

Supplementary Table 1: Venom gland proteomics

Gel Band	Mass (kDa)	Protein	Accession	Translation frame	Protein ID	SignalP	Peptides (>95%)	Expression (reads)	Coverage (%)	ProteinPilot Score (Total)
1	60	1	c29839_g1_i1	3	Chitinase	N	14	7378101	28.30	21.55
		2	c30148_g1_i2	3	Peptidase S1	Y	3	139510	14.18	5.37
		2	c30148_g1_i3	1	Peptidase S1	N	3	87362	18.18	5.37
		2	c30148_g1_i1	3	Peptidase S1	Y	3	364870	13.99	5.37
		2	c25117_g1_i1	3	Peptidase S1	N	2	301	29.10	4.03
		3	c30368_g1_i2	3	Peptidase S1 with LDLA domain	Y	2	995917	4.19	3.39
		3	c30675_g2_i2	4	Peptidase S1 with LDLA domain	Y	1	1228052	2.16	2
		3	c30675_g2_i1	5	Peptidase S1 with LDLA domain	N	1	434416	2.59	2
		3	c30675_g2_i4	6	Peptidase S1 with LDLA domain	N	1	933783	1.38	2
		3	c30675_g2_i3	5	Peptidase S1 with LDLA domain	Y	1	1612752	1.16	2
		3	c30368_g1_i3	3	Peptidase S1 with LDLA domain	Y	1	615193	1.39	2
		3	c29982_g3_i1	5	Peptidase S1 with LDLA domain	Y	1	381583	1.71	2
		3	c25446_g1_i4	2	Peptidase S1 with LDLA domain	N	1	14	7.29	2
2	50	1	c29839_g1_i1	3	Chitinase	N	8	7378101	21.44	10.24
		2	c27884_g1_i1	3	Chitinase	N	3	17222	18.18	3.76
		2	c28694_g4_i1	4	Chitinase	N	3	2471	13.30	3.33
		3	c30148_g1_i3	1	Peptidase S1	N	1	87362	12.46	3.23
		3	c30148_g1_i2	3	Peptidase S1	Y	1	139510	9.37	3.23
		3	c30148_g1_i1	3	Peptidase S1	Y	1	364870	9.58	3.23
		4	c57873_g1_i1	5	Thioredoxin	N	1	12	9.20	2.66
		5	c27020_g1_i1	4	CAP Protein	Y	1	67718	10.57	1.92
3	40	1	c29839_g1_i1	3	Chitinase	N	4	7378101	10.12	8.92
		2	c30148_g1_i3	1	Peptidase S1	N	3	87362	12.46	6
		2	c30148_g1_i2	3	Peptidase S1	Y	3	139510	9.37	6
		2	c30148_g1_i1	3	Peptidase S1	Y	3	364870	9.58	6
		2	c25117_g1_i1	3	Peptidase S1	N	2	301	14.93	4
		3	c27020_g1_i1	4	CAP Protein	Y	1	67718	4.57	2
4	37	1	c30148_g1_i2	3	Peptidase S1	Y	4	139510	13.67	8
		1	c30148_g1_i1	3	Peptidase S1	Y	4	364870	13.99	8
		1	c30148_g1_i3	1	Peptidase S1	N	3	87362	15.15	6
		2	c27577_g1_i3	3	Tropomyosin	N	2		10.21	4.62
		2	c27577_g1_i4	3	Tropomyosin	N	2		11.11	4.62
		3	c29839_g1_i1	3	Chitinase	N	2	7378101	3.09	3.12
		3	c28694_g3_i1	5	Chitinase	N	1	23414	7.58	1.4
		3	c28694_g2_i1	5	Chitinase	N	1	467	12.66	1.4
		3	c16904_g1_i1	1	Chitinase	N	1	0	13.33	1.4
5	30	1	c27020_g1_i1	4	CAP Protein	Y	35	67718	53.43	39.7
		2	c30148_g1_i3	1	Peptidase S1	N	4	87362	18.52	8.01
		2	c30148_g1_i2	3	Peptidase S1	Y	4	139510	11.39	8.01
		2	c30148_g1_i1	3	Peptidase S1	Y	4	364870	11.66	8.01
		3	c29839_g1_i1	3	Chitinase	N	3	7378101	5.49	4.01
		4	c30368_g1_i2	3	Peptidase S1 with LDLA domain	Y	3	995917	4.04	6
		4	c30675_g2_i3	5	Peptidase S1 with LDLA domain	Y	2	1612752	4.46	4
		4	c30675_g2_i2	4	Peptidase S1 with LDLA domain	Y	1	1228052	2.16	2
		4	c30675_g2_i1	5	Peptidase S1 with LDLA domain	N	1	434416	2.59	2
		4	c30368_g1_i3	3	Peptidase S1 with LDLA domain	Y	1	615193	1.39	2
		4	c29982_g3_i1	5	Peptidase S1 with LDLA domain	Y	1	381583	1.71	2
		4	c25446_g1_i4	2	Peptidase S1 with LDLA domain	N	1	14	7.29	2
		5	c18283_g1_i1	2	Prostasin	N	2	286704	8.79	4
					Chitin-binding domain containing protein	Y	2		3.28	3.48
		6	c29585_g1_i1	1	Peptidase S1	Y	3	316580	8.42	2.12
		7	c27960_g1_i1	1	Peptidase S1	Y	3	316580	8.42	2.12
		8	c30675_g2_i4	6	Peptidase S1 with LDLA domain	N	2	933783	5.32	4
		8	c30675_g2_i3	5	Peptidase S1 with LDLA domain	Y	2	1612752	4.46	4
		9	c57873_g1_i1	5	Thioredoxin	N	1	12	4.73	2
		10	c26920_g1_i1	5	Calycin	Y	1		2.48	2
		11	c24110_g1_i1	2	Carboxypeptidase M14A	Y	1	189506	2.46	2
6	26	1	c30148_g1_i1	3	Peptidase S1	Y	11	364870	22.80	19.13
		2	c27020_g1_i1	4	CAP protein	Y	9	67718	27.43	17.56
		3	c29839_g1_i1	3	Chitinase	N	7	7378101	19.90	14.51
		4	c29126_g1_i1	1	Peptidase S1	Y	6	72458	27.89	8.43
		5	c25996_g1_i1	2	Peptidase S1 with LDLA domain	Y	4	488359	13.24	7.13
		6	c18283_g1_i1	2	Prostasin	N	10	286704	33.85	6.83
		7	c27388_g1_i1	3	Peptidase S1 with LDLA domain	Y	3	228907	8.82	5.89
		8	c30368_g1_i2	3	Peptidase S1 with LDLA domain	Y	8	995917	14.44	9.27
		9	c29090_g1_i1	3	Peptidase S1	Y	3	140303	9.45	4.96
		10	c30675_g2_i3	5	Peptidase S1 with LDLA domain	Y	6	1612752	17.02	5.93
		10	c30675_g2_i4	6	Peptidase S1 with LDLA domain	N	6	933783	19.13	5.93
		10	c30675_g2_i2	4	Peptidase S1 with LDLA domain	Y	5	1228052	13.46	3.68

		10	c30675_g2_i1	5	Peptidase S1 with LDLA domain	N	5	434416	14.97	3.68
		11	c12686_g1_i1	3	Peptidase S1	N	3	103249	10.67	4.79
		12	c29091_g1_i2	2	Peptidase S1	Y	2	216342	12.86	4
		12	c29091_g1_i1	2	Peptidase S1	Y	1	75244	4.68	2
		13	c11081_g1_i1	5	Peptidase S1	N	2		41.51	3.44
		14	c29982_g5_i1	1	Peptidase S1	N	2	29390	7.28	3.24
		14	c29982_g4_i1	1	Peptidase S1	N	2	118055	5.85	3.24
		15	c29982_g1_i1	6	Peptidase S1	N	2	196885	14.04	3.1
		16	c27101_g1_i1	2	Peptidase S1	N	3	140921	17.19	3.64
		17	c29982_g2_i1	5	Peptidase S1 with LDLA domain	Y	4	191528	11.97	2.73
					Chitin-binding domain containing					
		18	c29585_g1_i1	1	protein	Y	2		7.29	2.37
		19	c28694_g4_i1	4	Chitinase	N	1	2471	13.83	2
		19	c27884_g1_i1	3	Chitinase	N	1	17222	14.69	2
		20	c27960_g1_i1	1	Peptidase S1	Y	3	316580	8.42	2
		21	c23479_g2_i1	1	Peptidase S1	N	2	68533	8.99	2
7	25	1	c30675_g2_i4	6	Peptidase S1 with LDLA domain	0.109	29	933783	26.82	28
		1	c30675_g2_i3	5	Peptidase S1 with LDLA domain	0.440 Y	29	1612752	22.48	28
		2	c30148_g1_i1	3	Peptidase S1	0.604 Y	14	364870	28.24	22.1
		2	c30148_g1_i2	3	Peptidase S1	0.602 Y	13	139510	25.82	22.1
		3	c18283_g1_i1	2	Prostasin	0.173	38	286704	39.79	24
		4	c30368_g1_i2	3	Peptidase S1 with LDLA domain	0.391 Y	20	995917	18.94	20.03
		5	c29982_g1_i1	6	Peptidase S1	0.098	7	196885	47.19	12
		6	c29839_g1_i1	3	Chitinase	0.21	6	7378101	9.61	12
					Chitin-binding domain containing					
		7	c29585_g1_i1	1	protein	0.450 Y	5		9.84	10
		8	c27057_g1_i2	1	Calycin	0.882 Y	4		13.73	8.05
		8	c27057_g1_i1	1	Calycin	0.882 Y	4		13.48	8.05
		9	c27960_g1_i1	1	Peptidase S1	0.444 Y	10	316580	27.55	10.04
		10	c57873_g1_i1	5	Thioredoxin	0.183	5	12	13.93	8
		11	c13598_g1_i1	5	Peptidase S1	0.438 Y	5	775049	19.06	8.01
		12	c25996_g1_i1	2	Peptidase S1 with LDLA domain	0.731 Y	2	488359	16.81	4.01
		13	c27884_g1_i1	3	Chitinase	0.274	2	17222	14.69	4
		13	c28694_g4_i1	4	Chitinase	0.327	1	2471	6.38	2
					Chitin-binding domain containing					
		14	c136843_g1_i1	2	protein	N	2		36.92	4
		15	c30148_g1_i3	1	Peptidase S1	0.328	11	87362	26.60	18.06
		16	c27030_g1_i2	2	Chitinase	0.107	4	4118	43.00	8
		16	c27030_g1_i1	3	Chitinase	0.112	3	18858	62.02	6
		17	c29982_g3_i1	5	Peptidase S1 with LDLA domain	0.791 Y	2	381583	7.58	4
		17	c29982_g2_i2	5	Peptidase S1 with LDLA domain	0.800 Y	1	88749	4.71	2
		18	c25446_g1_i4	2	Peptidase S1 with LDLA domain	0.126	3	14	16.67	4
		18	c30675_g2_i3	5	Peptidase S1 with LDLA domain	0.440 Y	29	1612752	22.48	28
		18	c30675_g2_i2	4	Peptidase S1 with LDLA domain	0.754 Y	20	1228052	14.45	20.03
		18	c30675_g2_i1	5	Peptidase S1 with LDLA domain	0.102	20	434416	17.37	20.03
		18	c25446_g1_i2	2	Peptidase S1 with LDLA domain	0.126	2	37	5.14	2
		18	c25446_g1_i1	2	Peptidase S1 with LDLA domain	0.126	2	39	6.62	2
		19	c27162_g1_i1	6	Peptidase S1	0.102	4	21533	20.95	4
		20	c27020_g1_i1	4	CAP protein	0.450 Y	1	67718	2.57	2
					Chitin-binding domain containing					
8	20	1	c29585_g1_i1	1	protein	0.450 Y	4		13.66	5.1
		2	c30148_g1_i2	3	Peptidase S1	0.602 Y	1	139510	15.44	3.15
		2	c30148_g1_i3	1	Peptidase S1	0.328	1	87362	18.18	3.15
		2	c30148_g1_i1	3	Peptidase S1	0.604 Y	1	364870	13.99	3.15
		2	c25117_g1_i1	3	Peptidase S1	0.104	0	301	27.61	1.17
					Chitin-binding domain containing					
9	15	3	c136843_g1_i1	2	protein		1		46.15	2.11
		1	c30148_g1_i1	3	Peptidase S1	0.602 Y	11	139510	16.96	9.5
		1	c30148_g1_i2	3	Peptidase S1	0.604 Y	11	364870	17.36	9.5
10	12	1	c30148_g1_i3	1	Peptidase S1	0.328	11	87362	18.18	7.1
		1	c30148_g1_i2	3	Peptidase S1	0.602 Y	4	139510	16.96	9.5
		1	c30148_g1_i1	3	Peptidase S1	0.604 Y	4	364870	17.36	9.5
		1	c30148_g1_i3	1	Peptidase S1	0.328	3	87362	18.18	7.1
		2	c29839_g1_i1	3	Chitinase	0.21	2	7378101	3.087	3.09
		2	c28694_g3_i1	5	Chitinase	0.107	1	23414	7.576	2
		2	c28694_g2_i1	5	Chitinase	0.112	1	467	12.66	2
		2	c16904_g1_i1	1	Chitinase	0.114	1	0	13.33	2
					13.6 kDa protein with no BLAST					
		3	c13428_g1_i2	3	hits (UniProt KB)	0.506 Y	1		2.896	1.59
		3	c13428_g1_i1	3	13.6 kDa protein with no BLAST	0.506 Y	1			
					hits (UniProt KB)				2.694	1.59

Supplementary Table 2: Venom gland tissue transcriptomics

Name of toxin protein family	ID of putative toxin contigs	Match via proteomics	Signal Peptide	Number of high-support contigs (reads > 25)	Lengths of contigs	Number of reads	FPKM
C1-like domain	c173255_g1_i1		yes	0 / 1	919	21	0.94
Calycin	c26920_g1_i1	yes	yes		1,158	81,138	2,880.98
	c27057_g1_i1	yes	yes		1,890	45,640	992.91
	c27057_g1_i2	yes	yes		1,847	35,449	789.15
	c23125_g1_i1	-	yes		1,018	297	12.00
	c27565_g1_i1	-	yes		1,017	206	8.33
	c24433_g1_i2	-	-		989	152	6.32
	c28078_g2_i1	-	yes		1,161	108	3.82
	c30135_g4_i1	-	yes		1,782	147	3.39
	c24433_g1_i3	-	-		594	45	3.11
	c1253_g1_i1	-	yes		1,246	78	2.57
	c28078_g1_i1	-	yes		2,080	119	2.35
	c83371_g1_i1	-	-		751	24	1.31
	c64218_g1_i1	-	-		595	11	0.76
	c179908_g1_i1	-	-		1,097	19	0.71
	c154025_g1_i1	-	-		383	1	0.11
<i>Total (high-support contigs)</i>				11 / 15		163,379	4,704.93
CAP	c27020_g1_i1	yes	yes		1,048	67,718	2,656.86
	c17634_g1_i1	-	yes		1,032	25,221	1,004.86
	c30341_g1_i1	-	yes		1,218	17,300	584.01
	c136857_g1_i1	-	yes		1,159	580	20.58
	c30174_g1_i3	-	-		1,663	434	10.73
	c23191_g1_i1	-	yes		1,692	313	7.61
	c27364_g1_i1	-	-		1,296	215	6.82
	c35027_g1_i1	-	yes		1,689	98	2.39
	c29302_g2_i1	-	yes		1,937	104	2.21
	c7719_g1_i1	-	yes		646	28	1.78
	c1310_g1_i2	-	yes		1,641	61	1.53
	c29302_g1_i1	-	yes		1,580	57	1.48
	c22705_g2_i1	-	yes		450	4	0.37
	c169637_g1_i1	-	-		278	0	0.00
<i>Total (high-support contigs)</i>				11 / 14		112,072	4,299.37
Chitinase	c29839_g1_i1	yes	yes		1,703	7,378,101	178,137.36
	c28694_g3_i1	yes	-		396	23,414	2,431.11
	c27030_g1_i1	yes	-		388	18,858	1,998.43
	c27884_g1_i1	yes	yes		424	17,222	1,670.10
	c136637_g1_i1	-	yes		311	9,301	1,229.69
	c27030_g1_i2	yes	-		300	4,118	564.40
	c28694_g4_i1	yes	yes		563	2,471	180.46
	c28694_g2_i1	yes	-		238	467	80.68
	c82743_g1_i1	-	-		169	144	35.03
	c28638_g1_i4	-	yes		1,750	821	19.29
	c11884_g1_i1	-	yes		440	85	7.94
	c30124_g1_i1	-	-		1,796	320	7.33
	c12847_g1_i1	-	-		1,341	72	2.21
	c28694_g1_i1	-	-		233	12	2.12
	c5675_g1_i1	-	-		1,109	40	1.48
	c137531_g1_i1	-	-		1,898	39	0.84
	c62314_g1_i1	-	-		203	4	0.81

	c121850_g1_i1	-	yes		633	8	0.52
	c94882_g1_i1	-	yes		326	4	0.50
	c30447_g1_i1	-	-		1,206	3	0.10
	c20352_g1_i1	-	yes		157	0	0.00
	c179482_g1_i1	-	-		262	0	0.00
	c71366_g1_i1	-	-		142	0	0.00
	c30754_g4_i1	-	-		246	0	0.00
	c161994_g1_i1	-	-		173	0	0.00
	c93866_g1_i1	-	-		163	0	0.00
	c16904_g1_i1	yes	-		225	0	0.00
	c93564_g1_i1	-	-		185	0	0.00
<i>Total (high-support contigs)</i>				13 / 28	7,455,394	186,364.04	
Colipase-like	c26403_g1_i1	-	yes		1,523	425	11.47
	c83533_g1_i1	-	-		632	6	0.39
	c69394_g1_i1	-	-		255	0	0.00
<i>Total (high-support contigs)</i>				1 / 3	425	11.47	
Cystatin	c30119_g1_i1	-	yes	1	2,699	162	2.47
Hyaluronidase	c28000_g2_i2	-	yes		1,299	630	19.94
	c28000_g2_i1	-	yes		1,299	347	10.98
	c26537_g1_i1	-	-		1,057	22	0.86
	c99311_g1_i1	-	-		491	8	0.67
	c26537_g1_i2	-	yes		477	7	0.60
	c84753_g1_i1	-	-		587	7	0.49
	c139045_g1_i1	-	yes		196	0	0.00
<i>Total (high-support contigs)</i>				2 / 7	977	30.93	
Kazal	c28644_g2_i2	-	yes		930	190	8.40
	c28848_g1_i2	-	-		1,797	333	7.62
	c28644_g2_i1	-	yes		539	68	5.19
	c28699_g2_i1	-	-		1,988	203	4.20
	c28699_g2_i2	-	-		1,973	200	4.17
	c30818_g8_i1	-	-		2,855	238	3.43
	c10145_g1_i1	-	-		1,333	65	2.00
	c30818_g8_i2	-	-		1,667	79	1.95
	c60227_g1_i1	-	yes		960	33	1.41
	c8461_g2_i1	-	-		1,381	40	1.19
	c22300_g1_i1	-	-		696	9	0.53
	c36870_g1_i1	-	-		447	3	0.28
<i>Total (high-support contigs)</i>				8 / 12	1,376	36.95	
Kunitz	c26909_g1_i1	-	-		2,790	19,756	291.15
	c26026_g2_i2	-	-		1,815	482	10.92
	c21419_g1_i1	-	-		1,209	120	4.08
	c2037_g1_i1	-	-		1,527	111	2.99
	c115833_g1_i1	-	-		1,255	65	2.13
	c2789_g1_i1	-	yes		548	23	1.73
	c92205_g1_i1	-	-		712	10	0.58
	c112161_g1_i1	-	-		745	9	0.50
<i>Total (high-support contigs)</i>				5 / 8	20,534	311.27	
Lectin	c72_g1_i1	-	-		1,469	82	2.30
	c4773_g1_i1	-	-		916	32	1.44
	c71342_g1_i1	-	-		471	15	1.31
	c31264_g1_i1	-	yes		1,355	32	0.97
	c43104_g1_i1	-	-		1,067	7	0.27
	c111380_g1_i1	-	-		411	2	0.20

Supplementary Table 2

<i>Total (high-support contigs)</i>				2 / 6	114	3,73
Metallopeptidase M12	c27520_g1_i1	-	yes	1,507	145,668	3,974.44
	c28947_g1_i1	-	yes	2,374	836	14.48
	c28592_g1_i2	-	yes	1,231	311	10.39
	c28592_g1_i1	-	-	1,276	298	9.60
	c16469_g1_i2	-	-	1,868	173	3.81
	c16469_g1_i1	-	-	1,917	174	3.73
	c37943_g1_i1	-	-	1,061	47	1.82
	c23132_g1_i1	-	-	1,012	38	1.54
	c140847_g1_i1	-	-	1,232	26	0.87
	c61570_g1_i1	-	-	547	7	0.53
	c61957_g1_i1	-	yes	432	5	0.48
	c46764_g1_i1	-	-	290	1	0.14
<i>Total (high-support contigs)</i>				8 / 12	147,545	4,019.82
Metallopeptidase M13	c27666_g1_i1	-	-	2,487	17,601	291.00
	c20542_g2_i1	-	-	1,700	37	0.89
	c89912_g1_i1	-	-	688	13	0.78
	c90181_g1_i1	-	-	815	14	0.71
	c112272_g1_i1	-	-	1,408	23	0.67
	c48921_g1_i1	-	-	156	2	0.53
<i>Total (high-support contigs)</i>				1 / 6	17,601	291.00
Metallopeptidase M14	c24110_g1_i1	yes	-	1,447	189,506	5,384.92
	c27520_g1_i1	-	-	1,507	145,668	3,974.44
	c27844_g2_i1	-	-	492	1,312	109.65
	c27232_g1_i1	-	yes	398	686	70.87
	c8150_g1_i1	-	yes	2,436	137	2.31
	c28686_g2_i1	-	-	1,401	47	1.38
	c12373_g1_i1	-	-	152	4	1.08
	c88597_g1_i1	-	-	220	4	0.75
	c137888_g1_i1	-	-	170	0	0.00
	c159732_g1_i1	-	-	159	0	0.00
<i>Total (high-support contigs)</i>				5 / 10	337,309	9,542.19
Peptidase S1	c13598_g1_i1	yes	yes	1,205	775,049	26,446.44
	c29982_g1_i1	yes	-	534	196,885	15,159.90
	c30148_g1_i1	yes	yes	1,140	364,870	13,160.07
	c27960_g1_i1	yes	yes	1,144	316,580	11,378.43
	c18283_g1_i1	yes	-	1,179	286,704	9,998.73
	c29982_g4_i1	yes	-	563	118,055	8,621.86
	c29091_g1_i2	yes	yes	1,100	216,342	8,086.73
	c27101_g1_i1	yes	-	1,141	140,921	5,078.26
	c30148_g1_i2	yes	yes	1,147	139,510	5,001.12
	c30148_g1_i3	yes	-	883	87,362	4,068.06
	c12686_g1_i1	yes	-	1,200	103,249	3,537.77
	c28042_g1_i1	yes	yes	1,155	84,621	3,012.46
	c27162_g1_i1	yes	-	313	21,533	2,828.69
	c29091_g1_i1	yes	yes	1,102	75,244	2,807.47
	c29982_g5_i1	yes	-	447	29,390	2,703.44
	c23479_g2_i1	yes	-	1,060	68,533	2,658.39
	c29090_g1_i1	yes	yes	2,238	140,303	2,577.70
	c29126_g1_i1	yes	yes	1,184	72,458	2,516.28
	c30416_g2_i1	-	yes	1,898	82,423	1,785.57
	c30416_g2_i2	-	yes	3,809	121,765	1,314.43
	c23479_g1_i1	-	-	453	9,314	845.40
	c29107_g2_i1	-	-	2,214	32,715	607.57

Supplementary Table 2

c13605_g1_i1	-	-	1,660	18,211	451.08
c17559_g1_i1	-	-	1,939	12,556	266.26
c21925_g2_i1	-	-	459	2,417	216.52
c25966_g1_i1	-	-	831	3,766	186.34
c20484_g1_i1	-	-	656	2,519	157.89
c21925_g1_i1	-	-	323	857	109.09
c28635_g1_i1	-	-	1,203	3,080	105.27
c25966_g2_i1	-	-	438	1,015	95.28
c29107_g1_i1	-	-	631	1,109	72.26
c17402_g1_i1	-	-	2,191	2,822	52.96
c26798_g1_i1	-	-	1,501	1,589	43.53
c165131_g1_i1	-	-	369	310	34.54
c25959_g2_i1	-	yes	522	424	33.40
c25117_g1_i1	yes	-	403	301	30.71
c27512_g1_i1	-	-	1,535	1,124	30.11
c27512_g1_i2	-	-	1,525	1,088	29.33
c29516_g1_i1	-	-	1,570	1,069	28.00
c163284_g1_i1	-	-	1,774	1,156	26.79
c18269_g1_i1	-	-	1,960	1,099	23.06
c19800_g1_i1	-	-	1,609	857	21.90
c25959_g1_i1	-	-	390	161	16.97
c28636_g1_i1	-	-	1,626	511	12.92
c26735_g1_i1	-	-	1,274	312	10.07
c28049_g1_i1	-	-	1,051	235	9.19
c21890_g2_i2	-	-	365	63	7.10
c28624_g1_i1	-	-	1,964	301	6.30
c24782_g2_i1	-	-	2,510	370	6.06
c28572_g1_i1	-	-	1,648	242	6.04
c28860_g1_i1	-	-	1,745	229	5.40
c28049_g1_i2	-	-	1,280	165	5.30
c29109_g1_i1	-	-	2,327	261	4.61
c29328_g1_i1	-	-	2,864	279	4.01
c16194_g1_i1	-	-	1,473	110	3.07
c12858_g1_i1	-	-	241	13	2.22
c25811_g1_i2	-	-	491	24	2.01
c5375_g2_i1	-	-	738	26	1.45
c165278_g1_i1	-	-	1,159	39	1.38
c24933_g1_i2	-	-	1,751	56	1.32
c90564_g1_i1	-	-	990	29	1.20
c7375_g2_i1	-	-	1,534	32	0.86
c5439_g1_i1	-	-	697	14	0.83
c141669_g1_i1	-	-	767	13	0.70
c9816_g1_i1	-	-	1,297	20	0.63
c44711_g1_i1	-	-	458	7	0.63
c99624_g1_i1	-	-	378	5	0.54
c165090_g1_i1	-	-	1,079	13	0.50
c37931_g1_i1	-	-	425	4	0.39
c56449_g1_i1	-	-	861	8	0.38
c166657_g1_i1	-	-	705	6	0.35
c2392_g2_i1	-	-	486	4	0.34
c11858_g1_i1	-	-	740	6	0.33
c148556_g1_i1	-	-	686	5	0.30
c96465_g1_i1	-	-	562	3	0.22
c187364_g1_i1	-	-	314	1	0.13

Supplementary Table 2

	c19937_g2_i1	-	yes	336	1	0.12
	c134251_g1_i1	-	-	313	0	0.00
	c136336_g1_i1	-	-	193	0	0.00
	c136382_g1_i1	-	yes	249	0	0.00
	c149051_g1_i1	-	yes	256	0	0.00
	c162416_g1_i1	-	yes	179	0	0.00
	c177612_g1_i1	-	yes	326	0	0.00
	c182909_g1_i1	-	-	289	0	0.00
	c186243_g1_i1	-	-	141	0	0.00
	c187083_g1_i1	-	-	381	0	0.00
	c22296_g1_i1	-	-	404	0	0.00
	c52848_g3_i1	-	yes	204	0	0.00
	c62183_g1_i1	-	-	368	0	0.00
	c73031_g1_i1	-	-	153	0	0.00
	c75035_g1_i1	-	-	168	0	0.00
	c81746_g1_i1	-	-	179	0	0.00
	c81784_g1_i1	-	-	159	0	0.00
	c82342_g1_i1	-	-	220	0	0.00
	c82379_g1_i1	-	-	340	0	0.00
	c84477_g1_i1	-	-	245	0	0.00
<i>Total (high-support contigs)</i>				55 / 96	3,544,434	136,306.15
Peptidase S1 - LDLA domain	c30675_g2_i3	yes	yes	1,795	1,612,752	36,942.66
	c30675_g2_i2	yes	yes	1,752	1,228,052	28,820.91
	c30675_g2_i4	yes	-	1,508	933,783	25,460.66
	c30368_g1_i2	yes	yes	1,910	995,917	21,439.51
	c30368_g1_i3	yes	yes	1,480	615,193	17,091.29
	c25996_g1_i1	yes	yes	1,410	488,359	14,241.15
	c29982_g3_i1	yes	yes	1,222	381,583	12,839.34
	c30675_g2_i1	yes	yes	1,456	434,416	12,267.88
	c29982_g2_i1	yes	yes	1,128	191,528	6,981.49
	c27388_g1_i1	yes	yes	2,016	228,907	4,668.67
	c25446_g1_i4	yes	-	288	14	2.00
<i>Total (high-support contigs)</i>				10 / 11	7,110,490	180,753.57
Peptidase S10	c29986_g1_i1	-	-	2,346	181,822	3,186.72
	c29849_g1_i1	-	-	3,440	512	6.12
	c29473_g5_i1	-	-	1,877	107	2.34
	c103962_g1_i1	-	-	183	2	0.45
<i>Total (high-support contigs)</i>				3 / 4	182,441	3,195.18
Phospholipase A2	c25267_g1_i1	-	yes	1,787	152	3.50
	c26550_g1_i1	-	-	932	60	2.65
	c17764_g1_i1	-	yes	1,612	38	0.97
	c1144_g1_i1	-	-	1,014	23	0.93
	c37684_g1_i1	-	-	259	0	0.00
<i>Total (high-support contigs)</i>				2 / 5	212	6.15
Serpín	c26358_g2_i1	-	yes	1,506	5,106	139.41
	c21812_g1_i1	-	yes	1,612	72	1.84
	c17839_g1_i2	-	-	1,367	31	0.93
	c17839_g1_i1	-	-	1,821	38	0.86
	c156108_g1_i1	-	-	146	0	0.00
<i>Total (high-support contigs)</i>				4 / 5	5,178	141.25
Sphingomyelinase	c60968_g1_i1	-	yes	1,224	33	1.11
	c88623_g1_i1	-	-	851	22	1.06
	c88354_g1_i1	-	-	837	3	0.15

Supplementary Table 2

Total (high-support contigs)				0 / 3	33	1.11	
VEGF-like	c29360_g3_i1	yes	yes	1,609	234,789	5,999.94	
	c26353_g1_i1	-	yes	2,323	1,095	19.38	
	c28217_g1_i2	-	yes	2,457	234	3.92	
	c28217_g1_i1	-	yes	2,481	236	3.91	
	c17785_g1_i2	-	yes	1,041	37	1.46	
	c113445_g1_i1	-	-	968	22	0.93	
	c90144_g1_i1	-	yes	972	13	0.55	
	c182771_g1_i1	-	-	260	0	0.00	
Total (high-support contigs)				4 / 8	236,354	6,027.15	
Xibalbin 1 (ICK)	c27367_g1_i1	yes	yes	728	126,395	7,138.77	
Total (high-support contigs)				1 / 1	126,395	7,138.77	
Xibalbin 2 (putative ICK)	c29772_g1_i1	yes	yes	773	1,412,448	75,130.80	
	c149924_g1_i1	-	yes	584	12	0.84	
	c27396_g1_i1	-	yes	354	0	0.00	
	c27396_g1_i2	-	-	293	0	0.00	
	c103283_g1_i1	-	-	158	0	0.00	
	c108798_g1_i1	-	-	181	0	0.00	
	Total (high-support contigs)				1 / 6	1,412,448	75,130.80
Xibalbin 3 (dICK)	c9387_g1_i1	yes	yes	790	145,444	7,569.96	
	c29843_g1_i2	yes	yes	1,640	151,439	3,796.81	
	c27340_g3_i1	-	-	328	116	14.54	
	c27303_g1_i2	-	yes	588	124	8.67	
	c27303_g1_i3	-	yes	909	130	5.88	
	c27303_g1_i1	-	yes	328	11	1.38	
	Total (high-support contigs)				5 / 6	297,253	11,395.87
Xibalbin 4 (putative CSab)	c18306_g1_i1	yes	yes	781	324,301	17,073.49	
	c26085_g1_i1	-	yes	1070	3,633	139.61	
	c26882_g2_i1	-	yes	1,062	2,458	95.17	
	c30070_g1_i1	-	yes	737	288	16.07	
	c30070_g1_i2	-	yes	1,535	258	6.91	
	c5499_g1_i1	-	yes	818	79	3.97	
	Total (high-support contigs)				6 / 6	331,017	17,335.21
Xibalbin 5 (putative CSab)	c28491_g1_i1	yes	yes	647	17,940	1,140.10	
	c74570_g1_i1	-	-	297	2	0.28	
Total (high-support contigs)				1 / 2	17,940	1,140.10	
Xibalbin 6 (CHH/ITP)	c13591_g1_i1	yes	-	1	1,321	3,443	107.17
Xibalbin 7 (sIGFBP-rp)	c13811_g1_i2	-	yes	632	55	3.58	
	c25812_g1_i1	-	yes	1,601	131	3.36	
	c13811_g1_i1	-	yes	601	46	3.15	
	c26493_g1_i3	-	yes	1,692	123	2.99	
	c23977_g2_i2	yes	yes	665	23	1.42	
	c26493_g1_i2	-	yes	890	22	1.02	
	c23977_g2_i1	yes	yes	687	9	0.54	
	Total (high-support contigs)				4 / 7	355	13.08
Xibalbin 8 (Unknown 1)	c23843_g2_i1	yes	yes	684	708	42.56	
	c77249_g1_i1	-	yes	301	1	0.14	
Total (high-support contigs)				1 / 2	708	42.56	
Xibalbin 09 (Unknown 2)	c23666_g1_i1	yes	yes	1	887	524,955	24,334.56
Xibalbin 10 (Unknown 3)	c25771_g1_i2	yes	yes	566	329,600	23,943.95	
	c25771_g1_i1	-	yes	545	180,730	13,635.11	
Total (high-support contigs)				2 / 2	510,330	37,579.07	

Supplementary Table 2

Xibalbin 11 (putative linear two-domain transcript)	c29407_g1_i2	yes	yes	715	564,966	32,489.37
	c29407_g1_i1	yes	yes	1,028	345,028	13,800.23
	c27729_g1_i1	-	yes	698	32,169	1,894.99
	c27729_g1_i2	-	yes	778	6,300	332.96
<i>Total (high-support contigs)</i>				4 / 4	948,463	48,517.55
Xibalbin 12 (Unknown)	c27075_g1_i1	-	yes	411	20,417	2,042.56
	c27075_g1_i2	-	yes	339	14,112	1,711.65
<i>Total (high-support contigs)</i>				2 / 2	34,529	3,754.21
Xibalbin 13 (ICK)	c29168_g1_i2	-	yes	1,966	597	12.49
	c29168_g1_i1	-	yes	2,050	519	10.41
<i>Total (high-support contigs)</i>				2 / 2	4,016	22.90

Supplementary Table 3: Whole body transcriptomics

Name of toxin protein family	ID of putative toxin contigs	Signal Peptide	Number of high-support contigs (reads > 25)	Lengths of contigs	Number of reads	FPKM
C1-like domain	c68643_g1_i1	yes		1,071	84	8.64
	c31704_g1_i1	yes		1,198	46	4.23
	c156732_g1_i1	yes		537	16	3.28
<i>Total</i>			2 / 3		130	12.86
Calycin	c42271_g1_i1	yes		733	25,283	3,797.90
	c39523_g1_i2	yes		1,110	10,189	1,010.71
	c37020_g1_i1	yes		906	8,303	1,009.08
	c41349_g4_i2	yes		1,570	10,951	768.02
	c39523_g1_i1	yes		938	5,923	695.28
	c1872_g1_i1	yes		2,642	12,459	519.24
	c40613_g2_i1	yes		775	3,498	496.98
	c14409_g1_i1	yes		741	2,921	434.04
	c39556_g2_i2	yes		881	1,665	208.09
	c1964_g1_i1	yes		1,001	1,794	197.34
	c38227_g1_i1	yes		1,544	2,316	165.16
	c40613_g1_i1	yes		1,435	1,960	150.39
	c29444_g2_i2	yes		656	829	139.15
	c38916_g1_i1	yes		2,725	1,960	79.20
	c38227_g1_i4	yes		390	276	77.92
	c30222_g1_i2	yes		1,169	534	50.30
	c40953_g3_i1	yes		1,971	855	47.76
	c39950_g3_i1	yes		980	268	30.11
	c30968_g2_i1	yes		1,153	309	29.51
	c38227_g1_i3	-		1,031	276	29.48
	c33342_g1_i1	yes		986	260	29.03
	c28551_g1_i1	yes		784	118	16.57
	c39950_g4_i1	yes		2,120	314	16.31
	c43200_g1_i1	yes		659	59	9.86
	c43013_g1_i1	yes		1,112	89	8.81
	c33878_g1_i1	yes		616	32	5.72
	c6754_g1_i1	-		637	30	5.19
	c56731_g1_i1	-		267	9	3.71
	c163658_g1_i1	-		284	8	3.10
	c98630_g1_i1	yes		762	20	2.89
	c153149_g1_i1	yes		276	6	2.39
	c79065_g1_i1	-		273	4	1.61
<i>Total</i>			27 / 32		93,471	10,027.14
CAP	c39648_g1_i1	yes		1,398	8,621	679.00
	c39316_g1_i1	yes		2,531	7,693	334.67
	c36696_g1_i1	yes		1,533	946	67.95
	c19356_g1_i1	yes		1,588	829	57.48
	c40495_g1_i2	-		1,427	609	46.99
	c35351_g1_i1	yes		967	290	33.02
	c30140_g1_i2	yes		1,371	139	11.16
	c29338_g1_i1	-		871	77	9.73

	c39513_g1_i1	yes	1,743	147	9.29
	c105183_g1_i1	-	948	49	5.69
	c120579_g1_i1	yes	674	20	3.27
	c179430_g1_i1	-	286	8	3.08
	c185465_g1_i1	-	286	5	1.92
	c101573_g1_i1	-	495	6	1.33
<i>Total</i>			10 / 14	19,400	1,254.99
Chitinase	c39564_g1_i1	yes	1,962	47,087	2,642.53
	c33934_g1_i1	yes	2,060	18,169	971.14
	c40224_g1_i1	yes	2,314	801	38.11
	c40216_g2_i1	yes	1,607	466	31.93
	c37725_g1_i1	yes	2,184	484	24.40
	c1616_g1_i1	yes	1,652	224	14.93
	c34447_g2_i1	-	661	56	9.33
	c34447_g1_i1	-	937	41	4.82
	c127858_g1_i1	-	299	8	2.95
<i>Total</i>			8 / 9	67,328	3,737.20
Colipase-like	c96280_g1_i1	yes	926	1,144	136.03
	c126351_g1_i1	yes	834	60	7.92
	c98001_g1_i1	yes	1,359	69	5.59
	c127271_g1_i1	yes	694	26	4.13
<i>Total</i>			4 / 4	1,299	153.67
Cystatin	c37574_g1_i1	-	2,700	1,065	43.43
	c8661_g1_i1	-	2,206	105	5.24
	c99564_g1_i1	-	1,091	36	3.63
	c77886_g1_i1	-	150	0	0.00
<i>Total</i>			3 / 4	1,206	52.31
Hyaluronidase	c40379_g1_i2	yes	1,184	151	14.04
	c31967_g2_i1	yes	1,211	119	10.82
	c40379_g1_i1	yes	1,284	102	8.75
	c28820_g1_i1	yes	264	9	3.75
	c47494_g1_i1	-	366	8	2.41
	c43222_g1_i1	-	400	6	1.65
	c111275_g1_i1	-	332	4	1.33
<i>Total</i>			3 / 7	372	33.61
Kazal	c40841_g1_i1	-	652	5,084	858.57
	c40841_g2_i1	-	1,681	12,103	792.76
	c40674_g1_i1	-	546	2,965	597.93
	c73313_g1_i1	yes	774	1,436	204.28
	c38149_g1_i1	yes	1,001	1,409	154.99
	c38149_g1_i2	yes	957	833	95.84
	c37585_g1_i2	-	1,534	549	39.41
	c40913_g3_i1	-	3,085	755	26.95
	c40913_g3_i2	-	2,595	509	21.60
	c29394_g1_i1	yes	1,365	201	16.21
	c151081_g1_i1	-	826	66	8.80
	c113609_g1_i1	yes	344	8	2.56
	c13750_g2_i1	-	618	13	2.32
	c8253_g2_i1	-	717	13	2.00
	c95379_g1_i1	yes	407	6	1.62
	c69644_g1_i1	-	293	3	1.13

Supplementary Table 3

<i>Total</i>			11 / 16	25,910	2,817.34
Kunitz	c41394_g2_i1	-	6,022	13,902	254.19
	c39736_g1_i1	-	2,724	2,103	85.01
	c36647_g1_i1	-	1,175	901	84.43
	c40229_g1_i1	-	3,064	1,703	61.20
	c39884_g2_i1	-	2,615	942	39.66
	c40838_g1_i2	-	3,230	1,016	34.63
	c40838_g1_i1	-	3,240	1,002	34.05
	c40913_g3_i1	-	3,085	755	26.95
	c40883_g1_i1	-	3,576	741	22.82
	c40913_g3_i2	-	2,595	509	21.60
	c37109_g1_i2	-	2,559	206	8.86
	c6455_g1_i1	-	1,089	82	8.29
	c17588_g1_i1	yes	2,247	120	5.88
	c99819_g1_i1	-	680	23	3.72
	c43688_g1_i1	-	1,297	43	3.65
	c175170_g1_i1	-	906	27	3.28
	c149176_g1_i1	-	1,191	35	3.24
	c31027_g3_i1	-	534	11	2.27
	c124181_g1_i1	yes	454	5	1.21
<i>Total</i>			16 / 19	24,087	697.74
Lectin	c3306_g1_i1	yes	1,020	11,353	1,225.54
	c38034_g1_i2	yes	903	7,367	898.30
	c38034_g1_i1	-	720	5,185	792.93
	c41421_g5_i2	-	2,744	14,360	576.22
	c33884_g1_i1	-	1,899	6,806	394.63
	c121397_g1_i1	-	1,474	770	57.52
	c39626_g1_i1	yes	1,482	261	19.39
	c41669_g1_i1	-	1,665	238	15.74
	c40169_g2_i1	-	1,149	142	13.61
	c34169_g1_i1	-	914	95	11.44
	c146039_g1_i1	-	1,111	110	10.90
	c173595_g1_i1	-	3,140	202	7.08
	c40169_g1_i1	-	1,082	60	6.11
	c23063_g1_i2	-	769	41	5.87
	c69970_g1_i1	yes	1,261	64	5.59
	c38285_g1_i1	-	1,897	92	5.34
	c174585_g1_i1	-	481	22	5.04
	c6021_g1_i1	-	457	20	4.82
	c80582_g1_i1	-	466	20	4.73
	c31371_g3_i1	-	405	17	4.62
	c44412_g1_i1	-	687	27	4.33
	c45488_g1_i1	-	695	27	4.28
	c31371_g1_i1	-	417	15	3.96
	c146790_g1_i1	yes	582	20	3.78
	c23063_g1_i1	-	732	25	3.76
	c46549_g1_i1	-	431	14	3.58
	c121773_g1_i1	-	436	14	3.54
	c31738_g2_i1	-	287	9	3.45
	c32349_g1_i1	-	417	13	3.43
	c95417_g1_i1	-	882	22	2.75

Supplementary Table 3

	c31371_g2_il	-	322	8	2.74
	c122717_g1_il	-	728	17	2.57
	c174091_g1_il	-	372	8	2.37
	c147606_g1_il	-	1,008	21	2.29
	c12041_g1_il	-	918	19	2.28
	c12041_g1_il	-	918	19	2.28
	c32349_g2_il	-	306	6	2.16
	c46354_g1_il	-	469	9	2.11
	c111370_g1_il	yes	433	8	2.03
	c121716_g1_il	-	715	13	2.00
	c114781_g1_il	-	351	6	1.88
	c148179_g1_il	-	247	4	1.78
	c55614_g1_il	-	262	4	1.68
	c183385_g1_il	-	334	5	1.65
	c125283_g1_il	-	271	4	1.63
	c105897_g1_il	-	475	7	1.62
	c95339_g1_il	-	277	4	1.59
	c25755_g1_il	-	208	3	1.59
	c15023_g1_il	-	169	2	1.30
	c100372_g1_il	-	234	2	0.94
	c18393_g1_il	-	187	0	0.00
<i>Total</i>			19 / 51	47,225	4,058.58
Metallopeptidase M12	c38819_g1_il	yes	1,853	11,265	669.38
	c40821_g1_i3	yes	1,859	4,370	258.83
	c40821_g1_i2	yes	1,829	4,281	257.72
	c40821_g1_il	yes	1,790	4,056	249.50
	c39128_g1_il	yes	2,799	5,379	211.60
	c38245_g1_il	yes	1,518	1,950	141.44
	c38587_g1_il	yes		834	106.90
	c36638_g2_il	-	672	596	97.66
	c29881_g1_il	yes	1,101	626	62.60
	c39901_g1_il	yes	3,065	1,633	58.66
	c29881_g1_i2	-	1,245	622	55.01
	c7262_g1_il	yes	1,914	595	34.23
	c38943_g1_i3	-	4,882	1,201	27.09
	c38943_g1_i2	-	4,894	1,149	25.85
	c38192_g1_il	-	2,134	131	6.76
	c125508_g1_il	yes	1,258	69	6.04
	c20701_g1_il	-	787	30	4.20
	c6166_g1_il	-	1,485	54	4.00
	c5983_g1_il	-	589	12	2.24
	c38192_g2_il	yes	624	11	1.94
	c134572_g1_il	-	479	8	1.84
	c48691_g1_il	-	360	6	1.84
	c156237_g1_il	-	434	7	1.78
	c51615_g1_il	yes	400	6	1.65
	c143471_g1_il	-	215	3	1.54
<i>Total</i>			19 / 25	38,853	2,279.72
Metallopeptidase M13	c40941_g3_il	yes	3,871	2,596	73.84
	c38812_g2_il	-	3,652	434	13.09
	c38809_g1_il	-	747	129	19.01

Supplementary Table 3

	c38809_g2_i1	-	2,276	320	15.48
	c36771_g1_i1	-	2,751	219	8.77
	c96701_g1_i1	-	1,994	147	8.12
	c28676_g1_i1	-	2,181	108	5.45
	c158946_g1_i1	-	243	7	3.17
	c120779_g1_i1	-	709	18	2.80
	c121332_g1_i1	-	643	16	2.74
	c122940_g1_i1	-	600	13	2.39
	c80464_g1_i1	-	505	9	1.96
	c29581_g3_i1	-	408	7	1.89
	c140065_g1_i1	-	464	7	1.66
	c137305_g1_i1	-	272	4	1.62
	c11088_g1_i1	-	445	6	1.48
	c147180_g1_i1	-	310	4	1.42
	c89109_g1_i1	-	286	3	1.15
	c22820_g1_i1	-	151	1	0.73
	c29581_g2_i1	-	196	1	0.56
	c22820_g2_i1	-	198	1	0.56
<i>Total</i>			8 / 21	3,966	146.14
Metallopeptidase M14	c39004_g1_i2	-	1,365	2,573	207.55
	c96470_g1_i1	-	1,804	2,962	180.79
	c39046_g1_i1	-	4,531	622	15.12
	c34863_g1_i2	yes	3,109	229	8.11
	c29585_g1_i1	-	832	54	7.15
	c125508_g1_i1	-	1,258	69	6.04
	c74890_g1_i1	-	725	28	4.25
	c7622_g1_i1	-	317	10	3.47
	c151706_g1_i1	-	260	7	2.96
	c72727_g1_i1	-	351	9	2.82
	c85284_g1_i1	-	253	6	2.61
	c43522_g1_i1	-	344	6	1.92
	c48691_g1_i1	-	360	6	1.84
	c69660_g1_i1	-	399	6	1.66
	c107555_g1_i1	yes	203	0	0.00
<i>Total</i>			7 / 15	6,537	429.00
Peptidase S1	c40947_g1_i1	-	908	26,544	3,218.84
	c40947_g1_i2	-	916	20,101	2,416.24
	c35347_g1_i1	-	981	17,078	1,916.84
	c40947_g1_i3	-	1,324	17,711	1,472.90
	c34883_g1_i1	-	994	13,011	1,441.26
	c36169_g1_i1	-	1,422	16,211	1,255.25
	c29879_g1_i1	-	1,522	6,271	453.67
	c39087_g1_i1	-	1,009	3,208	350.08
	c6983_g1_i1	-	1,657	3,013	200.21
	c40600_g1_i1	-	3,335	5,274	174.13
	c41381_g1_i2	-	2,480	3,839	170.45
	c41381_g1_i6	-	2,521	3,764	164.40
	c41381_g1_i9	-	2,484	3,685	163.34
	c28486_g1_i1	-	1,098	1,517	152.13
	c40236_g1_i1	-	1,698	1,860	120.61
	c29237_g1_i1	-	1,203	1,309	119.81

Supplementary Table 3

c40789_g1_i2	-	2,474	1,759	78.29
c40789_g1_i1	-	2,516	1,698	74.31
c38949_g1_i1	-	1,486	932	69.06
c13708_g1_i2	-	1,180	678	63.27
c7080_g1_i1	-	1,076	482	49.32
c13708_g1_i1	-	1,305	549	46.32
c39677_g1_i1	-	2,028	828	44.96
c31947_g1_i1	-	1,492	472	34.83
c27166_g1_i1	-	1,619	509	34.62
c38902_g1_i1	-	1,516	411	29.85
c39596_g1_i2	-	2,554	596	25.69
c120886_g1_i1	-	1,683	363	23.75
c8457_g1_i1	-	1,469	316	23.69
c39309_g1_i2	-	1,098	230	23.06
c41290_g3_i2	-	3,125	642	22.62
c37720_g1_i1	-	598	116	21.36
c39596_g1_i1	-	2,347	441	20.69
c34483_g1_i1	-	958	172	19.77
c37726_g1_i1	-	1,490	260	19.21
c37726_g1_i2	-	1,660	286	18.97
c37720_g3_i1	-	861	115	14.71
c41290_g2_i3	-	2,285	252	12.14
c7293_g1_i1	-	665	71	11.76
c37720_g3_i2	-	1,131	116	11.29
c8665_g1_i1	-	933	88	10.39
c32126_g1_i1	-	1,186	71	6.59
c7293_g2_i1	-	219	13	6.54
c25679_g1_i1	-	1,196	67	6.17
c15885_g1_i2	-	1,440	76	5.81
c15885_g1_i1	-	1,404	70	5.49
c6924_g1_i1	-	828	40	5.32
c134148_g1_i1	-	562	25	4.90
c41290_g1_i1	-	452	20	4.87
c145247_g1_i1	-	1,424	63	4.87
c37495_g2_i1	-	389	17	4.81
c10276_g2_i1	-	507	22	4.78
c35609_g2_i1	-	595	25	4.63
c122699_g1_i1	-	765	31	4.46
c14123_g1_i1	-	374	15	4.42
c44907_g1_i1	-	824	33	4.41
c9932_g2_i1	-	433	17	4.32
c148924_g1_i1	-	318	12	4.16
c36781_g1_i1	-	717	27	4.15
c35609_g1_i1	-	772	26	3.71
c69106_g1_i1	-	331	11	3.66
c158730_g1_i1	-	638	21	3.62
c106268_g1_i1	-	465	14	3.32
c35609_g2_i3	-	574	17	3.26
c154455_g1_i1	-	410	12	3.22
c124960_g1_i1	-	1,131	33	3.21
c126361_g1_i1	-	343	10	3.21

Supplementary Table 3

	c51355_g1_i1	-	279	8	3.16
	c5874_g1_i1	-	532	15	3.10
	c44537_g1_i1	-	836	23	3.03
	c103717_g1_i1	-	342	9	2.90
	c54183_g1_i1	-	687	18	2.88
	c11473_g1_i1	-	325	8	2.71
	c35609_g2_i2	-	501	12	2.64
	c177712_g1_i1	-	350	8	2.52
	c13003_g1_i1	-	396	9	2.50
	c71551_g1_i1	-	269	6	2.46
	c8447_g1_i1	-	866	19	2.42
	c140392_g1_i1	-	289	6	2.29
	c9932_g1_i1	-	167	3	1.98
	c155529_g1_i1	-	587	10	1.88
	c71020_g1_i1	-	369	6	1.79
	c133671_g1_i1	-	393	6	1.68
	c178180_g1_i1	-	344	5	1.60
	c174348_g1_i1	-	826	12	1.60
	c69216_g1_i1	-	696	10	1.58
	c123895_g1_i1	yes	372	5	1.48
	c88033_g1_i1	-	150	2	1.47
	c182508_g1_i1	-	150	2	1.47
	c4027_g1_i1	-	154	2	1.43
	c182887_g1_i1	-	315	4	1.40
	c158504_g1_i1	-	402	5	1.37
	c133015_g1_i1	-	251	3	1.32
	c188173_g1_i1	-	221	2	1.00
	c140274_g1_i1	-	142	1	0.78
	c185179_g1_i1	-	319	2	0.69
<i>Total</i>			54 / 96	157,365	14,657.79
Peptidase S1 - LDLA domain	c19670_g1_i1	-	1,506	460	33.63
	c41290_g2_i7	-	1,986	174	9.65
	c41290_g2_i5	-	4,402	420	10.51
	c41290_g2_i1	-	2,407	246	11.25
	c41290_g3_i1	-	2,939	670	25.10
	c41290_g3_i2	-	3,125	642	22.62
<i>Total</i>			6 / 6	2,612	112.76
Peptidase S10	c36911_g1_i1	-	3,284	720	24.14
	c171170_g1_i1	-	332	39	12.93
	c122754_g1_i1	-	1,082	65	6.61
	c170269_g1_i1	-	693	36	5.72
	c121851_g1_i1	-	1,327	49	4.07
	c12279_g1_i1	-	409	14	3.77
<i>Total</i>			5 / 6	909	53.48
Phospholipase A2	c40783_g1_i2	-	3,136	5,734	201.33
	c40783_g1_i1	-	3,133	5,149	180.96
	c36194_g1_i1	yes	958	754	86.66
	c35152_g1_i1	-	965	603	68.80
	c41269_g2_i1	yes	1,066	441	45.55
	c38299_g1_i2	yes	1,238	408	36.29
	c38299_g1_i1	yes	610	165	29.78

Supplementary Table 3

	c14022_g1_i1	yes	1,074	56	5.74
	c44309_g1_i1	yes	589	23	4.30
	c3302_g1_i1	-	926	26	3.09
	c3302_g1_i2	-	926	22	2.62
	c147416_g1_i1	-	573	12	2.31
<i>Total</i>			9 / 12	13,336	658.20
Serpin	c38500_g1_i2	-	1,835	618	37.08
	c40151_g1_i1	yes	1,738	510	32.31
	c38500_g1_i1	-	1,375	250	20.02
	c44653_g1_i1	yes	578	76	14.48
	c40233_g1_i2	-	1,217	140	12.67
	c40233_g1_i1	-	1,357	152	12.33
	c41454_g5_i3	-	1,833	142	8.53
	c41454_g5_i1	yes	1,657	127	8.44
	c41454_g5_i4	-	1,761	125	7.82
<i>Total</i>			9 / 9	2,140	153.67
Sphingomyelinase	c37208_g1_i1	yes	1,978	479	26.66
	c42331_g1_i1	yes	2,029	196	10.64
	c95721_g1_i1	yes	2,631	206	8.62
	c122187_g1_i1	-	1,330	61	5.05
	c44135_g1_i1	-	649	29	4.92
	c142423_g1_i1	-	336	5	1.64
	c33214_g1_i1	-	213	0	0.00
<i>Total</i>			5 / 7	971	55.89
VEGF-like	c29900_g1_i1	yes	2,348	575	26.96
	c32284_g1_i1	yes	877	184	23.10
	c8224_g1_i1	yes	1,142	85	8.20
	c102420_g1_i1	yes	1,144	66	6.35
	c123107_g1_i1	yes	346	16	5.09
	c29347_g1_i1	yes	764	34	4.90
	c88368_g1_i1	-	443	19	4.72
	c8330_g1_i1	yes	732	29	4.36
	c27914_g1_i1	-	545	21	4.24
	c30963_g3_i1	-	184	4	2.39
	c97173_g1_i1	-	175	1	0.63
<i>Total</i>			6 / 11	973	73.88
Xibalbin 5 (Putative CSab)	c69533_g1_i1	yes	802	35	4.81
Xibalbin 6 (CHH/ITP)	c170523_g1_i1	-	969	88	10.00
Xibalbin 7 (sIGFBP-rp)	c39061_g3_i1	yes	619	2,507	445.95
	c37504_g1_i1	yes	725	66	10.02
	c37504_g1_i2	yes	1,144	99	9.53
	c147484_g1_i1	yes	477	40	9.23
	c151081_g1_i1	yes	826	66	8.80
	c20493_g1_i1	yes	962	72	8.24
	c37504_g1_i3	yes	737	44	6.57
	c95379_g1_i1	yes	407	6	1.62
<i>Total</i>			7 / 8	2,894	498.34
Xibalbin 8 (Unknown 1)	c122822_g1_i1	yes	741	5,312	789.33

Supplementary Table 3

	c38865_g1_i1	yes		600	3,013	552.93
	c27492_g1_i1	yes		417	7	1.85
<i>Total</i>			2 / 3		8,325	1,342.26
Xibalbin 9 (Unknown 2)	c11438_g1_i1	yes	1	727	540	82
Xibalbin 13 (ICK)	c37192_g1_i4	yes		984	124	13.88
	c37192_g1_i2	yes		927	116	13.78
	c37192_g1_i3	yes		1,011	110	11.98
<i>Total</i>			3 / 3		350	39.63

Supplementary Table 4:

Novel remipede venom peptide families and peptides named according to the rational nomenclature for venom peptide toxins proposed by King et al. (2008). *Toxicon* 52: 264-276, and modified by Undheim et al. (2014). *Molecular Biology and Evolution* 31: 2124-2148.* The expression level of these transcripts did not satisfy the cut-off level. See main text for explanation.

Peptide family	Peptide	Transcript
Xibalbin 1	U-xibalbin1-Xtu1a	c27367_g1_i1
Xibalbin 2	U-xibalbin2-Xtu1a	c29772_g1_i1
Xibalbin 3	U-xibalbin3-Xtu1a	c9387_g1_i1
	U-xibalbin3-Xtu1b	c29843_g1_i2
Xibalbin 4	U-xibalbin4-Xtu1a	c18306_g1_i1
Xibalbin 5	U-xibalbin5-Xtu1a	c28491_g1_i1
Xibalbin 6	U-xibalbin6-Xtu1a	c13591_g1_i1
Xibalbin 7	U-xibalbin7-Xtu1a	c23977_g2_i2*
	U-xibalbin7-Xtu1b	c23977_g2_i1*
Xibalbin 8	U-xibalbin8-Xtu1a	c23843_g2_i1
Xibalbin 9	U-xibalbin9-Xtu1a	c23666_g1_i1
Xibalbin 10	U-xibalbin10-Xtu1a	c25771_g1_i2
Xibalbin 11	U-xibalbin11-Xtu1a	c29407_g1_i2
	U-xibalbin11-Xtu1b	c29407_g1_i1

Supplementary Table 5: Venom gland tissue transcriptome (SOAPdenovo-Tran contigs that match against secreted proteins [UniProtSL0243])

Nr.	Contig name	Read Numbers	Blast result (evalue=10 ⁻⁵ , BlastP, Nr database)	Seq. length	min. evalue	mean similarity	SignalP	InterProScan
1799	98935_length_138_cvg_113.1_tip_1_0	71	serine protease 56	46	1.94E-08	71.70%	0.123	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR009003 (SUPERFAMILY)
1	101333_length_141_cvg_61.0_tip_1_5	60	chitinase 3	47	2.70E-10	67.50%	0.121	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
2	102385_length_141_cvg_96.7_tip_0_4	59	serine protease like protein	47	6.55E-07	77.60%	0.174	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
3	102473_length_141_cvg_63.0_tip_0_4	25	serine protease like protein	47	2.91E-07	77.60%	0.188	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
4	102637_length_142_cvg_23.3_tip_1_5	0	zinc finger protein partial	47	6.80E-18	89.20%	0.107	IPR004457 (PFAM); PTHR10876 (PANTHER); PTHR10876:SF0 (PANTHER)
5	103713_length_142_cvg_7.4_tip_1_2	4	serine protease like protein	47	8.62E-07	74.90%	0.154	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
6	104322_length_143_cvg_5.2_tip_1_0	0	bile salt-activated lipase	48	4.23E-09	73.40%	0.172	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); PTHR11559:SF139 (PANTHER); IPR029058 (SUPERFAMILY)
7	104656_length_143_cvg_2.0_tip_1_1	0	insulin-degrading enzyme isoform x2	48	2.91E-11	80.20%	0.124	IPR011237 (G3DSA:3.30.830.GENE3D); IPR011249 (SUPERFAMILY)
8	105418_length_143_cvg_10.5_tip_1_3	0	stearoyl- desaturase partial	48	7.97E-14	83.70%	0.289	IPR015876 (PRINTS); PTHR11351 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
9	106280_length_144_cvg_6.2_tip_1_2	0	venom serine carboxypeptidase	48	1.06E-13	81.00%	0.098	IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11802:SF30 (PANTHER); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
10	106336_length_144_cvg_6.0_tip_1_0	0	---NA---	48			0.113	IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY)
11	107051_length_144_cvg_61.0_tip_1_1	47	mucin-22 isoform x4	48	4.61E-07	67.50%	0.1	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
12	108305_length_145_cvg_2.0_tip_1_2	2	hypothetical protein EGK_12522, partial	48	6.34E-08	75.00%	0.759 Y	SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
13	110726_length_146_cvg_3.0_tip_1_3	0	prophenoloxidase 1	49	2.55E-16	78.20%	0.109	IPR000896 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR013788 (PANTHER); PTHR11511:SF24 (PANTHER); IPR008922 (SUPERFAMILY)
14	110738_length_146_cvg_2.0_tip_1_0	0	alanine dehydrogenase	49	1.75E-21	100.00%	0.16	IPR007698 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR10160 (PANTHER); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
15	111644_length_147_cvg_60.0_tip_1_4	23	polycystic kidney disease protein 1-like 2-like	49	2.10E-06	70.50%	0.097	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
16	111700_length_147_cvg_2.0_tip_1_1	2	mre11 meiotic recombination 11 homolog a (cerevisiae) isoform cra_b	49	7.16E-15	85.70%	0.217	PTHR22878 (PANTHER)
17	111700_length_147_cvg_2.0_tip_1_3	2	polymerase (dna directed) isoform cra_c	49	1.88E-19	85.80%	0.329	PR02045 (PRINTS); PTHR12138 (PANTHER)
18	111700_length_147_cvg_2.0_tip_1_5	2	tak1-binding protein isoform cra_b	49	8.43E-14	79.50%	0.175	PTHR16213 (PANTHER)
19	114208_length_148_cvg_10.4_tip_1_4	1	serine proteinase stubble-like	49	1.22E-07	66.70%	0.111	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
20	114538_length_149_cvg_2.0_tip_1_0	0	histone h2b 1 2-like	50	1.81E-26	100.00%	0.111	IPR000558 (PRINTS); IPR000558 (SMART); IPR007125 (PFAM); IPR009072 (G3DSA:1.10.20.GENE3D); IPR000558 (PANTHER); IPR009072 (SUPERFAMILY)
21	115238_length_149_cvg_9.0_tip_1_0	2	chitinase 2	50	1.44E-10	68.50%	0.105	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF37 (PANTHER); PTHR11177 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
22	116894_length_150_cvg_4.5_tip_1_5	1	atrial natriuretic peptide-converting enzyme-like	50	3.03E-06	67.50%	0.119	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
24	118732_length_151_cvg_76.5_tip_0_2	76	secreted partial	50	2.34E-09	63.20%	0.102	IPR002557 (SMART); IPR002557 (PFAM); IPR002557 (G3DSA:2.170.140.GENE3D); PTHR23301 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY)
26	120362_length_152_cvg_14.7_tip_1_5	1	carboxypeptidase partial	50	1.02E-09	71.10%	0.097	G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
23	118192_length_151_cvg_60.8_tip_1_3	56	isoform h	51	4.58E-09	65.80%	0.106	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
25	119748_length_152_cvg_35.3_tip_1_0	25	---NA---	51			0.098	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)

27	120494_length_152_cvg_9.4_tip_1_3	9	low-density lipoprotein receptor-related protein 6 isoform 2	51	2.72E-11	73.10%	0.102	IPR002172 (SMART); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
28	121382_length_153_cvg_75.8_tip_1_1	2	carboxypeptidase b-like	51	7.06E-12	77.80%	0.126	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
29	121892_length_153_cvg_7.1_tip_1_3	2	low-density lipoprotein receptor-related protein 5	51	5.30E-08	63.22%	0.105	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
30	122044_length_153_cvg_3.0_tip_1_5	0	gelsolin-like allergen der f 16	51	1.67E-14	69.10%	0.108	IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR007122 (PANTHER); IPR030016 (PTHR11977:PANTHER); SSF55753 (SUPERFAMILY)
31	122840_length_154_cvg_6.7_tip_1_4	0	partial	51	1.38E-13	80.80%	0.106	Coil (COILS)
33	124508_length_155_cvg_2.0_tip_1_5	0	serine protease 45 isoform x5	51	6.33E-07	72.40%	0.281	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
32	123884_length_155_cvg_5.0_tip_1_3	0	alpha-carbonic anhydrase	52	5.88E-15	77.10%	0.265	IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); PTHR18952:SF92 (PANTHER); IPR023561 (PANTHER); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
34	124954_length_155_cvg_5.0_tip_1_3	3	venom allergen 3-like	52	1.73E-11	67.80%	0.129	IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (SUPERFAMILY)
35	125338_length_156_cvg_34.9_tip_1_4	13	serine protease easter	52	3.26E-07	74.20%	0.183	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24275 (PANTHER); IPR009003 (SUPERFAMILY)
36	125508_length_156_cvg_14.0_tip_1_5	13	chitinase 3	52	4.42E-09	63.90%	0.102	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
37	126180_length_156_cvg_41.2_tip_1_0	3	basement membrane-specific heparan sulfate proteoglycan core protein	52	3.37E-08	63.30%	0.1	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
38	127252_length_157_cvg_39.5_tip_1_2	124	proclotting enzyme-like	52	2.79E-10	72.00%	0.147	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24275 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
39	127822_length_157_cvg_45.2_tip_1_0	23	venom allergen 3	53	8.87E-09	78.33%	0.101	IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (SUPERFAMILY)
40	128010_length_157_cvg_3.6_tip_1_3	1	---NA---	53			0.199	no IPS match
41	128474_length_158_cvg_20.8_tip_1_3	7	transmembrane protease serine 11f	53	1.56E-08	64.10%	0.235	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24250 (PANTHER); IPR009003 (SUPERFAMILY)
42	130338_length_159_cvg_16.0_tip_1_4	0	serine proteinase stubble-like	53	2.25E-09	72.70%	0.154	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
43	130422_length_159_cvg_2.0_tip_1_4	0	serine endoprotease partial	53	3.99E-24	100.00%	0.107	IPR001940 (PRINTS); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR22939 (PANTHER); IPR009003 (SUPERFAMILY)
44	130464_length_159_cvg_14.8_tip_1_0	1	carboxypeptidase b-like	53	1.15E-10	71.30%	0.142	G3DSA:3.40.630.10 (GENE3D); SSF53187 (SUPERFAMILY)
45	130948_length_159_cvg_63.0_tip_0_3	3	probable serine carboxypeptidase cpvl	53	1.59E-11	72.00%	0.12	IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
46	133688_length_161_cvg_3.8_tip_1_4	0	alpha beta hydrolase domain-containing protein 17b-like	54	9.27E-30	99.00%	0.101	IPR029059 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR12277:SF55 (PANTHER); PTHR12277 (PANTHER); IPR029058 (SUPERFAMILY)
47	133740_length_161_cvg_63.0_tip_0_0	2	low quality protein: glutathione peroxidase 1-like	54	1.53E-22	84.20%	0.106	IPR012336 (G3DSA:3.40.30.GENE3D); PTHR11592:SF24 (PANTHER); IPR000889 (PANTHER); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
48	134146_length_162_cvg_3.5_tip_1_4	1	---NA---	54			0.105	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
49	134236_length_162_cvg_55.7_tip_1_5	2	very low-density lipoprotein receptor	54	8.68E-07	63.67%	0.191	G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (SUPERFAMILY)
50	134534_length_162_cvg_30.0_tip_1_5	3	serine protease 42-like	54	8.10E-07	71.40%	0.157	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
51	134664_length_162_cvg_4.0_tip_1_1	4	st14a protein	54	3.02E-06	69.00%	0.1	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
52	135072_length_162_cvg_8.5_tip_1_5	8	basement membrane-specific heparan sulfate proteoglycan core protein	54	2.27E-09	66.60%	0.103	IPR002172 (SMART); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
53	135316_length_162_cvg_2.0_tip_1_4	0	heat shock cognate 70	54	4.74E-20	85.80%	0.099	IPR029048 (G3DSA:1.20.1270.GENE3D); PTHR19375 (PANTHER); PTHR19375:SF142 (PANTHER); IPR029048 (SUPERFAMILY)
55	136372_length_163_cvg_2.0_tip_1_2	2	membrane alanyl aminopeptidase	54	2.73E-29	100.00%	0.168	IPR014782 (PRINTS); IPR014782 (PFAM); G3DSA:1.10.390.10 (GENE3D); PTHR11533:SF163 (PANTHER); IPR001930 (PANTHER); SSF55486 (SUPERFAMILY)
54	136174_length_163_cvg_2.2_tip_1_3	0	hypothetical protein Y032_0473g2095	55	1.01E-07	73.80%	0.122	no IPS match
56	136396_length_163_cvg_3.1_tip_1_0	0	heat shock cognate 71 kda protein	55	4.22E-27	93.40%	0.1	IPR013126 (PRINTS); G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); PTHR19375:SF155 (PANTHER); SSF53067 (SUPERFAMILY)
57	136832_length_163_cvg_2.0_tip_1_3	0	protein sda1 homolog	55	6.40E-20	91.00%	0.165	IPR027312 (PTHR12730:PANTHER); PTHR12730 (PANTHER)
58	136844_length_163_cvg_2.0_tip_1_0	0	elastin isoform x11	55	4.46E-08	66.14%	0.099	no IPS match
59	138652_length_165_cvg_2.1_tip_1_0	0	glyceraldehyde-3-phosphate dehydrogenase	55	2.64E-13	89.70%	0.123	IPR020831 (PANTHER); PTHR10836:SF31 (PANTHER)

60	139536_length_165_cvg_132.3_tip_0_1	473	low-density lipoprotein receptor-related protein 2-like	55	1.51E-06	71.50%	0.099	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
63	141944_length_167_cvg_2.0_tip_1_2	0	partial	55	3.22E-19	85.00%	0.096	IPR013320 (G3DSA:2.60.120.GENE3D); IPR001580 (PFAM); PTHR11073:SF5 (PANTHER); IPR001580 (PANTHER); IPR013320 (SUPERFAMILY)
61	140504_length_166_cvg_78.5_tip_1_0	5	urokinase-type plasminogen activator	56	1.43E-08	73.30%	0.31	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
62	141658_length_167_cvg_63.0_tip_1_3	31	chymotrypsin-like elastase family member 1	56	1.73E-08	65.90%	0.118	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
64	142817_length_168_cvg_109.6_tip_0_0	179	flocculation protein flo11 isoform x2	56	2.58E-07	76.80%	0.132	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
65	142839_length_168_cvg_2.0_tip_1_0	0	c4b-binding protein beta chain	56	3.17E-19	78.00%	0.121	G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); PTHR19325:SF340 (PANTHER); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY)
66	142999_length_168_cvg_4.6_tip_1_1	1	venom allergen 3- partial	56	8.58E-13	75.20%	0.104	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR018244 (PROSITE_PATTERNS); IPR014044 (SUPERFAMILY)
67	143039_length_168_cvg_7.0_tip_1_4	0	chitinase-related protein 1	56	1.89E-15	76.30%	0.114	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
68	143301_length_168_cvg_103.7_tip_1_4	4	low-density lipoprotein receptor-related protein 2	56	2.61E-08	64.30%	0.1	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
69	143319_length_168_cvg_10.3_tip_1_1	0	hemagglutinin amebocyte aggregation factor-like	56	2.36E-12	74.30%	0.108	PF14704 (PFAM); IPR026645 (PANTHER)
70	143575_length_168_cvg_32.3_tip_1_4	1	transmembrane protease serine 11f	56	3.72E-10	65.40%	0.105	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24275:SF50 (PANTHER); PTHR24275 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
71	143643_length_168_cvg_63.0_tip_0_3	170	flocculation protein flo11 isoform x1	56	3.63E-07	76.80%	0.133	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
76	145147_length_169_cvg_2.4_tip_1_1	0	hypothetical protein Y032_0580g260	56	2.10E-09	66.30%	0.102	no IPS match
77	145155_length_169_cvg_17.3_tip_1_1	37	---NA---	56			0.101	G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
72	144515_length_169_cvg_31.0_tip_1_3	130	---NA---	57			0.101	G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
73	144637_length_169_cvg_25.2_tip_1_3	2	agap000573-pb-like protein	57	7.35E-08	66.60%	0.11	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
74	145045_length_169_cvg_3.2_tip_0_0	0	hyaluronidase ph-20-like	57	5.38E-08	62.90%	0.101	IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
75	145135_length_169_cvg_2.3_tip_0_3	0	hyaluronidase- partial	57	6.11E-08	63.20%	0.1	IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); IPR018155 (PANTHER); IPR017853 (SUPERFAMILY)
78	145391_length_170_cvg_61.9_tip_1_3	81	acidic mammalian chitinase-like	57	8.22E-10	65.30%	0.117	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
79	146565_length_171_cvg_2.0_tip_1_1	0	cysteine-rich secretory protein 2	57	3.11E-26	85.60%	0.12	IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (SUPERFAMILY)
80	147255_length_171_cvg_2.6_tip_1_1	0	neurogenic locus notch	57	2.42E-24	96.00%	0.105	PR00010 (PRINTS); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24033 (PANTHER); PTHR24033:SF36 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
84	148789_length_172_cvg_2.0_tip_1_2	0	isoform a	57	1.27E-06	65.50%	0.102	IPR002223 (PRINTS); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY)
81	147787_length_172_cvg_56.0_tip_1_0	357	sortilin-related receptor	58	2.67E-07	62.60%	0.1	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); PTHR10529:SF222 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
82	147841_length_172_cvg_8.0_tip_1_0	0	hemagglutinin amebocyte aggregation factor-like	58	3.77E-10	64.60%	0.102	PF14704 (PFAM); IPR026645 (PANTHER)
83	148351_length_172_cvg_4.5_tip_1_3	0	histidine-rich glyco	58	5.00E-08	63.90%	0.098	no IPS match
85	149541_length_173_cvg_93.8_tip_1_0	248	isoform a	58	3.71E-06	57.67%	0.11	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
86	149543_length_173_cvg_63.0_tip_1_0	132	isoform a	58	3.71E-06	57.67%	0.11	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)

87	149725_length_173_cvg_115.5_tip_0_0	297	low-density lipoprotein receptor-related protein 1-like	58	1.28E-09	65.50%	0.099	IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
88	151099_length_174_cvg_42.2_tip_1_1	1	suppressor of tumorigenicity 14 protein homolog	58	8.20E-09	64.00%	0.101	IPR002172 (PRINTS); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
89	151199_length_174_cvg_59.3_tip_1_1	390	st14a protein	58	1.48E-06	63.57%	0.101	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
90	151427_length_174_cvg_2.6_tip_1_5	5	endo- -d-glucanase	58	5.15E-22	100.00%	0.12	IPR002037 (PFAM)
91	152010_length_175_cvg_21.0_tip_1_4	2	transmembrane protease serine 11a	58	8.67E-08	65.83%	0.105	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
93	152778_length_176_cvg_88.1_tip_0_5	30	probable serine carboxypeptidase cpvl isoform x5	58	2.01E-15	72.50%	0.104	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
95	153190_length_176_cvg_2.0_tip_1_5	0	enolase partial	58	2.58E-23	79.70%	0.118	IPR029065 (G3DSA:3.20.20.GENE3D); IPR020810 (PFAM); IPR000941 (PANTHER); IPR029065 (SUPERFAMILY)
92	152440_length_175_cvg_22.6_tip_1_0	3	clipb6 protein	59	8.03E-12	66.70%	0.127	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF72 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
94	152988_length_176_cvg_2.0_tip_1_3	1	ensangg00000017398 protein	59	2.37E-29	95.80%	0.099	IPR013126 (PRINTS); IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); PTHR19375:SF142 (PANTHER); SSF53067 (SUPERFAMILY)
96	154172_length_177_cvg_7.1_tip_1_1	0	granzyme a-like	59	6.05E-06	55.00%	0.1	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
97	154674_length_177_cvg_12.6_tip_1_5	0	carboxypeptidase b-like	59	1.41E-15	83.00%	0.1	IPR000834 (PRINTS); G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); PTHR11705:SF61 (PANTHER); SSF53187 (SUPERFAMILY)
98	155286_length_178_cvg_2.5_tip_1_2	24	chitinase 2	59	1.01E-09	61.90%	0.103	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF45 (PANTHER); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
99	155822_length_178_cvg_5.8_tip_1_3	1	---NA---	60			0.186	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); IPR029058 (SUPERFAMILY)
100	155898_length_178_cvg_60.3_tip_1_0	886	chitinase partial	60	3.69E-11	65.10%	0.103	IPR029070 (G3DSA:3.10.50.GENE3D); IPR029070 (SUPERFAMILY)
101	157098_length_179_cvg_3.8_tip_1_3	0	serine (or cysteine) proteinase clade b member	60	3.00E-09	65.60%	0.119	IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); IPR000215 (PANTHER); PTHR11461:SF52 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
102	157254_length_179_cvg_84.3_tip_0_3	308	chymotrypsin-like elastase family member 1	60	8.06E-09	61.90%	0.113	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
103	157808_length_179_cvg_35.0_tip_1_3	31	isoform a	60	5.71E-08	75.40%	0.227	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); IPR009003 (SUPERFAMILY)
104	158144_length_180_cvg_9.0_tip_1_4	0	dermatopontin 3	60	6.99E-10	69.20%	0.103	PF14704 (PFAM)
105	158236_length_180_cvg_62.0_tip_1_4	2290	acidic mammalian chitinase-like isoform x1	60	1.65E-10	64.00%	0.133	IPR013781 (G3DSA:3.20.20.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR029070 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
106	158352_length_180_cvg_16.3_tip_1_3	0	carboxypeptidase b-like	60	1.40E-16	75.70%	0.097	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
107	158546_length_180_cvg_3.3_tip_1_2	0	low-density lipoprotein receptor-related protein 2-like	60	3.71E-07	58.10%	0.114	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
109	159385_length_181_cvg_2.0_tip_1_1	0	nitrate reductase catalytic partial	60	8.13E-35	100.00%	0.118	IPR006656 (PFAM); G3DSA:3.40.228.10 (GENE3D); PTHR11615 (PANTHER); PTHR11615:SF123 (PANTHER); SSF53706 (SUPERFAMILY)
110	159581_length_181_cvg_62.1_tip_1_4	70	isoform f	60	2.92E-08	74.70%	0.135	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
111	160585_length_182_cvg_68.7_tip_1_5	85	chitinase	60	2.17E-06	71.00%	0.115	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
113	161237_length_182_cvg_62.0_tip_1_2	48	chitinase partial	60	5.61E-09	71.00%	0.102	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
108	159259_length_181_cvg_28.7_tip_1_3	9	low-density lipoprotein receptor-related protein 5	61	1.64E-07	65.30%	0.112	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PATTERNS); IPR002172 (SUPERFAMILY)
112	160629_length_182_cvg_2.0_tip_1_1	0	protein kinase dc2	61	1.28E-33	97.40%	0.096	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24353 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
114	161279_length_182_cvg_2.0_tip_1_3	0	polypeptide n-acetylgalactosaminyltransferase 2	61	1.39E-22	84.80%	0.186	G3DSA:2.80.10.50 (GENE3D); IPR000772 (PFAM); IPR000772 (PROSITE_PROFILES); IPR000772 (SUPERFAMILY)

115	161283_length_182_cvg_60.6_tip_1_3	2113	chitinase partial	61	1.47E-12	66.00%	0.145	IPR029070 (G3DSA:3.10.50.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); IPR029070 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
116	161522_length_183_cvg_61.5_tip_1_0	11	af117899_1ldlr-fut fusion protein	61	3.81E-06	72.67%	0.217	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
117	161528_length_183_cvg_28.8_tip_1_3	1	carboxypeptidase partial	61	2.42E-12	63.80%	0.304	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
118	161538_length_183_cvg_56.0_tip_1_2	10	---NA---	61			0.182	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
119	161564_length_183_cvg_2.0_tip_1_0	0	molecular chaperone partial	61	3.98E-35	99.80%	0.112	IPR013126 (PRINTS); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF173 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
120	161578_length_183_cvg_53.2_tip_1_5	9	serine protease 57	61	3.31E-06	58.30%	0.103	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
121	161584_length_183_cvg_19.2_tip_1_2	2	chymotrypsin-like elastase family member 2a	61	3.78E-06	63.50%	0.136	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
122	161654_length_183_cvg_61.0_tip_1_0	59	chitinase partial	61	5.12E-12	61.30%	0.101	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
123	161700_length_183_cvg_62.0_tip_1_1	49	chitinase 2	61	2.46E-11	62.80%	0.104	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
124	161704_length_183_cvg_31.8_tip_1_4	8	secreted salivary gland	61	1.52E-10	68.70%	0.112	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR009003 (SUPERFAMILY)
125	161716_length_183_cvg_45.2_tip_1_1	21	low-density lipoprotein receptor-related protein 2-like	61	5.32E-08	61.10%	0.098	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
126	161752_length_183_cvg_61.8_tip_1_1	59	chitotriosidase- partial	61	4.14E-09	61.60%	0.1	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
127	161762_length_183_cvg_35.3_tip_1_1	260	st14a protein	61	5.27E-08	64.70%	0.112	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
128	161782_length_183_cvg_61.0_tip_1_2	10	---NA---	61			0.21	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
129	161822_length_183_cvg_61.0_tip_1_4	75	chitinase 3	61	2.04E-09	62.40%	0.119	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
130	161826_length_183_cvg_28.4_tip_1_1	3	neurotrypsin- partial	61	1.19E-10	68.90%	0.134	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
131	161830_length_183_cvg_50.6_tip_1_5	216	low-density lipoprotein receptor-related protein 8	61	1.97E-11	65.00%	0.101	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
132	161832_length_183_cvg_11.7_tip_1_5	2	low quality protein: serine protease 55	61	8.65E-08	67.20%	0.108	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
133	161836_length_183_cvg_31.9_tip_1_4	159	low-density lipoprotein receptor-related protein 6 isoform x2	61	5.06E-10	68.30%	0.103	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
134	161868_length_183_cvg_38.4_tip_1_4	6	chitinase 1	61	1.02E-08	65.70%	0.174	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
135	161874_length_183_cvg_45.0_tip_1_3	2	chymotrypsin-like elastase family member 2a	61	2.26E-08	59.70%	0.136	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24258:SF97 (PANTHER); PTHR24258 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
136	161882_length_183_cvg_19.6_tip_1_3	2	zinc carboxypeptidase-like	61	1.05E-15	67.40%	0.117	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
137	161896_length_183_cvg_28.4_tip_1_2	185	transmembrane protease serine 11b	61	4.84E-07	61.80%	0.106	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF72 (PANTHER); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
138	161916_length_183_cvg_31.2_tip_1_2	5	suppressor of tumorigenicity 14 protein	61	6.65E-12	66.00%	0.193	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
139	161948_length_183_cvg_44.6_tip_1_5	10	---NA---	61			0.204	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
140	161960_length_183_cvg_10.2_tip_1_2	2	---NA---	61			0.098	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
141	161966_length_183_cvg_48.8_tip_1_1	2	transmembrane protease serine 11e	61	4.25E-10	68.30%	0.134	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24275 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
142	162006_length_183_cvg_34.0_tip_1_2	4	complement c1s subcomponent	61	1.27E-06	66.50%	0.106	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR009003 (SUPERFAMILY)
143	162010_length_183_cvg_39.7_tip_1_4	1	chymotrypsin-like elastase family member 2b	61	1.50E-09	66.70%	0.103	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24258:SF97 (PANTHER); PTHR24258 (PANTHER); IPR009003 (SUPERFAMILY)
144	162012_length_183_cvg_61.0_tip_1_1	54	chitinase 7 precursor	61	3.09E-08	61.60%	0.177	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)

145	162022_length_183_cvg_61.0_tip_1_5	48	chitinase partial	61	4.45E-08	68.00%	0.1	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
146	162030_length_183_cvg_43.2_tip_1_1	204	isoform a	61	3.64E-07	64.20%	0.109	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
147	162038_length_183_cvg_60.2_tip_1_1	43	chitinase partial	61	2.71E-12	68.60%	0.131	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
148	162040_length_183_cvg_60.2_tip_1_1	40	chitinase partial	61	1.71E-11	61.50%	0.105	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
149	162062_length_183_cvg_2.0_tip_1_2	0	zinc finger protein 2 homolog	61	5.30E-17	72.60%	0.162	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
150	162120_length_183_cvg_60.8_tip_1_4	53	chitinase partial	61	1.11E-10	70.00%	0.101	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
151	162144_length_183_cvg_29.7_tip_1_3	11	serine proteinase stubble-like	61	6.27E-10	61.00%	0.1	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR009003 (SUPERFAMILY)
152	162178_length_183_cvg_60.0_tip_1_5	1107	chitinase isoform a	61	6.04E-16	63.30%	0.101	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF45 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
153	162186_length_183_cvg_28.7_tip_1_2	0	venom serine carboxypeptidase-like	61	2.68E-17	68.00%	0.128	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
154	162190_length_183_cvg_53.6_tip_1_3	13	low-density lipoprotein receptor-related protein 6 isoform x2	61	2.55E-11	69.00%	0.102	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
155	162220_length_183_cvg_61.0_tip_1_1	82	chitinase 2	61	1.69E-12	64.10%	0.101	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF45 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
156	162266_length_183_cvg_31.0_tip_1_2	480	low-density lipoprotein receptor-related protein 2	61	1.85E-09	64.90%	0.099	IPR002172 (PRINTS); IPR002172 (SMART); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
157	162286_length_183_cvg_7.8_tip_1_1	0	---NA---	61			0.123	IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR014044 (SUPERFAMILY)
158	162410_length_183_cvg_26.2_tip_1_3	26	sortilin-related receptor containing ldlr class a repeats preproprotein	61	1.43E-06	62.00%	0.1	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
159	162414_length_183_cvg_33.6_tip_1_5	1	serine protease like protein	61	1.45E-12	64.50%	0.164	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF72 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
160	162434_length_183_cvg_60.2_tip_1_3	54	chitinase partial	61	2.63E-09	59.30%	0.1	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
161	162440_length_183_cvg_56.0_tip_1_4	11	granzyme a-like	61	5.72E-06	58.00%	0.112	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
162	162452_length_183_cvg_61.0_tip_1_3	9	low-density lipoprotein receptor-related protein 2-like	61	5.69E-13	68.00%	0.11	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); PTHR10529:SF222 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
163	162472_length_183_cvg_36.9_tip_1_0	0	chitinase partial	61	1.27E-16	71.70%	0.156	IPR001223 (PFAM); IPR029070 (G3DSA:3.10.50.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY); IPR029070 (SUPERFAMILY)
164	162496_length_183_cvg_59.6_tip_1_1	53	isoform k	61	7.61E-13	65.40%	0.108	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF45 (PANTHER); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
165	162544_length_183_cvg_18.6_tip_1_1	3	carboxypeptidase b	61	1.36E-10	62.90%	0.139	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
166	162546_length_183_cvg_60.0_tip_1_0	405	clip-domain serine protease	61	3.46E-06	77.33%	0.313	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); IPR009003 (SUPERFAMILY)
167	162564_length_183_cvg_41.0_tip_1_0	266	transcription activator brg1	61	2.25E-10	66.10%	0.1	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
168	162574_length_183_cvg_41.7_tip_1_5	156	sortilin-related receptor- partial	61	3.67E-08	59.30%	0.101	IPR002172 (SMART); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)

169	162596_length_183_cvg_26.1_tip_1_0	4	chymotrypsin-like elastase family member 1	61	1.52E-07	62.10%	0.145	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24258 (PANTHER); PTHR24258:SF97 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
170	162598_length_183_cvg_31.2_tip_1_4	9	granzyme a-like	61	4.74E-08	60.90%	0.106	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
171	162640_length_183_cvg_35.5_tip_1_3	3	plasma kallikrein	61	5.08E-08	61.60%	0.123	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24250 (PANTHER); PTHR24250:SF6 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
172	162682_length_183_cvg_60.2_tip_1_1	36	chitinase partial	61	1.59E-12	65.20%	0.107	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
173	162776_length_183_cvg_60.0_tip_1_5	40	chitinase partial	61	1.93E-10	71.00%	0.101	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
174	162800_length_183_cvg_61.0_tip_1_5	11	suppressor of tumorigenicity 14 protein	61	5.42E-09	67.80%	0.13	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR009003 (SUPERFAMILY)
175	162816_length_183_cvg_60.0_tip_1_2	66	isoform h	61	2.01E-13	67.80%	0.12	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
176	162826_length_183_cvg_42.6_tip_1_2	14	low-density lipoprotein receptor-related protein 2- partial	61	2.23E-10	63.60%	0.097	IPR002172 (PRINTS); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
177	162828_length_183_cvg_59.3_tip_1_5	32	chitinase partial	61	2.48E-09	68.10%	0.118	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
178	163819_length_184_cvg_84.4_tip_1_5	6	carboxypeptidase a2-like	61	4.06E-15	76.80%	0.106	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
179	164537_length_185_cvg_62.0_tip_1_0	239	probable chitinase 3	62	4.12E-13	68.60%	0.144	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
180	164579_length_185_cvg_14.9_tip_1_4	67	chitinase isoform a	62	1.38E-12	63.30%	0.106	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF45 (PANTHER); IPR017853 (SUPERFAMILY)
181	164733_length_185_cvg_59.0_tip_1_3	60	isoform h	62	1.09E-13	66.30%	0.116	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
182	165047_length_185_cvg_58.7_tip_1_4	69	brain chitinase and chia	62	7.44E-09	63.50%	0.104	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF45 (PANTHER); PTHR11177 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
183	165415_length_186_cvg_2.0_tip_1_4	2	outer membrane autotransporter barrel domain protein	62	1.21E-33	100.00%	0.111	IPR005546 (PFAM); IPR005546 (G3DSA:2.40.128.GENE3D); IPR005546 (SUPERFAMILY)
184	165911_length_186_cvg_36.8_tip_1_0	37	neurotrypsin- partial	62	7.20E-07	64.57%	0.138	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
185	167307_length_187_cvg_56.7_tip_1_1	87	peptidase s1 and s6 chymotrypsin hap	62	1.51E-11	73.40%	0.163	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
186	168596_length_188_cvg_19.3_tip_1_4	2	low quality protein: probable chitinase 3	63	1.09E-13	70.50%	0.103	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
187	168688_length_189_cvg_13.0_tip_1_4	0	leukocyte elastase inhibitor	63	2.20E-09	72.10%	0.133	G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
188	170656_length_190_cvg_2.0_tip_1_4	0	hypothetical protein DAPPUDRAFT_317027	63	5.33E-08	62.00%	0.135	IPR015420 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
189	171606_length_191_cvg_16.8_tip_1_5	1	---NA---	63			0.103	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
190	172110_length_192_cvg_2.0_tip_1_1	0	nad h:quinone oxidoreductase	64	1.27E-35	99.20%	0.156	IPR029039 (G3DSA:3.40.50.GENE3D); PTHR30546 (PANTHER); IPR029039 (SUPERFAMILY)
192	174052_length_193_cvg_5.8_tip_1_4	0	suppressor of tumorigenicity 14 protein	64	3.11E-11	72.70%	0.134	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR009003 (SUPERFAMILY)
193	174474_length_194_cvg_2.0_tip_1_2	0	chitinase partial	64	2.02E-06	47.00%	0.166	IPR029070 (G3DSA:3.10.50.GENE3D)
191	173640_length_193_cvg_2.0_tip_1_0	0	lysyl-trna synthetase	65	1.04E-28	90.80%	0.102	IPR004364 (PFAM); G3DSA:3.30.930.10 (GENE3D); PTHR22594:SF25 (PANTHER); IPR018150 (PANTHER); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY)
194	176070_length_195_cvg_63.0_tip_1_4	0	allergen 5	65	5.04E-13	74.80%	0.128	IPR002413 (PRINTS); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (SUPERFAMILY)
195	176198_length_195_cvg_56.2_tip_1_2	9	chymotrypsin-like elastase family member partial	65	2.17E-10	66.40%	0.259	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24275 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
196	176208_length_195_cvg_7.3_tip_1_4	4	serine protease	65	2.59E-08	69.80%	0.119	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF81 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
197	177798_length_197_cvg_3.1_tip_1_5	0	serine protease	65	2.50E-09	64.40%	0.104	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)

198	178412_length_197_cvg_84.0_tip_1_0	1163	trypsin-like protease	66	9.40E-08	61.70%	0.135	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
199	178612_length_198_cvg_63.8_tip_0_3	2	gamma-glutamyl hydrolase	66	4.32E-15	63.80%	0.098	IPR029062 (G3DSA:3.40.50.GENE3D); PTHR11315:SF0 (PANTHER); IPR015527 (PANTHER)
200	179098_length_198_cvg_2.0_tip_1_4	0	udp- c:polypeptide n-	66	5.24E-07	82.90%	0.112	no IPS match
201	181240_length_200_cvg_71.2_tip_0_3	698	proclotting enzyme	67	9.68E-14	69.40%	0.103	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
202	181262_length_200_cvg_2.4_tip_1_1	0	hypothetical protein Y032_0473g2095	67	1.99E-10	66.20%	0.109	no IPS match
203	181788_length_201_cvg_2.0_tip_1_1	0	alpha-amylase	67	1.55E-39	99.60%	0.158	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
204	181916_length_201_cvg_60.9_tip_1_1	41	chitinase-3-like protein 1	67	9.48E-14	65.40%	0.12	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
205	182700_length_202_cvg_2.0_tip_1_1	0	zinc finger protein 501-like	67	5.59E-09	69.60%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
206	183980_length_203_cvg_120.8_tip_1_3	15	venom allergen partial	68	3.67E-11	61.60%	0.117	IPR001283 (PRINTS); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR014044 (SUPERFAMILY)
207	184866_length_204_cvg_85.6_tip_1_1	22	urokinase-type plasminogen activator	68	2.57E-12	69.00%	0.14	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265:SF76 (PANTHER); PTHR24265 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
208	184962_length_204_cvg_2.0_tip_1_4	0	endothelin-converting enzyme 1-like	68	4.75E-20	83.60%	0.118	IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); PTHR11733:SF110 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
210	186520_length_205_cvg_61.0_tip_1_1	47	chitotriosidase- partial	68	1.31E-14	62.40%	0.104	IPR029070 (G3DSA:3.10.50.GENE3D); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF45 (PANTHER); IPR017853 (SUPERFAMILY)
209	186108_length_205_cvg_2.0_tip_1_0	0	serine threonine-protein kinase mark2-like isoform x10	69	6.33E-39	99.80%	0.109	G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24346 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
211	190393_length_209_cvg_9.0_tip_1_2	0	lysosomal acid phosphatase	69	4.69E-14	71.00%	0.517 Y	IPR000560 (PFAM); IPR029033 (G3DSA:3.40.50.GENE3D); PTHR11567:SF26 (PANTHER); PTHR11567 (PANTHER); IPR000560 (PROSITE_PATTERNS); SignalP-noTM (SIGNALP_EUK); IPR029033 (SUPERFAMILY)
212	190901_length_209_cvg_2.0_tip_1_5	0	von willebrand factor type egf and pentraxin domain-containing protein 1 isoform x1	69	1.06E-19	77.50%	0.128	IPR011641 (PFAM); G3DSA:2.10.50.10 (GENE3D); PTHR24049:SF6 (PANTHER); PTHR24049 (PANTHER); IPR009030 (SUPERFAMILY)
346	288445_length_332_cvg_4.5_tip_1_0	1	chitinase 7 precursor	69	3.13E-09	61.90%	0.101	IPR013781 (G3DSA:3.20.20.GENE3D)
213	191679_length_210_cvg_104.4_tip_0_4	2	neutral protease	70	2.32E-14	68.10%	0.112	IPR013856 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); SSF55486 (SUPERFAMILY)
214	192413_length_211_cvg_2.0_tip_1_2	0	glyceraldehyde-3-phosphate dehydrogenase c	70	1.94E-25	96.40%	0.105	IPR020828 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR10836:SF31 (PANTHER); IPR020831 (PANTHER); SSF51735 (SUPERFAMILY)
215	193737_length_212_cvg_2.0_tip_1_1	0	n-acetylated-alpha-linked acidic dipeptidase	71	4.95E-31	85.70%	0.107	G3DSA:3.40.630.10 (GENE3D); IPR007484 (PFAM); PTHR10404 (PANTHER); SSF53187 (SUPERFAMILY)
216	194686_length_213_cvg_2.0_tip_1_5	0	protein partial	71	3.11E-16	80.90%	0.16	IPR019154 (PFAM); PTHR21357 (PANTHER)
217	195332_length_213_cvg_2.0_tip_1_4	0	tryptophan-specific transport protein	71	8.96E-40	100.00%	0.14	IPR018227 (PFAM); PTHR32195 (PANTHER); PTHR32195:SF11 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
218	195482_length_213_cvg_2.0_tip_1_4	0	aael008198- partial	71	6.22E-17	66.30%	0.101	G3DSA:2.170.300.10 (GENE3D); PTHR24035 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES)
219	195916_length_214_cvg_4.0_tip_1_3	0	dimethylaniline monooxygenase	72	9.16E-22	75.90%	0.111	IPR020946 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR23023 (PANTHER); PTHR23023:SF4 (PANTHER); SSF51905 (SUPERFAMILY)
220	196852_length_215_cvg_2.0_tip_1_0	0	phosphoglucose partial	72	3.26E-45	98.80%	0.168	IPR001672 (PFAM); G3DSA:3.40.50.10490 (GENE3D); IPR001672 (PANTHER); PTHR11469:SF7 (PANTHER); IPR001672 (PROSITE_PROFILES); SSF53697 (SUPERFAMILY)
221	197384_length_215_cvg_2.0_tip_1_1	0	serine threonine-protein phosphatase 4 catalytic subunit	72	4.46E-43	98.00%	0.1	IPR006186 (PRINTS); IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); PTHR11668 (PANTHER); IPR029052 (SUPERFAMILY)
222	197766_length_216_cvg_87.7_tip_1_1	11	carboxypeptidase b-like	72	2.81E-21	76.10%	0.11	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY)
223	198108_length_216_cvg_63.0_tip_1_1	11	carboxypeptidase b-like	72	2.00E-20	77.90%	0.128	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY)

224	200410_length_218_cvg_2.0_tip_1_1	0	isoform g	73	1.93E-23	72.70%	0.14	G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325:SF340 (PANTHER); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
225	200875_length_219_cvg_3.8_tip_1_2	0	upf0669 protein c6orf120 homolog	73	3.07E-12	67.70%	0.809 Y	PTHR31703 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE)
226	203299_length_221_cvg_3.0_tip_1_3	2	xanthine dehydrogenase	74	3.27E-21	79.00%	0.103	IPR016169 (G3DSA:3.30.465.GENE3D); IPR002346 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR016166 (SUPERFAMILY)
227	204205_length_222_cvg_2.0_tip_1_3	0	basement membrane-specific heparan sulfate proteoglycan core protein	74	1.25E-26	81.80%	0.109	IPR002049 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR10574 (PANTHER); PTHR10574:SF252 (PANTHER); IPR002049 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY)
228	206453_length_224_cvg_2.0_tip_1_3	0	peptidyl-prolyl cis-trans rhodopsin-specific isozyme-like	75	1.03E-29	78.50%	0.134	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF11 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
229	206984_length_225_cvg_25.7_tip_1_2	0	xanthine dehydrogenase	75	3.94E-07	79.00%	0.226	IPR012675 (G3DSA:3.10.20.GENE3D)
230	209190_length_227_cvg_2.0_tip_1_5	0	proprotein convertase subtilisin kexin type 7	75	4.11E-31	85.10%	0.121	IPR000209 (PFAM); IPR000209 (G3DSA:3.40.50.GENE3D); PTHR10795:SF9 (PANTHER); IPR015500 (PANTHER); IPR023828 (PROSITE_PATTERNS); IPR000209 (SUPERFAMILY)
231	209490_length_227_cvg_2.5_tip_1_2	0	atp-binding component of a transport system	75	1.29E-40	98.10%	0.102	IPR012332 (G3DSA:2.160.20.GENE3D)
232	210110_length_228_cvg_4.4_tip_1_2	0	hypothetical protein Y032_0089g2326	76	5.56E-07	62.60%	0.106	no IPS match
233	210620_length_228_cvg_2.0_tip_1_4	0	zinc finger protein 676-like	76	6.78E-24	71.40%	0.119	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
235	211490_length_229_cvg_65.4_tip_1_1	115	chitinase 3	76	1.20E-17	64.90%	0.111	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
236	211668_length_229_cvg_54.1_tip_1_5	6	26kda protease	76	2.73E-16	65.90%	0.124	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
237	211962_length_229_cvg_47.2_tip_1_1	802	proclotting enzyme	76	2.09E-08	57.20%	0.106	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
238	212778_length_230_cvg_2.0_tip_1_2	0	low quality protein: protein flightless-1 homolog	76	2.33E-27	85.90%	0.169	PR00019 (PRINTS); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR007122 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
234	211482_length_229_cvg_59.4_tip_1_3	78	chitinase partial	77	2.37E-18	65.00%	0.122	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
239	213100_length_231_cvg_60.0_tip_1_4	81	chitinase 7 precursor	77	8.32E-08	55.80%	0.135	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
240	213684_length_231_cvg_2.0_tip_1_5	0	zinc finger protein 665-like isoform x6	77	5.69E-21	70.60%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
241	214176_length_232_cvg_90.1_tip_0_3	426	low-density lipoprotein receptor-related protein 2-like	78	3.51E-15	63.70%	0.1	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
242	215360_length_233_cvg_63.0_tip_1_3	17	serine protease 27-like	78	1.20E-10	63.70%	0.104	IPR001314 (PRINTS); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24258:SF97 (PANTHER); PTHR24258 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
243	216616_length_234_cvg_4.7_tip_1_1	0	hemagglutinin	78	3.02E-15	68.60%	0.1	IPR013856 (G3DSA:3.10.170.GENE3D); IPR013856 (PFAM); SSF55486 (SUPERFAMILY)
244	216696_length_234_cvg_123.1_tip_0_4	2107	low-density lipoprotein receptor-related protein 2-partial	78	1.88E-14	64.40%	0.098	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
246	217726_length_235_cvg_2.0_tip_1_2	2	coactosin-like protein isoform x1	78	7.41E-07	68.25%	0.143	no IPS match

245	217726_length_235_cvg_2.0_tip_1_0	2	neuronal thread protein ad7c-ntp	79	2.06E-19	62.80%	0.199	PF13900 (PFAM); PTHR16213 (PANTHER); PTHR16213:SF28 (PANTHER)
247	218528_length_236_cvg_4.1_tip_1_0	0	tab y 2 allergen	79	1.52E-08	65.20%	0.550 Y	IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-TM (SIGNALP_EUK); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
248	218614_length_236_cvg_3.7_tip_1_3	0	zinc finger protein 358	79	2.10E-17	64.40%	0.115	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
249	218837_length_237_cvg_5.2_tip_1_5	0	tyrosine-protein kinase wsck	79	6.35E-29	72.20%	0.469 Y	G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416 (PANTHER); IPR000719 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR011009 (SUPERFAMILY)
250	220301_length_238_cvg_61.5_tip_1_5	46	chitinase 8 precursor	79	7.14E-09	61.80%	0.108	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
256	221489_length_239_cvg_2.0_tip_1_2	0	laminin subunit gamma-1-like	79	6.01E-06	69.67%	0.237	IPR002049 (SMART); IPR002049 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
251	220495_length_238_cvg_2.0_tip_1_3	0	transposase	80	2.33E-09	64.30%	0.122	no IPS match
252	220881_length_239_cvg_63.0_tip_0_3	0	14-3-3 protein zeta isoform x1	80	7.90E-46	95.40%	0.111	IPR000308 (PRINTS); IPR023410 (PFAM); G3DSA:1.20.190.20 (GENE3D); IPR000308 (PANTHER); IPR023410 (SUPERFAMILY)
253	220883_length_239_cvg_37.0_tip_0_3	0	14-3-3 protein zeta isoform x1	80	1.06E-43	91.60%	0.108	IPR000308 (PRINTS); IPR023410 (PFAM); G3DSA:1.20.190.20 (GENE3D); IPR000308 (PANTHER); IPR023410 (SUPERFAMILY)
254	221143_length_239_cvg_63.0_tip_0_4	0	carboxypeptidase b	80	5.25E-26	69.70%	0.108	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
255	221301_length_239_cvg_96.7_tip_1_0	417	a chain crystal structure of porcine beta trypsin with % polydocanol	80	1.68E-13	67.80%	0.104	G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
257	221619_length_240_cvg_2.0_tip_1_1	0	gastrula zinc finger	80	1.33E-15	62.20%	0.114	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
258	221775_length_240_cvg_20.0_tip_0_5	0	partial	80	6.76E-42	93.90%	0.1	IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF146 (PANTHER); PTHR11711 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
259	222416_length_240_cvg_10.1_tip_1_2	0	odorrnanin-e1 antimicrobial peptide precursor	80	9.75E-06	61.00%	0.164	no IPS match
261	223378_length_241_cvg_2.0_tip_1_4	0	wd repeat domain isoform cra_c	80	8.19E-09	78.63%	0.127	no IPS match
262	223378_length_241_cvg_2.0_tip_1_5	0	low quality protein: lyr motif-containing protein partial	80	2.93E-12	79.60%	0.113	PF13900 (PFAM); PTHR16213 (PANTHER)
263	223830_length_242_cvg_2.0_tip_1_2	0	lysosomal alpha-mannosidase	80	4.46E-33	83.40%	0.11	IPR000602 (PFAM); IPR027291 (G3DSA:3.20.110.GENE3D); PTHR11607 (PANTHER); PTHR11607:SF3 (PANTHER); IPR011330 (SUPERFAMILY)
260	223378_length_241_cvg_2.0_tip_1_3	0	hypothetical calcr1-related pioneer protein	81	1.49E-09	72.00%	0.164	PTHR12138 (PANTHER)
264	224158_length_242_cvg_2.0_tip_1_1	0	peptidyl-prolyl cis-trans rhodopsin-specific isozyme	81	8.08E-31	78.70%	0.123	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
265	224530_length_243_cvg_2.0_tip_1_4	0	leukotriene a-4 partial	81	1.33E-35	83.50%	0.123	IPR014782 (PFAM); G3DSA:1.10.390.10 (GENE3D); PTHR11533:SF4 (PANTHER); IPR001930 (PANTHER); SSF55486 (SUPERFAMILY)
266	229941_length_249_cvg_3.4_tip_1_2	0	balbiani ring protein 3-like	83	4.91E-08	57.00%	0.101	IPR001506 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM)
267	230539_length_250_cvg_2.0_tip_1_2	0	choline partial	83	3.68E-51	100.00%	0.103	G3DSA:3.30.560.10 (GENE3D); G3DSA:3.50.50.60 (GENE3D); IPR007867 (PFAM); PTHR11552 (PANTHER); SSF51905 (SUPERFAMILY)
270	231865_length_251_cvg_2.0_tip_1_5	0	carbohydrate sulfotransferase 11-like isoform x1	83	1.59E-24	71.70%	0.118	IPR005331 (PFAM); IPR018011 (PANTHER); PTHR12137:SF29 (PANTHER)
268	231227_length_250_cvg_5.5_tip_1_0	0	zinc finger protein 502-like	84	4.09E-15	65.30%	0.102	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
269	231647_length_251_cvg_2.0_tip_1_1	2	3-hydroxyisobutyrate dehydrogenase	84	5.28E-37	90.60%	0.121	IPR029154 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR006115 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); PTHR22981 (PANTHER); PTHR22981:SF7 (PANTHER); IPR008927 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
271	233341_length_253_cvg_2.0_tip_1_1	0	adp-ribosylation factor 6	84	8.06E-30	98.90%	0.153	IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF151 (PANTHER); PTHR11711 (PANTHER); IPR027417 (SUPERFAMILY)

272	234371_length_254_cvg_40.0_tip_1_0	0	adp-ribosylation factor	85	2.43E-09	88.90%	0.218	IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF142 (PANTHER); IPR027417 (SUPERFAMILY)
273	234561_length_254_cvg_2.0_tip_1_3	0	tat (twin-arginine translocation) pathway signal sequence domain protein	85	6.66E-55	99.80%	0.101	IPR006963 (PFAM); G3DSA:3.40.50.740 (GENE3D); IPR006656 (PFAM); G3DSA:2.20.25.90 (GENE3D); PTHR11615 (PANTHER); PTHR11615:SF37 (PANTHER); IPR006963 (PROSITE_PROFILES); SSF53706 (SUPERFAMILY)
274	235091_length_255_cvg_12.0_tip_1_1	0	14-3-3 partial	85	3.61E-48	94.10%	0.106	IPR000308 (PRINTS); IPR023410 (SMART); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023410 (SUPERFAMILY)
275	235243_length_255_cvg_4.8_tip_1_5	0	nidogen- partial	85	3.23E-09	61.30%	0.157	IPR000716 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PFAM); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY)
276	236013_length_256_cvg_2.0_tip_1_1	2	von willebrand factor a domain-containing protein 8	85	6.56E-13	99.20%	0.194	PTHR21610 (PANTHER); PTHR21610:SF9 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
277	236653_length_257_cvg_2.0_tip_1_2	0	laminin subunit beta-1	85	6.24E-11	74.50%	0.1	IPR013015 (PROSITE_PROFILES)
278	237293_length_257_cvg_2.6_tip_1_3	0	inactive dipeptidyl	86	9.64E-27	80.50%	0.125	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001375 (PFAM); PTHR11731:SF103 (PANTHER); PTHR11731 (PANTHER); IPR029058 (SUPERFAMILY)
279	237309_length_257_cvg_2.0_tip_1_4	0	cathepsin o-like	86	4.93E-33	83.60%	0.116	G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); PTHR12411:SF287 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
280	238113_length_258_cvg_2.0_tip_1_1	0	nidogen-2 isoform x1	86	8.02E-34	82.70%	0.102	IPR000033 (SMART); IPR011042 (G3DSA:2.120.10.GENE3D); IPR000033 (PFAM); PTHR10529 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY)
281	239445_length_260_cvg_63.0_tip_1_3	827	trypsin-1-like isoform x1	87	2.12E-16	66.10%	0.157	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24255 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
282	239589_length_260_cvg_16.0_tip_1_0	4	venom protease-like	87	1.19E-06	60.00%	0.630 Y	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
283	240267_length_261_cvg_98.3_tip_0_5	1760	basement membrane-specific heparan sulfate proteoglycan core protein	87	5.78E-18	64.00%	0.103	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
284	242763_length_264_cvg_4.0_tip_1_4	4	attractin-like protein 1	88	4.02E-23	70.70%	0.105	PF13854 (PFAM); IPR015915 (G3DSA:2.120.10.GENE3D); IPR002165 (PFAM); PTHR10574:SF223 (PANTHER); PTHR10574 (PANTHER); SSF117281 (SUPERFAMILY)
285	242967_length_264_cvg_5.9_tip_1_5	0	-like protein 3	88	4.10E-20	74.10%	0.114	G3DSA:3.30.70.1500 (GENE3D); IPR002634 (PFAM); PTHR12735 (PANTHER); PTHR12735:SF4 (PANTHER); IPR002634 (SUPERFAMILY)
286	243335_length_265_cvg_3.4_tip_1_4	0	hypothetical protein, partial	88	4.45E-06	50.00%	0.390 Y	SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE)
287	243351_length_265_cvg_2.0_tip_1_2	0	dnaj homolog subfamily c member 18	88	3.16E-31	87.30%	0.102	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078:SF15 (PANTHER); PTHR24078 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
288	243423_length_265_cvg_81.6_tip_0_5	7	carboxypeptidase b-like	88	6.35E-29	75.60%	0.122	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
289	244475_length_266_cvg_2.0_tip_1_0	0	hemagglutinin	89	1.13E-09	55.20%	0.134	G3DSA:1.10.390.10 (GENE3D)
290	244758_length_266_cvg_2.0_tip_1_4	0	serine protease	89	1.49E-07	56.10%	0.098	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
291	246412_length_268_cvg_3.0_tip_1_4	0	6-phospho-beta- partial	89	2.41E-57	97.80%	0.148	IPR001360 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001360 (PANTHER); PTHR10353:SF35 (PANTHER); IPR017853 (SUPERFAMILY)
292	246604_length_269_cvg_4.0_tip_0_2	0	upf0364 protein c6orf211 homolog	89	9.87E-21	70.50%	0.123	IPR002791 (PFAM); PTHR12260:SF1 (PANTHER); PTHR12260 (PANTHER); IPR002791 (SUPERFAMILY)
293	246606_length_269_cvg_8.5_tip_0_2	0	upf0364 protein c6orf211 homolog	89	3.03E-19	68.70%	0.141	IPR002791 (PFAM); PTHR12260 (PANTHER); PTHR12260:SF1 (PANTHER); IPR002791 (SUPERFAMILY)
294	247188_length_269_cvg_2.0_tip_1_1	0	down syndrome cell adhesion molecule-like protein dscam2	90	2.01E-22	71.00%	0.135	IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR10489 (PANTHER); PTHR10489:SF567 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
295	247890_length_270_cvg_2.0_tip_1_5	0	tryptophan partial	90	3.39E-53	99.80%	0.148	IPR018227 (PFAM); PTHR32195 (PANTHER); PTHR32195:SF11 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)

298	249596_length_272_cvg_2.0_tip_1_2	0	gamma-aminobutyraldehyde dehydrogenase	90	1.10E-56	98.20%	0.102	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699:SF109 (PANTHER); PTHR11699 (PANTHER); IPR016161 (SUPERFAMILY)
296	248344_length_271_cvg_4.9_tip_1_0	0	family partial	91	6.30E-57	100.00%	0.121	IPR006664 (PRINTS); IPR006665 (PFAM); IPR006665 (G3DSA:3.30.1330.GENE3D); PTHR30128:SF0 (PANTHER); PTHR30128 (PANTHER); IPR006690 (PROSITE_PATTERNS); IPR006665 (PROSITE_PROFILES); IPR006665 (SUPERFAMILY)
297	249594_length_272_cvg_16.9_tip_0_0	0	zinc finger protein 235-like	91	1.59E-12	56.90%	0.12	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
299	250054_length_273_cvg_93.9_tip_0_0	2	annexin partial	91	1.50E-28	76.80%	0.11	Coil (COILS); IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); SSF47874 (SUPERFAMILY)
300	250320_length_273_cvg_84.9_tip_0_3	14	annexin partial	91	6.08E-29	78.60%	0.103	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (PFAM); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); SSF47874 (SUPERFAMILY)
301	250426_length_273_cvg_53.0_tip_1_0	0	isoform cra_b	91	1.38E-56	100.00%	0.128	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY)
302	251628_length_275_cvg_57.7_tip_1_2	15	low-density lipoprotein receptor-related protein 2	91	2.30E-14	64.50%	0.131	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
303	251756_length_275_cvg_60.0_tip_1_0	74	chitinase partial	92	1.24E-21	65.00%	0.104	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF45 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
304	252826_length_277_cvg_50.0_tip_1_2	0	adp-ribosylation factor 2	92	2.27E-13	100.00%	0.111	IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF145 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
305	254410_length_279_cvg_2.0_tip_1_2	0	plexin- partial	93	7.17E-41	84.80%	0.107	IPR001627 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22625 (PANTHER); PTHR22625:SF16 (PANTHER); IPR001627 (PROSITE_PROFILES); IPR001627 (SUPERFAMILY)
308	255670_length_280_cvg_2.8_tip_1_1	0	serine endoprotease partial	93	1.77E-57	100.00%	0.105	IPR001940 (PRINTS); PF13365 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR22939 (PANTHER); PTHR22939:SF79 (PANTHER); IPR009003 (SUPERFAMILY)
306	255344_length_280_cvg_3.0_tip_1_0	2	ankyrin repeat-containing protein	94	2.55E-12	59.40%	0.119	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
307	255456_length_280_cvg_2.0_tip_1_0	0	hemocyte protein-glutamine gamma-glutamyltransferase-like	94	3.58E-35	79.70%	0.104	IPR013783 (G3DSA:2.60.40.GENE3D); IPR002931 (G3DSA:3.90.260.GENE3D); IPR023608 (PANTHER); PTHR11590:SF40 (PANTHER); SSF54001 (SUPERFAMILY)
309	257696_length_283_cvg_8.6_tip_1_2	0	laccase 1	94	3.20E-34	76.00%	0.121	IPR008972 (G3DSA:2.60.40.GENE3D); IPR011707 (PFAM); PTHR11709 (PANTHER); PTHR11709:SF33 (PANTHER); IPR008972 (SUPERFAMILY)
311	260749_length_287_cvg_2.0_tip_1_2	2	---NA---	95			0.151	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
310	259772_length_286_cvg_2.0_tip_1_3	1	tyrosine-protein kinase-like 7	96	7.99E-25	71.70%	0.102	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
312	261405_length_288_cvg_2.0_tip_1_0	2	zinc c2h2 type domain-containing protein	96	3.05E-19	60.30%	0.102	IPR015880 (SMART); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
313	261963_length_289_cvg_2.0_tip_1_5	0	n-acetylmuramoyl-l-alanine partial	96	5.98E-62	100.00%	0.117	IPR002508 (SMART); IPR002508 (PFAM); IPR002508 (G3DSA:3.40.630.GENE3D); PTHR30404:SF0 (PANTHER); PTHR30404 (PANTHER); SSF53187 (SUPERFAMILY)

314	262447_length_290_cvg_3.9_tip_1_3	2	zinc finger protein ozf-like	97	1.48E-24	64.50%	0.192	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
315	263625_length_291_cvg_3.0_tip_1_1	1	zinc finger protein	97	6.20E-18	63.00%	0.111	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13909 (PFAM); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
316	263999_length_292_cvg_2.0_tip_1_1	1	polypeptide n-acetylgalactosaminyltransferase 9-like isoform x1	97	6.58E-41	91.40%	0.121	PTHR11675 (PANTHER)
317	265441_length_294_cvg_70.6_tip_1_4	92	serine (or cysteine) proteinase clade b member	98	5.69E-13	70.60%	0.113	G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); PTHR11461:SF52 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
318	265955_length_294_cvg_5.5_tip_1_2	0	zinc finger protein draculin	98	1.20E-12	57.00%	0.103	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
319	266815_length_295_cvg_4.0_tip_1_2	1	gamma-glutamyl hydrolase	98	6.47E-29	71.80%	0.113	IPR011697 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY)
320	267525_length_296_cvg_2.2_tip_1_4	1	n-acetylmuramoyl-l-alanine amidase family partial	99	1.17E-51	100.00%	0.101	IPR002508 (SMART); IPR002508 (PFAM); IPR002508 (G3DSA:3.40.630.GENE3D); PTHR30404 (PANTHER); PTHR30404:SF0 (PANTHER); SSF53187 (SUPERFAMILY)
321	267961_length_297_cvg_2.0_tip_1_5	0	bifunctional chitinase lysozyme domain protein	99	4.63E-54	99.80%	0.107	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
322	268179_length_297_cvg_2.0_tip_1_5	1	agrin-like isoform x2	99	9.40E-20	59.40%	0.121	G3DSA:2.40.50.120 (GENE3D); IPR004850 (PFAM); IPR004850 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY)
323	269203_length_299_cvg_3.0_tip_1_5	2	formate dehydrogenase h	99	8.09E-67	100.00%	0.102	G3DSA:2.20.25.90 (GENE3D); G3DSA:3.40.50.740 (GENE3D); IPR006656 (PFAM); PTHR11615:SF112 (PANTHER); PTHR11615 (PANTHER); IPR006963 (PROSITE_PROFILES); SSF53706 (SUPERFAMILY)
324	270615_length_300_cvg_4.0_tip_1_1	2	beta- -n-acetylgalactosaminyltransferase bre-4	100	1.02E-26	87.00%	0.105	IPR027791 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR003859 (PANTHER); PTHR19300:SF30 (PANTHER); IPR029044 (SUPERFAMILY)
325	270965_length_300_cvg_3.0_tip_1_3	2	protein sda1 homolog	100	4.89E-49	88.60%	0.121	IPR007949 (PFAM); PTHR12730 (PANTHER); IPR027312 (PTHR12730:PANTHER)
326	271585_length_300_cvg_3.3_tip_1_1	3	---NA---	100			0.151	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
327	273919_length_302_cvg_86.2_tip_0_3	586	venom allergen 3-like	101	8.31E-12	51.40%	0.119	IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR014044 (SUPERFAMILY)
328	274859_length_303_cvg_2.8_tip_1_1	2	histidine-rich glyco	101	1.33E-20	53.90%	0.113	no IPS match
329	275207_length_304_cvg_2.0_tip_1_2	1	serine protease 47 isoform x3	101	1.21E-13	56.10%	0.101	G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); PTHR24275:SF50 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
330	275259_length_304_cvg_3.0_tip_1_5	1	glycerophosphoryl diester phosphodiesterase domain protein	101	3.41E-64	100.00%	0.566 Y	IPR030395 (PFAM); IPR017946 (G3DSA:3.20.20.GENE3D); PTHR23344:SF7 (PANTHER); IPR004129 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR030395 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR017946 (SUPERFAMILY)
331	275481_length_305_cvg_2.0_tip_1_3	0	trna binding domain protein	102	1.31E-66	100.00%	0.096	IPR012340 (G3DSA:2.40.50.GENE3D); IPR002547 (PFAM); PTHR11586 (PANTHER); IPR002547 (PROSITE_PROFILES); IPR012340 (SUPERFAMILY)
332	275747_length_305_cvg_2.0_tip_1_0	0	hypothetical protein ZHAS_00020562	102	1.99E-26	67.50%	0.123	IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PFAM); PTHR12253 (PANTHER); IPR016090 (SUPERFAMILY)
333	275883_length_306_cvg_7.6_tip_0_1	1	bola-like protein 3	102	5.80E-12	90.70%	0.099	IPR002634 (PFAM); G3DSA:3.30.70.1500 (GENE3D); PTHR12735:SF4 (PANTHER); PTHR12735 (PANTHER); IPR002634 (SUPERFAMILY)

334	276413_length_307_cvg_7.9_tip_1_0	2	zinc finger partial	103	6.79E-21	60.00%	0.137	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
335	281827_length_318_cvg_44.5_tip_1_3	6	sjhgc07951 protein	106	6.57E-06	55.50%	0.222	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
336	282343_length_319_cvg_3.9_tip_1_0	3	retinol dehydrogenase 13	107	8.96E-27	75.80%	0.134	IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
337	283149_length_320_cvg_3.0_tip_1_4	2	zinc finger and scan domain-containing protein 2	107	2.65E-15	52.60%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
338	283595_length_321_cvg_95.8_tip_1_4	140	polycystic kidney disease protein 1-like 2-like	107	8.01E-10	57.60%	0.422 Y	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529:SF222 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
339	283883_length_322_cvg_2.0_tip_1_5	2	lim domain	107	1.04E-26	87.40%	0.099	IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR23257:SF94 (PANTHER); PTHR23257 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
340	285435_length_326_cvg_81.6_tip_0_2	2688	low quality protein: transmembrane protease serine 11g-like	108	2.64E-15	58.60%	0.117	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
341	285673_length_326_cvg_3.0_tip_1_2	3	12 kda fk506-binding protein	108	9.28E-44	88.40%	0.251	G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); PTHR10516:SF272 (PANTHER); IPR023566 (PANTHER); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY)
342	287179_length_329_cvg_6.0_tip_1_1	1	hemagglutinin amebocyte aggregation factor-like	110	3.64E-20	65.70%	0.111	PF14704 (PFAM); IPR026645 (PANTHER)
343	287459_length_330_cvg_2.4_tip_1_0	1	cell surface	110	5.39E-12	53.70%	0.153	no IPS match
344	287459_length_330_cvg_2.4_tip_1_4	1	collagen alpha type	110	3.84E-22	71.80%	0.12	IPR008160 (PFAM); PTHR24023:SF372 (PANTHER); PTHR24023 (PANTHER)
345	287467_length_330_cvg_2.0_tip_1_1	1	zinc finger protein 239	110	1.98E-19	61.80%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
347	288873_length_333_cvg_2.0_tip_1_3	1	actin-depolymerizing factor	111	1.26E-18	66.80%	0.102	IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007122 (PANTHER); IPR030004 (PTHR11977:PANTHER); SSF55753 (SUPERFAMILY)
348	288899_length_333_cvg_4.0_tip_1_3	2	#NAME?	111	5.42E-74	100.00%	0.136	IPR018389 (PFAM)
349	288911_length_333_cvg_56.7_tip_1_4	11	dnaj homolog subfamily b member 6-b isoform x1	111	8.92E-28	92.80%	0.105	Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24077 (PANTHER); PTHR24077:SF225 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
350	288981_length_333_cvg_84.3_tip_1_0	11554	proclotting enzyme-like isoform x1	111	1.57E-17	58.90%	0.149	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24272 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
351	289973_length_335_cvg_2.7_tip_1_0	2	zinc c2h2 type domain-containing protein	112	1.12E-07	50.90%	0.102	PF13465 (PFAM)
352	291251_length_338_cvg_2.0_tip_1_2	0	zinc c2h2 type domain-containing protein	112	7.59E-23	58.00%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

353	291367_length_338_cvg_2.0_tip_1_1	2	12 kda fk506-binding protein	113	1.00E-32	97.60%	0.11	G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); PTHR10516:SF260 (PANTHER); IPR023566 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY); TMhelix (TMHMM)
354	291931_length_340_cvg_2.0_tip_1_5	0	plasma alpha-l-fucosidase	113	6.88E-59	86.20%	0.117	IPR016286 (PRINTS); IPR000933 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR000933 (PFAM); PTHR10030:SF26 (PANTHER); IPR000933 (PANTHER); IPR017853 (SUPERFAMILY)
355	292487_length_341_cvg_4.0_tip_1_3	1	flavin-containing monooxygenase 2-like	114	3.28E-20	74.70%	0.113	PR00419 (PRINTS); G3DSA:3.50.50.60 (GENE3D); PF13450 (PFAM); PTHR23023:SF4 (PANTHER); PTHR23023 (PANTHER); SSF51905 (SUPERFAMILY)
356	293107_length_342_cvg_13.3_tip_1_0	7	peptidase s8	114	2.26E-09	66.80%	0.103	no IPS match
357	293741_length_344_cvg_2.2_tip_1_1	0	family protein	115	1.47E-48	99.40%	0.125	IPR004629 (PFAM); IPR004629 (TIGRFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
358	293975_length_344_cvg_4.6_tip_1_0	4	aldose reductase	115	8.19E-30	70.90%	0.151	IPR020471 (PRINTS); IPR023210 (G3DSA:3.20.20.GENE3D); IPR023210 (PFAM); PTHR11732:SF183 (PANTHER); IPR001395 (PANTHER); IPR023210 (SUPERFAMILY)
359	295365_length_347_cvg_2.0_tip_1_0	1	upf0378 protein k1aa0100	116	6.44E-48	83.70%	0.107	IPR019443 (PFAM); PTHR15678 (PANTHER); PTHR15678:SF6 (PANTHER)
360	296805_length_351_cvg_20.7_tip_0_0	10	low-density lipoprotein receptor 1	117	1.72E-08	51.70%	0.535 Y	IPR002172 (PRINTS); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
361	296989_length_351_cvg_4.0_tip_1_5	4	protein p21-like	117	1.31E-33	95.80%	0.099	IPR001938 (SMART); IPR001938 (G3DSA:2.60.110.GENE3D); IPR001938 (PFAM); IPR001938 (PANTHER); IPR001938 (PROSITE_PROFILES); IPR001938 (SUPERFAMILY)
362	297115_length_351_cvg_37.4_tip_0_5	15	dnaj homolog subfamily c member 4 isoform x4	117	5.02E-18	72.80%	0.112	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24077 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
364	297227_length_352_cvg_63.0_tip_0_1	154	muscle m-line assembly protein unc-89-like	117	2.03E-49	83.10%	0.106	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
363	297201_length_352_cvg_2.4_tip_1_3	1	zinc finger protein 235	118	2.13E-22	58.00%	0.114	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
365	298537_length_355_cvg_27.5_tip_1_5	13	low quality protein: twitchin-like	118	7.25E-44	82.80%	0.239	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
366	299003_length_356_cvg_7.9_tip_1_1	6	cyclophilin 2	119	3.95E-34	56.00%	0.1	IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF11 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
367	299539_length_357_cvg_3.3_tip_1_2	4	adamts-like protein 5	119	6.09E-10	71.80%	0.148	IPR010294 (PFAM); PTHR13723 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
368	300717_length_360_cvg_2.0_tip_1_5	1	partial	120	8.33E-81	100.00%	0.099	IPR001661 (PFAM); IPR001661 (PANTHER); PTHR23403:SF1 (PANTHER); IPR008928 (SUPERFAMILY)
369	300835_length_360_cvg_87.9_tip_0_3	66492	low-density lipoprotein receptor-related protein 5	120	6.96E-16	55.80%	0.103	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
370	301159_length_361_cvg_5.3_tip_1_5	4	heat shock protein 68-like	120	1.00E-28	70.70%	0.099	IPR029048 (G3DSA:1.20.1270.GENE3D); IPR013126 (PFAM); PTHR19375:SF155 (PANTHER); PTHR19375 (PANTHER); IPR029048 (SUPERFAMILY)
371	303032_length_365_cvg_2.0_tip_1_3	3	gamma-glutamyltranspeptidase 1	122	4.15E-13	76.10%	0.205	IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF15 (PANTHER); IPR029055 (SUPERFAMILY)
372	303208_length_365_cvg_7.4_tip_1_0	1	allergen 5	122	1.73E-08	72.60%	0.206	IPR002413 (PRINTS); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (SUPERFAMILY)
373	304080_length_368_cvg_2.0_tip_1_1	2	zinc finger	123	3.57E-64	92.10%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24391:SF9 (PANTHER); PTHR24391 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

374	304094_length_368_cvg_92.9_tip_1_3	76389	elastase 2 precursor	123	1.29E-21	61.70%	0.102	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
375	304280_length_368_cvg_4.9_tip_1_1	4	fat-like cadherin-related tumor suppressor partial	123	1.38E-43	73.30%	0.114	IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); PTHR24026:SF39 (PANTHER); PTHR24026 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)
376	304798_length_369_cvg_2.0_tip_1_2	2	von willebrand factor type egf and pentraxin domain-containing protein 1-like	123	1.33E-09	63.20%	0.1	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); PTHR19325 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); TMhelix (TMHMM)
377	305630_length_371_cvg_30.8_tip_1_2	38	transmembrane protease serine 9-like	123	1.15E-08	57.50%	0.139	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
378	305984_length_372_cvg_6.4_tip_1_0	2	heat shock cognate protein 70	124	1.15E-29	92.90%	0.305	IPR013126 (PFAM); IPR029048 (G3DSA:1.20.1270.GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029048 (SUPERFAMILY); TMhelix (TMHMM)
379	306170_length_373_cvg_51.4_tip_0_5	29	wnt inhibitory factor 1 precursor	124	2.28E-69	92.20%	0.123	IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PFAM); IPR000742 (PFAM); PTHR24838:SF276 (PANTHER); PTHR24838 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
380	306180_length_373_cvg_3.0_tip_1_1	4	cathepsin I	124	2.24E-29	71.30%	0.333	IPR013201 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR013201 (PFAM); IPR013128 (PANTHER); PTHR12411:SF289 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY)
381	307714_length_376_cvg_2.0_tip_1_4	2	hemagglutinin amebocyte aggregation factor-like	125	6.46E-18	68.40%	0.131	PF14704 (PFAM); IPR026645 (PANTHER)
382	308036_length_377_cvg_2.0_tip_1_1	3	lipophorin receptor	126	8.25E-25	68.60%	0.099	G3DSA:2.10.25.10 (GENE3D); PF14670 (PFAM); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); SSF57196 (SUPERFAMILY)
383	309180_length_380_cvg_2.0_tip_1_5	3	carbonic anhydrase isoform a	126	6.23E-11	57.60%	0.629 Y	IPR001148 (G3DSA:3.10.200.GENE3D); IPR001148 (PFAM); IPR023561 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001148 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR001148 (SUPERFAMILY)
384	309426_length_380_cvg_4.6_tip_1_2	6	vesicle-fusing atpase 1	126	2.57E-70	91.70%	0.104	IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); PTHR23078 (PANTHER); IPR027417 (SUPERFAMILY)
385	310200_length_382_cvg_2.0_tip_1_1	2	poxb regulator partial	127	2.75E-90	100.00%	0.137	IPR018149 (PRINTS); IPR004364 (PFAM); G3DSA:3.30.930.10 (GENE3D); IPR018150 (PANTHER); IPR004525 (PTHR22594:PANTHER); SSF55681 (SUPERFAMILY)
386	310352_length_382_cvg_3.0_tip_1_5	3	partial	127	1.46E-14	62.30%	0.108	IPR005203 (G3DSA:2.60.40.GENE3D); IPR005203 (PFAM); IPR013788 (PANTHER); PTHR11511:SF24 (PANTHER); IPR014756 (SUPERFAMILY)
387	310426_length_383_cvg_2.5_tip_1_1	3	zinc finger protein	128	1.28E-21	57.60%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
388	310984_length_384_cvg_2.9_tip_1_2	4	collagen alpha-1 chain-like	128	1.05E-18	61.40%	0.107	IPR008160 (PFAM); PTHR24023:SF379 (PANTHER); PTHR24023 (PANTHER)
389	310984_length_384_cvg_2.9_tip_1_5	4	collagen-like protein	128	7.74E-14	49.90%	0.147	no IPS match
390	311402_length_385_cvg_3.7_tip_1_2	4	adam 17-like protease	128	1.21E-32	67.10%	0.111	IPR024079 (G3DSA:3.40.390.GENE3D); PTHR11905:SF121 (PANTHER); PTHR11905 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
392	312112_length_386_cvg_3.0_tip_1_2	3	c-ter truncated protein	128	1.21E-86	99.80%	0.117	G3DSA:3.80.10.10 (GENE3D); SSF52058 (SUPERFAMILY)

393	312136_length_386_cvg_9.2_tip_1_2	8	von willebrand factor	128	8.21E-07	48.20%	0.102	no IPS match
391	311666_length_385_cvg_3.2_tip_1_0	4	tyrosine-protein kinase ryk-like	129	9.12E-14	84.30%	0.117	IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24416 (PANTHER); PTHR24416:SF256 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
424	326392_length_421_cvg_59.9_tip_1_0	206	hemagglutinin amebocyte aggregation factor-like	129	1.28E-14	66.90%	0.16	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
394	313369_length_389_cvg_3.1_tip_1_3	2	nedd4 family-interacting protein 1-like	130	6.49E-58	83.40%	0.126	IPR019325 (PFAM); PTHR13396 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
395	313647_length_390_cvg_7.1_tip_1_0	8	peptidase s8	130	2.47E-12	68.30%	0.361 Y	SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS)
396	313669_length_390_cvg_98.8_tip_1_0	768	carboxypeptidase a2-like	130	9.09E-11	57.90%	0.247	IPR003146 (PFAM); IPR003146 (G3DSA:3.30.70.GENE3D); PTHR11705 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009020 (SUPERFAMILY); TMhelix (TMHMM)
398	314219_length_391_cvg_2.6_tip_1_2	4	complement c1q-like protein 4 isoform x2	130	1.16E-06	52.50%	0.156	IPR001073 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY)
411	319977_length_405_cvg_12.5_tip_1_0	13	phospholipase a2 isozymes pa3a pa3b partial	130	7.38E-17	51.30%	0.104	IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PFAM); PTHR12253 (PANTHER); PTHR12253:SF8 (PANTHER); IPR016090 (SUPERFAMILY)
416	322165_length_410_cvg_54.8_tip_1_3	151	hemagglutinin amebocyte aggregation factor-like	130	4.32E-16	67.70%	0.177	PF14704 (PFAM); IPR026645 (PANTHER)
397	313973_length_391_cvg_65.6_tip_1_0	910	chitinase partial	131	3.19E-12	54.00%	0.105	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
399	314601_length_392_cvg_3.7_tip_1_1	2	tyrosine-protein kinase dnt-like	131	1.58E-24	85.40%	0.113	IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24416:SF302 (PANTHER); PTHR24416 (PANTHER); IPR011009 (SUPERFAMILY)
400	315893_length_395_cvg_2.0_tip_1_1	3	catalase-like isoform x1	132	1.93E-34	79.20%	0.32	IPR011614 (G3DSA:2.40.180.GENE3D); IPR011614 (PFAM); IPR018028 (PANTHER); IPR018028 (PROSITE_PROFILES); IPR020835 (SUPERFAMILY)
401	316635_length_397_cvg_16.8_tip_1_4	13	protein vein	132	1.40E-33	60.20%	0.126	IPR000742 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); PTHR11100 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR007110 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
403	316853_length_398_cvg_60.7_tip_0_5	46	PREDICTED: putative uncharacterized protein ART2-like, partial	132	2.01E-10	74.10%	0.114	no IPS match
402	316655_length_397_cvg_2.0_tip_1_3	2	venom serine carboxypeptidase-like	133	4.65E-27	69.40%	0.105	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); IPR001563 (PANTHER); IPR018202 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
404	317037_length_398_cvg_2.0_tip_1_3	2	tryptophan partial	133	5.76E-28	100.00%	0.106	IPR018227 (PFAM); IPR015422 (G3DSA:3.90.1150.GENE3D); PTHR32195:SF11 (PANTHER); PTHR32195 (PANTHER); IPR013061 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR015424 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
406	318163_length_401_cvg_2.0_tip_1_5	1	gelsolin	133	4.59E-34	74.60%	0.215	IPR029006 (G3DSA:3.40.20.GENE3D); IPR030004 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY)
405	318159_length_401_cvg_74.8_tip_0_0	91965	serine protease like protein	134	3.58E-22	57.30%	0.1	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
407	318371_length_401_cvg_2.4_tip_1_3	3	mam and ldl-receptor class a domain-containing protein 2-like	134	7.87E-12	56.80%	0.151	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
408	319001_length_403_cvg_63.0_tip_0_4	11756	ves g 5 allergen	134	2.94E-20	58.30%	0.105	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR014044 (SUPERFAMILY)
409	319263_length_403_cvg_2.0_tip_1_5	4	ectonucleoside triphosphate diphosphohydrolase 4-like isoform x2	134	8.04E-47	73.30%	0.118	IPR000407 (PFAM); PTHR11782:SF37 (PANTHER); IPR000407 (PANTHER); IPR000407 (PROSITE_PATTERNS)

410	319671_length_404_cvg_2.0_tip_1_0	3	zinc finger and scan domain-containing protein 2-like	135	2.18E-23	61.00%	0.123	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
412	320001_length_405_cvg_3.0_tip_1_2	4	lipophorin receptor	135	1.55E-51	79.00%	0.109	IPR000033 (SMART); IPR000033 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY)
413	320151_length_405_cvg_3.6_tip_1_5	3	neurogenic locus notch partial	135	7.02E-60	86.90%	0.112	PR00010 (PRINTS); IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR24033:SF36 (PANTHER); PTHR24033 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
414	320827_length_407_cvg_3.2_tip_1_1	5	b-cell lymphoma	136	4.45E-56	91.20%	0.113	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR23233:SF1 (PANTHER); PTHR23233 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
415	321041_length_408_cvg_3.0_tip_1_5	5	xanthine dehydrogenase	136	4.06E-35	68.60%	0.102	IPR016167 (G3DSA:3.30.43.GENE3D); IPR002346 (PFAM); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR016166 (SUPERFAMILY)
417	322195_length_410_cvg_2.0_tip_1_4	3	pa domain-containing protein	137	2.06E-44	77.70%	0.102	G3DSA:3.50.30.30 (GENE3D); IPR003137 (PFAM); PTHR22702 (PANTHER)
418	323039_length_412_cvg_3.0_tip_1_0	3	dermatopontin 2	138	8.63E-18	58.20%	0.247	PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
419	324163_length_415_cvg_2.0_tip_1_2	5	microtubule-associated serine threonine-protein kinase 3 isoform x1	138	1.18E-82	94.00%	0.131	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24356 (PANTHER); PTHR24356:SF36 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
420	324440_length_416_cvg_3.9_tip_1_3	4	7-alpha-hydroxysteroid dehydrogenase	139	6.64E-96	100.00%	0.103	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF166 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
421	325038_length_417_cvg_2.0_tip_1_2	3	gamma-glutamyltransferase	139	1.28E-93	99.70%	0.105	IPR000101 (PRINTS); IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF9 (PANTHER); IPR029055 (SUPERFAMILY)
422	325140_length_418_cvg_2.6_tip_1_1	4	gastrula zinc finger isoform x1	139	3.93E-46	71.30%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
423	325200_length_418_cvg_3.0_tip_1_5	4	astacin-like metalloprotease partial	139	2.73E-10	50.40%	0.849 Y	IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
425	327388_length_423_cvg_4.0_tip_1_5	4	hypothetical protein X975_25329, partial	141	4.14E-36	63.00%	0.099	PTHR23022 (PANTHER); PTHR23022:SF53 (PANTHER)
427	327842_length_424_cvg_2.0_tip_1_1	1	thioredoxin	141	2.31E-93	99.80%	0.343 Y	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005746 (TIGRFAM); IPR013766 (PFAM); PTHR10438:SF253 (PANTHER); IPR005746 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)

428	327904_length_424_cvg_6.1_tip_1_2	4	cytochrome p450 partial	141	4.12E-46	69.20%	0.1	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24291 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
426	327634_length_424_cvg_7.7_tip_1_0	11	PREDICTED: uncharacterized protein C15orf61-like	142	5.96E-41	77.60%	0.339	IPR029245 (PFAM)
429	328084_length_425_cvg_4.0_tip_1_4	1	serine protease inhibitor dipetalogastin precursor	142	9.12E-17	51.20%	0.102	IPR002350 (SMART); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); PTHR10913 (PANTHER); PTHR10913:SF46 (PANTHER); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
430	328158_length_425_cvg_102.8_tip_0_0	92927	clotting factor partial	142	9.89E-16	70.40%	0.119	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
431	328524_length_426_cvg_2.0_tip_1_2	3	protein flightless-1	142	7.70E-67	87.60%	0.131	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR007122 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
432	328884_length_426_cvg_2.0_tip_1_0	2	kelch-like ech-associated protein 1 isoform x2	142	5.79E-80	86.40%	0.102	IPR011705 (SMART); IPR011705 (PFAM); PTHR24412 (PANTHER); PTHR24412:SF1 (PANTHER)
437	329452_length_428_cvg_2.0_tip_1_2	2	low-density lipoprotein receptor-related protein 1b-like	142	1.54E-14	61.70%	0.269	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
433	329172_length_427_cvg_63.9_tip_0_0	105834	isoform a	143	3.13E-27	63.20%	0.111	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
434	329294_length_428_cvg_2.0_tip_1_4	2	aminoacylase-1-like isoform 1	143	4.33E-67	80.10%	0.138	IPR002933 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11014:SF8 (PANTHER); PTHR11014 (PANTHER); IPR001261 (PROSITE_PATTERNS); IPR001261 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY)
435	329356_length_428_cvg_2.0_tip_1_1	2	allatostatin precursor protein	143	3.55E-16	51.20%	0.098	no IPS match
436	329414_length_428_cvg_78.6_tip_0_3	104728	suppressor of tumorigenicity 14 protein isoform x3	143	7.80E-16	46.50%	0.098	IPR002172 (SMART); IPR002172 (PFAM); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256:SF96 (PANTHER); PTHR24256 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
438	329842_length_429_cvg_58.0_tip_1_0	84	zinc finger protein	143	4.11E-20	58.50%	0.104	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
439	330362_length_430_cvg_2.0_tip_1_2	1	leucine-rich repeat and guanylate kinase domain-containing partial	143	2.25E-13	68.10%	0.104	PR00019 (PRINTS); SM00365 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR025875 (PFAM); PTHR10588 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
440	330716_length_431_cvg_12.6_tip_1_5	15	sterile alpha motif domain-containing protein 13	143	2.79E-12	85.30%	0.125	IPR013761 (G3DSA:1.10.150.GENE3D); IPR021129 (PFAM); PTHR12247 (PANTHER); PTHR12247:SF66 (PANTHER); IPR013761 (SUPERFAMILY)
441	330878_length_432_cvg_2.0_tip_1_1	3	retinol dehydrogenase 11-like	144	7.43E-47	71.00%	0.315	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF305 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
442	331358_length_433_cvg_5.4_tip_1_5	6	phenoloxidase subunit a3-like	144	1.16E-31	60.40%	0.122	IPR005203 (PFAM); IPR005203 (G3DSA:2.60.40.GENE3D); PTHR11511:SF24 (PANTHER); IPR013788 (PANTHER); IPR014756 (SUPERFAMILY)
443	331514_length_433_cvg_3.0_tip_1_5	4	venom metalloproteinase 3-like	144	2.31E-09	47.70%	0.106	IPR006586 (SMART)
444	332144_length_435_cvg_2.0_tip_1_1	3	laminin beta 1	145	3.88E-60	73.70%	0.125	IPR002049 (SMART); IPR002049 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR10574 (PANTHER); PTHR10574:SF238 (PANTHER); IPR002049 (PROSITE_PROFILES); IPR013015 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)

445	332198_length_435_cvg_2.0_tip_1_1	3	attractin-like protein 1 isoform x1	145	1.25E-37	80.70%	0.121	PTHR10574 (PANTHER); PTHR10574:SF3 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
446	332482_length_436_cvg_7.1_tip_1_5	7	cysteine string isoform x1	145	5.38E-71	94.60%	0.162	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078:SF5 (PANTHER); PTHR24078 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
447	332770_length_436_cvg_37.2_tip_1_1	21	low-density lipoprotein receptor-related protein 2	145	5.80E-13	67.00%	0.1	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
448	333228_length_438_cvg_2.0_tip_1_5	3	cyclin dependent kinase 8	146	6.47E-95	97.30%	0.102	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24056 (PANTHER); PTHR24056:SF162 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
449	333868_length_439_cvg_2.9_tip_1_2	4	ejaculatory bulb-specific protein 3	146	7.83E-37	70.00%	0.554 Y	IPR005055 (G3DSA:1.10.2080.GENE3D); IPR005055 (PFAM); PTHR11257:SF4 (PANTHER); IPR005055 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-TM (SIGNALP_EUK); IPR005055 (SUPERFAMILY); TMhelix (TMHMM)
465	338474_length_450_cvg_3.0_tip_1_2	4	prostatic acid phosphatase-like	146	6.38E-13	56.00%	0.097	IPR029033 (G3DSA:3.40.50.GENE3D); PTHR11567:SF26 (PANTHER); PTHR11567 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029033 (SUPERFAMILY); TMhelix (TMHMM)
450	334092_length_440_cvg_9.7_tip_1_1	10	er protein gp78	147	7.95E-70	89.50%	0.544 Y	IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.30.30 (GENE3D); PTHR19375:SF157 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF53067 (SUPERFAMILY)
451	334888_length_442_cvg_3.0_tip_1_4	6	gram negative bacteria binding protein 1	147	7.17E-43	67.10%	0.102	IPR000757 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10963 (PANTHER); PTHR10963:SF4 (PANTHER); IPR013320 (SUPERFAMILY)
452	335456_length_443_cvg_2.0_tip_1_5	4	furin-like protease isoform 1-crr isoform x2	147	3.27E-13	46.29%	0.127	G3DSA:2.10.220.10 (GENE3D); IPR009030 (SUPERFAMILY)
517	352819_length_487_cvg_61.3_tip_1_1	756	ribosomal protein s26	147	2.02E-59	89.70%	0.106	IPR000892 (PFAM); IPR000892 (PANTHER); IPR000892 (PROSITE_PATTERNS)
453	335742_length_444_cvg_112.5_tip_0_2	146869	low-density lipoprotein receptor-related protein 2	148	1.36E-19	63.90%	0.492 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PROFILES); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
454	335776_length_444_cvg_2.3_tip_1_1	3	#NAME?	148	1.29E-52	81.50%	0.137	G3DSA:3.40.50.2000 (GENE3D); IPR001830 (PFAM); PTHR10788:SF6 (PANTHER); PTHR10788 (PANTHER); SSF53756 (SUPERFAMILY)
455	336054_length_445_cvg_2.6_tip_1_5	4	gels_homam ame: full= cytoplasmic ame: full=actin-depolymerizing factor short=adf	148	1.67E-40	78.30%	0.2	IPR007122 (SMART); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY)
456	336572_length_446_cvg_63.0_tip_0_2	178	vitellogenin receptor	148	3.10E-17	52.00%	0.127	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
457	336872_length_447_cvg_2.0_tip_1_1	3	protein lap4 isoform x4	149	8.02E-82	92.90%	0.103	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR025875 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); PTHR23155:SF31 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
458	337166_length_447_cvg_7.7_tip_1_1	9	serine protease nudel	149	2.27E-20	55.10%	0.129	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529:SF205 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

459	337188_length_447_cvg_2.0_tip_1_5	4	retinol dehydrogenase 13-like	149	1.02E-44	75.10%	0.243	IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316:SF305 (PANTHER); PTHR24316 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
460	337236_length_447_cvg_7.3_tip_0_1	4	low quality protein: otogelin	149	8.75E-08	49.00%	0.104	no IPS match
461	337516_length_448_cvg_8.0_tip_1_1	3	dehydrogenase reductase sdr family member 11-like	149	4.17E-14	86.50%	0.224	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF310 (PANTHER); SSF51735 (SUPERFAMILY)
462	337528_length_448_cvg_2.0_tip_1_4	4	basement membrane-specific heparan sulfate proteoglycan core protein	149	1.34E-16	64.00%	0.14	IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)
463	337658_length_448_cvg_89.7_tip_0_5	18805	low quality protein: probable chitinase 3	149	2.04E-35	71.30%	0.579 Y	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-TM (SIGNALP_EUK); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
464	338374_length_450_cvg_2.0_tip_1_0	2	calnexin isoform x2	150	1.35E-69	83.90%	0.106	IPR001580 (PRINTS); IPR009033 (G3DSA:2.10.250.GENE3D); IPR001580 (PFAM); IPR001580 (PANTHER); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR009033 (SUPERFAMILY)
466	338802_length_451_cvg_2.0_tip_1_4	3	lachesin	150	1.12E-50	73.20%	0.104	IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013106 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF43 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
468	338966_length_452_cvg_4.9_tip_1_5	5	alcohol dehydrogenase	150	3.60E-31	74.80%	0.106	IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); IPR001395 (PANTHER); PTHR11732:SF183 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
469	339140_length_452_cvg_82.0_tip_0_5	658959	probable chitinase 3	150	3.25E-32	69.20%	0.317	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
507	349207_length_478_cvg_3.0_tip_1_1	4	serine protease 52-like	150	2.03E-12	58.70%	0.212	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
467	338874_length_452_cvg_61.8_tip_1_0	43	agap012894-pa-like protein	151	5.72E-48	95.80%	0.113	IPR000558 (PRINTS); IPR000558 (SMART); IPR009072 (G3DSA:1.10.20.GENE3D); IPR007125 (PFAM); IPR000558 (PANTHER); IPR000558 (PROSITE_PATTERNS); IPR009072 (SUPERFAMILY)
470	339174_length_452_cvg_3.1_tip_1_1	4	14-3-3 protein	151	8.81E-31	90.20%	0.104	Coil (COILS); IPR000308 (PRINTS); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023410 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
471	339250_length_453_cvg_3.2_tip_1_4	4	mite allergen der f 3-like	151	6.67E-08	47.60%	0.14	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
472	339364_length_453_cvg_76.4_tip_1_3	67906	proclotting enzyme-like	151	2.07E-16	62.80%	0.116	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
473	339382_length_453_cvg_2.0_tip_1_1	4	3-hydroxy acid dehydrogenase	151	4.96E-40	99.50%	0.162	IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
474	339588_length_453_cvg_82.6_tip_1_3	34753	proclotting enzyme-like	151	2.01E-17	64.80%	0.119	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
475	339762_length_454_cvg_3.5_tip_1_1	2	maguk p55 subfamily member 6 isoform x1	151	6.31E-21	86.20%	0.269	IPR004172 (SMART); IPR014775 (PFAM); IPR004172 (PROSITE_PROFILES)
476	340068_length_455_cvg_5.5_tip_1_2	11	transcription factor e4f1-like	151	1.32E-36	60.30%	0.104	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

477	340320_length_455_cvg_5.0_tip_1_0	6	low quality protein: dnaj homolog subfamily c member 10-like	152	4.04E-17	70.40%	0.162	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR24078:SF3 (PANTHER); PTHR24078 (PANTHER); IPR017937 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
478	340492_length_456_cvg_2.0_tip_1_3	2	multiple epidermal growth factor-like domains protein 8	152	4.96E-33	66.70%	0.121	PTHR10574 (PANTHER); PTHR10574:SF3 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
479	340650_length_456_cvg_4.3_tip_1_5	6	down syndrome cell adhesion molecule-like protein dscam2 isoform x5	152	2.38E-59	68.80%	0.11	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR10489:SF567 (PANTHER); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
568	368844_length_532_cvg_4.3_tip_1_5	6	zinc finger protein 502	152	1.29E-32	60.20%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
480	341202_length_457_cvg_2.0_tip_1_3	3	serine threonine-protein phosphatase 6 regulatory ankyrin repeat subunit a- partial	153	1.40E-36	89.10%	0.105	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24158:SF22 (PANTHER); PTHR24158 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
481	341662_length_459_cvg_2.0_tip_1_4	2	peripheral plasma membrane protein cask isoform x2	153	3.17E-93	94.60%	0.102	IPR001452 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR011511 (PFAM); PTHR23122:SF7 (PANTHER); PTHR23122 (PANTHER); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY)
482	341882_length_459_cvg_62.6_tip_1_4	422	selenium-dependent glutathione peroxidase	153	2.12E-57	78.40%	0.115	IPR000889 (PRINTS); IPR000889 (PIRSF); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PFAM); PTHR11592:SF21 (PANTHER); IPR000889 (PANTHER); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
483	342038_length_460_cvg_5.3_tip_1_3	10	uncharacterized aarf domain-containing protein kinase 1	154	9.00E-26	70.40%	0.135	PTHR10566:SF58 (PANTHER); PTHR10566 (PANTHER)
484	342814_length_462_cvg_2.0_tip_1_1	3	apical endosomal glycoprotein	154	2.44E-19	68.60%	0.11	IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
485	342928_length_462_cvg_3.0_tip_1_4	4	hypothetical protein MDA_GLEAN10014894	154	7.37E-08	45.75%	0.12	no IPS match
486	343018_length_462_cvg_2.5_tip_1_3	3	PREDICTED: hypothetical protein LOC100647042	154	9.20E-18	52.70%	0.233	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24258:SF96 (PANTHER); PTHR24258 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
487	343032_length_462_cvg_2.1_tip_1_4	4	titin isoform x3	154	1.56E-31	63.60%	0.1	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
488	343066_length_462_cvg_106.9_tip_1_0	30526	chondroitin proteoglycan partial	154	7.25E-15	58.80%	0.1	IPR002557 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002557 (PFAM); PTHR23301 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY)
489	343076_length_462_cvg_4.8_tip_1_0	5	zinc finger protein	154	8.60E-29	55.60%	0.11	IPR015880 (SMART); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
490	343138_length_462_cvg_2.9_tip_1_0	6	lipase 3-like	154	3.20E-45	72.00%	0.183	IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11005 (PANTHER); PTHR11005:SF6 (PANTHER); IPR029058 (SUPERFAMILY)
491	343498_length_463_cvg_63.7_tip_0_5	1043398	chitinase partial	154	2.74E-40	63.00%	0.101	IPR011583 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
516	351721_length_484_cvg_2.0_tip_1_4	5	leucine-rich repeat protein soc-2 isoform x1	154	8.82E-64	82.50%	0.119	G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR16083 (PANTHER); PTHR16083:SF2 (PANTHER); SSF52075 (SUPERFAMILY)
492	343990_length_464_cvg_63.0_tip_0_4	401	uncharacterized oxidoreductase	155	8.03E-28	72.30%	0.133	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF237 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)

512	350945_length_482_cvg_2.6_tip_1_2	5	odorant-binding protein 4	155	1.25E-44	72.00%	0.101	IPR006170 (PRINTS); IPR006170 (SMART); IPR023316 (G3DSA:1.10.238.GENE3D); IPR006170 (PFAM); PTHR11857 (PANTHER); PTHR11857:SF4 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023316 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
493	344822_length_467_cvg_4.0_tip_1_4	6	peptidase partial	156	6.71E-06	70.50%	0.241	G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
494	344840_length_467_cvg_9.1_tip_1_0	16	ankyrin repeat domain-containing protein 32-like	156	2.25E-25	57.50%	0.162	IPR002110 (SMART); IPR020683 (PFAM); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24171 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
495	345792_length_469_cvg_2.4_tip_1_3	7	f379 retina specific protein	157	1.12E-08	70.00%	0.187	PR02045 (PRINTS); PTHR12138 (PANTHER)
496	345870_length_469_cvg_3.0_tip_1_3	7	dna-specific endonuclease partial	157	2.68E-48	99.80%	0.132	IPR007346 (PFAM); SSF54060 (SUPERFAMILY)
497	346016_length_470_cvg_90.8_tip_0_0	126651	low-density lipoprotein receptor-related protein 2	157	3.19E-32	61.10%	0.1	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
498	346482_length_471_cvg_82.5_tip_1_3	1404	transmembrane protease serine 9-like	157	2.31E-27	58.50%	0.113	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
499	346786_length_472_cvg_3.7_tip_1_3	5	upf0669 protein c6orf120 homolog	158	3.01E-23	63.00%	0.494 Y	PTHR31703 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM)
500	347108_length_473_cvg_2.0_tip_1_0	4	acid sphingomyelinase-like phosphodiesterase partial	158	3.36E-14	54.60%	0.101	PTHR10340 (PANTHER)
501	347640_length_474_cvg_2.0_tip_1_3	3	serine protease snake	158	1.53E-39	58.20%	0.149	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
502	347978_length_475_cvg_65.4_tip_1_4	108	peptidyl-prolyl cis-trans isomerase-like 1	158	1.12E-21	91.90%	0.115	IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
503	348527_length_476_cvg_4.0_tip_1_5	4	upf0364 protein c6orf211 homolog	158	4.43E-28	60.30%	0.103	IPR002791 (PFAM); PTHR12260:SF1 (PANTHER); PTHR12260 (PANTHER); IPR002791 (SUPERFAMILY)
504	348861_length_477_cvg_51.0_tip_1_2	87	bursicon alpha	159	4.24E-61	85.80%	0.607 Y	IPR004133 (PFAM); PTHR11339 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR006207 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK)
505	348889_length_477_cvg_4.0_tip_1_3	5	calcium calmodulin-dependent protein kinase	159	6.57E-94	92.10%	0.101	IPR008145 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:3.30.63.10 (GENE3D); IPR008145 (PFAM); PTHR23122:SF7 (PANTHER); PTHR23122 (PANTHER); IPR020590 (PROSITE_PATTERNS); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
506	348917_length_477_cvg_5.2_tip_1_5	7	glutamine-rich protein 2	159	1.62E-10	48.00%	0.197	SignalP-TM (SIGNALP_GRAM_POSITIVE)
508	349643_length_479_cvg_3.4_tip_1_2	5	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	159	2.82E-23	59.50%	0.097	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR003656 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
509	350293_length_481_cvg_4.1_tip_1_1	6	adam 17-like protease	160	1.60E-56	73.80%	0.663 Y	IPR002870 (PFAM); PTHR11905 (PANTHER); PTHR11905:SF121 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
510	350301_length_481_cvg_45.9_tip_1_2	84	maguk p55 subfamily member 6 isoform x1	160	9.46E-21	88.00%	0.099	IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23122 (PANTHER); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
511	350393_length_481_cvg_2.0_tip_1_4	3	transcriptional regulator partial	160	7.47E-112	99.90%	0.188	no IPS match

513	351333_length_483_cvg_3.0_tip_0_4	2	heat shock 70 kda protein 14	161	2.46E-38	65.30%	0.128	IPR013126 (PRINTS); G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF158 (PANTHER); PTHR19375 (PANTHER); SSF53067 (SUPERFAMILY)
514	351351_length_483_cvg_2.7_tip_1_5	5	peptidyl-prolyl cis-trans isomerase a	161	1.20E-81	100.00%	0.109	IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF195 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
515	351653_length_484_cvg_67.9_tip_1_0	1559	chitinase 2	162	5.57E-42	74.40%	0.336	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
518	352853_length_487_cvg_4.0_tip_1_4	10	tyrosine-protein kinase transmembrane receptor ror2	162	7.78E-67	92.10%	0.115	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416:SF63 (PANTHER); PTHR24416 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
519	353229_length_488_cvg_3.0_tip_1_2	5	neutral ceramidase-like	162	5.52E-59	70.70%	0.121	IPR006823 (PFAM); PTHR12670:SF1 (PANTHER); IPR006823 (PANTHER)
520	353415_length_489_cvg_3.0_tip_1_5	3	protein fem-1 homolog cg6966 isoform x1	163	4.51E-71	88.70%	0.166	IPR002110 (PRINTS); IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24173 (PANTHER); PTHR24173:SF15 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
521	353849_length_490_cvg_63.0_tip_0_5	47563	low-density lipoprotein receptor-related protein 5	163	6.72E-23	56.60%	0.885 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
522	355275_length_494_cvg_30.0_tip_1_0	36	polyubiquitin-b isoform x2	165	1.34E-110	99.00%	0.103	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY)
523	355307_length_494_cvg_5.6_tip_1_1	8	peroxiredoxin 1	165	6.41E-60	91.90%	0.108	IPR019479 (PFAM); IPR000866 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); IPR012336 (SUPERFAMILY)
524	356111_length_496_cvg_3.0_tip_1_4	3	neuropeptide f	165	8.16E-08	65.80%	0.209	IPR001955 (SMART); G3DSA:1.20.5.570 (GENE3D); IPR001955 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001955 (PROSITE_PROFILES); TMhelix (TMHMM)
525	356545_length_497_cvg_2.0_tip_1_3	5	venom serine protease bi-vsp-like	166	1.30E-45	68.40%	0.102	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF97 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
526	356687_length_497_cvg_2.9_tip_1_0	5	50-kda dystrophin-associated glycoprotein	166	4.86E-15	67.30%	0.117	IPR013783 (G3DSA:2.60.40.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR008908 (PFAM); IPR008908 (PANTHER); PTHR10132:SF14 (PANTHER); IPR016187 (SUPERFAMILY)
527	357067_length_498_cvg_69.0_tip_1_0	244	chymotrypsin-like elastase family member 2a	166	1.19E-13	55.60%	0.329	G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275:SF45 (PANTHER); PTHR24275 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
528	357261_length_499_cvg_2.3_tip_1_4	4	atp-dependent partial	166	6.85E-113	99.90%	0.162	G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23076:SF10 (PANTHER); PTHR23076 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)

529	358282_length_502_cvg_63.0_tip_0_4	376	inactive hydroxysteroid dehydrogenase-like protein 1	167	7.29E-68	78.40%	0.104	Coil (COILS); IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316:SF317 (PANTHER); PTHR24316 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
530	359418_length_505_cvg_5.3_tip_1_1	9	3-ketoacyl-acyl reductase	168	6.76E-86	99.20%	0.12	IPR002347 (PRINTS); IPR001227 (G3DSA:3.40.366.GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24312 (PANTHER); PTHR24312:SF0 (PANTHER); IPR016035 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
531	359528_length_505_cvg_2.0_tip_1_5	5	multiple epidermal growth factor-like domains protein 10 isoform x1	168	8.42E-34	69.00%	0.109	PR00011 (PRINTS); IPR002049 (SMART); G3DSA:2.170.300.10 (GENE3D); IPR013032 (PFAM); IPR002049 (PFAM); PTHR24035 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS)
534	359954_length_506_cvg_35.0_tip_0_2	66	histone h1	168	1.72E-40	76.70%	0.15	IPR005819 (PRINTS); IPR005818 (SMART); IPR011991 (G3DSA:1.10.10.GENE3D); IPR005818 (PFAM); PTHR11467 (PANTHER); IPR005818 (PROSITE_PROFILES); SSF46785 (SUPERFAMILY)
562	366934_length_526_cvg_2.7_tip_1_1	2	dscam splice variant	168	1.13E-26	70.00%	0.145	IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
532	359746_length_506_cvg_2.0_tip_1_1	6	mre11 meiotic recombination 11 homolog a (cerevisiae) isoform cra_b	169	6.91E-21	72.40%	0.146	PTHR22878 (PANTHER)
533	359746_length_506_cvg_2.0_tip_1_4	6	5 -nucleotidase domain containing isoform cra_d	169	2.09E-23	67.00%	0.201	PF13900 (PFAM); PTHR16213 (PANTHER)
535	360270_length_507_cvg_2.0_tip_1_5	4	zinc finger protein 530-like	169	5.75E-22	60.90%	0.167	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
536	360526_length_508_cvg_7.9_tip_1_2	12	mitochondrial import inner membrane translocase subunit tim8	169	2.92E-30	84.30%	0.107	IPR004217 (PFAM); IPR004217 (G3DSA:1.10.287.GENE3D); PTHR21535:SF25 (PANTHER); PTHR21535 (PANTHER); IPR004217 (SUPERFAMILY)
537	360562_length_508_cvg_2.0_tip_1_2	6	glucosidase 2 subunit beta	169	2.70E-63	70.70%	0.107	Coil (COILS); PF13015 (PFAM); IPR009011 (G3DSA:2.70.130.GENE3D); IPR026874 (PTHR12630:PANTHER); PTHR12630 (PANTHER); IPR009011 (SUPERFAMILY)
539	360628_length_508_cvg_2.5_tip_1_5	6	dnaj homolog subfamily c member 25 homolog	169	1.17E-63	81.20%	0.269	Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078:SF125 (PANTHER); PTHR24078 (PANTHER); IPR018253 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM)
538	360580_length_508_cvg_65.6_tip_1_0	245	chitinase 10 precursor	170	4.80E-41	69.20%	0.188	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
540	361324_length_510_cvg_57.5_tip_1_0	276	projectin short variant	170	1.49E-44	86.80%	0.196	IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
541	361506_length_510_cvg_2.0_tip_1_2	3	sp6-9 protein	170	1.98E-57	84.80%	0.159	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223:SF134 (PANTHER); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
542	361666_length_511_cvg_91.9_tip_1_2	123141	low-density lipoprotein receptor-related protein 5	170	1.03E-23	59.80%	0.420 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
543	361682_length_511_cvg_63.9_tip_0_2	462	gamma-glutamyl hydrolase-like	170	6.01E-48	72.40%	0.342 Y	IPR011697 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); PTHR11315:SF2 (PANTHER); IPR015527 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY); TMhelix (TMHMM)
544	361778_length_511_cvg_2.0_tip_1_0	2	serine threonine-protein kinase 17b-like	171	4.78E-91	85.50%	0.151	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24342 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)

545	361938_length_512_cvg_4.0_tip_1_0	6	kunitz bovine pancreatic trypsin inhibitor domain protein	171	2.46E-40	60.10%	0.106	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
546	362090_length_512_cvg_3.1_tip_1_0	8	hemocyte protein-glutamine gamma-glutamyltransferase-like	171	4.93E-25	63.90%	0.166	IPR001102 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR023608 (PANTHER); PTHR11590:SF40 (PANTHER); IPR014756 (SUPERFAMILY)
547	362276_length_513_cvg_2.9_tip_1_5	4	von willebrand factor c and egf domain-containing protein	171	1.03E-06	54.33%	0.107	IPR001007 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR001007 (PFAM); IPR001007 (PROSITE_PATTERNS); IPR001007 (PROSITE_PROFILES); SSF57603 (SUPERFAMILY)
548	362556_length_513_cvg_2.0_tip_1_3	5	lipophorin receptor	171	2.71E-91	85.50%	0.11	IPR000033 (SMART); IPR000033 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY)
549	362778_length_514_cvg_37.6_tip_1_5	49	vacuolar-sorting protein snf8-like	171	2.97E-71	90.40%	0.142	Coil (COILS); IPR007286 (PFAM); IPR011991 (G3DSA:1.10.10.GENE3D); IPR007286 (PANTHER); PTHR12806:SF0 (PANTHER); SSF46785 (SUPERFAMILY)
550	362968_length_515_cvg_3.4_tip_1_0	6	protein cbg27381	172	7.67E-44	61.50%	0.099	PF13358 (PFAM); PTHR23022:SF64 (PANTHER); PTHR23022 (PANTHER)
551	362996_length_515_cvg_12.8_tip_1_0	21	protein disulfide-isomerase a6	172	2.13E-52	74.30%	0.680 Y	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR005788 (TIGRFAM); PTHR18929 (PANTHER); PTHR18929:SF38 (PANTHER); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalIP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
552	363010_length_515_cvg_63.0_tip_0_0	173	---NA---	172			0.103	IPR008197 (PRINTS); IPR008197 (SMART); IPR008197 (PFAM); IPR008197 (G3DSA:4.10.75.GENE3D); IPR008197 (PROSITE_PROFILES); IPR008197 (PROSITE_PROFILES); IPR008197 (SUPERFAMILY)
553	363018_length_515_cvg_21.3_tip_0_3	40	prophenoloxidase activating factor	172	2.04E-57	69.10%	0.118	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
554	363678_length_517_cvg_8.5_tip_1_1	11	extracellular zinc metalloprotease	172	1.37E-08	44.50%	0.103	IPR011096 (PFAM); IPR025711 (PFAM)
555	363782_length_517_cvg_48.9_tip_1_5	81	serine protease	172	6.92E-09	64.90%	0.128	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
587	373648_length_546_cvg_12.4_tip_1_3	27	retinal dehydrogenase 1	172	2.14E-68	89.50%	0.101	IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699:SF145 (PANTHER); PTHR11699 (PANTHER); IPR016161 (SUPERFAMILY)
556	364314_length_518_cvg_3.0_tip_1_1	8	penicillin-binding protein partial	173	3.26E-116	99.50%	0.141	IPR001264 (PFAM); G3DSA:1.10.3810.10 (GENE3D); PTHR32282:SF1 (PANTHER); PTHR32282 (PANTHER); IPR023346 (SUPERFAMILY)
557	364844_length_520_cvg_7.2_tip_1_0	6	lpxtg-motif protein cell wall anchor domain protein	174	5.03E-11	49.10%	0.219	no IPS match
558	365050_length_521_cvg_19.3_tip_1_0	32	protein d2-like isoform x1	174	6.90E-64	77.40%	0.168	IPR008914 (G3DSA:3.90.280.GENE3D); IPR008914 (PFAM); PTHR11362 (PANTHER); IPR008914 (SUPERFAMILY)
559	365084_length_521_cvg_64.3_tip_0_0	3120	chitinase partial	174	7.87E-50	62.30%	0.107	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY); IPR029070 (SUPERFAMILY)
560	365278_length_521_cvg_93.5_tip_0_3	485	chitinase partial	174	3.31E-50	61.20%	0.11	IPR011583 (SMART); IPR029070 (G3DSA:3.10.50.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR029070 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
561	366424_length_524_cvg_5.1_tip_1_5	10	adp-ribosylation factor 1	174	4.72E-113	100.00%	0.122	IPR006689 (PRINTS); IPR024156 (SMART); IPR006687 (SMART); IPR005225 (TIGRFAM); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF104 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
571	370778_length_537_cvg_28.6_tip_1_2	48	prohormone-1-like	174	4.86E-33	78.40%	0.113	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
563	367302_length_527_cvg_11.8_tip_0_2	11	heat shock cognate 71 kda protein	175	6.35E-29	75.20%	0.104	IPR029048 (G3DSA:1.20.1270.GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR029048 (SUPERFAMILY)

581	372778_length_543_cvg_2.3_tip_1_0	4	upf0528 protein cg10038	181	2.16E-25	67.50%	0.114	IPR029058 (G3DSA:3.40.50.GENE3D); PTHR21357:SF4 (PANTHER); PTHR21357 (PANTHER); IPR029058 (SUPERFAMILY)
582	372808_length_543_cvg_2.0_tip_1_5	3	zinc finger protein 678-like	181	4.74E-24	56.30%	0.14	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
620	381064_length_569_cvg_4.2_tip_1_4	10	phosphoglycerate kinase	181	3.47E-66	92.40%	0.102	IPR001576 (PRINTS); IPR015901 (G3DSA:3.40.50.GENE3D); IPR001576 (PFAM); PTHR11406:SF6 (PANTHER); IPR001576 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001576 (SUPERFAMILY); TMhelix (TMHMM)
583	373132_length_544_cvg_4.7_tip_1_3	0	---NA---	182			0.222	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
584	373244_length_544_cvg_12.0_tip_1_3	18	otogelin- partial	182	6.97E-11	51.20%	0.101	no IPS match
585	373548_length_545_cvg_2.0_tip_1_1	4	peptidyl-glycine alpha-amidating monooxygenase partial	182	1.61E-56	64.50%	0.307	IPR000720 (PRINTS); PF03712 (PFAM); IPR014784 (G3DSA:2.60.120.GENE3D); PTHR10680 (PANTHER); PTHR10680:SF13 (PANTHER); IPR014783 (PROSITE_PATTERNS); IPR008977 (SUPERFAMILY)
586	373602_length_546_cvg_4.5_tip_1_2	9	pacifastin light chain	182	1.15E-16	50.10%	0.128	IPR008037 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); TMhelix (TMHMM)
588	373700_length_546_cvg_2.0_tip_1_2	2	calcium calmodulin-dependent protein kinase kinase 1-like isoform x2	182	1.73E-41	93.90%	0.125	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24347:SF141 (PANTHER); IPR020636 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
589	373730_length_546_cvg_2.0_tip_1_0	2	hypothetical protein DAPPUDRAFT_240129	182	3.27E-47	64.50%	0.132	IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
591	374124_length_547_cvg_4.4_tip_1_2	8	dbh-like monooxygenase protein 1	182	2.49E-30	57.40%	0.108	PF03712 (PFAM); IPR014784 (G3DSA:2.60.120.GENE3D); IPR000945 (PANTHER); IPR014783 (PROSITE_PATTERNS); IPR008977 (SUPERFAMILY)
592	374296_length_548_cvg_3.7_tip_1_2	13	apolipoprotein li-ii precursor	182	3.59E-17	50.50%	0.099	no IPS match
590	374088_length_547_cvg_2.0_tip_1_0	3	histone-lysine n-methyltransferase setmar isoform x2	183	1.85E-63	69.30%	0.109	IPR001888 (PFAM); IPR011991 (G3DSA:1.10.10.GENE3D); PTHR23016 (PANTHER); PTHR23016:SF3 (PANTHER)
593	374388_length_548_cvg_2.0_tip_1_3	6	short chain dehydrogenase reductase family protein	183	6.95E-132	100.00%	0.111	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF68 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
594	374820_length_549_cvg_2.0_tip_1_3	3	glycosyl hydrolases 31 family protein	183	8.08E-130	100.00%	0.1	IPR000322 (PFAM); IPR025887 (PFAM); PTHR22762:SF38 (PANTHER); PTHR22762 (PANTHER); IPR017853 (SUPERFAMILY); IPR011013 (SUPERFAMILY)
595	375008_length_550_cvg_66.0_tip_0_4	14274	venom serine carboxypeptidase-like	183	4.42E-42	73.50%	0.195	IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
596	375256_length_551_cvg_4.6_tip_1_2	7	myosin-binding protein fast-type-like	183	1.03E-37	65.00%	0.102	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR020675 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
597	375474_length_551_cvg_2.0_tip_1_3	9	membrane metallo-endopeptidase-like 1 isoform x2	184	2.18E-76	80.10%	0.125	IPR008753 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR11733:SF113 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
653	390544_length_601_cvg_62.6_tip_1_0	573	complement component 1 q subcomponent-binding mitochondrial	184	8.76E-11	78.90%	0.105	IPR003428 (PFAM); IPR003428 (G3DSA:3.10.280.GENE3D); PTHR10826 (PANTHER); PTHR10826:SF1 (PANTHER); IPR003428 (SUPERFAMILY)
600	376886_length_556_cvg_6.1_tip_1_1	13	anti-lipopolysaccharide partial	185	1.63E-19	66.10%	0.104	IPR024509 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024716 (PRODOM); TMhelix (TMHMM)
599	376866_length_556_cvg_5.5_tip_1_0	9	peroxisome biogenesis factor 10	186	2.76E-33	61.00%	0.127	IPR001841 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); PF13923 (PFAM); IPR025654 (PANTHER); IPR017907 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001841 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY)
601	377980_length_559_cvg_2.0_tip_1_2	3	glucose-6-phosphate partial	186	3.85E-114	100.00%	0.11	IPR001672 (PRINTS); IPR023096 (G3DSA:1.10.1390.GENE3D); G3DSA:3.40.50.10490 (GENE3D); IPR001672 (PFAM); PTHR11469:SF7 (PANTHER); IPR001672 (PANTHER); IPR018189 (PROSITE_PATTERNS); IPR001672 (PROSITE_PROFILES); SSF53697 (SUPERFAMILY)

603	378174_length_560_cvg_4.9_tip_1_5	6	fibroblast growth factor receptor-like 1	186	9.10E-27	64.00%	0.115	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19890 (PANTHER); PTHR19890:SF5 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
605	378428_length_560_cvg_3.0_tip_1_5	7	membrane metallo-endopeptidase-like 1	186	2.78E-22	86.20%	0.188	SSF55486 (SUPERFAMILY)
635	386754_length_588_cvg_57.6_tip_1_2	115	zinc finger protein zpr1	186	3.91E-73	80.30%	0.11	IPR004457 (SMART); IPR004457 (TIGRFAM); IPR004457 (PFAM); PTHR10876 (PANTHER); PTHR10876:SF0 (PANTHER)
602	378084_length_559_cvg_3.1_tip_1_3	6	hypothetical protein LOTGIDRAFT_201948	187	1.13E-71	74.30%	0.145	IPR007122 (PRINTS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR015628 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY)
606	378535_length_561_cvg_17.8_tip_1_4	29	calponin transgelin	187	1.70E-74	89.10%	0.347 Y	IPR001997 (PRINTS); IPR003096 (PRINTS); IPR001715 (SMART); IPR001715 (PFAM); IPR001715 (G3DSA:1.10.418.GENE3D); PTHR18959:SF51 (PANTHER); PTHR18959 (PANTHER); IPR001715 (PROSITE_PROFILES); IPR001715 (SUPERFAMILY)
608	378975_length_562_cvg_2.8_tip_1_1	6	latrophilin- partial	187	8.95E-51	91.90%	0.354 Y	IPR000832 (PFAM); PTHR12011:SF258 (PANTHER); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
609	378975_length_562_cvg_2.8_tip_1_2	6	latrophilin cirl-like isoform x1	187	3.09E-34	79.50%	0.176	IPR000832 (PFAM); PTHR12011:SF258 (PANTHER); PTHR12011 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
610	379319_length_563_cvg_5.8_tip_1_3	12	perq amino acid-rich with gyf domain-containing protein 2-like	188	3.46E-32	63.90%	0.112	IPR000884 (SMART); IPR000884 (PFAM); G3DSA:2.20.100.10 (GENE3D); PTHR11311 (PANTHER); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
611	379831_length_565_cvg_56.3_tip_1_2	147	14-3-3 zeta	188	3.75E-88	95.00%	0.124	Coil (COILS); IPR000308 (PRINTS); IPR023410 (SMART); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023409 (PROSITE_PATTERNS); IPR023410 (SUPERFAMILY)
612	379955_length_565_cvg_2.0_tip_1_0	4	poly -specific endoribonuclease homolog	189	3.35E-48	62.40%	0.1	IPR018998 (PFAM); PTHR12439 (PANTHER); SSF142877 (SUPERFAMILY)
613	380374_length_567_cvg_2.0_tip_1_1	6	transposable element tc3 partial	189	3.24E-35	57.40%	0.106	PTHR23022:SF53 (PANTHER); PTHR23022 (PANTHER)
614	380470_length_567_cvg_68.8_tip_1_1	1460	fk506-binding protein 2 isoform x1	189	1.32E-72	81.70%	0.294	G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); IPR023566 (PANTHER); PTHR10516:SF252 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY)
615	380582_length_567_cvg_19.0_tip_1_0	36	zinc finger protein 699-like	189	2.31E-20	55.90%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
616	380822_length_568_cvg_64.4_tip_0_2	40185	chitinase 2	189	9.95E-45	65.70%	0.162	IPR011583 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
617	380840_length_568_cvg_2.0_tip_1_1	4	sonic hedgehog protein a	189	4.98E-36	56.40%	0.108	IPR001657 (PRINTS); IPR003586 (SMART); IPR001767 (PFAM); IPR028992 (G3DSA:2.170.16.GENE3D); PTHR11889 (PANTHER); IPR028992 (SUPERFAMILY)
618	380888_length_568_cvg_30.6_tip_1_3	71	low-density lipoprotein receptor domain class a	190	1.61E-16	61.20%	0.17	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

619	380938_length_568_cvg_2.0_tip_1_3	5	voltage-dependent calcium channel type a subunit alpha-1 isoform x3	190	2.41E-101	90.20%	0.176	IPR002077 (PRINTS); IPR005821 (PFAM); IPR005448 (PTHR10037:PANTHER); PTHR10037 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF81324 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
621	381276_length_569_cvg_2.0_tip_1_4	2	lipase 3	190	1.33E-72	70.60%	0.161	IPR000073 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR006693 (PFAM); PTHR11005 (PANTHER); IPR029058 (SUPERFAMILY)
622	381888_length_571_cvg_2.0_tip_1_1	5	outer membrane autotransporter barrel domain protein	190	1.46E-133	100.00%	0.102	IPR005546 (G3DSA:2.40.128.GENE3D); IPR006315 (TIGRFAM); IPR005546 (PFAM); PTHR12338 (PANTHER); IPR005546 (PROSITE_PROFILES); IPR005546 (SUPERFAMILY)
623	382056_length_572_cvg_2.4_tip_1_2	5	metabotropic gaba-b receptor subtype isoform b	190	3.69E-21	96.10%	0.243	G3DSA:3.40.50.2300 (GENE3D); PTHR10519:SF3 (PANTHER); IPR002455 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR028082 (SUPERFAMILY)
631	385762_length_584_cvg_3.4_tip_1_0	6	low quality protein: zinc finger protein 333	190	2.39E-22	65.10%	0.316	IPR015880 (SMART); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
624	382814_length_575_cvg_90.4_tip_1_4	27006	basement membrane-specific heparan sulfate proteoglycan core protein	192	1.15E-24	60.70%	0.535 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
625	384012_length_579_cvg_2.9_tip_1_3	5	otopettrin-2 isoform x1	193	3.51E-62	76.70%	0.218	IPR004878 (PFAM); IPR004878 (PANTHER); PTHR21522:SF37 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
626	385008_length_582_cvg_18.6_tip_1_2	35	cytochrome p450 partial	194	1.61E-62	69.30%	0.148	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24305 (PANTHER); PTHR24305:SF49 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
627	385244_length_583_cvg_12.0_tip_1_1	16	acetylcholine receptor subunit alpha-type acr-16	194	1.78E-40	59.70%	0.610 Y	IPR006201 (PRINTS); IPR002394 (PRINTS); IPR006202 (PFAM); IPR006202 (G3DSA:2.70.170.GENE3D); IPR006201 (PANTHER); PTHR18945:SF490 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-TM (SIGNALP_EUK); IPR006202 (SUPERFAMILY)
628	385324_length_583_cvg_2.2_tip_1_2	6	alpha c-terminal all-beta domain protein	194	8.14E-137	98.00%	0.118	IPR017853 (SUPERFAMILY)
630	385556_length_584_cvg_3.0_tip_1_5	6	cysteine-rich with egf-like domain protein 2	194	3.31E-21	72.90%	0.112	IPR021852 (PFAM); PTHR24838:SF251 (PANTHER); PTHR24838 (PANTHER)
632	385970_length_585_cvg_2.0_tip_1_3	4	low quality protein: protein lap4-like	195	1.67E-90	82.60%	0.131	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR016313 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
633	386018_length_585_cvg_27.0_tip_1_2	59	dehydrogenase reductase sdr family member 11 isoform x1	195	8.03E-42	73.60%	0.105	IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)

634	386026_length_585_cvg_13.4_tip_1_0	27	zinc finger protein 227	195	5.64E-53	70.00%	0.118	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
636	387006_length_589_cvg_9.3_tip_1_1	21	kazal-type serine protease inhibitor domain-containing protein 1	196	3.51E-37	59.70%	0.430 Y	IPR002350 (SMART); IPR000867 (SMART); IPR002350 (PFAM); IPR000867 (PFAM); G3DSA:3.30.60.30 (GENE3D); PTHR14186:SF9 (PANTHER); IPR011390 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR000867 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); IPR009030 (SUPERFAMILY); TMhelix (TMHMM)
637	387016_length_589_cvg_4.4_tip_1_1	9	leukocyte elastase inhibitor isoform x2	196	1.31E-38	56.30%	0.101	IPR023796 (SMART); IPR023796 (PFAM); G3DSA:3.30.497.10 (GENE3D); G3DSA:2.30.39.10 (GENE3D); IPR000215 (PANTHER); IPR023796 (SUPERFAMILY)
639	387218_length_589_cvg_3.0_tip_1_5	5	otogelin- partial	196	2.32E-13	44.30%	0.12	no IPS match
667	393627_length_612_cvg_77.0_tip_1_0	6665	ubiquitin-60s ribosomal protein l40	196	1.58E-85	99.10%	0.104	IPR019956 (PRINTS); IPR000626 (SMART); IPR001975 (PFAM); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR011332 (SUPERFAMILY)
638	387142_length_589_cvg_2.7_tip_1_3	4	vitellogenin fused with superoxide dismutase	197	3.60E-07	52.00%	0.11	no IPS match
640	387262_length_589_cvg_2.7_tip_1_0	8	catalase peroxidase partial	197	1.36E-136	99.90%	0.104	IPR002016 (PRINTS); G3DSA:1.10.520.10 (GENE3D); G3DSA:1.10.420.10 (GENE3D); IPR002016 (PFAM); PTHR30555 (PANTHER); PTHR30555:SF0 (PANTHER); IPR019793 (PROSITE_PATTERNS); IPR010255 (SUPERFAMILY)
641	388034_length_592_cvg_2.8_tip_1_4	5	cyclin-dependent kinase 1 isoform x1	197	1.70E-110	94.50%	0.098	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24056 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
642	388178_length_592_cvg_2.0_tip_1_4	4	zinc finger protein	197	4.26E-38	57.20%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY);
643	388308_length_593_cvg_2.0_tip_1_0	6	low quality protein: mucin-19	198	1.73E-11	44.60%	0.165	SSF141571 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
644	388582_length_594_cvg_3.0_tip_1_1	5	serine protease	198	4.35E-13	65.30%	0.14	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
645	388582_length_594_cvg_3.0_tip_1_3	5	exosporium glycoprotein	198	7.47E-25	72.90%	0.297	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
646	388718_length_594_cvg_62.4_tip_1_1	1475	chymotrypsin-like protease ctrl-1	198	5.28E-16	56.40%	0.245	IPR001314 (PRINTS); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24259 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
647	388978_length_595_cvg_6.0_tip_1_2	16	pc3-like endoprotease variant b-like	198	2.22E-38	63.00%	0.102	IPR015500 (PRINTS); IPR000209 (PFAM); IPR000209 (G3DSA:3.40.50.GENE3D); IPR015500 (PANTHER); PTHR10795:SF310 (PANTHER); IPR023827 (PROSITE_PATTERNS); IPR000209 (SUPERFAMILY)

648	389222_length_596_cvg_6.5_tip_1_2	17	secreted salivary gland	198	2.70E-10	70.80%	0.251	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF85 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
673	396057_length_621_cvg_93.1_tip_1_0	2757	glyceraldehyde-3-phosphate dehydrogenase	198	3.19E-11	89.10%	0.121	IPR020831 (PANTHER); PTHR10836:SF31 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
649	389278_length_596_cvg_3.6_tip_1_1	7	protein creg1	199	1.96E-57	76.60%	0.106	PF13883 (PFAM); IPR012349 (G3DSA:2.30.110.GENE3D); PTHR13343 (PANTHER); PTHR13343:SF12 (PANTHER); IPR012349 (SUPERFAMILY)
650	389306_length_596_cvg_5.4_tip_1_1	6	protein will die slowly	199	3.96E-141	98.90%	0.118	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847:SF308 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
651	389926_length_598_cvg_2.0_tip_1_5	6	tyrosine-protein phosphatase partial	199	5.91E-25	50.90%	0.106	IPR000242 (PRINTS); IPR000242 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134 (PANTHER); PTHR19134:SF81 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
682	399076_length_632_cvg_6.0_tip_1_5	10	mesencephalic astrocyte-derived neurotrophic factor homolog	199	6.92E-73	85.00%	0.166	IPR019345 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR12990 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF68906 (SUPERFAMILY); TMhelix (TMHMM)
652	390444_length_600_cvg_2.7_tip_1_4	10	annexin b10-like	200	2.63E-39	80.10%	0.107	IPR018502 (SMART); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); SSF47874 (SUPERFAMILY)
654	391011_length_602_cvg_91.8_tip_0_3	1967	carboxypeptidase b-like	201	7.31E-83	68.70%	0.107	IPR000834 (SMART); G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
655	391067_length_603_cvg_62.5_tip_1_5	3082	ubiquitin-40s ribosomal protein s27a-like	201	4.35E-94	95.50%	0.241	IPR019956 (PRINTS); IPR000626 (SMART); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); IPR002906 (PFAM); PTHR10666:SF99 (PANTHER); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR011332 (SUPERFAMILY)
656	391107_length_603_cvg_5.8_tip_1_0	9	calcium calmodulin-dependent protein kinase type 1	201	1.88E-53	97.10%	0.1	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24347:SF116 (PANTHER); IPR020636 (PANTHER); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
657	391227_length_603_cvg_6.2_tip_1_5	13	neogenin isoform x3	201	9.99E-12	74.20%	0.109	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
658	391877_length_606_cvg_3.4_tip_1_1	6	proactivator polypeptide	202	3.01E-64	67.30%	0.127	IPR008373 (PRINTS); IPR003119 (SMART); IPR008139 (SMART); IPR011001 (G3DSA:1.10.225.GENE3D); IPR003119 (PFAM); IPR007856 (PFAM); IPR008138 (PFAM); PTHR11480 (PANTHER); PTHR11480:SF3 (PANTHER); IPR003119 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR011001 (SUPERFAMILY)
660	392439_length_608_cvg_2.0_tip_1_2	6	phenoloxidase subunit a3	202	1.90E-62	65.80%	0.102	IPR000896 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); PTHR11511:SF24 (PANTHER); IPR013788 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR002227 (PROSITE_PATTERNS); IPR008922 (SUPERFAMILY)
659	392419_length_608_cvg_22.7_tip_1_4	55	vp302_lycmc ame: full=venom protein 302 flags: precursor	203	2.24E-14	55.80%	0.718 Y	PTHR14186:SF8 (PANTHER); IPR011390 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR000867 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009030 (SUPERFAMILY)
661	392483_length_608_cvg_2.0_tip_1_4	4	lysine--trna partial	203	2.86E-146	100.00%	0.101	IPR018149 (PRINTS); IPR004365 (PFAM); G3DSA:3.30.930.10 (GENE3D); IPR012340 (G3DSA:2.40.50.GENE3D); IPR004364 (PFAM); IPR018150 (PANTHER); PTHR22594:SF25 (PANTHER); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY); IPR012340 (SUPERFAMILY)

662	392707_length_609_cvg_24.5_tip_1_2	54	zinc finger and btb domain-containing protein 48	203	4.67E-19	53.00%	0.098	IPR015880 (SMART); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
663	392841_length_609_cvg_15.7_tip_1_0	44	bone morphogenetic protein 5 8 precursor	203	1.44E-42	91.20%	0.119	IPR001839 (SMART); IPR001839 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); IPR015615 (PANTHER); PTHR11848:SF137 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
664	393101_length_610_cvg_2.0_tip_1_1	6	protein sidekick-1	203	9.76E-12	50.40%	0.167	IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
665	393355_length_611_cvg_3.2_tip_1_2	5	---NA---	203			0.149	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
666	393579_length_612_cvg_35.8_tip_0_3	63	serine protease nudel	204	1.29E-16	51.90%	0.1	IPR002172 (SMART); IPR001190 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR017448 (G3DSA:3.10.250.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR001190 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR017448 (SUPERFAMILY)
668	393999_length_614_cvg_69.2_tip_1_2	24117	venom allergen 3-like	204	1.27E-25	53.40%	0.305	IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM)
669	394141_length_614_cvg_2.7_tip_1_2	11	prostaglandin-endoperoxide synthase 2	204	2.37E-92	77.40%	0.106	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11903:SF10 (PANTHER); PTHR11903 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
697	402288_length_644_cvg_55.1_tip_1_0	2371	peptidase s8	205	1.07E-17	61.00%	0.301	IPR007280 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
713	407048_length_663_cvg_2.9_tip_1_1	19	serine proteinase stubble- partial	205	2.27E-23	64.20%	0.104	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
670	395019_length_617_cvg_3.5_tip_1_0	4	serpin i2	206	4.04E-09	66.40%	0.163	G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); PTHR11461:SF52 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
688	400532_length_637_cvg_6.5_tip_1_3	15	---NA---	206			0.153	IPR000742 (SMART); IPR023413 (G3DSA:2.40.155.GENE3D); IPR024731 (PFAM); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
671	395833_length_620_cvg_2.6_tip_1_0	7	isocitrate dehydrogenase	207	3.28E-66	82.80%	0.187	IPR024084 (PFAM); IPR024084 (G3DSA:3.40.718.GENE3D); IPR001804 (PANTHER); PTHR11835:SF42 (PANTHER); SSF53659 (SUPERFAMILY); TMhelix (TMHMM)
672	395985_length_621_cvg_63.0_tip_1_4	339	probable chitinase 3	207	9.80E-54	65.30%	0.222	IPR011583 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR001579 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
674	396271_length_622_cvg_2.0_tip_1_2	4	glutathione peroxidase 6	207	2.79E-13	67.40%	0.107	IPR012336 (G3DSA:3.40.30.GENE3D); PTHR11592:SF21 (PANTHER); IPR000889 (PANTHER); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)

675	397317_length_626_cvg_2.0_tip_1_5	6	leucomyosuppressin precursor	208	4.44E-15	68.90%	0.768 Y	SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
696	402278_length_644_cvg_10.7_tip_1_5	24	transcription factor sp4-like	208	3.71E-72	84.20%	0.11	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR030450 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
676	397615_length_627_cvg_3.4_tip_1_3	8	retinol dehydrogenase 13	209	6.33E-66	69.70%	0.126	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); SSF51735 (SUPERFAMILY)
677	398396_length_630_cvg_2.0_tip_1_5	4	f-box wd repeat-containing protein 7	210	7.27E-111	96.90%	0.115	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22844 (PANTHER); PTHR22844:SF116 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
678	398764_length_631_cvg_4.0_tip_1_5	8	hypothetical protein Y032_0655g1201	210	1.11E-45	56.20%	0.097	PF13358 (PFAM); PTHR23022:SF64 (PANTHER); PTHR23022 (PANTHER)
679	398852_length_632_cvg_3.0_tip_1_2	7	carcinolectin 5b partial	210	6.13E-28	72.60%	0.108	IPR002181 (SMART); IPR002181 (PFAM); IPR014715 (G3DSA:4.10.530.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
681	399036_length_632_cvg_3.3_tip_1_2	12	---NA---	210			0.27	IPR029058 (G3DSA:3.40.50.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
680	398890_length_632_cvg_14.8_tip_1_0	23	protein shifted	211	4.47E-19	67.20%	0.105	IPR000742 (SMART); IPR013032 (PFAM); G3DSA:2.170.300.10 (GENE3D); PTHR24838 (PANTHER); PTHR24838:SF276 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
683	399116_length_632_cvg_4.8_tip_1_4	13	hemocyte protein-glutamine gamma-glutamyltransferase-like	211	7.67E-43	71.00%	0.122	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR008958 (PFAM); PTHR11590:SF40 (PANTHER); IPR023608 (PANTHER); IPR008958 (SUPERFAMILY); IPR008958 (SUPERFAMILY)
684	399290_length_633_cvg_2.0_tip_1_3	6	ankyrin repeat domain protein	211	7.44E-15	57.60%	0.107	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
711	406510_length_661_cvg_11.6_tip_1_4	32	xanthine dehydrogenase	211	1.16E-67	84.40%	0.101	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)
685	399988_length_636_cvg_6.7_tip_1_3	17	aldehyde oxidase	212	1.94E-17	80.90%	0.108	IPR002888 (PFAM); IPR002888 (G3DSA:1.10.150.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF65 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002888 (SUPERFAMILY)
686	400146_length_636_cvg_5.2_tip_1_3	12	sodium channel protein type 5 subunit alpha	212	4.72E-09	72.80%	0.136	IPR028820 (PTHR10037:PANTHER); PTHR10037 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
689	400548_length_637_cvg_2.0_tip_1_2	6	sugar partial	212	1.42E-155	100.00%	0.103	IPR013781 (G3DSA:3.20.20.GENE3D); IPR006047 (PFAM); G3DSA:3.90.400.10 (GENE3D); IPR015902 (PANTHER); PTHR10357:SF132 (PANTHER); IPR017853 (SUPERFAMILY)

687	400354_length_637_cvg_56.6_tip_0_3	120	phenoloxidase subunit a3	213	2.76E-62	63.70%	0.138	IPR013788 (PRINTS); IPR005204 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR000896 (PFAM); PTHR11511:SF4 (PANTHER); IPR013788 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR005204 (SUPERFAMILY); IPR008922 (SUPERFAMILY)
690	400566_length_638_cvg_2.6_tip_1_3	7	circumsporozoite protein	213	7.62E-30	45.70%	0.137	no IPS match
691	400566_length_638_cvg_2.6_tip_1_4	7	---NA---	213			0.104	no IPS match
692	400664_length_638_cvg_2.8_tip_1_0	7	protein cbg25835	213	3.25E-20	57.00%	0.113	PTHR23022:SF64 (PANTHER); PTHR23022 (PANTHER)
694	401352_length_641_cvg_2.0_tip_1_2	7	mitogen-activated protein kinase kinase kinase 7-like	213	4.40E-47	86.50%	0.374 Y	IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR23257 (PANTHER); IPR017441 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR011009 (SUPERFAMILY)
693	401270_length_640_cvg_17.4_tip_0_3	39	serine protease 44-like	214	4.82E-35	77.20%	0.245	Coil (COILS); G3DSA:2.40.10.10 (GENE3D); PF11600 (PFAM); IPR001254 (PFAM); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
695	402128_length_644_cvg_2.2_tip_1_4	4	xanthine dehydrogenase	215	1.62E-22	90.80%	0.371 Y	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008274 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
698	402434_length_645_cvg_2.6_tip_1_0	6	gastrula zinc finger	215	2.42E-24	61.30%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
699	402960_length_647_cvg_4.1_tip_1_0	10	clotting factor partial	216	8.72E-25	63.90%	0.248	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
700	403058_length_648_cvg_2.9_tip_1_3	7	hypothetical protein Y032_0001g415	216	2.20E-45	57.80%	0.114	PF13358 (PFAM); PTHR23022 (PANTHER); PTHR23022:SF64 (PANTHER)
701	403364_length_649_cvg_5.3_tip_1_2	6	alcohol dehydrogenase	216	2.67E-16	69.90%	0.128	IPR023210 (G3DSA:3.20.20.GENE3D); PTHR11732:SF183 (PANTHER); IPR001395 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023210 (SUPERFAMILY); TMhelix (TMHMM)
702	403658_length_650_cvg_2.8_tip_1_5	7	glucose dehydrogenase	216	1.91E-51	64.10%	0.127	IPR000172 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR11552:SF77 (PANTHER); PTHR11552 (PANTHER); IPR000172 (PROSITE_PATTERNS); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY)
721	408426_length_669_cvg_7.5_tip_1_5	19	---NA---	216			0.111	G3DSA:2.40.10.10 (GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
703	404582_length_653_cvg_6.5_tip_1_5	21	multiple ankyrin repeats single kh domain	217	3.67E-74	90.60%	0.135	Coil (COILS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR23206 (PANTHER); PTHR23206:SF4 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
704	404856_length_654_cvg_4.3_tip_1_5	14	5 -nucleotidase	218	8.15E-72	82.80%	0.111	IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11575:SF7 (PANTHER); IPR006179 (PANTHER); IPR029052 (SUPERFAMILY)
722	408538_length_669_cvg_91.4_tip_0_0	5878	c-type lectin	218	6.33E-33	51.70%	0.13	IPR002557 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR002557 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
734	412054_length_685_cvg_5.7_tip_1_3	17	protein disulfide	218	1.53E-109	79.70%	0.106	PR00421 (PRINTS); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF85 (PANTHER); PTHR18929 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
705	405384_length_656_cvg_81.8_tip_1_1	1287	hornerin isoform x2	219	1.47E-29	50.20%	0.123	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

706	405648_length_658_cvg_10.2_tip_1_4	28	gamma-interferon-inducible lysosomal thiol reductase	219	1.40E-19	58.20%	0.255	IPR004911 (PFAM); IPR004911 (PANTHER); PTHR13234:SF8 (PANTHER)
732	411764_length_684_cvg_5.3_tip_1_4	17	zinc finger protein partial	219	1.54E-23	59.20%	0.128	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
707	406110_length_659_cvg_2.6_tip_1_0	7	hsp70 family protein	220	1.51E-157	99.90%	0.131	IPR013126 (PRINTS); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); PTHR19375:SF151 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
708	406298_length_660_cvg_2.0_tip_1_5	5	twitchin- partial	220	9.81E-99	80.80%	0.113	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
710	406388_length_661_cvg_3.7_tip_1_2	12	zinc finger protein	220	8.53E-29	57.60%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
712	406790_length_662_cvg_2.0_tip_1_5	7	zinc finger and scan domain-containing protein 22	220	1.55E-32	55.20%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
709	406376_length_661_cvg_100.9_tip_0_3	160937	low-density lipoprotein receptor-related protein 2	221	8.70E-37	59.10%	0.109	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
714	407216_length_664_cvg_2.0_tip_1_4	6	acyloxyacyl hydrolase	221	4.95E-70	64.30%	0.11	IPR001087 (PFAM); IPR013830 (G3DSA:3.40.50.GENE3D); PTHR15010 (PANTHER); IPR013830 (SUPERFAMILY)
716	407286_length_664_cvg_3.3_tip_1_4	11	semaphorin-1a isoform x1	221	1.37E-12	89.10%	0.356 Y	IPR015943 (G3DSA:2.130.10.GENE3D); IPR001627 (PFAM); IPR027231 (PANTHER); PTHR11036:SF66 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001627 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
715	407234_length_664_cvg_63.2_tip_1_3	347	macrophage migration inhibitory factor	222	2.37E-39	69.80%	0.135	IPR001398 (PFAM); G3DSA:3.30.429.10 (GENE3D); IPR001398 (PANTHER); PTHR11954:SF6 (PANTHER); IPR001398 (PRODOM); IPR014347 (SUPERFAMILY)
717	407458_length_665_cvg_10.9_tip_1_4	24	maguk p55 subfamily member partial	222	3.06E-23	87.60%	0.248	Coil (COILS); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23122:SF32 (PANTHER); PTHR23122 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)

748	415401_length_701_cvg_78.9_tip_1_3	812	myophilin-like isoform 2	234	5.07E-100	85.00%	0.103	IPR003096 (PRINTS); IPR001715 (SMART); IPR001715 (PFAM); IPR001715 (G3DSA:1.10.418.GENE3D); PTHR18959 (PANTHER); IPR000557 (PROSITE_PATTERNS); IPR000557 (PROSITE_PROFILES); IPR001715 (PROSITE_PROFILES); IPR001715 (SUPERFAMILY)
749	415499_length_702_cvg_47.8_tip_1_1	117	a-kinase anchor protein partial	234	1.01E-21	56.50%	0.098	Coil (COILS)
752	415927_length_704_cvg_3.0_tip_1_2	12	wnt10 protein	234	3.04E-34	80.60%	0.13	IPR005817 (PFAM); PTHR12027:SF89 (PANTHER); IPR005817 (PANTHER)
777	421213_length_729_cvg_3.2_tip_1_2	13	zinc finger protein	234	1.79E-31	57.30%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13912 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
751	415791_length_703_cvg_8.1_tip_1_0	21	zinc finger protein	235	2.61E-54	69.70%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
753	415949_length_704_cvg_82.8_tip_1_1	946	serine protease 27-like	235	1.65E-43	54.80%	0.116	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
754	415953_length_704_cvg_2.7_tip_1_1	9	ganglioside-induced differentiation-associated protein 2	235	3.28E-56	70.70%	0.252	IPR002589 (SMART); IPR002589 (PFAM); G3DSA:3.40.220.10 (GENE3D); PTHR11106 (PANTHER); PTHR11106:SF59 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002589 (PROSITE_PROFILES); SSF52949 (SUPERFAMILY)
755	416033_length_704_cvg_5.7_tip_1_3	16	zinc finger protein 850-like	235	7.97E-41	59.00%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
756	416121_length_705_cvg_2.0_tip_1_4	6	adhesive serine protease	235	2.89E-26	67.30%	0.12	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
757	416121_length_705_cvg_2.0_tip_1_5	6	trypsin- partial	235	5.87E-12	73.40%	0.15	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24258:SF4 (PANTHER); PTHR24258 (PANTHER); IPR009003 (SUPERFAMILY)
758	416133_length_705_cvg_68.3_tip_0_1	128445	chitinase partial	235	9.04E-60	63.30%	0.106	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY); IPR029070 (SUPERFAMILY)

805	425325_length_749_cvg_4.2_tip_1_5	13	zinc finger protein 226-like	235	8.23E-33	60.20%	0.123	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
759	416639_length_707_cvg_2.0_tip_1_3	7	proclotting enzyme	236	3.44E-20	76.50%	0.122	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
760	417027_length_709_cvg_4.0_tip_1_5	14	peptidyl-prolyl cis-trans isomerase-like 4	236	3.15E-76	84.20%	0.108	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF156 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
762	417143_length_709_cvg_2.2_tip_1_2	6	twitchin isoform x4	236	2.40E-116	85.60%	0.199	PR00014 (PRINTS); IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF142 (PANTHER); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
763	417373_length_710_cvg_3.5_tip_1_2	13	trypsin 3	236	1.84E-32	63.40%	0.125	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24260 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
761	417119_length_709_cvg_2.5_tip_1_3	11	epidermal growth factor-like protein 7	237	1.29E-29	49.90%	0.117	Coil (COILS); Coil (COILS); IPR001881 (SMART); IPR000742 (SMART); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); PTHR14949 (PANTHER); PTHR14949:SF14 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
764	417581_length_711_cvg_4.3_tip_1_3	16	proprotein convertase subtilisin kexin type 7	237	4.37E-68	58.50%	0.645 Y	IPR002884 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); PTHR10795:SF9 (PANTHER); IPR015500 (PANTHER); SignalP-noTM (SIGNALP_EUK); IPR008979 (SUPERFAMILY)
765	417847_length_712_cvg_4.3_tip_1_0	14	sortilin-related receptor	238	1.41E-17	80.70%	0.739 Y	G3DSA:2.130.10.140 (GENE3D); PTHR12106 (PANTHER); PTHR12106:SF7 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF110296 (SUPERFAMILY); TMhelix (TMHMM)
766	418055_length_713_cvg_2.0_tip_1_4	6	tyrosine-protein kinase receptor tie-1-like isoform x1	238	2.03E-09	63.30%	0.114	G3DSA:2.10.25.10 (GENE3D); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES)
768	418611_length_716_cvg_5.7_tip_1_1	15	probable nuclear transport factor 2 isoform x1	239	2.37E-63	81.90%	0.138	G3DSA:3.10.450.50 (GENE3D); IPR002075 (PFAM); PTHR12612 (PANTHER); IPR018222 (PROSITE_PROFILES); SSF54427 (SUPERFAMILY)
769	418797_length_717_cvg_2.2_tip_1_0	9	limbic system-associated membrane protein	239	3.71E-92	68.40%	0.1	IPR003961 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PF13895 (PFAM); PTHR19831:SF40 (PANTHER); PTHR19831 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
770	418907_length_717_cvg_63.6_tip_1_4	5047	granulins- partial	239	3.40E-36	53.10%	0.626 Y	IPR000118 (SMART); IPR000118 (PFAM); PTHR12274 (PANTHER); PTHR12274:SF1 (PANTHER); IPR000118 (PROSITE_PATTERNS); IPR000118 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF57277 (SUPERFAMILY); SSF57277 (SUPERFAMILY); TMhelix (TMHMM)

783	422189_length_734_cvg_3.6_tip_1_1	17	transcription factor e4f1-like	245	4.47E-17	75.90%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
784	422293_length_734_cvg_21.3_tip_1_0	69	gastrula zinc finger protein	245	1.25E-30	57.00%	0.105	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13912 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
786	422487_length_735_cvg_3.2_tip_1_4	14	down syndrome cell adhesion molecule-like protein dscam2	245	7.82E-20	63.90%	0.18	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF580 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
787	422715_length_737_cvg_2.0_tip_1_2	7	protein kinase c-binding protein nell1-like isoform x2	245	1.05E-58	61.80%	0.107	IPR001007 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR001007 (PFAM); PTHR24042 (PANTHER); PTHR24042:SF4 (PANTHER); IPR001007 (PROSITE_PATTERNS); IPR001007 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); SSF57603 (SUPERFAMILY); SSF57603 (SUPERFAMILY)
788	422727_length_737_cvg_4.2_tip_1_3	9	serrate partial	246	3.80E-28	77.60%	0.285	IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24044 (PANTHER); PTHR24044:SF222 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
789	423171_length_739_cvg_4.7_tip_1_5	14	upf0364 protein c6orf211 homolog	246	3.21E-74	69.10%	0.197	IPR002791 (PFAM); PTHR12260 (PANTHER); PTHR12260:SF1 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002791 (SUPERFAMILY)
790	423527_length_740_cvg_39.3_tip_1_5	150	marginal zone b- and b1-cell-specific	246	1.21E-44	56.40%	0.18	PTHR15881:SF1 (PANTHER); PTHR15881 (PANTHER)
791	423649_length_741_cvg_5.2_tip_1_4	14	prostaglandin f synthase-like isoform x4	247	1.39E-77	72.90%	0.102	IPR020471 (PRINTS); IPR023210 (G3DSA:3.20.20.GENE3D); IPR023210 (PFAM); IPR020471 (PIRSF); PTHR11732:SF133 (PANTHER); IPR001395 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
792	423767_length_742_cvg_4.1_tip_1_4	12	protein cbg17465	247	1.09E-18	56.50%	0.206	PTHR23022 (PANTHER); PTHR23022:SF64 (PANTHER)
793	423843_length_742_cvg_2.2_tip_1_0	7	---NA---	248			0.131	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
794	423893_length_742_cvg_2.5_tip_1_3	8	alpha-l- partial	248	2.71E-06	68.29%	0.137	no IPS match
795	424183_length_743_cvg_2.0_tip_1_4	6	secreted frizzled-related protein 5-like	248	7.98E-19	77.60%	0.148	IPR020067 (G3DSA:1.10.2000.GENE3D); IPR015526 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020067 (SUPERFAMILY); TMhelix (TMHMM)
796	424227_length_744_cvg_8.4_tip_1_0	17	zinc metalloprotease	248	2.46E-10	59.20%	0.205	G3DSA:1.10.390.10 (GENE3D); TMhelix (TMHMM)
797	424569_length_745_cvg_7.7_tip_1_5	27	von willebrand factor like 1	248	1.50E-09	43.10%	0.101	no IPS match
817	426883_length_758_cvg_35.2_tip_1_1	148	lysine--trna ligase isoform x2	248	4.01E-79	94.30%	0.111	G3DSA:3.30.930.10 (GENE3D); IPR004364 (PFAM); IPR018150 (PANTHER); PTHR22594:SF4 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
798	424657_length_746_cvg_2.0_tip_1_0	6	pdz domain-containing protein 2	249	7.80E-16	82.20%	0.099	IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
799	424833_length_747_cvg_3.9_tip_1_2	18	collagen alpha-1 partial	249	5.34E-23	52.60%	0.101	IPR008160 (PFAM); PTHR24023:SF379 (PANTHER); PTHR24023 (PANTHER)
800	424833_length_747_cvg_3.9_tip_1_5	18	collagen-like protein	249	1.82E-21	44.30%	0.218	no IPS match
801	425089_length_748_cvg_3.7_tip_1_4	11	protein partial	249	1.54E-16	57.40%	0.111	no IPS match
802	425111_length_748_cvg_6.4_tip_1_1	19	zinc metalloproteinase nas-13	249	3.85E-31	60.90%	0.169	IPR001506 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)
803	425141_length_748_cvg_61.9_tip_1_4	210	hypothetical protein BRAFLDRAFT_71031	249	1.20E-15	50.50%	0.106	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)

804	425317_length_749_cvg_2.4_tip_1_3	12	pt repeat family protein	250	1.50E-12	65.30%	0.638 Y	SignalIP-noTM (SIGNALP_EUK)
806	425493_length_750_cvg_2.5_tip_1_1	9	zinc finger protein gfi-1b-like isoform x2	250	6.21E-23	72.40%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
807	425591_length_750_cvg_2.4_tip_1_5	6	hemocyanin subunit	250	2.61E-11	54.70%	0.11	IPR005204 (G3DSA:1.20.1370.GENE3D); IPR005204 (PFAM); IPR005204 (SUPERFAMILY)
809	425989_length_753_cvg_64.9_tip_1_5	544	protein twin sister of ft	251	2.28E-24	59.50%	0.142	IPR008914 (G3DSA:3.90.280.GENE3D); IPR008914 (PFAM); PTHR11362 (PANTHER); IPR001858 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008914 (SUPERFAMILY)
811	426635_length_756_cvg_4.6_tip_1_1	17	epidermal growth factor-like protein 8-like	252	1.20E-21	61.70%	0.26	IPR011489 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011489 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM)
812	426683_length_757_cvg_7.7_tip_1_2	26	phospholipase a-2-activating	252	4.29E-100	75.20%	0.11	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19849 (PANTHER); PTHR19849:SF0 (PANTHER); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
813	426729_length_757_cvg_6.3_tip_1_1	22	retinol dehydrogenase 13-like	252	3.71E-99	76.60%	0.109	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320:SF55 (PANTHER); PTHR24320 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
815	426751_length_757_cvg_2.0_tip_1_2	6	zinc finger protein partial	252	5.53E-67	75.90%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
841	430955_length_781_cvg_12.4_tip_1_4	40	peptidyl-prolyl cis-trans isomerase-like 6	252	6.44E-18	61.70%	0.103	IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF210 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
816	426761_length_757_cvg_30.1_tip_1_3	63	gastrula zinc finger isoform x1	253	1.92E-35	61.30%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
818	427391_length_760_cvg_9.5_tip_1_3	29	peroxidase isoform x2	254	8.58E-14	65.10%	0.104	IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
819	427557_length_761_cvg_4.4_tip_1_0	15	heat shock protein 70 a1-like	254	4.19E-161	95.50%	0.1	IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.90.640.10 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF142 (PANTHER); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
820	427827_length_763_cvg_9.6_tip_1_4	23	adp-ribosylation factor-like protein 5b	254	2.15E-60	97.10%	0.152	IPR006689 (PRINTS); IPR024156 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF146 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
821	427873_length_763_cvg_6.5_tip_1_5	17	cre-ptr-16 protein	254	5.49E-22	56.80%	0.246	PTHR23022 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
822	428007_length_764_cvg_3.4_tip_1_0	11	serine protease easter	255	3.04E-50	59.80%	0.15	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF85 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

823	428181_length_765_cvg_28.7_tip_1_3	111	l-xylulose reductase	255	5.35E-90	80.60%	0.12	IPR002198 (PRINTS); IPR002347 (PRINTS); PF13561 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24311:SF6 (PANTHER); PTHR24311 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
824	428377_length_766_cvg_14.2_tip_1_1	39	prenylcysteine oxidase-like	255	2.88E-61	64.20%	0.211	PF13450 (PFAM); IPR010795 (PFAM); G3DSA:3.50.50.60 (GENE3D); IPR017046 (PANTHER); SSF51905 (SUPERFAMILY)
825	428525_length_767_cvg_41.4_tip_1_0	95	suppressor of tumorigenicity 14 protein	256	5.71E-07	64.86%	0.155	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
826	428585_length_767_cvg_2.0_tip_1_1	9	penicillin-binding protein partial	256	0	99.40%	0.144	IPR012338 (G3DSA:3.40.710.GENE3D); IPR012340 (G3DSA:2.40.50.GENE3D); IPR001460 (PFAM); PTHR32282:SF5 (PANTHER); PTHR32282 (PANTHER); IPR012338 (SUPERFAMILY)
828	428969_length_769_cvg_4.8_tip_1_1	22	peptidyl-prolyl cis-trans	256	3.58E-57	71.20%	0.098	IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); PTHR11071:SF193 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
827	428943_length_769_cvg_9.5_tip_1_0	35	niemann-pick type c1 domain-containing	257	6.40E-58	72.50%	0.114	Coil (COILS); Coil (COILS); PTHR19237:SF20 (PANTHER); PTHR19237 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
829	429347_length_772_cvg_6.0_tip_1_1	15	carbohydrate sulfotransferase 11-like	257	1.68E-43	68.50%	0.098	IPR005331 (PFAM); PTHR12137:SF29 (PANTHER); IPR018011 (PANTHER); TMhelix (TMHMM); TMhelix (TMHMM)
830	429715_length_774_cvg_6.7_tip_1_0	18	neurofilament medium polypeptide	258	8.48E-13	54.20%	0.096	no IPS match
831	429789_length_774_cvg_3.1_tip_1_0	11	mam and ldl-receptor class a domain-containing protein 2-like	258	8.70E-41	60.50%	0.149	IPR000998 (SMART); IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PATTERNS); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
832	429789_length_774_cvg_3.1_tip_1_2	11	mlrp2_acrmi ame: full=mam and ldl-receptor class a domain-containing protein 2 ame: full=skeletal organic matrix mam and ldl-receptor 2 short=som mam and ldl-receptor partial	258	1.40E-07	55.86%	0.107	IPR000998 (PFAM); PTHR23282 (PANTHER); PTHR23282:SF75 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
833	429855_length_775_cvg_12.4_tip_1_5	34	esterase fe4	258	6.22E-91	70.60%	0.547 Y	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR019826 (PROSITE_PATTERNS); IPR019819 (PROSITE_PATTERNS); SignalP-noTM (SIGNALP_EUK); IPR029058 (SUPERFAMILY)
834	430241_length_777_cvg_3.5_tip_1_4	17	trafficking protein particle complex subunit 1	259	1.30E-62	86.10%	0.167	IPR007233 (PFAM); G3DSA:3.30.450.70 (GENE3D); PTHR23249:SF16 (PANTHER); IPR007233 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011012 (SUPERFAMILY); TMhelix (TMHMM)
835	430243_length_777_cvg_61.3_tip_1_0	817	superoxide dismutase	259	5.37E-78	85.20%	0.171	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); PTHR10003:SF33 (PANTHER); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY); TMhelix (TMHMM)
836	430251_length_777_cvg_76.7_tip_0_1	2443	annexin b10-like	259	1.14E-83	69.70%	0.104	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); SSF47874 (SUPERFAMILY)
837	430289_length_777_cvg_6.7_tip_1_3	22	gamma-glutamyl hydrolase-like	259	1.84E-57	68.00%	0.114	IPR011697 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER); PTHR11315:SF2 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY); TMhelix (TMHMM)
838	430315_length_777_cvg_102.3_tip_1_3	225214	secreted salivary gland	259	7.88E-34	54.40%	0.104	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

839	430805_length_780_cvg_2.0_tip_1_2	9	vitellogenin receptor	260	6.85E-50	56.00%	0.12	IPR002172 (PRINTS); IPR001881 (SMART); IPR000742 (SMART); IPR002172 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001881 (PFAM); PTHR10529 (PANTHER); PTHR10529:SF204 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
840	430951_length_781_cvg_2.6_tip_1_4	11	hypothetical protein Y032_0322g2447	260	2.00E-24	52.50%	0.185	PTHR23022:SF64 (PANTHER); PTHR23022 (PANTHER)
842	431395_length_784_cvg_3.0_tip_1_1	9	low quality protein: zinc finger protein 233	261	2.79E-67	67.00%	0.116	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
843	431465_length_784_cvg_2.7_tip_1_5	7	leukotriene a-4 hydrolase	261	2.16E-76	75.60%	0.096	IPR014782 (PRINTS); IPR014782 (PFAM); IPR001930 (PANTHER); PTHR11533:SF4 (PANTHER); SSF63737 (SUPERFAMILY)
844	431471_length_784_cvg_2.5_tip_1_4	7	zinc finger protein 699-like isoform x1	261	3.66E-38	59.00%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
854	435732_length_810_cvg_21.3_tip_1_0	73	trafficking protein particle complex subunit 1 isoform x1	262	7.57E-07	71.00%	0.231	IPR007233 (PFAM)
860	436234_length_814_cvg_21.4_tip_1_2	66	spondin-2 isoform x1	262	9.11E-13	75.30%	0.166	IPR009465 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009465 (PROSITE_PROFILES); TMhelix (TMHMM)
845	432175_length_788_cvg_8.0_tip_1_3	26	---NA---	263			0.104	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
846	432275_length_789_cvg_3.3_tip_1_3	9	repetitive proline-rich cell wall protein 2-like isoform x2	263	3.77E-28	51.90%	0.137	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF141571 (SUPERFAMILY)
855	435846_length_811_cvg_11.9_tip_1_2	32	hemagglutinin	263	1.75E-27	57.00%	0.135	IPR001570 (PFAM); IPR007280 (PFAM); G3DSA:1.10.390.10 (GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
847	433549_length_796_cvg_62.9_tip_1_2	1381	protein disulfide-isomerase a3	265	1.76E-102	76.90%	0.354 Y	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); PF13848 (PFAM); IPR013766 (PFAM); IPR005788 (TIGRFAM); PTHR18929:SF74 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
848	433855_length_798_cvg_4.7_tip_1_5	19	neutral ceramidase	266	5.14E-62	65.80%	0.108	IPR006823 (PFAM); IPR006823 (PANTHER); PTHR12670:SF1 (PANTHER)
869	437874_length_825_cvg_72.1_tip_1_2	666	protein them6	266	1.41E-25	54.90%	0.149	IPR029069 (G3DSA:3.10.129.GENE3D); PF13279 (PFAM); PTHR12475 (PANTHER); IPR029069 (SUPERFAMILY); TMhelix (TMHMM)

849	434079_length_800_cvg_4.1_tip_1_1	14	proactivator polypeptide	267	1.56E-10	71.90%	0.119	IPR008139 (SMART); IPR008138 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR11480:SF3 (PANTHER); PTHR11480 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008139 (PROSITE_PROFILES); IPR011001 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
871	438794_length_831_cvg_61.8_tip_1_1	782	hemagglutinin amebocyte aggregation factor-like	267	5.86E-38	57.90%	0.229	PF14704 (PFAM); IPR026645 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
896	441963_length_853_cvg_16.5_tip_1_4	58	epididymal secretory protein e1	267	3.03E-23	58.80%	0.133	IPR003172 (SMART); IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306 (PANTHER); PTHR11306:SF3 (PANTHER); IPR014756 (SUPERFAMILY)
850	435057_length_806_cvg_2.5_tip_1_0	7	ligand of numb protein x 2	269	1.97E-41	67.40%	0.131	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
851	435088_length_806_cvg_11.4_tip_1_1	34	cysteine-rich motor neuron 1	269	3.23E-41	59.90%	0.141	IPR000867 (SMART); IPR000867 (PFAM); PTHR14186:SF8 (PANTHER); IPR011390 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000867 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
852	435248_length_807_cvg_4.2_tip_1_1	15	low quality protein: zinc finger protein 233	269	1.56E-32	60.80%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
853	435330_length_808_cvg_2.0_tip_1_1	8	exostosin 1-like protein	269	2.96E-116	79.40%	0.113	IPR004263 (PFAM); PTHR11062 (PANTHER); PTHR11062:SF7 (PANTHER)
856	435974_length_812_cvg_5.4_tip_1_5	19	zinc finger protein 665-like	270	1.44E-58	62.60%	0.099	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
878	439269_length_835_cvg_4.2_tip_1_4	16	developmental protein cactus	270	2.70E-25	70.70%	0.114	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24139:SF26 (PANTHER); PTHR24139 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM)
857	436060_length_813_cvg_2.6_tip_1_4	14	nepriysin 2 isoform x3	271	1.66E-104	72.00%	0.1	IPR018497 (PRINTS); IPR018497 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000718 (PANTHER); PTHR11733:SF113 (PANTHER); SSF55486 (SUPERFAMILY)
858	436116_length_813_cvg_85.8_tip_0_3	2705088	isoform k	271	6.99E-42	48.30%	0.105	IPR002557 (SMART); IPR001223 (PFAM); IPR029070 (G3DSA:3.10.50.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002557 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF133 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR017853 (SUPERFAMILY); IPR029070 (SUPERFAMILY); IPR002557 (SUPERFAMILY)

873	438903_length_832_cvg_3.3_tip_1_3	13	krueppel-like factor 5	278	1.87E-46	96.20%	0.103	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
874	439057_length_833_cvg_6.3_tip_1_3	21	integral membrane protein 2c	278	1.20E-91	66.60%	0.14	IPR007084 (SMART); IPR007084 (PFAM); PTHR10962:SF1 (PANTHER); PTHR10962 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007084 (PROSITE_PROFILES); TMhelix (TMHMM)
875	439061_length_833_cvg_2.9_tip_1_1	11	neural cell adhesion molecule 1	278	1.63E-32	54.90%	0.477 Y	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19831:SF40 (PANTHER); PTHR19831 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
877	439197_length_834_cvg_2.6_tip_1_4	8	cathepsin partial	278	4.20E-30	83.60%	0.146	G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); IPR013128 (PANTHER); PTHR12411:SF289 (PANTHER); IPR025661 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
904	443595_length_865_cvg_48.1_tip_1_4	422	histone h2a-like	279	1.68E-79	96.80%	0.221	IPR002119 (PRINTS); IPR002119 (SMART); IPR009072 (G3DSA:1.10.20.GENE3D); IPR007125 (PFAM); PTHR23430:SF45 (PANTHER); PTHR23430 (PANTHER); IPR002119 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009072 (SUPERFAMILY); TMhelix (TMHMM)
879	440019_length_840_cvg_2.9_tip_1_2	11	spondin-1	280	3.58E-94	68.50%	0.136	IPR002223 (PRINTS); IPR000884 (SMART); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); G3DSA:2.20.100.10 (GENE3D); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); IPR002223 (PFAM); PTHR11311 (PANTHER); PTHR11311:SF11 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
880	440147_length_841_cvg_19.6_tip_1_3	75	Adrenodoxin, mitochondrial	281	2.89E-52	76.80%	0.148	IPR001055 (PRINTS); IPR012675 (G3DSA:3.10.20.GENE3D); IPR001041 (PFAM); PTHR23426:SF21 (PANTHER); PTHR23426 (PANTHER); IPR018298 (PROSITE_PATTERNS); IPR001041 (PROSITE_PROFILES); IPR001041 (SUPERFAMILY)
882	440359_length_842_cvg_11.8_tip_1_0	52	thioredoxin 2	281	1.56E-35	71.30%	0.284	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR10438:SF235 (PANTHER); IPR005746 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
883	440477_length_843_cvg_5.9_tip_1_2	18	zinc finger protein 226-like	281	6.58E-43	57.00%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
884	440519_length_843_cvg_59.8_tip_1_5	682	lipophorin receptor isoform c	281	3.94E-13	54.60%	0.476 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); PTHR10529:SF208 (PANTHER); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)

885	440573_length_844_cvg_6.8_tip_1_2	19	n-acetylglucosamine-6-sulfatase-like isoform x3	281	5.52E-98	71.90%	0.206	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342:SF208 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM)
886	440625_length_844_cvg_4.9_tip_1_5	16	variable charge x-linked protein 3b	281	2.27E-10	58.10%	0.258	no IPS match
887	440641_length_844_cvg_36.4_tip_0_5	119	acyl- delta desaturase	281	7.07E-118	82.70%	0.108	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351:SF28 (PANTHER); PTHR11351 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
888	440795_length_845_cvg_5.0_tip_1_5	18	cyclin-dependent kinase 6	281	3.82E-132	79.20%	0.096	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24056:SF180 (PANTHER); PTHR24056 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
905	443797_length_866_cvg_14.9_tip_1_2	61	otogelin-like protein	281	2.65E-09	44.10%	0.101	no IPS match
889	440897_length_846_cvg_4.1_tip_1_5	14	dehydrogenase reductase sdr family protein 7-like	282	1.09E-101	78.40%	0.293	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF325 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
890	441101_length_848_cvg_64.9_tip_0_0	226	zinc finger protein gfi-1b	283	2.38E-22	55.40%	0.104	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
891	441257_length_849_cvg_4.0_tip_1_4	22	protein cbg17465	283	9.56E-07	55.33%	0.122	no IPS match
892	441267_length_849_cvg_4.5_tip_1_2	18	c4b-binding protein beta	283	1.31E-119	77.10%	0.11	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); PTHR19325:SF312 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
893	441805_length_852_cvg_2.2_tip_1_5	13	serine partial	284	1.49E-36	63.10%	0.107	IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); PTHR11802:SF30 (PANTHER); IPR029058 (SUPERFAMILY)
894	441891_length_853_cvg_2.0_tip_1_0	6	epsilon-sarcoglycan isoform x2	285	1.25E-60	65.50%	0.113	IPR001304 (PFAM); IPR008908 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR008908 (PANTHER); PTHR10132:SF14 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
895	441955_length_853_cvg_3.8_tip_1_0	13	thioredoxin domain-containing protein 11	285	1.46E-38	54.80%	0.129	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929:SF61 (PANTHER); PTHR18929 (PANTHER); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
897	442037_length_854_cvg_7.7_tip_1_0	19	chorion peroxidase-like	285	1.11E-101	68.50%	0.139	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
898	442107_length_855_cvg_79.0_tip_0_2	212877	plasma kallikrein	285	4.96E-48	55.90%	0.124	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
899	442159_length_855_cvg_4.3_tip_1_2	16	collagen alpha-1 chain-like	285	1.81E-87	81.60%	0.127	IPR000885 (SMART); IPR000885 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF444 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000885 (PRODOM); IPR000885 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
900	442625_length_858_cvg_8.1_tip_1_1	23	hypothetical protein L798_15262	286	4.89E-12	77.00%	0.334	IPR029245 (PFAM)

909	444575_length_871_cvg_4.5_tip_1_2	21	calumenin	290	4.65E-14	85.10%	0.429 Y	IPR011992 (G3DSA:1.10.238.GENE3D); IPR018247 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
911	444933_length_874_cvg_51.0_tip_1_3	145	adp-ribosylation factor-like protein 16	292	1.30E-41	67.80%	0.145	IPR006687 (SMART); IPR024156 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF42 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
912	445613_length_879_cvg_4.8_tip_1_2	15	zinc finger protein	293	3.06E-42	54.50%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
913	445673_length_880_cvg_9.3_tip_1_2	39	hypothetical protein BRAFLDRAFT_125057	293	7.15E-09	46.00%	0.112	no IPS match
938	448897_length_906_cvg_9.8_tip_1_3	53	spermatogenesis-associated protein 5	293	4.49E-141	82.30%	0.104	Coil (COILS); IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23077:SF27 (PANTHER); PTHR23077 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
914	445711_length_880_cvg_56.5_tip_1_0	461	ecdysteroid-regulated 16 kda protein	294	1.42E-17	54.20%	0.393 Y	IPR003172 (SMART); IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306 (PANTHER); IPR014756 (SUPERFAMILY)
915	445811_length_881_cvg_6.8_tip_1_4	28	alcohol dehydrogenase	294	1.44E-58	65.90%	0.16	IPR020471 (PRINTS); IPR023210 (G3DSA:3.20.20.GENE3D); IPR023210 (PFAM); PTHR11732:SF183 (PANTHER); IPR001395 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023210 (SUPERFAMILY); TMhelix (TMHMM)
916	445989_length_882_cvg_17.7_tip_1_2	68	adp-ribosylation factor-like protein 2	294	4.78E-109	93.70%	0.551 Y	IPR006689 (PRINTS); IPR003579 (SMART); IPR006687 (SMART); IPR024156 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711:SF26 (PANTHER); PTHR11711 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
936	448597_length_903_cvg_3.0_tip_1_1	14	striatin- partial	294	2.49E-140	88.60%	0.118	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR15653 (PANTHER); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
954	451101_length_924_cvg_63.3_tip_1_5	23025	translationally-controlled tumor protein	294	4.03E-71	79.40%	0.274	IPR018105 (PRINTS); IPR018105 (PFAM); IPR011323 (G3DSA:2.170.150.GENE3D); IPR018105 (PANTHER); IPR011057 (SUPERFAMILY)
917	446083_length_883_cvg_4.0_tip_1_3	14	lipophorin receptor	295	2.88E-28	71.80%	0.323	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
918	446161_length_883_cvg_4.3_tip_1_0	13	peptidyl-prolyl cis-trans isomerase-like 2	295	7.36E-141	79.50%	0.102	Coil (COILS); IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF147 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
923	446629_length_887_cvg_7.0_tip_1_5	23	venom dipeptidyl peptidase 4 isoform x3	295	1.03E-26	71.40%	0.103	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001375 (PFAM); PTHR11731:SF93 (PANTHER); PTHR11731 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY)
922	446575_length_886_cvg_5.2_tip_1_0	23	nucleobindin-2-like isoform x5	296	3.03E-54	74.10%	0.103	IPR011992 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR19237 (PANTHER); PTHR19237:SF20 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)

924	446803_length_889_cvg_3.9_tip_1_4	19	immunoglobulin-like and fibronectin type iii domain containing 7	296	7.97E-18	55.90%	0.156	IPR026966 (PFAM); PTHR10489 (PANTHER); PTHR10489:SF553 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
925	446805_length_889_cvg_16.9_tip_1_1	61	calnexin-like isoform x2	296	1.89E-91	78.50%	0.102	IPR001580 (PRINTS); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001580 (PFAM); PTHR11073:SF1 (PANTHER); IPR001580 (PANTHER); IPR018124 (PROSITE_PATTERNS); IPR013320 (SUPERFAMILY)
927	446899_length_889_cvg_5.9_tip_1_2	32	tyrosine-protein kinase receptor tie-1	296	1.69E-18	57.90%	0.185	G3DSA:2.170.300.10 (GENE3D); PTHR24416:SF125 (PANTHER); PTHR24416 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
926	446897_length_889_cvg_18.1_tip_1_3	63	hemagglutinin amebocyte aggregation factor-like	297	1.29E-29	57.60%	0.269	PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
928	447037_length_890_cvg_4.7_tip_1_0	21	zinc finger protein 420-like	297	3.48E-41	56.80%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
931	447621_length_895_cvg_42.7_tip_1_1	131	protein shifted isoform x1	298	7.43E-81	87.70%	0.145	IPR013309 (PRINTS); IPR003306 (SMART); IPR003306 (PFAM); PTHR24838 (PANTHER); PTHR24838:SF276 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003306 (PRODOM); IPR003306 (PROSITE_PROFILES); TMhelix (TMHMM)
932	447653_length_895_cvg_59.9_tip_1_2	7269	plasma kallikrein	298	7.74E-38	54.10%	0.214	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
933	447777_length_896_cvg_10.6_tip_1_5	36	stromal cell-derived factor 2	298	5.28E-95	75.50%	0.448 Y	IPR016093 (SMART); IPR016093 (PFAM); G3DSA:2.80.10.50 (GENE3D); IPR027005 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016093 (PROSITE_PROFILES); IPR016093 (PROSITE_PROFILES); IPR016093 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR016093 (SUPERFAMILY)
949	450611_length_920_cvg_9.8_tip_1_2	36	nad h-hydrate epimerase-like	299	1.33E-109	77.00%	0.195	IPR004443 (G3DSA:3.40.50.GENE3D); IPR004443 (PFAM); IPR004443 (TIGRFAM); PTHR13232 (PANTHER); IPR004443 (PROSITE_PROFILES); IPR004443 (HAMAP); IPR004443 (SUPERFAMILY)
934	448147_length_899_cvg_5.0_tip_1_3	18	cathepsin l-associated protein	300	2.63E-62	59.40%	0.510 Y	IPR000782 (SMART); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY); TMhelix (TMHMM)
935	448499_length_902_cvg_2.0_tip_1_4	7	glucose partial	301	0	100.00%	0.149	IPR018391 (SMART); IPR027295 (G3DSA:2.140.10.GENE3D); PF13360 (PFAM); IPR002372 (PFAM); PTHR32303 (PANTHER); PTHR32303:SF2 (PANTHER); IPR001479 (PROSITE_PATTERNS); IPR011047 (SUPERFAMILY)
937	448643_length_904_cvg_49.6_tip_1_0	191	serine protease inhibitor kazal-type 6-like isoform x1	302	4.25E-09	61.43%	0.614 Y	IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); IPR002350 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002350 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

939	449317_length_909_cvg_3.4_tip_1_2	19	serine proteinase	303	1.72E-40	50.70%	0.246	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
940	449371_length_910_cvg_2.6_tip_1_5	8	ecdysis triggering hormone receptor isoform a	303	8.02E-71	81.80%	0.1	IPR000276 (PRINTS); IPR000276 (PFAM); G3DSA:1.20.1070.10 (GENE3D); PTHR24243 (PANTHER); PTHR24243:SF102 (PANTHER); IPR000276 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017452 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
941	449375_length_910_cvg_3.0_tip_1_2	10	serine-aspartate repeat protein f	303	2.09E-18	42.80%	0.363	Y no IPS match
943	449375_length_910_cvg_3.0_tip_1_5	10	collagen alpha-1 chain	303	3.84E-16	60.20%	0.114	IPR008160 (PFAM)
942	449375_length_910_cvg_3.0_tip_1_3	10	collagen alpha-1 chain	304	3.28E-20	58.60%	0.101	IPR008160 (PFAM); PTHR24023:SF372 (PANTHER); PTHR24023 (PANTHER)
944	449511_length_911_cvg_20.1_tip_1_0	77	zinc finger protein	304	4.50E-30	54.20%	0.113	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
945	449841_length_914_cvg_5.1_tip_1_1	25	carbonyl reductase	305	1.30E-123	74.60%	0.121	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF58 (PANTHER); SSF51735 (SUPERFAMILY)
946	450099_length_916_cvg_64.1_tip_1_1	867	glutathione peroxidase 7	305	2.61E-75	71.00%	0.168	IPR000889 (PRINTS); IPR000889 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PANTHER); PTHR11592:SF10 (PANTHER); IPR029759 (PROSITE_PATTERNS); IPR029760 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
947	450357_length_918_cvg_4.3_tip_1_2	16	retinol dehydrogenase 13-like	306	7.66E-32	74.60%	0.134	PTHR24320:SF55 (PANTHER); PTHR24320 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
948	450493_length_919_cvg_2.6_tip_1_1	10	zinc finger protein	306	3.51E-15	54.60%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
950	450633_length_920_cvg_4.6_tip_1_0	25	carboxypeptidase q isoform x2	307	1.93E-93	74.80%	0.262	IPR003137 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR12053 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); TMhelix (TMHMM)
951	450693_length_921_cvg_11.6_tip_1_0	42	zinc finger protein 420-like	307	4.97E-18	44.30%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

966	453228_length_943_cvg_5.4_tip_1_5	28	wnt1-inducible-signaling pathway protein 3	314	8.68E-15	50.30%	0.223	IPR000867 (SMART); IPR000867 (PFAM); PTHR11348 (PANTHER); IPR000867 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
980	455475_length_964_cvg_12.4_tip_1_3	52	adiponectin receptor protein	314	3.97E-21	77.70%	0.101	IPR004254 (PFAM); PTHR20855:Sf15 (PANTHER); IPR004254 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
965	453212_length_943_cvg_5.6_tip_1_3	32	low quality protein: titin-like	315	1.55E-177	87.90%	0.099	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR010939 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:Sf149 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
967	453368_length_944_cvg_7.0_tip_1_0	37	thioredoxin-dependent peroxide reductase	315	4.63E-127	84.70%	0.476 Y	IPR019479 (PFAM); IPR000866 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10681 (PANTHER); PTHR10681:Sf101 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalIP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY)
968	453592_length_946_cvg_17.0_tip_1_5	66	wd repeat domain 5	315	6.32E-53	86.40%	0.102	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847:Sf308 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
969	453752_length_948_cvg_2.0_tip_1_3	10	tyrosine-protein kinase hopscotch	316	1.36E-93	66.50%	0.116	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR016253 (PIRSF); IPR001245 (PFAM); PTHR24418 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
970	454160_length_951_cvg_5.2_tip_1_0	16	collagen triple helix repeat family protein	317	2.17E-11	52.90%	0.135	no IPS match
971	454160_length_951_cvg_5.2_tip_1_4	16	pneumococcal surface protein c	317	3.41E-10	48.90%	0.112	no IPS match
972	454174_length_951_cvg_40.2_tip_1_5	162	casein kinase ii subunit alpha	317	0	96.10%	0.098	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24054:Sf28 (PANTHER); PTHR24054 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
973	454452_length_954_cvg_3.0_tip_1_5	19	collagen alpha 1 chain	318	9.92E-57	55.70%	0.125	IPR016186 (G3DSA:3.10.100.GENE3D); IPR010515 (PFAM); IPR026917 (PTHr24023:PANTHER); PTHr24023 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
974	454796_length_958_cvg_5.8_tip_1_5	23	tyrosine-protein phosphatase 69d-like	319	6.36E-140	80.00%	0.133	IPR000242 (PRINTS); IPR000242 (SMART); IPR003595 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134:Sf227 (PANTHER); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
975	454810_length_958_cvg_12.8_tip_1_4	77	stereocilin	319	5.83E-19	47.00%	0.1	IPR026061 (PTHr23412:PANTHER); IPR026664 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
976	454903_length_959_cvg_4.2_tip_1_3	15	zinc finger protein	320	6.06E-45	57.40%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PTHR24409:Sf14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

978	455123_length_961_cvg_6.8_tip_1_4	22	zinc finger protein 76	320	3.08E-89	67.60%	0.151	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR11389 (PANTHER); PTHR11389:SF448 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
979	455197_length_961_cvg_10.9_tip_1_2	45	prenylcysteine oxidase-like	320	1.07E-61	57.20%	0.099	IPR010795 (PFAM); IPR017046 (PANTHER)
983	455595_length_965_cvg_4.0_tip_1_2	19	retinol dehydrogenase 13	321	2.41E-70	70.90%	0.114	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320:SF55 (PANTHER); PTHR24320 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
981	455539_length_965_cvg_4.0_tip_1_0	16	hypothetical protein BRAFLDRAFT_203178	322	2.71E-26	69.30%	0.099	IPR008979 (G3DSA:2.60.120.GENE3D); IPR006104 (PFAM); PTHR10066 (PANTHER); IPR028369 (PTHR10066:PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008979 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
982	455559_length_965_cvg_2.7_tip_1_4	16	ser thr protein	322	1.46E-153	85.50%	0.129	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); IPR020675 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
984	455709_length_966_cvg_2.0_tip_1_1	10	hypoxanthine partial	322	1.95E-147	100.00%	0.146	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF64 (PANTHER); IPR008274 (SUPERFAMILY)
985	455769_length_967_cvg_3.2_tip_1_4	13	secreted salivary gland	322	9.03E-31	50.40%	0.107	IPR023307 (G3DSA:2.170.15.GENE3D); IPR004991 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF56973 (SUPERFAMILY)
1057	463991_length_1058_cvg_4.4_tip_1_0	23	high affinity nerve growth factor	322	9.00E-32	73.70%	0.175	IPR020635 (SMART); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418 (PANTHER); PTHR24418:SF198 (PANTHER); IPR008266 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011009 (SUPERFAMILY)
986	455925_length_969_cvg_2.0_tip_1_3	9	periplasmic endochitinase	323	0	99.70%	0.141	IPR003610 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR003610 (PFAM); IPR003610 (G3DSA:2.10.10.GENE3D); IPR017853 (SUPERFAMILY); IPR003610 (SUPERFAMILY)
987	455925_length_969_cvg_2.0_tip_1_4	9	chi11_metan ame: full=endochitinase 11 ame: full=chitinase 11 flags: precursor	323	1.30E-06	77.00%	0.146	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
988	456087_length_970_cvg_11.0_tip_1_2	55	peroxisomal trans-2-enoyl- reductase-like	323	3.32E-128	74.70%	0.131	IPR002347 (PRINTS); PF13561 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24317 (PANTHER); SSF51735 (SUPERFAMILY)
989	456095_length_970_cvg_2.5_tip_1_3	13	neural ectodermal development factor imp-12	324	3.74E-44	51.40%	0.809 Y	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
990	456115_length_970_cvg_4.0_tip_1_3	14	zinc finger protein 347 isoform x1	324	1.26E-57	69.00%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
991	456291_length_972_cvg_11.8_tip_1_5	53	bone morphogenetic protein 4	324	5.39E-14	46.40%	0.112	Coil (COILS); IPR001111 (PFAM); IPR015615 (PANTHER)
992	456497_length_974_cvg_47.1_tip_1_2	225	zinc finger protein zpr1	324	1.14E-127	73.80%	0.185	IPR004457 (SMART); IPR004457 (PFAM); IPR004457 (TIGRFAM); PTHR10876:SF0 (PANTHER); PTHR10876 (PANTHER)

993	456537_length_974_cvg_4.5_tip_1_5	24	gastrula zinc finger protein	324	1.25E-22	56.80%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1022	458903_length_999_cvg_36.3_tip_1_5	147	subtilisin-like serine protease	324	8.29E-13	56.00%	0.510 Y	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_EUK)
994	456555_length_975_cvg_70.9_tip_1_4	15826	anti-lipopolysaccharide factor	325	3.10E-33	68.60%	0.411 Y	IPR024509 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024716 (PRODOM); TMhelix (TMHMM); TMhelix (TMHMM)
995	456779_length_977_cvg_3.0_tip_1_3	13	zinc finger protein	326	7.98E-15	56.10%	0.113	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24375:SF106 (PANTHER); PTHR24375 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
996	456819_length_977_cvg_61.8_tip_1_0	376	adp-ribosylation factor-like protein 1	326	8.92E-118	95.90%	0.134	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR003579 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); IPR006689 (PFAM); PTHR11711:SF41 (PANTHER); PTHR11711 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
997	456875_length_978_cvg_3.1_tip_1_4	18	zinc finger	326	1.22E-70	69.50%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PTHR24391 (PANTHER); PTHR24391:SF9 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
998	456899_length_978_cvg_22.4_tip_1_4	89	apolipoprotein d-like	326	2.80E-42	60.20%	0.246	IPR003057 (PRINTS); IPR000566 (PFAM); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612:SF7 (PANTHER); PTHR10612 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)
999	457017_length_979_cvg_3.6_tip_1_1	15	dnaj homolog subfamily c member 21-like	326	1.55E-140	81.50%	0.122	Coil (COILS); Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF150 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1000	457113_length_980_cvg_76.7_tip_1_5	62696	chymotrypsinogen 2-like	326	2.46E-46	56.50%	0.31	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1001	457123_length_980_cvg_5.8_tip_1_3	26	trypsin theta	327	4.33E-19	52.80%	0.107	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1002	457203_length_981_cvg_5.4_tip_1_2	26	immunoglobulin superfamily dcc subclass member 3-like	327	7.51E-40	65.00%	0.105	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1023	459023_length_1001_cvg_29.5_tip_1_3	126	aminoacyl trna synthase complex-interacting multifunctional protein partial	330	3.46E-100	68.30%	0.101	Coil (COILS); IPR002547 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); PTHR11586 (PANTHER); PTHR11586:SF1 (PANTHER); IPR002547 (PROSITE_PROFILES); IPR012340 (SUPERFAMILY)
1015	458115_length_991_cvg_4.7_tip_1_3	23	rac protein kinase drac-	331	3.92E-162	86.90%	0.121	IPR000961 (SMART); IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); IPR017892 (PFAM); PTHR24351 (PANTHER); PTHR24351:SF64 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000961 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1016	458135_length_991_cvg_72.9_tip_1_3	247454	prostasin- partial	331	7.65E-47	55.70%	0.132	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1017	458187_length_992_cvg_63.0_tip_0_0	596	14-3-3 partial	331	2.98E-28	100.00%	0.113	IPR023410 (PFAM); G3DSA:1.20.190.20 (GENE3D); IPR000308 (PANTHER); IPR023409 (PROSITE_PATTERNS); IPR023410 (SUPERFAMILY)
1018	458195_length_992_cvg_68.2_tip_1_1	2323	probable chitinase 3	331	1.66E-72	53.40%	0.098	IPR011583 (SMART); IPR002557 (SMART); IPR001223 (PFAM); IPR002557 (G3DSA:2.170.140.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); IPR002557 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR029070 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR002557 (SUPERFAMILY)
1019	458399_length_994_cvg_16.1_tip_1_2	74	lysosomal acid phosphatase	331	2.34E-86	67.10%	0.099	IPR029033 (G3DSA:3.40.50.GENE3D); IPR000560 (PFAM); PTHR11567:SF26 (PANTHER); PTHR11567 (PANTHER); IPR000560 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029033 (SUPERFAMILY)
1020	458575_length_995_cvg_9.3_tip_1_5	46	tolloid-like protein 2 isoform x1	331	3.03E-160	74.70%	0.106	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF557 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
1021	458817_length_998_cvg_3.2_tip_1_2	15	histone h2a	332	4.40E-78	99.80%	0.131	IPR002119 (PRINTS); IPR002119 (SMART); IPR007125 (PFAM); IPR009072 (G3DSA:1.10.20.GENE3D); PTHR23430:SF45 (PANTHER); PTHR23430 (PANTHER); IPR002119 (PROSITE_PATTERNS); IPR009072 (SUPERFAMILY)
1034	460605_length_1018_cvg_9.7_tip_1_0	46	a disintegrin and metalloproteinase with thrombospondin motifs 2	333	5.91E-15	48.80%	0.104	IPR002870 (PFAM); PTHR13723 (PANTHER)
1024	459545_length_1006_cvg_2.5_tip_1_4	14	af425264_1lysozyme precursor	335	5.60E-42	71.80%	0.421 Y	IPR001916 (PRINTS); IPR001916 (SMART); G3DSA:1.10.530.10 (GENE3D); IPR001916 (PFAM); PTHR11407:SF4 (PANTHER); PTHR11407 (PANTHER); IPR019799 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001916 (PROSITE_PROFILES); IPR023346 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1040	461805_length_1032_cvg_58.9_tip_1_2	317	alpha-aminoadipic semialdehyde dehydrogenase	335	7.06E-164	84.80%	0.117	IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699:SF144 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
1025	459615_length_1007_cvg_64.9_tip_1_0	761	torsin-1b-like isoform x1	336	2.01E-77	66.90%	0.253	IPR001270 (PRINTS); IPR010448 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR010448 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1026	459749_length_1008_cvg_3.5_tip_1_5	15	sortilin-related receptor-like	336	3.90E-52	55.30%	0.465 Y	IPR013783 (G3DSA:2.60.40.GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR003961 (SUPERFAMILY); TMhelix (TMHMM)
1027	459809_length_1009_cvg_37.2_tip_1_2	2816	alkaline serine protease	336	3.87E-20	66.80%	0.236	Coil (COILS); IPR007280 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1029	460111_length_1012_cvg_3.7_tip_1_4	18	hyaluronidase- partial	337	5.63E-57	61.50%	0.121	IPR018155 (PRINTS); IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PANTHER); PTHR11769:SF8 (PANTHER); IPR017853 (SUPERFAMILY)

1030	460119_length_1012_cvg_8.3_tip_1_1	38	prolow-density lipoprotein receptor-related protein 1-like	337	3.41E-31	54.70%	0.103	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1031	460391_length_1015_cvg_10.4_tip_1_4	48	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	338	2.59E-31	51.90%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24375:SF106 (PANTHER); PTHR24375 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
1032	460507_length_1017_cvg_37.0_tip_1_2	62	ensangp00000031746-like partial	339	8.20E-78	92.80%	0.232	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1033	460545_length_1017_cvg_65.4_tip_1_1	1025	---NA---	339			0.187	no IPS match
1062	464363_length_1063_cvg_54.0_tip_1_1	333	isoamyl acetate-hydrolyzing esterase 1 homolog	339	2.20E-73	65.70%	0.118	IPR013830 (G3DSA:3.40.50.GENE3D); IPR001087 (PFAM); PTHR14209 (PANTHER); IPR013830 (SUPERFAMILY)
1047	462625_length_1041_cvg_55.3_tip_1_3	339	beta-mannosidase	340	8.69E-70	60.20%	0.114	IPR013781 (G3DSA:3.20.20.GENE3D); IPR028369 (PTHR10066:PANTHER); PTHR10066 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006102 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR006102 (SUPERFAMILY)
1035	461089_length_1023_cvg_2.4_tip_1_4	15	dnaj homolog dnj-5	341	4.36E-132	71.60%	0.208	IPR001623 (PRINTS); IPR001623 (SMART); PF14901 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078:SF141 (PANTHER); PTHR24078 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1036	461141_length_1024_cvg_3.7_tip_1_5	21	aael001398- partial	341	2.90E-111	76.30%	0.156	Coil (COILS); IPR001849 (SMART); IPR001452 (SMART); IPR011993 (G3DSA:2.30.29.GENE3D); IPR001452 (PFAM); G3DSA:2.30.30.40 (GENE3D); PTHR12845 (PANTHER); PTHR12845:SF5 (PANTHER); IPR001849 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); SSF50729 (SUPERFAMILY); IPR001452 (SUPERFAMILY)
1037	461185_length_1025_cvg_21.3_tip_1_5	66	otogelin-like protein	341	6.30E-09	47.10%	0.099	no IPS match
1050	462795_length_1043_cvg_7.3_tip_1_4	42	dynein heavy chain axonemal	341	4.47E-11	60.80%	0.27	no IPS match
1039	461571_length_1029_cvg_7.6_tip_1_2	46	peptidyl-prolyl cis-trans isomerase h	343	5.42E-125	95.40%	0.111	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF58 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1041	462245_length_1037_cvg_5.6_tip_1_0	22	adamts-like protein 4 isoform x1	346	1.24E-22	56.70%	0.205	IPR000884 (SMART); IPR000884 (PFAM); G3DSA:2.20.100.10 (GENE3D); PTHR13723 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1042	462307_length_1038_cvg_50.6_tip_1_1	694	peptidyl-prolyl cis-trans isomerase-like 3	346	2.52E-96	91.00%	0.146	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)

1056	463949_length_1058_cvg_15.4_tip_1_3	53	fibroblast growth factor receptor partial	353	8.31E-16	67.40%	0.101	IPR013783 (G3DSA:2.60.40.GENE3D); IPR028174 (PTHR24416:PANTHER); PTHR24416 (PANTHER); SSF48726 (SUPERFAMILY)
1058	464049_length_1059_cvg_5.4_tip_1_5	24	tyrosine-protein phosphatase lar isoform x1	353	8.30E-28	74.50%	0.118	IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR19134 (PANTHER); PTHR19134:SF199 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1059	464191_length_1061_cvg_6.4_tip_1_3	34	aromatic hydrocarbon receptor	354	3.40E-13	62.50%	0.172	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1060	464303_length_1062_cvg_2.5_tip_1_3	13	zinc finger protein 235-like isoform x1	354	1.12E-31	61.20%	0.285	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1061	464335_length_1062_cvg_2.1_tip_1_5	17	xanthine dehydrogenase oxidase	354	1.95E-23	80.40%	0.623 Y	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); SignalP-noTM (SIGNALP_EUK); IPR008274 (SUPERFAMILY)
1080	466451_length_1089_cvg_68.9_tip_1_0	537	glycosyl-phosphatidylinositol-linked carbonic anhydrase	354	3.78E-85	63.40%	0.167	IPR001148 (SMART); IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); IPR023561 (PANTHER); IPR018338 (PROSITE_PATTERNS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
1063	464691_length_1067_cvg_19.6_tip_1_5	85	insulin-like growth factor-binding protein 7 precursor	355	6.42E-37	64.90%	0.162	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR011390 (PANTHER); PTHR14186:SF9 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1064	464757_length_1068_cvg_7.4_tip_1_2	39	5-hydroxyisourate hydrolase	356	1.90E-33	68.20%	0.1	IPR000895 (PRINTS); IPR023416 (SMART); IPR023416 (G3DSA:2.60.40.GENE3D); IPR023416 (PFAM); IPR014306 (TIGRFAM); PTHR10395:SF8 (PANTHER); PTHR10395 (PANTHER); IPR023418 (PROSITE_PATTERNS); IPR023416 (SUPERFAMILY)
1065	464981_length_1070_cvg_7.4_tip_1_5	40	zinc finger protein 699-like	356	8.56E-34	55.70%	0.106	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1089	467121_length_1098_cvg_12.2_tip_1_5	70	protein spaetzle	356	8.86E-28	51.90%	0.141	PTHR23199 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029034 (SUPERFAMILY); TMhelix (TMHMM)
1066	465025_length_1070_cvg_3.0_tip_1_3	15	otogelin	357	1.29E-14	44.40%	0.11	no IPS match
1067	465069_length_1071_cvg_62.7_tip_1_1	782	thioredoxin 1	357	4.84E-49	83.30%	0.254	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005746 (TIGRFAM); IPR013766 (PFAM); IPR005746 (PANTHER); IPR017937 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1068	465169_length_1072_cvg_107.3_tip_0_4	61379	proclotting enzyme-like	357	4.08E-50	55.20%	0.860 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1070	465191_length_1073_cvg_32.3_tip_1_3	153	peroxiredoxin partial	358	8.00E-116	83.50%	0.143	IPR000866 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); G3DSA:3.30.1020.10 (GENE3D); IPR019479 (PFAM); PTHR10681 (PANTHER); PTHR10681:SF77 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
1071	465395_length_1075_cvg_3.5_tip_1_1	17	galectin partial	358	8.14E-70	67.20%	0.099	IPR001079 (SMART); IPR001079 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001079 (PFAM); PTHR11346 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001079 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
1072	465495_length_1076_cvg_4.1_tip_1_5	25	scp-like extracellular domain containing protein 1	358	1.92E-47	52.30%	0.574 Y	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR002172 (SMART); IPR014044 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1073	465689_length_1079_cvg_7.3_tip_1_0	36	transposase	360	1.12E-42	57.50%	0.205	no IPS match
1074	465743_length_1079_cvg_53.0_tip_1_3	383	peptidoglycan recognition protein 3 short class	360	4.51E-58	65.10%	0.810 Y	IPR002502 (SMART); IPR006619 (SMART); IPR002502 (G3DSA:3.40.80.GENE3D); IPR002502 (PFAM); IPR015510 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR002502 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1075	465757_length_1080_cvg_6.3_tip_1_0	29	beta-mannosidase	360	7.42E-130	69.90%	0.121	IPR013781 (G3DSA:3.20.20.GENE3D); IPR006103 (PFAM); IPR013812 (G3DSA:2.60.40.GENE3D); PTHR10066 (PANTHER); IPR028369 (PTHR10066:PANTHER); IPR017853 (SUPERFAMILY); IPR006102 (SUPERFAMILY)
1117	469523_length_1132_cvg_61.6_tip_1_1	3070	eukaryotic translation initiation factor 3 subunit i-like	360	0	84.20%	0.173	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19877 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR027525 (HAMAP); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1076	465869_length_1081_cvg_3.6_tip_1_0	20	xanthine dehydrogenase partial	361	2.63E-180	81.50%	0.145	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR008274 (SUPERFAMILY)
1077	465995_length_1083_cvg_9.0_tip_1_1	30	syntaxin-16 isoform x4	361	1.40E-104	70.80%	0.155	IPR000727 (SMART); IPR006011 (PFAM); G3DSA:1.20.58.70 (GENE3D); IPR000727 (PFAM); PTHR19957:SF83 (PANTHER); PTHR19957 (PANTHER); IPR006012 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000727 (PROSITE_PROFILES); IPR010989 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1078	466097_length_1084_cvg_3.1_tip_1_5	14	clip-domain serine family d	361	1.02E-08	75.60%	0.12	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24264:SF9 (PANTHER); PTHR24264 (PANTHER); IPR009003 (SUPERFAMILY)
1105	468399_length_1115_cvg_68.0_tip_1_5	673	scp-like extracellular domain containing protein 2	361	1.97E-06	65.25%	0.789 Y	IPR002413 (PRINTS); IPR014044 (G3DSA:3.40.33.GENE3D); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK)

1079	466227_length_1086_cvg_8.2_tip_1_5	41	venom serine carboxypeptidase-like	362	1.32E-12	65.30%	0.119	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); IPR001563 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1081	466557_length_1090_cvg_4.1_tip_1_1	24	chondroitin sulfate synthase 1	363	2.88E-111	64.50%	0.101	IPR029044 (G3DSA:3.90.550.GENE3D); IPR008428 (PFAM); PTHR12369 (PANTHER); PTHR12369:SF11 (PANTHER); IPR029044 (SUPERFAMILY)
1102	468229_length_1113_cvg_3.2_tip_1_4	16	zinc finger protein 239- partial	364	1.18E-49	57.20%	0.13	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1082	466729_length_1093_cvg_2.0_tip_1_0	14	tissue factor pathway inhibitor	365	1.88E-55	50.10%	0.794 Y	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
1083	466769_length_1094_cvg_99.5_tip_1_0	213697	isoform a	365	2.63E-44	53.50%	0.776 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1084	466899_length_1095_cvg_6.2_tip_1_3	27	neuronal cell adhesion	365	1.34E-111	70.20%	0.138	PR00014 (PRINTS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489:SF553 (PANTHER); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
1085	466909_length_1095_cvg_2.0_tip_1_3	14	u4 u6 small nuclear ribonucleoprotein prp4	365	0	84.20%	0.122	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR027106 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1086	466923_length_1096_cvg_58.6_tip_1_2	355	aldose reductase-like	365	4.20E-137	77.50%	0.101	IPR020471 (PRINTS); IPR023210 (G3DSA:3.20.20.GENE3D); IPR023210 (PFAM); IPR001395 (PANTHER); PTHR11732:SF202 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
1087	466951_length_1096_cvg_3.3_tip_1_1	22	5 -nucleotidase	365	1.04E-125	70.80%	0.106	IPR008334 (PFAM); IPR008334 (G3DSA:3.90.780.GENE3D); IPR006179 (PANTHER); PTHR11575:SF7 (PANTHER); IPR008334 (SUPERFAMILY)
1088	467011_length_1097_cvg_4.5_tip_1_1	26	ves g 5 allergen	366	1.01E-46	53.20%	0.104	IPR001283 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR014044 (SUPERFAMILY)

1098	468075_length_1111_cvg_5.0_tip_1_4	30	adp-ribosylation factor-like protein 3	370	1.32E-109	93.90%	0.227	IPR006689 (PRINTS); IPR024156 (SMART); IPR003579 (SMART); IPR006687 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF124 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1100	468141_length_1112_cvg_8.4_tip_1_5	37	gastrula zinc finger	370	7.04E-31	57.40%	0.109	IPR015880 (SMART); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
1099	468097_length_1111_cvg_3.4_tip_1_0	21	ankyrin repeat domain-containing protein 5-like	371	2.04E-18	47.80%	0.1	PTHR23022:SF64 (PANTHER); PTHR23022 (PANTHER)
1101	468191_length_1112_cvg_76.6_tip_1_3	4330	glyceraldehyde 3-phosphate dehydrogenase	371	1.36E-11	90.90%	0.128	IPR020831 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1103	468245_length_1113_cvg_2.7_tip_1_1	17	metallophosphoesterase domain-containing protein 1	371	1.59E-116	81.20%	0.107	IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR12905 (PANTHER); IPR029052 (SUPERFAMILY)
1124	469853_length_1137_cvg_10.9_tip_1_4	72	chitinase partial	371	1.46E-66	67.10%	0.144	IPR002557 (SMART); IPR029070 (G3DSA:3.10.50.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002557 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR029070 (SUPERFAMILY)
1104	468297_length_1114_cvg_2.7_tip_1_0	12	upf0364 protein c6orf211 homolog	372	9.35E-96	60.50%	0.101	Coil (COILS); IPR002791 (PFAM); PTHR12260:SF1 (PANTHER); PTHR12260 (PANTHER); IPR002791 (SUPERFAMILY)
1106	468431_length_1115_cvg_6.3_tip_1_1	36	preproneuropeptide f i	372	1.58E-17	63.75%	0.142	IPR020392 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001955 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1107	468461_length_1116_cvg_3.8_tip_1_2	24	cysteine-rich with egf-like domain protein 2	372	3.58E-48	67.30%	0.112	IPR006212 (SMART); PTHR24838:SF13 (PANTHER); PTHR24838 (PANTHER); IPR018097 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009030 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1109	468545_length_1117_cvg_25.3_tip_1_1	109	thioredoxin 2	372	2.69E-34	70.70%	0.14	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10438:SF235 (PANTHER); IPR005746 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
1133	470195_length_1143_cvg_20.4_tip_1_0	127	dehydrogenase reductase sdr family member 11-like	372	1.90E-42	73.30%	0.109	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1146	471119_length_1158_cvg_69.2_tip_1_2	1338	guanine nucleotide-binding protein subunit beta-like protein	372	0	93.20%	0.136	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19868:SF0 (PANTHER); PTHR19868 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)

1108	468519_length_1117_cvg_12.9_tip_1_0	66	zinc finger protein	373	1.24E-35	56.90%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
1110	468657_length_1118_cvg_4.0_tip_1_4	21	zinc finger protein 420-like	373	1.80E-37	61.10%	0.098	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1119	469579_length_1133_cvg_22.4_tip_1_4	109	e3 ubiquitin-protein ligase rnf185-like isoform x2	373	1.31E-86	81.00%	0.1	IPR001841 (SMART); PF13923 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); PTHR12313:SF3 (PANTHER); PTHR12313 (PANTHER); IPR017907 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001841 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1156	471717_length_1167_cvg_82.4_tip_1_4	24389	venom allergen 3-like	373	5.77E-45	50.10%	0.174	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM)
1111	469029_length_1124_cvg_73.7_tip_1_2	2389	gamma-glutamyl hydrolase	374	3.14E-30	68.00%	0.1	IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY)
1151	471559_length_1164_cvg_6.2_tip_1_1	39	dentin matrix protein 4-like	374	0	85.00%	0.099	IPR009581 (PFAM); IPR024869 (PANTHER); PTHR12450:SF8 (PANTHER) PR00421 (PRINTS); IPR005788 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PF13848 (PFAM); IPR013766 (PFAM); PTHR18929:SF60 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1112	469049_length_1124_cvg_63.0_tip_0_3	4759	protein disulfide-isomerase a3	375	1.13E-113	82.50%	0.119	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929:SF81 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1127	469959_length_1138_cvg_12.7_tip_1_0	78	thioredoxin-related transmembrane protein 1	375	7.31E-102	71.20%	0.462 Y	IPR001079 (SMART); IPR001079 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001079 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR11346 (PANTHER); IPR001079 (PROSITE_PROFILES); IPR001079 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1113	469171_length_1126_cvg_95.8_tip_1_0	9527	low quality protein: galectin-4	376	5.64E-51	50.50%	0.410 Y	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); IPR000718 (PANTHER); PTHR11733:SF113 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1114	469195_length_1127_cvg_4.8_tip_1_1	25	membrane metallo-endopeptidase-like 1-like	376	1.01E-91	84.90%	0.148	

1165	472193_length_1174_cvg_60.5_tip_1_2	602	mitochondrial acyl carrier protein 1 isoform b	376	1.40E-42	85.30%	0.115	IPR009081 (PFAM); IPR009081 (G3DSA:1.10.1200.GENE3D); PTHR20863 (PANTHER); PTHR20863:SF5 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003231 (PRODOM); IPR003231 (HAMAP); IPR009081 (PROSITE_PROFILES); IPR009081 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1116	469515_length_1132_cvg_4.5_tip_1_1	30	zinc finger protein	377	2.12E-57	66.20%	0.177	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1149	471387_length_1162_cvg_66.7_tip_1_2	2739	thioredoxin peroxidase	377	1.67E-118	88.20%	0.107	IPR012336 (G3DSA:3.40.30.GENE3D); IPR019479 (PFAM); IPR000866 (PFAM); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1118	469563_length_1133_cvg_5.5_tip_1_3	29	heat shock 70 kda protein 14	378	1.80E-105	61.60%	0.163	IPR013126 (PRINTS); IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.90.640.10 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF158 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY)
1120	469627_length_1133_cvg_4.0_tip_1_1	26	fasciclin-3 isoform x2	378	7.93E-29	46.00%	0.241	IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013162 (PFAM); PTHR11640 (PANTHER); PTHR11640:SF52 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1145	471109_length_1158_cvg_52.1_tip_1_5	305	pacifastin light chain	378	3.33E-16	51.40%	0.102	IPR008037 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1121	469707_length_1135_cvg_7.6_tip_1_0	53	transcription initiation factor tfiid subunit 5	379	1.35E-126	84.70%	0.303	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19879 (PANTHER); PTHR19879:SF1 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1122	469837_length_1137_cvg_6.4_tip_1_1	49	kettin protein	379	8.76E-167	75.20%	0.104	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF149 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)

1134	470201_length_1143_cvg_64.3_tip_1_1	3385	ion transport peptide isoform x2	381	1.74E-30	77.70%	0.106	IPR000346 (PRINTS); IPR001166 (PRINTS); IPR001166 (G3DSA:1.10.2010.GENE3D); IPR001166 (PFAM); IPR018251 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR001166 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1135	470241_length_1143_cvg_4.7_tip_1_3	18	multiple pdz domain	381	3.47E-110	75.80%	0.113	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964 (PANTHER); PTHR19964:SF34 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
1136	470241_length_1143_cvg_4.7_tip_1_5	18	multiple pdz domain	381	4.62E-31	91.70%	0.182	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR19964 (PANTHER); PTHR19964:SF10 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
1155	471657_length_1166_cvg_8.8_tip_1_3	54	basement membrane-specific heparan sulfate proteoglycan core isoform x4	381	1.10E-86	77.00%	0.14	IPR013106 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013106 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR23279 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1157	471857_length_1169_cvg_64.4_tip_1_0	651	histone -like	381	2.50E-80	99.20%	0.174	IPR002119 (PRINTS); IPR002119 (SMART); IPR007125 (PFAM); IPR009072 (G3DSA:1.10.20.GENE3D); PTHR23430:SF34 (PANTHER); PTHR23430 (PANTHER); IPR002119 (PROSITE_PATTERNS); IPR009072 (SUPERFAMILY)
1137	470347_length_1145_cvg_9.5_tip_1_0	42	dnaj homolog subfamily c member 30-like	382	1.10E-26	51.20%	0.123	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF171 (PANTHER); IPR018253 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1166	472231_length_1175_cvg_23.1_tip_1_0	141	i-type lysozyme	382	1.86E-35	64.50%	0.117	IPR008597 (PFAM); IPR008597 (PANTHER); IPR018247 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1138	470457_length_1147_cvg_6.5_tip_1_3	26	zinc c2h2 type domain-containing protein	383	6.69E-19	57.90%	0.101	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1139	470533_length_1148_cvg_4.8_tip_1_1	25	zinc finger protein 585a-like isoform x1	383	5.02E-23	48.90%	0.098	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1140	470587_length_1149_cvg_62.8_tip_0_1	725	prolyl 3-hydroxylase 1-like isoform x2	383	1.14E-112	68.80%	0.098	IPR011990 (G3DSA:1.25.40.GENE3D); PTHR13986 (PANTHER); PTHR13986:SF8 (PANTHER)
1141	470639_length_1150_cvg_61.9_tip_1_4	528	nucleoporin seh1 isoform x2	383	0	85.20%	0.339	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR11024:SF3 (PANTHER); PTHR11024 (PANTHER); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)

1142	470717_length_1151_cvg_3.0_tip_1_4	15	leucine rich repeat protein	384	1.51E-25	54.80%	0.274	PR00019 (PRINTS); SM00365 (SMART); IPR003591 (SMART); SM00364 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
1163	472107_length_1173_cvg_50.8_tip_1_5	357	leucine-rich repeat-containing protein 57	384	7.97E-93	75.70%	0.116	PR00019 (PRINTS); IPR003591 (SMART); IPR025875 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
1143	470847_length_1154_cvg_3.5_tip_1_0	20	vacuolar protein sorting-associated protein 4a-like	385	0	89.30%	0.121	IPR007330 (SMART); IPR003593 (SMART); IPR007330 (G3DSA:1.20.58.GENE3D); IPR003959 (PFAM); G3DSA:1.10.8.60 (GENE3D); IPR007330 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23074 (PANTHER); PTHR23074:Sf72 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR007330 (SUPERFAMILY); IPR027417 (SUPERFAMILY)
1144	471095_length_1158_cvg_7.2_tip_1_5	36	von willebrand factor like 2	386	4.31E-09	42.20%	0.107	no IPS match
1147	471201_length_1159_cvg_8.3_tip_1_1	39	trypsin-like serine proteinase 2	386	1.88E-61	56.70%	0.824 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALLP_EUK); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1148	471203_length_1159_cvg_24.0_tip_1_2	139	wd repeat domain-containing protein 83	386	4.26E-100	78.70%	0.139	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22842 (PANTHER); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1162	472025_length_1172_cvg_67.6_tip_1_3	557	glutaminyl-peptide cyclotransferase-like	387	2.60E-116	68.90%	0.645 Y	G3DSA:3.40.630.10 (GENE3D); IPR007484 (PFAM); PTHR12283 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALLP_EUK); SSF53187 (SUPERFAMILY)
1150	471555_length_1164_cvg_4.6_tip_1_0	33	sphingomyelin phosphodiesterase	388	7.06E-101	65.60%	0.261	IPR008139 (SMART); IPR011001 (G3DSA:1.10.225.GENE3D); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR10340:Sf13 (PANTHER); PTHR10340 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008139 (PROSITE_PROFILES); IPR011001 (SUPERFAMILY); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
1153	471609_length_1165_cvg_3.6_tip_1_2	16	partial	388	1.29E-146	99.50%	0.101	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342 (PANTHER); PTHR10342:Sf22 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)
1154	471641_length_1166_cvg_3.0_tip_1_2	22	hyaluronidase precursor	388	9.01E-83	59.90%	0.108	Coil (COILS); IPR001329 (PRINTS); IPR018155 (PRINTS); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); PTHR11769:Sf8 (PANTHER); IPR018155 (PANTHER); IPR017853 (SUPERFAMILY)
1152	471607_length_1165_cvg_58.7_tip_1_0	516	tropinone reductase 2-like	389	2.77E-122	76.40%	0.103	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR013968 (SMART); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:Sf111 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY)
1158	471887_length_1170_cvg_13.1_tip_1_0	57	alpha-mannosidase partial	390	3.00E-156	72.90%	0.109	G3DSA:2.70.98.30 (GENE3D); IPR011682 (PFAM); PTHR11607:Sf22 (PANTHER); PTHR11607 (PANTHER); IPR011013 (SUPERFAMILY)

1159	471903_length_1170_cvg_13.8_tip_1_3	59	fk506-binding protein 2	390	3.52E-66	84.70%	0.247	G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); PTHR10516:SF134 (PANTHER); IPR023566 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1160	471913_length_1170_cvg_5.8_tip_1_1	32	dipeptidyl peptidase 9	390	0	82.30%	0.126	IPR002469 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001375 (PFAM); IPR002469 (G3DSA:2.140.10.GENE3D); PTHR11731 (PANTHER); PTHR11731:SF110 (PANTHER); IPR029058 (SUPERFAMILY); SSF82171 (SUPERFAMILY)
1161	472003_length_1172_cvg_23.2_tip_1_3	72	sparc	391	1.62E-115	77.40%	0.206	Coil (COILS); Coil (COILS); IPR003645 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR019577 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR13866:SF14 (PANTHER); PTHR13866 (PANTHER); IPR001999 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF47473 (SUPERFAMILY); SSF100895 (SUPERFAMILY); TMhelix (TMHMM)
1164	472175_length_1174_cvg_4.6_tip_0_1	25	zinc finger protein 2 homolog	391	3.69E-143	63.60%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1167	472299_length_1176_cvg_12.0_tip_1_3	68	calbindin- partial	392	1.90E-56	82.50%	0.142	IPR002048 (SMART); IPR011992 (G3DSA:1.10.238.GENE3D); IPR002048 (PFAM); IPR014710 (G3DSA:2.60.120.GENE3D); PTHR19972 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); TMhelix (TMHMM)
1168	472397_length_1178_cvg_10.0_tip_1_0	27	fas1_scham ame: full=fasciclin-1 ame: full=fasciclin i short=fas i short=fcn flags: precursor	393	5.52E-104	63.60%	0.105	IPR000782 (SMART); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900 (PANTHER); PTHR10900:SF73 (PANTHER); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY)
1169	472399_length_1178_cvg_63.8_tip_1_0	750127	serine protease 27-like	393	4.81E-42	55.00%	0.484 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1170	472427_length_1179_cvg_50.4_tip_1_4	321	meprin a subunit beta	393	3.44E-51	58.50%	0.196	IPR001506 (PRINTS); IPR006026 (SMART); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1171	472541_length_1181_cvg_3.0_tip_1_2	18	plasma alpha-l-fucosidase	393	7.44E-63	81.40%	0.768 Y	IPR016286 (PRINTS); IPR000933 (SMART); IPR000933 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR000933 (PANTHER); PTHR10030:SF26 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-TM (SIGNALP_EUK); IPR017853 (SUPERFAMILY)

1180	473371_length_1195_cvg_14.7_tip_1_5	79	low quality protein: agrin	398	8.47E-40	52.10%	0.400 Y	IPR002350 (SMART); G3DSA:2.40.50.120 (GENE3D); IPR004850 (PFAM); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); PTHR10913 (PANTHER); PTHR10913:SF45 (PANTHER); IPR002350 (PROSITE_PROFILES); IPR004850 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); IPR008993 (SUPERFAMILY); TMhelix (TMHMM)
1181	473465_length_1197_cvg_8.2_tip_1_5	53	endonuclease mitochondrial	399	9.97E-127	84.00%	0.156	IPR020821 (SMART); IPR001604 (SMART); IPR020821 (G3DSA:3.40.570.GENE3D); IPR001604 (PFAM); PTHR13966 (PANTHER); IPR018524 (PROSITE_PATTERNS); SSF54060 (SUPERFAMILY)
1182	473507_length_1198_cvg_57.2_tip_1_3	584	neuferricin -like protein	400	3.09E-81	67.30%	0.326	IPR001199 (PFAM); IPR001199 (G3DSA:3.10.120.GENE3D); PTHR10281:SF4 (PANTHER); PTHR10281 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001199 (SUPERFAMILY)
1183	473565_length_1199_cvg_5.7_tip_1_3	24	alpha- -mannosyl-glycoprotein 4-beta-n-acetylglucosaminyltransferase partial	400	6.77E-41	55.30%	0.164	IPR006759 (PFAM); PTHR12062:SF5 (PANTHER); IPR006759 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1184	473571_length_1199_cvg_63.0_tip_1_0	15319	calreticulin	400	0	83.70%	0.323	Coil (COILS); IPR001580 (PRINTS); IPR009169 (PIRSF); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001580 (PFAM); PTHR11073:SF8 (PANTHER); IPR001580 (PANTHER); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009033 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
1185	473741_length_1202_cvg_3.1_tip_1_5	19	early growth response	400	4.58E-83	70.40%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223:SF80 (PANTHER); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1186	473803_length_1203_cvg_85.9_tip_1_0	98515	transmembrane protease serine 4	401	1.78E-41	52.40%	0.496 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1187	473853_length_1205_cvg_4.7_tip_1_2	27	melanopsin-like isoform x1	401	1.04E-74	60.00%	0.106	IPR000276 (PRINTS); IPR000276 (PFAM); G3DSA:1.20.1070.10 (GENE3D); PTHR24242:SF154 (PANTHER); PTHR24242 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017452 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1188	473919_length_1206_cvg_6.4_tip_1_0	32	nardilysin-like isoform x2	402	5.11E-98	66.10%	0.15	IPR011237 (G3DSA:3.30.830.GENE3D); IPR007863 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); PTHR11851 (PANTHER); PTHR11851:SF108 (PANTHER); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY)
1189	473961_length_1206_cvg_6.6_tip_1_1	49	endoplasmic reticulum resident protein 44 isoform x2	402	0	81.40%	0.154	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PF13848 (PFAM); PTHR18929 (PANTHER); PTHR18929:SF49 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1190	473987_length_1207_cvg_7.3_tip_1_4	38	transcription termination factor rho	402	3.22E-09	62.90%	0.108	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)

1214	475455_length_1236_cvg_8.2_tip_1_4	49	ras-related protein rab-4b	403	5.25E-135	94.30%	0.236	IPR001806 (PRINTS); IPR003579 (SMART); IPR024156 (SMART); IPR003578 (SMART); IPR020849 (SMART); IPR002041 (SMART); IPR001806 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR24073 (PANTHER); PTHR24073:SF387 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1191	474127_length_1210_cvg_90.4_tip_1_0	414780	suppressor of tumorigenicity 14 protein homolog	404	4.56E-43	50.50%	0.316	IPR001314 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1193	474273_length_1212_cvg_15.5_tip_1_4	61	39s ribosomal protein mitochondrial	404	2.93E-101	70.30%	0.312	IPR008914 (G3DSA:3.90.280.GENE3D); IPR008914 (PFAM); PTHR11362:SF16 (PANTHER); PTHR11362 (PANTHER); IPR008914 (SUPERFAMILY)
1207	475245_length_1231_cvg_16.6_tip_1_3	70	dehydrogenase reductase sdr family member 7	404	7.23E-109	67.50%	0.141	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF31 (PANTHER); PTHR24322 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1195	474493_length_1217_cvg_3.4_tip_1_2	29	krueppel-like factor 13	405	1.46E-50	84.30%	0.247	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1200	474927_length_1225_cvg_62.8_tip_1_1	1386	glutaredoxin- partial	405	3.20E-143	78.20%	0.238	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR002109 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR004480 (TIGRFAM); PTHR10293:SF40 (PANTHER); IPR004480 (PANTHER); IPR002109 (PROSITE_PROFILES); IPR002109 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1196	474739_length_1222_cvg_3.4_tip_1_1	18	zinc finger protein 239-like	407	2.55E-29	47.40%	0.109	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1197	474779_length_1223_cvg_12.2_tip_1_5	55	uv radiation resistance-associated gene protein	407	9.09E-40	66.40%	0.097	Coil (COILS); PTHR15157 (PANTHER)
1198	474875_length_1224_cvg_4.7_tip_1_0	30	von willebrand factor type egf and pentraxin domain-containing protein 1-like	408	4.39E-13	46.40%	0.101	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1199	474897_length_1225_cvg_54.7_tip_1_1	591	histone 1o	408	2.21E-29	71.80%	0.119	IPR005819 (PRINTS); IPR005818 (SMART); IPR005818 (PFAM); IPR011991 (G3DSA:1.10.10.GENE3D); PTHR11467 (PANTHER); IPR005818 (PROSITE_PROFILES); SSF46785 (SUPERFAMILY)
1201	474959_length_1226_cvg_3.4_tip_1_4	18	dnaj homolog subfamily b member 9	409	1.42E-61	56.10%	0.186	Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24077 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)

1202	475091_length_1228_cvg_6.8_tip_0_4	39	coagulation factor xi	409	1.68E-64	61.90%	0.124	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1203	475119_length_1229_cvg_18.4_tip_1_1	94	ankyrin repeat family a protein 2	410	8.32E-73	67.70%	0.204	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); PTHR24124 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1204	475165_length_1230_cvg_4.4_tip_1_2	32	fukutin-related partial	410	1.20E-26	72.00%	0.286	IPR007074 (PFAM); PTHR13627 (PANTHER); PTHR13627:SF25 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1205	475171_length_1230_cvg_12.1_tip_1_5	66	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	410	1.02E-37	54.20%	0.131	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24375 (PANTHER); PTHR24375:SF106 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1206	475175_length_1230_cvg_65.9_tip_1_3	1197	hemagglutinin	410	6.36E-93	67.80%	0.114	IPR023612 (PRINTS); G3DSA:1.10.390.10 (GENE3D); IPR013856 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); IPR001570 (PFAM); IPR007280 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1222	475901_length_1245_cvg_19.6_tip_1_2	117	ankyrin repeat domain-containing protein 16-like	410	2.31E-112	63.60%	0.104	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24181:SF20 (PANTHER); PTHR24181 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1209	475349_length_1233_cvg_35.6_tip_1_4	154	ligand of numb protein x 2	411	2.40E-55	69.10%	0.166	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1238	477460_length_1278_cvg_91.2_tip_1_1	6691	transmembrane protease serine 6 isoform x2	418	1.57E-40	53.40%	0.155	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1231	476467_length_1256_cvg_8.8_tip_1_0	40	hemocytin	419	3.55E-38	46.60%	0.102	IPR001846 (PFAM); IPR014853 (PFAM); IPR001846 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY)
1232	476524_length_1258_cvg_6.5_tip_1_3	47	phosphatidylinositol -trisphosphate 3-phosphatase and dual-specificity protein phosphatase pten isoform x4	420	8.25E-123	70.90%	0.118	IPR003595 (SMART); G3DSA:2.60.40.1110 (GENE3D); IPR000340 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR014020 (PFAM); PTHR12305 (PANTHER); IPR016130 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029023 (PROSITE_PROFILES); IPR014020 (PROSITE_PROFILES); IPR000008 (SUPERFAMILY); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)
1233	476786_length_1263_cvg_16.3_tip_1_4	81	zinc finger protein 300-like isoform x1	421	1.65E-18	60.60%	0.13	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR026590 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1242	477978_length_1290_cvg_12.6_tip_1_0	87	adenosine deaminase-like protein	422	1.49E-108	69.70%	0.097	G3DSA:3.20.20.140 (GENE3D); IPR001365 (PFAM); PTHR11409:SF21 (PANTHER); PTHR11409 (PANTHER); SSF51556 (SUPERFAMILY)
1234	477142_length_1271_cvg_12.3_tip_1_4	64	p38 mitogen-activated protein kinase	424	1.09E-127	90.00%	0.108	Coil (COILS); IPR008352 (PRINTS); IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24055:SF110 (PANTHER); PTHR24055 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1235	477200_length_1272_cvg_3.1_tip_1_1	23	prolyl 3-hydroxylase 2-like isoform x1	424	3.30E-105	68.90%	0.103	Coil (COILS); IPR006620 (SMART); IPR005123 (PFAM); PTHR14049 (PANTHER); PTHR14049:SF9 (PANTHER); IPR005123 (PROSITE_PROFILES)
1236	477370_length_1276_cvg_5.7_tip_1_3	24	agap000560-pa-like protein	426	0	74.50%	0.13	IPR003593 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); PTHR23076:SF47 (PANTHER); PTHR23076 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1237	477392_length_1277_cvg_2.3_tip_1_4	18	-like protein subfamily c member 11	426	0	81.50%	0.102	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078:SF159 (PANTHER); PTHR24078 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1239	477520_length_1279_cvg_2.0_tip_1_2	13	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	426	3.97E-41	54.70%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1240	477702_length_1284_cvg_4.6_tip_1_4	22	neuroglian-like isoform 2	428	0	80.00%	0.108	IPR003598 (SMART); IPR003599 (SMART); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489:SF553 (PANTHER); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1254	478894_length_1312_cvg_35.7_tip_1_0	196	gamma-glutamyl hydrolase	428	7.53E-100	65.80%	0.546 Y	IPR011697 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR029062 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1252	478752_length_1309_cvg_2.4_tip_1_2	19	cytochrome p450 cyp44	436	6.34E-145	65.30%	0.099	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24291:SF1 (PANTHER); PTHR24291 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
1271	479790_length_1333_cvg_59.8_tip_1_3	588	huga_polan ame: full=hyaluronidase short=hya ame: full=hyaluronoglucosaminidase ame: allergen=pol a 2 flags: partial	436	8.44E-72	57.00%	0.262	IPR001329 (PRINTS); IPR018155 (PRINTS); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); PTHR11769:SF8 (PANTHER); IPR018155 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1253	478810_length_1310_cvg_2.9_tip_1_1	25	---NA---	437			0.173	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1265	479538_length_1326_cvg_63.3_tip_1_4	5958	ferritin	437	2.13E-83	84.70%	0.275	Coil (COILS); IPR008331 (PFAM); IPR012347 (G3DSA:1.20.1260.GENE3D); IPR001519 (PANTHER); IPR014034 (PROSITE_PATTERNS); IPR014034 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1267	479624_length_1328_cvg_5.4_tip_1_4	39	zinc finger protein 571- partial	437	4.98E-30	52.30%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1276	480012_length_1338_cvg_5.6_tip_1_0	36	guanine nucleotide-binding protein subunit beta-5	438	2.20E-90	92.80%	0.127	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR016346 (PANTHER); PTHR19850:SF12 (PANTHER); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
1255	479036_length_1316_cvg_5.8_tip_1_1	47	prophenol oxidase activating enzyme precursor	439	3.37E-48	52.10%	0.156	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR022700 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF54 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1257	479090_length_1317_cvg_6.3_tip_1_2	41	glucose dehydrogenase	439	1.01E-39	81.10%	0.127	G3DSA:3.30.560.10 (GENE3D); IPR007867 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR11552:SF68 (PANTHER); PTHR11552 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY)
1258	479118_length_1317_cvg_4.6_tip_1_5	28	cyclin-c	439	9.44E-166	90.90%	0.118	IPR013763 (SMART); IPR006671 (PFAM); IPR013763 (G3DSA:1.10.472.GENE3D); IPR015429 (PANTHER); IPR013763 (SUPERFAMILY); IPR013763 (SUPERFAMILY)
1259	479134_length_1317_cvg_59.0_tip_1_2	430	epoxide hydrolase 4	439	6.69E-104	62.00%	0.099	IPR000073 (PRINTS); IPR000639 (PRINTS); IPR000073 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR10992:SF721 (PANTHER); PTHR10992 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1260	479224_length_1319_cvg_6.7_tip_1_5	26	otogelin-like protein	439	2.04E-15	45.30%	0.102	no IPS match

[illegible]

1279	480236_length_1344_cvg_3.9_tip_1_1	30	threonine synthase-like 2	448	3.96E-108	72.50%	0.141	G3DSA:3.40.50.1100 (GENE3D); IPR029144 (G3DSA:3.90.1380.GENE3D); IPR029144 (PFAM); PTHR10314 (PANTHER); IPR027457 (PTHR10314:PANTHER); IPR001926 (SUPERFAMILY)
1280	480238_length_1344_cvg_54.3_tip_1_4	452	superoxide dismutase	448	2.39E-43	66.30%	0.147	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY)
1281	480276_length_1346_cvg_4.7_tip_1_5	38	gpi-anchor transamidase	448	1.88E-106	75.40%	0.106	IPR001096 (PRINTS); IPR001096 (PFAM); IPR001096 (PANTHER); IPR028361 (PTHR12000:PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1282	480454_length_1352_cvg_5.4_tip_1_1	36	leukocyte elastase inhibitor a-like	451	5.64E-49	56.60%	0.128	IPR023796 (SMART); IPR023796 (PFAM); G3DSA:3.30.497.10 (GENE3D); IPR000215 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023796 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1283	480460_length_1352_cvg_2.0_tip_1_1	16	early growth response	451	3.99E-114	57.00%	0.103	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR10042 (PANTHER); PTHR10042:SF24 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1286	480662_length_1357_cvg_6.8_tip_1_4	52	cleavage stimulation factor subunit 1-like	452	0	85.70%	0.138	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22840 (PANTHER); PTHR22840:SF8 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1287	480764_length_1359_cvg_6.4_tip_1_1	46	activated cdc42 kinase 1 isoform x2	453	0	79.70%	0.229	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); G3DSA:2.30.30.40 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR030220 (PTHR24418:PANTHER); PTHR24418 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1288	480844_length_1362_cvg_62.0_tip_1_2	395	cyclin-g-associated kinase-like	454	9.20E-155	78.50%	0.172	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR23172:SF19 (PANTHER); PTHR23172 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1290	480888_length_1363_cvg_55.7_tip_1_1	663	cathepsin I	454	0	80.90%	0.139	IPR000668 (PRINTS); IPR000668 (SMART); IPR013201 (SMART); IPR000668 (PFAM); IPR013201 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR013128 (PANTHER); PTHR12411:SF57 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
1289	480874_length_1363_cvg_8.3_tip_1_0	66	lysyl-trna synthetase	455	0	85.80%	0.11	Coil (COILS); IPR018149 (PRINTS); IPR004364 (PFAM); IPR004365 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); IPR002313 (TIGRFAM); G3DSA:3.30.930.10 (GENE3D); IPR018150 (PANTHER); PTHR22594:SF4 (PANTHER); IPR006195 (PROSITE_PROFILES); IPR012340 (SUPERFAMILY); SSF55681 (SUPERFAMILY)
1291	480944_length_1365_cvg_78.9_tip_1_2	134111	carboxypeptidase b-like	455	6.11E-127	62.40%	0.395	IPR000834 (PRINTS); IPR000834 (SMART); IPR000834 (PFAM); IPR003146 (PFAM); G3DSA:3.40.630.10 (GENE3D); IPR003146 (G3DSA:3.30.70.GENE3D); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY); IPR009020 (SUPERFAMILY)

1292	480978_length_1366_cvg_5.6_tip_1_5	33	alk tyrosine kinase receptor isoform x1	455	9.06E-112	58.40%	0.124	IPR002172 (SMART); IPR000998 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PFAM); IPR002172 (PFAM); PTHR23282 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1306	481774_length_1390_cvg_10.9_tip_1_0	63	gamma-interferon-inducible lysosomal thiol reductase	455	4.09E-48	57.80%	0.251	IPR004911 (PFAM); PTHR13234:SF8 (PANTHER); IPR004911 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1307	481780_length_1391_cvg_63.6_tip_1_5	401	copper chaperone for superoxide dismutase	455	1.71E-111	77.00%	0.434 Y	IPR001424 (PRINTS); IPR006121 (PFAM); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); G3DSA:3.30.70.100 (GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR006121 (PROSITE_PROFILES); IPR001424 (SUPERFAMILY); IPR006121 (SUPERFAMILY)
1295	481114_length_1369_cvg_3.3_tip_1_1	31	mam and ldl-receptor class a domain-containing protein 1	456	8.76E-35	46.60%	0.104	IPR002172 (PRINTS); IPR002172 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR23282 (PANTHER); PTHR23282:SF67 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1297	481134_length_1370_cvg_90.6_tip_1_2	176340	carboxypeptidase b-like	456	1.31E-126	62.00%	0.723 Y	IPR000834 (PRINTS); IPR000834 (SMART); G3DSA:3.40.630.10 (GENE3D); IPR003146 (G3DSA:3.30.70.GENE3D); IPR003146 (PFAM); IPR000834 (PFAM); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF53187 (SUPERFAMILY); IPR009020 (SUPERFAMILY)
1314	482070_length_1400_cvg_62.4_tip_1_2	3335	adp-ribosylation factor-like protein 8b-a	456	7.72E-124	97.70%	0.114	IPR006689 (PRINTS); IPR006687 (SMART); IPR003579 (SMART); IPR024156 (SMART); IPR006689 (PFAM); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF122 (PANTHER); PTHR11711 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1293	481090_length_1369_cvg_3.2_tip_1_3	27	upf0454 protein c12orf49 homolog	457	1.59E-106	76.00%	0.102	IPR019352 (PFAM); IPR019352 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1294	481112_length_1369_cvg_3.0_tip_1_0	22	zinc finger protein	457	1.45E-22	59.40%	0.166	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1296	481132_length_1370_cvg_2.6_tip_1_1	23	endothelin-converting enzyme 1 isoform x2	457	2.66E-150	66.30%	0.191	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); IPR008753 (PFAM); IPR029733 (PTHR11733:PANTHER); IPR000718 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1298	481206_length_1373_cvg_18.9_tip_1_5	132	15-hydroxyprostaglandin dehydrogenase	457	7.56E-64	63.10%	0.121	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24310 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY)

1312	482004_length_1398_cvg_10.5_tip_1_5	82	wd repeat-containing protein 3	466	2.37E-143	69.20%	0.357 Y	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19853:SF0 (PANTHER); PTHR19853 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
1315	482076_length_1400_cvg_3.1_tip_1_5	25	fat-like cadherin-related tumor suppressor homolog isoform x1	466	1.93E-143	76.20%	0.106	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); PTHR24026:SF39 (PANTHER); PTHR24026 (PANTHER); IPR020894 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); TMhelix (TMHMM)
1329	482860_length_1423_cvg_106.2_tip_1_2	138989	transmembrane protease serine 4	466	4.08E-39	52.40%	0.106	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1327	482802_length_1422_cvg_5.2_tip_1_0	32	interstitial collagenase	467	7.09E-24	61.10%	0.153	IPR018487 (SMART); IPR000585 (G3DSA:2.110.10.GENE3D); IPR018487 (PFAM); PTHR10201 (PANTHER); IPR018486 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR018487 (PROSITE_PROFILES); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY)
1334	483152_length_1431_cvg_59.0_tip_1_5	431	cytolysin src-1-like isoform x2	467	7.84E-25	51.20%	0.111	IPR015926 (G3DSA:2.60.270.GENE3D); IPR009104 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR015926 (SUPERFAMILY); TMhelix (TMHMM)
1317	482188_length_1403_cvg_5.6_tip_1_1	33	nucleolar protein 58-like	468	0	83.60%	0.166	IPR012976 (SMART); IPR002687 (PFAM); IPR012976 (PFAM); IPR012974 (PFAM); PTHR10894 (PANTHER); IPR002687 (PROSITE_PROFILES); SSF89124 (SUPERFAMILY)
1318	482370_length_1409_cvg_42.8_tip_1_3	505	cyclin-h	470	7.64E-157	81.70%	0.121	IPR013763 (SMART); IPR013763 (G3DSA:1.10.472.GENE3D); IPR013763 (G3DSA:1.10.472.GENE3D); IPR006671 (PFAM); IPR027081 (TIGRFAM); IPR015429 (PANTHER); IPR027081 (PTHR10026:PANTHER); IPR013763 (SUPERFAMILY); IPR013763 (SUPERFAMILY)
1319	482376_length_1409_cvg_8.8_tip_1_4	55	scp-like extracellular domain containing protein 1	470	6.33E-37	49.50%	0.101	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR014044 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR014044 (G3DSA:3.40.33.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1320	482402_length_1410_cvg_16.6_tip_1_4	112	zinc finger protein 431-like isoform x2	470	1.99E-37	53.40%	0.115	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1321	482456_length_1412_cvg_62.8_tip_1_3	14361	disulfide isomerase	471	0	81.70%	0.622 Y	PR00421 (PRINTS); IPR005788 (TIGRFAM); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PF13848 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005792 (TIGRFAM); PTHR18929 (PANTHER); PTHR18929:SF48 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)

1322	482486_length_1413_cvg_17.5_tip_1_2	125	tho complex subunit 3	471	0	86.90%	0.104	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR011659 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22839 (PANTHER); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1323	482516_length_1414_cvg_2.3_tip_1_2	22	kae1 qri7 required for threonylcarbamoyladenine t a37 formation in trna	471	5.73E-35	99.60%	0.111	IPR000905 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR11735 (PANTHER); SSF53067 (SUPERFAMILY)
1324	482552_length_1415_cvg_6.9_tip_1_1	66	beta-galactosidase and hygromycin phosphotransferase fusion protein	472	0	100.00%	0.124	IPR006101 (PRINTS); IPR006103 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR013812 (G3DSA:2.60.40.GENE3D); IPR008979 (G3DSA:2.60.120.GENE3D); IPR006102 (PFAM); IPR006104 (PFAM); PTHR10066:SF57 (PANTHER); PTHR10066 (PANTHER); IPR023232 (PROSITE_PATTERNS); IPR023230 (PROSITE_PATTERNS); IPR006102 (SUPERFAMILY); IPR008979 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1325	482658_length_1417_cvg_11.2_tip_1_2	80	mitochondrial cardiolipin hydrolase-like	472	1.28E-60	66.40%	0.151	G3DSA:3.30.870.10 (GENE3D); IPR025202 (PFAM); PTHR21248 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001736 (PROSITE_PROFILES); SSF56024 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1339	483386_length_1441_cvg_8.1_tip_1_3	56	arylsulfatase b-like	473	6.23E-143	66.20%	0.285	IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); IPR000917 (PFAM); PTHR10342:SF206 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR017850 (SUPERFAMILY)
1328	482836_length_1422_cvg_63.1_tip_0_3	205020	suppressor of tumorigenicity 14 protein	474	9.87E-70	51.60%	0.103	IPR002172 (PRINTS); IPR001254 (SMART); IPR002172 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
1357	484108_length_1466_cvg_80.7_tip_1_0	170597	suppressor of tumorigenicity 14 protein homolog isoform x2	474	1.76E-52	45.80%	0.104	IPR002172 (PRINTS); IPR001254 (SMART); IPR002172 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256:SF106 (PANTHER); PTHR24256 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1330	482912_length_1424_cvg_12.8_tip_1_0	80	sparc-related modular calcium-binding protein 1-like isoform x2	475	5.65E-124	56.90%	0.103	IPR000716 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR000716 (PFAM); IPR019577 (PFAM); IPR002350 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR12352 (PANTHER); PTHR12352:SF3 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY); SSF47473 (SUPERFAMILY); SSF47473 (SUPERFAMILY)

1331	482978_length_1427_cvg_55.6_tip_1_5	346	probable cytosolic iron-sulfur protein assembly protein cioa1	475	2.60E-167	80.30%	0.099	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19920:SF0 (PANTHER); PTHR19920 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR028608 (HAMAP); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1332	483076_length_1429_cvg_30.1_tip_1_5	165	cytochrome p450	476	4.55E-90	77.60%	0.107	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24290 (PANTHER); PTHR24290:SF0 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY)
1347	483674_length_1449_cvg_49.5_tip_1_3	336	hypothetical protein DAPPUDRAFT_196945	476	5.35E-89	64.80%	0.149	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
1333	483082_length_1429_cvg_2.1_tip_1_0	23	endoplasmic reticulum mannosyl-oligosaccharide - alpha-mannosidase	477	4.70E-135	81.30%	0.105	IPR001382 (PRINTS); IPR001382 (PFAM); IPR001382 (G3DSA:1.50.10.GENE3D); PTHR11742:SF7 (PANTHER); IPR001382 (PANTHER); IPR001382 (SUPERFAMILY)
1335	483156_length_1432_cvg_9.8_tip_1_4	71	lachesin	477	9.25E-88	66.30%	0.116	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831:SF43 (PANTHER); PTHR19831 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1336	483158_length_1432_cvg_8.1_tip_1_1	41	syntaxin-12	477	4.29E-95	72.00%	0.196	IPR006011 (SMART); IPR000727 (SMART); PF14523 (PFAM); G3DSA:1.20.58.70 (GENE3D); IPR000727 (PFAM); PTHR19957 (PANTHER); PTHR19957:SF87 (PANTHER); IPR006012 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000727 (PROSITE_PROFILES); IPR010989 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1337	483218_length_1434_cvg_8.3_tip_1_2	53	limbic system-associated membrane protein	478	4.55E-150	69.70%	0.122	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF47 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1338	483352_length_1439_cvg_61.2_tip_1_5	2986	muscle m-line assembly protein unc-89-like	479	5.04E-158	75.90%	0.103	Coil (COILS); IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF148 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1362	484396_length_1476_cvg_61.0_tip_1_4	641	hyaluronidase-like	480	2.93E-73	56.90%	0.105	IPR018155 (PRINTS); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); PTHR11769:SF8 (PANTHER); IPR018155 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY)
1340	483392_length_1441_cvg_5.7_tip_1_0	40	apical endosomal glycoprotein	481	5.92E-15	46.20%	0.131	IPR000998 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1341	483480_length_1444_cvg_63.5_tip_1_2	10717	st14a protein	481	5.16E-44	50.30%	0.852	Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR002172 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1359	484188_length_1468_cvg_25.3_tip_1_0	210	kielin chordin-like protein	481	1.10E-34	48.20%	0.316		IPR001791 (SMART); IPR013320 (SUPERFAMILY)
1342	483544_length_1446_cvg_72.0_tip_1_2	1785	26kda protease	482	4.36E-46	56.90%	0.306		IPR001314 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1343	483580_length_1447_cvg_9.2_tip_1_2	71	3-ketodihydrosphingosine reductase	482	1.95E-119	71.70%	0.117		IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320:SF1 (PANTHER); PTHR24320 (PANTHER); IPR020904 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1344	483614_length_1448_cvg_18.2_tip_1_1	127	pitslr serine threonine-protein kinase cdc2l1	483	0	88.10%	0.102		IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24056:SF107 (PANTHER); PTHR24056 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1345	483628_length_1448_cvg_9.8_tip_1_1	68	protein kinase domain-containing cytoplasmic	483	2.02E-104	58.60%	0.142		IPR022049 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR26392 (PANTHER); PTHR26392:SF71 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1346	483648_length_1449_cvg_9.0_tip_1_4	69	adiponectin receptor protein	483	0	80.70%	0.138		IPR004254 (PFAM); IPR004254 (PANTHER); PTHR20855:SF15 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1348	483684_length_1450_cvg_13.3_tip_1_4	89	zinc finger protein 239- partial	483	1.05E-56	66.00%	0.102		IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1350	483712_length_1451_cvg_10.6_tip_1_5	83	retinol dehydrogenase 12	483	2.72E-95	61.10%	0.215	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); PTHR24320:SF55 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1349	483686_length_1450_cvg_23.0_tip_1_0	161	zinc finger protein 235-like	484	5.76E-40	49.10%	0.1	IPR015880 (SMART); IPR003656 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1351	483730_length_1451_cvg_60.5_tip_1_1	1617	ribosome biogenesis protein wdr12 homolog	484	1.58E-180	74.50%	0.134	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR012972 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19855 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR028599 (HAMAP); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1352	483792_length_1454_cvg_10.2_tip_1_5	56	vanin-like protein 1	484	3.96E-38	52.20%	0.166	IPR003010 (PFAM); IPR003010 (G3DSA:3.60.110.GENE3D); IPR012101 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003010 (PROSITE_PROFILES); IPR003010 (SUPERFAMILY); TMhelix (TMHMM)
1363	484408_length_1477_cvg_66.4_tip_0_1	92717	transmembrane protease serine 6	484	5.90E-45	49.40%	0.834 Y	IPR001314 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
1364	484492_length_1480_cvg_39.5_tip_1_4	224	trans-l-3-hydroxyproline dehydratase	484	1.05E-143	76.00%	0.301	G3DSA:3.10.310.10 (GENE3D); G3DSA:3.10.310.10 (GENE3D); IPR008794 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54506 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1353	483806_length_1455_cvg_18.5_tip_1_1	152	leucine-rich repeat protein 1 isoform x2	485	2.22E-120	64.10%	0.246	PR00019 (PRINTS); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)

									IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_P
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1373	484904_length_1494_cvg_57.6_tip_1_4	500	platelet-activating factor acetylhydrolase	487	2.00E-102	57.20%	0.192	Coil (COILS); IPR005065 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR005065 (PANTHER); IPR029058 (SUPERFAMILY)
1356	484074_length_1465_cvg_27.4_tip_1_5	193	epidermal retinol dehydrogenase 2-like isoform x2	488	6.37E-112	71.70%	0.102	Coil (COILS); IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316 (PANTHER); PTHR24316:SF289 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1358	484112_length_1466_cvg_22.0_tip_1_1	167	upf0378 protein kiaa0100	489	8.84E-62	54.20%	0.091	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1371	484844_length_1492_cvg_6.7_tip_1_2	44	zinc finger protein 84-like isoform x2	489	1.28E-62	55.10%	0.098	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1376	484986_length_1497_cvg_36.0_tip_1_3	250	n-acetylglucosamine-6- partial	490	4.38E-71	53.00%	0.117	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342:SF208 (PANTHER); PTHR10342 (PANTHER); IPR017850 (SUPERFAMILY)
1360	484350_length_1474_cvg_8.0_tip_1_1	59	exocyst complex component 6	491	0	82.20%	0.242	Coil (COILS); Coil (COILS); IPR007225 (PFAM); IPR007225 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1366	484512_length_1481_cvg_10.2_tip_1_4	89	apolipoprotein d	494	1.38E-07	45.60%	0.129	IPR012674 (G3DSA:2.40.128.GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011038 (SUPERFAMILY)
1369	484680_length_1486_cvg_5.7_tip_1_1	53	aldehyde mitochondrial	495	0	85.60%	0.105	IPR016162 (G3DSA:3.40.605.GENE3D); IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699:SF151 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
1372	484878_length_1493_cvg_2.0_tip_1_2	14	maltase a2-like isoform x1	497	1.48E-83	53.20%	0.1	IPR006589 (SMART); IPR006047 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR10357:SF133 (PANTHER); IPR015902 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY)
1374	484924_length_1495_cvg_19.2_tip_1_3	137	d-aspartate oxidase	499	1.82E-98	63.70%	0.114	IPR006076 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR023209 (PANTHER); PTHR11530:SF0 (PANTHER); IPR006181 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51971 (SUPERFAMILY); SSF54373 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1390	486004_length_1539_cvg_6.5_tip_1_0	48	acidic phospholipase a2 pa4 isoform x2	513	1.00E-42	56.90%	0.898 Y	IPR001211 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR12253 (PANTHER); IPR013090 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR016090 (SUPERFAMILY)
1391	486082_length_1541_cvg_8.6_tip_1_2	73	bola-like protein ddb_g0274169	513	9.51E-47	82.00%	0.144	IPR002634 (G3DSA:3.30.300.GENE3D); IPR002634 (PFAM); PTHR12735 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002634 (SUPERFAMILY)
1398	486310_length_1551_cvg_22.0_tip_1_3	221	serine proteinase stubble-like	513	2.38E-69	56.40%	0.099	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1410	486648_length_1564_cvg_38.0_tip_1_1	248	zinc finger protein 569-like	513	1.85E-25	47.90%	0.181	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1392	486106_length_1542_cvg_6.8_tip_1_4	59	folate receptor alpha-like	514	3.66E-80	68.10%	0.299	IPR018143 (PFAM); PTHR10517:SF3 (PANTHER); IPR004269 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1393	486138_length_1543_cvg_37.2_tip_1_2	302	proclotting enzyme	514	8.60E-128	65.80%	0.111	IPR001314 (PRINTS); IPR006604 (SMART); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF81 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1394	486148_length_1543_cvg_5.2_tip_1_4	47	patj-like protein	514	0	77.20%	0.1	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964:SF34 (PANTHER); PTHR19964 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
1395	486166_length_1545_cvg_11.1_tip_1_2	60	26s protease regulatory subunit 8	515	0	97.10%	0.1	Coil (COILS); IPR003593 (SMART); IPR005937 (TIGRFAM); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:1.10.8.60 (GENE3D); PTHR23073 (PANTHER); PTHR23073:SF12 (PANTHER); IPR003960 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY)
1396	486286_length_1549_cvg_4.2_tip_1_2	32	nas-15 protein	516	1.21E-46	59.80%	0.101	IPR001506 (PRINTS); IPR006026 (SMART); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1397	486288_length_1550_cvg_6.1_tip_1_5	42	allatostatin neuropeptide precursor	516	2.31E-44	53.60%	0.097	IPR010276 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)

1399	486358_length_1553_cvg_2.4_tip_1_1	29	e3 ubiquitin-protein ligase mib2	518	0	70.00%	0.424 Y	Coil (COILS); IPR001841 (SMART); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); PF13920 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR013083 (G3DSA:3.30.40.GENE3D); IPR002110 (PFAM); PTHR24202:SF4 (PANTHER); PTHR24202 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR001841 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR001841 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1400	486420_length_1555_cvg_2.0_tip_1_4	27	ly6 plaur domain-containing protein 6b-like isoform x1	518	2.64E-38	74.90%	0.112	G3DSA:2.10.60.10 (GENE3D); PTHR31171 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF57302 (SUPERFAMILY)
1421	487016_length_1581_cvg_66.7_tip_1_2	1169	chitinase domain-containing protein 1 isoform x1	518	2.97E-149	70.30%	0.13	IPR011583 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF135 (PANTHER); PTHR11177 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1401	486424_length_1555_cvg_63.6_tip_1_3	1357	ferritin 1-like protein a	519	3.11E-45	64.60%	0.256	IPR008331 (PFAM); IPR012347 (G3DSA:1.20.1260.GENE3D); PTHR11431:SF29 (PANTHER); IPR001519 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY)
1402	486466_length_1557_cvg_24.2_tip_1_1	175	polycomb protein eed	519	0	86.10%	0.104	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR10253 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1403	486472_length_1557_cvg_11.1_tip_1_3	75	sh3 domain-containing ring finger protein 3 isoform x1	519	3.94E-68	52.50%	0.116	IPR001452 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR001452 (PFAM); PTHR10661 (PANTHER); PTHR10661:SF7 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); TMhelix (TMHMM)
1404	486474_length_1557_cvg_27.4_tip_1_4	147	tropinone reductase 2-like	519	4.42E-134	83.50%	0.168	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF111 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1405	486484_length_1557_cvg_2.9_tip_1_1	29	dipeptidyl peptidase 1 isoform x1	519	0	71.30%	0.684 Y	IPR000668 (PRINTS); IPR000668 (SMART); IPR014882 (PFAM); IPR000668 (PFAM); IPR014882 (G3DSA:2.40.128.GENE3D); G3DSA:3.90.70.10 (GENE3D); IPR013128 (PANTHER); PTHR12411:SF314 (PANTHER); IPR000169 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); SignalP-noTM (SIGNALP_EUK); IPR014882 (SUPERFAMILY); SSF54001 (SUPERFAMILY)
1416	486860_length_1575_cvg_49.2_tip_1_5	395	dnaj homolog subfamily c member 9	519	1.54E-85	75.60%	0.113	Coil (COILS); Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078:SF166 (PANTHER); PTHR24078 (PANTHER); IPR018253 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1419	486986_length_1580_cvg_18.7_tip_1_2	159	---NA---	519			0.101	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1407	486542_length_1560_cvg_20.6_tip_1_3	143	tl5a_tactr ame: full=techylectin-5a flags: precursor	520	5.15E-54	60.80%	0.106	Coil (COILS); IPR002181 (SMART); IPR002181 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); IPR014715 (G3DSA:4.10.530.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)

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1418	486924_length_1577_cvg_13.0_tip_1_5	91	serine protease mitochondrial	525	2.06E-130	73.50%	0.125	IPR001940 (PRINTS); IPR001478 (SMART); G3DSA:2.40.10.10 (GENE3D); PF13365 (PFAM); IPR001478 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR22939:SF69 (PANTHER); PTHR22939 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
1417	486912_length_1577_cvg_71.0_tip_1_0	659	transcription factor sp5-like	526	9.69E-74	53.80%	0.29	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR23223 (PANTHER); PTHR23223:SF15 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1420	486992_length_1580_cvg_3.7_tip_1_1	29	dehydrogenase reductase sdr family member 11-like	527	2.70E-102	74.50%	0.13	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF310 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1432	487456_length_1607_cvg_63.0_tip_1_2	855	serine protease snake	527	3.88E-75	54.10%	0.446 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR006604 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24260:SF46 (PANTHER); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1422	487042_length_1583_cvg_20.6_tip_1_4	209	beta- -galactosyltransferase 7	528	1.03E-126	72.30%	0.526 Y	IPR003859 (PRINTS); IPR027791 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027995 (PFAM); PTHR19300:SF1 (PANTHER); IPR003859 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR029044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1423	487134_length_1588_cvg_8.5_tip_1_1	75	neuropsin-like protein	529	2.13E-18	61.20%	0.104	IPR010850 (PFAM); IPR011390 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR010850 (PRODOM); IPR009030 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1426	487238_length_1593_cvg_18.7_tip_1_5	154	arylsulfatase a-like	531	0	68.20%	0.440 Y	G3DSA:3.30.1120.10 (GENE3D); IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PF14707 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF22 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM)
1427	487240_length_1593_cvg_66.8_tip_1_3	2640	twitchin isoform x1	531	1.58E-137	70.40%	0.1	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)

1428	487328_length_1598_cvg_13.6_tip_1_4	133	pdz domain-containing protein 11	533	4.33E-50	76.90%	0.105	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR14063 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
1438	487638_length_1617_cvg_9.7_tip_1_4	72	serine proteinase inhibitor b3	533	5.43E-73	53.90%	0.186	IPR023796 (SMART); IPR023796 (PFAM); G3DSA:3.30.497.10 (GENE3D); G3DSA:2.30.39.10 (GENE3D); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023796 (SUPERFAMILY); TMhelix (TMHMM)
1429	487412_length_1604_cvg_15.0_tip_1_4	105	gamma-aminobutyric acid type b receptor subunit 1 isoform x1	535	0	75.80%	0.097	Coil (COILS); PR01176 (PRINTS); IPR002456 (PRINTS); IPR017978 (PFAM); PTHR10519:SF3 (PANTHER); IPR002455 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017978 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1430	487450_length_1606_cvg_48.3_tip_1_4	342	transmembrane protease serine 6	535	1.55E-49	53.00%	0.912 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR002172 (SMART); IPR001254 (PFAM); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1454	487998_length_1634_cvg_11.8_tip_1_4	117	acetylcholine receptor subunit alpha-type acr-16	535	6.06E-112	59.90%	0.171	IPR006201 (PRINTS); IPR006202 (PFAM); IPR006029 (PFAM); IPR027361 (G3DSA:1.20.120.GENE3D); IPR006202 (G3DSA:2.70.170.GENE3D); PTHR18945:SF490 (PANTHER); IPR006201 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006029 (SUPERFAMILY); IPR006202 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1431	487454_length_1607_cvg_12.5_tip_1_3	97	wd40 repeat-containing protein smu1	536	0	93.90%	0.105	IPR020472 (PRINTS); IPR006594 (SMART); IPR006595 (SMART); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22848 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR006594 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR006595 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1433	487470_length_1607_cvg_4.3_tip_1_4	42	serine threonine-protein kinase nek7	536	2.76E-178	91.00%	0.145	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24362 (PANTHER); PTHR24362:SF228 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1434	487506_length_1610_cvg_8.7_tip_1_5	76	26s protease regulatory subunit 6b	536	0	96.20%	0.098	Coil (COILS); IPR003593 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:1.10.8.60 (GENE3D); IPR005937 (TIGRFAM); IPR003959 (PFAM); PTHR23073:SF8 (PANTHER); PTHR23073 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)

1440	487690_length_1619_cvg_35.6_tip_1_1	292	hydroxysteroid (17-beta)	536	1.15E-78	62.00%	0.107	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF68 (PANTHER); PTHR24316 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1444	487764_length_1622_cvg_10.8_tip_1_0	90	neuroendocrine partial	536	1.88E-108	62.30%	0.13	IPR002884 (PFAM); IPR000209 (G3DSA:3.40.50.GENE3D); IPR008979 (G3DSA:2.60.120.GENE3D); IPR000209 (PFAM); PTHR10795:SF340 (PANTHER); IPR015500 (PANTHER); IPR023828 (PROSITE_PATTERNS); IPR000209 (SUPERFAMILY); IPR008979 (SUPERFAMILY)
1435	487590_length_1614_cvg_52.5_tip_1_5	357	cartilage intermediate layer protein 2-like	538	8.32E-18	43.90%	0.109	IPR025155 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1437	487618_length_1616_cvg_5.0_tip_1_5	41	serine threonine-protein phosphatase pp1-beta catalytic subunit	538	0	97.30%	0.115	IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668:SF204 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029052 (SUPERFAMILY)
1436	487608_length_1615_cvg_16.3_tip_1_3	115	flavin-containing monooxygenase fmo gs-ox4-like isoform x1	539	8.10E-134	62.90%	0.308	IPR000960 (PRINTS); IPR020946 (PFAM); G3DSA:3.50.50.60 (GENE3D); G3DSA:3.50.50.60 (GENE3D); PTHR23023:SF4 (PANTHER); PTHR23023 (PANTHER); SSF51905 (SUPERFAMILY); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
1439	487678_length_1619_cvg_73.4_tip_0_5	137565	venom serine carboxypeptidase-like	539	1.89E-59	58.30%	0.102	IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); IPR018202 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
1441	487710_length_1620_cvg_11.6_tip_1_5	85	carbohydrate sulfotransferase 11-like	540	1.54E-66	55.10%	0.642 Y	IPR005331 (PFAM); IPR018011 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
1442	487734_length_1621_cvg_5.2_tip_1_5	48	aldehyde dimeric nadp-preferring isoform x4	540	0	74.30%	0.108	IPR012394 (PIRSF); IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF15 (PANTHER); IPR029510 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM)
1443	487762_length_1622_cvg_32.7_tip_1_2	265	notchless protein homolog 1	540	0	83.20%	0.115	IPR001632 (PRINTS); IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR012972 (PFAM); PTHR19848:SF0 (PANTHER); PTHR19848 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR011047 (SUPERFAMILY)
1464	488288_length_1650_cvg_26.2_tip_1_1	267	dermatopontin 2	540	2.97E-37	58.70%	0.574 Y	PF14704 (PFAM); IPR026645 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); TMhelix (TMHMM)
1445	487780_length_1623_cvg_44.9_tip_1_5	293	ras-related protein rab-10	541	1.76E-116	92.90%	0.182	IPR001806 (PRINTS); IPR024156 (SMART); IPR003579 (SMART); IPR002041 (SMART); IPR020849 (SMART); IPR003578 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); IPR001806 (PFAM); PTHR24073:SF456 (PANTHER); PTHR24073 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)

1453	487928_length_1630_cvg_3.4_tip_1_4	27	titin- partial	543	1.92E-22	52.00%	0.111	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1466	488386_length_1656_cvg_7.5_tip_0_1	78	transducin beta-like protein 2	544	1.69E-136	73.50%	0.105	Coil (COILS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22847:SF380 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1455	488042_length_1637_cvg_3.4_tip_1_2	28	aspartate--trna mitochondrial	545	0	72.50%	0.102	IPR002312 (PRINTS); G3DSA:3.30.930.10 (GENE3D); IPR004364 (PFAM); IPR004115 (G3DSA:3.30.1360.GENE3D); IPR004524 (TIGRFAM); IPR029351 (PFAM); IPR004524 (PTHR22594:PANTHER); IPR018150 (PANTHER); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY); IPR004115 (SUPERFAMILY)
1465	488360_length_1655_cvg_57.1_tip_1_0	535	phosphoglycerate kinase	546	0	87.40%	0.142	IPR001576 (PRINTS); IPR015824 (G3DSA:3.40.50.GENE3D); IPR015901 (G3DSA:3.40.50.GENE3D); IPR001576 (PFAM); IPR001576 (PANTHER); PTHR11406:SF6 (PANTHER); IPR015911 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001576 (HAMAP); IPR001576 (SUPERFAMILY)
1456	488116_length_1641_cvg_12.1_tip_1_0	129	sulfhydryl oxidase 2-like	547	9.50E-63	60.60%	0.135	IPR017905 (G3DSA:1.20.120.GENE3D); IPR017905 (PFAM); PTHR22897 (PANTHER); PTHR22897:SF8 (PANTHER); IPR017905 (PROSITE_PROFILES); IPR017905 (SUPERFAMILY)
1457	488116_length_1641_cvg_12.1_tip_1_1	129	sulfhydryl oxidase 1-like	547	5.07E-34	64.60%	0.118	IPR012336 (G3DSA:3.40.30.GENE3D); PTHR22897 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
1487	488918_length_1689_cvg_61.8_tip_1_2	795	er membrane protein complex subunit 10	547	9.38E-72	63.70%	0.18	IPR029615 (PTHR21397:PANTHER); PTHR21397 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1458	488172_length_1645_cvg_7.0_tip_1_5	59	ga-binding protein subunit beta-2	548	4.33E-101	57.40%	0.122	Coil (COILS); IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24193:SF73 (PANTHER); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1459	488196_length_1646_cvg_39.1_tip_1_3	367	polyubiquitin-c-like isoform 2	549	2.52E-155	99.00%	0.102	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1460	488230_length_1647_cvg_2.5_tip_1_3	24	isoform cra_b	549	9.92E-76	78.50%	0.136	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24348 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1461	488230_length_1647_cvg_2.5_tip_1_5	24	serine threonine-protein kinase ulk3	549	5.59E-93	66.50%	0.417 Y	Coil (COILS); IPR007330 (SMART); IPR002290 (SMART); IPR007330 (G3DSA:1.20.58.GENE3D); IPR000719 (PFAM); IPR007330 (PFAM); IPR007330 (G3DSA:1.20.58.GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24348 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR007330 (SUPERFAMILY); IPR011009 (SUPERFAMILY); IPR007330 (SUPERFAMILY)

1480	488714_length_1677_cvg_25.3_tip_1_3	186	3-hydroxyisobutyrate mitochondrial	559	5.52E-151	81.30%	0.306	IPR013328 (G3DSA:1.10.1040.GENE3D); IPR011548 (TIGRFAM); IPR006115 (PFAM); IPR029154 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22981 (PANTHER); PTHR22981:SF51 (PANTHER); IPR002204 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR008927 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
1482	488762_length_1679_cvg_4.1_tip_1_2	37	basement membrane-specific heparan sulfate proteoglycan core isoform x2	559	4.72E-104	75.40%	0.145	IPR013106 (SMART); IPR003598 (SMART); IPR003599 (SMART); IPR013106 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR23279 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1483	488774_length_1680_cvg_35.5_tip_1_1	274	zinc finger protein	560	1.90E-15	61.00%	0.1	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1495	489138_length_1706_cvg_28.1_tip_1_3	1128	adp-ribosylation factor-related protein 1	560	1.52E-123	94.40%	0.22	IPR001806 (PRINTS); IPR006687 (SMART); IPR003579 (SMART); IPR024156 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); IPR005225 (TIGRFAM); PTHR11711 (PANTHER); PTHR11711:SF19 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1484	488816_length_1683_cvg_5.9_tip_1_1	76	cd109 antigen-like isoform x2	561	0	74.80%	0.168	IPR009048 (G3DSA:2.60.40.GENE3D); IPR011626 (PFAM); IPR008930 (G3DSA:1.50.10.GENE3D); IPR009048 (PFAM); PTHR11412:SF84 (PANTHER); PTHR11412 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008930 (SUPERFAMILY); IPR009048 (SUPERFAMILY); TMhelix (TMHMM)
1496	489166_length_1707_cvg_9.6_tip_1_0	103	aael005189- partial	561	3.87E-128	69.30%	0.129	IPR003112 (SMART); IPR003112 (PFAM); PTHR23192:SF33 (PANTHER); PTHR23192 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003112 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM)
1485	488842_length_1685_cvg_11.5_tip_1_0	165	hemocyte protein-glutamine gamma-glutamyltransferase-like	562	0	72.10%	0.145	IPR002931 (SMART); IPR002931 (PFAM); IPR002931 (G3DSA:3.90.260.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR008958 (PFAM); IPR023608 (PIRSF); IPR013783 (G3DSA:2.60.40.GENE3D); IPR023608 (PANTHER); PTHR11590:SF40 (PANTHER); IPR008958 (SUPERFAMILY); SSF54001 (SUPERFAMILY); IPR008958 (SUPERFAMILY)
1486	488890_length_1688_cvg_9.6_tip_1_5	70	sepiapterin reductase-like	562	1.75E-80	63.70%	0.114	IPR002347 (PRINTS); IPR006393 (TIGRFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24318 (PANTHER); PTHR24318:SF1 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY)
1501	489258_length_1713_cvg_40.4_tip_1_1	357	46 kda fk506-binding nuclear protein	562	7.78E-47	73.40%	0.248	Coil (COILS); G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); IPR023566 (PANTHER); IPR001179 (PROSITE_PROFILES); IPR024057 (SUPERFAMILY); SSF54534 (SUPERFAMILY)

1488	488944_length_1691_cvg_61.4_tip_1_2	720	protein tumorous imaginal mitochondrial-like isoform x2	563	0	75.10%	0.199	IPR001623 (PRINTS); IPR001623 (SMART); IPR001305 (G3DSA:2.10.230.GENE3D); IPR001305 (PFAM); IPR001623 (PFAM); IPR002939 (PFAM); G3DSA:2.60.260.20 (GENE3D); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24076 (PANTHER); PTHR24076:SF79 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR012724 (HAMAP); IPR001305 (PROSITE_PROFILES); IPR001305 (SUPERFAMILY); IPR001623 (SUPERFAMILY); IPR008971 (SUPERFAMILY); IPR008971 (SUPERFAMILY)
1504	489370_length_1722_cvg_7.2_tip_1_1	90	wd repeat-containing protein 3	565	0	78.20%	0.114	Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR007148 (PFAM); PTHR19853 (PANTHER); PTHR19853:SF0 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1489	489026_length_1698_cvg_4.7_tip_1_4	51	centromeric protein	566	1.74E-103	66.60%	0.276	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR027881 (PFAM); PTHR15742 (PANTHER); PTHR15742:SF0 (PANTHER)
1490	489042_length_1699_cvg_6.2_tip_1_2	40	guanine nucleotide-binding protein g g subunit beta-1 isoform x1	566	0	98.40%	0.159	IPR001632 (PRINTS); IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR016346 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMHMM); TMhelix (TMHMM)
1515	489604_length_1739_cvg_68.2_tip_1_4	2297	bola-like protein 2-like	566	1.16E-33	83.10%	0.261	IPR002634 (G3DSA:3.30.300.GENE3D); IPR002634 (PFAM); PTHR12735:SF2 (PANTHER); PTHR12735 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002634 (SUPERFAMILY)
1491	489048_length_1699_cvg_4.2_tip_1_3	40	wee1-like protein kinase	567	0	74.30%	0.257	IPR002290 (SMART); IPR017164 (PIRSF); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR11042:SF69 (PANTHER); PTHR11042 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1492	489070_length_1700_cvg_74.4_tip_1_1	19098	tissue factor pathway inhibitor 2	567	3.91E-31	62.20%	0.136	Coil (COILS); IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1493	489096_length_1702_cvg_13.3_tip_1_4	104	zinc finger protein 235-like	567	2.32E-28	43.50%	0.099	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1494	489106_length_1703_cvg_8.6_tip_1_2	61	low quality protein: selenoprotein h	567	1.62E-18	63.70%	0.102	IPR020478 (PRINTS); IPR017956 (SMART); IPR011893 (PFAM); IPR011893 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR017956 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)

1506	489406_length_1724_cvg_64.9_tip_1_5	835	di-n-acetylchitinase	574	5.24E-114	63.10%	0.469 Y	IPR011583 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF146 (PANTHER); PTHR11177 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1505	489386_length_1723_cvg_13.0_tip_1_0	82	apolipoprotein d-like	575	1.43E-57	62.20%	0.127	IPR003057 (PRINTS); IPR000566 (PFAM); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612:SF7 (PANTHER); PTHR10612 (PANTHER); IPR022272 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)
1507	489412_length_1725_cvg_3.8_tip_1_0	51	fmrf_musdo ame: full=fmrfamide neuropeptides contains: ame: full= amide-2 contains: ame: full= amide-3 contains: ame: full= amide-4 contains: ame: full= amide-5 contains: ame: full= amide-6 contains: ame: full= amide-7 contains: ame: full= amide-8 ame: full= amide-10 contains: ame: full= amide-9 ame: full= amide-11 ame: full= amide-12 ame: full= amide-13 contains: ame: full= amide-14 contains: ame: full= amide-15 contains: ame: full= amide-17 contains: ame: full= amide-16 contains: ame: full= amide-18 flags: precursor	575	1.65E-19	58.10%	0.609 Y	IPR002544 (PFAM); PTHR20986 (PANTHER); PTHR20986:SF1 (PANTHER); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
1508	489444_length_1727_cvg_8.3_tip_1_5	90	integrin-linked protein kinase	575	0	87.10%	0.236	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR016253 (PIRSF); G3DSA:1.10.510.10 (GENE3D); IPR002110 (PFAM); IPR020683 (PFAM); IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR23257:SF30 (PANTHER); PTHR23257 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1509	489474_length_1729_cvg_3.0_tip_1_5	24	von willebrand factor like 1	576	1.07E-20	39.50%	0.102	IPR001007 (PROSITE_PATTERNS); PD968187 (PRODOM); IPR001007 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY)
1511	489504_length_1732_cvg_5.9_tip_1_2	54	---NA---	577			0.12	IPR002350 (SMART); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1520	489852_length_1756_cvg_60.5_tip_1_5	1153	serine protease easter-like	577	1.62E-71	54.70%	0.217	IPR001314 (PRINTS); IPR006604 (SMART); IPR001254 (SMART); IPR022700 (PFAM); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); PTHR24260:SF3 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1539	490204_length_1781_cvg_68.8_tip_1_5	6700	cathepsin b	577	4.14E-164	78.80%	0.13	IPR000668 (PRINTS); IPR000668 (SMART); IPR012599 (PFAM); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR015643 (PTHR12411:PANTHER); IPR013128 (PANTHER); IPR025661 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1523	489904_length_1760_cvg_25.2_tip_1_5	162	wd repeat-containing protein 61	586	1.16E-139	87.30%	0.103	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22841 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
1528	490034_length_1768_cvg_5.4_tip_1_4	59	multiple inositol polyphosphate phosphatase 1	586	1.23E-71	59.50%	0.202	IPR029033 (G3DSA:3.40.50.GENE3D); IPR000560 (PFAM); PTHR20963 (PANTHER); PTHR20963:SF8 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029033 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1524	489922_length_1761_cvg_17.3_tip_1_2	154	von willebrand domain-containing protein	587	1.16E-120	54.40%	0.241	IPR002035 (G3DSA:3.40.50.GENE3D); PF13768 (PFAM); PTHR10338 (PANTHER); PTHR10338:SF95 (PANTHER); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
1525	489930_length_1761_cvg_29.6_tip_1_0	231	factor d-like protein	587	2.01E-79	50.70%	0.108	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1543	490318_length_1790_cvg_61.0_tip_1_2	713	atpase family aaa domain-containing protein 1-b	588	1.68E-164	77.60%	0.122	IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); PTHR23074 (PANTHER); PTHR23074:SF20 (PANTHER); IPR003960 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY)
1526	490004_length_1766_cvg_10.6_tip_1_0	78	von willebrand domain-containing protein	589	5.18E-90	61.20%	0.099	Coil (COILS); IPR013694 (SMART); IPR013694 (PFAM); PTHR10338 (PANTHER); PTHR10338:SF95 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR013694 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1527	490022_length_1767_cvg_56.8_tip_1_3	493	golgi-associated plant pathogenesis-related protein 1	589	2.39E-157	62.40%	0.103	IPR001283 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); PTHR10334:SF189 (PANTHER); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); IPR014044 (SUPERFAMILY); IPR014044 (SUPERFAMILY)
1545	490388_length_1795_cvg_9.4_tip_1_1	87	peptidyl-alpha-hydroxyglycine alpha-amidating lyase 2-like	590	1.18E-109	60.50%	0.208	IPR000720 (PRINTS); IPR011042 (G3DSA:2.120.10.GENE3D); IPR001258 (PFAM); PTHR10680 (PANTHER); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); SSF101898 (SUPERFAMILY)
1549	490454_length_1798_cvg_50.8_tip_1_3	517	prophenoloxidase activating factor	590	2.15E-131	65.60%	0.106	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF95 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1534	490114_length_1775_cvg_2.3_tip_1_1	20	zinc finger protein 37-like	592	6.09E-19	52.10%	0.101	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY);
1548	490430_length_1797_cvg_38.0_tip_1_3	394	superoxide dismutase	592	8.81E-62	68.70%	0.203	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY); IPR001424 (SUPERFAMILY); TMhelix (TMHMM)
1536	490156_length_1778_cvg_4.0_tip_1_1	39	fez family zinc finger protein 2	593	0	80.10%	0.103	Coil (COILS); IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1537	490162_length_1778_cvg_4.1_tip_1_4	28	cgmp-dependent protein isozyme 2 forms cd4 t1 t3a t3b isoform x2	593	0	90.20%	0.105	Coil (COILS); IPR002374 (PRINTS); IPR002290 (SMART); IPR000595 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000595 (PFAM); IPR000719 (PFAM); IPR014710 (G3DSA:2.60.120.GENE3D); IPR002374 (PIRSF); IPR014710 (G3DSA:2.60.120.GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24353:SF65 (PANTHER); PTHR24353 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR000595 (PROSITE_PROFILES); IPR000595 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); IPR018490 (SUPERFAMILY); IPR018490 (SUPERFAMILY)
1538	490178_length_1779_cvg_5.5_tip_1_4	46	cation channel sperm-associated protein 2	593	1.56E-72	54.60%	0.132	Coil (COILS); IPR005821 (PFAM); IPR027359 (G3DSA:1.20.120.GENE3D); PTHR10037 (PANTHER); IPR028747 (PTHR10037:PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF81324 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1553	490528_length_1803_cvg_19.4_tip_1_3	162	zinc finger protein 37 homolog isoform x1	593	2.31E-57	64.00%	0.132	IPR015880 (SMART); IPR000210 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); G3DSA:3.30.710.10 (GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013069 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR000210 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); IPR011333 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)

1565	491000_length_1841_cvg_9.8_tip_1_4	126	puromycin-sensitive aminopeptidase	593	3.49E-101	80.00%	0.113	Coil (COILS); IPR024571 (PFAM); IPR001930 (PANTHER); PTHR11533:SF163 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1540	490220_length_1783_cvg_6.1_tip_1_5	53	nitrilase and fragile histidine triad fusion protein hit	594	0	69.50%	0.112	Coil (COILS); IPR003010 (G3DSA:3.60.110.GENE3D); IPR001310 (PFAM); IPR011146 (G3DSA:3.30.428.GENE3D); IPR003010 (PFAM); PTHR23088:SF5 (PANTHER); PTHR23088 (PANTHER); IPR019808 (PROSITE_PATTERNS); IPR001110 (PROSITE_PATTERNS); IPR011146 (PROSITE_PROFILES); IPR003010 (PROSITE_PROFILES); IPR003010 (SUPERFAMILY); IPR011146 (SUPERFAMILY)
1541	490258_length_1785_cvg_21.6_tip_1_0	229	villin-1-like isoform x2	595	0	66.30%	0.1	IPR007122 (PRINTS); IPR003128 (SMART); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR003128 (PFAM); IPR003128 (G3DSA:1.10.950.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007122 (PANTHER); IPR003128 (PROSITE_PROFILES); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF82754 (SUPERFAMILY); IPR003128 (SUPERFAMILY)
1552	490520_length_1803_cvg_23.2_tip_1_2	206	lamin dm0-like isoform x1	596	1.17E-170	74.40%	0.148	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); G3DSA:1.20.5.170 (GENE3D); IPR001322 (G3DSA:2.60.40.GENE3D); IPR001322 (PFAM); IPR001664 (PFAM); IPR027696 (PTHR23239:PANTHER); IPR001664 (PANTHER); IPR018039 (PROSITE_PATTERNS); SSF64593 (SUPERFAMILY); IPR001322 (SUPERFAMILY)
1544	490344_length_1791_cvg_57.0_tip_1_5	877	n-acetylated-alpha-linked acidic dipeptidase	597	3.38E-143	59.60%	0.136	IPR007484 (PFAM); G3DSA:3.50.30.30 (GENE3D); IPR007365 (G3DSA:1.20.930.GENE3D); G3DSA:3.40.630.10 (GENE3D); IPR007365 (PFAM); PTHR10404 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); IPR007365 (SUPERFAMILY); SSF52025 (SUPERFAMILY)
1546	490422_length_1797_cvg_17.8_tip_1_2	180	acyl- delta desaturase	599	1.88E-128	72.50%	0.304	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351 (PANTHER); PTHR11351:SF28 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1547	490426_length_1797_cvg_14.2_tip_1_1	118	zinc finger protein	599	6.28E-32	53.10%	0.134	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1559	490836_length_1826_cvg_28.3_tip_1_5	233	c protein immunoglobulin-a-binding beta antigen	599	8.34E-33	56.40%	0.298	G3DSA:2.160.10.10 (GENE3D); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1551	490470_length_1799_cvg_8.8_tip_1_1	96	plexin domain-containing protein 2-like	600	3.99E-117	70.40%	0.335	IPR016201 (SMART); G3DSA:3.30.1680.10 (GENE3D); PTHR13055 (PANTHER); PTHR13055:SF12 (PANTHER)
1554	490552_length_1805_cvg_2.2_tip_1_1	27	hypothetical protein BRAFLDRAFT_125057	602	3.29E-12	47.10%	0.107	no IPS match

1568	491080_length_1847_cvg_3.9_tip_1_5	38	chitinase 1 precursor	615	0	70.50%	0.128	IPR002557 (SMART); IPR011583 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR002557 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF144 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR017853 (SUPERFAMILY); IPR029070 (SUPERFAMILY); IPR002557 (SUPERFAMILY)
1583	491356_length_1872_cvg_15.8_tip_1_1	174	a disintegrin and metalloproteinase with thrombospondin motifs 18	615	1.58E-60	55.10%	0.112	IPR006586 (SMART); IPR001590 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR13723 (PANTHER); IPR001590 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY)
1569	491124_length_1851_cvg_14.5_tip_1_2	135	rna-binding protein 5-like	617	4.61E-151	64.90%	0.106	Coil (COILS); IPR000467 (SMART); IPR000467 (PFAM); PTHR13948 (PANTHER); IPR000467 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES)
1570	491130_length_1852_cvg_12.4_tip_1_4	101	secreted frizzled-related protein 3	617	1.01E-78	59.70%	0.254	Coil (COILS); IPR020067 (SMART); IPR018933 (SMART); G3DSA:2.40.50.120 (GENE3D); IPR020067 (PFAM); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR018933 (PFAM); PTHR11309:SF83 (PANTHER); IPR015526 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020067 (PROSITE_PROFILES); IPR001134 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY); IPR020067 (SUPERFAMILY)
1571	491144_length_1852_cvg_5.1_tip_1_4	58	flavin-containing monooxygenase fmo gs-ox3	617	2.52E-141	64.30%	0.273	IPR000960 (PRINTS); G3DSA:3.50.50.60 (GENE3D); G3DSA:3.50.50.60 (GENE3D); IPR020946 (PFAM); PTHR23023 (PANTHER); PTHR23023:SF4 (PANTHER); SSF51905 (SUPERFAMILY); SSF51905 (SUPERFAMILY)
1579	491274_length_1864_cvg_57.3_tip_1_3	812	tribbles homolog 2	617	1.53E-121	71.70%	0.11	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR22961:SF4 (PANTHER); IPR024104 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1573	491178_length_1855_cvg_5.5_tip_1_3	47	dual specificity mitogen-activated protein kinase kinase 4-like	619	0	89.90%	0.117	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24360:SF46 (PANTHER); PTHR24360 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1574	491208_length_1857_cvg_8.9_tip_1_4	104	scp-like extracellular domain containing protein 1	619	1.91E-69	60.30%	0.237	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); PTHR10334:SF174 (PANTHER); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR014044 (SUPERFAMILY); TMhelix (TMHMM)
1576	491210_length_1858_cvg_7.9_tip_1_2	79	#NAME?	619	5.14E-46	71.60%	0.215	IPR001830 (PFAM); G3DSA:3.40.50.2000 (GENE3D); PTHR10788:SF6 (PANTHER); PTHR10788 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53756 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1575	491210_length_1858_cvg_7.9_tip_1_0	79	trehalose 6-phosphate synthase 1	620	4.53E-28	68.90%	0.364 Y	IPR001830 (PFAM); G3DSA:3.40.50.2000 (GENE3D); G3DSA:3.40.50.2000 (GENE3D); PTHR10788:SF6 (PANTHER); PTHR10788 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SSF53756 (SUPERFAMILY)
1593	491566_length_1895_cvg_10.1_tip_1_5	84	transposable element tcb1 partial	621	6.00E-25	60.70%	0.122	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

1595	491592_length_1897_cvg_31.6_tip_1_2	271	low quality protein: hemocytin-like	621	4.77E-75	53.50%	0.114	IPR006207 (SMART); IPR006208 (PFAM); PTHR11339:SF229 (PANTHER); PTHR11339 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006207 (PROSITE_PROFILES); SSF57603 (SUPERFAMILY); SSF57603 (SUPERFAMILY)
1580	491326_length_1869_cvg_6.1_tip_1_5	51	insulin-degrading enzyme	623	2.93E-178	72.80%	0.113	IPR007863 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); IPR011237 (G3DSA:3.30.830.GENE3D); PTHR11851:SF85 (PANTHER); PTHR11851 (PANTHER); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY)
1581	491342_length_1871_cvg_27.1_tip_1_4	453904	suppressor of tumorigenicity 14 protein	624	2.70E-51	52.30%	0.126	IPR001314 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1582	491352_length_1872_cvg_30.3_tip_1_1	311	angiotensin-converting enzyme	624	0	78.10%	0.133	IPR001548 (PRINTS); IPR001548 (PFAM); PTHR10514:SF17 (PANTHER); IPR001548 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1596	491594_length_1897_cvg_41.0_tip_1_5	360	probable cytochrome p450 49a1	624	6.74E-137	60.50%	0.146	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24305 (PANTHER); PTHR24305:SF49 (PANTHER); IPR017972 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1584	491412_length_1879_cvg_4.8_tip_1_2	60	wd repeat-containing protein 37	626	0	77.10%	0.12	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19855:SF12 (PANTHER); PTHR19855 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1585	491418_length_1879_cvg_41.5_tip_1_4	361	serine threonine-protein kinase grp-like	626	0	74.50%	0.129	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24344 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1586	491458_length_1883_cvg_9.4_tip_1_1	78	serine threonine-protein kinase osr1 isoform x2	628	0	83.30%	0.111	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.10.20.90 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); IPR024678 (PFAM); PTHR24361:SF201 (PANTHER); PTHR24361 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1587	491470_length_1884_cvg_5.4_tip_1_1	54	97 kda heat shock	628	0	78.90%	0.126	IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.90.640.10 (GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF78 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY)
1588	491480_length_1885_cvg_31.5_tip_1_2	248	carbohydrate sulfotransferase 11	628	5.95E-30	49.40%	0.098	IPR005331 (PFAM); IPR018011 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)

1594	491580_length_1897_cvg_15.6_tip_1_1	107	arginine abc periplasmic arginine-binding protein	632	0	99.40%	0.126	IPR001320 (SMART); IPR001638 (SMART); PF00497 (PFAM); IPR005768 (TIGRFAM); G3DSA:3.40.190.10 (GENE3D); G3DSA:3.40.190.10 (GENE3D); PTHR18966:SF152 (PANTHER); PTHR18966 (PANTHER); IPR018313 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53850 (SUPERFAMILY)
1597	491630_length_1903_cvg_18.7_tip_1_5	192	btb poz domain-containing protein 17	634	0	75.30%	0.142	IPR000210 (SMART); IPR011705 (SMART); G3DSA:3.30.710.10 (GENE3D); IPR013069 (PFAM); IPR011705 (PFAM); PTHR24410:SF9 (PANTHER); PTHR24410 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000210 (PROSITE_PROFILES); IPR011333 (SUPERFAMILY); TMhelix (TMHMM)
1598	491634_length_1903_cvg_3.0_tip_1_2	31	zinc finger protein 436-like isoform x2	634	5.85E-42	59.70%	0.321	IPR000210 (SMART); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013069 (PFAM); G3DSA:3.30.710.10 (GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR000210 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); IPR011333 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
1599	491638_length_1903_cvg_30.6_tip_1_3	343	protein disulfide-isomerase a6	635	1.61E-140	81.70%	0.102	PR00421 (PRINTS); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005788 (TIGRFAM); PTHR18929:SF38 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
1600	491674_length_1907_cvg_4.7_tip_1_3	48	sortilin-related I(dlr class) a repeats-containing-like isoform x2	636	0	69.90%	0.114	IPR002172 (PRINTS); IPR002172 (SMART); IPR000742 (SMART); IPR000033 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR000033 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR12106:SF7 (PANTHER); PTHR12106 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY)
1611	491958_length_1937_cvg_17.7_tip_1_0	152	adp-ribosylation factor-like protein 4a	638	7.82E-109	86.80%	0.114	IPR006689 (PRINTS); IPR024156 (SMART); IPR003579 (SMART); IPR006687 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR11711 (PANTHER); PTHR11711:SF121 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1615	492050_length_1948_cvg_50.0_tip_1_2	652	peptidylglycine alpha-hydroxylating monooxygenase	639	1.50E-167	78.10%	0.157	IPR000720 (PRINTS); IPR000323 (G3DSA:2.60.120.GENE3D); IPR000323 (PFAM); PF03712 (PFAM); IPR014784 (G3DSA:2.60.120.GENE3D); PTHR10680 (PANTHER); IPR014783 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008977 (SUPERFAMILY); IPR008977 (SUPERFAMILY); IPR008977 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1603	491808_length_1920_cvg_5.8_tip_1_2	65	antigen partial	640	0	99.10%	0.184	IPR024973 (PFAM); IPR012332 (G3DSA:2.160.20.GENE3D); PTHR12338 (PANTHER); IPR011050 (SUPERFAMILY)
1604	491846_length_1924_cvg_60.1_tip_1_1	8613	retinal dehydrogenase 1-like	641	0	82.10%	0.207	IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF145 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM)
1610	491948_length_1937_cvg_22.4_tip_1_3	207	gtp-binding protein sar1	641	5.09E-123	93.90%	0.249	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR006689 (PFAM); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF133 (PANTHER); PTHR11711 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006687 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1605	491878_length_1927_cvg_13.8_tip_1_2	152	serine threonine-protein phosphatase 6 regulatory ankyrin repeat subunit c-like	642	8.46E-96	55.00%	0.123	IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1616	492058_length_1949_cvg_61.8_tip_1_1	554	u8-agatoxin-ao1a-like isoform x2	642	3.78E-32	78.10%	0.366 Y	IPR004169 (PFAM); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF57059 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1618	492108_length_1954_cvg_20.3_tip_1_1	268	mitochondrial 10-formyltetrahydrofolate dehydrogenase	643	0	91.80%	0.134	IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF118 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
1606	491908_length_1932_cvg_24.5_tip_1_0	163	agap005714-pa-like protein	644	1.06E-156	50.20%	0.1	IPR000436 (SMART); IPR001881 (SMART); IPR000742 (SMART); IPR003410 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); PF14670 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR023413 (G3DSA:2.40.155.GENE3D); PTHR24034 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR003410 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR009030 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1607	491922_length_1934_cvg_57.3_tip_1_3	629	wd repeat-containing protein 86-like	645	8.52E-128	65.60%	0.118	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22844:SF166 (PANTHER); PTHR22844 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR011047 (SUPERFAMILY); TMhelix (TMHMM)

1609	491946_length_1937_cvg_48.6_tip_1_5	571	zinc finger protein 239-like	645	3.55E-26	53.40%	0.138	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1622	492202_length_1966_cvg_63.6_tip_1_5	1552	hypothetical protein TcasGA2_TC013968	645	1.82E-10	46.29%	0.136	Coil (COILS); PTHR11008:SF13 (PANTHER); PTHR11008 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020234 (PRODOM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1608	491932_length_1936_cvg_17.9_tip_1_0	182	cytochrome p450	646	0	69.90%	0.33	Coil (COILS); IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24290:SF0 (PANTHER); PTHR24290 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
1612	491968_length_1939_cvg_57.0_tip_1_2	489	cell recognition protein caspr4 isoform 5	646	1.08E-66	54.10%	0.103	IPR001073 (SMART); IPR001073 (PFAM); IPR000885 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); IPR008983 (G3DSA:2.60.120.GENE3D); PTHR10127:SF575 (PANTHER); PTHR10127 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY); IPR002181 (SUPERFAMILY); IPR002181 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1625	492252_length_1972_cvg_13.9_tip_1_4	246	coatomer subunit alpha	647	0	81.70%	0.109	IPR010714 (PFAM); IPR006692 (PFAM); PTHR19876 (PANTHER)
1613	492018_length_1944_cvg_26.8_tip_1_3	265	ankyrin-1-like isoform x3	648	0	80.20%	0.108	IPR002110 (PRINTS); IPR001496 (SMART); IPR002110 (SMART); IPR001496 (SMART); IPR002110 (PFAM); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR001496 (PFAM); PTHR24133 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001496 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); SSF158235 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1614	492038_length_1946_cvg_59.0_tip_1_0	789	ddb1- and cul4-associated factor 13-like	649	0	80.80%	0.104	IPR001680 (SMART); IPR001680 (PFAM); IPR007287 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22851:SF0 (PANTHER); PTHR22851 (PANTHER); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)

1623	492218_length_1968_cvg_44.2_tip_1_3	554	hypothetical protein L798_04491	649	4.36E-34	63.40%	0.107	IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR21104 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1619	492124_length_1956_cvg_7.0_tip_1_3	97	esterase fe4	652	1.61E-65	70.80%	0.108	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR019826 (PROSITE_PATTERNS); IPR019819 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
1620	492124_length_1956_cvg_7.0_tip_1_4	97	venom carboxylesterase-6	652	1.09E-38	53.10%	0.137	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1621	492184_length_1963_cvg_3.8_tip_1_1	52	iron zinc purple acid phosphatase-like protein	654	0	75.30%	0.297	IPR015914 (G3DSA:2.60.40.GENE3D); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); IPR025733 (PFAM); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY); IPR008963 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1624	492240_length_1970_cvg_7.8_tip_1_5	75	calcium calmodulin-dependent protein kinase ii isoform a	656	0	93.60%	0.138	IPR002290 (SMART); IPR013543 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:3.10.450.50 (GENE3D); PTHR24347:SF108 (PANTHER); IPR020636 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); SSF54427 (SUPERFAMILY); IPR011009 (SUPERFAMILY)
1633	492442_length_1999_cvg_58.9_tip_1_2	2859	hemagglutinin amebocyte aggregation factor-like	657	1.22E-39	61.10%	0.159	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1631	492378_length_1989_cvg_61.9_tip_1_4	1087	lissencephaly-1 homolog	658	0	90.90%	0.171	Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR006594 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR006594 (PFAM); IPR001680 (PFAM); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017252 (HAMAP); SSF109925 (SUPERFAMILY); IPR017986 (SUPERFAMILY)
1626	492276_length_1975_cvg_2.7_tip_1_0	35	peroxisomal multifunctional enzyme type 2	659	0	71.90%	0.139	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR013968 (SMART); PF13452 (PFAM); IPR003033 (G3DSA:3.30.1050.GENE3D); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002539 (PFAM); IPR029069 (G3DSA:3.10.129.GENE3D); IPR029069 (G3DSA:3.10.129.GENE3D); PTHR24316:SF2 (PANTHER); PTHR24316 (PANTHER); IPR020904 (PROSITE_PATTERNS); IPR029069 (SUPERFAMILY); SSF51735 (SUPERFAMILY); IPR029069 (SUPERFAMILY)
1627	492346_length_1986_cvg_2.9_tip_1_4	42	transmembrane protease serine partial	662	1.07E-12	76.50%	0.101	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

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1656	493030_length_2095_cvg_6.5_tip_1_3	86	probable chitinase 3	699	3.08E-133	56.50%	0.266	IPR011583 (SMART); IPR002557 (SMART); IPR002557 (PFAM); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR001579 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR017853 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR029070 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1658	493048_length_2098_cvg_62.9_tip_1_4	5871	heat shock 70 kda protein cognate 3	699	0	95.00%	0.102	Coil (COILS); Coil (COILS); IPR013126 (PRINTS); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.90.640.10 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); IPR013126 (PFAM); PTHR19375:SF157 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); IPR029048 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1659	493056_length_2099_cvg_8.0_tip_1_2	86	mannosyl-oligosaccharide -alpha-mannosidase ia isoform x1	699	1.32E-53	87.40%	0.109	IPR001382 (PRINTS); IPR001382 (PFAM); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PANTHER); PTHR11742:SF6 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001382 (SUPERFAMILY); TMhelix (TMHMM)
1663	493190_length_2123_cvg_3.0_tip_1_1	39	zinc finger protein 850-like isoform x1	699	2.15E-32	54.50%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007527 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY);
1665	493218_length_2132_cvg_4.2_tip_1_2	45	neural cell adhesion molecule 1-b	702	1.88E-71	57.20%	0.103	IPR003599 (SMART); IPR003961 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF48 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1660	493102_length_2109_cvg_28.7_tip_1_0	306	dehydrogenase reductase sdr family member 11-like	703	3.58E-111	77.10%	0.165	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR013968 (SMART); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF78 (PANTHER); IPR020904 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1662	493162_length_2121_cvg_2.0_tip_1_5	27	glutaminy-peptide cyclotransferase	707	2.90E-39	68.60%	0.133	IPR007484 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR12283 (PANTHER); SSF53187 (SUPERFAMILY)

1679	493508_length_2197_cvg_10.8_tip_1_1	115	cyclin-dependent kinase 9-like	732	0	93.40%	0.109	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24056 (PANTHER); PTHR24056:SF158 (PANTHER); IPR008271 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1688	493638_length_2224_cvg_6.3_tip_1_2	109	krueppel-like factor 3 isoform x1	732	1.26E-61	71.20%	0.139	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); PTHR23223:SF132 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1692	493678_length_2235_cvg_58.9_tip_1_1	722	vegetative cell wall protein gp1-like	732	4.28E-14	48.90%	0.162	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1693	493678_length_2235_cvg_58.9_tip_1_3	722	muc19_human ame: full=mucin-19 short=muc-19 flags: partial	732	1.21E-33	50.70%	0.099	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1680	493512_length_2198_cvg_13.8_tip_1_0	150	nicotinic acetylcholine receptor subunit alpha10	733	6.59E-105	59.10%	0.675 Y	IPR006201 (PRINTS); IPR006029 (PFAM); IPR006202 (PFAM); IPR027361 (G3DSA:1.20.120.GENE3D); IPR006202 (G3DSA:2.70.170.GENE3D); PTHR18945:SF490 (PANTHER); IPR006201 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR006202 (SUPERFAMILY); IPR006029 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1689	493640_length_2225_cvg_28.7_tip_1_1	253	dnaj homolog subfamily c member 7	733	0	74.80%	0.109	IPR001623 (PRINTS); IPR019734 (SMART); IPR001623 (SMART); PF13414 (PFAM); IPR019734 (PFAM); IPR001623 (PFAM); IPR013105 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF140 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR001623 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); SSF48452 (SUPERFAMILY); SSF48452 (SUPERFAMILY)

1690	493650_length_2230_cvg_52.7_tip_1_3	1148	adp-ribosylation factor 1	744	2.23E-126	98.70%	0.313	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR003579 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR11711 (PANTHER); PTHR11711:SF118 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1691	493674_length_2234_cvg_3.6_tip_1_2	51	nephrin isoform x1	744	1.09E-158	65.40%	0.101	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013162 (PFAM); IPR013098 (PFAM); PTHR11640:SF31 (PANTHER); PTHR11640 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1699	493740_length_2254_cvg_26.6_tip_1_2	360	ectoderm-expressed 3	744	3.92E-154	57.30%	0.135	IPR001944 (PRINTS); IPR001944 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR008979 (G3DSA:2.60.120.GENE3D); IPR001944 (PANTHER); PTHR23421:SF13 (PANTHER); IPR019801 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY); IPR008979 (SUPERFAMILY)
1704	493768_length_2263_cvg_19.3_tip_1_5	224	coatomer subunit beta isoform x2	744	0	78.20%	0.129	IPR006692 (PFAM); PTHR19876 (PANTHER); PTHR19876:SF2 (PANTHER); IPR011044 (SUPERFAMILY)
1694	493680_length_2235_cvg_12.4_tip_1_2	122	zinc finger protein 77-like isoform x2	745	1.06E-29	56.30%	0.15	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1695	493686_length_2240_cvg_62.9_tip_1_4	6242	hemocyanin subunit type 1 precursor	747	0	75.50%	0.372	IPR013788 (PRINTS); IPR005203 (G3DSA:2.60.40.GENE3D); IPR000896 (PFAM); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR005204 (PFAM); IPR005203 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR013788 (PANTHER); PTHR11511:SF5 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); IPR002227 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005204 (SUPERFAMILY); IPR008922 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
1696	493706_length_2246_cvg_5.6_tip_1_1	66	lachesin-like isoform x1	749	2.91E-86	73.00%	0.32	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR23279:SF12 (PANTHER); PTHR23279 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)

									Coil (COILS); IPR001547 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR31308 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY)
1697	493726_length_2251_cvg_10.8_tip_1_4	120	glycoside catalytic core	750	8.25E-94	54.00%	0.173		IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR019826 (PROSITE_PATTERNS); IPR019819 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR029058 (SUPERFAMILY)
1698	493738_length_2253_cvg_15.0_tip_1_5	155	venom carboxylesterase-6 isoform x2	751	2.24E-137	58.20%	0.909	Y	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
1701	493746_length_2255_cvg_4.0_tip_1_0	58	cytochrome p450 2j6-like	752	9.31E-105	56.00%	0.146		IPR002223 (PRINTS); IPR003645 (SMART); IPR002223 (SMART); IPR008197 (SMART); IPR002223 (PFAM); IPR008197 (G3DSA:4.10.75.GENE3D); IPR008197 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008197 (PROSITE_PROFILES); IPR008197 (PROSITE_PROFILES); IPR008197 (PROSITE_PROFILES); IPR008197 (PROSITE_PROFILES); IPR008197 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR008197 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1703	493758_length_2261_cvg_19.4_tip_1_0	306	egf domain protein	754	1.65E-11	41.60%	0.467	Y	IPR002618 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR002618 (PANTHER); IPR016267 (PTHR11952:PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1705	493778_length_2267_cvg_53.8_tip_1_0	567	utp--glucose-1-phosphate uridylyltransferase-like	756	0	84.40%	0.108		IPR029033 (G3DSA:3.40.50.GENE3D); IPR000560 (PFAM); PTHR20963 (PANTHER); PTHR20963:Sf8 (PANTHER); IPR000560 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029033 (SUPERFAMILY); TMhelix (TMHMM)
1706	493828_length_2280_cvg_32.5_tip_1_2	939	multiple inositol polyphosphate phosphatase 1	760	1.94E-142	61.20%	0.29		IPR001839 (SMART); IPR001111 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001839 (PFAM); PTHR11848:Sf131 (PANTHER); IPR015615 (PANTHER); IPR017948 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1707	493852_length_2287_cvg_3.7_tip_1_2	42	transforming growth factor beta superfamily signaling ligand	762	3.21E-87	54.20%	0.151		IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24152 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1711	493940_length_2317_cvg_39.4_tip_1_5	443	myotrophin-like isoform 2	764	6.55E-53	84.20%	0.141		IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24152 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1713	493972_length_2326_cvg_48.4_tip_1_5	665	facilitated trehalose transporter tret1-like isoform x1	766	5.31E-111	58.80%	0.11	IPR003663 (PRINTS); G3DSA:1.20.1250.20 (GENE3D); IPR003663 (TIGRFAM); IPR005828 (PFAM); PTHR24063 (PANTHER); IPR005829 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020846 (PROSITE_PROFILES); SSF141571 (SUPERFAMILY); IPR020846 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1708	493900_length_2307_cvg_50.2_tip_1_5	597	low quality protein: hemocytin	769	1.09E-79	47.10%	0.819 Y	IPR001846 (SMART); IPR001846 (PFAM); IPR014853 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR11339 (PANTHER); PTHR11339:SF25 (PANTHER); IPR001846 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002919 (SUPERFAMILY)
1709	493908_length_2309_cvg_10.0_tip_1_2	141	neuropeptides capa receptor-like	769	1.38E-149	74.00%	0.327	Coil (COILS); IPR005390 (PRINTS); IPR000276 (PRINTS); IPR000276 (PFAM); G3DSA:1.20.1070.10 (GENE3D); PTHR24243 (PANTHER); PTHR24243:SF107 (PANTHER); IPR000276 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017452 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1710	493912_length_2309_cvg_3.2_tip_1_1	49	probable chitinase 3	770	4.44E-130	56.80%	0.106	IPR011583 (SMART); IPR002557 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR002557 (PFAM); IPR029070 (G3DSA:3.10.50.GENE3D); IPR001223 (PFAM); IPR002557 (G3DSA:2.170.140.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR001579 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR002557 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1721	494088_length_2364_cvg_65.4_tip_1_5	46408	heat shock cognate protein 70	773	0	94.80%	0.179	Coil (COILS); IPR013126 (PRINTS); IPR029048 (G3DSA:1.20.1270.GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.30.30 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.90.640.10 (GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029048 (SUPERFAMILY)

1712	493964_length_2323_cvg_13.9_tip_1_5	187	poc1 centriolar protein homolog a	774	0	73.40%	0.231	Coil (COILS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847:SF319 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1717	494042_length_2347_cvg_9.0_tip_1_1	95	zinc finger protein 501 isoform x2	774	6.80E-11	60.30%	0.172	IPR000210 (SMART); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013069 (PFAM); G3DSA:3.30.710.10 (GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR000210 (PROSITE_PROFILES); IPR011333 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
1714	493994_length_2334_cvg_5.1_tip_1_4	57	cadherin egf lag seven-pass g-type receptor 1-like isoform x6	778	2.63E-35	44.10%	0.151	IPR000832 (PFAM); PTHR12011:SF74 (PANTHER); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1715	494014_length_2341_cvg_45.5_tip_1_4	478	iduronate 2-sulfatase	780	0	67.60%	0.462 Y	G3DSA:3.30.1120.10 (GENE3D); IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342:SF185 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017850 (SUPERFAMILY)
1716	494016_length_2341_cvg_17.7_tip_1_3	202	wd repeat-containing protein 82	781	0	94.80%	0.18	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19861:SF2 (PANTHER); PTHR19861 (PANTHER); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1728	494156_length_2388_cvg_7.9_tip_1_4	110	membrane-associated guanylate ww and pdz domain-containing protein 1-like isoform x1	796	4.10E-35	81.40%	0.161	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR10316:SF40 (PANTHER); PTHR10316 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1736	494282_length_2452_cvg_51.4_tip_1_5	868	heat shock 70 kda protein cognate 5	800	0	89.00%	0.22	Coil (COILS); IPR013126 (PRINTS); G3DSA:3.30.30.30 (GENE3D); G3DSA:3.90.640.10 (GENE3D); IPR012725 (TIGRFAM); IPR029048 (G3DSA:1.20.1270.GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); PTHR19375:SF173 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR012725 (HAMAP); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
1731	494218_length_2425_cvg_7.6_tip_1_3	91	phospholipase a2	809	1.44E-26	48.90%	0.161	IPR016090 (SMART); IPR016090 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PANTHER); PTHR11716:SF45 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016090 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1732	494230_length_2433_cvg_32.0_tip_1_0	1145	beta- -n-acetylgalactosaminyltransferase bre-4	811	1.40E-121	66.60%	0.323	IPR003859 (PRINTS); IPR027791 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR009053 (G3DSA:1.10.287.GENE3D); IPR027995 (PFAM); IPR004127 (PFAM); IPR003859 (PANTHER); PTHR19300:SF30 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009053 (SUPERFAMILY); IPR029044 (SUPERFAMILY); TMhelix (TMHMM)
1733	494232_length_2433_cvg_9.6_tip_1_1	137	carboxypeptidase e	811	0	73.90%	0.138	IPR000834 (PRINTS); IPR000834 (SMART); IPR014766 (G3DSA:2.60.40.GENE3D); PF13620 (PFAM); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11532:SF41 (PANTHER); PTHR11532 (PANTHER); IPR000834 (PROSITE_PATTERNS); IPR000834 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); IPR008969 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1734	494234_length_2434_cvg_63.2_tip_1_3	1092	pdgf- and vegf-related factor 1-like precursor	812	7.84E-53	55.80%	0.159	IPR000072 (SMART); IPR000072 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); PTHR11633 (PANTHER); PTHR11633:SF1 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000072 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1741	494322_length_2472_cvg_12.8_tip_1_2	170	mitogen-activated protein kinase 15-like	814	0	73.00%	0.151	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24055:SF79 (PANTHER); PTHR24055 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR003527 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1746	494368_length_2489_cvg_89.6_tip_1_0	17714	membrane metallo-endopeptidase-like 1-like	816	0	67.50%	0.146	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR008753 (PFAM); IPR018497 (PFAM); IPR000718 (PANTHER); PTHR11733:SF113 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1737	494290_length_2454_cvg_4.2_tip_1_1	97	ectonucleoside triphosphate diphosphohydrolase 2-like isoform x4	818	2.62E-105	54.30%	0.168	IPR000407 (PFAM); IPR000407 (PANTHER); IPR000407 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1743	494354_length_2483_cvg_12.6_tip_1_4	155	leucine-rich repeat-containing protein 47-like	819	8.81E-173	67.80%	0.121	IPR003591 (SMART); IPR005146 (SMART); SM00364 (SMART); IPR025875 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR005146 (PFAM); PTHR10947 (PANTHER); PTHR10947:SF2 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1738	494300_length_2458_cvg_5.1_tip_1_0	77	eukaryotic translation initiation factor 2-alpha kinase 3	820	1.36E-112	52.50%	0.173	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR11042 (PANTHER); PTHR11042:SF86 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1739	494302_length_2458_cvg_66.9_tip_1_3	22192	enolase	820	0	89.50%	0.196	IPR000941 (PRINTS); IPR029017 (G3DSA:3.30.390.GENE3D); IPR020811 (PFAM); IPR000941 (TIGRFAM); IPR029065 (G3DSA:3.20.20.GENE3D); IPR020810 (PFAM); IPR000941 (PANTHER); IPR020809 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000941 (HAMAP); IPR029017 (SUPERFAMILY); IPR029065 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1744	494356_length_2483_cvg_48.3_tip_1_0	1135	extracellular matrix protein partial	820	5.62E-22	40.10%	0.106	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001007 (PROSITE_PROFILES); IPR006207 (PROSITE_PROFILES); TMhelix (TMHMM)
1740	494320_length_2472_cvg_63.9_tip_1_1	837	zinc metalloproteinase nas-13-like isoform 1	824	7.99E-133	54.80%	0.291	IPR001506 (PRINTS); IPR003582 (SMART); IPR006026 (SMART); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR003582 (PFAM); PTHR10127 (PANTHER); PTHR10127:SF550 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003582 (PROSITE_PROFILES); IPR003582 (PROSITE_PROFILES); IPR003582 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1754	494442_length_2523_cvg_56.4_tip_1_0	863	alpha beta hydrolase domain-containing protein 13	824	1.76E-137	75.10%	0.129	IPR029058 (G3DSA:3.40.50.GENE3D); IPR029059 (PFAM); PTHR12277 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1742	494342_length_2478_cvg_16.0_tip_1_0	193	n-sulphoglucosamine partial	826	0	78.30%	0.127	Coil (COILS); IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); PTHR10342 (PANTHER); PTHR10342:SF76 (PANTHER); IPR024607 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017850 (SUPERFAMILY)
1750	494414_length_2513_cvg_14.3_tip_1_2	223	inversin-like isoform x3	827	1.96E-58	74.30%	0.219	IPR002110 (SMART); IPR000048 (SMART); IPR000048 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24178 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR000048 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1745	494366_length_2486_cvg_10.5_tip_1_3	109	group 3 secretory phospholipase a2	829	1.07E-45	68.30%	0.137	IPR001211 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR12253 (PANTHER); IPR016090 (SUPERFAMILY)
1752	494420_length_2515_cvg_60.2_tip_1_3	1991	hemocyanin subunit type 2 precursor	830	0	73.10%	0.881 Y	IPR013788 (PRINTS); IPR005203 (PFAM); IPR000896 (PFAM); IPR005204 (PFAM); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005203 (G3DSA:2.60.40.GENE3D); IPR013788 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR002227 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR008922 (SUPERFAMILY); IPR014756 (SUPERFAMILY); IPR005204 (SUPERFAMILY); TMhelix (TMHMM)
1747	494378_length_2498_cvg_32.0_tip_1_4	374	e3 ubiquitin-protein ligase hakai	833	6.69E-75	74.20%	0.326	PTHR13480:SF0 (PANTHER); PTHR13480 (PANTHER); IPR017907 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001841 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1748	494396_length_2502_cvg_14.6_tip_1_3	177	glucosylceramidase-like	834	3.74E-180	66.20%	0.111	IPR001139 (PRINTS); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001139 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); PTHR11069:SF7 (PANTHER); IPR001139 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); SSF51011 (SUPERFAMILY)
1749	494412_length_2512_cvg_4.6_tip_1_2	72	telomerase protein component 1-like	837	2.62E-36	42.10%	0.101	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR017986 (SUPERFAMILY)

1756	494494_length_2568_cvg_55.2_tip_1_5	17610	suppressor of tumorigenicity 14 partial	856	2.10E-67	53.40%	0.738 Y	IPR002172 (PRINTS); IPR001254 (SMART); IPR002172 (SMART); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1757	494510_length_2578_cvg_56.0_tip_1_3	709	cathepsin d	860	0	80.70%	0.655 Y	IPR001461 (PRINTS); IPR012848 (PFAM); IPR021109 (G3DSA:2.40.70.GENE3D); IPR021109 (G3DSA:2.40.70.GENE3D); IPR001461 (PFAM); PTHR13683:SF230 (PANTHER); IPR001461 (PANTHER); IPR001969 (PROSITE_PATTERNS); IPR001969 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR021109 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1758	494518_length_2581_cvg_39.6_tip_1_2	714	tyrosine-protein phosphatase non-receptor type 9 isoform x1	860	0	67.70%	0.287	IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR001251 (G3DSA:3.40.525.GENE3D); IPR001251 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134:SF232 (PANTHER); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR001251 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); IPR001251 (SUPERFAMILY)
1761	494560_length_2635_cvg_10.4_tip_1_4	138	polypeptide n-acetylgalactosaminyltransferase 5 isoform x2	870	0	85.90%	0.101	IPR000772 (SMART); IPR000772 (PFAM); IPR001173 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); G3DSA:2.80.10.50 (GENE3D); PTHR11675 (PANTHER); PTHR11675:SF39 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000772 (PROSITE_PROFILES); IPR029044 (SUPERFAMILY); IPR000772 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1760	494540_length_2614_cvg_6.6_tip_1_2	83	aminopeptidase n	871	0	100.00%	0.375 Y	IPR014782 (PRINTS); IPR012779 (TIGRFAM); IPR024601 (G3DSA:1.25.50.GENE3D); G3DSA:1.10.390.10 (GENE3D); IPR024601 (PFAM); IPR014782 (PFAM); PTHR11533:SF152 (PANTHER); IPR001930 (PANTHER); SSF63737 (SUPERFAMILY); SSF55486 (SUPERFAMILY)
1763	494574_length_2650_cvg_15.9_tip_1_1	195	exocyst complex component 3	877	0	74.20%	0.135	Coil (COILS); IPR010326 (PFAM); IPR010326 (PANTHER); PTHR21292:SF1 (PANTHER)
1765	494582_length_2662_cvg_21.5_tip_1_0	266	vitellogenin 2	879	2.10E-66	43.80%	0.129	IPR001846 (SMART); IPR015255 (PFAM); IPR001846 (PFAM); PTHR23345:SF1 (PANTHER); PTHR23345 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001846 (PROSITE_PROFILES); IPR015819 (SUPERFAMILY)
1766	494590_length_2671_cvg_20.0_tip_1_3	260	zinc finger protein 239- partial	880	9.82E-52	60.10%	0.136	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1762	494566_length_2642_cvg_17.9_tip_1_3	294	serine threonine-protein phosphatase 6 catalytic subunit	881	0	93.80%	0.164	IPR006186 (PRINTS); IPR006186 (SMART); IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); PTHR11668 (PANTHER); PTHR11668:SF24 (PANTHER); IPR006186 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
1764	494576_length_2652_cvg_28.8_tip_1_3	563	hemagglutinin	884	6.30E-90	66.00%	0.113	IPR023612 (PRINTS); IPR007280 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); G3DSA:1.10.390.10 (GENE3D); IPR013856 (PFAM); IPR001570 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1767	494594_length_2687_cvg_54.2_tip_1_0	1848	cell surface protein	896	1.12E-13	42.70%	0.396 Y	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1768	494602_length_2700_cvg_12.4_tip_1_2	138	#NAME?	900	1.50E-116	99.80%	0.17	IPR002180 (PFAM); IPR002180 (TIGRFAM); IPR000728 (PFAM); IPR016188 (G3DSA:3.30.1330.GENE3D); IPR002180 (G3DSA:3.40.50.GENE3D); IPR002180 (PANTHER); PTHR21058:SF0 (PANTHER); IPR002180 (HAMAP); IPR016188 (SUPERFAMILY); IPR002180 (SUPERFAMILY)
1770	494614_length_2713_cvg_32.5_tip_1_3	433	zinc finger protein	900	5.30E-30	51.80%	0.121	Coil (COILS); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1769	494604_length_2701_cvg_15.9_tip_1_3	231	dnaj homolog subfamily b member 11	901	0	84.50%	0.733 Y	IPR001623 (PRINTS); IPR001623 (SMART); IPR002939 (PFAM); G3DSA:2.60.260.20 (GENE3D); IPR001623 (G3DSA:1.10.287.GENE3D); G3DSA:2.60.260.20 (GENE3D); IPR001623 (PFAM); PTHR24077 (PANTHER); PTHR24077:SF210 (PANTHER); IPR018253 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR008971 (SUPERFAMILY); IPR008971 (SUPERFAMILY); IPR001623 (SUPERFAMILY)
1771	494624_length_2732_cvg_3.2_tip_1_0	52	cd109 antigen	911	0	64.00%	0.105	IPR008930 (G3DSA:1.50.10.GENE3D); IPR011626 (PFAM); PTHR11412 (PANTHER); PTHR11412:SF85 (PANTHER); IPR008930 (SUPERFAMILY)
1772	494632_length_2737_cvg_7.2_tip_1_0	122	kr domain protein	913	5.29E-148	99.00%	0.359 Y	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF265 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
1773	494646_length_2769_cvg_9.7_tip_1_2	134	fimbrial family protein	923	3.44E-120	99.50%	0.734 Y	IPR000259 (G3DSA:2.60.40.GENE3D); IPR000259 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR008966 (SUPERFAMILY)
1774	494648_length_2772_cvg_6.8_tip_1_0	156	angiotensin-converting enzyme-like	924	2.05E-162	61.70%	0.271	Coil (COILS); IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1775	494654_length_2789_cvg_49.8_tip_1_1	9780	intestinal mucin-like	930	1.59E-24	40.90%	0.1	IPR006207 (SMART); IPR001007 (SMART); IPR001007 (PFAM); IPR001007 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001007 (PROSITE_PROFILES); IPR006207 (PROSITE_PROFILES)

1776	494658_length_2792_cvg_37.7_tip_1_0	450	map kinase-interacting serine threonine-protein kinase 1	931	0	81.40%	0.12	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24349 (PANTHER); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1778	494688_length_2881_cvg_24.9_tip_1_2	642	hemocytin isoform x1	951	3.85E-26	41.20%	0.118	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006207 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM)
1777	494686_length_2881_cvg_32.9_tip_1_0	1056	gamma-glutamyltransferase 7	961	1.91E-108	54.80%	0.225	IPR000101 (PRINTS); IPR000101 (PFAM); PTHR11686:SF18 (PANTHER); IPR000101 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029055 (SUPERFAMILY); TMhelix (TMHMM)
1780	494714_length_2926_cvg_18.0_tip_1_4	327	vitellogenin receptor	967	3.98E-83	45.10%	0.106	IPR002172 (PRINTS); IPR002172 (SMART); IPR001881 (SMART); IPR000033 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR10529 (PANTHER); PTHR10529:SF204 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1779	494712_length_2921_cvg_36.2_tip_1_5	512	titin- partial	973	3.93E-148	72.50%	0.111	PR00014 (PRINTS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF142 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1781	494728_length_2965_cvg_14.9_tip_1_3	200	transducin beta-like protein 3	974	9.14E-175	69.00%	0.103	Coil (COILS); Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR013934 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19854 (PANTHER); PTHR19854:SF15 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1782	494732_length_2973_cvg_42.5_tip_1_0	2428	receptor-type tyrosine-protein phosphatase n2	991	0	87.30%	0.232	IPR000242 (PRINTS); IPR000242 (SMART); IPR003595 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134:SF2 (PANTHER); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1784	494748_length_3081_cvg_12.5_tip_1_4	231	serine threonine-protein phosphatase 2a catalytic subunit alpha isoform	1018	0	97.10%	0.1	Coil (COILS); IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668 (PANTHER); PTHR11668:SF216 (PANTHER); IPR006186 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029052 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1783	494746_length_3076_cvg_16.5_tip_1_5	183	neutral alpha-glucosidase ab-like	1025	0	73.80%	0.125	IPR025887 (PFAM); IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF54 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51011 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR011013 (SUPERFAMILY)
1785	494762_length_3126_cvg_12.6_tip_1_3	165	atp-dependent rna helicase ddx1	1035	0	83.50%	0.14	IPR014001 (SMART); IPR001650 (SMART); IPR003877 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR001650 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR011545 (PFAM); IPR003877 (PFAM); PTHR24031 (PANTHER); PTHR24031:SF211 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014014 (PROSITE_PROFILES); IPR001650 (PROSITE_PROFILES); IPR001870 (PROSITE_PROFILES); IPR014001 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1786	494766_length_3145_cvg_18.6_tip_1_1	382	basement membrane-specific heparan sulfate proteoglycan core protein	1048	6.20E-96	58.40%	0.102	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013151 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1787	494770_length_3157_cvg_69.1_tip_1_1	12425	plasminogen activator spa	1052	8.89E-58	55.50%	0.231	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1788	494776_length_3200_cvg_5.9_tip_1_1	91	zinc finger protein	1067	6.37E-37	59.40%	0.109	Coil (COILS); IPR015880 (SMART); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

Supplementary Table 5

1794	494844_length_3965_cvg_29.6_tip_1_1	1103	neutral and basic amino acid transport protein rbat	1322	3.57E-160	56.50%	0.189	IPR006589 (SMART); G3DSA:3.90.400.10 (GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR006047 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); PTHR10357:SF77 (PANTHER); IPR015902 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1795	494846_length_3995_cvg_22.9_tip_1_2	2782	long form-like	1322	0	86.30%	0.123	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR002928 (PFAM); PTHR13140:SF164 (PANTHER); PTHR13140 (PANTHER); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY)
1796	494848_length_4019_cvg_62.7_tip_1_2	179426	levansucrase	1339	0	99.30%	0.146	IPR023296 (G3DSA:2.115.10.GENE3D); IPR003469 (PFAM); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023296 (SUPERFAMILY); TMhelix (TMHMM)
1797	494848_length_4019_cvg_62.7_tip_1_5	179426	hypothetical protein ECP02989421_5334	1339	6.03E-84	83.90%	0.119	Coil (COILS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1798	494854_length_4495_cvg_43.9_tip_1_5	7406	myosin heavy chain isoform 2	1498	0	90.00%	0.107	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR002928 (PFAM); G3DSA:1.20.5.340 (GENE3D); PTHR13140:SF364 (PANTHER); PTHR13140 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); TMhelix (TMHMM)

Supplementary Table 6: Whole body transcriptome (SOAPdenovo-Tran contigs that match against secreted proteins [UniProtSL0243])

Nr.	Contig name	Read Numbers	Blast result (evalue= 10^{-5} , BlastP, Nr database)	Seq. length	min. evalue	mean similarity	SignalP	InterProScan
2290	55825_length_139_cvg_14.0_tip_0_5	0	phospholipase b-like 2	46	1.08E-15	86.70%	0.098	IPR007000 (PFAM); PTHR12370:SF3 (PANTHER); IPR007000 (PANTHER)
2291	55827_length_139_cvg_9.3_tip_0_5	0	phospholipase b-like 2	46	6.75E-13	80.90%	0.099	IPR007000 (PFAM)
2292	56659_length_141_cvg_63.0_tip_0_0	0	---NA---	47			0.115	PF14704 (PFAM)
2293	56661_length_141_cvg_63.0_tip_0_0	0	hemagglutinin amebocyte aggregation factor	47	2.38E-06	65.00%	0.114	PF14704 (PFAM)
2294	56779_length_141_cvg_8.3_tip_1_4	0	---NA---	47			0.11	IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR002223 (SUPERFAMILY)
2296	57979_length_142_cvg_2.0_tip_1_1	1	very low-density lipoprotein receptor	47	9.80E-12	72.90%	0.104	IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (SUPERFAMILY)
2297	58471_length_142_cvg_2.0_tip_1_5	2	notch 2	47	3.22E-07	67.00%	0.148	IPR011641 (PFAM)
2299	59727_length_142_cvg_4.6_tip_1_4	2	dipeptidyl peptidase 1	47	1.59E-16	84.20%	0.1	IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF314 (PANTHER); IPR013128 (PANTHER); IPR000169 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
2300	59761_length_142_cvg_2.0_tip_1_4	1	reelin-like isoform x4	47	7.42E-08	77.89%	0.106	no IPS match
2301	60087_length_142_cvg_2.0_tip_1_2	2	tyrosine-protein kinase btk29a	47	4.31E-21	95.20%	0.26	IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418:SF162 (PANTHER); PTHR24418 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2302	60507_length_142_cvg_2.0_tip_1_1	1	proclotting enzyme	47	1.10E-11	75.60%	0.138	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
2303	61187_length_142_cvg_3.0_tip_1_1	1	tachykinins isoform x3	47	3.85E-10	76.60%	0.107	no IPS match
2305	61595_length_143_cvg_2.0_tip_1_2	2	polypeptide n-acetylgalactosaminyltransferase 5 isoform x2	47	8.62E-24	93.40%	0.183	PTHR11675 (PANTHER); PTHR11675:SF21 (PANTHER)
2308	62575_length_143_cvg_2.6_tip_1_2	2	er degradation-enhancing alpha-mannosidase-like protein 1	47	2.09E-19	92.80%	0.095	IPR001382 (PFAM); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PANTHER); PTHR11742:SF25 (PANTHER); IPR001382 (SUPERFAMILY)
2311	63651_length_143_cvg_2.0_tip_1_2	2	xanthine dehydrogenase	47	8.20E-19	93.40%	0.109	IPR012675 (G3DSA:3.10.20.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR001041 (SUPERFAMILY)
2312	63711_length_143_cvg_4.0_tip_1_2	0	retinol dehydrogenase 14-like	47	4.95E-12	78.00%	0.109	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF305 (PANTHER); PTHR24316 (PANTHER); SSF51735 (SUPERFAMILY)
2314	64527_length_143_cvg_2.0_tip_1_2	1	dentin matrix protein 4- partial	47	5.03E-21	94.80%	0.103	IPR029207 (PFAM); PTHR12450:SF8 (PANTHER); IPR024869 (PANTHER)
2295	57913_length_142_cvg_2.0_tip_1_3	1	von willebrand factor a domain-containing protein 8- partial	48	7.13E-19	92.20%	0.095	IPR011704 (PFAM); PTHR21610 (PANTHER); PTHR21610:SF9 (PANTHER)
2298	59651_length_142_cvg_2.0_tip_1_3	2	protein fam132a	48	3.28E-09	77.90%	0.2	no IPS match
2304	61511_length_143_cvg_2.0_tip_1_1	1	---NA---	48			0.156	no IPS match
2306	62125_length_143_cvg_2.9_tip_1_0	1	ubiquitin carboxyl-terminal hydrolase	48	9.26E-11	68.00%	0.104	no IPS match
2307	62573_length_143_cvg_3.0_tip_1_1	1	alpha beta hydrolase domain-containing protein 17c	48	1.04E-16	92.20%	0.477 Y	PTHR12277:SF52 (PANTHER); PTHR12277 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
2309	63159_length_143_cvg_2.0_tip_1_3	2	matrix metalloproteinase-14-like	48	6.04E-20	87.80%	0.115	IPR000585 (G3DSA:2.110.10.GENE3D); IPR018487 (PFAM); PTHR10201:SF135 (PANTHER); PTHR10201 (PANTHER); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY)
2310	63567_length_143_cvg_2.0_tip_1_0	1	epidermal growth factor receptor isoform x1	48	8.09E-21	90.40%	0.102	G3DSA:2.10.220.10 (GENE3D); PTHR24416:SF95 (PANTHER); PTHR24416 (PANTHER)
2313	64021_length_143_cvg_2.0_tip_1_4	1	fic domain-containing partial	48	6.07E-21	93.80%	0.106	IPR003812 (G3DSA:1.10.3290.GENE3D); IPR003812 (PFAM); PTHR13504:SF12 (PANTHER); PTHR13504 (PANTHER); IPR003812 (PROSITE_PROFILES); IPR003812 (SUPERFAMILY)
2315	64691_length_143_cvg_3.0_tip_1_0	3	ring finger and spry domain-containing protein 1-like	48	2.00E-20	92.40%	0.098	PTHR13363 (PANTHER)
2316	65057_length_144_cvg_2.0_tip_1_2	1	matrix metalloproteinase	48	1.50E-10	69.20%	0.144	IPR021190 (PRINTS); IPR001818 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10201 (PANTHER); SSF55486 (SUPERFAMILY)
2317	65739_length_144_cvg_3.0_tip_1_2	3	de-cadherin-like isoform x2	48	7.32E-09	73.70%	0.096	no IPS match
2318	65967_length_144_cvg_2.0_tip_1_5	2	adenylate cyclase type 8 isoform x2	48	6.93E-23	93.80%	0.124	IPR001054 (G3DSA:3.30.70.GENE3D); IPR001054 (PFAM); PTHR11920:SF236 (PANTHER); PTHR11920 (PANTHER); IPR018297 (PROSITE_PATTERNS); IPR001054 (PROSITE_PROFILES); IPR029787 (SUPERFAMILY)

2319	66459_length_144_cvg_2.0_tip_1_2	2	receptor-type tyrosine-protein phosphatase kappa-like	48	4.22E-16	85.10%	0.1	IPR000242 (PRINTS); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134:SF227 (PANTHER); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
2320	67017_length_144_cvg_2.0_tip_1_0	2	beta- -galactosyltransferase 1-like	48	2.83E-12	71.60%	0.103	IPR027791 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
2321	67221_length_144_cvg_2.0_tip_1_1	1	tyrosine-protein kinase transmembrane receptor ror1-like	48	2.11E-19	86.90%	0.1	G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416 (PANTHER); PTHR24416:SF309 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2322	67235_length_144_cvg_6.2_tip_1_4	0	---NA---	48			0.113	IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (SUPERFAMILY)
2323	67577_length_144_cvg_2.0_tip_1_1	2	epidermal growth factor receptor isoform x2	48	1.17E-16	89.00%	0.097	IPR000494 (G3DSA:3.80.20.GENE3D); SSF52058 (SUPERFAMILY)
2324	68047_length_144_cvg_2.3_tip_1_5	0	ubiquitin carboxyl-terminal hydrolase	48	4.84E-11	69.38%	0.103	no IPS match
2326	69411_length_145_cvg_2.0_tip_1_1	2	partial	48	1.47E-23	99.40%	0.106	IPR011614 (G3DSA:2.40.180.GENE3D); IPR011614 (PFAM); IPR018028 (PANTHER); IPR020835 (SUPERFAMILY)
2325	68553_length_145_cvg_2.0_tip_1_3	1	zinc finger and scan domain-containing protein 2-like	49	2.24E-17	84.40%	0.147	IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2327	69591_length_145_cvg_2.0_tip_1_3	2	cre-bli-4 protein	49	6.85E-10	75.60%	0.101	IPR000209 (G3DSA:3.40.50.GENE3D); IPR000209 (SUPERFAMILY)
2328	70853_length_145_cvg_2.0_tip_1_3	2	fibrillin-2-like	49	7.15E-19	91.20%	0.116	G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); PTHR24039:SF20 (PANTHER); IPR011398 (PANTHER); IPR000152 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY)
2329	71019_length_145_cvg_2.0_tip_1_0	1	moxd1 homolog 1-like	49	7.03E-08	67.70%	0.146	IPR000323 (G3DSA:2.60.120.GENE3D); IPR000323 (PFAM); IPR008977 (SUPERFAMILY)
2330	73573_length_146_cvg_2.0_tip_1_3	1	polypeptide n-acetylgalactosaminyltransferase 5 isoform x1	49	1.34E-22	93.90%	0.126	PTHR11675:SF21 (PANTHER); PTHR11675 (PANTHER); IPR029044 (SUPERFAMILY)
2331	73881_length_146_cvg_62.1_tip_1_3	21	leucine-rich repeat-containing protein 45- partial	49	2.14E-06	70.00%	0.248	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
2332	74393_length_146_cvg_2.0_tip_1_0	2	---NA---	49			0.106	IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
2333	74545_length_146_cvg_3.0_tip_1_0	1	furin-like protease isoforms 1 1-x 2-like	49	1.12E-18	88.80%	0.113	IPR000209 (G3DSA:3.40.50.GENE3D); IPR015500 (PANTHER); PTHR10795:SF71 (PANTHER); IPR000209 (SUPERFAMILY)
2334	74645_length_146_cvg_2.0_tip_1_0	2	14/03/2003	49	1.06E-13	88.70%	0.102	G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023410 (SUPERFAMILY)
2335	75617_length_147_cvg_3.0_tip_1_5	1	protein 5nuc-like	49	2.64E-15	82.20%	0.096	IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11575:SF21 (PANTHER); IPR006179 (PANTHER); IPR029052 (SUPERFAMILY)
2336	75849_length_147_cvg_3.0_tip_1_0	0	dopamine beta hydroxylase	49	4.12E-09	66.20%	0.101	IPR005018 (PFAM); IPR000945 (PANTHER); PTHR10157:SF23 (PANTHER); IPR005018 (PROSITE_PROFILES)
2337	76097_length_147_cvg_2.0_tip_1_3	1	serine threonine-protein kinase tao1 isoform x1	49	1.54E-24	95.50%	0.112	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24361:SF259 (PANTHER); PTHR24361 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2338	77657_length_147_cvg_3.0_tip_1_5	3	endothelial lipase	49	5.92E-11	75.00%	0.206	IPR013818 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR000734 (PANTHER); IPR029058 (SUPERFAMILY)
2341	80069_length_148_cvg_5.0_tip_1_5	0	collagen type iv	49	6.43E-20	87.20%	0.137	IPR001442 (SMART); IPR001442 (G3DSA:2.170.240.GENE3D); IPR001442 (PFAM); PTHR24023:SF397 (PANTHER); PTHR24023 (PANTHER); IPR001442 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
2342	80565_length_148_cvg_2.0_tip_1_5	0	vitellogenin partial	49	1.28E-14	85.40%	0.098	no IPS match
2344	81249_length_148_cvg_2.0_tip_1_2	2	bone morphogenetic protein 10	49	2.59E-20	82.80%	0.149	IPR001839 (SMART); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001839 (PFAM); IPR015615 (PANTHER); PTHR11848:SF146 (PANTHER); IPR017948 (PROSITE_PATTERNS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)
2345	82099_length_149_cvg_2.0_tip_1_2	2	epidermal growth factor receptor	49	2.85E-11	74.60%	0.126	IPR006212 (SMART); G3DSA:2.10.220.10 (GENE3D); PF14843 (PFAM); IPR009030 (SUPERFAMILY)
2346	82301_length_149_cvg_2.0_tip_1_5	1	lysosomal pro-x	49	2.71E-16	81.50%	0.101	IPR008758 (PFAM); PTHR11010:SF31 (PANTHER); IPR008758 (PANTHER)
2348	82517_length_149_cvg_4.0_tip_1_5	1	isoform a	49	2.85E-19	84.40%	0.11	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF144 (PANTHER); PTHR11177 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
2349	82575_length_149_cvg_2.0_tip_1_2	1	carboxypeptidase s	49	6.53E-13	83.00%	0.104	G3DSA:3.40.630.10 (GENE3D); PTHR11014 (PANTHER); PTHR11014:SF66 (PANTHER); SSF53187 (SUPERFAMILY)
2339	78887_length_148_cvg_3.0_tip_1_3	0	lysosomal pro-x carboxypeptidase	50	5.75E-17	84.00%	0.098	IPR008758 (PFAM); PTHR11010:SF11 (PANTHER); IPR008758 (PANTHER)
2340	79833_length_148_cvg_2.0_tip_1_0	2	---NA---	50			0.101	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
2343	81157_length_148_cvg_2.0_tip_1_3	2	---NA---	50			0.096	no IPS match

2347	82389_length_149_cvg_2.0_tip_1_1	3	isoform b	50	5.36E-21	92.20%	0.097	G3DSA:3.30.200.20 (GENE3D); IPR001245 (PFAM); PTHR24418 (PANTHER); PTHR24418:SF0 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2350	82673_length_149_cvg_6.0_tip_1_4	0	---NA---	50			0.103	PF14704 (PFAM)
2351	83441_length_149_cvg_2.0_tip_1_4	3	peptidyl-prolyl cis-trans isomerase a- partial	50	7.60E-20	87.20%	0.145	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
2352	83571_length_149_cvg_2.0_tip_1_0	2	zinc finger protein	50	2.22E-19	85.20%	0.096	IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR23228 (PANTHER); PTHR23228:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2353	83839_length_149_cvg_2.0_tip_1_1	3	serine protease nudel	50	2.42E-21	82.10%	0.12	IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (SUPERFAMILY)
2354	87869_length_150_cvg_2.0_tip_1_4	2	laminin subunit alpha	50	1.55E-16	77.20%	0.117	G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF39 (PANTHER)
2355	87911_length_150_cvg_3.0_tip_1_4	2	chondroitin sulfate synthase 1-like	50	1.34E-20	91.80%	0.1	IPR008428 (PFAM); PTHR12369 (PANTHER); PTHR12369:SF11 (PANTHER)
2356	88159_length_150_cvg_3.0_tip_1_4	1	aael007486- partial	50	2.38E-17	85.50%	0.117	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR019826 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
2357	88747_length_150_cvg_3.0_tip_1_0	2	calcium-activated chloride channel regulator 4-like	50	7.39E-09	64.80%	0.121	IPR013642 (PFAM)
2358	88941_length_150_cvg_2.0_tip_1_3	2	von willebrand factor type egf and pentraxin domain-containing protein 1	50	4.72E-13	80.00%	0.107	IPR001881 (SMART); IPR000742 (SMART); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24049:SF6 (PANTHER); PTHR24049 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
2359	89473_length_150_cvg_4.0_tip_1_1	3	basement membrane-specific heparan sulfate proteoglycan core protein	50	5.77E-12	75.70%	0.105	no IPS match
2360	89787_length_150_cvg_2.0_tip_1_4	1	dopamine beta-hydroxylase	50	1.79E-06	67.40%	0.112	IPR000945 (PANTHER)
2361	90033_length_150_cvg_4.0_tip_1_4	2	glyceraldehyde-3-phosphate partial	50	2.57E-20	91.20%	0.104	IPR020831 (PRINTS); IPR020829 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020831 (PANTHER); IPR020830 (PROSITE_PATTERNS); SSF55347 (SUPERFAMILY)
2362	90143_length_150_cvg_2.0_tip_1_3	1	fibrillin-2-like	50	3.08E-17	83.10%	0.122	G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); PTHR24039:SF20 (PANTHER); IPR011398 (PANTHER); SSF57196 (SUPERFAMILY)
2363	92997_length_150_cvg_2.0_tip_1_3	1	sialate o-acetyltransferase isoform x1	50	4.23E-10	78.90%	0.177	IPR005181 (PFAM)
2364	93721_length_150_cvg_2.0_tip_1_0	3	sushi von willebrand factor type a egf pentraxin domain-containing partial	50	9.78E-08	60.60%	0.111	IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY)
2365	93927_length_150_cvg_4.0_tip_1_4	4	heat shock protein 70	50	1.58E-16	84.80%	0.103	IPR013126 (PFAM); IPR029047 (G3DSA:2.60.34.GENE3D); PTHR19375:SF156 (PANTHER); PTHR19375 (PANTHER); IPR029047 (SUPERFAMILY)
2366	94339_length_151_cvg_3.0_tip_1_5	5	xanthine dehydrogenase partial	50	2.62E-24	94.40%	0.098	IPR002888 (PFAM); IPR002888 (G3DSA:1.10.150.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR002888 (SUPERFAMILY)
2367	95511_length_151_cvg_2.0_tip_1_2	4	syntaxin 1a	50	9.32E-19	83.10%	0.102	Coil (COILS); G3DSA:1.20.58.70 (GENE3D); IPR006011 (PFAM); IPR010989 (SUPERFAMILY)
2368	95759_length_152_cvg_2.0_tip_1_0	2	secreted protein with kunitz	51	2.22E-18	76.50%	0.114	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY)
2369	95975_length_152_cvg_102.6_tip_1_0	308	trypsin-like serine proteinase 1	51	1.20E-09	64.50%	0.32	G3DSA:2.40.10.10 (GENE3D); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009003 (SUPERFAMILY)
2370	96301_length_152_cvg_5.2_tip_1_3	0	heat shock protein partial	51	7.87E-23	95.30%	0.11	G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.90.640.10 (GENE3D); PTHR19375:SF137 (PANTHER); PTHR19375 (PANTHER); SSF53067 (SUPERFAMILY)
2371	97170_length_153_cvg_3.0_tip_1_3	4	kielin chordin-like protein	51	9.36E-17	78.70%	0.14	IPR014853 (SMART); IPR014853 (PFAM); PTHR11339 (PANTHER)
2372	98334_length_154_cvg_2.0_tip_1_2	2	receptor-type tyrosine-protein phosphatase mu	51	1.80E-10	73.10%	0.105	IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
2	102236_length_158_cvg_3.0_tip_1_2	3	protein cbg25156	52	5.14E-06	54.00%	0.102	IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
2373	98804_length_155_cvg_2.0_tip_1_1	2	deoxyribonuclease-1-like 2-like	52	2.24E-10	81.10%	0.099	IPR005135 (G3DSA:3.60.10.GENE3D); IPR016202 (PANTHER); IPR005135 (SUPERFAMILY)
2374	99236_length_155_cvg_36.2_tip_0_0	28	egcse_cyano ame: full=endoglycoceramidase short=egc case ame: full=glycosphingolipid-specific enzyme short=gsl-specific enzyme flags: precursor	52	1.16E-11	80.33%	0.102	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)

2375	99238_length_155_cvg_63.0_tip_0_0	95	egcse_cyano ame: full=endoglycoceramidase short=egcase ame: full=glycosphingolipid-specific enzyme short=gsl-specific enzyme flags: precursor	52	1.16E-11	80.33%	0.102	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
2376	99640_length_155_cvg_2.0_tip_1_1	2	Af1-cadherin	52	1.81E-06	67.50%	0.106	no IPS match
1	102208_length_158_cvg_2.0_tip_1_4	2	---NA---	53			0.104	IPR008160 (PFAM)
3	103152_length_159_cvg_2.0_tip_1_4	0	variable lymphocyte receptor a	53	1.94E-06	69.00%	0.128	PR00019 (PRINTS); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
4	103416_length_160_cvg_4.0_tip_1_1	4	proclotting enzyme	53	7.72E-10	65.40%	0.136	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260:SF3 (PANTHER); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
6	104090_length_160_cvg_3.0_tip_1_4	4	secretory phospholipase a2 receptor	53	1.82E-06	65.33%	0.1	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
5	103454_length_160_cvg_63.0_tip_1_0	573	serine protease inhibitor dipetalogastin-like	54	3.24E-06	72.00%	0.099	IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY)
7	104256_length_161_cvg_2.0_tip_1_3	0	transforming growth factor-beta-induced protein ig-h3	54	5.16E-20	72.70%	0.103	IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900 (PANTHER); PTHR10900:SF73 (PANTHER); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY)
8	104358_length_161_cvg_62.0_tip_0_0	15	colostrum trypsin inhibitor-like	54	2.06E-13	74.70%	0.101	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY)
9	104644_length_161_cvg_63.0_tip_0_3	248	glyceraldehyde-3-phosphate dehydrogenase	54	2.54E-13	89.70%	0.123	PTHR10836:SF31 (PANTHER); IPR020831 (PANTHER)
10	104710_length_161_cvg_3.7_tip_1_3	2	xylosyltransferase 1-like	54	4.86E-12	63.60%	0.102	no IPS match
11	104890_length_161_cvg_2.0_tip_1_0	2	leucomyosuppressin precursor	54	8.56E-23	81.50%	0.247	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS)
12	105574_length_162_cvg_2.0_tip_1_5	1	epidermal growth factor receptor isoform x1	54	6.73E-29	100.00%	0.131	G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416 (PANTHER); PTHR24416:SF95 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
13	105650_length_162_cvg_63.0_tip_0_4	24	fibroleukin-like isoform x1	54	5.25E-07	68.00%	0.106	IPR002181 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
14	105984_length_163_cvg_4.0_tip_1_1	4	hyaluronidase- partial	54	9.85E-09	70.90%	0.102	IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); IPR018155 (PANTHER); PTHR11769:SF8 (PANTHER); IPR017853 (SUPERFAMILY)
15	106044_length_163_cvg_3.0_tip_1_5	3	---NA---	54			0.104	IPR013642 (PFAM)
16	106196_length_163_cvg_2.0_tip_1_4	1	down syndrome cell adhesion	54	5.55E-22	90.00%	0.114	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF567 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
17	106244_length_163_cvg_2.0_tip_1_2	1	peptidyl-alpha-hydroxyglycine alpha-amidating lyase 1	54	2.03E-10	70.30%	0.107	IPR001258 (PFAM)
18	106402_length_163_cvg_3.4_tip_1_4	1	peptidyl-prolyl cis-trans isomerase nima-interacting 1-like	54	6.32E-23	82.80%	0.11	G3DSA:3.10.50.40 (GENE3D); PTHR10657 (PANTHER); SSF54534 (SUPERFAMILY)
20	106972_length_164_cvg_2.0_tip_1_2	2	attractin-like protein 1	54	7.18E-23	94.80%	0.193	PTHR10574:SF3 (PANTHER); PTHR10574 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
19	106958_length_164_cvg_2.0_tip_1_4	1	cub and sushi domain-containing protein 1	55	1.52E-07	53.80%	0.1	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY)
21	106986_length_164_cvg_9.0_tip_1_1	4	adenosine deaminase cecr1-like	55	3.33E-19	84.10%	0.108	IPR001365 (PFAM); G3DSA:3.20.20.140 (GENE3D); PTHR11409 (PANTHER); PTHR11409:SF39 (PANTHER); SSF51556 (SUPERFAMILY)
22	108732_length_166_cvg_28.2_tip_0_5	4	techlectin- partial	55	9.16E-12	72.90%	0.127	IPR002181 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); PTHR19143 (PANTHER); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
23	108752_length_166_cvg_62.0_tip_0_4	13	hemagglutinin amebocyte aggregation factor-like	55	9.40E-10	66.50%	0.102	PF14704 (PFAM); IPR026645 (PANTHER)
24	108754_length_166_cvg_63.0_tip_0_4	44	hemagglutinin amebocyte aggregation factor-like	55	1.79E-08	63.40%	0.099	PF14704 (PFAM); PTHR15040:SF3 (PANTHER); IPR026645 (PANTHER)
25	109168_length_167_cvg_63.0_tip_0_0	31	---NA---	56			0.152	no IPS match
26	109720_length_168_cvg_2.0_tip_1_2	1	laminin a	56	1.32E-17	75.70%	0.1	G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); IPR013032 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
27	110249_length_168_cvg_4.0_tip_1_2	6	er degradation-enhancing alpha-mannosidase-like protein 2	56	7.56E-27	92.20%	0.202	IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); IPR001382 (PANTHER); PTHR11742:SF37 (PANTHER); IPR001382 (SUPERFAMILY)
28	110419_length_168_cvg_2.0_tip_1_3	0	carboxypeptidase a2-like	56	1.43E-14	73.80%	0.13	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
29	110659_length_169_cvg_29.0_tip_1_4	1	hemagglutinin amebocyte aggregation factor-like	56	1.73E-10	70.90%	0.105	PF14704 (PFAM); IPR026645 (PANTHER)

30	110727_length_169_cvg_2.2_tip_1_2	4	ankyrin domain-containing protein	56	5.83E-09	68.50%	0.138	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); PF13857 (PFAM); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
32	111137_length_169_cvg_2.0_tip_1_5	3	imaginal disc growth factor	56	1.95E-23	86.80%	0.134	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR017853 (SUPERFAMILY)
31	110923_length_169_cvg_122.7_tip_0_3	596	anti-lipopolysaccharide factor isoform 7	57	4.20E-15	73.60%	0.118	IPR024509 (PFAM); IPR024716 (PRODOM)
33	111991_length_171_cvg_2.0_tip_1_3	1	neurogenic locus protein partial	57	6.03E-16	70.50%	0.11	IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); PTHR24033:SF0 (PANTHER); PTHR24033 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
34	112135_length_171_cvg_63.0_tip_1_5	88	---NA---	57			0.097	G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY)
35	112379_length_171_cvg_2.0_tip_1_2	2	low quality protein: von willebrand factor type egf and pentraxin domain-containing protein 1	57	9.43E-18	79.20%	0.112	PR00010 (PRINTS); IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24049 (PANTHER); PTHR24049:SF6 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
36	113019_length_172_cvg_2.0_tip_1_1	2	tyrosine-protein kinase src64b isoform x1	57	3.50E-21	86.20%	0.11	IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
37	113913_length_174_cvg_63.0_tip_1_2	510	partial	58	1.37E-16	80.80%	0.117	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24264 (PANTHER); IPR009003 (SUPERFAMILY)
38	114249_length_174_cvg_63.0_tip_0_5	75	hemagglutinin amebocyte aggregation factor-like	58	1.37E-10	66.80%	0.119	PF14704 (PFAM); IPR026645 (PANTHER)
39	114309_length_174_cvg_4.0_tip_1_4	5	proprotein convertase subtilisin kexin type 5	58	2.66E-11	71.20%	0.108	G3DSA:3.30.70.850 (GENE3D)
40	114729_length_175_cvg_2.0_tip_1_4	2	acid sphingomyelinase-like phosphodiesterase 3a	58	1.88E-07	57.67%	0.794 Y	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE)
41	115223_length_176_cvg_11.0_tip_1_5	9	peptidase m4	58	1.58E-09	69.50%	0.099	IPR023612 (PRINTS); IPR013856 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); SSF55486 (SUPERFAMILY)
42	115267_length_176_cvg_20.0_tip_1_2	15	hemagglutinin amebocyte aggregation factor-like	58	3.77E-10	64.60%	0.102	PF14704 (PFAM); IPR026645 (PANTHER)
43	115341_length_176_cvg_2.5_tip_1_0	2	alcohol dehydrogenase	59	1.51E-13	69.80%	0.127	IPR023210 (G3DSA:3.20.20.GENE3D); PTHR11732:SF183 (PANTHER); IPR001395 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
44	115509_length_176_cvg_63.0_tip_0_0	265	chitinase partial	59	1.26E-15	70.00%	0.147	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR029070 (G3DSA:3.10.50.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR029070 (SUPERFAMILY)
45	115511_length_176_cvg_63.0_tip_0_0	158	chitinase partial	59	6.65E-16	69.00%	0.146	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR029070 (SUPERFAMILY)
46	115799_length_177_cvg_4.0_tip_1_4	4	cysteine-rich with egf-like domain protein 2	59	1.02E-12	79.60%	0.101	no IPS match
47	116507_length_178_cvg_2.0_tip_1_5	1	proprotein convertase subtilisin kexin type	59	1.39E-17	77.00%	0.11	G3DSA:3.30.70.850 (GENE3D); PTHR10795:SF325 (PANTHER); IPR015500 (PANTHER); IPR009020 (SUPERFAMILY)
48	116763_length_178_cvg_2.0_tip_1_1	1	hexamerin 1	59	1.23E-21	85.30%	0.1	IPR005203 (PFAM); IPR005203 (G3DSA:2.60.40.GENE3D); PTHR11511:SF5 (PANTHER); IPR013788 (PANTHER); IPR014756 (SUPERFAMILY)
49	117133_length_179_cvg_2.0_tip_1_3	2	---NA---	60			0.1	IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
50	117839_length_180_cvg_4.0_tip_1_2	4	glyceraldehyde-3-phosphate dehydrogenase	60	1.59E-23	88.30%	0.159	G3DSA:3.30.360.10 (GENE3D); IPR020829 (PFAM); PTHR10836:SF31 (PANTHER); IPR020831 (PANTHER); SSF55347 (SUPERFAMILY)
51	117991_length_180_cvg_3.0_tip_1_4	1	peripheral plasma membrane protein cask isoform x5	60	2.59E-32	96.00%	0.113	IPR011511 (PFAM); G3DSA:2.30.30.40 (GENE3D); PTHR23122 (PANTHER); PTHR23122:SF7 (PANTHER); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY)
52	118069_length_180_cvg_12.1_tip_0_0	4	angiopoietin-1 isoform x1	60	2.60E-12	68.60%	0.108	IPR002181 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); PTHR19143 (PANTHER); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
53	118075_length_180_cvg_2.0_tip_1_5	2	zinc c2h2 type	60	8.11E-09	68.60%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
54	118147_length_180_cvg_23.0_tip_0_0	4	microfibril-associated glycoprotein 4-like	60	4.71E-12	68.20%	0.118	IPR002181 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); PTHR19143 (PANTHER); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
55	118417_length_181_cvg_32.8_tip_1_5	10	glycosyl hydrolase family cellulase	60	2.73E-13	68.50%	0.098	IPR001547 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR31308 (PANTHER); IPR017853 (SUPERFAMILY)

56	118419_length_181_cvg_63.0_tip_1_5	61	glycosyl hydrolase family cellulase	60	9.00E-14	68.00%	0.098	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001547 (PFAM); PTHR31308 (PANTHER); IPR017853 (SUPERFAMILY)
58	119217_length_182_cvg_2.0_tip_1_5	3	peptidyl-alpha-hydroxyglycine alpha-amidating lyase 2-like	60	3.15E-12	68.60%	0.098	PTHR10680 (PANTHER)
57	118701_length_181_cvg_3.0_tip_1_3	2	endothelin-converting enzyme 1 isoform x2	61	3.91E-22	82.30%	0.311	IPR018497 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR11733:SF124 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
59	119432_length_183_cvg_2.0_tip_1_4	1	probable serine carboxypeptidase cpvl	61	3.46E-21	85.00%	0.143	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); PTHR11802:SF30 (PANTHER); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
60	119548_length_183_cvg_10.8_tip_1_2	59	---NA---	61			0.222	TMhelix (TMHMM)
61	121708_length_187_cvg_2.0_tip_1_3	1	membrane metallo-endopeptidase-like 1 isoform x2	63	8.56E-21	85.80%	0.114	IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); PTHR11733:SF111 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
62	122478_length_188_cvg_3.0_tip_1_1	2	cade_drome ame: full=de-cadherin ame: full=protein shotgun flags: precursor	63	4.02E-09	59.90%	0.111	IPR013320 (G3DSA:2.60.120.GENE3D)
63	122908_length_189_cvg_2.0_tip_1_1	1	moxd1 homolog 2-like	63	3.72E-09	64.70%	0.141	PF03712 (PFAM); IPR014784 (G3DSA:2.60.120.GENE3D); IPR000945 (PANTHER); IPR014783 (PROSITE_PATTERNS); IPR008977 (SUPERFAMILY)
65	124034_length_191_cvg_2.0_tip_1_5	2	insulin-like growth factor-binding protein complex acid labile chain	63	4.88E-16	82.80%	0.113	IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); PTHR24365:SF83 (PANTHER); SSF52058 (SUPERFAMILY)
66	124064_length_191_cvg_12.5_tip_0_5	7	ankyrin domain-containing protein	63	2.26E-10	67.10%	0.134	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
64	123634_length_190_cvg_2.0_tip_1_3	3	aldehyde oxidase	64	1.41E-19	81.00%	0.11	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF65 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)
67	124910_length_192_cvg_2.0_tip_1_4	1	protein kinase related to protein kinase isoform e	64	3.14E-39	100.00%	0.098	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24357:SF80 (PANTHER); PTHR24357 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
68	125060_length_193_cvg_3.0_tip_1_0	1	zinc finger protein 235-like	65	1.07E-11	64.60%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
69	125208_length_193_cvg_3.2_tip_1_3	6	predicted protein	65	3.20E-08	48.50%	0.115	no IPS match
70	126392_length_195_cvg_3.0_tip_1_3	2	heat shock protein partial	65	7.35E-37	99.80%	0.1	G3DSA:3.90.640.10 (GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); PTHR19375:SF142 (PANTHER); SSF53067 (SUPERFAMILY)
71	126710_length_195_cvg_2.0_tip_1_2	3	latrophilin cirl isoform x1	65	7.59E-21	78.00%	0.117	IPR000922 (PFAM); PTHR12011 (PANTHER); PTHR12011:SF260 (PANTHER); IPR000922 (PROSITE_PROFILES)
72	127202_length_196_cvg_4.8_tip_1_4	2	gly-xaa carboxypeptidase	65	1.45E-13	72.90%	0.107	IPR011650 (G3DSA:3.30.70.GENE3D); IPR011650 (PFAM); PTHR11014 (PANTHER); PTHR11014:SF66 (PANTHER)
73	127602_length_197_cvg_2.0_tip_1_2	4	low quality protein: zinc finger protein 233	65	1.52E-15	68.10%	0.105	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
74	128210_length_198_cvg_21.3_tip_0_0	17	stearoyl- desaturase partial	66	3.32E-28	88.10%	0.263	IPR015876 (PRINTS); PTHR11351 (PANTHER); PTHR11351:SF28 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
75	128230_length_198_cvg_34.0_tip_0_3	18	fatty acid	66	2.45E-28	87.40%	0.262	IPR015876 (PRINTS); PTHR11351 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
77	128768_length_199_cvg_2.0_tip_1_2	2	protein kinase c-binding protein nell1-like	66	4.08E-21	84.90%	0.148	PTHR24042:SF4 (PANTHER); PTHR24042 (PANTHER)
76	128360_length_199_cvg_2.9_tip_1_3	3	xanthine dehydrogenase oxidase	67	1.05E-26	82.80%	0.106	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)
78	128970_length_200_cvg_2.0_tip_1_3	3	zinc finger partial	67	3.74E-07	58.30%	0.102	PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF20 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
79	129482_length_201_cvg_2.0_tip_1_0	0	angiotensin-converting enzyme	67	5.20E-30	85.80%	0.113	IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); SSF55486 (SUPERFAMILY)
80	130160_length_202_cvg_3.6_tip_1_5	5	epididymal sperm-binding protein 1	67	3.97E-07	58.33%	0.113	IPR000562 (SMART); IPR000562 (G3DSA:2.10.10.GENE3D); IPR000562 (PFAM); IPR000562 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY)
81	130698_length_203_cvg_3.0_tip_1_1	2	lysosomal alpha-glucosidase-like	68	6.55E-27	83.70%	0.108	IPR000322 (PFAM); PTHR22762:SF69 (PANTHER); PTHR22762 (PANTHER); IPR017853 (SUPERFAMILY)

82	132066_length_206_cvg_2.0_tip_1_5	2	ankyrin repeat domain-containing protein 49	68	4.98E-09	64.70%	0.555 Y	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24188 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR020683 (SUPERFAMILY)
83	133900_length_210_cvg_2.0_tip_1_5	3	gastrula zinc finger protein - partial	70	4.74E-16	69.10%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
84	133914_length_210_cvg_11.8_tip_1_0	18	glucose dehydrogenase	70	1.41E-09	75.90%	0.24	IPR000172 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR11552:SF77 (PANTHER); PTHR11552 (PANTHER); IPR000172 (PROSITE_PATTERNS); SSF51905 (SUPERFAMILY)
85	134808_length_212_cvg_84.8_tip_1_3	563	---NA---	71			0.316	IPR000716 (G3DSA:4.10.800.GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000716 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR000716 (SUPERFAMILY); TMhelix (TMHMM)
86	134910_length_212_cvg_4.0_tip_1_0	0	ectonucleotide pyrophosphatase phosphodiesterase family member 3	71	7.18E-12	73.40%	0.156	IPR002591 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); IPR024873 (PANTHER); IPR017850 (SUPERFAMILY)
87	134978_length_212_cvg_2.0_tip_1_0	2	aminopeptidase n	71	1.99E-14	64.30%	0.114	G3DSA:1.10.390.10 (GENE3D); PTHR11533:SF148 (PANTHER); IPR001930 (PANTHER); SSF55486 (SUPERFAMILY)
88	135286_length_212_cvg_2.0_tip_1_1	1	plexin- partial	71	2.10E-30	87.60%	0.099	IPR015943 (G3DSA:2.130.10.GENE3D); IPR001627 (PFAM); PTHR22625 (PANTHER); PTHR22625:SF16 (PANTHER); IPR001627 (PROSITE_PROFILES); IPR001627 (SUPERFAMILY); TMhelix (TMHMM)
89	135342_length_213_cvg_4.0_tip_1_2	7	allatostatin neuropeptide precursor	71	9.50E-12	69.40%	0.105	IPR010276 (PFAM)
90	135558_length_213_cvg_17.0_tip_1_2	17	serpin b10	71	1.28E-12	68.30%	0.137	IPR023796 (PFAM); G3DSA:3.30.497.10 (GENE3D); IPR000215 (PANTHER); IPR023796 (SUPERFAMILY)
91	135936_length_214_cvg_4.0_tip_1_5	6	neuroligin- x- partial	71	1.65E-08	62.40%	0.279	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR029058 (SUPERFAMILY)
93	136164_length_214_cvg_104.9_tip_0_1	593	unnamed protein product	71	1.62E-06	60.00%	0.182	IPR002350 (SMART); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY)
92	136140_length_214_cvg_2.0_tip_1_0	4	lactase-phlorizin hydrolase	72	1.90E-23	77.80%	0.109	IPR001360 (PRINTS); IPR001360 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001360 (PANTHER); IPR017853 (SUPERFAMILY)
94	136796_length_216_cvg_2.0_tip_1_3	2	serine proteinase stubble-like	72	7.24E-21	73.00%	0.118	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
95	137262_length_216_cvg_2.0_tip_1_0	2	---NA---	72			0.13	no IPS match
96	137368_length_217_cvg_3.9_tip_1_5	28	glutamine-rich protein 2	72	3.69E-09	63.00%	0.102	PR01217 (PRINTS)
97	137538_length_217_cvg_2.0_tip_1_4	5	---NA---	72			0.103	IPR014020 (PFAM); G3DSA:2.60.40.1110 (GENE3D); IPR000008 (SUPERFAMILY)
98	137568_length_217_cvg_63.0_tip_0_5	504	probable endoglycoceramidase	72	2.77E-21	70.40%	0.119	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001547 (PFAM); PTHR31308 (PANTHER); IPR017853 (SUPERFAMILY)
99	137624_length_217_cvg_3.0_tip_1_4	4	glyceraldehyde-3-phosphate dehydrogenase	72	9.07E-17	72.80%	0.102	IPR020828 (SMART); IPR020828 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020831 (PANTHER); SSF51735 (SUPERFAMILY)
100	137784_length_218_cvg_25.7_tip_1_1	33	hemagglutinin amebocyte aggregation factor-like	73	2.41E-13	63.70%	0.108	PF14704 (PFAM); IPR026645 (PANTHER)
101	138088_length_218_cvg_2.0_tip_1_4	3	ankyrin repeat domain-containing protein 29-like	73	2.35E-12	63.50%	0.103	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24188 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
102	138150_length_218_cvg_2.0_tip_1_0	2	transferrin	73	9.85E-16	70.60%	0.099	IPR001156 (PRINTS); IPR001156 (PFAM); G3DSA:3.40.190.10 (GENE3D); PTHR11485:SF18 (PANTHER); PTHR11485 (PANTHER); IPR001156 (PROSITE_PROFILES); SSF53850 (SUPERFAMILY)
103	138792_length_219_cvg_2.0_tip_1_3	3	fad-linked sulfhydryl oxidase partial	73	3.12E-32	81.00%	0.155	IPR017905 (PFAM); IPR017905 (G3DSA:1.20.120.GENE3D); PTHR12645 (PANTHER); IPR017905 (PROSITE_PROFILES); IPR017905 (SUPERFAMILY)
104	138936_length_220_cvg_2.0_tip_1_2	4	peptidyl-prolyl cis-trans cyclophilin-type family	73	1.49E-34	88.50%	0.122	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
105	139150_length_220_cvg_2.0_tip_1_3	4	gamma-glutamyl hydrolase-like	74	1.43E-15	75.30%	0.105	IPR029062 (G3DSA:3.40.50.GENE3D); IPR011697 (PFAM); PTHR11315:SF2 (PANTHER); IPR015527 (PANTHER)
106	139391_length_221_cvg_4.1_tip_1_3	6	---NA---	74			0.107	IPR001846 (PFAM); IPR001846 (PROSITE_PROFILES)
107	139997_length_222_cvg_3.0_tip_1_0	5	colostrum trypsin inhibitor-like	74	5.32E-16	71.50%	0.103	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY)

108	140211_length_222_cvg_9.5_tip_1_3	12	insulin-like receptor	74	2.66E-29	80.20%	0.107	G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416 (PANTHER); PTHR24416:SF254 (PANTHER); IPR011009 (SUPERFAMILY)
109	140481_length_223_cvg_2.0_tip_1_4	1	phosphodiesterase i	74	9.33E-15	62.90%	0.178	IPR017849 (G3DSA:3.40.720.GENE3D); IPR002591 (PFAM); IPR024873 (PANTHER); IPR017850 (SUPERFAMILY)
110	140609_length_223_cvg_2.0_tip_1_5	4	ankyrin repeat and sterile alpha motif domain-containing protein 1b	74	9.38E-27	93.20%	0.107	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24174 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
111	140885_length_223_cvg_2.0_tip_1_2	4	endothelial zinc finger protein induced by tumor necrosis factor partial	74	7.77E-17	64.90%	0.112	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
112	141043_length_224_cvg_3.0_tip_1_4	4	sparc-related modular calcium-binding protein partial	75	4.48E-21	73.90%	0.1	IPR019577 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR12352 (PANTHER); IPR018247 (PROSITE_PATTERNS); SSF47473 (SUPERFAMILY)
113	141131_length_224_cvg_2.0_tip_1_3	4	low density lipoprotein receptor-related protein 5 isoform cra_a	75	4.36E-06	57.00%	0.103	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
114	141465_length_225_cvg_15.8_tip_1_0	24	transcriptional regulator atrx homolog	75	3.24E-09	60.00%	0.1	no IPS match
115	141927_length_225_cvg_3.0_tip_1_0	4	esterase e4-like	75	3.48E-25	78.10%	0.201	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559 (PANTHER); IPR029058 (SUPERFAMILY)
120	142911_length_227_cvg_37.8_tip_1_5	53	gram positive anchor	75	3.77E-11	55.00%	0.176	no IPS match
121	143127_length_227_cvg_2.0_tip_1_2	3	signal cub and egf-like domain-containing protein 1 isoform x1	75	1.23E-20	79.20%	0.123	PTHR24046 (PANTHER); PTHR24046:SF4 (PANTHER)
116	142017_length_226_cvg_2.0_tip_1_0	3	low quality protein: kinase d-interacting substrate of 220 kda-like	76	6.50E-32	85.30%	0.105	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24139 (PANTHER); PTHR24139:SF10 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
117	142265_length_226_cvg_115.4_tip_1_0	2726	anti-lipopolysaccharide factor isoform 7	76	1.47E-08	57.50%	0.909 Y	IPR024509 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR024716 (PRODOM); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); TMhelix (TMHMM)
118	142449_length_226_cvg_3.0_tip_1_3	6	carboxypeptidase b-like	76	3.85E-25	78.80%	0.137	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705:SF61 (PANTHER); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
119	142567_length_227_cvg_2.0_tip_1_1	3	er degradation-enhancing alpha-mannosidase-like 3	76	3.42E-31	90.80%	0.108	IPR001382 (PFAM); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PANTHER); PTHR11742:SF38 (PANTHER); IPR001382 (SUPERFAMILY)
122	143285_length_228_cvg_2.0_tip_1_3	3	lutropin-choriogonadotropic hormone receptor	76	3.10E-06	59.50%	0.113	G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
123	143623_length_228_cvg_2.0_tip_1_5	3	aael015439- partial	76	5.13E-30	79.20%	0.163	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); PTHR24256:SF103 (PANTHER); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
124	143747_length_228_cvg_3.0_tip_1_5	6	d chain coupling of remote alternating-access transport mechanisms for protons and substrates in the multidrug efflux pump acrb	76	3.13E-13	62.20%	0.144	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24182 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
125	144217_length_229_cvg_9.2_tip_1_5	11	PREDICTED: hyaluronidase-1-like	76	2.47E-06	63.00%	0.105	IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
126	144573_length_230_cvg_2.0_tip_1_3	3	heat shock protein partial	77	2.36E-35	88.10%	0.104	IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); PTHR19375:SF137 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
127	145295_length_231_cvg_2.0_tip_1_2	5	prolyl 4- beta subunit	77	7.18E-18	70.60%	0.113	IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929 (PANTHER); PTHR18929:SF74 (PANTHER); IPR012336 (SUPERFAMILY)
128	145327_length_231_cvg_2.0_tip_1_3	3	zinc finger protein 109	77	2.31E-14	60.20%	0.146	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
129	145649_length_231_cvg_3.0_tip_1_3	5	zinc c2h2 type	77	3.25E-11	62.50%	0.118	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)

130	145901_length_232_cvg_2.0_tip_1_4	4	fat-like cadherin-related tumor suppressor homolog isoform x3	77	3.34E-13	63.80%	0.114	IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); PTHR24028 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY)
131	145965_length_232_cvg_2.0_tip_1_1	2	zinc finger protein 502-like	77	2.12E-14	67.00%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
133	146185_length_232_cvg_2.0_tip_1_4	7	26s protease regulatory subunit 6a-b	77	1.32E-45	99.60%	0.102	IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23073:SF7 (PANTHER); PTHR23073 (PANTHER); IPR027417 (SUPERFAMILY)
135	146945_length_233_cvg_2.4_tip_1_5	6	gamma-glutamyl hydrolase	77	1.78E-13	63.80%	0.116	IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER)
132	145969_length_232_cvg_2.0_tip_1_3	4	beta- -n-acetylgalactosaminyltransferase bre-4	78	4.90E-42	88.40%	0.128	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); PTHR19300:SF30 (PANTHER); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
134	146727_length_233_cvg_2.0_tip_1_3	5	pancreatic triacylglycerol lipase-like	78	2.12E-28	78.60%	0.108	IPR013818 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR000734 (PANTHER); IPR029058 (SUPERFAMILY)
136	147193_length_234_cvg_2.0_tip_1_1	1	carboxypeptidase b-like	78	3.05E-21	80.70%	0.148	IPR000834 (PRINTS); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY)
137	147511_length_234_cvg_2.0_tip_1_1	5	phospholipase a2 isozyme partial	78	1.90E-09	67.10%	0.098	IPR001211 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); IPR016090 (SUPERFAMILY)
138	147779_length_234_cvg_2.0_tip_1_1	4	syntaxin partial	78	9.56E-18	78.90%	0.1	Coil (COILS); IPR000727 (SMART); IPR000727 (PFAM); G3DSA:1.20.5.110 (GENE3D); IPR028669 (PTHR19957:PANTHER); PTHR19957 (PANTHER); IPR006012 (PROSITE_PATTERNS); IPR000727 (PROSITE_PROFILES); IPR010989 (SUPERFAMILY)
139	147899_length_234_cvg_2.0_tip_1_0	3	vacuolar-sorting protein snf8-like	78	3.01E-18	92.20%	0.19	Coil (COILS); IPR007286 (PFAM); PTHR12806:SF0 (PANTHER); IPR007286 (PANTHER)
140	148541_length_235_cvg_12.0_tip_1_1	2	vktti_najna ame: full=kunitz-type serine protease inhibitor ame: full=venom trypsin inhibitor	78	1.60E-14	72.40%	0.122	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY)
141	149653_length_236_cvg_2.0_tip_1_1	4	zinc c2h2 type domain-containing protein	79	4.73E-18	62.80%	0.108	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
142	149803_length_237_cvg_2.0_tip_1_5	5	plexin- partial	79	1.62E-40	96.80%	0.404 Y	IPR013548 (PFAM); PTHR22625 (PANTHER); IPR008936 (SUPERFAMILY)
143	150497_length_237_cvg_12.2_tip_1_4	20	adp-ribosylation factor	79	8.89E-10	88.80%	0.249	IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711:SF142 (PANTHER); PTHR11711 (PANTHER); IPR027417 (SUPERFAMILY)
144	150837_length_238_cvg_2.0_tip_1_1	3	zinc finger protein 543	79	1.13E-12	57.30%	0.111	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
145	150891_length_238_cvg_2.7_tip_1_2	4	cd4-specific ankyrin repeat protein	79	3.34E-10	61.10%	0.118	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
146	151231_length_238_cvg_2.0_tip_1_5	3	endothelin-converting enzyme 1 isoform x3	79	1.48E-24	79.20%	0.394 Y	IPR008753 (PFAM); G3DSA:1.10.1380.10 (GENE3D); IPR029733 (PTHR11733:PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
147	151369_length_238_cvg_2.0_tip_1_2	3	mam and ldl-receptor class a domain-containing protein 1-like	79	3.15E-10	58.38%	0.118	IPR000998 (PFAM); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
148	151459_length_238_cvg_3.0_tip_1_4	4	protein creg1	79	8.82E-20	74.90%	0.12	IPR012349 (G3DSA:2.30.110.GENE3D); PF13883 (PFAM); PTHR13343:SF17 (PANTHER); PTHR13343 (PANTHER); IPR012349 (SUPERFAMILY)
149	151739_length_239_cvg_45.0_tip_1_3	62	14-3-3 protein zeta isoform x1	80	1.06E-43	91.60%	0.108	IPR000308 (PRINTS); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023410 (SUPERFAMILY)
150	152047_length_239_cvg_2.9_tip_1_4	8	n-sulphoglucosamine sulphohydrolase	80	2.21E-22	86.20%	0.115	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342 (PANTHER); PTHR10342:SF76 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)
151	152999_length_240_cvg_2.0_tip_1_0	5	low-density lipoprotein receptor-related protein 2	80	9.38E-38	85.80%	0.107	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
152	153083_length_240_cvg_2.0_tip_1_5	5	basement membrane-specific heparan sulfate proteoglycan core protein	80	2.05E-25	65.90%	0.108	IPR013783 (G3DSA:2.60.40.GENE3D)
153	153595_length_241_cvg_63.0_tip_0_2	3159	probable chitinase 3	80	1.66E-24	72.50%	0.099	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF109 (PANTHER); IPR017853 (SUPERFAMILY)

154	153649_length_241_cvg_3.0_tip_1_5	7	---	80	0.099	IPR002413 (PRINTS); IPR014044 (G3DSA:3.40.33.GENE3D)				
155	153699_length_241_cvg_2.0_tip_1_1	1	serine threonine-protein kinase 10 isoform x3	80	5.31E-45	95.20%	0.108	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24361:SF249 (PANTHER); PTHR24361 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)		
156	153789_length_241_cvg_2.4_tip_1_5	5	chemosensory protein 1 partial	80	1.13E-31	80.30%	0.107	IPR005055 (PFAM); IPR005055 (G3DSA:1.10.2080.GENE3D); IPR005055 (PANTHER); PTHR11257:SF4 (PANTHER); IPR005055 (SUPERFAMILY)		
157	154119_length_241_cvg_2.0_tip_1_2	4	fibrillin-2-like isoform x2	80	2.88E-32	81.90%	0.141	IPR017878 (PFAM); IPR017878 (G3DSA:3.90.290.GENE3D); IPR011398 (PANTHER); IPR017878 (PROSITE_PROFILES); IPR017878 (SUPERFAMILY)		
158	154173_length_241_cvg_2.0_tip_1_2	4	zinc finger and btb domain-containing protein	80	5.33E-14	62.70%	0.106	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)		
159	154475_length_241_cvg_2.0_tip_1_3	5	ankyrin repeat-containing protein	81	1.63E-07	65.00%	0.105	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)		
160	154631_length_242_cvg_3.0_tip_1_0	5	af296336_1collagen-like surface protein	81	8.84E-06	56.00%	0.1	IPR008160 (PFAM)		
161	154955_length_242_cvg_2.0_tip_1_0	3	prenylcysteine oxidase	81	2.84E-13	62.60%	0.097	IPR010795 (PFAM); IPR017046 (PANTHER)		
162	155341_length_242_cvg_2.0_tip_1_3	3	d chain in silico and in vitro co-evolution of a high affinity complementary protein-protein interface	81	5.59E-10	62.80%	0.112	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)		
163	155465_length_242_cvg_2.0_tip_1_4	7	neurogenic locus notch homolog protein 3-like	81	2.41E-32	76.80%	0.133	IPR004094 (G3DSA:2.10.22.GENE3D); IPR004094 (PFAM); PTHR19441 (PANTHER); PTHR19441:SF10 (PANTHER); IPR004094 (PROSITE_PROFILES); IPR011061 (SUPERFAMILY)		
164	155839_length_243_cvg_3.0_tip_1_3	7	gastrula zinc finger	81	1.72E-23	73.50%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)		
165	155869_length_243_cvg_2.0_tip_1_0	4	low quality protein: cadherin-related tumor suppressor-like	81	1.37E-08	62.70%	0.126	IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)		
166	156013_length_243_cvg_2.0_tip_1_2	6	chemosensory protein-14	81	2.58E-39	89.00%	0.105	IPR005055 (PFAM); IPR005055 (G3DSA:1.10.2080.GENE3D); PTHR11257:SF4 (PANTHER); IPR005055 (PANTHER); IPR005055 (SUPERFAMILY)		
167	156111_length_243_cvg_2.0_tip_1_2	7	xanthine dehydrogenase oxidase	81	9.87E-28	77.60%	0.111	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR008274 (SUPERFAMILY)		
168	156173_length_243_cvg_2.0_tip_1_2	4	papain family cysteine protease	81	1.77E-29	78.30%	0.145	IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF15 (PANTHER); IPR013128 (PANTHER); SSF54001 (SUPERFAMILY)		
169	156369_length_243_cvg_2.0_tip_1_5	5	down syndrome cell adhesion molecule-like protein dscam2	81	1.37E-25	74.90%	0.163	IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF580 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)		
170	156399_length_243_cvg_2.0_tip_1_2	5	trehalase isoform x3	81	1.92E-15	66.70%	0.105	PTHR23403:SF1 (PANTHER); IPR001661 (PANTHER); IPR008928 (SUPERFAMILY)		
171	156445_length_243_cvg_4.0_tip_1_3	7	5 -nucleotidase-like	81	4.02E-20	71.10%	0.122	IPR029052 (G3DSA:3.60.21.GENE3D); IPR006179 (PANTHER); PTHR11575:SF21 (PANTHER); IPR006146 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)		
172	156507_length_243_cvg_13.0_tip_1_0	22	plasma alpha-l-fucosidase-like	81	1.05E-28	78.80%	0.581 Y	IPR013781 (G3DSA:3.20.20.GENE3D); IPR000933 (PFAM); PTHR10030:SF26 (PANTHER); IPR000933 (PANTHER); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-TM (SIGNALP_EUK); IPR017853 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)		
173	156993_length_243_cvg_2.7_tip_1_4	5	von willebrand factor type egf and pentraxin domain-containing protein 1-like	81	1.35E-19	73.00%	0.106	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY)		
174	157621_length_244_cvg_2.6_tip_1_1	4	dnaj homolog subfamily c member 3-like	81	1.17E-33	85.80%	0.106	IPR019734 (SMART); PF13414 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY)		
175	157681_length_244_cvg_2.5_tip_1_4	4	membrane metallo-endopeptidase-like 1 isoform x4	81	1.22E-12	62.40%	0.102	G3DSA:1.10.1380.10 (GENE3D); IPR008753 (PFAM); PTHR11733:SF111 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)		

176	157713_length_244_cvg_2.0_tip_1_2	4	tyrosine-protein kinase src42a	81	1.36E-11	59.60%	0.205	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24373 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
177	157865_length_244_cvg_2.9_tip_1_4	4	endothelin-converting enzyme, putative	81	6.34E-06	62.00%	0.104	IPR008753 (PFAM); G3DSA:1.10.1380.10 (GENE3D); SSF55486 (SUPERFAMILY)
183	159332_length_245_cvg_2.0_tip_1_2	6	phospholipase b-like 2	81	7.94E-31	84.20%	0.123	IPR007000 (PFAM); PTHR12370:SF3 (PANTHER); IPR007000 (PANTHER)
178	157985_length_244_cvg_119.9_tip_0_0	5053	kazal-type protease inhibitor	82	3.46E-12	56.00%	0.112	IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); IPR002350 (PFAM); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
179	158298_length_244_cvg_2.0_tip_1_0	5	sortilin-related receptor-like	82	2.15E-28	81.60%	0.132	G3DSA:2.130.10.140 (GENE3D); PTHR12106:SF7 (PANTHER); PTHR12106 (PANTHER); SSF110296 (SUPERFAMILY)
180	158366_length_245_cvg_2.0_tip_1_3	4	c-type lectin ctl- partial	82	7.62E-07	55.70%	0.894 Y	IPR016186 (G3DSA:3.10.100.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001304 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR016187 (SUPERFAMILY)
181	158552_length_245_cvg_3.0_tip_1_1	7	parkinson disease 7 domain-containing protein 1	82	2.14E-17	82.80%	0.101	IPR029062 (G3DSA:3.40.50.GENE3D); IPR029062 (SUPERFAMILY)
182	159262_length_245_cvg_2.0_tip_1_4	4	core histone macro-	82	1.55E-34	86.20%	0.107	IPR002119 (PRINTS); IPR002119 (SMART); IPR009072 (G3DSA:1.10.20.GENE3D); IPR007125 (PFAM); PTHR23430 (PANTHER); PTHR23430:SF33 (PANTHER); IPR009072 (SUPERFAMILY)
184	159406_length_245_cvg_2.0_tip_1_4	5	thrombospondin type-1 domain-containing protein 4	82	3.18E-28	56.40%	0.108	IPR000884 (SMART); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); PTHR13723 (PANTHER); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
185	159576_length_245_cvg_2.0_tip_1_3	5	trehalose 6-phosphate synthase 1a isoform	82	7.54E-36	91.30%	0.097	G3DSA:3.40.50.2000 (GENE3D); IPR001830 (PFAM); PTHR10788:SF6 (PANTHER); PTHR10788 (PANTHER); SSF53756 (SUPERFAMILY)
186	159872_length_246_cvg_2.0_tip_1_3	7	vitellogenin partial	82	1.08E-17	58.50%	0.101	no IPS match
189	161756_length_247_cvg_3.0_tip_1_1	7	tyrosine-protein phosphatase	82	6.19E-36	84.80%	0.132	IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
190	162168_length_247_cvg_63.0_tip_0_4	4625	trypsin 3	82	1.52E-29	77.80%	0.114	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
193	163066_length_248_cvg_4.0_tip_1_5	9	probable carboxypeptidase pm20d1	82	4.56E-20	66.70%	0.138	IPR011650 (G3DSA:3.30.70.GENE3D); IPR011650 (PFAM); PTHR11014 (PANTHER); PTHR11014:SF66 (PANTHER); TMhelix (TMHMM)
194	163226_length_248_cvg_2.0_tip_1_5	3	agap003656-pa-like protein	82	6.32E-30	81.80%	0.111	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
187	161218_length_247_cvg_2.0_tip_1_3	5	achain 3ank: a designed ankyrin repeat protein with three identical consensus repeats	83	6.61E-13	65.60%	0.112	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
188	161490_length_247_cvg_2.0_tip_1_3	4	peptidyl-prolyl cis-trans isomerase h	83	6.37E-45	95.00%	0.105	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); PTHR11071:SF58 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
191	162352_length_248_cvg_2.0_tip_1_0	5	hypothetical protein Y032_0312g2164	83	6.13E-11	63.10%	0.106	no IPS match
192	162710_length_248_cvg_2.0_tip_1_0	4	adp-dependent glucokinase-like	83	6.39E-24	73.30%	0.107	IPR007666 (PFAM); IPR029056 (G3DSA:3.40.1190.GENE3D); IPR007666 (PANTHER); PTHR21208:SF1 (PANTHER); IPR007666 (PROSITE_PROFILES); IPR029056 (SUPERFAMILY)
195	163295_length_248_cvg_2.4_tip_1_1	5	insulin-like growth factor-binding protein complex acid labile chain	83	3.96E-11	61.50%	0.139	PR00019 (PRINTS); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
196	163613_length_249_cvg_2.0_tip_1_1	6	carboxypeptidase d	83	4.14E-18	68.30%	0.108	PF13620 (PFAM); IPR014766 (G3DSA:2.60.40.GENE3D); PTHR11532 (PANTHER); IPR027062 (PTHR11532:PANTHER); IPR008969 (SUPERFAMILY)
197	163879_length_249_cvg_2.0_tip_1_1	4	brevican core protein	83	1.15E-11	52.00%	0.125	IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
198	164509_length_249_cvg_2.0_tip_1_1	6	zinc finger protein 420-like	83	3.28E-14	64.60%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)

199	164761_length_249_cvg_2.0_tip_1_0	2	follistatin-related protein 5	83	1.14E-40	87.80%	0.098	IPR011992 (G3DSA:1.10.238.GENE3D); PTHR10913:SF14 (PANTHER); PTHR10913 (PANTHER); IPR018247 (PROSITE_PATTERNS); SSF47473 (SUPERFAMILY)
200	165005_length_250_cvg_4.5_tip_1_2	6	glucose dehydrogenase	83	2.13E-16	65.70%	0.101	IPR007867 (PFAM); G3DSA:3.30.560.10 (GENE3D); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); SSF54373 (SUPERFAMILY)
201	165059_length_250_cvg_2.0_tip_1_4	4	nucleolar protein partial	83	6.52E-31	80.30%	0.113	PTHR10894 (PANTHER)
202	165317_length_250_cvg_3.0_tip_1_5	6	leucine-rich repeats containing	83	9.13E-19	62.70%	0.112	IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
203	165351_length_250_cvg_2.0_tip_1_5	7	neutral endopeptidase	83	1.26E-24	72.50%	0.113	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); PTHR11733:SF113 (PANTHER); IPR000718 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
205	166061_length_250_cvg_3.0_tip_1_4	7	isoform cra_c	83	1.91E-10	66.80%	0.136	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24264 (PANTHER); PTHR24264:SF9 (PANTHER); IPR009003 (SUPERFAMILY)
206	166185_length_250_cvg_2.0_tip_1_2	7	low-density lipoprotein	83	1.21E-34	84.60%	0.13	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); PTHR10529:SF204 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
204	166041_length_250_cvg_2.7_tip_1_0	7	heat shock cognate 71 kda	84	5.72E-30	84.10%	0.178	IPR013126 (PRINTS); IPR013126 (PFAM); G3DSA:3.30.30.30 (GENE3D); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
207	166767_length_251_cvg_2.0_tip_1_1	5	protein lap1-like	84	9.95E-25	78.30%	0.097	IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR025875 (PFAM); PTHR23155 (PANTHER); PTHR23155:SF466 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52075 (SUPERFAMILY)
208	166999_length_251_cvg_2.0_tip_1_4	5	agrn partial	84	5.06E-13	62.70%	0.113	IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
209	167047_length_251_cvg_3.0_tip_1_0	6	#NAME?	84	2.59E-23	83.30%	0.418 Y	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24077 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
210	167061_length_251_cvg_3.0_tip_1_4	8	mam and ldl-receptor class a domain-containing protein 1	84	1.97E-13	57.20%	0.102	IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PFAM); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
211	167177_length_251_cvg_3.0_tip_1_4	7	zinc finger protein rotund isoform x1	84	2.75E-48	98.00%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR016608 (PTHR11389:PANTHER); PTHR11389 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
212	167645_length_251_cvg_2.0_tip_1_4	7	mam and ldl-receptor class a domain-containing protein 1	84	2.54E-13	62.70%	0.405 Y	IPR000998 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR23282 (PANTHER); PTHR23282:SF75 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
213	167831_length_252_cvg_2.0_tip_1_5	4	laminin subunit alpha	84	1.19E-35	88.60%	0.098	IPR008211 (SMART); IPR008211 (PFAM); PTHR10574:SF39 (PANTHER); PTHR10574 (PANTHER); IPR008211 (PROSITE_PROFILES)
214	167865_length_252_cvg_2.9_tip_1_5	7	iron zinc purple acid phosphatase-like protein	84	7.51E-39	85.80%	0.143	IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); IPR029052 (SUPERFAMILY)
215	168045_length_252_cvg_3.0_tip_1_0	6	protein disulfide-isomerase partial	84	5.09E-27	72.60%	0.107	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929 (PANTHER); PTHR18929:SF56 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
216	168115_length_252_cvg_3.0_tip_1_5	8	zinc finger protein 429-like isoform x2	84	1.05E-39	90.10%	0.114	IPR015880 (SMART); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
217	168207_length_252_cvg_2.0_tip_1_0	5	serine protease like protein	84	2.25E-22	67.40%	0.259	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF94 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

218	168229_length_252_cvg_3.0_tip_1_4	5	muscle ankyrin repeat protein 3	84	1.89E-09	57.80%	0.117	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
219	168643_length_252_cvg_2.4_tip_1_3	3	phosphoglycerate kinase	84	8.23E-17	60.60%	0.103	IPR001576 (PFAM); IPR015901 (G3DSA:3.40.50.GENE3D); IPR001576 (PANTHER); PTHR11406:SF6 (PANTHER); IPR001576 (SUPERFAMILY)
220	168973_length_252_cvg_2.0_tip_1_2	6	zinc c2h2 type domain-containing protein	84	6.40E-15	58.40%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
222	169329_length_253_cvg_5.0_tip_1_4	6	laminin subunit gamma-1	84	8.37E-13	69.30%	0.104	no IPS match
224	169869_length_253_cvg_2.0_tip_1_2	5	a disintegrin and metalloproteinase with thrombospondin motifs 12 isoform x1	84	2.16E-09	64.60%	0.1	IPR002870 (PFAM); PTHR11905 (PANTHER)
227	171233_length_254_cvg_2.0_tip_1_5	4	zinc finger protein	84	2.98E-13	60.40%	0.107	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
229	171623_length_254_cvg_3.3_tip_1_2	10	achain 3ank: a designed ankyrin repeat protein with three identical consensus repeats	84	1.55E-14	62.30%	0.132	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24193 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
221	169169_length_253_cvg_2.0_tip_1_0	6	attractin-like protein 1 isoform x1	85	1.82E-25	74.80%	0.12	IPR015915 (G3DSA:2.120.10.GENE3D); PF13418 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF3 (PANTHER); SSF117281 (SUPERFAMILY)
223	169741_length_253_cvg_3.0_tip_1_0	9	collagen alpha-1 chain-like	85	4.49E-10	62.30%	0.104	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF372 (PANTHER)
225	170415_length_253_cvg_2.0_tip_1_0	6	aldehyde mitochondrial precursor	85	2.82E-37	85.10%	0.113	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); IPR015657 (PTHR11699:PANTHER); IPR016161 (SUPERFAMILY)
226	170917_length_254_cvg_2.0_tip_1_3	2	retinol dehydrogenase 14 isoform x2	85	4.01E-27	80.70%	0.106	IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY)
228	171329_length_254_cvg_2.0_tip_1_3	3	mucin-19 isoform x1	85	2.66E-08	59.80%	0.169	IPR001846 (PFAM); IPR001846 (PROSITE_PROFILES)
230	171683_length_254_cvg_3.9_tip_1_0	10	c-type mannose receptor 2	85	1.04E-06	62.57%	0.111	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
231	171863_length_255_cvg_2.0_tip_1_0	5	signal cub and egf-like domain-containing protein partial	85	1.30E-18	67.60%	0.113	IPR001881 (SMART); IPR000742 (SMART); PF14670 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR026823 (PFAM); PTHR24034 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
232	171907_length_255_cvg_2.0_tip_1_4	6	group xv phospholipase a2	85	3.53E-40	84.70%	0.107	IPR003386 (PFAM); PTHR11440 (PANTHER); PTHR11440:SF47 (PANTHER)
233	171921_length_255_cvg_2.9_tip_1_1	9	thyroglobulin type-1 repeat-containing domain protein	85	3.69E-19	65.70%	0.108	IPR000716 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PFAM); PTHR12352 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY)
234	171959_length_255_cvg_4.0_tip_1_5	14	---NA---	85			0.114	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
235	172043_length_255_cvg_2.0_tip_1_1	6	glucose dehydrogenase	85	2.45E-30	77.20%	0.166	G3DSA:3.50.50.60 (GENE3D); IPR000172 (PFAM); PTHR11552:SF77 (PANTHER); PTHR11552 (PANTHER); IPR000172 (PROSITE_PATTERNS); SSF51905 (SUPERFAMILY)
236	172289_length_255_cvg_17.0_tip_1_1	23	14-3-3 partial	85	3.61E-48	94.10%	0.106	IPR000308 (PRINTS); IPR023410 (SMART); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023410 (SUPERFAMILY)
237	172529_length_255_cvg_3.0_tip_1_2	9	collagen alpha-1 chain isoform x1	85	2.71E-07	63.70%	0.751 Y	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF372 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK)
238	172529_length_255_cvg_3.0_tip_1_5	9	hypothetical protein	85	2.12E-06	51.00%	0.103	no IPS match
239	172807_length_255_cvg_3.0_tip_1_1	7	ecotropic virus integration site 1 protein	85	5.33E-13	62.30%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)

240	172905_length_255_cvg_2.0_tip_1_4	7	laminin subunit gamma- partial	85	1.10E-39	83.30%	0.1	IPR008211 (SMART); IPR008979 (G3DSA:2.60.120.GENE3D); IPR008211 (PFAM); PTHR10574:SF228 (PANTHER); PTHR10574 (PANTHER); IPR008211 (PROSITE_PROFILES)
241	173453_length_256_cvg_2.0_tip_1_4	4	receptor-type tyrosine-protein phosphatase kappa	85	7.99E-39	82.60%	0.113	IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); PTHR19134:SF227 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
242	174007_length_256_cvg_2.0_tip_1_1	8	molting fluid carboxypeptidase a precursor	85	4.16E-29	74.20%	0.11	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
249	175291_length_257_cvg_2.0_tip_1_2	6	notch-regulated ankyrin repeat-containing protein	85	1.75E-32	74.40%	0.112	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); PF13857 (PFAM); PTHR24203 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
243	174331_length_256_cvg_4.6_tip_1_3	9	protein sda1 homolog	86	4.88E-33	86.50%	0.161	IPR012977 (PFAM); IPR027312 (PTHR12730:PANTHER); PTHR12730 (PANTHER)
244	174991_length_257_cvg_3.0_tip_1_1	7	oocyte zinc finger protein 6	86	4.26E-17	59.70%	0.103	IPR015880 (SMART); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PANTHER); PTHR19134:SF227 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
245	175015_length_257_cvg_2.0_tip_1_3	7	zinc finger protein	86	8.16E-13	60.30%	0.107	IPR015880 (SMART); PF12874 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
246	175203_length_257_cvg_2.0_tip_1_4	3	neural-cadherin- partial	86	1.86E-38	90.10%	0.103	IPR000233 (PFAM); IPR027397 (G3DSA:4.10.900.GENE3D); PTHR24027:SF251 (PANTHER); PTHR24027 (PANTHER)
247	175219_length_257_cvg_3.0_tip_1_3	7	enolase	86	1.32E-34	86.80%	0.118	IPR000941 (PRINTS); IPR020810 (PFAM); IPR029065 (G3DSA:3.20.20.GENE3D); IPR000941 (PANTHER); IPR029065 (SUPERFAMILY)
248	175233_length_257_cvg_2.0_tip_1_4	5	zinc finger protein partial	86	5.46E-18	61.70%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
250	175461_length_257_cvg_12.5_tip_1_0	19	adp-ribosylation factor 2	86	1.61E-13	99.70%	0.133	IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF145 (PANTHER); PTHR11711 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
251	175837_length_258_cvg_6.0_tip_1_4	15	plexin domain-containing protein 2	86	4.77E-30	81.00%	0.118	PTHR13055 (PANTHER); PTHR13055:SF12 (PANTHER)
252	175879_length_258_cvg_2.0_tip_1_4	3	pro-epidermal growth factor	86	1.29E-28	72.30%	0.101	IPR000742 (SMART); IPR001881 (SMART); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PF14670 (PFAM); PTHR24034 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
253	176117_length_258_cvg_2.0_tip_1_5	4	afadin isoform x3	86	3.03E-43	93.10%	0.108	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR10398 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
254	176407_length_258_cvg_3.0_tip_1_4	7	ldlr2-a protein	86	1.07E-11	65.40%	0.121	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
255	176943_length_258_cvg_2.0_tip_1_3	4	apical endosomal glyco	86	4.84E-21	66.60%	0.113	IPR000998 (PFAM); PTHR23282 (PANTHER); PTHR23282:SF75 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
256	177043_length_259_cvg_2.9_tip_1_2	8	c-terminal tandem repeated domain in type 4 procollagen	86	2.06E-13	67.90%	0.109	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF379 (PANTHER)
259	177133_length_259_cvg_8.0_tip_1_4	13	serpin b12	86	4.36E-12	74.10%	0.108	IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); PTHR11461:SF52 (PANTHER); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
261	177457_length_259_cvg_4.0_tip_1_1	9	retinol dehydrogenase 11-like	86	4.24E-17	61.80%	0.501 Y	PTHR24320 (PANTHER); PTHR24320:SF59 (PANTHER); SignalIP-noTM (SIGNALP_EUK)

262	177821_length_259_cvg_6.0_tip_1_5	16	zinc finger partial	86	9.23E-15	62.70%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
263	178049_length_259_cvg_2.0_tip_1_4	3	sialate o- partial	86	3.65E-19	67.80%	0.12	IPR005181 (PFAM); PTHR22901 (PANTHER); IPR013830 (SUPERFAMILY)
265	179285_length_260_cvg_3.0_tip_1_2	6	tyrosine-protein kinase wsck	86	5.04E-24	62.20%	0.157	IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24416 (PANTHER); PTHR24416:SF95 (PANTHER); IPR011009 (SUPERFAMILY)
257	177043_length_259_cvg_2.9_tip_1_3	8	cell surface	87	3.29E-12	56.60%	0.124	no IPS match
258	177107_length_259_cvg_2.1_tip_1_0	5	heat shock protein 70	87	1.64E-23	66.70%	0.104	Coil (COILS); IPR013126 (PFAM); IPR029047 (G3DSA:2.60.34.GENE3D); PTHR19375 (PANTHER); PTHR19375:SF156 (PANTHER); IPR029047 (SUPERFAMILY)
260	177377_length_259_cvg_9.3_tip_1_3	20	hemagglutinin amebocyte aggregation factor-like	87	4.08E-16	67.60%	0.177	PF14704 (PFAM); IPR026645 (PANTHER)
264	179139_length_260_cvg_3.0_tip_1_4	8	macrophage mannose receptor 1	87	2.55E-13	58.00%	0.112	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
266	179607_length_261_cvg_62.2_tip_0_4	275	angiopoietin-4 isoform x2	87	2.10E-19	70.30%	0.103	IPR002181 (SMART); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
267	179781_length_261_cvg_52.0_tip_1_3	107	---NA---	87			0.914 Y	IPR014044 (G3DSA:3.40.33.GENE3D); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM)
268	180769_length_262_cvg_2.0_tip_1_4	5	PREDICTED: uncharacterized protein C4orf29 homolog isoform X5	87	6.29E-34	81.10%	0.116	IPR019149 (PFAM); PTHR13617 (PANTHER)
269	180967_length_262_cvg_3.0_tip_1_2	7	aquaporin	87	1.20E-27	71.90%	0.211	IPR000425 (PRINTS); IPR000425 (PFAM); IPR023271 (G3DSA:1.20.1080.GENE3D); IPR000425 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023271 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
270	181025_length_262_cvg_2.0_tip_1_5	4	hormone-sensitive lipase	87	7.78E-33	75.60%	0.207	IPR013094 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR23025 (PANTHER); PTHR23025:SF3 (PANTHER); IPR029058 (SUPERFAMILY)
271	181171_length_262_cvg_2.0_tip_1_5	6	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	87	1.86E-22	69.70%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
272	181231_length_262_cvg_2.0_tip_1_5	4	basement membrane-specific heparan sulfate proteoglycan core protein	87	2.02E-28	73.30%	0.1	G3DSA:2.10.25.10 (GENE3D); PTHR10574 (PANTHER); PTHR10574:SF252 (PANTHER)
274	181721_length_262_cvg_2.0_tip_1_1	6	extracellular serine threonine protein kinase fam20c isoform x1	87	9.00E-18	72.10%	0.152	PTHR12450:SF8 (PANTHER); IPR024869 (PANTHER)
275	181775_length_263_cvg_4.0_tip_1_5	10	millepora cytotoxin-1-like	87	1.92E-07	65.14%	0.102	PF14704 (PFAM); IPR026645 (PANTHER)
276	182183_length_263_cvg_2.0_tip_1_2	6	krueppel-like factor 13	87	1.70E-13	62.30%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
277	182245_length_263_cvg_2.0_tip_1_2	4	zinc finger protein 254-like	87	6.90E-20	68.70%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
278	182273_length_263_cvg_2.0_tip_1_2	5	zinc c2h2 type domain-containing protein	87	1.08E-15	59.50%	0.1	IPR015880 (SMART); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
279	182317_length_263_cvg_2.0_tip_1_2	3	mam and ldl-receptor class a domain-containing protein 2-like	87	9.52E-24	72.70%	0.103	IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)

273	181569_length_262_cvg_3.0_tip_1_0	7	transferrin	88	4.55E-19	64.30%	0.099	IPR001156 (PRINTS); G3DSA:3.40.190.10 (GENE3D); IPR001156 (PFAM); PTHR11485 (PANTHER); IPR001156 (PROSITE_PROFILES); SSF53850 (SUPERFAMILY)
280	182529_length_263_cvg_4.0_tip_1_3	8	fras1-related extracellular matrix protein 1 isoform x1	88	5.24E-12	56.50%	0.167	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
281	182805_length_264_cvg_25.4_tip_1_0	55	aldose reductase	88	6.70E-27	85.40%	0.364 Y	IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); PTHR11732:SF173 (PANTHER); IPR001395 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
282	182807_length_264_cvg_3.9_tip_1_3	7	endo-beta- -glucanase	88	1.96E-14	80.00%	0.22	IPR012341 (G3DSA:1.50.10.GENE3D); IPR001701 (PFAM); PTHR22298 (PANTHER); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR008928 (SUPERFAMILY)
283	182895_length_264_cvg_2.0_tip_1_4	7	serine protease nudel	88	1.07E-43	89.10%	0.113	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
284	182909_length_264_cvg_2.0_tip_1_0	5	hemicentin-1 precursor	88	6.59E-29	73.80%	0.142	PR01705 (PRINTS); IPR000884 (SMART); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); PTHR19897 (PANTHER); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
285	183009_length_264_cvg_2.7_tip_1_5	6	wilms tumor partial	88	1.63E-26	69.80%	0.125	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
286	183023_length_264_cvg_2.0_tip_1_0	7	trehalase-like isoform x1	88	6.01E-26	70.30%	0.116	IPR001661 (PFAM); IPR001661 (PANTHER); PTHR23403:SF1 (PANTHER); IPR018232 (PROSITE_PATTERNS); IPR008928 (SUPERFAMILY)
287	183287_length_264_cvg_2.8_tip_1_4	6	zinc finger protein 431 isoform x2	88	6.86E-18	68.50%	0.146	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
288	183293_length_264_cvg_4.0_tip_1_5	12	thioredoxin domain-containing protein 11	88	4.06E-22	63.10%	0.111	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929 (PANTHER); PTHR18929:SF61 (PANTHER); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
289	183395_length_264_cvg_9.8_tip_1_0	21	alpha-esterase 47 isoform I	88	2.91E-11	72.50%	0.496 Y	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
292	184509_length_265_cvg_12.0_tip_1_2	33	melanoma-associated antigen e1- partial	88	6.88E-10	67.10%	0.428 Y	SignalP-TM (SIGNALP_GRAM_POSITIVE)
293	184667_length_265_cvg_4.0_tip_1_5	11	ribonuclease oy-like	88	2.72E-18	61.10%	0.112	IPR001568 (PFAM); IPR001568 (G3DSA:3.90.730.GENE3D); IPR001568 (PANTHER); IPR001568 (SUPERFAMILY)
295	185267_length_266_cvg_3.0_tip_1_5	4	ring finger and spry domain-containing protein 1-like	88	4.92E-35	79.80%	0.148	IPR003877 (PFAM); PTHR13363 (PANTHER); IPR001870 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
290	184341_length_265_cvg_2.0_tip_1_0	6	hypothetical protein Phum_PHUM426340	89	4.69E-20	67.10%	0.133	IPR003410 (PFAM); PTHR24273:SF29 (PANTHER); PTHR24273 (PANTHER); IPR003410 (PROSITE_PROFILES)
291	184497_length_265_cvg_3.8_tip_1_3	15	urokinase-type plasminogen activator	89	3.23E-06	82.30%	0.148	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
294	184747_length_265_cvg_5.0_tip_1_0	10	nuclear transport	89	2.79E-21	86.80%	0.121	IPR002075 (PFAM); G3DSA:3.10.450.50 (GENE3D); PTHR12612 (PANTHER); IPR018222 (PROSITE_PROFILES); SSF54427 (SUPERFAMILY)
296	185457_length_266_cvg_2.0_tip_1_4	4	nad h-hydrate epimerase-like	89	2.80E-38	78.90%	0.106	IPR004443 (PFAM); IPR004443 (G3DSA:3.40.50.GENE3D); PTHR13232 (PANTHER); IPR004443 (PROSITE_PROFILES); IPR004443 (SUPERFAMILY)
297	185923_length_266_cvg_6.0_tip_1_3	12	cd109 antigen-like isoform x1	89	1.08E-35	77.70%	0.108	IPR002890 (PFAM); PTHR11412:SF84 (PANTHER); PTHR11412 (PANTHER)
298	185997_length_267_cvg_3.0_tip_1_2	9	heat shock protein	89	7.68E-42	91.50%	0.112	IPR029048 (G3DSA:1.20.1270.GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); IPR029047 (SUPERFAMILY)
299	186277_length_267_cvg_2.0_tip_1_0	6	slit-like partial	89	4.88E-19	65.50%	0.247	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
300	186389_length_267_cvg_2.0_tip_1_2	5	receptor tyrosine phosphatase type r2a	89	3.37E-30	79.90%	0.134	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19134 (PANTHER); PTHR19134:SF199 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
301	186531_length_267_cvg_2.0_tip_1_3	6	transmembrane protease serine 12	89	8.34E-19	75.60%	0.148	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24264:SF9 (PANTHER); PTHR24264 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)

302	186723_length_267_cvg_66.1_tip_1_3	225	plasma alpha-l-fucosidase-like	89	2.29E-26	77.60%	0.731 Y	IPR000933 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR000933 (PANTHER); PTHR10030:SF26 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017853 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
303	186757_length_267_cvg_2.0_tip_1_1	5	short-chain dehydrogenase	89	1.76E-22	71.50%	0.440 Y	IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF308 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
304	186821_length_267_cvg_2.0_tip_1_5	4	zinc finger protein	89	7.77E-17	59.00%	0.102	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
305	187119_length_268_cvg_2.0_tip_1_1	6	spermatogenesis-associated protein 5	89	3.98E-48	92.80%	0.105	IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23077 (PANTHER); PTHR23077:SF27 (PANTHER); IPR027417 (SUPERFAMILY)
306	187171_length_268_cvg_2.0_tip_1_5	5	zinc finger protein	89	2.80E-15	58.20%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
308	187339_length_268_cvg_3.0_tip_1_2	7	c-terminal tandem repeated domain in type 4 procollagen	89	8.48E-10	63.20%	0.098	IPR008160 (PFAM); PTHR24023:SF379 (PANTHER); PTHR24023 (PANTHER)
310	187415_length_268_cvg_2.0_tip_1_4	6	wd repeat-containing protein 37-like	89	3.26E-47	92.80%	0.104	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19855 (PANTHER); PTHR19855:SF12 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
312	187625_length_268_cvg_2.0_tip_1_4	6	---NA---	89			0.107	no IPS match
313	187661_length_268_cvg_2.0_tip_1_5	3	glucose dehydrogenase	89	3.27E-23	71.10%	0.143	G3DSA:3.50.50.60 (GENE3D); IPR000172 (PFAM); PTHR11552:SF77 (PANTHER); PTHR11552 (PANTHER); SSF51905 (SUPERFAMILY)
314	187993_length_269_cvg_3.2_tip_1_5	7	zinc finger protein 235	89	5.31E-15	61.20%	0.099	IPR015880 (SMART); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
316	188235_length_269_cvg_8.4_tip_1_2	23	prolow-density lipoprotein receptor-related protein 1-like	89	4.64E-08	64.00%	0.359 Y	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
319	188575_length_269_cvg_2.0_tip_1_5	4	dnaj homolog subfamily c member 30-like	89	4.76E-21	73.30%	0.113	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF171 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
307	187283_length_268_cvg_2.0_tip_1_0	6	er degradation-enhancing alpha-mannosidase-like 1	90	7.88E-40	84.40%	0.105	IPR001382 (PFAM); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PANTHER); PTHR11742:SF25 (PANTHER); IPR001382 (SUPERFAMILY)
309	187339_length_268_cvg_3.0_tip_1_3	7	hypothetical protein, partial	90	1.75E-09	48.80%	0.119	no IPS match
311	187461_length_268_cvg_2.0_tip_1_3	6	leucine-rich repeat-containing protein 58	90	5.52E-10	60.40%	0.103	G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52075 (SUPERFAMILY)
315	188197_length_269_cvg_4.0_tip_1_1	12	proprotein convertase subtilisin kexin type	90	5.34E-30	79.00%	0.106	IPR002884 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); PTHR10795:SF71 (PANTHER); IPR015500 (PANTHER); IPR008979 (SUPERFAMILY)
317	188275_length_269_cvg_2.0_tip_1_4	7	convoluted-like protein	90	3.52E-15	66.30%	0.101	G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); PTHR24365:SF83 (PANTHER); SSF52058 (SUPERFAMILY)
318	188403_length_269_cvg_4.3_tip_1_3	9	immunoglobulin i-set domain-containing protein	90	1.14E-20	65.90%	0.113	IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
320	188879_length_269_cvg_3.0_tip_1_3	14	coagulation factor v	90	2.97E-09	64.90%	0.113	no IPS match
321	189091_length_270_cvg_3.0_tip_1_5	10	dappu_318553-like protein	90	1.55E-22	68.00%	0.127	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
322	189153_length_270_cvg_4.5_tip_1_2	14	collagen alpha-1 chain	90	2.56E-10	57.80%	0.099	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF379 (PANTHER)

323	189199_length_270_cvg_5.0_tip_1_5	13	krueppel-like factor 13	90	1.65E-45	85.70%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
324	189217_length_270_cvg_2.0_tip_1_2	6	abl interactor 2 isoform x1	90	5.75E-40	85.60%	0.119	IPR001452 (PRINTS); IPR001452 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR001452 (PFAM); IPR028457 (PANTHER); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY)
325	189585_length_270_cvg_4.0_tip_1_1	14	transforming growth factor-beta-induced protein ig-h3-like	90	5.57E-30	68.20%	0.102	IPR000782 (PFAM); IPR000782 (G3DSA:2.30.180.GENE3D); PTHR10900:SF73 (PANTHER); PTHR10900 (PANTHER); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY)
326	189631_length_270_cvg_3.0_tip_1_5	6	cyclin-dependent kinase 2-like	90	5.04E-54	95.90%	0.201	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24056 (PANTHER); PTHR24056:SF168 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
327	189721_length_270_cvg_4.0_tip_1_2	12	alpha-2-macroglobulin-like isoform x1	90	2.61E-14	60.20%	0.105	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
328	189949_length_271_cvg_4.0_tip_1_2	12	titin isoform x1	90	2.23E-32	77.50%	0.106	IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF149 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
331	190273_length_271_cvg_2.0_tip_1_5	5	aldehyde dehydrogenase family 16 member a1-like	90	2.25E-42	93.20%	0.099	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699:SF98 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
332	190347_length_271_cvg_2.0_tip_1_1	8	clipd6 protein	90	8.41E-12	58.00%	0.129	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265:SF76 (PANTHER); PTHR24265 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
333	190471_length_271_cvg_2.0_tip_1_2	3	keratin-associated protein 5-9-like	90	2.23E-07	56.43%	0.322	no IPS match
334	190477_length_271_cvg_4.0_tip_1_2	9	heat shock protein 70	90	1.52E-19	67.60%	0.103	G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); SSF53067 (SUPERFAMILY)
335	190497_length_271_cvg_6.0_tip_1_2	7	striatin- partial	90	5.48E-54	97.30%	0.114	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR15653 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
338	191023_length_272_cvg_2.0_tip_1_2	6	zinc finger protein 235	90	3.10E-13	57.20%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR002219 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
341	191333_length_272_cvg_4.0_tip_1_2	9	titin- partial	90	5.46E-43	88.00%	0.098	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF149 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
329	189955_length_271_cvg_3.0_tip_1_3	8	glyoxal reductase	91	2.29E-27	72.30%	0.107	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); PTHR11732:SF133 (PANTHER); IPR001395 (PANTHER); IPR023210 (SUPERFAMILY)
330	190181_length_271_cvg_2.0_tip_1_3	4	aldehyde oxidase	91	6.95E-23	71.20%	0.126	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF65 (PANTHER); IPR008274 (SUPERFAMILY)
336	190535_length_271_cvg_9.2_tip_1_0	21	zinc finger protein 235-like	91	5.69E-22	67.20%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
337	190807_length_272_cvg_2.0_tip_1_0	10	polypeptide n-acetylgalactosaminyltransferase 2	91	6.35E-21	60.60%	0.104	PTHR11675 (PANTHER); PTHR11675:SF24 (PANTHER)
339	191089_length_272_cvg_2.0_tip_1_3	6	protein flightless-1	91	3.09E-40	86.90%	0.165	IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029919 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY)
340	191129_length_272_cvg_2.3_tip_1_3	8	heat shock 70 kda protein cognate 4	91	4.77E-21	88.70%	0.104	IPR013126 (PRINTS); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF155 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)

342	191811_length_273_cvg_19.9_tip_0_0	36	annexin partial	91	1.50E-28	76.80%	0.11	Coil (COILS); IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (PFAM); PTHR10502 (PANTHER); IPR018252 (PROSITE PATTERNS); SSF47874 (SUPERFAMILY)
343	191813_length_273_cvg_34.0_tip_0_0	60	annexin partial	91	6.08E-29	78.60%	0.103	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (PFAM); PTHR10502 (PANTHER); IPR018252 (PROSITE PATTERNS); SSF47874 (SUPERFAMILY)
344	191951_length_273_cvg_68.5_tip_1_3	217	isoform cra_b	91	1.38E-56	100.00%	0.128	IPR019956 (PRINTS); IPR000626 (SMART); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); G3DSA:3.10.20.90 (GENE3D); PTHR10666 (PANTHER); IPR019954 (PROSITE PATTERNS); IPR000626 (PROSITE PROFILES); IPR029071 (SUPERFAMILY)
345	192287_length_274_cvg_2.0_tip_1_4	5	hemimentin- partial	91	4.42E-34	81.40%	0.148	IPR023413 (G3DSA:2.40.155.GENE3D); IPR006605 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF158 (PANTHER); IPR006605 (PROSITE PROFILES); IPR009017 (SUPERFAMILY)
346	192597_length_274_cvg_2.0_tip_1_1	7	roundabout homolog 1-like isoform x3	91	3.43E-06	52.40%	0.102	IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR007110 (PROSITE PROFILES); SSF48726 (SUPERFAMILY)
349	193401_length_275_cvg_2.0_tip_1_2	7	perlucin 8	91	3.26E-06	61.00%	0.114	IPR016186 (G3DSA:3.10.100.GENE3D); IPR016187 (SUPERFAMILY)
352	193489_length_275_cvg_2.0_tip_1_2	7	protein pbmucl2- partial	91	4.38E-12	44.10%	0.156	no IPS match
354	193603_length_275_cvg_3.2_tip_1_5	11	ubiquitin family partial	91	1.74E-55	97.90%	0.168	IPR019956 (PRINTS); IPR000626 (SMART); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); G3DSA:3.10.20.90 (GENE3D); PTHR10666 (PANTHER); IPR019954 (PROSITE PATTERNS); IPR000626 (PROSITE PROFILES); IPR029071 (SUPERFAMILY)
347	193227_length_275_cvg_2.0_tip_1_3	6	---NA---	92			0.576 Y	IPR012674 (G3DSA:2.40.128.GENE3D); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_EUK); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)
348	193317_length_275_cvg_3.0_tip_1_0	8	heat shock cognate 71 kda protein	92	1.38E-21	96.00%	0.114	IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); PTHR19375:SF155 (PANTHER); IPR018181 (PROSITE PATTERNS); SSF53067 (SUPERFAMILY)
350	193453_length_275_cvg_2.4_tip_1_3	9	deoxyribonuclease-2-alpha isoform x3	92	7.09E-15	55.60%	0.133	IPR004947 (PFAM); IPR004947 (PANTHER)
351	193467_length_275_cvg_2.2_tip_1_1	8	phospholipase b-like lamina ancestor	92	1.61E-26	68.20%	0.172	IPR007000 (PFAM); IPR007000 (PANTHER); PTHR12370:SF3 (PANTHER)
353	193569_length_275_cvg_2.0_tip_1_3	8	hemocytin	92	1.22E-21	67.90%	0.104	G3DSA:2.10.25.10 (GENE3D)
355	193645_length_275_cvg_2.0_tip_1_4	2	zinc finger protein partial	92	3.51E-37	81.40%	0.118	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR19818 (PANTHER); PTHR19818:SF68 (PANTHER); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PROFILES); IPR007087 (PROSITE PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
356	193663_length_275_cvg_2.0_tip_1_0	7	zinc finger protein gfi-1b isoform x2	92	1.31E-15	61.90%	0.108	IPR015880 (SMART); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PROFILES); IPR007087 (PROSITE PROFILES); SSF57667 (SUPERFAMILY)
357	193683_length_275_cvg_2.0_tip_1_1	6	protein creg1	92	8.85E-20	74.00%	0.113	IPR012349 (G3DSA:2.30.110.GENE3D); PF13883 (PFAM); PTHR13343 (PANTHER); PTHR13343:SF17 (PANTHER); IPR012349 (SUPERFAMILY)
358	193949_length_276_cvg_7.8_tip_1_5	26	krueppel-like factor 15	92	1.40E-19	87.00%	0.122	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); PTHR23223:SF146 (PANTHER); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PROFILES); SSF57667 (SUPERFAMILY)
359	194175_length_276_cvg_2.0_tip_1_0	3	fat-like cadherin-related tumor suppressor homolog	92	5.82E-28	70.70%	0.101	IPR002126 (PRINTS); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); PTHR24026 (PANTHER); PTHR24026:SF39 (PANTHER); IPR020894 (PROSITE PATTERNS); IPR002126 (PROSITE PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
360	194203_length_276_cvg_2.3_tip_1_1	5	lysosomal pro-x partial	92	1.67E-37	82.30%	0.113	IPR008758 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11010:SF11 (PANTHER); IPR008758 (PANTHER); IPR029058 (SUPERFAMILY)
361	194363_length_276_cvg_2.0_tip_1_3	8	isoform c	92	6.49E-36	82.20%	0.121	IPR000716 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PFAM); PTHR12036 (PANTHER); IPR000716 (PROSITE PATTERNS); IPR000716 (PROSITE PROFILES); IPR000716 (SUPERFAMILY)
362	194735_length_277_cvg_3.0_tip_1_2	7	carboxypeptidase pm20d1	92	1.33E-29	72.90%	0.098	PTHR11014:SF66 (PANTHER); PTHR11014 (PANTHER)
370	195593_length_278_cvg_4.9_tip_1_5	13	vanin-like protein 1	92	1.63E-26	69.40%	0.137	IPR003010 (G3DSA:3.60.110.GENE3D); IPR012101 (PANTHER); IPR003010 (SUPERFAMILY)

363	195085_length_278_cvg_4.0_tip_1_4	10	neprilysin-2 isoform x3	93	2.51E-33	76.90%	0.255	IPR018497 (PRINTS); IPR018497 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000718 (PANTHER); PTHR11733:SF113 (PANTHER); SSF55486 (SUPERFAMILY)
364	195145_length_278_cvg_6.0_tip_1_4	21	ankyrin repeat domain-containing protein 16	93	4.11E-16	63.90%	0.241	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
365	195201_length_278_cvg_3.0_tip_1_1	7	fat-like cadherin-related tumor suppressor homolog	93	6.22E-42	89.20%	0.108	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); PTHR24026 (PANTHER); PTHR24026:SF39 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY)
366	195327_length_278_cvg_5.3_tip_1_1	17	low-density lipoprotein receptor-related protein 2	93	8.02E-42	86.60%	0.133	IPR000033 (SMART); IPR011042 (G3DSA:2.120.10.GENE3D); IPR000033 (PFAM); PTHR10529:SF210 (PANTHER); PTHR10529 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY)
367	195353_length_278_cvg_3.0_tip_1_4	8	serine threonine-protein kinase ulk3 isoform x1	93	3.48E-38	81.40%	0.111	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24348 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
368	195399_length_278_cvg_54.7_tip_1_1	179	---NA---	93			0.105	no IPS match
369	195575_length_278_cvg_2.0_tip_1_3	7	low-density lipoprotein receptor-related protein partial	93	9.44E-15	60.10%	0.118	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
371	195843_length_279_cvg_12.0_tip_1_0	30	---NA---	93			0.099	no IPS match
372	196005_length_279_cvg_3.0_tip_1_0	10	matrix metalloproteinase 1 isoform 1	93	1.72E-34	77.80%	0.113	IPR018487 (SMART); IPR018487 (PFAM); IPR000585 (G3DSA:2.110.10.GENE3D); PTHR10201 (PANTHER); PTHR10201:SF131 (PANTHER); IPR018487 (PROSITE_PROFILES); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY)
373	196093_length_279_cvg_2.0_tip_1_4	4	zinc finger protein 628	93	1.14E-29	76.40%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
374	196169_length_279_cvg_3.0_tip_1_0	11	metabotropic gaba-b receptor subtype isoform b	93	4.15E-39	86.10%	0.16	IPR002456 (PRINTS); G3DSA:3.40.50.2300 (GENE3D); IPR001828 (PFAM); PTHR10519:SF3 (PANTHER); IPR002455 (PANTHER); IPR028082 (SUPERFAMILY)
375	196549_length_280_cvg_2.0_tip_1_2	5	cysteine peptidase c	93	2.39E-26	79.00%	0.119	IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF286 (PANTHER); IPR013128 (PANTHER); SSF54001 (SUPERFAMILY)
376	196601_length_280_cvg_3.0_tip_1_4	9	peroxisome biogenesis factor 1-like	93	2.23E-52	93.30%	0.24	IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); IPR025653 (PTHR23077:PANTHER); PTHR23077 (PANTHER); IPR027417 (SUPERFAMILY)
377	196671_length_280_cvg_2.0_tip_1_5	5	glypican- partial	93	1.13E-08	80.57%	0.125	IPR001863 (PFAM)
378	196755_length_280_cvg_93.4_tip_0_2	194	muc19_human ame: full=mucin-19 short=muc-19 flags: partial	93	9.48E-07	49.00%	0.119	no IPS match
380	197279_length_281_cvg_12.6_tip_1_2	15	bola-like protein 3	93	5.66E-23	76.40%	0.107	G3DSA:3.30.70.1500 (GENE3D); IPR002634 (PFAM); PTHR12735 (PANTHER); PTHR12735:SF4 (PANTHER); IPR002634 (SUPERFAMILY)
379	196973_length_281_cvg_2.0_tip_1_0	6	elastase	94	2.13E-20	64.20%	0.097	IPR023612 (PRINTS); IPR013856 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); SSF55486 (SUPERFAMILY)
381	197575_length_282_cvg_2.0_tip_1_1	7	st14a protein	94	1.74E-09	55.90%	0.141	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
382	197833_length_282_cvg_3.0_tip_1_4	8	serine threonine-protein kinase kin4	94	1.16E-41	81.20%	0.104	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24359 (PANTHER); PTHR24359:SF18 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
383	197843_length_282_cvg_2.0_tip_1_0	8	zinc finger protein 492-like	94	7.27E-28	76.00%	0.13	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
384	198269_length_283_cvg_4.0_tip_1_1	9	leucine-rich repeat-containing protein 58-like	94	1.58E-31	79.70%	0.108	SM00364 (SMART); IPR003591 (SMART); IPR025875 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52075 (SUPERFAMILY)
385	198529_length_283_cvg_18.2_tip_0_5	41	golgin subfamily a member 6-like protein 22	94	8.21E-09	52.20%	0.101	no IPS match

386	198611_length_283_cvg_3.0_tip_1_5	8	u5 small nuclear ribonucleoprotein 40 kda	94	9.69E-47	85.40%	0.108	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
387	198777_length_284_cvg_3.0_tip_1_5	7	phospholipase b-like 2	94	6.80E-30	73.90%	0.101	IPR007000 (PFAM); IPR007000 (PANTHER)
389	199253_length_284_cvg_3.0_tip_1_5	9	c-type lectin domain family 4 member m-like	94	3.26E-19	60.00%	0.146	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22801 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
390	199263_length_284_cvg_3.0_tip_1_5	10	krueppel-like factor partial	94	1.50E-37	86.80%	0.195	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
388	199067_length_284_cvg_2.0_tip_1_1	7	carboxypeptidase e	95	6.68E-28	65.90%	0.114	PF13620 (PFAM); IPR014766 (G3DSA:2.60.40.GENE3D); PTHR11532:SF41 (PANTHER); PTHR11532 (PANTHER); IPR008969 (SUPERFAMILY)
391	199589_length_285_cvg_2.0_tip_1_0	6	ankyrin repeat	95	1.04E-18	59.50%	0.127	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24188 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
392	199851_length_285_cvg_4.0_tip_1_2	10	xanthine dehydrogenase-like	95	5.34E-31	79.00%	0.105	IPR000674 (PFAM); IPR000674 (G3DSA:3.90.1170.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR000674 (SUPERFAMILY)
395	200073_length_286_cvg_4.8_tip_1_5	13	basement membrane-specific heparan sulfate proteoglycan core protein	95	4.82E-24	66.70%	0.104	IPR000034 (PFAM); IPR000034 (PROSITE_PROFILES)
397	200207_length_286_cvg_3.4_tip_1_5	4	zinc finger protein 850-like	95	2.51E-15	63.90%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
393	199867_length_286_cvg_2.0_tip_1_0	4	acid sphingomyelinase-like phosphodiesterase 3b	96	2.26E-20	56.20%	0.241	IPR029052 (G3DSA:3.60.21.GENE3D); PTHR10340 (PANTHER); IPR029052 (SUPERFAMILY)
394	199935_length_286_cvg_2.0_tip_1_3	4	von willebrand factor type egf and pentraxin domain-containing protein 1 isoform x2	96	2.59E-30	76.80%	0.102	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
396	200095_length_286_cvg_2.0_tip_1_3	5	macrophage mannose receptor 1-like	96	6.01E-07	48.14%	0.104	IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803:SF16 (PANTHER); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
398	200413_length_287_cvg_6.0_tip_1_3	15	dnaj homolog subfamily c member 21-like	96	7.17E-36	87.30%	0.129	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF150 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
399	200589_length_287_cvg_2.0_tip_1_0	5	homeotic protein spalt-major-like	96	6.32E-59	97.00%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR23233 (PANTHER); PTHR23233:SF49 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
400	200803_length_287_cvg_3.0_tip_1_4	9	venom serine carboxypeptidase-like	96	4.64E-15	61.70%	0.195	IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
401	201041_length_288_cvg_2.9_tip_1_2	11	zinc c2h2 type domain-containing protein	96	8.75E-15	58.30%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
402	201145_length_288_cvg_2.0_tip_1_4	6	serine threonine-protein kinase osr1 isoform x1	96	2.02E-53	94.50%	0.485 Y	G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24361 (PANTHER); PTHR24361:SF201 (PANTHER); IPR000719 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR011009 (SUPERFAMILY)
403	201345_length_288_cvg_2.0_tip_1_4	4	transport and golgi organization protein 1	96	1.83E-17	65.00%	0.413 Y	G3DSA:2.30.30.40 (GENE3D); IPR001452 (SUPERFAMILY)

404	201455_length_289_cvg_2.0_tip_1_1	3	basement membrane-specific heparan sulfate proteoglycan core protein	96	4.75E-11	59.30%	0.105	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529:SF3 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
405	201465_length_289_cvg_2.0_tip_1_4	5	fat-like cadherin-related tumor suppressor-like protein	96	7.97E-38	87.80%	0.1	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); PTHR24026:SF39 (PANTHER); PTHR24026 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY)
406	201801_length_289_cvg_30.0_tip_1_4	81	plasma alpha-l-fucosidase-like	96	3.21E-26	79.50%	0.606 Y	IPR013781 (G3DSA:3.20.20.GENE3D); IPR000933 (PFAM); IPR000933 (PANTHER); PTHR10030:SF26 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017853 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
408	202485_length_290_cvg_3.7_tip_1_5	10	ankyrin repeat	96	2.77E-19	60.50%	0.127	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
407	201849_length_289_cvg_7.8_tip_1_3	37	leucine-rich repeats and immunoglobulin-like domains protein 3 isoform x2	97	3.47E-10	54.00%	0.112	no IPS match
409	202487_length_290_cvg_3.9_tip_1_1	14	glucose dehydrogenase	97	7.00E-23	74.80%	0.1	G3DSA:3.50.50.60 (GENE3D); IPR000172 (PFAM); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); IPR000172 (PROSITE_PATTERNS); SSF51905 (SUPERFAMILY)
410	202663_length_291_cvg_2.0_tip_1_4	5	zinc finger protein	97	1.59E-13	52.90%	0.101	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24375:SF106 (PANTHER); PTHR24375 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
411	202865_length_291_cvg_5.5_tip_1_3	21	achain structural determinants for improved thermal stability of designed ankyrin repeat proteins with a redesigned c- capping	97	2.86E-14	63.10%	0.141	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24188 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
412	202903_length_291_cvg_4.0_tip_1_0	11	low-density lipoprotein receptor-related protein 2	97	7.71E-34	77.20%	0.107	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
413	203111_length_292_cvg_2.0_tip_1_2	6	aael012493- partial	97	2.84E-36	80.20%	0.114	IPR006652 (SMART); IPR015915 (G3DSA:2.120.10.GENE3D); IPR006652 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF3 (PANTHER); SSF117281 (SUPERFAMILY)
416	203233_length_292_cvg_4.0_tip_1_1	10	adp-ribosylation factor-like protein 4c	97	1.95E-54	92.20%	0.156	IPR006689 (PRINTS); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR11711:SF121 (PANTHER); PTHR11711 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
418	203411_length_292_cvg_2.5_tip_1_4	10	low affinity immunoglobulin epsilon fc receptor	97	7.88E-15	55.30%	0.183	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
414	203131_length_292_cvg_4.7_tip_1_0	11	alcohol dehydrogenase	98	5.41E-13	69.90%	0.13	IPR023210 (G3DSA:3.20.20.GENE3D); IPR001395 (PANTHER); PTHR11732:SF144 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
415	203181_length_292_cvg_3.9_tip_1_0	9	coagulation factor x- partial	98	6.74E-14	59.10%	0.103	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
417	203409_length_292_cvg_3.0_tip_1_0	9	---NA---	98			0.103	Coil (COILS); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016187 (SUPERFAMILY)
419	203787_length_293_cvg_3.0_tip_1_1	9	zinc finger and scan domain-containing protein 2-like isoform x1	98	1.87E-49	86.40%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
420	204119_length_294_cvg_2.0_tip_1_2	5	cbl-interacting protein kinase 16-like isoform x1	98	3.43E-45	86.10%	0.122	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24342 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)

421	204223_length_294_cvg_2.0_tip_1_3	5	sucrase- intestinal-like	98	1.86E-18	60.30%	0.1	PTHR22762:SF69 (PANTHER); PTHR22762 (PANTHER); IPR011013 (SUPERFAMILY)
422	204269_length_294_cvg_2.0_tip_1_0	7	receptor-type tyrosine-protein phosphatase kappa	98	1.06E-45	84.80%	0.117	IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134:SF227 (PANTHER); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
423	204527_length_294_cvg_2.0_tip_1_5	7	low-density lipoprotein	98	5.33E-28	70.40%	0.103	IPR000742 (SMART); IPR001881 (SMART); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10529:SF204 (PANTHER); PTHR10529 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
425	205001_length_296_cvg_3.9_tip_1_2	17	heat shock cognate 71 kda	98	9.06E-50	98.00%	0.186	IPR013126 (PRINTS); G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF142 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
427	205261_length_296_cvg_4.0_tip_1_5	11	tyrosine-protein phosphatase lar isoform x1	98	1.56E-35	80.00%	0.102	PR00014 (PRINTS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR19134:SF204 (PANTHER); PTHR19134 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
424	204979_length_296_cvg_8.0_tip_1_4	21	pacifastin-related peptide precursor	99	5.92E-10	58.22%	0.626 Y	IPR008037 (PFAM); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY)
426	205107_length_296_cvg_2.8_tip_1_0	9	gamma-glutamyltranspeptidase 1	99	7.43E-35	75.80%	0.098	IPR000101 (PRINTS); IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF15 (PANTHER); IPR029055 (SUPERFAMILY)
428	205423_length_296_cvg_2.8_tip_1_4	11	peripheral plasma membrane protein partial	99	4.19E-39	81.30%	0.598 Y	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24347:SF136 (PANTHER); IPR020636 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
429	205491_length_297_cvg_3.0_tip_1_3	8	macrophage mannose receptor 1-like	99	9.94E-11	55.30%	0.108	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); PTHR22803:SF16 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR016187 (SUPERFAMILY)
430	206035_length_298_cvg_5.0_tip_1_2	16	peptidyl-prolyl cis-trans isomerase d	99	4.09E-21	67.90%	0.121	Coil (COILS); IPR019734 (SMART); IPR011990 (G3DSA:1.25.40.GENE3D); PF13414 (PFAM); IPR023566 (PANTHER); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY)
431	206209_length_298_cvg_3.8_tip_1_2	10	peptidyl-prolyl cis-trans isomerase nima-interacting 1-like	99	4.75E-39	91.90%	0.101	IPR000297 (PFAM); G3DSA:3.10.50.40 (GENE3D); PTHR10657 (PANTHER); IPR023058 (PROSITE_PATTERNS); IPR000297 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY)
432	206401_length_298_cvg_3.0_tip_1_5	12	zinc finger protein 525-like	99	8.32E-14	57.60%	0.121	IPR015880 (SMART); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
433	206523_length_299_cvg_2.0_tip_1_5	6	ring finger and spry domain-containing protein 1-like	99	1.00E-38	80.50%	0.098	PTHR13363 (PANTHER)
434	206945_length_299_cvg_2.0_tip_1_5	5	low-density lipoprotein	99	3.95E-27	65.70%	0.133	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
435	207021_length_300_cvg_3.9_tip_1_2	12	zinc finger protein 629 isoform x1	100	9.63E-25	78.20%	0.102	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); PTHR23223:SF130 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
436	207225_length_300_cvg_3.0_tip_1_3	10	melanoma-associated antigen e1- partial	100	2.66E-15	65.60%	0.142	SignalP-TM (SIGNALP_GRAM_POSITIVE)
437	207615_length_301_cvg_4.0_tip_1_2	13	xanthine dehydrogenase isoform x1	100	2.17E-26	74.30%	0.099	IPR000674 (PFAM); IPR000674 (G3DSA:3.90.1170.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR000674 (SUPERFAMILY)
438	208039_length_302_cvg_5.0_tip_1_5	18	collagen alpha-5 chain-like	100	2.36E-06	69.00%	0.131	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
439	208073_length_302_cvg_2.0_tip_1_2	5	lysosomal alpha-glucosidase-like	100	3.34E-55	89.40%	0.147	IPR000322 (PFAM); PTHR22762:SF7 (PANTHER); PTHR22762 (PANTHER); IPR030459 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
441	208365_length_302_cvg_3.0_tip_1_5	8	fukutin-related protein	100	3.27E-09	62.40%	0.098	no IPS match

440	208273_length_302_cvg_9.0_tip_1_0	26	group iii secreted phospholipase	101	1.96E-21	60.10%	0.137	IPR001211 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR12253 (PANTHER); IPR016090 (SUPERFAMILY)
442	208379_length_302_cvg_3.0_tip_1_0	9	serine protease	101	1.29E-18	60.60%	0.101	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
443	208419_length_303_cvg_38.8_tip_1_0	112	actin-depolymerizing factor	101	5.92E-37	75.10%	0.102	IPR007122 (PRINTS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY)
444	208669_length_303_cvg_3.0_tip_1_2	9	zinc finger protein	101	1.39E-59	95.30%	0.105	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23228:SF26 (PANTHER); PTHR23228 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
445	208755_length_303_cvg_2.0_tip_1_0	6	cd4-specific ankyrin repeat protein	101	1.53E-15	54.30%	0.103	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
446	208879_length_304_cvg_88.6_tip_0_3	1828	kazal-type serine proteinase inhibitor 4	102	8.63E-10	53.30%	0.108	IPR002350 (SMART); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
447	209385_length_305_cvg_2.0_tip_1_0	7	angiogenic factor with g patch and fha domains 1-like	102	4.46E-14	63.00%	0.118	no IPS match
448	209417_length_305_cvg_2.0_tip_1_1	3	zinc finger protein 239- partial	102	2.99E-19	60.20%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
449	210005_length_306_cvg_5.0_tip_1_3	18	peptidyl-prolyl cis-trans isomerase-like	102	3.98E-39	86.50%	0.612 Y	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR0020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR029000 (SUPERFAMILY)
450	210057_length_306_cvg_4.0_tip_1_2	12	carboxypeptidase b-like	102	2.53E-12	54.70%	0.1	IPR003146 (PFAM); IPR003146 (G3DSA:3.30.70.GENE3D); PTHR11705 (PANTHER); IPR009020 (SUPERFAMILY)
451	210063_length_306_cvg_7.0_tip_1_1	27	very low-density lipoprotein receptor-like	102	1.11E-09	53.90%	0.114	IPR002172 (SMART); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
452	210285_length_307_cvg_2.0_tip_1_1	4	carboxypeptidase d-like	102	8.26E-16	71.50%	0.143	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); SSF53187 (SUPERFAMILY)
453	210557_length_307_cvg_2.0_tip_1_4	6	polypeptide n-acetylgalactosaminyltransferase 5 isoform x2	102	1.87E-45	82.40%	0.1	IPR000772 (SMART); G3DSA:2.80.10.50 (GENE3D); IPR000772 (PFAM); PTHR11675:SF39 (PANTHER); PTHR11675 (PANTHER); IPR000772 (PROSITE_PROFILES); IPR000772 (SUPERFAMILY)
455	210767_length_308_cvg_3.7_tip_1_2	13	vesicle-fusing atpase 1-like	102	8.38E-32	76.40%	0.122	IPR003338 (SMART); G3DSA:2.40.40.20 (GENE3D); IPR003338 (PFAM); PTHR23078 (PANTHER); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009010 (SUPERFAMILY)
456	210841_length_308_cvg_3.0_tip_1_2	10	aqp_aedae ame: full=aquaporin	102	4.97E-20	70.00%	0.242	IPR000425 (PRINTS); IPR023271 (G3DSA:1.20.1080.GENE3D); IPR000425 (PFAM); IPR000425 (PANTHER); PTHR19139:SF45 (PANTHER); IPR022357 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023271 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
454	210689_length_307_cvg_7.0_tip_1_3	14	heat shock protein partial	103	7.78E-55	90.10%	0.101	G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF142 (PANTHER); SSF53067 (SUPERFAMILY)
457	210867_length_308_cvg_15.7_tip_1_3	59	huga_polan ame: full=hyaluronidase short=hya ame: full=hyaluronoglucosaminidase ame: allergen=pol a 2 flags: partial	103	1.14E-09	61.10%	0.366 Y	IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
458	210911_length_308_cvg_8.6_tip_1_4	27	folistatin-related protein 5-like	103	7.23E-50	83.80%	0.107	PTHR10913 (PANTHER); PTHR10913:SF14 (PANTHER)
459	211137_length_308_cvg_3.6_tip_1_0	9	reticulocalbin-2-like isoform x1	103	1.85E-32	75.30%	0.104	IPR002048 (SMART); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); PTHR10827:SF48 (PANTHER); PTHR10827 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)

460	211175_length_308_cvg_5.1_tip_1_4	16	vitellogenic carboxypeptidase	103	6.49E-33	73.60%	0.108	IPR001563 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
461	211267_length_309_cvg_2.0_tip_1_1	6	dna polymerase alpha catalytic subunit	103	8.26E-28	71.00%	0.119	IPR000101 (PRINTS); IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF18 (PANTHER); IPR029055 (SUPERFAMILY); TMhelix (TMHMM)
462	211443_length_309_cvg_11.0_tip_1_2	30	cd109 antigen	103	3.47E-32	74.20%	0.137	IPR011625 (PFAM); PTHR11412 (PANTHER); PTHR11412:SF84 (PANTHER)
463	211605_length_309_cvg_3.0_tip_1_1	10	neuroigin- y-linked isoform x1	103	6.47E-46	84.60%	0.142	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); PTHR11559:SF157 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY)
464	211607_length_309_cvg_2.0_tip_1_0	6	lactose-binding lectin I-2-like	103	5.08E-10	58.60%	0.111	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
465	211609_length_309_cvg_2.4_tip_1_5	12	mitochondrial cardiolipin hydrolase	103	5.35E-37	70.80%	0.122	G3DSA:3.30.870.10 (GENE3D); IPR025202 (PFAM); PTHR21248 (PANTHER); IPR001736 (PROSITE_PROFILES); SSF56024 (SUPERFAMILY)
466	212195_length_311_cvg_2.0_tip_1_2	6	fez family zinc finger protein 2	103	6.26E-61	95.80%	0.121	IPR015880 (SMART); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
467	212245_length_311_cvg_2.0_tip_1_1	4	hindsight transcription factor-like protein	104	5.24E-50	86.20%	0.11	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23233:SF42 (PANTHER); PTHR23233 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
468	212339_length_311_cvg_2.1_tip_1_4	6	macrophage mannose receptor 1-like	104	1.28E-13	51.90%	0.159	IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803:SF16 (PANTHER); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
469	212991_length_312_cvg_2.0_tip_1_1	6	low quality protein: zinc finger protein 665	104	3.61E-23	67.40%	0.101	IPR015880 (SMART); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
470	213125_length_313_cvg_2.0_tip_1_4	9	partial	104	1.12E-11	52.10%	0.155	IPR000372 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR000372 (PFAM)
471	213149_length_313_cvg_2.0_tip_1_4	6	hypothetical protein	104	7.98E-13	61.20%	0.101	G3DSA:1.20.120.20 (GENE3D); SSF47162 (SUPERFAMILY)
472	213357_length_313_cvg_2.1_tip_1_1	12	cubilin	104	1.01E-19	60.00%	0.155	IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
473	213497_length_314_cvg_4.0_tip_1_2	14	adiponectin receptor protein	104	6.58E-41	90.20%	0.307	IPR004254 (PFAM); IPR004254 (PANTHER); PTHR20855:SF15 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
474	213513_length_314_cvg_4.7_tip_1_1	6	achain crystal structure of engineered northeast structural genomics consortium target	105	7.53E-16	60.60%	0.099	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
475	213531_length_314_cvg_2.0_tip_1_0	7	epidermal growth factor receptor	105	3.10E-39	77.80%	0.101	IPR000494 (G3DSA:3.80.20.GENE3D); IPR000494 (PFAM); PTHR24416 (PANTHER); PTHR24416:SF88 (PANTHER); SSF52058 (SUPERFAMILY)
476	213597_length_314_cvg_2.3_tip_1_1	8	beta- -galactosyltransferase 3-like	105	3.72E-38	72.10%	0.126	IPR003859 (PRINTS); IPR027995 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
477	213665_length_314_cvg_3.0_tip_1_4	8	inversin protein	105	7.73E-42	80.00%	0.141	IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24178 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)

478	213687_length_314_cvg_3.0_tip_1_1	10	zinc finger protein 316-like isoform x2	105	1.28E-15	61.40%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
479	213955_length_315_cvg_3.0_tip_1_2	9	lipophorin receptor	105	1.63E-54	88.40%	0.261	IPR000033 (SMART); IPR000033 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY)
480	214523_length_316_cvg_2.9_tip_1_2	13	tryptase-like isoform x1	105	1.21E-31	75.20%	0.193	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); PTHR24268:SF95 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
481	214607_length_316_cvg_2.0_tip_1_1	7	protein flightless-1	105	1.64E-46	83.10%	0.123	IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007122 (PANTHER); IPR029919 (PTHR11977:PANTHER); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY)
482	214615_length_316_cvg_2.0_tip_1_4	6	c-type lectin domain family 4 member e-like	105	9.66E-12	54.30%	0.106	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802:SF216 (PANTHER); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
483	214669_length_316_cvg_2.0_tip_1_2	8	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	105	4.29E-20	64.60%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
484	214687_length_316_cvg_2.0_tip_1_2	7	mam domain-containing glycosylphosphatidylinositol anchor protein 1	105	2.49E-14	58.20%	0.102	IPR000998 (PRINTS); IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
485	214699_length_316_cvg_4.0_tip_1_4	11	lachesin-like isoform x1	105	3.18E-49	83.90%	0.099	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013106 (PFAM); IPR013098 (PFAM); PTHR19831:SF43 (PANTHER); PTHR19831 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
486	214833_length_317_cvg_48.0_tip_1_2	200	serine protease	105	3.89E-15	72.40%	0.121	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
487	214877_length_317_cvg_2.0_tip_1_5	6	tyrosine-protein phosphatase non-receptor type 9-like	105	1.54E-47	84.30%	0.099	IPR000242 (PRINTS); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134 (PANTHER); PTHR19134:SF232 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
488	215163_length_317_cvg_2.0_tip_1_4	8	zinc finger protein	106	7.15E-16	55.70%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
489	215167_length_317_cvg_4.2_tip_1_0	16	cysteine proteinase cg12163	106	2.13E-59	91.00%	0.107	G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); PTHR12411:SF316 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
490	215261_length_317_cvg_3.0_tip_1_1	9	glycoside hydrolase family 1	106	1.04E-30	80.20%	0.109	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001360 (PFAM); IPR001360 (PANTHER); IPR018120 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
491	215343_length_318_cvg_2.0_tip_1_3	9	insulin-like growth factor-binding protein complex acid labile subunit	106	2.28E-18	62.60%	0.116	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PFAM); PTHR24365 (PANTHER); SSF52058 (SUPERFAMILY)
492	215355_length_318_cvg_2.0_tip_1_3	7	group xv phospholipase a2-like	106	7.02E-34	69.90%	0.126	PTHR11440:SF47 (PANTHER); PTHR11440 (PANTHER)
493	215401_length_318_cvg_2.6_tip_1_1	12	zinc finger protein 358	106	1.21E-21	60.10%	0.127	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
494	215779_length_319_cvg_87.0_tip_1_4	3019	protein npc2 homolog	106	3.72E-09	67.00%	0.109	IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306 (PANTHER); PTHR11306:SF3 (PANTHER); IPR014756 (SUPERFAMILY)
495	215921_length_319_cvg_4.0_tip_1_2	12	leucine-rich repeat-containing protein 70 isoform x1	106	6.55E-13	57.90%	0.104	IPR003591 (SMART); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); SSF52058 (SUPERFAMILY)
496	216109_length_319_cvg_2.5_tip_1_1	7	extensin-like protein:near transporter	106	1.43E-17	72.90%	0.125	no IPS match

499	216281_length_320_cvg_3.0_tip_1_5	9	ecdysteroid-regulated 16 kda	106	1.18E-25	73.80%	0.132	IPR003172 (G3DSA:2.60.40.GENE3D); IPR003172 (PFAM); PTHR11306:SF0 (PANTHER); PTHR11306 (PANTHER); IPR014756 (SUPERFAMILY)
497	216143_length_319_cvg_4.0_tip_1_3	13	neuroendocrine convertase 2	107	6.37E-65	97.50%	0.102	IPR000209 (PFAM); IPR000209 (G3DSA:3.40.50.GENE3D); PTHR10795:SF11 (PANTHER); IPR015500 (PANTHER); IPR022398 (PROSITE_PATTERNS); IPR000209 (SUPERFAMILY)
498	216157_length_320_cvg_2.0_tip_1_1	8	zinc finger protein 665-like isoform x1	107	3.72E-16	62.10%	0.116	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
500	216465_length_320_cvg_3.0_tip_1_0	8	neurogenic locus notch homolog protein 1 isoform x1	107	6.77E-29	78.50%	0.099	IPR008197 (PRINTS); IPR008197 (SMART); IPR008197 (G3DSA:4.10.75.GENE3D); IPR008197 (PFAM); PTHR19441 (PANTHER); PTHR19441:SF10 (PANTHER); IPR008197 (PROSITE_PROFILES); IPR008197 (SUPERFAMILY)
501	216589_length_320_cvg_2.0_tip_1_0	8	transmembrane protease serine partial	107	1.44E-19	69.10%	0.228	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF81 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
502	216869_length_321_cvg_2.0_tip_1_0	9	mlrp2_acrmi ame: full=mam and ldl-receptor class a domain-containing protein 2 ame: full=skeletal organic matrix mam and ldl-receptor 2 short=som mam and ldl-receptor partial	107	7.00E-22	61.80%	0.111	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PFAM); IPR002172 (PFAM); PTHR23282:SF75 (PANTHER); PTHR23282 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
503	216967_length_321_cvg_2.0_tip_1_1	9	discoidin domain-containing receptor partial	107	4.02E-43	79.40%	0.107	IPR020635 (SMART); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24416 (PANTHER); PTHR24416:SF210 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
504	217059_length_322_cvg_7.0_tip_1_4	23	esterase fe4	107	5.57E-32	67.70%	0.101	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559 (PANTHER); IPR019819 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
505	217111_length_322_cvg_3.0_tip_1_4	12	papilin isoform x2	107	4.78E-44	82.50%	0.112	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
506	217381_length_322_cvg_2.0_tip_1_5	9	zinc finger protein 282	107	1.21E-18	57.70%	0.128	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
507	217667_length_323_cvg_2.0_tip_1_2	8	platelet glycoprotein v	107	3.31E-16	57.00%	0.132	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373:SF12 (PANTHER); PTHR24373 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
508	217683_length_323_cvg_5.0_tip_1_3	16	plexin- partial	108	2.79E-52	85.60%	0.098	IPR016201 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR002165 (PFAM); G3DSA:3.30.1680.10 (GENE3D); PTHR22625:SF16 (PANTHER); PTHR22625 (PANTHER); IPR016201 (SUPERFAMILY); IPR001627 (SUPERFAMILY)
509	217733_length_323_cvg_23.0_tip_1_1	71	---NA---	108			0.125	IPR008197 (SMART); IPR008197 (PFAM); IPR008197 (G3DSA:4.10.75.GENE3D); IPR008197 (PROSITE_PROFILES); IPR008197 (SUPERFAMILY)
510	217857_length_323_cvg_2.0_tip_1_4	6	dorsal-ventral patterning protein partial	108	1.33E-27	62.70%	0.122	IPR001007 (SMART); IPR001007 (PFAM); PTHR11339:SF223 (PANTHER); PTHR11339 (PANTHER); SSF57603 (SUPERFAMILY)
511	217871_length_324_cvg_63.0_tip_1_1	2038	---NA---	108			0.134	no IPS match
512	218203_length_324_cvg_5.0_tip_1_4	15	cd4-specific ankyrin repeat protein	108	1.38E-10	69.70%	0.122	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24182 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
514	218323_length_325_cvg_18.7_tip_0_5	50	wnt inhibitory factor 1 precursor	108	9.96E-61	93.40%	0.123	IPR000742 (SMART); IPR000742 (PFAM); IPR013111 (PFAM); IPR013032 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24838:SF276 (PANTHER); PTHR24838 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
515	218469_length_325_cvg_2.0_tip_1_5	4	protein kinase brain isozyme	108	7.76E-69	99.50%	0.134	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24357:SF75 (PANTHER); PTHR24357 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)

516	218515_length_325_cvg_4.0_tip_1_5	11	reelin- partial	108	4.43E-26	70.70%	0.126	PTHR11841 (PANTHER)
517	218571_length_325_cvg_3.0_tip_1_4	8	low quality protein: carboxypeptidase n subunit 2	108	4.91E-08	54.70%	0.122	IPR003591 (SMART); PF13516 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373:SF100 (PANTHER); PTHR24373 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
519	218729_length_326_cvg_2.0_tip_1_2	11	endonuclease mitochondrial	108	3.35E-32	67.80%	0.107	IPR001604 (PFAM); IPR020821 (G3DSA:3.40.570.GENE3D); PTHR13966 (PANTHER); SSF54060 (SUPERFAMILY)
521	218787_length_326_cvg_2.0_tip_1_5	7	leucine-rich transmembrane	108	1.50E-09	59.60%	0.099	PR00019 (PRINTS); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
522	218873_length_326_cvg_8.7_tip_1_5	27	14-3-3 protein	108	2.19E-51	84.60%	0.107	IPR000308 (PRINTS); IPR023410 (SMART); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023410 (SUPERFAMILY)
523	218943_length_326_cvg_3.0_tip_1_5	10	---NA---	108			0.157	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR000436 (SUPERFAMILY)
513	218307_length_325_cvg_76.8_tip_0_0	1229	venom allergen 3-like	109	6.02E-15	50.30%	0.122	IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR014044 (SUPERFAMILY)
518	218661_length_325_cvg_2.0_tip_1_0	7	low quality protein: titin-like	109	6.35E-45	78.20%	0.103	IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF149 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
520	218749_length_326_cvg_5.0_tip_1_3	15	beta- -galactosyltransferase 5	109	1.19E-17	67.20%	0.099	Coil (COILS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027995 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
524	219005_length_326_cvg_3.0_tip_1_3	9	vanin-like protein 1 isoform x1	109	8.10E-10	53.60%	0.106	IPR012101 (PANTHER); PTHR10609:SF14 (PANTHER)
525	219139_length_327_cvg_3.0_tip_1_3	9	gastrula zinc finger protein	109	5.52E-21	61.10%	0.103	IPR015880 (SMART); IPR008598 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
526	219635_length_328_cvg_2.0_tip_1_3	8	vascular endothelial growth factor receptor 1-like	110	2.06E-53	91.90%	0.152	IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416:SF298 (PANTHER); PTHR24416 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
527	219875_length_329_cvg_3.1_tip_1_4	9	peptidyl-prolyl cis-trans isomerase g-like	110	7.53E-31	70.30%	0.098	IPR000072 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); PTHR21719:SF1 (PANTHER); PTHR21719 (PANTHER); IPR000072 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)
528	220621_length_330_cvg_2.0_tip_1_0	5	leucine-rich repeat-containing protein 47-like	110	1.35E-25	67.80%	0.11	IPR003591 (SMART); SM00364 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR10947:SF2 (PANTHER); PTHR10947 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
529	220687_length_331_cvg_3.0_tip_1_2	10	mam and ldl-receptor class a domain-containing protein 2-like	110	3.00E-10	50.60%	0.117	IPR000998 (PFAM); PTHR23282:SF75 (PANTHER); PTHR23282 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
530	220711_length_331_cvg_6.0_tip_1_2	24	chemosensory protein	110	4.25E-42	81.30%	0.834 Y	IPR005055 (G3DSA:1.10.2080.GENE3D); IPR005055 (PFAM); IPR005055 (PANTHER); PTHR11257:SF4 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR005055 (SUPERFAMILY)
531	221085_length_332_cvg_4.0_tip_1_3	11	attractin-like protein 1-like	111	6.44E-31	68.10%	0.111	IPR016201 (SMART); IPR002165 (PFAM); PTHR10574:SF3 (PANTHER); PTHR10574 (PANTHER)
532	221173_length_332_cvg_3.7_tip_1_0	10	alcohol dehydrogenase	111	2.40E-29	68.40%	0.13	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); IPR001395 (PANTHER); PTHR11732:SF144 (PANTHER); IPR023210 (SUPERFAMILY)
533	221235_length_332_cvg_2.0_tip_1_4	6	chondroitin sulfate	111	7.24E-53	85.80%	0.12	IPR003378 (PFAM); PTHR12369 (PANTHER); PTHR12369:SF11 (PANTHER)
534	221721_length_333_cvg_3.0_tip_1_1	9	reelin	111	2.77E-27	66.00%	0.105	G3DSA:2.10.25.10 (GENE3D); IPR013111 (PFAM); IPR006149 (PFAM); PTHR11841 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY)
536	221925_length_334_cvg_3.0_tip_1_1	12	achain kringle 2 domain of human plasminogen: nmr solution structure of trans-4-aminomethylcyclohexane-1-carboxylic acid complex	111	8.26E-25	67.20%	0.1	PR00018 (PRINTS); IPR000001 (SMART); IPR000001 (PFAM); G3DSA:2.40.20.10 (GENE3D); PTHR24259 (PANTHER); IPR018056 (PROSITE_PATTERNS); IPR000001 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY)
537	222013_length_334_cvg_2.0_tip_1_1	8	growth differentiation factor 8	111	9.42E-30	69.20%	0.105	IPR001111 (PFAM); IPR015615 (PANTHER); IPR015616 (PTHR11848:PANTHER)

535	221893_length_334_cvg_2.0_tip_1_3	7	tyrosine kinase receptor cad96ca	112	1.38E-53	89.60%	0.281	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416:SF268 (PANTHER); PTHR24416 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
538	222423_length_335_cvg_4.0_tip_1_4	13	protein will die slowly	112	9.92E-73	98.20%	0.105	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847:SF308 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
539	222889_length_336_cvg_2.0_tip_1_2	9	low quality protein: sco-spondin	112	6.71E-12	54.10%	0.695 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529:SF204 (PANTHER); PTHR10529 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
540	222983_length_337_cvg_2.0_tip_1_4	8	scavenger partial	112	1.11E-47	82.70%	0.115	IPR001695 (PFAM); PTHR19331 (PANTHER); PTHR19331:SF77 (PANTHER); IPR001190 (PROSITE_PROFILES)
541	223121_length_337_cvg_2.0_tip_1_5	6	fibrillin-2-like	112	1.07E-47	84.10%	0.117	IPR000742 (SMART); IPR001881 (SMART); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR011398 (PANTHER); PTHR24039:SF20 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
542	223239_length_337_cvg_7.2_tip_1_4	22	serine protease p69	112	2.11E-21	59.80%	0.105	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); PTHR24260:SF45 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
543	223547_length_338_cvg_2.0_tip_1_0	7	laminin subunit alpha	113	2.70E-43	80.60%	0.109	IPR002049 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF39 (PANTHER); IPR002049 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
544	223559_length_338_cvg_2.0_tip_1_1	7	calcium activated chlorine	113	3.38E-15	53.80%	0.102	IPR015394 (PFAM); PTHR10579 (PANTHER); PTHR10579:SF43 (PANTHER)
545	223841_length_339_cvg_4.0_tip_1_4	16	growth differentiation factor 8-like	113	1.32E-65	84.20%	0.101	IPR001839 (SMART); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001839 (PFAM); IPR015616 (PTHR11848:PANTHER); IPR015615 (PANTHER); IPR017948 (PROSITE_PATTERNS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)
546	223995_length_339_cvg_3.7_tip_1_5	13	lysosomal pro-x carboxypeptidase-like	113	4.32E-27	75.90%	0.198	IPR008758 (PFAM); IPR008758 (PANTHER); PTHR11010:SF11 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
547	224017_length_339_cvg_3.9_tip_1_1	14	xanthine dehydrogenase oxidase	113	4.32E-51	84.00%	0.105	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)
548	224037_length_339_cvg_7.0_tip_1_2	25	cda2 isoform a	113	5.86E-50	83.70%	0.246	IPR002172 (SMART); IPR002557 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); PTHR11177:SF136 (PANTHER); PTHR11177 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002557 (SUPERFAMILY)
549	224075_length_339_cvg_16.0_tip_1_5	31	acyl- delta desaturase	113	3.23E-55	83.10%	0.507 Y	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351 (PANTHER); PTHR11351:SF28 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM)
553	224635_length_341_cvg_22.7_tip_0_2	39	cytochrome p450 3a11-like	113	4.99E-36	73.60%	0.125	IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24292 (PANTHER); PTHR24292:SF24 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
555	224743_length_341_cvg_5.2_tip_1_2	18	gastrula zinc finger	113	7.84E-20	62.10%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
550	224163_length_340_cvg_8.0_tip_1_0	16	basement membrane-specific heparan sulfate proteoglycan core protein	114	1.95E-25	56.20%	0.101	IPR003599 (SMART); IPR003598 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

551	224375_length_340_cvg_7.0_tip_1_3	25	von willebrand factor a domain-containing protein 8-like	114	1.33E-54	85.00%	0.121	PTHR21610 (PANTHER); PTHR21610:SF9 (PANTHER); IPR002035 (SUPERFAMILY)
552	224557_length_341_cvg_14.3_tip_0_3	35	egf domain protein	114	5.25E-12	48.10%	0.101	IPR002223 (G3DSA:4.10.410.GENE3D); IPR023413 (G3DSA:2.40.155.GENE3D); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
554	224699_length_341_cvg_2.0_tip_1_3	6	voltage-gated sodium partial	114	2.31E-57	91.60%	0.276	IPR005821 (PFAM); IPR027359 (G3DSA:1.20.120.GENE3D); PTHR10037 (PANTHER); IPR028814 (PTHR10037:PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF81324 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
556	224827_length_342_cvg_2.0_tip_1_3	7	low quality protein: titin-like	114	6.36E-49	86.00%	0.103	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF149 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
557	224915_length_342_cvg_7.0_tip_1_4	23	er degradation-enhancing alpha-mannosidase-like protein 2-like	114	1.56E-57	89.50%	0.1	IPR001382 (PRINTS); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); PTHR11742:SF37 (PANTHER); IPR001382 (PANTHER); IPR001382 (SUPERFAMILY)
558	224987_length_342_cvg_2.0_tip_1_0	9	secreted frizzled-related protein 3	114	1.94E-31	71.10%	0.27	IPR020067 (SMART); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR020067 (PFAM); IPR015526 (PANTHER); PTHR11309:SF83 (PANTHER); IPR020067 (PROSITE_PROFILES); IPR020067 (SUPERFAMILY)
559	225111_length_342_cvg_4.0_tip_1_1	16	maguk p55 subfamily member 7 isoform x4	114	1.81E-54	91.40%	0.1	IPR008145 (SMART); IPR008145 (PFAM); G3DSA:3.30.63.10 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23122 (PANTHER); PTHR23122:SF14 (PANTHER); IPR020590 (PROSITE_PATTERNS); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
561	225377_length_343_cvg_4.0_tip_1_2	15	maguk p55 subfamily member 7 isoform x1	114	6.25E-60	90.20%	0.113	IPR001452 (PRINTS); IPR001452 (SMART); IPR011511 (PFAM); G3DSA:2.30.30.40 (GENE3D); PTHR23122:SF14 (PANTHER); PTHR23122 (PANTHER); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY)
560	225305_length_343_cvg_2.0_tip_1_0	6	gastrula zinc finger	115	1.26E-20	63.40%	0.102	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
562	225475_length_343_cvg_4.0_tip_1_0	15	neuroendocrine convertase 2	115	1.45E-59	85.70%	0.1	IPR002884 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); IPR015500 (PANTHER); PTHR10795:SF11 (PANTHER); IPR008979 (SUPERFAMILY)
563	225633_length_344_cvg_2.0_tip_1_1	11	gamma-glutamyltranspeptidase 1-like	115	1.48E-45	78.90%	0.103	IPR000101 (PRINTS); IPR000101 (PFAM); PTHR11686:SF15 (PANTHER); IPR000101 (PANTHER); IPR029055 (SUPERFAMILY)
564	225965_length_345_cvg_2.0_tip_1_4	10	protein yellow-like	115	8.80E-20	60.70%	0.112	IPR017996 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D)
565	225989_length_345_cvg_2.0_tip_1_1	11	spermatogenesis-associated protein 5-like	115	4.86E-45	80.60%	0.143	Coil (COILS); G3DSA:1.10.8.60 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); PTHR23077:SF27 (PANTHER); PTHR23077 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
566	226157_length_345_cvg_11.0_tip_1_2	42	collagen alpha-2 partial	115	3.96E-66	89.20%	0.132	IPR001442 (SMART); IPR001442 (PFAM); IPR001442 (G3DSA:2.170.240.GENE3D); PTHR24023:SF397 (PANTHER); PTHR24023 (PANTHER); IPR001442 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
567	226203_length_345_cvg_3.8_tip_1_0	13	zinc c2h2 type	115	9.90E-16	57.70%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
568	226251_length_345_cvg_2.2_tip_1_2	8	pr domain zinc finger protein 1 isoform x2	115	7.06E-21	65.00%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

569	226415_length_346_cvg_2.8_tip_1_5	8	zinc finger protein 891	115	2.01E-21	61.10%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
571	226789_length_347_cvg_2.0_tip_1_5	8	zinc finger protein 45-like	115	1.07E-24	59.10%	0.111	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
573	226903_length_347_cvg_7.0_tip_1_2	27	26s protease regulatory subunit 6b	115	3.77E-75	99.90%	0.106	IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); PTHR23073 (PANTHER); IPR027417 (SUPERFAMILY)
575	226927_length_347_cvg_2.0_tip_1_2	9	matrix metalloproteinase	115	7.60E-22	79.10%	0.102	IPR018487 (SMART); IPR018487 (PFAM); IPR000585 (G3DSA:2.110.10.GENE3D); PTHR10201 (PANTHER); PTHR10201:SF131 (PANTHER); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY)
576	226973_length_347_cvg_5.4_tip_1_2	21	low-density lipoprotein receptor-related protein 2	115	7.80E-60	86.30%	0.172	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
570	226665_length_347_cvg_2.0_tip_1_3	6	otopetrin-2 isoform x1	116	1.38E-22	63.50%	0.122	IPR004878 (PFAM); PTHR21522:SF37 (PANTHER); IPR004878 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
572	226857_length_347_cvg_2.0_tip_1_3	8	zinc finger protein 777- partial	116	6.09E-14	72.70%	0.122	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
574	226905_length_347_cvg_2.0_tip_1_0	6	endothelin-converting enzyme	116	1.94E-63	89.40%	0.118	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); IPR000718 (PANTHER); IPR029733 (PTHR11733:PANTHER); SSF55486 (SUPERFAMILY)
577	227059_length_348_cvg_3.0_tip_1_3	13	gastrula zinc finger	116	3.03E-23	61.30%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
578	227095_length_348_cvg_2.0_tip_1_3	6	---NA---	116			0.109	no IPS match
579	227153_length_348_cvg_2.8_tip_1_0	10	matrix metalloproteinase-9	116	8.65E-11	47.50%	0.161	IPR000562 (SMART); IPR000562 (PFAM); IPR000562 (G3DSA:2.10.10.GENE3D); IPR000562 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY)
580	227213_length_348_cvg_3.0_tip_1_5	9	sortilin-related receptor-like isoform x2	116	7.26E-32	65.90%	0.108	G3DSA:2.130.10.140 (GENE3D); PTHR12106:SF7 (PANTHER); PTHR12106 (PANTHER); SSF110296 (SUPERFAMILY)
581	227261_length_348_cvg_3.4_tip_1_5	12	kielin chordin-like protein	116	4.18E-11	43.00%	0.103	G3DSA:2.10.70.10 (GENE3D); SSF57603 (SUPERFAMILY); SSF57603 (SUPERFAMILY)
582	227341_length_348_cvg_2.0_tip_1_0	4	titin isoform x1	116	1.46E-34	68.30%	0.099	IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR020675 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
583	227533_length_349_cvg_2.0_tip_1_2	5	doublecortin-like protein kinase	116	3.73E-43	76.30%	0.592 Y	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24347:SF49 (PANTHER); IPR020636 (PANTHER); IPR000719 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR011009 (SUPERFAMILY)
585	227571_length_349_cvg_3.0_tip_1_2	9	laccase-1-like isoform x1	116	2.47E-47	79.00%	0.124	IPR011706 (PFAM); IPR008972 (G3DSA:2.60.40.GENE3D); PTHR11709:SF33 (PANTHER); PTHR11709 (PANTHER); IPR002355 (PROSITE_PATTERNS); IPR002355 (PROSITE_PATTERNS); IPR008972 (SUPERFAMILY)
588	227687_length_349_cvg_2.0_tip_1_4	7	de-cadherin-like isoform x1	116	6.28E-19	57.90%	0.11	IPR002126 (G3DSA:2.60.40.GENE3D); IPR015919 (SUPERFAMILY)
591	228041_length_350_cvg_6.1_tip_1_2	13	upf0764 protein c16orf89 homolog	116	6.29E-10	49.00%	0.176	no IPS match
584	227559_length_349_cvg_3.5_tip_1_3	14	down syndrome cell adhesion molecule-like protein dscam2 isoform x29	117	1.64E-59	90.00%	0.11	IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF567 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)

586	227641_length_349_cvg_5.2_tip_1_3	12	serine (or cysteine) proteinase clade b member	117	1.09E-12	71.10%	0.113	G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); PTHR11461:SF52 (PANTHER); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
587	227665_length_349_cvg_2.0_tip_1_0	7	fasciclin-2 isoform x4	117	1.65E-15	54.70%	0.13	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
589	227881_length_350_cvg_2.0_tip_1_3	12	cubilin, partial	117	8.92E-27	59.00%	0.118	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
590	227923_length_350_cvg_2.0_tip_1_3	7	aael005189- partial	117	1.42E-33	68.50%	0.31	IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19831:SF50 (PANTHER); PTHR19831 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
592	228081_length_351_cvg_3.0_tip_1_3	13	phospholipase a2-like	117	2.95E-18	65.90%	0.101	IPR016090 (G3DSA:1.20.90.GENE3D); IPR016090 (PFAM); IPR013090 (PROSITE_PATTERNS); IPR016090 (SUPERFAMILY)
593	228127_length_351_cvg_3.0_tip_1_5	9	plexin-a4	117	2.19E-68	97.30%	0.109	IPR013548 (PFAM); PTHR22625 (PANTHER)
594	228175_length_351_cvg_3.0_tip_1_3	10	gastrula zinc finger protein - partial	117	2.44E-24	61.10%	0.105	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
595	228499_length_352_cvg_2.0_tip_1_3	4	dlp hdl-bgbp precursor	118	5.73E-37	75.40%	0.1	IPR015255 (PFAM); IPR015817 (G3DSA:2.20.50.GENE3D); PTHR23345 (PANTHER); PTHR23345:SF11 (PANTHER); IPR015819 (SUPERFAMILY)
596	228609_length_352_cvg_3.0_tip_1_3	11	growth differentiation factor 8-like	118	1.23E-08	67.00%	0.107	IPR001839 (SMART); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001839 (PFAM); IPR015615 (PANTHER); PTHR11848:SF126 (PANTHER); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)
597	228679_length_353_cvg_3.0_tip_1_0	9	bone morphogenetic protein receptor type-2	118	1.58E-48	79.80%	0.139	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR23255:SF52 (PANTHER); IPR000333 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
598	228775_length_353_cvg_2.0_tip_1_1	10	achain crystal structure of anti-il4 darpin 44c12v5	118	1.19E-14	60.40%	0.108	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
599	228811_length_353_cvg_2.0_tip_1_4	8	low-density lipoprotein	118	2.88E-40	68.00%	0.104	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
600	228893_length_353_cvg_3.0_tip_1_0	5	hypothetical protein, partial	118	1.06E-11	49.40%	0.154	no IPS match
601	228893_length_353_cvg_3.0_tip_1_3	5	collagen alpha-1 chain	118	1.15E-34	76.50%	0.112	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF164 (PANTHER)
602	229133_length_354_cvg_2.2_tip_1_2	9	protein rtoa- partial	118	6.98E-12	57.80%	0.121	SignalP-TM (SIGNALP_GRAM_POSITIVE)
603	229263_length_354_cvg_3.6_tip_1_0	13	zinc c2h2 type domain-containing protein	118	7.72E-16	58.30%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
609	229860_length_356_cvg_2.6_tip_1_2	8	zinc finger protein 699-like isoform x2	118	3.25E-22	61.80%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
610	229898_length_356_cvg_2.0_tip_1_2	10	moxd1 homolog 1	118	2.92E-31	67.30%	0.097	IPR014784 (G3DSA:2.60.120.GENE3D); PF03712 (PFAM); IPR000945 (PANTHER); IPR008977 (SUPERFAMILY)
604	229396_length_355_cvg_3.8_tip_1_3	16	tyrosine-protein kinase src64b	119	2.61E-61	90.20%	0.118	IPR001245 (PRINTS); IPR020635 (SMART); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)

605	229518_length_355_cvg_2.0_tip_1_0	9	limbic system-associated membrane protein	119	3.71E-40	74.40%	0.108	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF45 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
606	229700_length_356_cvg_3.0_tip_1_1	10	phosphatidylinositol -trisphosphate 3-phosphatase and dual-specificity protein phosphatase pten	119	2.69E-46	86.70%	0.214	IPR029021 (G3DSA:3.90.190.GENE3D); PTHR12305 (PANTHER); IPR029023 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
607	229786_length_356_cvg_7.0_tip_1_1	29	frizzled-4	119	3.60E-49	87.10%	0.145	IPR020067 (SMART); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR020067 (PFAM); IPR015526 (PANTHER); IPR026551 (PTHR11309:PANTHER); IPR020067 (PROSITE_PROFILES); IPR020067 (SUPERFAMILY)
608	229800_length_356_cvg_3.0_tip_1_1	13	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein	119	1.43E-14	51.50%	0.136	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
611	229988_length_357_cvg_2.0_tip_1_4	7	zinc finger	119	1.48E-62	85.90%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23228 (PANTHER); PTHR23228:SF78 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
612	230108_length_357_cvg_3.0_tip_1_2	10	thrombospondin type-1 domain-containing protein 4-like	119	3.43E-41	77.10%	0.106	IPR010294 (PFAM); PTHR13723 (PANTHER)
613	230162_length_357_cvg_2.0_tip_1_1	9	zinc finger protein 519- partial	119	3.21E-23	60.00%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
614	230196_length_357_cvg_6.4_tip_1_2	22	hypothetical protein JL09_g3666	119	1.23E-07	54.00%	0.102	no IPS match
615	230340_length_357_cvg_3.5_tip_1_2	12	maguk p55 subfamily member 5	119	5.48E-44	79.50%	0.108	G3DSA:2.30.30.40 (GENE3D); PTHR23122 (PANTHER); PTHR23122:SF32 (PANTHER)
617	230394_length_358_cvg_2.0_tip_1_1	9	xanthine dehydrogenase oxidase isoform x1	119	2.71E-54	82.90%	0.164	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR022407 (PROSITE_PATTERNS); IPR008274 (SUPERFAMILY)
618	230436_length_358_cvg_3.0_tip_1_5	13	transient receptor potential channel pyrexia-like	119	2.19E-51	88.20%	0.129	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24133 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
620	230594_length_358_cvg_2.0_tip_1_2	8	subfamily member 17	119	3.63E-45	82.30%	0.105	Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF153 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
616	230384_length_358_cvg_3.0_tip_1_3	13	Le-cadherin	120	4.56E-28	61.00%	0.109	no IPS match
619	230496_length_358_cvg_2.4_tip_1_3	8	chorion peroxidase	120	2.17E-48	72.00%	0.112	IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
621	230728_length_359_cvg_2.0_tip_1_3	10	protein ndnf-like	120	2.30E-17	49.30%	0.12	IPR013783 (G3DSA:2.60.40.GENE3D)
622	230872_length_359_cvg_21.7_tip_0_3	63	nidogen-2 isoform x2	120	3.18E-15	59.70%	0.101	IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR023413 (G3DSA:2.40.155.GENE3D); IPR024731 (PFAM); IPR020901 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY)
623	231046_length_360_cvg_2.0_tip_1_1	9	beta- -n-acetylgalactosaminyltransferase bre-4-like	120	4.79E-43	69.20%	0.123	IPR027791 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
624	231272_length_360_cvg_3.0_tip_1_1	11	gastrula zinc finger protein - partial	120	5.78E-42	68.70%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

625	231286_length_361_cvg_3.0_tip_1_5	11	lysosomal pro-x carboxypeptidase-like	120	2.03E-21	75.00%	0.134	IPR008758 (PFAM); PTHR11010:SF11 (PANTHER); IPR008758 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
626	231358_length_361_cvg_2.0_tip_1_1	9	zinc finger protein 37-like	120	3.07E-16	60.00%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
627	231392_length_361_cvg_7.1_tip_1_4	24	lysosomal alpha-glucosidase-like	120	4.72E-51	78.00%	0.109	IPR000322 (PFAM); PTHR22762:SF7 (PANTHER); PTHR22762 (PANTHER); IPR017853 (SUPERFAMILY)
628	231532_length_361_cvg_2.5_tip_1_4	10	limbic system-associated membrane protein	120	3.14E-34	67.50%	0.098	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831:SF47 (PANTHER); PTHR19831 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
631	231628_length_362_cvg_4.0_tip_1_5	17	nardilysin-like isoform x1	120	5.02E-34	72.10%	0.125	IPR011237 (G3DSA:3.30.830.GENE3D); IPR007863 (PFAM); PTHR11851 (PANTHER); PTHR11851:SF108 (PANTHER); IPR011249 (SUPERFAMILY)
629	231560_length_361_cvg_4.7_tip_1_0	20	c4b-binding protein beta	121	8.43E-58	83.70%	0.181	IPR013783 (G3DSA:2.60.40.GENE3D); SSF48726 (SUPERFAMILY)
630	231590_length_361_cvg_2.0_tip_1_0	5	proprotein convertase subtilisin kexin type 7 isoform x2	121	7.64E-55	81.50%	0.106	IPR000209 (PFAM); IPR000209 (G3DSA:3.40.50.GENE3D); IPR015500 (PANTHER); PTHR10795:SF9 (PANTHER); IPR000209 (SUPERFAMILY)
632	231698_length_362_cvg_60.5_tip_0_3	467	blastula protease 10-like	121	4.46E-37	69.10%	0.108	IPR001506 (PRINTS); IPR006026 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)
633	231738_length_362_cvg_2.0_tip_1_4	7	ring finger and spry domain-containing protein 1-like	121	4.95E-15	81.10%	0.12	IPR001841 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); PF13920 (PFAM); IPR001841 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY)
634	231760_length_362_cvg_2.0_tip_1_3	8	cartilage oligomeric matrix protein isoform x1	121	3.72E-26	58.90%	0.1	Coil (COILS); IPR024665 (PFAM)
635	231876_length_362_cvg_2.0_tip_1_4	10	carbohydrate sulfotransferase 11 isoform x1	121	4.59E-19	64.80%	0.128	IPR005531 (PFAM); PTHR12137:SF29 (PANTHER); IPR018011 (PANTHER)
636	232106_length_363_cvg_7.4_tip_1_3	25	peptidase inhibitor 16	121	2.30E-14	54.70%	0.151	IPR001283 (PRINTS); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR014044 (SUPERFAMILY)
637	232128_length_363_cvg_2.0_tip_1_1	9	nedd4 family-interacting protein 1-like	121	5.46E-43	68.30%	0.269	IPR019325 (PFAM); PTHR13396 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
638	232190_length_363_cvg_3.0_tip_1_5	7	heat shock protein 70	121	3.14E-44	80.10%	0.097	Coil (COILS); IPR029048 (G3DSA:1.20.1270.GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); IPR029048 (SUPERFAMILY); IPR029047 (SUPERFAMILY)
639	232216_length_363_cvg_6.0_tip_1_1	23	trafficking protein particle complex subunit 1	121	1.70E-63	86.80%	0.167	IPR007233 (PFAM); G3DSA:3.30.450.70 (GENE3D); PTHR23249:SF16 (PANTHER); IPR007233 (PANTHER); IPR011012 (SUPERFAMILY)
641	232338_length_364_cvg_3.7_tip_1_2	14	trafficking protein particle complex subunit 1-like isoform x3	121	2.34E-08	71.00%	0.112	IPR007233 (PFAM)
643	232506_length_364_cvg_3.6_tip_1_2	14	mam and ldl-receptor class a domain-containing protein c10orf112-like	121	2.84E-06	52.50%	0.103	IPR000998 (PFAM); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
640	232244_length_364_cvg_2.0_tip_1_0	8	low-density lipoprotein receptor-related protein 4-like	122	6.83E-06	63.17%	0.119	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
642	232426_length_364_cvg_2.0_tip_1_0	7	h aca ribonucleoprotein complex non-core subunit naf1	122	3.70E-48	79.30%	0.379 Y	G3DSA:2.40.10.230 (GENE3D); IPR007504 (PFAM); PTHR31991 (PANTHER); IPR009000 (SUPERFAMILY)
644	232852_length_366_cvg_2.0_tip_1_3	10	inversin- partial	122	3.09E-40	73.40%	0.143	IPR002110 (SMART); IPR020683 (PFAM); PF13637 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24178 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
645	232870_length_366_cvg_3.0_tip_1_2	13	secreted frizzled-related protein 3	122	5.59E-16	59.00%	0.137	Coil (COILS); IPR018933 (SMART); G3DSA:2.40.50.120 (GENE3D); IPR018933 (PFAM); PTHR11309:SF83 (PANTHER); IPR015526 (PANTHER); IPR001134 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY)
646	232906_length_366_cvg_3.0_tip_1_3	13	dehydrogenase reductase sdr family member on chromosome x	122	3.17E-33	68.60%	0.114	IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); SSF51735 (SUPERFAMILY)
647	232944_length_366_cvg_4.2_tip_1_4	16	laccase 1 isoform x1	122	1.85E-42	73.70%	0.13	IPR008972 (G3DSA:2.60.40.GENE3D); IPR001117 (PFAM); PTHR11709:SF33 (PANTHER); PTHR11709 (PANTHER); IPR008972 (SUPERFAMILY)
648	233048_length_366_cvg_3.0_tip_1_0	10	exocyst complex component 7	122	6.07E-37	77.70%	0.105	PTHR12542:SF7 (PANTHER); IPR004140 (PANTHER)

649	233188_length_367_cvg_3.0_tip_1_4	12	gamma-glutamyltranspeptidase 1-like	122	2.08E-23	57.10%	0.238	IPR000101 (PRINTS); IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF18 (PANTHER); IPR029055 (SUPERFAMILY)
650	233386_length_368_cvg_2.0_tip_1_2	8	rega-1 protein	122	2.59E-08	52.20%	0.129	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19831 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
652	233436_length_368_cvg_2.0_tip_1_2	7	deoxyribonuclease-2- partial	122	2.97E-17	67.60%	0.115	IPR004947 (PFAM); IPR004947 (PANTHER)
651	233418_length_368_cvg_5.0_tip_1_0	16	metalloprotease i	123	6.43E-16	57.10%	0.118	IPR013856 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D)
653	233498_length_368_cvg_3.0_tip_1_4	12	zinc finger protein 628	123	1.22E-10	71.60%	0.114	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
654	233610_length_369_cvg_3.0_tip_1_1	13	dnaj homolog subfamily c member 11	123	2.60E-55	90.00%	0.103	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF159 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
655	233618_length_369_cvg_2.0_tip_1_0	8	zinc finger partial	123	4.06E-23	58.00%	0.098	IPR015880 (SMART); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
656	233818_length_369_cvg_2.0_tip_1_0	8	vascular endothelial growth factor receptor 1	123	4.07E-15	47.30%	0.141	PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); SSF48726 (SUPERFAMILY)
657	233826_length_369_cvg_2.0_tip_1_0	10	cardioactive peptide	123	2.67E-11	60.50%	0.106	IPR024276 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024276 (PRODOM); TMhelix (TMHMM)
658	233848_length_369_cvg_2.0_tip_1_1	9	membrane metallo-endopeptidase-like 1-like	123	3.16E-33	69.80%	0.108	G3DSA:1.10.1380.10 (GENE3D); IPR008753 (PFAM); IPR000718 (PANTHER); PTHR11733:SF113 (PANTHER); SSF55486 (SUPERFAMILY)
661	234068_length_370_cvg_2.9_tip_1_4	11	endochitinase isoform x1	123	4.71E-45	86.20%	0.104	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF144 (PANTHER); IPR017853 (SUPERFAMILY)
659	233910_length_370_cvg_43.9_tip_1_3	155	thioredoxin 1	124	8.45E-38	85.50%	0.126	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005746 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
660	234056_length_370_cvg_3.0_tip_1_3	10	protein fam3c-like	124	1.48E-31	65.30%	0.113	PTHR14592:SF7 (PANTHER); IPR026101 (PANTHER)
662	234082_length_370_cvg_4.5_tip_0_0	16	protein creg1	124	9.68E-50	74.40%	0.117	PF13883 (PFAM); IPR012349 (G3DSA:2.30.110.GENE3D); PTHR13343 (PANTHER); PTHR13343:SF12 (PANTHER); IPR012349 (SUPERFAMILY)
663	234256_length_371_cvg_2.0_tip_1_1	7	n-alpha-acetyltransferase auxiliary subunit	124	3.12E-35	64.70%	0.176	IPR019183 (PFAM); PTHR22767 (PANTHER); PTHR22767:SF3 (PANTHER)
664	234290_length_371_cvg_2.0_tip_1_1	6	irregular chiasm c-roughest protein isoform x1	124	1.58E-42	71.60%	0.135	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11640 (PANTHER); PTHR11640:SF54 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
665	234380_length_371_cvg_2.0_tip_1_1	10	glucose dehydrogenase	124	1.31E-37	68.70%	0.108	IPR000172 (PFAM); G3DSA:3.30.560.10 (GENE3D); G3DSA:3.50.50.60 (GENE3D); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); SSF51905 (SUPERFAMILY)
666	234434_length_371_cvg_21.3_tip_0_1	93	acyl- delta desaturase	124	3.98E-65	87.00%	0.478 Y	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351:SF28 (PANTHER); PTHR11351 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM)
667	234488_length_372_cvg_5.0_tip_1_2	16	chitinase 1a	124	2.48E-58	82.50%	0.137	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR029070 (G3DSA:3.10.50.GENE3D); PTHR11177:SF144 (PANTHER); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
668	234628_length_372_cvg_2.0_tip_1_1	12	97 kda heat shock protein isoform x2	124	7.30E-42	87.80%	0.133	G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.30.30 (GENE3D); PTHR19375:SF78 (PANTHER); PTHR19375 (PANTHER); SSF53067 (SUPERFAMILY)
669	234878_length_373_cvg_2.0_tip_1_4	8	basement membrane-specific heparan sulfate proteoglycan core protein	124	1.68E-31	65.10%	0.103	IPR018031 (SMART); IPR000034 (PFAM); PTHR10574:SF39 (PANTHER); PTHR10574 (PANTHER); IPR000034 (PROSITE_PROFILES)
670	234888_length_373_cvg_9.0_tip_1_4	28	dipeptidyl peptidase 9	124	1.41E-66	91.40%	0.186	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001375 (PFAM); PTHR11731:SF110 (PANTHER); PTHR11731 (PANTHER); IPR029058 (SUPERFAMILY)
671	234934_length_373_cvg_5.6_tip_1_1	23	calbindin-32 isoform x2	124	2.67E-75	98.00%	0.106	IPR002048 (SMART); IPR011992 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); IPR002048 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR19972 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)

672	235024_length_373_cvg_2.0_tip_1_2	7	zinc finger protein	124	1.16E-24	56.00%	0.13	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
675	235188_length_374_cvg_3.0_tip_1_2	9	hemacentin-2	124	1.26E-23	63.00%	0.109	IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR026823 (PFAM); PTHR19897:SF158 (PANTHER); PTHR19897 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
673	235044_length_374_cvg_3.0_tip_1_0	11	epidermal growth factor receptor-like	125	1.18E-37	66.20%	0.104	IPR006212 (SMART); G3DSA:2.10.220.10 (GENE3D); IPR009030 (SUPERFAMILY)
674	235134_length_374_cvg_4.0_tip_1_4	14	reelin-like isoform x4	125	8.08E-42	63.40%	0.105	PTHR11841 (PANTHER)
676	235232_length_374_cvg_2.7_tip_1_3	11	chondroitin sulfate	125	1.33E-43	74.30%	0.165	IPR029044 (G3DSA:3.90.550.GENE3D); IPR008428 (PFAM); PTHR12369:SF11 (PANTHER); PTHR12369 (PANTHER); IPR029044 (SUPERFAMILY)
677	235398_length_375_cvg_8.0_tip_1_3	36	zinc finger protein 3-like isoform x1	125	3.43E-17	68.80%	0.117	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
678	235448_length_375_cvg_2.0_tip_1_4	10	dual specificity testis-specific protein kinase 2	125	3.36E-57	83.70%	0.15	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR23257 (PANTHER); PTHR23257:SF324 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
679	235462_length_375_cvg_5.7_tip_1_2	35	va52_dolma ame: full=venom allergen ame: full=allergen dol m v-a ame: full=antigen 5 form 2 short=ag5-2 ame: full=cysteine-rich venom protein short=crvp ame: allergen=dol m flags: precursor	125	1.26E-06	56.40%	0.31	IPR014044 (G3DSA:3.40.33.GENE3D)
680	235512_length_375_cvg_2.7_tip_1_1	10	zinc finger protein	125	2.37E-22	58.50%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
681	235564_length_376_cvg_5.4_tip_1_1	21	zinc finger protein zpr1	125	3.25E-48	77.10%	0.1	IPR004457 (SMART); IPR004457 (TIGRFAM); IPR004457 (PFAM); PTHR10876 (PANTHER); PTHR10876:SF0 (PANTHER)
682	235900_length_377_cvg_3.5_tip_1_2	19	trypsin-1-like isoform x2	125	6.54E-27	69.70%	0.33	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
683	236088_length_377_cvg_3.0_tip_1_2	12	limbic system-associated membrane protein	125	4.88E-42	69.30%	0.119	IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF47 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
684	236220_length_378_cvg_3.0_tip_1_4	13	wd sam and u-box domain-containing protein 1-like isoform x1	126	1.28E-27	61.80%	0.133	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
686	236576_length_379_cvg_2.0_tip_1_5	5	integrin alpha-ps1 isoform x2	126	1.43E-50	79.90%	0.119	IPR000413 (PRINTS); IPR013519 (SMART); G3DSA:2.130.10.130 (GENE3D); IPR013517 (PFAM); PTHR23220:SF77 (PANTHER); PTHR23220 (PANTHER); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); SSF69318 (SUPERFAMILY)
685	236356_length_379_cvg_3.0_tip_1_3	12	complement c1q tumor necrosis factor-related protein 4	127	1.46E-11	51.00%	0.129	IPR001073 (SMART); IPR001073 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); PTHR22923 (PANTHER); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY)
687	236904_length_381_cvg_5.0_tip_1_3	19	heat shock protein partial	127	9.54E-78	96.10%	0.113	G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.90.640.10 (GENE3D); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)

688	237056_length_381_cvg_5.0_tip_1_3	26	tyrosine-protein phosphatase 69d	127	4.04E-49	80.40%	0.138	IPR003595 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134:SF277 (PANTHER); PTHR19134 (PANTHER); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
689	237070_length_381_cvg_2.0_tip_1_2	9	thromboxane a synthase-like protein	127	2.11E-39	69.30%	0.171	IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24292 (PANTHER); PTHR24292:SF24 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
690	237278_length_382_cvg_3.0_tip_1_2	13	polypeptide n-acetylgalactosaminyltransferase 5 isoform x1	127	3.47E-40	75.30%	0.101	PTHR11675:SF21 (PANTHER); PTHR11675 (PANTHER)
691	237386_length_383_cvg_8.6_tip_1_5	32	dnaj protein homolog 1-like	127	2.39E-35	96.10%	0.147	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24077 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
692	237414_length_383_cvg_3.0_tip_1_0	13	retinoid-inducible serine carboxypeptidase	128	4.84E-32	68.20%	0.114	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); PTHR11802:SF30 (PANTHER); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
693	237622_length_383_cvg_4.0_tip_1_3	18	mam and ldl-receptor class a domain-containing protein 1-like	128	1.27E-35	63.30%	0.114	IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
694	237654_length_384_cvg_4.0_tip_1_2	16	epidermal growth factor receptor	128	4.06E-73	94.00%	0.117	IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24416:SF95 (PANTHER); PTHR24416 (PANTHER); IPR017441 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
695	237700_length_384_cvg_2.0_tip_1_4	9	zinc finger protein 665-like	128	8.24E-48	72.90%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
696	237708_length_384_cvg_77.3_tip_1_0	768	hypothetical protein BRAFLDRAFT_77846	128	8.30E-22	62.90%	0.426 Y	IPR013781 (G3DSA:3.20.20.GENE3D); PTHR31308 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
697	238136_length_386_cvg_5.6_tip_1_5	24	protein disulfide-isomerase a6	128	6.37E-57	80.90%	0.117	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929:SF38 (PANTHER); PTHR18929 (PANTHER); IPR012336 (SUPERFAMILY)
698	238286_length_386_cvg_3.1_tip_1_2	11	collagen alpha-1 chain	128	2.09E-18	61.80%	0.1	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF379 (PANTHER)
699	238286_length_386_cvg_3.1_tip_1_4	11	collagen-like protein	129	3.74E-12	47.80%	0.165	no IPS match
700	238448_length_387_cvg_2.0_tip_1_2	6	low-density lipoprotein receptor-related protein 2	129	6.98E-38	71.80%	0.103	IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); IPR001881 (PFAM); PTHR10529 (PANTHER); IPR018097 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY)
703	239032_length_389_cvg_10.8_tip_1_2	35	hemagglutinin proteinase	129	1.99E-15	50.30%	0.108	IPR013856 (G3DSA:3.10.170.GENE3D); IPR013856 (PFAM)
704	239156_length_389_cvg_4.0_tip_1_5	19	senseless- isoform a	129	1.16E-19	53.10%	0.101	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
701	238796_length_388_cvg_2.2_tip_1_0	11	vascular non-inflammatory molecule 3-like	130	3.68E-13	54.00%	0.105	IPR003010 (G3DSA:3.60.110.GENE3D); IPR003010 (PFAM); IPR012101 (PANTHER); IPR003010 (PROSITE_PROFILES); IPR003010 (SUPERFAMILY)
702	239030_length_389_cvg_2.0_tip_1_0	9	trypsin- partial	130	5.65E-40	65.50%	0.158	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24258 (PANTHER); PTHR24258:SF4 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
705	239264_length_390_cvg_5.5_tip_1_2	21	lipase 3-like	130	5.95E-35	69.10%	0.094	IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11005:SF6 (PANTHER); PTHR11005 (PANTHER); IPR029058 (SUPERFAMILY)
706	239272_length_390_cvg_2.0_tip_1_1	10	very low-density lipoprotein partial	130	6.12E-12	48.70%	0.108	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

707	239390_length_390_cvg_2.0_tip_1_2	7	tyrosine-protein phosphatase 69d-like	130	1.73E-46	76.50%	0.218	IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134 (PANTHER); PTHR19134:SF261 (PANTHER); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
708	239480_length_390_cvg_2.8_tip_1_3	11	granzyme c	130	1.24E-23	61.20%	0.104	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
711	239736_length_391_cvg_3.0_tip_1_5	11	apolipoprotein d-like	130	1.64E-08	61.60%	0.141	IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)
713	239962_length_392_cvg_2.0_tip_1_2	7	uncharacterized protein ZBAI_02902	130	3.61E-11	61.90%	0.097	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
709	239524_length_391_cvg_2.2_tip_1_0	13	prolyl 3-hydroxylase 2	131	1.21E-23	75.00%	0.107	Coil (COILS); PTHR14049:SF9 (PANTHER); PTHR14049 (PANTHER)
710	239566_length_391_cvg_4.0_tip_1_0	17	maguk p55 subfamily member 5	131	4.98E-72	92.00%	0.107	Coil (COILS); Coil (COILS); IPR008145 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR008145 (PFAM); PTHR23122 (PANTHER); PTHR23122:SF32 (PANTHER); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
712	239872_length_392_cvg_2.0_tip_1_4	10	lipoprotein receptor	131	3.35E-23	68.30%	0.325	IPR000832 (PFAM); PTHR12011:SF260 (PANTHER); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
714	240232_length_393_cvg_10.0_tip_1_0	44	upf0669 protein c6orf120 homolog	131	3.73E-38	66.40%	0.106	PTHR31703 (PANTHER)
715	240286_length_393_cvg_2.0_tip_1_5	11	heat shock 70 kda protein 14	131	6.68E-50	73.40%	0.225	G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.90.640.10 (GENE3D); PTHR19375:SF158 (PANTHER); PTHR19375 (PANTHER); SSF53067 (SUPERFAMILY); TMhelix (TMHMM)
716	240302_length_394_cvg_3.0_tip_1_5	14	achain nmr solution dynamics and binding properties of the krigle iv type 8 module of apolipoprotein	131	7.52E-31	64.30%	0.709 Y	PR00018 (PRINTS); IPR000001 (SMART); G3DSA:2.40.20.10 (GENE3D); IPR000001 (PFAM); PTHR24259 (PANTHER); IPR018056 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000001 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR013806 (SUPERFAMILY)
717	240326_length_394_cvg_2.0_tip_1_1	8	transforming growth factor-beta-induced protein ig-h3-like isoform x6	131	6.59E-43	68.10%	0.193	IPR000782 (SMART); IPR000782 (PFAM); IPR000782 (G3DSA:2.30.180.GENE3D); PTHR10900 (PANTHER); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY)
719	240442_length_394_cvg_2.3_tip_1_1	8	polypeptide n-acetylgalactosaminyltransferase partial	131	5.58E-68	83.90%	0.104	G3DSA:2.80.10.50 (GENE3D); IPR000772 (PFAM); PTHR11675 (PANTHER); PTHR11675:SF24 (PANTHER); IPR000772 (PROSITE_PROFILES); IPR000772 (SUPERFAMILY); IPR029044 (SUPERFAMILY)
722	240666_length_395_cvg_2.0_tip_1_5	10	calcium-activated chloride channel regulator 2	131	1.07E-17	52.20%	0.101	IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10579 (PANTHER); PTHR10579:SF43 (PANTHER)
718	240360_length_394_cvg_2.0_tip_1_0	8	attractin-like protein 1 isoform x1	132	1.28E-41	73.70%	0.149	G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013111 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10574 (PANTHER); PTHR10574:SF3 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES)
720	240582_length_395_cvg_11.9_tip_1_3	31	low quality protein: mucin-2-like	132	5.77E-07	44.29%	0.119	PR01217 (PRINTS); IPR001846 (PFAM); IPR001846 (PROSITE_PROFILES)
721	240612_length_395_cvg_3.0_tip_1_1	12	mlrp1_acrmi ame: full=mam and ldl-receptor class a domain-containing protein 1 ame: full=skeletal organic matrix mam and ldl-receptor 1 short=som mam and ldl-receptor partial	132	1.74E-16	64.40%	0.322	IPR000998 (PFAM); PTHR23282 (PANTHER); PTHR23282:SF75 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
723	240740_length_395_cvg_7.3_tip_1_3	35	ectonucleoside triphosphate diphosphohydrolase 5 isoform x2	132	5.93E-22	69.50%	0.14	IPR000407 (PFAM); IPR000407 (PANTHER); PTHR11782:SF30 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
724	240796_length_396_cvg_2.0_tip_1_5	7	neural cell adhesion molecule 1 isoform 2	132	1.67E-12	49.20%	0.143	IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
725	240826_length_396_cvg_27.0_tip_1_5	98	twitchin isoform x5	132	9.73E-44	76.00%	0.098	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897:SF155 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)

726	240874_length_396_cvg_3.0_tip_1_1	15	cytokine receptor	132	4.13E-23	59.50%	0.142	IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
728	241066_length_397_cvg_2.0_tip_1_2	10	wnt-receptor frizzled-like protein variant 2	132	4.31E-75	88.60%	0.111	IPR020067 (SMART); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR020067 (PFAM); IPR026561 (PTHR11309:PANTHER); IPR015526 (PANTHER); IPR020067 (PROSITE_PROFILES); IPR020067 (SUPERFAMILY)
730	241142_length_397_cvg_111.6_tip_1_2	6720	dermatopontin 2	132	1.93E-16	60.80%	0.297	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
731	241170_length_397_cvg_3.0_tip_1_5	12	meprin a	132	1.43E-24	53.30%	0.104	G3DSA:2.170.300.10 (GENE3D); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF580 (PANTHER); IPR000859 (PROSITE_PROFILES)
732	241208_length_397_cvg_2.5_tip_1_1	15	sco-spondin isoform x1	132	4.03E-17	52.80%	0.101	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); PTHR10529 (PANTHER); PTHR10529:SF208 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
733	241226_length_397_cvg_2.0_tip_1_1	12	ectonucleoside triphosphate diphosphohydrolase 7	132	8.38E-23	72.60%	0.314	IPR000407 (PFAM); IPR000407 (PANTHER); PTHR11782:SF37 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
727	241028_length_397_cvg_2.0_tip_1_0	6	down syndrome cell adhesion molecule-like protein dscam2	133	2.01E-62	88.00%	0.106	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR10489:SF567 (PANTHER); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
729	241076_length_397_cvg_9.1_tip_1_0	50	kallikrein-14- partial	133	2.26E-26	68.70%	0.102	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
734	241466_length_398_cvg_3.0_tip_1_1	12	15-hydroxyprostaglandin dehydrogenase	133	4.00E-64	78.10%	0.112	IPR002198 (PRINTS); IPR002424 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24310 (PANTHER); SSF51735 (SUPERFAMILY)
735	241486_length_398_cvg_3.3_tip_1_4	15	peptidyl-prolyl cis-trans isomerase cwc27 homolog	133	2.84E-76	90.00%	0.16	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PIRSF); IPR024936 (PANTHER); PTHR11071:SF152 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
736	241638_length_399_cvg_3.5_tip_1_2	13	ubiquitin thioesterase partial	133	7.40E-19	55.10%	0.288	no IPS match
737	241706_length_399_cvg_5.8_tip_1_0	27	glucose dehydrogenase	133	2.09E-17	92.20%	0.122	G3DSA:3.50.50.60 (GENE3D); IPR007867 (PFAM); PTHR11552 (PANTHER); PTHR11552:SF90 (PANTHER); SSF51905 (SUPERFAMILY)
739	241854_length_400_cvg_4.0_tip_1_4	17	latrophilin cir1-like isoform x1	133	3.19E-12	54.00%	0.126	IPR000203 (PFAM); PTHR12011 (PANTHER); IPR000203 (PROSITE_PROFILES)
738	241836_length_400_cvg_2.0_tip_1_3	7	neurotrypsin isoform x1	134	2.99E-45	70.50%	0.109	IPR001190 (PRINTS); IPR017448 (SMART); IPR001190 (PFAM); IPR017448 (G3DSA:3.10.250.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR19331 (PANTHER); IPR001190 (PROSITE_PROFILES); IPR017448 (SUPERFAMILY)
740	242326_length_402_cvg_3.0_tip_1_3	13	gastrula zinc finger protein - partial	134	3.39E-39	66.90%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
741	242444_length_402_cvg_2.0_tip_1_5	9	gastrula zinc finger	134	4.15E-40	64.10%	0.13	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

742	242546_length_403_cvg_2.0_tip_1_5	12	eph receptor tyrosine	134	1.84E-84	92.30%	0.273	IPR001245 (PRINTS); IPR020635 (SMART); IPR013761 (G3DSA:1.10.150.GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416 (PANTHER); PTHR24416:SF263 (PANTHER); IPR001660 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
744	242696_length_403_cvg_3.0_tip_1_4	15	translocation protein sec63 homolog	134	6.44E-58	77.90%	0.125	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); IPR027137 (PANTHER); PTHR24075:SF0 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM)
745	242768_length_404_cvg_4.0_tip_1_2	18	calbindin isoform a	134	7.69E-85	93.50%	0.104	IPR002048 (SMART); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); PTHR19972 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)
743	242676_length_403_cvg_3.0_tip_1_0	13	retinol dehydrogenase 13	135	1.51E-38	74.40%	0.166	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF305 (PANTHER); PTHR24316 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
746	242790_length_404_cvg_4.0_tip_1_3	21	peptidyl-prolyl cis-trans isomerase h-like	135	2.42E-56	96.00%	0.1	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF58 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
747	242856_length_404_cvg_2.0_tip_1_0	10	gastrula zinc finger protein	135	2.77E-17	51.80%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
748	242940_length_405_cvg_76.9_tip_1_2	614	epidermal retinol dehydrogenase partial	135	9.51E-22	71.10%	0.117	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF246 (PANTHER); PTHR24316 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
749	242952_length_405_cvg_28.0_tip_1_3	120	poly -specific endoribonuclease homolog	135	4.19E-20	62.50%	0.325	IPR018998 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF142877 (SUPERFAMILY); TMhelix (TMHMM)
750	243024_length_405_cvg_4.0_tip_1_3	20	dnaj homolog dnj-5	135	7.72E-67	85.30%	0.11	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF141 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
753	243376_length_406_cvg_5.0_tip_1_2	24	chemosensory protein	135	4.77E-49	77.70%	0.499 Y	IPR005055 (PFAM); IPR005055 (G3DSA:1.10.2080.GENE3D); PTHR11257:SF2 (PANTHER); IPR005055 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR005055 (SUPERFAMILY)
754	243422_length_407_cvg_5.0_tip_1_2	24	carboxypeptidase n catalytic chain	135	4.46E-23	57.60%	0.269	G3DSA:3.40.630.10 (GENE3D); IPR014766 (G3DSA:2.60.40.GENE3D); PF13620 (PFAM); PTHR11532 (PANTHER); PTHR11532:SF50 (PANTHER); SSF53187 (SUPERFAMILY); IPR008969 (SUPERFAMILY)
751	243206_length_406_cvg_2.0_tip_1_0	7	---NA---	136			0.127	IPR008979 (G3DSA:2.60.120.GENE3D); IPR000421 (PFAM); IPR000421 (PROSITE_PATTERNS); IPR000421 (PROSITE_PROFILES); IPR008979 (SUPERFAMILY)
752	243346_length_406_cvg_3.0_tip_1_0	14	tyrosine-protein kinase hopscotch	136	5.86E-42	70.50%	0.117	IPR001245 (PRINTS); IPR020635 (SMART); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418:SF216 (PANTHER); PTHR24418 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
755	243480_length_407_cvg_2.0_tip_1_1	8	isoform a	136	1.01E-45	67.30%	0.101	IPR005331 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR018011 (PANTHER); PTHR12137:SF30 (PANTHER)
756	243512_length_407_cvg_7.0_tip_1_1	28	cuticular protein	136	2.78E-30	75.40%	0.104	TMhelix (TMHMM)
757	243630_length_408_cvg_2.0_tip_1_1	11	laminin subunit gamma-1	136	2.36E-53	76.40%	0.109	IPR018031 (SMART); IPR000034 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF231 (PANTHER); IPR000034 (PROSITE_PROFILES)
758	243634_length_408_cvg_2.2_tip_1_3	11	multicopper oxidase	136	9.66E-41	67.20%	0.103	IPR008972 (G3DSA:2.60.40.GENE3D); IPR008972 (G3DSA:2.60.40.GENE3D); IPR011707 (PFAM); PTHR11709:SF33 (PANTHER); PTHR11709 (PANTHER); IPR008972 (SUPERFAMILY)

759	243692_length_408_cvg_3.8_tip_1_4	16	down syndrome cell adhesion molecule-like partial	136	4.44E-55	79.10%	0.105	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF567 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
760	243802_length_408_cvg_3.0_tip_1_5	17	receptor-type tyrosine-protein phosphatase kappa-like	136	2.29E-35	65.90%	0.108	IPR000242 (PRINTS); IPR000242 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
761	244404_length_411_cvg_4.3_tip_1_0	22	matrix metalloproteinase-14 isoform x1	137	2.70E-18	57.00%	0.105	IPR018487 (SMART); IPR000585 (G3DSA:2.110.10.GENE3D); IPR018487 (PFAM); PTHR10201:SF131 (PANTHER); PTHR10201 (PANTHER); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY)
762	244486_length_412_cvg_3.5_tip_1_2	16	protein phosphatase 1 regulatory subunit 16a isoform x3	137	2.62E-70	89.00%	0.12	IPR002110 (SMART); PF13857 (PFAM); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24186 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
765	244870_length_413_cvg_2.0_tip_1_5	9	death-associated protein kinase partial	137	6.79E-47	68.20%	0.196	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR22964:SF46 (PANTHER); IPR020675 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
767	244928_length_413_cvg_2.0_tip_1_2	8	isoform c	137	7.35E-16	66.20%	0.102	IPR019149 (PFAM); PTHR13617 (PANTHER)
763	244754_length_413_cvg_17.9_tip_1_1	70	nidogen- partial	138	1.92E-15	51.00%	0.112	IPR000716 (SMART); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); PTHR12352 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY)
764	244820_length_413_cvg_4.0_tip_1_0	16	adp-ribosylation factor-like protein 2	138	4.49E-26	89.20%	0.12	IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF26 (PANTHER); PTHR11711 (PANTHER); IPR027417 (SUPERFAMILY)
766	244898_length_413_cvg_27.6_tip_1_0	159	inter-alpha-trypsin inhibitor heavy chain h3-like	138	3.81E-30	67.00%	0.105	PTHR10338:SF24 (PANTHER); PTHR10338 (PANTHER)
768	245048_length_414_cvg_3.3_tip_1_0	17	conserved hypothetical protein	138	8.11E-35	71.60%	0.107	IPR011030 (G3DSA:1.25.10.GENE3D); IPR015255 (PFAM); IPR001747 (PFAM); IPR015817 (G3DSA:2.20.50.GENE3D); PTHR23345 (PANTHER); PTHR23345:SF11 (PANTHER); IPR011030 (SUPERFAMILY); IPR015819 (SUPERFAMILY)
769	245114_length_414_cvg_2.0_tip_1_5	8	protein twisted gastrulation	138	3.82E-16	76.40%	0.169	IPR006761 (PFAM); PTHR12312:SF15 (PANTHER); IPR006761 (PANTHER)
772	245214_length_415_cvg_38.0_tip_1_2	189	cathepsin I	138	1.11E-37	89.20%	0.102	IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF57 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
773	245290_length_415_cvg_6.0_tip_1_2	23	laminin subunit gamma- partial	138	4.56E-28	62.70%	0.104	Coil (COILS); Coil (COILS)
775	245358_length_416_cvg_2.8_tip_1_5	14	plexin- partial	138	1.80E-66	84.50%	0.1	IPR015943 (G3DSA:2.130.10.GENE3D); IPR001627 (PFAM); PTHR22625:SF16 (PANTHER); PTHR22625 (PANTHER); IPR001627 (PROSITE_PROFILES); IPR001627 (SUPERFAMILY)
776	245384_length_416_cvg_2.0_tip_1_5	10	zinc finger protein 239- partial	138	5.33E-36	60.10%	0.105	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
777	245440_length_416_cvg_2.0_tip_1_5	8	peptidyl-glycine alpha-amidating monooxygenase partial	138	8.46E-45	65.70%	0.183	IPR000720 (PRINTS); IPR014784 (G3DSA:2.60.120.GENE3D); PF03712 (PFAM); PTHR10680:SF13 (PANTHER); PTHR10680 (PANTHER); IPR014783 (PROSITE_PATTERNS); IPR008977 (SUPERFAMILY)
778	245454_length_416_cvg_2.0_tip_1_2	7	cytokine receptor	138	4.61E-38	72.70%	0.125	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)

770	245158_length_415_cvg_2.0_tip_1_0	8	big brain	139	5.81E-45	73.00%	0.424 Y	IPR000425 (PRINTS); IPR000425 (PFAM); IPR023271 (G3DSA:1.20.1080.GENE3D); IPR000425 (PANTHER); PTHR19139:SF85 (PANTHER); IPR022357 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023271 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
771	245160_length_415_cvg_3.0_tip_1_3	12	venom allergen 3-like	139	7.59E-24	51.80%	0.141	IPR001283 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR014044 (SUPERFAMILY)
774	245294_length_415_cvg_73.7_tip_0_3	2392	otogelin- partial	139	3.86E-06	47.00%	0.117	no IPS match
779	245708_length_417_cvg_63.0_tip_0_0	594	kunitz bovine pancreatic trypsin inhibitor domain protein	139	1.29E-36	62.70%	0.102	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
780	245764_length_417_cvg_2.0_tip_1_5	10	zinc finger protein 45-like	139	2.69E-16	62.50%	0.15	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
781	245782_length_417_cvg_2.0_tip_1_0	10	u5 small nuclear ribonucleoprotein 40 kda protein	139	7.74E-90	98.80%	0.101	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
783	246012_length_418_cvg_3.8_tip_1_2	20	tyrosine-protein phosphatase lar isoform x4	139	1.45E-69	86.40%	0.109	PR00014 (PRINTS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR19134 (PANTHER); PTHR19134:SF204 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
782	245848_length_418_cvg_5.9_tip_1_0	26	phospholipase b-like partial	140	9.17E-67	80.60%	0.1	IPR007000 (PFAM); PTHR12370:SF3 (PANTHER); IPR007000 (PANTHER)
784	246118_length_419_cvg_4.3_tip_1_4	21	integrin beta-ps	140	8.93E-36	64.70%	0.105	G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013111 (PFAM); IPR015812 (PANTHER); PTHR10082:SF16 (PANTHER); IPR015812 (PROSITE_PATTERNS); IPR015812 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY); IPR012896 (SUPERFAMILY)
785	246120_length_419_cvg_2.9_tip_1_0	15	tripartite motif-containing protein 2-like isoform x5	140	1.58E-68	85.40%	0.097	IPR011042 (G3DSA:2.120.10.GENE3D); IPR001258 (PFAM); PTHR24103 (PANTHER); PTHR24103:SF1 (PANTHER); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); SSF101898 (SUPERFAMILY)
786	246292_length_420_cvg_3.2_tip_1_2	15	venom serine carboxypeptidase-like	140	1.72E-27	67.30%	0.107	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); IPR001563 (PANTHER); IPR018202 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
787	246312_length_420_cvg_4.0_tip_1_5	19	zinc finger protein 358	140	4.48E-29	58.70%	0.101	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
788	246364_length_420_cvg_3.0_tip_1_1	15	basement membrane-specific heparan sulfate proteoglycan core protein	140	8.09E-17	55.50%	0.143	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
789	246500_length_421_cvg_7.6_tip_1_4	43	carbonic anhydrase 1	140	1.05E-50	70.50%	0.108	IPR001148 (SMART); IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); IPR023561 (PANTHER); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)

790	246830_length_422_cvg_3.0_tip_1_2	13	basement membrane-specific heparan sulfate proteoglycan core protein	140	7.32E-47	69.90%	0.121	IPR002049 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF148 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
791	246870_length_422_cvg_2.7_tip_1_2	13	glutamyl aminopeptidase	140	4.04E-14	53.30%	0.114	IPR024571 (PFAM); IPR001930 (PANTHER); PTHR11533:SF165 (PANTHER) IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY)
792	246894_length_423_cvg_13.6_tip_1_4	47	ubiquitin family protein	141	1.44E-72	94.30%	0.139	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
795	247390_length_425_cvg_3.5_tip_1_2	21	zinc finger protein 26-like	141	4.37E-22	55.80%	0.12	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24202 (PANTHER); PTHR24202:SF52 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
793	247138_length_424_cvg_2.0_tip_1_0	8	e3 ubiquitin-protein ligase partial	142	2.53E-80	94.40%	0.135	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
794	247334_length_425_cvg_4.0_tip_1_1	20	very low-density lipoprotein receptor-like	142	3.54E-21	64.20%	0.103	IPR001073 (PRINTS); IPR001073 (SMART); IPR008983 (G3DSA:2.60.120.GENE3D); IPR001073 (PFAM); PTHR22923:SF51 (PANTHER); PTHR22923 (PANTHER); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY)
796	247430_length_425_cvg_2.0_tip_1_3	14	complement component q subcomponent-like protein	142	5.91E-28	62.30%	0.102	IPR014853 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR002919 (SUPERFAMILY)
797	247494_length_425_cvg_91.9_tip_0_3	1593	c-binding protein	142	7.49E-09	46.80%	0.135	PR00011 (PRINTS); IPR002049 (SMART); IPR013032 (PFAM); G3DSA:2.170.300.10 (GENE3D); IPR002049 (PFAM); PTHR24035 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES)
798	247510_length_426_cvg_8.8_tip_1_3	36	multiple epidermal growth factor-like domains protein 10 isoform x1	142	3.90E-42	70.50%	0.107	Coil (COILS); IPR006011 (SMART); G3DSA:1.20.58.70 (GENE3D); IPR006011 (PFAM); IPR028669 (PTHR19957:PANTHER); PTHR19957 (PANTHER); IPR010989 (SUPERFAMILY)
799	247606_length_426_cvg_3.0_tip_1_4	17	syntaxin 1a	142	1.39E-96	99.30%	0.101	G3DSA:2.10.25.10 (GENE3D); PTHR19897:SF158 (PANTHER); PTHR19897 (PANTHER)
800	247666_length_426_cvg_4.0_tip_1_1	18	hemimentin- partial	142	1.70E-55	65.50%	0.106	no IPS match
801	247838_length_427_cvg_2.0_tip_1_2	13	repetin	142	2.47E-14	48.20%	0.1	IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803:SF16 (PANTHER); PTHR22803 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
802	247886_length_427_cvg_3.9_tip_1_5	21	macrophage mannose receptor 1	142	5.82E-31	60.40%	0.123	IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); PTHR24026:SF41 (PANTHER); PTHR24026 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY)
803	247934_length_428_cvg_2.0_tip_1_4	9	cadherin-related tumor suppressor	143	1.51E-45	71.80%	0.101	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
804	247950_length_428_cvg_6.1_tip_1_3	27	cd4-specific ankyrin repeat protein	143	3.15E-10	69.30%	0.112	IPR025887 (PFAM); IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF57 (PANTHER); IPR011013 (SUPERFAMILY)
805	247964_length_428_cvg_3.0_tip_1_4	15	lysosomal alpha-glucosidase-like isoform x1	143	9.82E-67	81.40%	0.116	

806	247994_length_428_cvg_2.0_tip_1_0	9	receptor-type tyrosine-protein phosphatase partial	143	6.07E-27	62.90%	0.107	IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
807	248020_length_428_cvg_4.9_tip_1_4	18	n-acetylglucosamine-6-sulfatase-like isoform x3	143	2.34E-65	76.00%	0.106	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342 (PANTHER); PTHR10342:SF208 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)
808	248256_length_430_cvg_2.0_tip_1_2	11	5 - partial	143	2.22E-29	69.90%	0.106	IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11575:SF21 (PANTHER); IPR006179 (PANTHER); IPR006146 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
809	248522_length_431_cvg_3.0_tip_1_1	12	transcriptional repressor ctcfi-like isoform x1	144	6.64E-83	93.50%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24375 (PANTHER); PTHR24375:SF1 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
810	248626_length_431_cvg_18.0_tip_1_0	103	glycosyl-phosphatidylinositol-linked carbonic anhydrase	144	5.69E-15	54.20%	0.34	IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); IPR023561 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
811	248652_length_431_cvg_3.0_tip_1_3	14	hemagglutinin amebocyte aggregation factor-like	144	2.02E-39	61.00%	0.14	PF14704 (PFAM); IPR026645 (PANTHER)
812	248662_length_431_cvg_3.4_tip_1_1	16	adam 17-like protease	144	1.34E-46	70.80%	0.106	IPR002870 (PFAM); PTHR11905:SF121 (PANTHER); PTHR11905 (PANTHER)
813	248728_length_432_cvg_3.6_tip_1_4	16	prostaglandin f synthase-like	144	9.46E-39	73.30%	0.291	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); PTHR11732:SF133 (PANTHER); IPR001395 (PANTHER); IPR023210 (SUPERFAMILY)
814	248748_length_432_cvg_5.0_tip_1_5	27	serine protease	144	6.64E-09	65.40%	0.129	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
815	248864_length_432_cvg_55.0_tip_1_0	459	kallikrein-11 isoform x2	144	2.64E-21	65.20%	0.101	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
816	248936_length_433_cvg_7.7_tip_1_2	34	latrophilin-2-like isoform x3	144	1.41E-21	51.70%	0.498 Y	IPR000832 (PFAM); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
818	248982_length_433_cvg_2.0_tip_1_5	10	papilin isoform x1	144	1.68E-45	66.00%	0.101	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
819	249056_length_433_cvg_2.8_tip_1_2	14	dnaj homolog subfamily c member 3	144	3.27E-51	72.00%	0.103	Coil (COILS); IPR019734 (SMART); PF13414 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR24078:SF132 (PANTHER); PTHR24078 (PANTHER); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY)
820	249062_length_433_cvg_3.6_tip_1_5	23	meprin a subunit beta-like	144	6.10E-29	61.30%	0.268	IPR001506 (PRINTS); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)
821	249102_length_434_cvg_5.0_tip_1_5	24	calcium calmodulin-dependent serine protein kinase	144	1.26E-46	73.60%	0.099	IPR001478 (SMART); IPR001478 (PFAM); G3DSA:2.30.30.40 (GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR23122 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
823	249306_length_434_cvg_3.4_tip_1_5	26	peptidoglycan linked protein	144	5.07E-08	49.63%	0.164	no IPS match
817	248976_length_433_cvg_2.0_tip_1_0	11	sh3 domain protein	145	7.14E-08	66.00%	0.102	no IPS match
822	249250_length_434_cvg_2.0_tip_1_4	7	adam 17-like protease	145	2.36E-73	86.80%	0.1	PTHR11905:SF121 (PANTHER); PTHR11905 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
825	249530_length_436_cvg_3.0_tip_1_1	16	deoxyribonuclease- partial	145	1.44E-31	64.70%	0.114	IPR016202 (PRINTS); IPR016202 (SMART); IPR005135 (G3DSA:3.60.10.GENE3D); IPR016202 (PANTHER); IPR005135 (SUPERFAMILY)

826	249672_length_436_cvg_8.5_tip_1_1	24	heterochromatin-associated protein ment- partial	145	1.11E-10	77.40%	0.107	IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); PTHR11461:SF52 (PANTHER); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023796 (SUPERFAMILY)
828	249838_length_437_cvg_53.4_tip_1_5	2778	ribosomal protein s26	145	1.78E-59	89.80%	0.107	IPR000892 (PFAM); IPR000892 (PANTHER); IPR000892 (PROSITE_PATTERNS)
830	249868_length_437_cvg_2.2_tip_1_5	8	leucine-rich repeat neuronal protein 2	145	7.77E-19	53.70%	0.101	G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373:SF111 (PANTHER); PTHR24373 (PANTHER); SSF52058 (SUPERFAMILY)
824	249526_length_436_cvg_2.0_tip_1_0	15	vascular endothelial growth factor receptor partial	146	7.62E-17	49.00%	0.137	IPR003598 (SMART); IPR003599 (SMART); IPR013106 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
827	249676_length_436_cvg_5.0_tip_1_0	26	low-density lipoprotein receptor-related protein 1b	146	8.20E-14	57.50%	0.106	IPR002172 (SMART); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
829	249844_length_437_cvg_4.0_tip_1_4	16	myosin light chain smooth muscle	146	2.88E-67	86.20%	0.1	Coil (COILS); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF150 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
831	249900_length_437_cvg_5.8_tip_1_1	23	disintegrin and metalloproteinase domain-containing protein 10 isoform x1	146	5.90E-39	69.90%	0.111	IPR001762 (SMART); IPR001762 (G3DSA:4.10.70.GENE3D); IPR001762 (PFAM); PTHR11905:SF4 (PANTHER); PTHR11905 (PANTHER); IPR001762 (PROSITE_PROFILES); IPR001762 (SUPERFAMILY)
832	250054_length_438_cvg_4.8_tip_1_2	21	gamma-glutamyl hydrolase a-like isoform x3	146	7.41E-23	61.40%	0.114	IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY)
834	250112_length_439_cvg_6.6_tip_1_4	36	heat shock protein	146	7.82E-64	83.70%	0.101	IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); IPR029047 (G3DSA:2.60.34.GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
835	250228_length_440_cvg_2.0_tip_1_5	8	calcium-activated chloride channel regulator 1-like	146	2.88E-28	61.00%	0.136	IPR002035 (G3DSA:3.40.50.GENE3D); PF13519 (PFAM); PTHR10579:SF8 (PANTHER); PTHR10579 (PANTHER); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
833	250100_length_439_cvg_2.9_tip_1_0	15	cationic trypsin- partial	147	1.53E-30	56.30%	0.105	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
836	250340_length_440_cvg_38.6_tip_1_3	189	hemagglutinin amebocyte aggregation factor-like	147	1.23E-27	65.70%	0.113	PF14704 (PFAM); IPR026645 (PANTHER); TMhelix (TMHMM)
837	250380_length_441_cvg_2.8_tip_1_0	12	zinc finger protein 420-like	147	3.61E-33	62.80%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
838	250440_length_441_cvg_8.0_tip_1_5	43	alpha-2-macroglobulin-like protein 1 isoform x2	147	2.17E-21	54.10%	0.191	IPR011625 (PFAM); PTHR11412 (PANTHER); PTHR11412:SF80 (PANTHER)
839	250466_length_441_cvg_4.0_tip_1_3	13	trypsinogen 2	147	5.53E-28	72.40%	0.102	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
840	250554_length_442_cvg_4.0_tip_1_1	22	disintegrin and metalloproteinase domain-containing protein 10 isoform x3	147	2.38E-45	67.90%	0.162	PTHR11905:SF4 (PANTHER); PTHR11905 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
841	250628_length_442_cvg_13.7_tip_1_1	46	leukocyte elastase inhibitor	147	7.38E-26	55.70%	0.101	G3DSA:3.30.497.10 (GENE3D); IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); IPR000215 (PANTHER); PTHR11461:SF141 (PANTHER); IPR023796 (SUPERFAMILY)
842	250648_length_442_cvg_3.0_tip_1_1	13	polypeptide n-acetylgalactosaminyltransferase 2	147	1.62E-12	55.50%	0.103	IPR000772 (PFAM); G3DSA:2.80.10.50 (GENE3D); PTHR11675 (PANTHER); PTHR11675:SF24 (PANTHER); IPR000772 (PROSITE_PROFILES); IPR000772 (SUPERFAMILY)
843	250772_length_443_cvg_4.6_tip_1_5	23	interstitial collagenase	147	2.13E-58	74.30%	0.105	IPR021190 (PRINTS); IPR006026 (SMART); IPR001818 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10201 (PANTHER); SSF55486 (SUPERFAMILY)
844	251008_length_444_cvg_4.0_tip_1_0	21	heat shock 70 kda protein cognate 4- partial	148	1.17E-25	79.70%	0.121	Coil (COILS); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); SSF53067 (SUPERFAMILY)
845	251064_length_444_cvg_7.0_tip_1_3	35	cyclin-g-associated kinase	148	6.63E-54	77.40%	0.106	IPR029021 (G3DSA:3.90.190.GENE3D); IPR000340 (PFAM); PTHR23172 (PANTHER); PTHR23172:SF19 (PANTHER); IPR029023 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)

846	251098_length_444_cvg_4.0_tip_1_3	19	c-type mannose receptor 2	148	1.59E-11	48.20%	0.108	IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
848	251174_length_445_cvg_3.0_tip_1_2	18	histone-lysine n-methyltransferase prdm9	148	6.85E-39	65.60%	0.097	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
849	251450_length_446_cvg_5.0_tip_1_5	22	calcium calmodulin-dependent protein kinase	148	7.64E-88	92.30%	0.128	IPR008145 (SMART); G3DSA:3.30.63.10 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR008145 (PFAM); PTHR23122 (PANTHER); PTHR23122:SF7 (PANTHER); IPR020590 (PROSITE_PATTERNS); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
847	251166_length_445_cvg_3.9_tip_1_3	15	beta-ketoacyl partial	149	1.14E-12	54.20%	0.1	SignalP-TM (SIGNALP_GRAM_POSITIVE)
850	251728_length_447_cvg_3.4_tip_1_4	16	g protein-coupled receptor kinase 2	149	1.78E-91	94.00%	0.103	Coil (COILS); IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24355:SF24 (PANTHER); PTHR24355 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
852	251978_length_449_cvg_4.0_tip_1_5	17	serine threonine-protein kinase genghis khan isoform x1	149	5.57E-81	98.50%	0.118	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR22988 (PANTHER); PTHR22988:SF2 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
851	251738_length_448_cvg_2.0_tip_1_3	13	matrix metalloproteinase-17 isoform x2	150	2.08E-29	52.40%	0.104	IPR000585 (G3DSA:2.110.10.GENE3D); IPR018487 (PFAM); IPR001818 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10201:SF135 (PANTHER); PTHR10201 (PANTHER); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY); SSF55486 (SUPERFAMILY)
853	252028_length_449_cvg_4.2_tip_1_3	18	von willebrand factor type egf and pentraxin domain-containing protein 1-like isoform x2	150	1.41E-34	62.20%	0.112	IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR19325 (PANTHER); PTHR19325:SF43 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
854	252070_length_450_cvg_8.6_tip_1_0	35	locomotion-related protein hikaru genki	150	1.84E-23	48.60%	0.12	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
855	252158_length_450_cvg_3.0_tip_1_1	21	low-density lipoprotein receptor-related protein 2	150	6.76E-07	64.75%	0.147	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
856	252202_length_450_cvg_3.0_tip_1_0	11	slei family protein	150	7.06E-17	52.60%	0.096	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
857	252272_length_451_cvg_3.2_tip_1_0	18	cysteine proteinase	151	1.36E-58	76.20%	0.112	IPR000668 (SMART); IPR013201 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); PTHR12411:SF316 (PANTHER); IPR013128 (PANTHER); IPR000169 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
858	252600_length_452_cvg_11.0_tip_1_3	70	dermatopontin 2	151	2.34E-07	76.50%	0.166	PF14704 (PFAM); IPR026645 (PANTHER)
859	252744_length_453_cvg_81.7_tip_0_1	741	fibrinogen-related protein	151	4.74E-44	66.90%	0.104	IPR002181 (SMART); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PFAM); IPR014715 (G3DSA:4.10.530.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
860	252914_length_454_cvg_3.5_tip_1_3	15	lysosomal pro-x carboxypeptidase	152	3.80E-10	79.00%	0.117	PTHR11010:SF11 (PANTHER); IPR008758 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
861	253336_length_457_cvg_4.0_tip_1_4	20	dnak protein	152	1.39E-77	88.30%	0.119	IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
863	253506_length_457_cvg_4.1_tip_1_1	23	heat shock 70 kda protein 14	152	2.63E-28	52.90%	0.148	IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); PTHR19375:SF158 (PANTHER); IPR029047 (SUPERFAMILY)

865	253680_length_458_cvg_3.0_tip_1_5	18	pro-phenol oxidase subunit 2	152	3.78E-41	62.70%	0.11	IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005203 (G3DSA:2.60.40.GENE3D); IPR000896 (PFAM); IPR005203 (PFAM); PTHR11511:SF24 (PANTHER); IPR013788 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR002227 (PROSITE_PATTERNS); IPR014756 (SUPERFAMILY); IPR008922 (SUPERFAMILY)
862	253386_length_457_cvg_2.0_tip_1_3	11	leucine-rich repeat-containing protein 15-like	153	7.65E-37	65.70%	0.101	IPR003591 (SMART); SM00365 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PATTERNS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
864	253582_length_458_cvg_4.7_tip_1_0	25	collagen alpha-1 chain isoform x5	153	1.50E-10	50.10%	0.136	IPR010515 (PFAM)
866	253902_length_460_cvg_3.0_tip_1_5	13	gastrula zinc finger protein	153	9.58E-15	59.20%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
867	253922_length_460_cvg_2.0_tip_1_4	6	von willebrand factor type egf and pentraxin domain-containing protein 1	153	4.39E-28	54.50%	0.1	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
868	254136_length_461_cvg_110.7_tip_0_1	52567	hc subunit partial	154	8.99E-100	77.00%	0.1	IPR000896 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005203 (G3DSA:2.60.40.GENE3D); IPR005203 (PFAM); PTHR11511:SF5 (PANTHER); IPR013788 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR002227 (PROSITE_PATTERNS); IPR008922 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
869	254348_length_463_cvg_2.7_tip_1_5	15	ww domain-containing oxidoreductase-like	154	5.14E-48	80.80%	0.124	IPR001202 (SMART); IPR001202 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); G3DSA:2.20.70.10 (GENE3D); PTHR24310:SF30 (PANTHER); PTHR24310 (PANTHER); IPR001202 (PROSITE_PROFILES); SSF51735 (SUPERFAMILY); IPR001202 (SUPERFAMILY)
870	254370_length_463_cvg_7.0_tip_1_2	36	von willebrand factor a domain-containing protein 8	154	4.46E-44	84.40%	0.107	PTHR21610:SF9 (PANTHER); PTHR21610 (PANTHER)
871	254442_length_463_cvg_3.2_tip_1_2	17	protein flightless-1-like	154	2.73E-49	94.50%	0.102	IPR007122 (PRINTS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR029919 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY)
872	254482_length_463_cvg_2.0_tip_1_5	13	adp-ribosylation factor-like protein 2	154	1.10E-71	95.90%	0.285	IPR006689 (PRINTS); IPR024156 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); IPR005225 (TIGRFAM); PTHR11711 (PANTHER); PTHR11711:SF26 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
874	254574_length_464_cvg_2.0_tip_1_5	9	zinc finger protein partial	154	1.09E-69	81.20%	0.101	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
873	254526_length_464_cvg_2.7_tip_1_0	11	fibrillin-2-like	155	2.37E-61	77.50%	0.101	IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); PTHR24039:SF20 (PANTHER); IPR011398 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
875	254678_length_465_cvg_9.1_tip_1_1	43	spindolin-related protein	155	2.96E-40	57.80%	0.102	G3DSA:2.70.50.50 (GENE3D); IPR004302 (PFAM); IPR014756 (SUPERFAMILY)
876	254710_length_465_cvg_27.0_tip_1_0	100	atrial natriuretic peptide-converting enzyme	155	5.47E-08	53.70%	0.519 Y	IPR002172 (PRINTS); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-TM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
877	254736_length_465_cvg_3.0_tip_1_4	15	laminin subunit alpha	155	1.71E-64	74.70%	0.096	no IPS match

882	255068_length_467_cvg_49.0_tip_1_5	328	projectin short variant	155	1.08E-44	87.10%	0.32	IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF155 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
878	254914_length_466_cvg_4.9_tip_1_3	28	ankyrin repeat and socs box protein 3-like isoform x1	156	2.53E-28	56.10%	0.131	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
879	254916_length_466_cvg_3.4_tip_1_3	23	cognate 70 kda heat shock partial	156	9.15E-101	99.10%	0.134	IPR013126 (PRINTS); IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR029047 (SUPERFAMILY)
880	255002_length_467_cvg_3.0_tip_1_0	14	multicopper oxidase- isoform a	156	1.59E-65	76.10%	0.116	IPR008972 (G3DSA:2.60.40.GENE3D); IPR011707 (PFAM); PTHR11709:SF33 (PANTHER); PTHR11709 (PANTHER); IPR008972 (SUPERFAMILY)
881	255040_length_467_cvg_2.5_tip_1_1	21	calcium calmodulin-dependent serine protein kinase	156	9.61E-16	66.50%	0.116	IPR014775 (PFAM); IPR004172 (PROSITE_PROFILES); SSF101288 (SUPERFAMILY)
883	255154_length_468_cvg_5.7_tip_1_1	36	tissue factor pathway inhibitor 2 precursor	156	3.47E-13	64.80%	0.126	IPR002223 (PRINTS); IPR002223 (SMART); IPR008037 (PFAM); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR002223 (SUPERFAMILY); TMhelix (TMHMM)
884	255184_length_468_cvg_2.0_tip_1_4	9	low-density lipoprotein receptor-related protein partial	156	1.02E-28	55.60%	0.121	IPR000033 (SMART); IPR011042 (G3DSA:2.120.10.GENE3D); IPR000033 (PFAM); PTHR10529 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY)
885	255306_length_468_cvg_2.6_tip_1_3	24	zinc finger protein 311	156	8.16E-28	58.80%	0.11	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
886	255310_length_468_cvg_3.2_tip_1_2	17	calcium calmodulin-dependent protein kinase	156	2.68E-24	90.40%	0.12	IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23122:SF7 (PANTHER); PTHR23122 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
887	255322_length_468_cvg_71.7_tip_1_5	1907	epididymal secretory protein e1	156	7.58E-12	56.70%	0.112	IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306 (PANTHER); IPR014756 (SUPERFAMILY)
888	255450_length_469_cvg_12.0_tip_1_2	58	hemagglutinin	156	2.26E-44	68.60%	0.103	G3DSA:1.10.390.10 (GENE3D); IPR001570 (PFAM); SSF55486 (SUPERFAMILY)
890	255652_length_470_cvg_2.1_tip_1_5	13	hypothetical protein LOTGIDRAFT_122202, partial	156	9.18E-08	56.75%	0.105	IPR013182 (PFAM)
889	255652_length_470_cvg_2.1_tip_1_3	13	dna-directed rna polymerase	157	6.62E-14	66.80%	0.1	no IPS match
891	255752_length_471_cvg_3.0_tip_1_0	17	collagen alpha-1 chain	157	1.05E-30	65.10%	0.106	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF379 (PANTHER)
892	255752_length_471_cvg_3.0_tip_1_4	17	threonine-rich gpi-anchored partial	157	7.93E-24	46.80%	0.107	PTHR24023:SF405 (PANTHER); PTHR24023 (PANTHER)
893	255788_length_471_cvg_25.5_tip_1_0	127	type iv secretion protein	157	3.77E-16	45.50%	0.235	SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE)
894	255862_length_472_cvg_4.0_tip_1_1	22	upf0764 protein c16orf89 homolog	157	3.45E-11	51.30%	0.108	no IPS match
895	255908_length_472_cvg_3.0_tip_1_4	16	plexin partial	157	1.30E-92	94.80%	0.1	Coil (COILS); IPR013548 (PFAM); PTHR22625 (PANTHER); PTHR22625:SF16 (PANTHER)
896	255934_length_472_cvg_2.0_tip_1_4	10	dnak protein	157	2.60E-83	91.20%	0.117	IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.90.640.10 (GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY)

897	255982_length_472_cvg_2.0_tip_1_1	11	zinc finger protein 558	157	9.54E-18	62.10%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
898	256082_length_473_cvg_2.9_tip_1_0	24	iron zinc purple acid phosphatase-like isoform x1	158	3.69E-76	81.40%	0.117	IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); IPR015914 (G3DSA:2.60.40.GENE3D); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); IPR008963 (SUPERFAMILY); IPR029052 (SUPERFAMILY)
899	256254_length_474_cvg_2.0_tip_1_1	15	heat shock partial	158	1.07E-66	82.30%	0.104	Coil (COILS); Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF125 (PANTHER); IPR018253 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM)
900	256320_length_474_cvg_3.0_tip_1_3	18	serine beta-lactamase-like protein mitochondrial isoform x2	158	1.08E-53	75.00%	0.12	Coil (COILS); IPR012338 (G3DSA:3.40.710.GENE3D); IPR001466 (PFAM); PTHR22935:SF64 (PANTHER); PTHR22935 (PANTHER); IPR012338 (SUPERFAMILY)
902	256498_length_475_cvg_3.4_tip_1_5	16	zinc finger protein	158	1.23E-25	55.50%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
901	256356_length_475_cvg_4.0_tip_1_3	21	alpha- partial	159	5.46E-39	65.90%	0.117	IPR001599 (PFAM); PTHR11412:SF80 (PANTHER); PTHR11412 (PANTHER); IPR014756 (SUPERFAMILY)
904	257126_length_479_cvg_2.0_tip_1_2	12	ccr4-not transcription complex subunit 6-like isoform x7	159	6.27E-62	80.90%	0.121	IPR003591 (SMART); IPR025875 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR12121:SF35 (PANTHER); PTHR12121 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
903	257014_length_478_cvg_4.0_tip_1_0	24	zinc finger protein 64 isoform x2	160	3.08E-59	77.80%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
905	257166_length_479_cvg_4.0_tip_1_0	22	dehydrogenase reductase sdr family member 11	160	7.92E-59	77.30%	0.191	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF310 (PANTHER); SSF51735 (SUPERFAMILY)
906	257470_length_481_cvg_4.6_tip_1_2	24	allatostatin precursor protein	160	4.96E-25	57.70%	0.099	IPR010276 (PFAM)
908	257508_length_482_cvg_6.9_tip_1_2	40	zinc finger protein 502	160	4.14E-37	60.00%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
909	257518_length_482_cvg_3.0_tip_1_5	18	tyrosine-protein phosphatase non-receptor	160	1.88E-43	69.90%	0.19	IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
907	257490_length_482_cvg_2.0_tip_1_3	11	macrophage mannose receptor 1-like isoform 2	161	5.55E-25	51.90%	0.119	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803 (PANTHER); PTHR22803:SF16 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
910	257626_length_483_cvg_2.7_tip_1_5	14	alpha-mannosidase 2x	161	6.04E-47	75.20%	0.102	IPR027291 (G3DSA:3.20.110.GENE3D); IPR000602 (PFAM); PTHR11607:SF4 (PANTHER); PTHR11607 (PANTHER); IPR011330 (SUPERFAMILY)

911	258184_length_486_cvg_3.4_tip_1_0	27	low-density lipoprotein receptor-related protein 1b-like	162	5.66E-09	74.10%	0.102	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
912	258288_length_487_cvg_3.0_tip_1_2	16	ankyrin repeat and sam domain-containing protein 6-like	162	7.07E-35	62.20%	0.609 Y	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); PTHR10627 (PANTHER); PTHR10627:SF2 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR020683 (SUPERFAMILY)
913	258484_length_488_cvg_2.0_tip_1_2	8	zinc finger protein	162	6.95E-26	55.80%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
914	258486_length_488_cvg_4.0_tip_1_5	23	low quality protein: basement membrane-specific heparan sulfate proteoglycan core	162	4.03E-57	72.10%	0.096	IPR018031 (SMART); IPR000034 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF252 (PANTHER); IPR000034 (PROSITE_PROFILES)
915	258490_length_488_cvg_57.0_tip_1_3	973	protein	163	2.00E-23	72.60%	0.115	IPR002181 (SMART); IPR014715 (G3DSA:4.10.530.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
916	258510_length_488_cvg_4.0_tip_1_0	28	sucrase- intestinal-like	163	8.87E-31	57.10%	0.104	IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF7 (PANTHER); IPR017853 (SUPERFAMILY)
917	258606_length_489_cvg_2.6_tip_1_1	12	sialate o-acetylerase-like	163	1.66E-15	57.10%	0.192	PTHR22901 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
918	258638_length_489_cvg_2.5_tip_1_3	16	endo-b- -glucanase	163	6.88E-56	76.80%	0.232	IPR012341 (G3DSA:1.50.10.GENE3D); IPR001701 (PFAM); PTHR22298 (PANTHER); PTHR22298:SF17 (PANTHER); IPR018221 (PROSITE_PATTERNS); IPR008928 (SUPERFAMILY)
919	258676_length_490_cvg_42.0_tip_1_5	188	cell wall anchor partial	163	3.37E-17	40.00%	0.244	SSF141571 (SUPERFAMILY)
921	258788_length_491_cvg_2.7_tip_1_2	19	integrin-linked protein kinase	163	2.05E-50	90.40%	0.148	IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR23257:SF30 (PANTHER); PTHR23257 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
920	258772_length_490_cvg_12.2_tip_1_0	64	anti-lipopolysaccharide partial	164	4.44E-20	68.30%	0.11	IPR024509 (PFAM); IPR024716 (PRODOM)
922	259082_length_493_cvg_3.0_tip_1_5	22	5 -nucleotidase-like	164	9.80E-45	62.70%	0.112	IPR006179 (PRINTS); IPR008334 (PFAM); IPR008334 (G3DSA:3.90.780.GENE3D); IPR006179 (PANTHER); PTHR11575:SF21 (PANTHER); IPR008334 (SUPERFAMILY)
924	259344_length_494_cvg_3.0_tip_1_5	18	lachesin	164	4.48E-76	81.40%	0.129	IPR003599 (SMART); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF43 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
923	259312_length_494_cvg_63.0_tip_1_3	605	polyubiquitin-b isoform x1	165	3.14E-111	100.00%	0.102	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY)
925	259428_length_495_cvg_46.7_tip_1_3	320	low affinity immunoglobulin epsilon fc receptor	165	6.18E-19	51.60%	0.113	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
927	259944_length_499_cvg_2.0_tip_1_4	13	xanthine dehydrogenase	166	5.33E-45	64.80%	0.101	IPR016167 (G3DSA:3.30.43.GENE3D); IPR002888 (G3DSA:1.10.150.GENE3D); IPR002346 (PFAM); IPR002888 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR016166 (SUPERFAMILY); IPR002888 (SUPERFAMILY)

926	259912_length_499_cvg_5.4_tip_1_3	24	zinc finger protein	167	2.16E-30	56.30%	0.105	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
928	260112_length_500_cvg_3.9_tip_1_1	23	acid sphingomyelinase-like phosphodiesterase 3b	167	1.13E-37	61.90%	0.218	IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); PTHR10340 (PANTHER); PTHR10340:SF14 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY)
929	260114_length_500_cvg_5.6_tip_1_1	26	low-density lipoprotein receptor-related protein 2	167	8.33E-67	79.00%	0.102	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
930	260158_length_500_cvg_2.6_tip_1_3	20	clotting factor partial	167	7.42E-31	63.70%	0.136	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
931	260210_length_501_cvg_2.0_tip_1_2	13	tyrosine-protein kinase abl	167	4.41E-55	71.00%	0.133	G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24418 (PANTHER); PTHR24418:SF87 (PANTHER); IPR011009 (SUPERFAMILY)
932	260252_length_501_cvg_5.4_tip_1_2	29	multiple epidermal growth factor-like domains partial	167	3.34E-61	69.00%	0.119	PR00011 (PRINTS); IPR000742 (SMART); G3DSA:2.170.300.10 (GENE3D); IPR002049 (PFAM); PTHR24035 (PANTHER); PTHR24035:SF4 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR011489 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES)
933	260262_length_501_cvg_2.9_tip_1_5	19	ankyrin repeat protein partial	167	3.37E-23	54.60%	0.16	IPR002110 (SMART); IPR020683 (PFAM); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
934	260440_length_502_cvg_2.0_tip_1_4	17	ga-binding protein subunit beta-2	167	4.11E-68	81.90%	0.148	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); PTHR24193 (PANTHER); PTHR24193:SF72 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
935	260520_length_503_cvg_3.0_tip_1_5	15	leucine-rich repeat protein soc-2 homolog	167	8.95E-98	93.70%	0.111	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR23155 (PANTHER); IPR027036 (PTHR23155:PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
936	260748_length_505_cvg_4.0_tip_1_1	23	pancreatic triacylglycerol lipase	168	1.89E-24	58.90%	0.585 Y	IPR029058 (G3DSA:3.40.50.GENE3D); IPR013818 (PFAM); IPR000734 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR029058 (SUPERFAMILY)
937	260948_length_506_cvg_6.0_tip_1_1	34	von willebrand factor type egf and pentraxin domain-containing protein 1	169	3.33E-10	42.70%	0.101	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
942	261358_length_509_cvg_10.0_tip_1_2	43	low quality protein: tenascin	169	1.04E-25	65.00%	0.106	IPR002181 (SMART); IPR014715 (G3DSA:4.10.530.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
938	261150_length_508_cvg_3.5_tip_1_3	18	---NA---	170			0.122	IPR001073 (PRINTS); IPR001073 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY); IPR008983 (SUPERFAMILY)

939	261190_length_508_cvg_3.7_tip_1_0	22	rac protein kinase drac-	170	3.02E-93	87.60%	0.366 Y	IPR000961 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); IPR017892 (PFAM); PTHR24351 (PANTHER); PTHR24351:SF64 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
940	261192_length_508_cvg_6.0_tip_1_0	31	mannosyl-oligosaccharide -alpha-mannosidase ib	170	4.08E-94	89.00%	0.2	IPR001382 (PRINTS); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); IPR001382 (PANTHER); PTHR11742:SF37 (PANTHER); IPR001382 (SUPERFAMILY)
941	261272_length_509_cvg_4.0_tip_1_0	23	von willebrand factor a domain-containing protein partial	170	1.50E-28	55.60%	0.103	PTHR21610:SF9 (PANTHER); PTHR21610 (PANTHER)
943	261400_length_509_cvg_2.8_tip_1_4	13	u4 u6 small nuclear ribonucleoprotein prp4	170	4.56E-76	88.50%	0.238	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR027106 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
944	261410_length_509_cvg_6.0_tip_1_1	33	phospholipase b-like partial	170	1.65E-76	77.70%	0.136	IPR007000 (PFAM); IPR007000 (PANTHER); PTHR12370:SF3 (PANTHER)
945	261436_length_510_cvg_4.3_tip_1_3	39	parkinson disease 7 domain-containing	170	2.24E-73	72.70%	0.256	IPR002818 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); IPR029062 (SUPERFAMILY)
946	261456_length_510_cvg_2.9_tip_1_5	16	vitellogenin receptor	170	7.09E-18	47.90%	0.127	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
948	261652_length_511_cvg_2.0_tip_1_2	16	peptidyl-prolyl cis-trans isomerase-like 4	170	1.62E-77	80.80%	0.103	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF156 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
950	261702_length_511_cvg_4.0_tip_1_5	27	low quality protein: cubilin- partial	170	3.50E-43	58.80%	0.231	IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
951	261730_length_512_cvg_4.0_tip_1_5	22	arylsulfatase b	170	2.16E-35	57.30%	0.102	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); G3DSA:3.30.1120.10 (GENE3D); PTHR10342:SF206 (PANTHER); PTHR10342 (PANTHER); IPR017850 (SUPERFAMILY)
952	261800_length_512_cvg_86.0_tip_1_2	4982	cathepsin l2	170	1.19E-77	80.90%	0.103	IPR000668 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); IPR013128 (PANTHER); PTHR12411:SF265 (PANTHER); IPR025661 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
947	261570_length_511_cvg_12.8_tip_1_0	71	signal cub and egf-like domain-containing protein 2	171	4.56E-09	50.70%	0.113	IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR024731 (PFAM); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR009030 (SUPERFAMILY)
949	261688_length_511_cvg_9.0_tip_1_0	45	zinc finger protein 233	171	3.06E-32	57.00%	0.113	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
953	261878_length_513_cvg_6.2_tip_1_2	39	cubilin isoform x2	171	1.78E-31	56.70%	0.107	IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
954	261944_length_513_cvg_3.0_tip_1_2	15	aael017480- partial	171	2.77E-27	56.10%	0.145	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
955	262022_length_514_cvg_6.1_tip_1_3	37	wd repeat-containing protein 61	172	1.22E-89	90.80%	0.109	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22841 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
956	262080_length_514_cvg_38.0_tip_1_0	165	low-density lipoprotein receptor-related protein partial	172	3.72E-07	64.50%	0.12	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)

957	262116_length_515_cvg_4.6_tip_1_0	26	von willebrand factor a domain-containing protein 8	172	2.37E-20	58.40%	0.114	PTHR21610 (PANTHER); PTHR21610:SF9 (PANTHER) IPR002001 (PRINTS); IPR000832 (PRINTS); IPR000832 (PFAM); G3DSA:1.20.1070.10 (GENE3D); PTHR12011 (PANTHER); PTHR12011:SF249 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017981 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
958	262156_length_515_cvg_3.2_tip_1_0	25	diuretic hormone receptor-like isoform x1	172	3.76E-65	77.10%	0.141	G3DSA:1.10.390.10 (GENE3D); IPR001570 (PFAM); SSF55486 (SUPERFAMILY) IPR003172 (SMART); IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306 (PANTHER); PTHR11306:SF4 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR014756 (SUPERFAMILY); TMhelix (TMHMM) IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR001164 (PFAM); PTHR23180 (PANTHER); PTHR23180:SF229 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); SSF57863 (SUPERFAMILY); IPR020683 (SUPERFAMILY)
959	262328_length_516_cvg_33.6_tip_1_2	192	hemagglutinin	172	8.87E-44	70.80%	0.098	IPR019565 (PFAM); IPR008930 (G3DSA:1.50.10.GENE3D); PTHR11412 (PANTHER); IPR019742 (PROSITE_PATTERNS); IPR008930 (SUPERFAMILY)
960	262426_length_517_cvg_15.7_tip_1_0	93	md-2-related lipid-recognition	173	2.45E-24	53.50%	0.785 Y	IPR001863 (PFAM); IPR001863 (PANTHER)
961	262740_length_519_cvg_2.9_tip_1_5	17	centaurin-gamma 1a	173	2.02E-74	72.10%	0.164	PTHR21610 (PANTHER); PTHR21610:SF9 (PANTHER)
962	262746_length_519_cvg_7.0_tip_1_5	46	alpha-2-macroglobulin-like protein 1	173	1.37E-53	71.10%	0.105	IPR013548 (PFAM); PTHR22625 (PANTHER); IPR008936 (SUPERFAMILY)
963	262750_length_519_cvg_3.9_tip_1_0	29	glypican-5 isoform x5	173	1.06E-33	57.10%	0.192	IPR002110 (PRINTS); IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24144 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
964	262808_length_520_cvg_6.0_tip_1_2	34	von willebrand factor a domain-containing protein 8-like	173	3.31E-85	85.80%	0.125	IPR002110 (PRINTS); IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24144 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
965	262902_length_520_cvg_3.0_tip_1_4	18	plexin- partial	173	7.77E-99	93.70%	0.144	IPR002110 (PRINTS); IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24144 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
966	263080_length_522_cvg_6.0_tip_1_2	34	ankyrin repeat domain-containing protein 49-like	174	1.41E-56	71.10%	0.134	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22844 (PANTHER); PTHR22844:SF166 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
967	263084_length_522_cvg_14.0_tip_1_0	83	wd repeat-containing protein 86-like	174	4.95E-43	72.50%	0.16	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24291 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
968	263164_length_522_cvg_8.9_tip_1_5	50	cytochrome p450 partial	174	4.43E-52	66.60%	0.1	Coil (COILS); IPR000582 (PRINTS); IPR029045 (G3DSA:3.90.226.GENE3D); IPR000582 (PFAM); IPR014352 (G3DSA:1.20.80.GENE3D); IPR001753 (PFAM); PTHR23310 (PANTHER); PTHR23310:SF55 (PANTHER); IPR022408 (PROSITE_PATTERNS); IPR000582 (PROSITE_PROFILES); IPR029045 (SUPERFAMILY); IPR000582 (SUPERFAMILY)
969	263188_length_522_cvg_3.2_tip_1_5	24	enoyl- delta isomerase mitochondrial	174	6.37E-45	67.20%	0.179	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF114 (PANTHER); IPR016161 (SUPERFAMILY)
971	263214_length_523_cvg_5.2_tip_1_4	39	betaine aldehyde dehydrogenase	174	6.74E-36	80.20%	0.128	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
972	263216_length_523_cvg_3.0_tip_1_4	16	low quality protein: low-density lipoprotein receptor-related protein 1- partial	174	3.22E-23	56.10%	0.354 Y	IPR011496 (PFAM); PTHR13170 (PANTHER); PTHR13170:SF17 (PANTHER); IPR017853 (SUPERFAMILY)
970	263212_length_523_cvg_2.0_tip_1_3	14	bifunctional protein ncoat isoform x2	175	1.03E-81	92.20%	0.201	PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
973	263374_length_524_cvg_42.1_tip_1_3	228	hemagglutinin amebocyte aggregation factor-like	175	1.37E-23	57.40%	0.194	

974	263484_length_524_cvg_2.1_tip_1_1	20	adenosine deaminase cecr1-like	175	1.07E-34	63.50%	0.367 Y	IPR013659 (PFAM); PTHR11409:SF39 (PANTHER); PTHR11409 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SSF51556 (SUPERFAMILY); TMhelix (TMHMM)
975	263584_length_525_cvg_2.8_tip_1_0	23	map kinase-activated protein kinase 2	175	2.39E-102	88.90%	0.113	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24349:SF64 (PANTHER); PTHR24349 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
976	263706_length_526_cvg_5.6_tip_1_1	41	protein disulfide-isomerase a4-like	175	1.03E-57	67.40%	0.916 Y	PR00421 (PRINTS); IPR013766 (PFAM); IPR005788 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF56 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR012336 (SUPERFAMILY)
977	263732_length_526_cvg_54.5_tip_1_0	1385	ubiquitin-60s ribosomal protein I40	176	1.59E-85	99.20%	0.16	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); IPR001975 (PFAM); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR011332 (SUPERFAMILY)
978	263748_length_527_cvg_3.8_tip_1_1	22	low quality protein: reelin-like	176	2.57E-29	54.50%	0.219	PTHR11841 (PANTHER)
979	263918_length_528_cvg_5.4_tip_1_3	33	ga-binding protein subunit beta-2	176	2.51E-10	68.30%	0.117	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24182 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
984	264200_length_530_cvg_19.5_tip_1_5	141	hypothetical protein	176	7.03E-13	50.40%	0.383 Y	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
980	264012_length_529_cvg_15.4_tip_1_0	79	lysosomal alpha-mannosidase-like	177	7.20E-31	67.60%	0.137	IPR011682 (PFAM); G3DSA:2.60.40.1360 (GENE3D); PTHR11607:SF3 (PANTHER); PTHR11607 (PANTHER); IPR011013 (SUPERFAMILY)
981	264042_length_529_cvg_22.6_tip_1_0	166	bone sialoprotein-binding partial	177	1.76E-08	49.00%	0.106	no IPS match
982	264096_length_529_cvg_2.9_tip_1_3	16	achain crystal structure of engineered northeast structural genomics consortium target	177	1.12E-11	64.60%	0.123	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24182 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
983	264134_length_530_cvg_2.0_tip_1_0	18	beta-glucuronidase isoform x2	177	1.00E-74	75.60%	0.127	IPR006101 (PRINTS); IPR006103 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR10066:SF51 (PANTHER); PTHR10066 (PANTHER); IPR023230 (PROSITE_PATTERNS); IPR023232 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
985	264300_length_531_cvg_6.1_tip_1_1	39	sortilin-related receptor	177	1.73E-10	41.60%	0.1	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
986	264324_length_531_cvg_3.9_tip_1_0	30	zinc finger protein	177	4.77E-18	55.90%	0.103	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR003656 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
987	264366_length_532_cvg_3.0_tip_1_1	21	short neuropeptide f	177	1.51E-22	68.60%	0.211	no IPS match
990	264526_length_533_cvg_3.9_tip_1_5	25	integrin alpha-ps2-like	177	1.62E-39	61.30%	0.141	IPR000413 (PRINTS); IPR013519 (SMART); G3DSA:2.130.10.130 (GENE3D); IPR013517 (PFAM); PTHR23220 (PANTHER); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); SSF69318 (SUPERFAMILY)
988	264492_length_533_cvg_32.3_tip_0_4	206	neurotransmitter gated ion channel	178	4.54E-53	66.30%	0.139	IPR006202 (PFAM); IPR006202 (G3DSA:2.70.170.GENE3D); IPR027361 (G3DSA:1.20.120.GENE3D); PTHR18945:SF490 (PANTHER); IPR006201 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006202 (SUPERFAMILY); IPR006029 (SUPERFAMILY); TMhelix (TMHMM)

989	264508_length_533_cvg_3.7_tip_1_1	22	serine threonine-protein phosphatase 6 regulatory ankyrin repeat subunit c-like	178	9.02E-28	54.70%	0.136	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
991	264620_length_534_cvg_2.1_tip_1_5	16	dentin sialophosphoprotein isoform x1	178	1.32E-59	71.20%	0.107	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
992	264668_length_534_cvg_3.0_tip_1_4	18	aldehyde dehydrogenase	178	5.94E-66	69.00%	0.183	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); IPR015657 (PTHR11699:PANTHER); IPR016161 (SUPERFAMILY); TMhelix (TMHMM)
995	264776_length_535_cvg_2.7_tip_1_4	16	zinc finger protein 239-like	178	2.05E-24	60.00%	0.106	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
997	264798_length_536_cvg_17.6_tip_1_2	105	membrane glycoprotein lig-	178	2.46E-23	52.60%	0.106	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR026906 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
993	264700_length_535_cvg_17.3_tip_1_0	93	apolipoprotein d-like	179	8.20E-34	61.20%	0.363 Y	IPR003057 (PRINTS); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612:SF7 (PANTHER); PTHR10612 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)
994	264740_length_535_cvg_2.0_tip_1_3	15	caseinolytic peptidase b protein homolog	179	7.79E-53	75.70%	0.099	IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
996	264778_length_535_cvg_11.0_tip_1_0	64	ribosome biogenesis protein wdr12 homolog	179	5.03E-83	80.40%	0.157	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19855 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
998	264824_length_536_cvg_5.9_tip_1_4	34	low affinity immunoglobulin epsilon fc receptor-like	179	3.28E-17	46.40%	0.132	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
999	265016_length_537_cvg_2.0_tip_1_3	15	chorion peroxidase	179	2.84E-25	67.80%	0.12	IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
1001	265202_length_539_cvg_19.7_tip_1_2	109	peptidyl-prolyl cis-trans isomerase b	179	3.66E-43	54.60%	0.109	IPR024936 (PIRSF); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF78 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1002	265266_length_539_cvg_3.9_tip_1_2	26	aael017046- partial	179	2.08E-59	74.30%	0.920 Y	IPR021190 (PRINTS); IPR002477 (PFAM); IPR002477 (G3DSA:1.10.101.GENE3D); IPR001818 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10201:SF131 (PANTHER); PTHR10201 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR002477 (SUPERFAMILY); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1000	265166_length_539_cvg_4.6_tip_1_4	29	low quality protein: neurogenic locus notch homolog protein 3-like	180	8.45E-52	65.50%	0.101	IPR000742 (SMART); IPR013032 (PFAM); G3DSA:2.10.25.10 (GENE3D)
1003	265272_length_539_cvg_4.0_tip_1_3	26	alcohol dehydrogenase	180	1.32E-51	71.80%	0.182	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); IPR001395 (PANTHER); PTHR11732:SF183 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
1004	265302_length_540_cvg_4.2_tip_1_0	26	attractin-like protein 1	180	3.81E-81	79.80%	0.1	G3DSA:2.10.25.10 (GENE3D); PTHR10574:SF3 (PANTHER); PTHR10574 (PANTHER)

1005	265314_length_540_cvg_73.1_tip_1_4	1003	carboxypeptidase b-like	180	1.69E-64	71.80%	0.118	IPR000834 (SMART); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
1006	265338_length_540_cvg_2.0_tip_1_3	16	peroxisomal biogenesis factor 7	180	2.14E-81	76.10%	0.102	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22850 (PANTHER); PTHR22850:SF98 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1007	265358_length_540_cvg_5.3_tip_1_2	40	alpha-2-macroglobulin-like protein 1	180	1.37E-21	47.80%	0.22	IPR011625 (PFAM); PTHR11412 (PANTHER)
1008	265556_length_542_cvg_61.6_tip_1_0	18917	vitellogenin 2	181	1.31E-22	53.40%	0.540 Y	IPR015816 (G3DSA:2.30.230.GENE3D); IPR001747 (PFAM); PTHR23345 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_EUK); IPR015819 (SUPERFAMILY); TMhelix (TMHMM)
1009	265608_length_542_cvg_5.3_tip_1_3	29	c4b-binding protein beta	181	6.74E-59	66.40%	0.108	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); PTHR19325:SF312 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1010	265698_length_543_cvg_3.4_tip_1_5	22	gastrula zinc finger	181	9.02E-23	63.50%	0.097	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1011	265786_length_544_cvg_4.0_tip_1_2	28	peroxidasin homolog	181	1.69E-16	46.40%	0.112	IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
1012	265804_length_544_cvg_2.0_tip_1_5	13	von willebrand factor d and egf domain-containing	181	7.04E-47	58.10%	0.118	IPR000742 (SMART); IPR000742 (PFAM); G3DSA:2.170.300.10 (GENE3D); IPR013032 (PFAM); PTHR24838 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
1013	265840_length_544_cvg_2.2_tip_1_1	22	group xiia secretory phospholipase a2	181	1.80E-52	63.10%	0.659 Y	IPR016090 (G3DSA:1.20.90.GENE3D); IPR010711 (PFAM); PTHR12824:SF8 (PANTHER); IPR010711 (PANTHER); IPR013090 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR016090 (SUPERFAMILY); TMhelix (TMHMM)
1014	265852_length_544_cvg_2.0_tip_1_1	11	rna polymerase ii largest subunit	181	7.19E-47	84.90%	0.097	PR01217 (PRINTS); IPR000684 (PFAM); IPR000684 (PROSITE_PATTERNS); IPR000684 (PROSITE_PATTERNS); IPR000684 (PROSITE_PATTERNS); IPR000684 (PROSITE_PATTERNS); IPR000684 (PROSITE_PATTERNS); IPR000684 (PROSITE_PATTERNS); IPR000684 (PROSITE_PATTERNS); IPR000684 (PROSITE_PATTERNS); IPR000684 (PROSITE_PATTERNS); IPR000684 (PROSITE_PATTERNS)
1015	265928_length_545_cvg_3.4_tip_1_1	25	dehydrogenase reductase sdr family protein 7-like	182	8.87E-87	84.10%	0.104	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF325 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY)
1016	266006_length_546_cvg_11.4_tip_1_3	62	serpin b3	182	1.86E-29	67.10%	0.123	G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); G3DSA:3.30.497.10 (GENE3D); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
1017	266082_length_546_cvg_3.5_tip_1_1	22	mam and ldl-receptor class a domain-containing protein 1-like	182	4.22E-15	48.00%	0.119	IPR000998 (SMART); IPR000998 (PFAM); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
1021	266184_length_547_cvg_25.1_tip_1_2	88	gamma-glutamyl hydrolase-like	182	3.57E-24	69.70%	0.203	IPR011697 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); PTHR11315:SF2 (PANTHER); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES)
1023	266228_length_548_cvg_12.2_tip_1_5	57	hypothetical protein	182	2.31E-08	74.17%	0.117	IPR010790 (PFAM)

1018	266112_length_547_cvg_3.0_tip_1_3	22	isoform b	183	8.95E-31	65.60%	0.518 Y	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320:SF38 (PANTHER); PTHR24320 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1019	266146_length_547_cvg_6.3_tip_1_0	44	muscle m-line assembly protein unc-89	183	1.80E-47	66.90%	0.103	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1020	266150_length_547_cvg_27.9_tip_1_3	174	translocase of inner mitochondrial membrane 8 homolog b	183	2.05E-33	78.30%	0.124	IPR004217 (G3DSA:1.10.287.GENE3D); IPR004217 (PFAM); PTHR21535 (PANTHER); PTHR21535:SF25 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR004217 (SUPERFAMILY); TMhelix (TMHMM)
1022	266212_length_547_cvg_3.0_tip_1_3	18	insulin receptor	183	7.00E-102	88.00%	0.103	IPR001245 (PRINTS); IPR020635 (SMART); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24416:SF254 (PANTHER); PTHR24416 (PANTHER); IPR002011 (PROSITE_PATTERNS); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1024	266258_length_548_cvg_3.0_tip_1_3	18	venom protease-like	183	2.11E-43	59.00%	0.267	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF81 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1025	266274_length_548_cvg_2.0_tip_1_4	16	antigen 5 scp domain-containing	183	9.84E-12	56.50%	0.311	IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR014044 (SUPERFAMILY)
1026	266284_length_548_cvg_60.0_tip_1_0	514	---NA---	183			0.187	Coil (COILS); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); TMhelix (TMHMM)
1027	266370_length_549_cvg_3.3_tip_1_4	20	third variable lymphocyte receptor	183	2.55E-11	51.00%	0.18	G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); SSF52058 (SUPERFAMILY)
1028	266408_length_549_cvg_4.0_tip_1_4	28	low quality protein: titin-like	183	2.83E-47	62.10%	0.101	IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1029	266458_length_550_cvg_9.6_tip_1_4	66	integrin-linked protein kinase	183	5.15E-42	91.20%	0.227	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR23257:SF30 (PANTHER); PTHR23257 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM)
1032	266642_length_551_cvg_13.8_tip_1_2	74	beta- -n-acetylgalactosaminyltransferase bre-4-like	183	1.75E-49	58.90%	0.145	IPR003859 (PRINTS); IPR027791 (PFAM); IPR027995 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR003859 (PANTHER); PTHR19300:SF30 (PANTHER); IPR029044 (SUPERFAMILY)
1030	266478_length_550_cvg_3.9_tip_1_3	23	transmembrane protease serine 9	184	2.84E-16	53.20%	0.106	IPR002172 (SMART); IPR001254 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
1031	266550_length_551_cvg_3.0_tip_1_3	16	von willebrand factor	184	1.07E-10	47.20%	0.12	IPR001846 (PFAM); PTHR11339 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001846 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1033	266666_length_552_cvg_80.8_tip_1_3	4434	glyceraldehyde 3-phosphate dehydrogenase	184	3.14E-12	90.80%	0.128	IPR020831 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1034	266750_length_552_cvg_3.2_tip_1_4	17	cytochrome p450 2u1-like	184	2.24E-58	67.40%	0.666 Y	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300 (PANTHER); SignalP-noTM (SIGNALP_EUK); IPR001128 (SUPERFAMILY)
1035	266754_length_552_cvg_3.8_tip_1_5	28	fibronectin type 3 and ankyrin repeat domains protein 1	184	2.95E-42	69.50%	0.455 Y	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); PTHR24183:SF1 (PANTHER); PTHR24183 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR020683 (SUPERFAMILY)

1036	266804_length_553_cvg_17.0_tip_1_3	120	fatty acid binding protein	185	2.55E-54	75.10%	0.157	IPR000463 (PRINTS); IPR012674 (G3DSA:2.40.128.GENE3D); IPR000566 (PFAM); PTHR11955 (PANTHER); IPR000463 (PROSITE_PATTERNS); IPR011038 (SUPERFAMILY)
1037	267028_length_555_cvg_4.0_tip_1_4	25	isoform b	185	1.17E-11	63.20%	0.116	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF94 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
1038	267034_length_555_cvg_2.0_tip_1_2	13	deleted in autism protein 1 homolog	185	1.74E-34	54.40%	0.114	IPR022049 (PFAM); PTHR32073 (PANTHER); PTHR32073:SF7 (PANTHER); IPR020519 (PRODOM)
1039	267106_length_556_cvg_2.0_tip_1_2	12	CG4553	185	2.82E-24	61.70%	0.142	Coil (COILS); Coil (COILS); IPR010487 (PFAM); PTHR21133 (PANTHER); PTHR21133:SF0 (PANTHER)
1040	267130_length_556_cvg_2.5_tip_1_5	14	#NAME?	185	3.12E-84	79.80%	0.124	G3DSA:3.40.50.2000 (GENE3D); IPR023214 (G3DSA:3.40.50.GENE3D); IPR001830 (PFAM); PTHR10788:SF6 (PANTHER); PTHR10788 (PANTHER); SSF53756 (SUPERFAMILY)
1041	267146_length_556_cvg_5.0_tip_1_2	34	sco- partial	185	1.40E-33	61.20%	0.148	IPR000421 (SMART); IPR000421 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); PTHR24543 (PANTHER); IPR000421 (PROSITE_PATTERNS); IPR000421 (PROSITE_PROFILES); IPR008979 (SUPERFAMILY)
1042	267160_length_556_cvg_2.0_tip_1_5	14	zinc finger protein 184-like	185	1.97E-43	64.80%	0.115	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1044	267644_length_560_cvg_2.0_tip_1_2	15	intersectin-2 isoform x1	186	3.34E-66	75.00%	0.107	IPR001452 (PRINTS); PR00499 (PRINTS); IPR001452 (SMART); IPR001452 (PFAM); G3DSA:2.30.30.40 (GENE3D); G3DSA:2.30.30.40 (GENE3D); PTHR11216:SF59 (PANTHER); PTHR11216 (PANTHER); IPR001452 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); IPR001452 (SUPERFAMILY)
1045	267646_length_560_cvg_3.1_tip_1_5	21	ectonucleotide pyrophosphatase phosphodiesterase family member 6	186	5.03E-43	58.10%	0.1	IPR017849 (G3DSA:3.40.720.GENE3D); IPR002591 (PFAM); IPR024873 (PANTHER); IPR017850 (SUPERFAMILY)
1043	267468_length_559_cvg_2.0_tip_1_3	12	protein cbfa2t1-like isoform x5	187	2.77E-69	78.30%	0.125	Coil (COILS); Coil (COILS); IPR013289 (PRINTS); IPR002893 (PFAM); PTHR10379 (PANTHER); IPR002893 (PROSITE_PATTERNS); IPR002893 (PROSITE_PROFILES); SSF144232 (SUPERFAMILY)
1046	267704_length_561_cvg_8.2_tip_1_4	43	reticulocalbin-2	187	1.36E-45	69.90%	0.412 Y	IPR011992 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR10827:SF48 (PANTHER); PTHR10827 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)
1047	267760_length_561_cvg_3.2_tip_1_0	21	zinc finger protein 628 isoform x1	187	9.99E-16	57.20%	0.137	Coil (COILS); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1048	267766_length_561_cvg_2.9_tip_1_4	23	hornerin isoform x2	187	4.62E-18	46.80%	0.141	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1049	267780_length_561_cvg_2.9_tip_1_1	18	elastase 2b	187	7.99E-22	55.40%	0.099	G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
1051	267848_length_562_cvg_50.9_tip_1_4	742	hemagglutinin amebocyte aggregation factor-like	187	2.70E-10	72.20%	0.108	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1052	267910_length_562_cvg_2.0_tip_1_5	16	upf0764 protein c1orf89 homolog	187	2.71E-21	52.20%	0.183	no IPS match
1053	267914_length_562_cvg_4.2_tip_1_5	31	dentin sialophosphoprotein isoform x1	187	5.39E-40	59.30%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1050	267828_length_562_cvg_2.0_tip_1_0	15	zinc finger protein 77-like	188	9.68E-15	65.90%	0.118	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1054	268168_length_565_cvg_2.0_tip_1_4	14	17-beta-hydroxysteroid dehydrogenase type partial	188	2.18E-80	72.20%	0.106	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316 (PANTHER); PTHR24316:SF215 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
1055	268356_length_567_cvg_2.0_tip_1_1	11	adp-ribosylation factor-like protein 3-like	189	2.15E-72	67.00%	0.329	IPR006689 (PRINTS); IPR024156 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711:SF15 (PANTHER); PTHR11711 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1056	268400_length_567_cvg_4.0_tip_1_3	28	carboxypeptidase a2-like	189	3.15E-35	59.00%	0.642 Y	G3DSA:3.40.630.10 (GENE3D); IPR003146 (G3DSA:3.30.70.GENE3D); IPR000834 (PFAM); IPR003146 (PFAM); PTHR11705 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR009020 (SUPERFAMILY); SSF53187 (SUPERFAMILY)
1057	268548_length_568_cvg_3.0_tip_1_1	21	protein toll	189	6.89E-26	49.90%	0.909 Y	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SSF52058 (SUPERFAMILY)
1060	268704_length_569_cvg_56.5_tip_1_5	2643	ubiquitin-40s ribosomal protein s27a-like	189	3.41E-94	96.10%	0.244	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR002906 (PFAM); IPR000626 (PFAM); PTHR10666:SF99 (PANTHER); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR011332 (SUPERFAMILY)
1058	268584_length_568_cvg_6.9_tip_1_3	49	contactin-associated protein like 5-1	190	2.81E-69	73.70%	0.103	G3DSA:2.10.25.10 (GENE3D); PTHR10127:SF346 (PANTHER); PTHR10127 (PANTHER); IPR000742 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
1059	268676_length_569_cvg_8.6_tip_1_0	52	epithelial chloride channel partial	190	6.47E-34	63.10%	0.138	IPR013642 (PFAM); PTHR10579:SF8 (PANTHER); PTHR10579 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1061	268728_length_570_cvg_6.4_tip_1_1	40	dna-directed rna polymerase ii subunit rpb1	190	4.36E-07	53.00%	0.104	PR01217 (PRINTS)
1062	268848_length_571_cvg_5.5_tip_1_1	30	adenosine deaminase cecr1	190	1.83E-57	62.90%	0.157	G3DSA:3.20.20.140 (GENE3D); IPR001365 (PFAM); PTHR11409:SF39 (PANTHER); PTHR11409 (PANTHER); SSF51556 (SUPERFAMILY)
1063	268930_length_571_cvg_3.0_tip_1_3	21	hemocyte protein-glutamine gamma-glutamyltransferase-like	191	3.27E-79	76.50%	0.105	IPR013783 (G3DSA:2.60.40.GENE3D); IPR002931 (PFAM); IPR002931 (G3DSA:3.90.260.GENE3D); IPR023608 (PANTHER); PTHR11590:SF40 (PANTHER); SSF54001 (SUPERFAMILY)
1064	268934_length_572_cvg_2.0_tip_1_0	19	transforming growth factor-beta-induced protein ig-h3-like	191	7.07E-82	66.00%	0.102	IPR000782 (SMART); IPR000782 (PFAM); IPR000782 (G3DSA:2.30.180.GENE3D); PTHR10900:SF73 (PANTHER); PTHR10900 (PANTHER); IPR011489 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY)
1065	269042_length_572_cvg_4.3_tip_1_3	28	hemagglutinin	191	4.34E-27	54.60%	0.175	G3DSA:2.60.120.380 (GENE3D); G3DSA:1.10.390.10 (GENE3D); IPR001570 (PFAM); IPR007280 (PFAM); SSF55486 (SUPERFAMILY)
1066	269072_length_573_cvg_2.9_tip_1_5	20	sucrase- intestinal	191	2.23E-33	57.80%	0.103	PTHR22762 (PANTHER); PTHR22762:SF7 (PANTHER); IPR011013 (SUPERFAMILY)
1067	269194_length_574_cvg_2.0_tip_1_1	15	collagen-like protein	191	3.82E-19	46.40%	0.12	no IPS match
1068	269194_length_574_cvg_2.0_tip_1_4	15	collagen alpha-1 chain	191	1.56E-27	57.60%	0.128	IPR008160 (PFAM); PTHR24023 (PANTHER)
1069	269224_length_574_cvg_14.0_tip_1_3	88	serine protease nudel-like	192	6.28E-07	52.00%	0.102	IPR002172 (SMART); IPR003014 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:3.50.4.10 (GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
1070	269402_length_576_cvg_3.0_tip_1_1	24	myosin heavy chain variant c	192	5.05E-113	98.50%	0.112	Coil (COILS); Coil (COILS); IPR002928 (PFAM); PTHR13140 (PANTHER); PTHR13140:SF364 (PANTHER); SSF57997 (SUPERFAMILY)
1071	269534_length_577_cvg_4.0_tip_1_2	33	hypothetical protein KGM_21983	192	1.03E-41	57.70%	0.114	IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)

1072	269592_length_577_cvg_2.0_tip_1_5	13	zinc finger protein ozf	192	3.86E-79	59.30%	0.103	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1074	269632_length_578_cvg_3.0_tip_1_5	23	protein kinase c epsilon partial	192	1.06E-127	95.50%	0.096	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24357:SF73 (PANTHER); PTHR24357 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1075	269690_length_578_cvg_47.9_tip_1_2	228	---NA---	192			0.182	TMhelix (TMHMM); TMhelix (TMHMM)
1073	269610_length_578_cvg_5.1_tip_1_4	30	cell recognition protein caspr4 isoform 5	193	1.88E-39	55.60%	0.13	PTHR10127 (PANTHER); PTHR10127:SF575 (PANTHER)
1076	269710_length_579_cvg_5.1_tip_1_4	41	isoform b	193	6.99E-89	76.30%	0.681 Y	IPR002172 (SMART); IPR002557 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002557 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF136 (PANTHER); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002557 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1077	269718_length_579_cvg_2.0_tip_1_2	15	endothelin-converting enzyme 1-like	193	3.31E-44	53.20%	0.106	IPR018497 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR11733:SF124 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
1078	269724_length_579_cvg_9.0_tip_1_3	63	perlucin-like protein	193	7.30E-22	54.70%	0.137	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
1079	269776_length_579_cvg_3.0_tip_1_3	26	spermatogenesis-associated protein 20	193	4.65E-58	80.90%	0.134	IPR012336 (G3DSA:3.40.30.GENE3D); IPR004879 (PFAM); PTHR12145 (PANTHER); PTHR12145:SF11 (PANTHER); IPR012336 (SUPERFAMILY)
1080	269816_length_580_cvg_3.7_tip_1_2	26	lysosomal pro-x carboxypeptidase	193	2.83E-80	71.10%	0.244	IPR008758 (PFAM); IPR008758 (PANTHER); PTHR11010:SF11 (PANTHER)
1081	269822_length_580_cvg_65.2_tip_1_2	6630	cathepsin l1-like	193	2.65E-76	80.70%	0.101	IPR000668 (SMART); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF265 (PANTHER); IPR013128 (PANTHER); IPR025661 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
1083	269944_length_581_cvg_34.0_tip_1_2	296	histone h2a-like	193	1.03E-79	97.30%	0.316	IPR002119 (PRINTS); IPR002119 (SMART); IPR007125 (PFAM); IPR009072 (G3DSA:1.10.20.GENE3D); PTHR23430:SF45 (PANTHER); PTHR23430 (PANTHER); IPR002119 (PROSITE_PATTERNS); IPR009072 (SUPERFAMILY)
1082	269942_length_581_cvg_5.5_tip_1_3	44	39s ribosomal protein mitochondrial	194	5.45E-83	74.20%	0.102	IPR008914 (G3DSA:3.90.280.GENE3D); IPR008914 (PFAM); PTHR11362 (PANTHER); PTHR11362:SF16 (PANTHER); IPR008914 (SUPERFAMILY)
1084	270030_length_582_cvg_7.0_tip_1_4	53	ankyrin repeat partial	194	6.68E-37	60.40%	0.115	IPR002110 (SMART); PF13637 (PFAM); PF13857 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1085	270168_length_583_cvg_2.0_tip_1_4	16	cysteine-rich with egf-like domain protein 2	194	1.75E-73	69.60%	0.109	G3DSA:2.170.300.10 (GENE3D); IPR001881 (PFAM); PTHR24838:SF13 (PANTHER); PTHR24838 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
1086	270176_length_584_cvg_4.0_tip_1_1	27	adrenodoxin-like mitochondrial	195	1.44E-77	85.00%	0.191	IPR001055 (PRINTS); IPR001041 (PFAM); IPR012675 (G3DSA:3.10.20.GENE3D); PTHR23426 (PANTHER); PTHR23426:SF1 (PANTHER); IPR018298 (PROSITE_PATTERNS); IPR001041 (PROSITE_PROFILES); IPR001041 (SUPERFAMILY)
1087	270184_length_584_cvg_2.0_tip_1_0	20	ankyrin repeat domain-containing protein 39	195	5.24E-54	67.50%	0.221	IPR002110 (SMART); PF13637 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PF13857 (PFAM); PTHR24148 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)

1088	270266_length_585_cvg_19.7_tip_1_2	146	adiponectin receptor protein	195	8.19E-56	83.30%	0.204	IPR004254 (PFAM); PTHR20855:SF15 (PANTHER); IPR004254 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1089	270294_length_585_cvg_2.2_tip_1_1	15	guanine nucleotide-binding protein subunit beta-5	195	3.14E-128	93.20%	0.107	IPR020472 (PRINTS); IPR001632 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR016346 (PANTHER); PTHR19850:SF12 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1090	270364_length_585_cvg_14.5_tip_1_4	104	iron zinc purple acid phosphatase-like partial	195	3.79E-62	71.20%	0.27	IPR003961 (PFAM); IPR015914 (G3DSA:2.60.40.GENE3D); IPR029052 (G3DSA:3.60.21.GENE3D); IPR018946 (PFAM); PTHR22953 (PANTHER); PTHR22953:SF9 (PANTHER); IPR008963 (SUPERFAMILY); TMhelix (TMHMM)
1091	270476_length_587_cvg_7.2_tip_1_2	48	alpha-mannosidase 2x	195	6.13E-98	81.50%	0.102	IPR000602 (PFAM); IPR027291 (G3DSA:3.20.110.GENE3D); PTHR11607 (PANTHER); PTHR11607:SF4 (PANTHER); IPR011330 (SUPERFAMILY)
1092	270540_length_587_cvg_2.3_tip_1_4	23	zinc finger protein 1 homolog	196	1.28E-16	54.10%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1093	270670_length_589_cvg_4.0_tip_1_2	31	tkl protein kinase	196	3.95E-44	54.30%	0.098	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1094	270678_length_589_cvg_3.9_tip_1_1	23	adenylate cyclase type 9	196	2.06E-52	84.20%	0.254	IPR001054 (PFAM); IPR001054 (G3DSA:3.30.70.GENE3D); PTHR11920:SF272 (PANTHER); PTHR11920 (PANTHER); IPR018297 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001054 (PROSITE_PROFILES); IPR029787 (SUPERFAMILY); TMhelix (TMHMM)
1095	270730_length_589_cvg_4.2_tip_1_1	26	gastrula zinc finger isoform x1	196	6.55E-63	68.50%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1098	270758_length_590_cvg_2.0_tip_1_5	12	collagen alpha-1 chain	196	6.42E-45	59.30%	0.103	IPR008160 (PFAM); PTHR24023 (PANTHER)
1100	270820_length_590_cvg_3.4_tip_1_5	23	low-density lipoprotein receptor-related protein 2	196	2.28E-94	83.90%	0.102	IPR000742 (SMART); IPR001881 (SMART); IPR002172 (SMART); IPR026823 (PFAM); IPR002172 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10529 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
1096	270744_length_589_cvg_5.7_tip_1_0	33	disks large 1 tumor suppressor protein	197	1.15E-86	86.60%	0.113	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); IPR016313 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
1097	270758_length_590_cvg_2.0_tip_1_1	12	c protein immunoglobulin-a-binding beta antigen	197	4.79E-27	43.80%	0.138	PTHR24023 (PANTHER); PTHR24023:SF405 (PANTHER)
1099	270790_length_590_cvg_48.9_tip_0_3	299	amine oxidase	197	1.03E-67	70.70%	0.112	IPR001613 (PRINTS); IPR002937 (PFAM); G3DSA:3.90.660.10 (GENE3D); PTHR10742 (PANTHER); PTHR10742:SF253 (PANTHER); SSF54373 (SUPERFAMILY); SSF51905 (SUPERFAMILY)

1113	271624_length_599_cvg_4.5_tip_1_0	39	aael003561- partial	200	2.18E-26	51.80%	0.263	IPR001211 (PRINTS); IPR016090 (SMART); IPR016090 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR11716:SF45 (PANTHER); IPR001211 (PANTHER); IPR013090 (PROSITE_PATTERNS); IPR013090 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016090 (SUPERFAMILY); TMhelix (TMHMM)
1114	271688_length_600_cvg_5.0_tip_1_0	43	zinc finger protein ozf-like isoform x2	200	5.58E-40	60.00%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1115	271696_length_600_cvg_3.8_tip_1_4	28	contactin-associated 2 precursor	200	3.85E-29	53.20%	0.104	IPR008983 (G3DSA:2.60.120.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); IPR001073 (PFAM); PTHR10127:SF575 (PANTHER); PTHR10127 (PANTHER); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY); IPR002181 (SUPERFAMILY)
1116	271758_length_600_cvg_59.4_tip_1_4	718	plasminogen activator spa	200	1.63E-36	56.40%	0.444 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1117	271804_length_601_cvg_3.5_tip_1_2	21	heat shock protein 70	200	1.86E-22	74.80%	0.1	IPR029048 (G3DSA:1.20.1270.GENE3D); PTHR19375 (PANTHER); PTHR19375:SF155 (PANTHER); IPR029048 (SUPERFAMILY)
1118	271810_length_601_cvg_14.8_tip_1_5	110	plasminogen activator spa	200	5.36E-28	55.50%	0.366 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1119	271856_length_602_cvg_73.4_tip_1_3	5433	cathepsin l2 cysteine protease	201	9.07E-62	68.60%	0.348 Y	IPR000668 (SMART); IPR013201 (SMART); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR013201 (PFAM); PTHR12411:SF57 (PANTHER); IPR013128 (PANTHER); IPR000169 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY)
1120	271870_length_602_cvg_3.9_tip_1_3	33	sucrase- intestinal-like	201	1.31E-43	70.40%	0.298	IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF7 (PANTHER); IPR017853 (SUPERFAMILY)
1121	271922_length_602_cvg_2.0_tip_1_3	14	tolloid-like protein 2 isoform x1	201	9.01E-73	68.50%	0.132	IPR002172 (SMART); IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10127:SF557 (PANTHER); PTHR10127 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1122	272074_length_604_cvg_4.0_tip_1_4	38	sortilin-related receptor-like	201	2.84E-66	66.20%	0.131	PTHR12106 (PANTHER); PTHR12106:SF7 (PANTHER)
1123	272226_length_606_cvg_7.5_tip_1_3	53	nf-kappa-b inhibitor	202	8.37E-63	66.20%	0.143	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24139 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1125	272328_length_607_cvg_5.6_tip_1_2	44	mitochondrial import inner membrane translocase subunit tim13	202	9.92E-44	86.30%	0.171	IPR004217 (PFAM); IPR004217 (G3DSA:1.10.287.GENE3D); PTHR19338 (PANTHER); IPR004217 (SUPERFAMILY)
1126	272382_length_607_cvg_17.8_tip_1_2	138	myotrophin-like isoform 2	202	1.51E-55	84.20%	0.14	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24152 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)

1138	273030_length_615_cvg_20.8_tip_1_0	107	protein shifted	205	6.42E-19	68.90%	0.105	IPR000742 (SMART); G3DSA:2.170.300.10 (GENE3D); IPR013032 (PFAM); PTHR24838 (PANTHER); PTHR24838:SF276 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES)
1139	273038_length_615_cvg_2.0_tip_1_3	21	c-type lectin domain family 4 member g-like isoform x2	205	1.56E-09	45.80%	0.112	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
1140	273040_length_615_cvg_4.9_tip_1_3	42	glucose dehydrogenase	205	5.11E-55	68.70%	0.156	IPR000172 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); IPR000172 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
1141	273046_length_615_cvg_2.0_tip_1_3	13	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphex133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	205	2.16E-92	68.80%	0.113	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1142	273062_length_615_cvg_2.0_tip_1_2	19	leukotriene a-4 hydrolase	205	1.28E-71	73.10%	0.135	IPR014782 (PRINTS); IPR014782 (PFAM); PTHR11533:SF4 (PANTHER); IPR001930 (PANTHER); SSF63737 (SUPERFAMILY)
1143	273112_length_616_cvg_9.4_tip_1_1	81	---NA---	205			0.118	no IPS match
1144	273200_length_617_cvg_3.0_tip_1_5	22	serine protease snake	205	3.67E-14	54.50%	0.143	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF81 (PANTHER); PTHR24268 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
1145	273282_length_618_cvg_60.2_tip_1_0	468	thioredoxin peroxidase 2	206	5.01E-10	85.60%	0.101	IPR012336 (G3DSA:3.40.30.GENE3D); IPR019479 (PFAM); PTHR10681 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (SUPERFAMILY)
1146	273362_length_618_cvg_36.4_tip_1_3	223	type iv secretion protein	206	3.40E-23	45.50%	0.206	no IPS match
1147	273366_length_618_cvg_3.0_tip_1_5	25	epithelial chloride channel partial	206	3.63E-15	48.40%	0.099	IPR002035 (G3DSA:3.40.50.GENE3D); PTHR10579:SF8 (PANTHER); PTHR10579 (PANTHER); IPR002035 (SUPERFAMILY)
1148	273368_length_619_cvg_5.9_tip_1_5	48	trypsinogen 1	206	1.73E-39	58.60%	0.215	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1149	273384_length_619_cvg_3.0_tip_1_0	23	map kinase-activated protein kinase 2	207	2.99E-102	87.70%	0.126	IPR002290 (SMART); IPR027442 (G3DSA:4.10.1170.GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24349 (PANTHER); PTHR24349:SF63 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1150	273412_length_619_cvg_3.0_tip_1_0	23	alpha-mannosidase 2	207	7.43E-117	84.10%	0.104	IPR000602 (PFAM); IPR027291 (G3DSA:3.20.110.GENE3D); PTHR11607 (PANTHER); PTHR11607:SF22 (PANTHER); IPR011330 (SUPERFAMILY)
1151	273486_length_620_cvg_4.2_tip_1_0	38	sortilin-related I(dlr class) a repeats-containing-like isoform x2	207	5.88E-72	66.40%	0.101	PTHR12106 (PANTHER); PTHR12106:SF7 (PANTHER)
1152	273576_length_621_cvg_3.0_tip_1_3	19	receptor-type tyrosine-protein phosphatase partial	207	2.10E-17	51.50%	0.2	IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1153	273602_length_621_cvg_8.1_tip_1_4	62	leucine-rich repeat-containing protein 57	207	4.16E-72	77.70%	0.099	IPR003591 (SMART); IPR025875 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR23155 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)

1154	273632_length_622_cvg_3.2_tip_1_4	24	lysosomal pro-x carboxypeptidase	207	2.86E-82	72.00%	0.105	IPR008758 (PFAM); IPR008758 (PANTHER); PTHR11010:SF11 (PANTHER); IPR029058 (SUPERFAMILY)
1155	273726_length_623_cvg_3.4_tip_1_5	26	limulus clotting factor partial	207	4.36E-28	50.70%	0.122	G3DSA:2.40.10.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR026823 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1156	273824_length_624_cvg_2.0_tip_1_4	18	ryanodine receptor 44f	208	1.61E-96	83.10%	0.113	IPR003032 (PFAM); IPR003877 (PFAM); IPR015925 (PANTHER); PTHR13715:SF74 (PANTHER); IPR001870 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
1157	273856_length_625_cvg_2.0_tip_1_1	18	receptor-type tyrosine-protein phosphatase f	208	4.51E-81	78.80%	0.1	PR00014 (PRINTS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
1158	274000_length_627_cvg_2.0_tip_1_0	13	tyrosine-protein kinase btk29a isoform x3	209	5.10E-126	92.10%	0.112	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24418 (PANTHER); PTHR24418:SF162 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1159	274060_length_627_cvg_7.5_tip_1_3	53	venom carboxylesterase-6-like	209	2.91E-50	52.30%	0.104	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559:SF198 (PANTHER); PTHR11559 (PANTHER); IPR029058 (SUPERFAMILY)
1182	275450_length_645_cvg_8.7_tip_1_5	56	protoporphyrin ix magnesium chelatase	209	2.64E-17	60.20%	0.12	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1160	274216_length_629_cvg_3.0_tip_1_3	27	latrophilin-3- partial	210	1.85E-18	60.70%	0.162	IPR000832 (PFAM); PTHR12011:SF222 (PANTHER); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1161	274290_length_630_cvg_7.8_tip_1_0	61	spondin-1-like	210	1.54E-79	68.50%	0.233	IPR000884 (SMART); IPR000884 (PFAM); IPR009465 (PFAM); G3DSA:2.20.100.10 (GENE3D); PTHR11311 (PANTHER); IPR009465 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY)
1162	274328_length_630_cvg_6.3_tip_1_5	56	peptidyl-prolyl cis-trans isomerase-like 1	210	2.55E-79	92.50%	0.103	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1163	274382_length_631_cvg_3.0_tip_1_4	29	serine threonine-protein kinase sgk1 isoform x1	210	1.55E-122	89.00%	0.097	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24356 (PANTHER); PTHR24356:SF121 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1164	274388_length_631_cvg_22.1_tip_1_2	146	cytochrome p450 partial	210	2.37E-54	67.70%	0.1	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24305 (PANTHER); PTHR24305:SF49 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
1165	274394_length_631_cvg_5.1_tip_1_2	40	xanthine dehydrogenase	210	4.81E-81	83.40%	0.178	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)
1166	274404_length_631_cvg_5.3_tip_1_4	27	---NA---	210			0.118	Coil (COILS)
1167	274430_length_632_cvg_37.4_tip_1_2	330	poly -specific endoribonuclease homolog	210	1.38E-57	65.90%	0.116	IPR018998 (PFAM); PTHR12439 (PANTHER); SSF142877 (SUPERFAMILY)
1168	274538_length_633_cvg_8.0_tip_1_5	59	von willebrand factor a domain-containing protein 8-like	211	9.92E-48	80.70%	0.116	IPR011704 (PFAM); PTHR21610:SF9 (PANTHER); PTHR21610 (PANTHER)
1170	274602_length_634_cvg_3.9_tip_1_5	37	aael005189- partial	211	3.12E-80	69.20%	0.115	IPR003112 (SMART); IPR003112 (PFAM); PTHR23192 (PANTHER); PTHR23192:SF33 (PANTHER); IPR003112 (PROSITE_PROFILES); SSF50993 (SUPERFAMILY)
1171	274662_length_634_cvg_4.1_tip_1_5	33	pdz domain-containing protein 11	211	2.10E-52	76.90%	0.106	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR14063 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
1169	274598_length_634_cvg_23.2_tip_1_0	125	alpha-n-acetylgalactosaminidase isoform x4	212	4.66E-92	85.50%	0.15	IPR002241 (PRINTS); IPR000111 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); PTHR11452 (PANTHER); PTHR11452:SF23 (PANTHER); IPR000111 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY)

1172	274828_length_637_cvg_12.8_tip_1_2	84	trypsin-like serine proteinase	212	1.81E-54	60.50%	0.285	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1173	274938_length_638_cvg_8.5_tip_1_2	67	coatomer subunit beta partial	212	5.30E-143	95.20%	0.11	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19876 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1175	275080_length_640_cvg_50.8_tip_1_2	314	muscle-specific protein 20	213	2.06E-84	86.10%	0.464 Y	IPR003096 (PRINTS); IPR001997 (PRINTS); IPR001715 (SMART); IPR000557 (PFAM); IPR001715 (PFAM); IPR001715 (G3DSA:1.10.418.GENE3D); PTHR18959 (PANTHER); PTHR18959:SF51 (PANTHER); IPR001715 (PROSITE_PROFILES); IPR000557 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR001715 (SUPERFAMILY)
1179	275192_length_641_cvg_86.6_tip_1_2	9375	chitinase partial	213	5.06E-80	75.60%	0.307	IPR011583 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1174	275060_length_640_cvg_10.5_tip_1_3	69	---NA---	214			0.145	no IPS match
1176	275116_length_641_cvg_3.7_tip_1_0	40	serine protease snake	214	5.86E-08	58.70%	0.103	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
1177	275146_length_641_cvg_2.5_tip_1_4	23	cysteine protease inhibitor	214	2.67E-21	50.60%	0.098	IPR000010 (SMART); IPR000010 (PFAM); G3DSA:3.10.450.10 (GENE3D); G3DSA:3.10.450.10 (GENE3D); PTHR11413:SF26 (PANTHER); IPR027214 (PANTHER); IPR018073 (PROSITE_PATTERNS); SSF54403 (SUPERFAMILY); SSF54403 (SUPERFAMILY)
1178	275170_length_641_cvg_2.0_tip_1_4	14	fibronectin type-iii domain-containing protein 3a-like isoform x5	214	1.52E-73	74.10%	0.143	PR00014 (PRINTS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19900 (PANTHER); PTHR19900:SF50 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
1180	275410_length_644_cvg_2.9_tip_1_4	26	eukaryotic translation initiation factor 2-alpha kinase partial	215	2.48E-79	72.00%	0.1	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR11042:SF86 (PANTHER); PTHR11042 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1181	275424_length_644_cvg_8.2_tip_1_4	54	tyrosine-protein kinase dnt-like	215	6.34E-114	83.10%	0.107	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR001245 (PFAM); PTHR24416 (PANTHER); PTHR24416:SF256 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1183	275488_length_646_cvg_35.0_tip_1_4	268	peptidase s8	215	3.24E-25	69.80%	0.378 Y	IPR007280 (PFAM); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TMhelix (TMHMM)
1184	275542_length_646_cvg_3.0_tip_1_2	23	thrombospondin type-1 domain-containing protein partial	215	8.02E-36	64.00%	0.125	IPR000884 (SMART); IPR010909 (PFAM); IPR000884 (PFAM); G3DSA:2.20.100.10 (GENE3D); PTHR13723 (PANTHER); IPR010909 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY)
1185	275630_length_648_cvg_2.4_tip_1_4	27	zinc finger protein 226-like	216	2.91E-30	58.00%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1186	275650_length_648_cvg_4.0_tip_1_2	32	lactase-phlorizin hydrolase-like	216	2.02E-71	67.50%	0.112	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001360 (PFAM); IPR001360 (PANTHER); IPR017853 (SUPERFAMILY)
1188	275706_length_649_cvg_5.0_tip_1_2	37	protein cbg06875	216	6.09E-17	62.10%	0.144	PTHR11660:SF46 (PANTHER); PTHR11660 (PANTHER)

1189	275756_length_649_cvg_64.9_tip_1_5	6486	cathepsin l2 cysteine protease	216	7.14E-64	69.10%	0.172	IPR000668 (SMART); IPR013201 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR013201 (PFAM); IPR000668 (PFAM); IPR013128 (PANTHER); PTHR12411:SF57 (PANTHER); IPR000169 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY)
1187	275700_length_649_cvg_3.6_tip_1_0	26	c3orf33 protein	217	6.65E-23	45.30%	0.15	IPR016071 (G3DSA:2.40.50.GENE3D); IPR016071 (SUPERFAMILY)
1190	275852_length_650_cvg_63.0_tip_0_0	869	kunitz bovine pancreatic trypsin inhibitor domain protein	217	2.58E-51	58.80%	0.11	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
1191	275932_length_651_cvg_7.5_tip_1_2	59	apolipoprotein d-like	217	3.65E-34	56.70%	0.213	IPR000566 (PFAM); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612 (PANTHER); PTHR10612:SF7 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011038 (SUPERFAMILY)
1192	275936_length_651_cvg_3.0_tip_1_3	22	low quality protein: maltase- intestinal-like	217	2.74E-54	59.90%	0.154	IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF76 (PANTHER); IPR017853 (SUPERFAMILY); SSF51011 (SUPERFAMILY)
1193	276038_length_653_cvg_5.6_tip_1_5	36	camp-dependent protein kinase catalytic subunit	217	3.28E-148	97.10%	0.109	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24353 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1194	276048_length_653_cvg_7.9_tip_1_0	68	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 3-like	218	2.94E-98	82.20%	0.147	IPR006620 (SMART); IPR005123 (PFAM); PTHR14650:SF1 (PANTHER); PTHR14650 (PANTHER); IPR005123 (PROSITE_PROFILES)
1195	276136_length_654_cvg_7.2_tip_1_0	56	chitinase 5 isoform x1	218	2.48E-57	57.30%	0.104	IPR002557 (SMART); IPR002557 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); IPR001223 (PFAM); IPR002557 (G3DSA:2.170.140.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF144 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY); IPR029070 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1196	276140_length_654_cvg_21.0_tip_1_1	169	epithelial chloride channel partial	218	3.29E-45	55.30%	0.131	IPR013642 (PFAM); PTHR10579:SF8 (PANTHER); PTHR10579 (PANTHER)
1197	276150_length_654_cvg_3.5_tip_1_1	26	gastrula zinc finger	218	2.51E-37	54.60%	0.097	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1198	276156_length_654_cvg_4.6_tip_1_4	34	basement membrane-specific heparan sulfate proteoglycan core partial	218	3.30E-24	66.40%	0.103	IPR003599 (SMART); IPR003598 (SMART); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
1199	276170_length_655_cvg_69.3_tip_1_5	2551	vp302_lycmc ame: full=venom protein 302 flags: precursor	218	2.68E-14	55.50%	0.779 Y	IPR011390 (PANTHER); PTHR14186:SF8 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR000867 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR009030 (SUPERFAMILY)
1200	276270_length_656_cvg_7.0_tip_1_3	53	fibrillin-2-like	219	7.63E-32	52.60%	0.1	PTHR24039:SF20 (PANTHER); IPR011398 (PANTHER)
1201	276334_length_657_cvg_12.8_tip_1_5	89	low-density lipoprotein receptor	219	1.29E-19	60.20%	0.132	IPR002172 (PRINTS); IPR002172 (SMART); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1202	276384_length_658_cvg_2.6_tip_1_2	19	neuroligin-2-like isoform x1	219	1.60E-88	76.30%	0.11	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559 (PANTHER); PTHR11559:SF157 (PANTHER); IPR029058 (SUPERFAMILY)
1203	276554_length_660_cvg_47.0_tip_1_5	372	hemagglutinin amebocyte aggregation factor-like	220	2.76E-30	57.60%	0.446 Y	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS)

1204	276570_length_660_cvg_3.5_tip_1_1	29	low quality protein: cubilin	220	8.05E-31	52.00%	0.122	IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
1205	276728_length_663_cvg_4.0_tip_1_5	34	neuropilin and tolloid-like protein 2	221	1.63E-74	65.50%	0.106	IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127:SF572 (PANTHER); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
1206	276758_length_663_cvg_54.6_tip_1_0	2120	chymotrypsin-like elastase family member 2a-like	221	1.37E-25	62.10%	0.176	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1207	276804_length_664_cvg_74.3_tip_1_1	10802	trypsin-like serine proteinase 2	221	3.95E-31	60.40%	0.154	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1228	277930_length_680_cvg_60.7_tip_1_3	1293	clotting factor b-like	221	3.75E-48	64.00%	0.105	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1208	276928_length_666_cvg_3.0_tip_1_2	27	cysteine proteinase	222	1.78E-30	54.60%	0.157	IPR000010 (SMART); G3DSA:3.10.450.10 (GENE3D); IPR000010 (PFAM); IPR027214 (PANTHER); IPR018073 (PROSITE_PATTERNS); IPR020381 (PRODOM); SSF54403 (SUPERFAMILY); SSF54403 (SUPERFAMILY)
1209	276934_length_666_cvg_6.8_tip_1_3	50	hyaluronidase-like	222	1.15E-49	57.00%	0.104	IPR018155 (PRINTS); IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PANTHER); PTHR11769:SF8 (PANTHER); IPR017853 (SUPERFAMILY)
1210	276950_length_666_cvg_3.3_tip_1_4	30	isoamyl acetate-hydrolyzing esterase 1 homolog	222	1.33E-70	66.90%	0.25	IPR001087 (PFAM); IPR013830 (G3DSA:3.40.50.GENE3D); PTHR14209 (PANTHER); IPR013830 (SUPERFAMILY)
1211	277028_length_667_cvg_22.9_tip_1_2	174	micos complex subunit mic27	222	7.69E-28	55.60%	0.173	IPR019166 (PFAM); PTHR14564:SF1 (PANTHER); PTHR14564 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1213	277066_length_667_cvg_26.0_tip_1_1	81	46 kda fk506-binding nuclear protein	222	1.21E-48	72.80%	0.106	G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); IPR023566 (PANTHER); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY)
1216	277102_length_668_cvg_8.0_tip_1_5	72	hemocyte protein-glutamine gamma-glutamyltransferase-like	222	6.63E-46	70.20%	0.11	IPR008958 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11590:SF40 (PANTHER); IPR023608 (PANTHER); IPR008958 (SUPERFAMILY); IPR008958 (SUPERFAMILY)
1212	277046_length_667_cvg_5.0_tip_1_0	40	uv radiation resistance-associated gene protein	223	5.43E-21	62.00%	0.123	Coil (COILS); PTHR15157 (PANTHER)
1214	277086_length_668_cvg_51.6_tip_1_1	527	epididymal secretory protein e1	223	8.15E-31	57.80%	0.423 Y	IPR003172 (SMART); IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014756 (SUPERFAMILY); TMhelix (TMHMM)
1215	277092_length_668_cvg_5.0_tip_1_0	41	beta- -galactosyltransferase 7	223	1.48E-102	81.60%	0.171	IPR003859 (PRINTS); IPR027995 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR003859 (PANTHER); PTHR19300:SF1 (PANTHER); IPR029044 (SUPERFAMILY)
1217	277232_length_670_cvg_2.0_tip_1_2	22	irregular chiasm c-roughest protein isoform x1	223	2.14E-92	76.00%	0.099	IPR003598 (SMART); IPR013162 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11640:SF54 (PANTHER); PTHR11640 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1218	277238_length_670_cvg_16.1_tip_1_5	152	thermolysin catalytic domain partial	223	1.66E-12	48.10%	0.367 Y	IPR025711 (PFAM); IPR011096 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1219	277258_length_670_cvg_4.1_tip_1_1	42	n-acetyllactosaminide 3-alpha-galactosyltransferase	223	1.49E-21	63.90%	0.441 Y	IPR029044 (G3DSA:3.90.550.GENE3D); IPR027995 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)

1220	277324_length_671_cvg_2.1_tip_1_0	17	von willebrand factor type egf and pentraxin domain-containing protein partial	224	6.63E-53	53.40%	0.116	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1221	277442_length_674_cvg_3.0_tip_1_3	27	abnormal spindle-like microcephaly-associated protein homolog	225	3.54E-67	65.10%	0.112	IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19900 (PANTHER); PTHR19900:SF44 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1222	277456_length_674_cvg_2.2_tip_1_4	23	fizzy-related protein homolog	225	2.58E-142	95.40%	0.1	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19918:SF6 (PANTHER); PTHR19918 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR011047 (SUPERFAMILY)
1223	277470_length_674_cvg_62.7_tip_1_3	19099	nidogen-2 isoform x5	225	6.59E-23	54.70%	0.653 Y	IPR000716 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PFAM); IPR022339 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY)
1224	277728_length_677_cvg_5.0_tip_1_2	40	ecto-nox disulfide-thiol exchanger 2	225	5.74E-39	69.60%	0.103	PTHR16001 (PANTHER)
1225	277738_length_678_cvg_5.7_tip_1_2	51	all-trans-retinol -reductase	226	1.15E-76	70.70%	0.311	PF13450 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR10668:SF61 (PANTHER); PTHR10668 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
1226	277760_length_678_cvg_40.4_tip_1_1	601	mucin-5ac- partial	226	1.67E-10	49.40%	0.28	IPR025155 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1227	277768_length_678_cvg_63.4_tip_1_4	781	thioredoxin peroxidase	226	4.64E-112	90.60%	0.116	IPR012336 (G3DSA:3.40.30.GENE3D); IPR000866 (PFAM); IPR019479 (PFAM); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1229	277944_length_681_cvg_61.3_tip_1_2	2140	hypothetical protein DAPPUDRAFT_312473	227	1.89E-07	65.00%	0.101	IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); PTHR10334:SF153 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1230	277960_length_681_cvg_3.1_tip_1_4	25	probable serine carboxypeptidase cpvl	227	2.60E-50	59.00%	0.116	IPR001563 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); IPR001563 (PANTHER); PTHR11802:SF30 (PANTHER); IPR018202 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
1231	277968_length_681_cvg_8.9_tip_1_2	64	cytochrome p450 partial	227	1.34E-66	67.10%	0.146	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24305:SF49 (PANTHER); PTHR24305 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY)
1232	277970_length_681_cvg_2.9_tip_1_5	27	cub and sushi domain-containing protein 3-like	227	9.30E-09	47.20%	0.278	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); PTHR22991:SF23 (PANTHER); PTHR22991 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
1233	277972_length_681_cvg_3.0_tip_1_1	28	ectonucleotide pyrophosphatase phosphodiesterase family member 7-like	227	1.77E-62	57.50%	0.098	IPR002591 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); IPR024873 (PANTHER); IPR017850 (SUPERFAMILY)
1234	277984_length_681_cvg_3.4_tip_1_1	29	rna polymerase ii-associated protein 3	227	3.45E-28	52.90%	0.124	Coil (COILS); IPR019734 (SMART); PF13414 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR22904 (PANTHER); PTHR22904:SF292 (PANTHER); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY)

1235	278004_length_681_cvg_5.0_tip_1_4	45	low-density lipoprotein receptor-related protein 2	227	2.23E-38	57.20%	0.101	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1236	278014_length_681_cvg_5.0_tip_1_0	41	phenoloxidase subunit a3-like	227	3.51E-47	62.50%	0.098	IPR005203 (PFAM); IPR005203 (G3DSA:2.60.40.GENE3D); IPR013788 (PANTHER); PTHR11511:SF24 (PANTHER); IPR014756 (SUPERFAMILY)
1237	278134_length_683_cvg_5.9_tip_1_1	40	camp-dependent protein kinase catalytic	228	3.25E-124	86.40%	0.106	IPR000961 (SMART); IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR017892 (PFAM); IPR000719 (PFAM); PTHR24357:SF70 (PANTHER); PTHR24357 (PANTHER); IPR000961 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1238	278136_length_683_cvg_3.8_tip_1_3	29	low quality protein: abc transporter f family member 4-like	228	2.42E-08	55.00%	0.112	Coil (COILS); Coil (COILS)
1239	278138_length_683_cvg_45.1_tip_1_1	471	macrophage migration inhibitory factor	228	2.90E-39	69.80%	0.114	G3DSA:3.30.429.10 (GENE3D); IPR001398 (PFAM); PTHR11954:SF6 (PANTHER); IPR001398 (PANTHER); IPR001398 (PRODOM); IPR014347 (SUPERFAMILY)
1240	278320_length_686_cvg_4.5_tip_1_5	36	serine protease mitochondrial	228	8.85E-98	78.00%	0.11	IPR001940 (PRINTS); G3DSA:2.40.10.10 (GENE3D); PF13365 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR22939 (PANTHER); IPR009003 (SUPERFAMILY)
1241	278328_length_686_cvg_21.9_tip_1_0	169	guanine nucleotide-binding protein g g subunit beta-1	229	3.32E-122	97.80%	0.125	Coil (COILS); IPR001632 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR016346 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1242	278344_length_686_cvg_3.0_tip_1_3	26	protein gdap2 homolog	229	2.99E-83	73.20%	0.106	IPR002589 (SMART); G3DSA:3.40.220.10 (GENE3D); IPR002589 (PFAM); PTHR11106 (PANTHER); PTHR11106:SF59 (PANTHER); IPR002589 (PROSITE_PROFILES); SSF52949 (SUPERFAMILY)
1243	278366_length_687_cvg_6.4_tip_1_0	51	keratin-associated protein 5-9-like	229	2.20E-12	67.30%	0.095	no IPS match
1244	278438_length_688_cvg_6.7_tip_1_4	52	otopetrin-2 isoform x1	229	1.29E-84	77.70%	0.142	IPR004878 (PFAM); IPR004878 (PANTHER); PTHR21522:SF37 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1245	278582_length_690_cvg_3.0_tip_1_1	28	chondroitin sulfate	230	3.87E-72	69.60%	0.101	IPR008428 (PFAM); PTHR12369:SF11 (PANTHER); PTHR12369 (PANTHER)
1246	278628_length_690_cvg_79.7_tip_1_0	4134	dermatopontin 2	230	3.28E-38	58.90%	0.25	PF14704 (PFAM); IPR026645 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TMhelix (TMHMM)
1247	278632_length_690_cvg_21.0_tip_1_5	182	diuretic hormone class 2-like	230	1.39E-29	73.30%	0.15	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1248	278780_length_693_cvg_2.9_tip_1_3	28	very low-density lipoprotein receptor-like isoform x1	231	2.34E-19	43.60%	0.101	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1249	278786_length_693_cvg_39.0_tip_1_3	311	cytosolic non-specific dipeptidase	231	1.40E-109	84.00%	0.133	G3DSA:3.40.630.10 (GENE3D); IPR002933 (PFAM); PTHR11014:SF51 (PANTHER); PTHR11014 (PANTHER); IPR001261 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY)
1250	278906_length_694_cvg_5.9_tip_1_0	58	hemocyte protein-glutamine gamma-glutamyltransferase-like	232	6.44E-100	78.90%	0.146	IPR013783 (G3DSA:2.60.40.GENE3D); IPR002931 (G3DSA:3.90.260.GENE3D); IPR008958 (PFAM); IPR023608 (PANTHER); PTHR11590:SF40 (PANTHER); SSF54001 (SUPERFAMILY); IPR008958 (SUPERFAMILY)
1251	279026_length_697_cvg_4.0_tip_1_5	36	protein phosphatase 1 regulatory subunit 27	232	2.72E-61	70.90%	0.133	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24179 (PANTHER); PTHR24179:SF23 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)

1252	279050_length_697_cvg_4.0_tip_1_1	38	mitogen-activated protein kinase kinase kinase 4	232	9.90E-99	79.40%	0.11	IPR002290 (SMART); IPR000719 (PFAM); IPR016253 (PIRSF); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24360:SF47 (PANTHER); PTHR24360 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1253	279084_length_697_cvg_3.8_tip_1_3	32	fk506-binding protein 2	233	2.19E-67	84.70%	0.28	IPR001179 (PFAM); G3DSA:3.10.50.40 (GENE3D); IPR023566 (PANTHER); PTHR10516:SF134 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY); TMhelix (TMHMM)
1254	279092_length_698_cvg_3.4_tip_1_4	31	serine threonine-protein phosphatase 6 regulatory ankyrin repeat subunit c-like	233	1.81E-46	55.60%	0.112	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1255	279194_length_699_cvg_6.0_tip_1_3	49	succinate-semialdehyde mitochondrial	233	6.56E-105	79.10%	0.103	IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699:SF49 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
1257	279274_length_700_cvg_18.9_tip_1_1	106	protein	233	4.08E-29	83.10%	0.146	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1256	279266_length_700_cvg_82.0_tip_1_3	1240	nidogen-related basement membrane protein	234	5.72E-07	52.00%	0.103	IPR000716 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PFAM); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY)
1258	279308_length_701_cvg_24.9_tip_1_0	171	protein spaetzle	234	8.59E-17	51.50%	0.099	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029034 (SUPERFAMILY); TMhelix (TMHMM)
1259	279366_length_702_cvg_3.0_tip_1_5	20	kelch-like protein diablo	234	3.29E-136	95.00%	0.108	IPR011705 (SMART); IPR000210 (SMART); G3DSA:3.30.710.10 (GENE3D); IPR011705 (PFAM); IPR013069 (PFAM); PTHR24412 (PANTHER); IPR000210 (PROSITE_PROFILES); IPR011333 (SUPERFAMILY)
1260	279376_length_703_cvg_3.2_tip_1_1	33	folistatin-related protein 5- partial	234	2.36E-136	88.70%	0.098	PTHR10913 (PANTHER); PTHR10913:SF14 (PANTHER); SSF63825 (SUPERFAMILY)
1262	279402_length_703_cvg_5.6_tip_1_4	61	carcinolectin 5b partial	234	2.15E-43	65.20%	0.109	IPR002181 (SMART); IPR002181 (PFAM); IPR014715 (G3DSA:4.10.530.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
1261	279380_length_703_cvg_2.0_tip_1_3	18	zinc finger x-linked protein zxdb	235	6.17E-90	72.80%	0.101	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR19818 (PANTHER); PTHR19818:SF68 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1264	279606_length_706_cvg_11.6_tip_1_5	88	membrane glycoprotein lig-	235	1.72E-16	47.20%	0.1	G3DSA:3.80.10.10 (GENE3D); PTHR24373 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1265	279630_length_706_cvg_3.0_tip_1_4	27	carboxypeptidase e-like	235	2.29E-118	81.50%	0.133	IPR000834 (SMART); G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11532:SF41 (PANTHER); PTHR11532 (PANTHER); IPR000834 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY)
1263	279578_length_706_cvg_6.2_tip_1_0	45	protein bowel	236	1.90E-105	82.30%	0.115	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR14196:SF0 (PANTHER); PTHR14196 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1266	279660_length_707_cvg_3.0_tip_1_1	26	zinc finger protein 26-like	236	3.25E-39	55.70%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1267	279692_length_707_cvg_36.0_tip_1_4	297	26s proteasome non-atpase regulatory subunit 10	236	2.84E-81	71.60%	0.142	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24199 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1268	279732_length_708_cvg_10.8_tip_1_2	68	uncharacterized oxidoreductase	236	1.29E-62	69.10%	0.099	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF237 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1269	279790_length_709_cvg_8.7_tip_1_2	70	biotinidase	236	4.20E-29	54.40%	0.214	IPR003010 (G3DSA:3.60.110.GENE3D); IPR003010 (PFAM); IPR012101 (PANTHER); PTHR10609:SF14 (PANTHER); IPR003010 (PROSITE_PROFILES); IPR003010 (SUPERFAMILY)
1270	279854_length_710_cvg_27.8_tip_1_0	182	induced during granule regeneration 1	237	1.10E-14	50.14%	0.103	no IPS match
1271	279856_length_710_cvg_62.8_tip_1_4	1397	pacifastin light chain	237	6.30E-17	50.40%	0.846 Y	IPR008037 (PFAM); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); TMhelix (TMHMM)
1272	279926_length_711_cvg_66.3_tip_1_3	732	hemagglutinin amebocyte aggregation factor-like	237	1.50E-40	62.60%	0.677 Y	PF14704 (PFAM); IPR026645 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
1274	280040_length_713_cvg_9.0_tip_1_5	76	peptidoglycan recognition protein 3 short class	237	6.63E-59	64.70%	0.878 Y	IPR002502 (SMART); IPR006619 (SMART); IPR002502 (G3DSA:3.40.80.GENE3D); IPR002502 (PFAM); IPR015510 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR002502 (SUPERFAMILY); TMhelix (TMHMM)
1273	280038_length_713_cvg_4.0_tip_1_3	49	vitellogenin- partial	238	2.77E-14	44.70%	0.109	PTHR23345 (PANTHER); PTHR23345:SF1 (PANTHER); IPR001846 (PROSITE_PROFILES)
1275	280314_length_717_cvg_3.0_tip_1_4	39	plexin domain-containing protein 2-like	239	1.08E-37	46.20%	0.183	IPR016201 (SMART); G3DSA:3.30.1680.10 (GENE3D); PTHR13055 (PANTHER); PTHR13055:SF12 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016201 (SUPERFAMILY); TMhelix (TMHMM)
1276	280328_length_718_cvg_10.9_tip_0_5	68	marginal zone b- and b1-cell-specific protein	239	1.76E-43	59.10%	0.105	PTHR15881 (PANTHER); PTHR15881:SF1 (PANTHER)
1277	280358_length_718_cvg_3.1_tip_1_4	27	prenylcysteine oxidase-like	239	6.22E-52	61.70%	0.128	IPR010795 (PFAM); IPR017046 (PANTHER)
1278	280388_length_719_cvg_7.0_tip_1_3	61	receptor-type tyrosine-protein phosphatase n2	240	9.18E-157	92.50%	0.11	IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134 (PANTHER); PTHR19134:SF2 (PANTHER); IPR016130 (PROSITE_PATTERNS); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
1279	280396_length_719_cvg_11.8_tip_1_1	85	protein them6	240	7.53E-25	55.30%	0.137	PF13279 (PFAM); IPR029069 (G3DSA:3.10.129.GENE3D); PTHR12475 (PANTHER); IPR029069 (SUPERFAMILY)
1280	280500_length_720_cvg_4.0_tip_1_3	33	protein tag-53	240	6.40E-66	58.50%	0.113	IPR016201 (SMART); IPR015915 (G3DSA:2.120.10.GENE3D); IPR002165 (PFAM); PF13854 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF3 (PANTHER); SSF117281 (SUPERFAMILY)
1281	280550_length_721_cvg_3.0_tip_1_5	34	probable gpi-anchored adhesin-like protein pga55	240	3.07E-57	75.00%	0.144	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR11324 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)

1282	280568_length_722_cvg_8.6_tip_1_1	84	receptor-type tyrosine-protein phosphatase f-like isoform x1	241	5.97E-48	70.70%	0.138	IPR000242 (PRINTS); IPR000242 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)
1283	280648_length_723_cvg_3.2_tip_1_4	34	glucose dehydrogenase	241	4.63E-54	65.10%	0.161	IPR007867 (PFAM); IPR000172 (PFAM); G3DSA:3.30.560.10 (GENE3D); G3DSA:3.50.50.60 (GENE3D); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); SSF54373 (SUPERFAMILY); SSF51905 (SUPERFAMILY)
1284	280670_length_723_cvg_4.2_tip_1_3	35	interleukin-1 receptor-associated kinase 4	241	1.19E-86	69.50%	0.106	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24420 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1285	280696_length_724_cvg_10.6_tip_1_4	87	coiled-coil domain-containing protein partial	241	3.12E-15	50.20%	0.113	SignalP-TM (SIGNALP_GRAM_POSITIVE)
1286	280706_length_724_cvg_6.0_tip_1_4	53	protein disulfide-isomerase a6	241	2.16E-83	74.30%	0.251	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005788 (TIGRFAM); IPR013766 (PFAM); PTHR18929:SF38 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1287	280712_length_724_cvg_4.3_tip_1_4	38	serine protease easter	241	2.71E-37	60.30%	0.103	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1289	280726_length_724_cvg_4.0_tip_1_4	40	carboxypeptidase b	241	1.03E-97	68.20%	0.15	IPR000834 (SMART); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
1290	280800_length_725_cvg_4.0_tip_1_2	35	tyrosine-protein kinase hopscotch	241	2.43E-79	67.20%	0.108	IPR001245 (PRINTS); IPR020635 (SMART); IPR016253 (PIRSF); IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24418 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1288	280716_length_724_cvg_33.4_tip_1_0	265	adp-ribosylation factor 2	242	3.69E-105	95.80%	0.115	IPR006689 (PRINTS); IPR024156 (SMART); IPR006687 (SMART); IPR005225 (TIGRFAM); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF153 (PANTHER); PTHR11711 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1291	280838_length_726_cvg_11.0_tip_1_5	80	hypoxia up-regulated protein 1 isoform x1	242	1.08E-95	80.30%	0.303	IPR013126 (PRINTS); G3DSA:3.30.30.30 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); PTHR19375:SF90 (PANTHER); SSF53067 (SUPERFAMILY)
1292	280880_length_727_cvg_59.2_tip_0_3	632	low quality protein: mucin-19	243	6.57E-16	43.20%	0.133	SignalP-TM (SIGNALP_GRAM_POSITIVE)
1293	280924_length_727_cvg_12.1_tip_1_0	128	membrane metallo-endopeptidase-like 1-like	243	2.35E-27	54.10%	0.151	IPR008753 (PFAM); G3DSA:1.10.1380.10 (GENE3D); IPR000718 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1294	280974_length_728_cvg_7.2_tip_1_3	81	ankyrin repeat and mynd domain-containing protein 2	243	1.90E-91	71.60%	0.099	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24150 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1295	281142_length_731_cvg_57.0_tip_1_3	693	granulins- partial	244	4.22E-36	53.10%	0.552 Y	IPR000118 (SMART); IPR000118 (PFAM); PTHR12274 (PANTHER); PTHR12274:SF1 (PANTHER); IPR000118 (PROSITE_PATTERNS); IPR000118 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF57277 (SUPERFAMILY); SSF57277 (SUPERFAMILY); TMhelix (TMHMM)
1296	281144_length_731_cvg_31.0_tip_1_3	286	protein twin sister of ft	244	1.93E-24	59.50%	0.164	IPR008914 (PFAM); IPR008914 (G3DSA:3.90.280.GENE3D); PTHR11362 (PANTHER); IPR001858 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008914 (SUPERFAMILY)
1297	281254_length_733_cvg_6.2_tip_1_1	59	fat-like cadherin-related tumor suppressor homolog isoform x3	244	6.25E-88	70.90%	0.101	IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24026 (PANTHER); PTHR24026:SF39 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)

1298	281370_length_736_cvg_10.7_tip_1_2	97	aael007448- partial	245	1.77E-57	72.00%	0.105	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001375 (PFAM); PTHR11731 (PANTHER); PTHR11731:SF103 (PANTHER); IPR029058 (SUPERFAMILY)
1299	281374_length_736_cvg_3.1_tip_1_2	38	cadherin-related family member partial	245	7.28E-18	50.70%	0.101	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
1301	281410_length_736_cvg_2.8_tip_1_1	31	lysosomal alpha-glucosidase-like	245	8.69E-41	60.90%	0.118	PTHR22762 (PANTHER); PTHR22762:SF7 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1300	281388_length_736_cvg_4.4_tip_1_0	42	multiple pdz domain	246	1.35E-56	61.20%	0.148	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964 (PANTHER); PTHR19964:SF34 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
1302	281486_length_738_cvg_64.1_tip_1_1	1935	14-3-3 protein zeta isoform x1	246	8.18E-139	96.00%	0.122	Coil (COILS); IPR000308 (PRINTS); IPR023410 (SMART); IPR023410 (PFAM); G3DSA:1.20.190.20 (GENE3D); IPR000308 (PIRSF); IPR000308 (PANTHER); IPR023409 (PROSITE_PATTERNS); IPR023410 (SUPERFAMILY)
1303	281500_length_738_cvg_3.0_tip_1_0	25	sh3 and multiple ankyrin repeat domains protein partial	246	2.65E-125	87.80%	0.142	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24135 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1304	281580_length_739_cvg_5.0_tip_1_1	47	dehydrogenase reductase sdr family member 11-like	246	1.78E-12	72.00%	0.106	PTHR24322 (PANTHER); PTHR24322:SF310 (PANTHER)
1306	281614_length_740_cvg_6.9_tip_1_5	74	3-hydroxybutyrate dehydrogenase type 2	246	1.18E-87	84.30%	0.114	IPR002347 (PRINTS); IPR002198 (PRINTS); PF13561 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24321 (PANTHER); PTHR24321:SF3 (PANTHER); IPR020904 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1308	281634_length_740_cvg_5.4_tip_1_2	44	zinc finger protein 726	246	3.04E-37	66.30%	0.105	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1305	281586_length_739_cvg_59.2_tip_1_3	903	pacifastin light chain	247	1.04E-16	51.00%	0.425 Y	IPR008037 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); TMhelix (TMHMM)
1307	281624_length_740_cvg_55.0_tip_1_0	687	ras-related protein rab-1a	247	3.18E-134	94.30%	0.178	IPR001806 (PRINTS); IPR003579 (SMART); IPR003578 (SMART); IPR020849 (SMART); IPR002041 (SMART); IPR024156 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); IPR001806 (PFAM); PTHR24073 (PANTHER); PTHR24073:SF455 (PANTHER); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1309	281782_length_743_cvg_3.0_tip_1_4	29	acyl- -binding domain-containing protein 5 isoform x3	248	2.43E-39	65.90%	0.128	IPR000582 (PRINTS); IPR000582 (PFAM); IPR014352 (G3DSA:1.20.80.GENE3D); PTHR23310:SF14 (PANTHER); PTHR23310 (PANTHER); IPR000582 (PROSITE_PROFILES); IPR000582 (SUPERFAMILY)
1310	281810_length_744_cvg_4.0_tip_1_3	37	cyclin-g-associated kinase-like	248	4.89E-101	79.90%	0.159	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR23172 (PANTHER); PTHR23172:SF19 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1311	281824_length_744_cvg_95.4_tip_0_3	2633	blastula protease 10-like	248	9.34E-33	50.40%	0.158	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR001506 (PFAM); IPR000859 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF580 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)

1312	281826_length_744_cvg_2.0_tip_1_3	22	gastrula zinc finger protein - partial	248	2.16E-48	54.00%	0.145	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1313	281858_length_745_cvg_4.4_tip_1_0	50	---NA---	249			0.105	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
1314	281878_length_746_cvg_2.7_tip_1_4	36	zinc finger	249	9.19E-29	58.10%	0.133	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1315	281924_length_746_cvg_6.8_tip_1_3	60	galectin partial	249	1.12E-60	69.70%	0.098	IPR001079 (SMART); IPR001079 (SMART); IPR001079 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR11346 (PANTHER); IPR001079 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
1316	281972_length_748_cvg_2.9_tip_1_1	29	hypothetical protein	249	6.15E-11	45.00%	0.125	no IPS match
1317	281972_length_748_cvg_2.9_tip_1_4	29	tachykinins isoform x1	249	2.14E-41	54.20%	0.118	no IPS match
1318	282054_length_749_cvg_72.8_tip_0_3	3764	hypothetical protein BRAFLDRAFT_77844	250	7.20E-47	55.60%	0.149	IPR001547 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR31308 (PANTHER); IPR017853 (SUPERFAMILY)
1319	282090_length_750_cvg_67.4_tip_1_4	1503	hemagglutinin amebocyte aggregation factor-like	250	2.58E-39	61.40%	0.116	PF14704 (PFAM); IPR026645 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1320	282098_length_750_cvg_2.0_tip_1_2	20	variable lymphocyte receptor a	250	2.85E-10	51.10%	0.116	IPR003591 (SMART); SM00364 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1321	282162_length_751_cvg_15.9_tip_1_4	154	ribosome biogenesis protein wdr12 homolog	250	2.77E-89	71.50%	0.103	IPR001680 (SMART); IPR012972 (PFAM); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19855 (PANTHER); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1322	282216_length_753_cvg_62.0_tip_1_3	1433	kazal-type serine proteinase inhibitor 3	251	3.29E-24	56.90%	0.572 Y	IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); PTHR10913:SF46 (PANTHER); PTHR10913 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1323	282228_length_753_cvg_5.7_tip_1_2	50	myosin light chain	251	1.60E-100	76.00%	0.108	IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013098 (PFAM); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1324	282234_length_753_cvg_52.2_tip_1_1	454	annexin b10-like	251	8.53E-84	69.70%	0.103	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); SSF47874 (SUPERFAMILY)

1326	282324_length_754_cvg_4.8_tip_1_5	47	cuticlin- partial	251	3.31E-133	81.80%	0.109	IPR001507 (SMART); IPR001507 (PFAM); PTHR22907:SF1 (PANTHER); PTHR22907 (PANTHER); IPR001507 (PROSITE_PROFILES)
1325	282276_length_754_cvg_2.1_tip_1_3	24	gamma-aminobutyric acid type b receptor subunit 1	252	8.53E-134	86.60%	0.223	PR01176 (PRINTS); IPR002456 (PRINTS); IPR017978 (PFAM); IPR002455 (PANTHER); PTHR10519:SF3 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1327	282388_length_756_cvg_55.3_tip_1_1	1503	apolipoprotein d-like	252	5.13E-14	46.10%	0.438 Y	IPR000566 (PFAM); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612 (PANTHER); PTHR10612:SF10 (PANTHER); IPR011038 (SUPERFAMILY)
1328	282460_length_757_cvg_4.0_tip_1_2	38	receptor-type tyrosine-protein phosphatase kappa	252	1.87E-94	74.40%	0.208	IPR000242 (PRINTS); IPR000242 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134:SF252 (PANTHER); PTHR19134 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)
1329	282484_length_758_cvg_6.0_tip_1_0	58	l-xylulose reductase	253	2.67E-92	78.50%	0.112	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PF13561 (PFAM); PTHR24311:SF6 (PANTHER); PTHR24311 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
1330	282492_length_758_cvg_66.5_tip_1_3	1104	af425264_1lysozyme precursor	253	2.80E-46	63.90%	0.132	IPR001916 (PRINTS); IPR000974 (PRINTS); IPR001916 (SMART); G3DSA:1.10.530.10 (GENE3D); IPR001916 (PFAM); PTHR11407 (PANTHER); IPR019799 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001916 (PROSITE_PROFILES); IPR023346 (SUPERFAMILY)
1331	282494_length_758_cvg_3.0_tip_1_3	32	3-hydroxyisobutyrate dehydrogenase	253	1.10E-113	85.30%	0.134	IPR029154 (PFAM); IPR006115 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); IPR011548 (TIGRFAM); IPR015815 (PIRSF); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22981:SF51 (PANTHER); PTHR22981 (PANTHER); IPR008927 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
1334	282648_length_761_cvg_75.0_tip_1_2	15917	trypsinogen 2	253	8.60E-99	72.90%	0.816 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1336	282660_length_761_cvg_13.3_tip_1_5	150	slit homolog 1	253	1.61E-51	67.10%	0.271	IPR003591 (SMART); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24373 (PANTHER); PTHR24373:SF98 (PANTHER); SSF52058 (SUPERFAMILY)
1332	282606_length_760_cvg_10.1_tip_1_3	95	peptidyl-prolyl cis-trans isomerase-like 3	254	1.69E-97	91.00%	0.145	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1333	282608_length_760_cvg_8.8_tip_1_3	96	hemocytin isoform x2	254	1.85E-08	43.20%	0.109	IPR014853 (PFAM); IPR001846 (PROSITE_PROFILES)
1335	282656_length_761_cvg_3.0_tip_1_0	33	sialate o-acetyltransferase isoform x1	254	2.89E-70	60.10%	0.338	IPR005181 (PFAM); PTHR22901 (PANTHER); IPR013830 (SUPERFAMILY)
1337	282764_length_763_cvg_2.3_tip_1_4	28	papilin isoform x2	254	3.21E-75	66.00%	0.124	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
1338	282834_length_764_cvg_17.8_tip_1_5	164	epoxide hydrolase 4-like	254	8.34E-58	67.60%	0.104	IPR000639 (PRINTS); IPR000073 (PRINTS); IPR000073 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR10992:SF721 (PANTHER); PTHR10992 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)

1339	282860_length_764_cvg_2.0_tip_1_4	24	mitogen-activated protein kinase erk-	255	3.00E-145	87.10%	0.107	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24360 (PANTHER); PTHR24360:SF15 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1340	282982_length_767_cvg_15.4_tip_1_4	195	na(+) h(+) exchange regulatory cofactor nhe-rf2	256	2.30E-56	73.60%	0.161	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR14191 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
1341	283054_length_768_cvg_11.0_tip_1_0	102	serpin b3-like	256	8.79E-46	53.30%	0.171	IPR023796 (SMART); G3DSA:2.30.39.10 (GENE3D); G3DSA:3.30.497.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); IPR023796 (SUPERFAMILY)
1343	283096_length_769_cvg_65.2_tip_1_2	1112	ferritin	256	7.28E-86	84.70%	0.726 Y	Coil (COILS); IPR008331 (PFAM); IPR012347 (G3DSA:1.20.1260.GENE3D); IPR001519 (PANTHER); IPR014034 (PROSITE_PATTERNS); IPR014034 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR009040 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009078 (SUPERFAMILY)
1342	283084_length_769_cvg_22.7_tip_1_0	193	ectonucleoside triphosphate diphosphohydrolase 5-partial	257	1.81E-19	81.90%	0.156	IPR000407 (PFAM); IPR000407 (PANTHER)
1344	283142_length_770_cvg_10.5_tip_1_3	129	pdz domain-containing protein gipc3	257	1.22E-141	85.80%	0.11	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR12259 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
1345	283236_length_772_cvg_4.7_tip_1_2	45	zinc finger protein 431-like isoform x2	257	8.18E-34	55.90%	0.1	IPR015880 (SMART); PF13912 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1346	283428_length_776_cvg_14.7_tip_1_1	119	collagen alpha type	259	5.31E-54	70.60%	0.111	IPR010515 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR24023:SF461 (PANTHER); PTHR24023 (PANTHER); IPR016187 (SUPERFAMILY)
1347	283462_length_777_cvg_3.8_tip_1_0	31	zinc finger protein 271-like	259	2.78E-71	66.80%	0.099	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1348	283470_length_777_cvg_2.6_tip_1_3	26	heat-shock protein 105	259	8.36E-127	81.30%	0.123	IPR013126 (PRINTS); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.90.640.10 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF78 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
1384	284792_length_807_cvg_6.4_tip_1_1	75	virulence metalloprotease	259	1.10E-18	54.40%	0.286	IPR011096 (PFAM); IPR025711 (PFAM); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1349	283644_length_780_cvg_10.8_tip_1_3	122	glutathione peroxidase 7	260	7.44E-76	71.80%	0.12	IPR000889 (PRINTS); IPR000889 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PANTHER); PTHR11592:SF10 (PANTHER); IPR029759 (PROSITE_PATTERNS); IPR029760 (PROSITE_PATTERNS); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
1350	283702_length_782_cvg_2.0_tip_1_2	25	glutamate synthase	260	2.96E-143	88.70%	0.102	PR00419 (PRINTS); PF13450 (PFAM); IPR028261 (PFAM); G3DSA:1.10.1060.10 (GENE3D); G3DSA:3.50.50.60 (GENE3D); PTHR11938 (PANTHER); PTHR11938:SF61 (PANTHER); IPR009051 (SUPERFAMILY); SSF51971 (SUPERFAMILY)

1363	284020_length_788_cvg_2.1_tip_1_3	22	asparagine-rich zinc finger protein azf1-like isoform x2	263	5.63E-65	69.00%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1364	284028_length_789_cvg_6.4_tip_1_1	62	insulin-like growth factor binding protein 7-like protein	263	2.79E-08	51.80%	0.636 Y	IPR000867 (SMART); IPR000867 (PFAM); IPR011390 (PANTHER); PTHR14186:SF8 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR000867 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009030 (SUPERFAMILY); TMhelix (TMHMM)
1365	284038_length_789_cvg_60.9_tip_1_1	80801	soma ferritin-like	263	2.07E-74	80.50%	0.113	IPR012347 (G3DSA:1.20.1260.GENE3D); IPR008331 (PFAM); IPR001519 (PANTHER); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY)
1366	284116_length_790_cvg_2.9_tip_1_5	30	periostin- partial	263	2.47E-23	50.10%	0.363 Y	IPR000782 (SMART); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900 (PANTHER); PTHR10900:SF72 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY)
1367	284208_length_792_cvg_42.2_tip_1_0	303	probable nuclear transport factor 2 isoform x1	264	3.98E-47	82.00%	0.097	IPR002075 (PFAM); G3DSA:3.10.450.50 (GENE3D); PTHR12612 (PANTHER); IPR018222 (PROSITE_PROFILES); SSF54427 (SUPERFAMILY)
1368	284316_length_794_cvg_12.4_tip_1_4	92	tunicate retinoic acid-inducible modular protease	265	7.10E-13	48.40%	0.133	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR003014 (PFAM); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); SSF57414 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1369	284342_length_795_cvg_59.0_tip_1_1	1132	pacifastin light chain	265	6.92E-16	51.90%	0.474 Y	IPR008197 (PRINTS); IPR008197 (SMART); IPR008197 (PFAM); IPR008197 (G3DSA:4.10.75.GENE3D); IPR008037 (PFAM); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008197 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008197 (SUPERFAMILY); TMhelix (TMHMM)
1370	284350_length_795_cvg_59.9_tip_1_5	9361	unnamed protein product	265	1.58E-09	73.00%	0.148	no IPS match
1371	284378_length_796_cvg_3.5_tip_1_0	40	adp-ribosylation factor-like protein 1	266	5.11E-90	95.50%	0.104	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); IPR006689 (PFAM); PTHR11711:SF41 (PANTHER); PTHR11711 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1372	284434_length_798_cvg_10.9_tip_1_4	133	beta-galactosidase-1-like protein 2	266	1.21E-77	69.50%	0.148	IPR001944 (PRINTS); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001944 (PFAM); PTHR23421:SF66 (PANTHER); IPR001944 (PANTHER); IPR019801 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
1373	284462_length_798_cvg_3.3_tip_1_5	33	e3 ubiquitin-protein ligase sh3rf1	266	3.43E-29	56.70%	0.106	IPR001452 (PRINTS); IPR001452 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR001452 (PFAM); PTHR10661 (PANTHER); PTHR10661:SF66 (PANTHER); IPR001452 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR001452 (SUPERFAMILY)
1376	284530_length_800_cvg_4.5_tip_1_5	43	ves g 5 allergen	266	4.88E-44	51.40%	0.467 Y	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR014044 (SUPERFAMILY); TMhelix (TMHMM)
1374	284508_length_800_cvg_4.0_tip_1_4	41	probable chitinase	267	1.07E-20	50.40%	0.138	IPR011583 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
1375	284526_length_800_cvg_4.6_tip_1_3	54	estradiol 17-beta-dehydrogenase 12	267	1.45E-40	67.00%	0.12	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316:SF68 (PANTHER); PTHR24316 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1377	284536_length_801_cvg_4.8_tip_1_5	58	calcium-activated chloride channel regulator 1-like	267	5.11E-25	53.80%	0.106	PTHR10579 (PANTHER); PTHR10579:SF8 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)

1392	284976_length_811_cvg_19.9_tip_1_2	188	pneumococcal surface protein c	270	2.91E-13	44.90%	0.455 Y	SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
1395	284992_length_812_cvg_4.9_tip_1_5	58	neurexin-4 isoform x1	270	4.25E-31	48.70%	0.491 Y	Coil (COILS); IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10083 (PANTHER); IPR029858 (PTHR10083:PANTHER); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002223 (SUPERFAMILY)
1390	284942_length_811_cvg_5.0_tip_1_0	46	laminin subunit gamma-1	271	2.36E-62	66.90%	0.105	Coil (COILS); Coil (COILS); Coil (COILS); PTHR10574:SF228 (PANTHER); PTHR10574 (PANTHER)
1391	284970_length_811_cvg_11.8_tip_1_3	95	dipeptidyl peptidase 1 isoform x1	271	4.43E-80	83.00%	0.102	IPR000668 (SMART); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); G3DSA:2.40.50.170 (GENE3D); PTHR12411:SF314 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
1393	284984_length_812_cvg_12.6_tip_1_3	116	peptidyl-prolyl cis-trans isomerase cyp11 isoform x1	271	2.84E-106	88.20%	0.133	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF229 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1394	284990_length_812_cvg_2.0_tip_1_4	28	thrombospondin type-1 domain-containing protein 4-like	271	1.44E-67	63.60%	0.122	IPR000884 (SMART); IPR000884 (PFAM); G3DSA:2.20.100.10 (GENE3D); PTHR13723 (PANTHER); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
1396	285024_length_813_cvg_10.7_tip_1_4	82	peptidase inhibitor 16	271	8.28E-06	52.00%	0.106	IPR014044 (G3DSA:3.40.33.GENE3D); IPR018244 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1397	285030_length_813_cvg_3.4_tip_1_1	37	calponin homology domain containing	271	9.47E-67	58.60%	0.136	Coil (COILS); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); PTHR23155:SF423 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52075 (SUPERFAMILY)
1398	285036_length_813_cvg_5.0_tip_1_3	50	protein twisted gastrulation	271	7.73E-83	78.40%	0.142	IPR006761 (PFAM); PTHR12312:SF15 (PANTHER); IPR006761 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1399	285054_length_814_cvg_14.7_tip_1_0	112	abhydrolase domain-containing protein partial	272	4.73E-121	75.70%	0.137	IPR029059 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR12277:SF44 (PANTHER); PTHR12277 (PANTHER); IPR029058 (SUPERFAMILY)
1400	285078_length_815_cvg_4.3_tip_1_0	44	apolipoprotein partial	272	2.31E-53	55.30%	0.103	PR00018 (PRINTS); IPR000001 (SMART); G3DSA:2.40.20.10 (GENE3D); IPR000001 (PFAM); PTHR24259 (PANTHER); IPR018056 (PROSITE_PATTERNS); IPR018056 (PROSITE_PATTERNS); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY)
1401	285114_length_815_cvg_9.4_tip_1_1	89	cysteine string protein	272	3.60E-100	75.80%	0.233	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078:SF5 (PANTHER); PTHR24078 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1402	285124_length_816_cvg_50.3_tip_1_5	873	Adrenodoxin, mitochondrial	272	2.53E-52	76.90%	0.123	IPR001055 (PRINTS); IPR001041 (PFAM); IPR012675 (G3DSA:3.10.20.GENE3D); PTHR23426 (PANTHER); PTHR23426:SF21 (PANTHER); IPR018298 (PROSITE_PATTERNS); IPR001041 (PROSITE_PROFILES); IPR001041 (SUPERFAMILY)
1403	285134_length_816_cvg_4.7_tip_1_4	53	carboxypeptidase m isoform x2	272	1.57E-41	69.50%	0.219	PF13620 (PFAM); IPR014766 (G3DSA:2.60.40.GENE3D); IPR027062 (PTHR11532:PANTHER); PTHR11532 (PANTHER); IPR008969 (SUPERFAMILY)
1404	285168_length_817_cvg_3.0_tip_1_4	39	zinc finger protein 350-like isoform x1	272	9.55E-46	79.80%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1405	285190_length_817_cvg_6.4_tip_1_4	88	gamma-interferon-inducible lysosomal thiol reductase	272	7.12E-44	51.30%	0.322	IPR004911 (PFAM); IPR004911 (PANTHER); PTHR13234:SF8 (PANTHER)

1406	285202_length_818_cvg_5.9_tip_1_2	52	lipophorin receptor	272	2.51E-74	63.30%	0.121	IPR000742 (SMART); IPR000033 (SMART); IPR001881 (SMART); IPR002172 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); IPR002172 (PFAM); IPR000033 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY); IPR009030 (SUPERFAMILY)
1407	285226_length_818_cvg_3.6_tip_1_4	53	zona pellucida-binding protein 2-like isoform x2	273	1.09E-07	49.00%	0.119	G3DSA:2.10.50.10 (GENE3D); IPR011641 (PFAM)
1408	285240_length_819_cvg_6.0_tip_1_3	66	insulin-like growth factor-binding protein 7 precursor	273	4.55E-74	58.90%	0.544 Y	IPR002350 (SMART); IPR003598 (SMART); IPR000867 (SMART); IPR000867 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR002350 (PFAM); IPR013098 (PFAM); IPR011390 (PANTHER); PTHR14186:SF9 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000867 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); SSF48726 (SUPERFAMILY); IPR009030 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
1409	285248_length_819_cvg_8.7_tip_1_4	99	trypsinogen 2	273	2.07E-93	67.20%	0.520 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1410	285254_length_819_cvg_42.8_tip_1_3	373	kielin chordin-like protein	273	2.67E-18	40.00%	0.784 Y	IPR001846 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR11339 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001846 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF57603 (SUPERFAMILY); TMhelix (TMHMM)
1411	285268_length_819_cvg_3.8_tip_1_3	51	multiple pdz domain	273	1.13E-89	67.70%	0.096	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR19964 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
1412	285270_length_819_cvg_3.2_tip_1_4	33	carbonyl reductase	273	6.10E-93	74.50%	0.125	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF58 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1413	285286_length_820_cvg_16.7_tip_1_3	141	reelin- partial	274	5.10E-52	69.20%	0.107	PTHR11841 (PANTHER)
1415	285328_length_821_cvg_56.9_tip_1_0	1286	carboxypeptidase	274	2.39E-52	59.20%	0.25	IPR000834 (PRINTS); IPR000834 (SMART); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); IPR003146 (PFAM); IPR003146 (G3DSA:3.30.70.GENE3D); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY); IPR009020 (SUPERFAMILY)
1416	285354_length_821_cvg_49.6_tip_1_0	444	phosphatidylinositol 4-phosphate 3-kinase c2 domain-containing subunit beta- partial	274	7.60E-17	43.00%	0.107	G3DSA:1.20.120.20 (GENE3D); SSF47162 (SUPERFAMILY)
1417	285402_length_822_cvg_6.0_tip_1_3	59	e3 ubiquitin-protein ligase mib2	274	1.75E-138	79.80%	0.102	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24202 (PANTHER); PTHR24202:SF4 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)

1418	285494_length_824_cvg_6.0_tip_1_1	62	probable cytosolic iron-sulfur protein assembly protein ciao1 isoform x1	275	3.51E-134	82.90%	0.101	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19920:SF0 (PANTHER); PTHR19920 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1419	285512_length_825_cvg_5.7_tip_1_4	58	alpha-mannosidase partial	275	3.15E-111	74.30%	0.101	G3DSA:2.70.98.30 (GENE3D); IPR011682 (PFAM); PTHR11607:SF22 (PANTHER); PTHR11607 (PANTHER); IPR011013 (SUPERFAMILY)
1420	285562_length_826_cvg_3.0_tip_1_1	37	aldehyde dehydrogenase family 9 member a1-b-like	275	5.35E-124	77.90%	0.122	IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699:SF114 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
1421	285566_length_826_cvg_4.5_tip_1_5	52	hook dna-binding motif-containing protein 1	275	5.79E-07	52.00%	0.098	no IPS match
1422	285582_length_827_cvg_3.2_tip_1_5	40	anti-lipopolysaccharide factor like protein	275	6.84E-15	57.50%	0.161	IPR024509 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024716 (PRODOM); TMhelix (TMHMM); TMhelix (TMHMM)
1423	285602_length_828_cvg_2.1_tip_1_3	27	adam 10	276	2.06E-145	83.60%	0.141	IPR024079 (G3DSA:3.40.390.GENE3D); PF13688 (PFAM); PTHR11905 (PANTHER); PTHR11905:SF4 (PANTHER); IPR001590 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY)
1424	285638_length_828_cvg_3.7_tip_1_0	47	iduronate 2-sulfatase-like	276	2.72E-83	59.70%	0.118	G3DSA:3.30.1120.10 (GENE3D); IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342:SF185 (PANTHER); PTHR10342 (PANTHER); IPR017850 (SUPERFAMILY)
1425	285766_length_832_cvg_2.0_tip_1_5	36	iduronate 2- partial	277	1.70E-114	77.60%	0.630 Y	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342:SF185 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017850 (SUPERFAMILY)
1426	285832_length_834_cvg_7.0_tip_1_1	62	maltase- intestinal-like	278	9.63E-61	58.30%	0.15	IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF7 (PANTHER); SSF51011 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1427	285844_length_834_cvg_10.5_tip_1_1	106	dnaj homolog subfamily c member 9	278	2.53E-89	75.10%	0.116	Coil (COILS); Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF166 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1428	285904_length_836_cvg_7.5_tip_1_0	92	cytolysin src-1-like isoform x2	279	2.05E-25	51.00%	0.114	IPR009104 (PFAM); IPR015926 (G3DSA:2.60.270.GENE3D); IPR015926 (SUPERFAMILY)
1429	285924_length_836_cvg_4.7_tip_1_0	43	alpha-mannosidase 2	279	9.21E-139	78.50%	0.102	IPR015341 (SMART); IPR000602 (PFAM); IPR015341 (PFAM); IPR015341 (G3DSA:1.20.1270.GENE3D); IPR027291 (G3DSA:3.20.110.GENE3D); PTHR11607 (PANTHER); PTHR11607:SF22 (PANTHER); IPR028995 (SUPERFAMILY); IPR011330 (SUPERFAMILY)
1430	285934_length_836_cvg_2.8_tip_1_1	28	lpxtg motif protein	279	1.68E-09	54.00%	0.174	Coil (COILS)
1431	285992_length_838_cvg_4.0_tip_1_1	45	low quality protein: mucin-19	279	7.12E-07	53.00%	0.142	CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1432	285994_length_838_cvg_5.5_tip_1_4	51	ectonucleoside triphosphate diphosphohydrolase 5 isoform x2	279	5.84E-101	67.00%	0.168	IPR000407 (PFAM); PTHR11782:SF35 (PANTHER); IPR000407 (PANTHER)
1433	286034_length_839_cvg_3.0_tip_1_5	38	arylsulfatase a-like	279	7.51E-114	71.30%	0.686 Y	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF22 (PANTHER); IPR024607 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017850 (SUPERFAMILY)
1434	286050_length_840_cvg_7.9_tip_1_0	103	macrophage mannose receptor 1-like	280	2.07E-26	48.90%	0.117	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803 (PANTHER); PTHR22803:SF16 (PANTHER); IPR018378 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1435	286074_length_840_cvg_8.0_tip_1_5	67	flavin-containing monooxygenase fmo gs-ox-like 4	280	4.25E-102	66.20%	0.103	IPR000960 (PRINTS); G3DSA:3.50.50.60 (GENE3D); G3DSA:3.50.50.60 (GENE3D); IPR020946 (PFAM); PTHR23023:SF4 (PANTHER); PTHR23023 (PANTHER); SSF51905 (SUPERFAMILY); SSF51905 (SUPERFAMILY)

1447	286356_length_847_cvg_2.4_tip_1_2	34	pancreatic lipase-related protein	282	4.73E-29	57.40%	0.114	IPR013818 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR000734 (PANTHER); IPR029058 (SUPERFAMILY)
1448	286362_length_847_cvg_61.9_tip_1_5	4885	hemagglutinin amebocyte aggregation factor-like	282	8.79E-38	57.70%	0.152	PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1449	286658_length_855_cvg_4.0_tip_1_5	47	kielin130 protein	285	4.73E-13	46.00%	0.12	IPR001846 (PFAM); IPR001846 (PROSITE_PROFILES)
1451	286706_length_856_cvg_3.0_tip_1_1	41	carbonic anhydrase 1	285	3.31E-33	68.40%	0.129	IPR001148 (SMART); IPR001148 (G3DSA:3.10.200.GENE3D); IPR001148 (PFAM); IPR023561 (PANTHER); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
1450	286686_length_856_cvg_3.2_tip_1_0	32	proteinase inhibitor i4 serpin	286	5.00E-11	53.30%	0.114	IPR023796 (PFAM); G3DSA:3.30.497.10 (GENE3D); IPR000215 (PANTHER); IPR023796 (SUPERFAMILY)
1452	286758_length_857_cvg_62.8_tip_1_4	834	cre-nas-7 protein	286	7.86E-34	53.90%	0.903 Y	IPR001506 (PRINTS); IPR006026 (SMART); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1453	286908_length_861_cvg_4.0_tip_1_4	45	carboxypeptidase d-like	287	1.31E-101	69.40%	0.443 Y	Coil (COILS); IPR000834 (PRINTS); IPR000834 (SMART); G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); IPR015567 (PTHR11532:PANTHER); PTHR11532 (PANTHER); IPR000834 (PROSITE_PATTERNS); IPR000834 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SSF53187 (SUPERFAMILY)
1455	286970_length_863_cvg_57.7_tip_1_5	1108	blastula protease 10-like	287	1.46E-30	56.20%	0.546 Y	IPR001506 (PRINTS); IPR006026 (SMART); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127:SF580 (PANTHER); PTHR10127 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1454	286934_length_862_cvg_4.3_tip_1_3	40	aael005189- partial	288	9.88E-32	74.00%	0.108	IPR003112 (PFAM); PTHR23192 (PANTHER); PTHR23192:SF33 (PANTHER); IPR003112 (PROSITE_PROFILES)
1456	286996_length_864_cvg_6.0_tip_1_2	57	collagen alpha 1 chain	288	4.51E-50	69.30%	0.114	IPR010515 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR026917 (PTHR24023:PANTHER); PTHR24023 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016187 (SUPERFAMILY)
1485	288156_length_900_cvg_7.8_tip_1_1	75	peptidyl-alpha-hydroxyglycine alpha-amidating lyase 2-like	288	5.44E-31	60.60%	0.139	IPR001258 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR10680 (PANTHER); SSF63825 (SUPERFAMILY)
1457	287060_length_866_cvg_54.2_tip_1_1	619	trypsinogen 2	289	3.18E-70	59.00%	0.882 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009003 (SUPERFAMILY)
1458	287066_length_866_cvg_3.0_tip_1_1	31	omega-amidase nit2-like	289	7.19E-142	83.20%	0.101	IPR003010 (PFAM); IPR003010 (G3DSA:3.60.110.GENE3D); PTHR23088:SF20 (PANTHER); PTHR23088 (PANTHER); IPR003010 (PROSITE_PROFILES); IPR003010 (SUPERFAMILY)
1459	287076_length_867_cvg_32.0_tip_1_1	334	sparc	289	7.39E-112	78.70%	0.109	Coil (COILS); Coil (COILS); IPR003645 (SMART); IPR011992 (G3DSA:1.10.238.GENE3D); G3DSA:3.30.60.30 (GENE3D); IPR019577 (PFAM); PTHR13866:SF14 (PANTHER); PTHR13866 (PANTHER); IPR001999 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); SSF47473 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
1460	287102_length_867_cvg_12.9_tip_1_4	142	u8-agatoxin-ao1a-like isoform x2	289	3.62E-35	73.00%	0.702 Y	IPR004169 (PFAM); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-TM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_NEGATIVE); SSF57059 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1461	287158_length_869_cvg_67.3_tip_1_4	7534	zinc metalloproteinase nas-13	290	2.73E-63	58.30%	0.797 Y	IPR001506 (PRINTS); IPR006026 (SMART); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF55486 (SUPERFAMILY)
1462	287202_length_870_cvg_5.8_tip_1_1	68	coagulation factor x-like	290	8.91E-28	57.20%	0.138	IPR001314 (PRINTS); IPR001254 (SMART); IPR002172 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24265 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1463	287228_length_871_cvg_3.0_tip_1_0	35	chorion peroxidase-like	291	4.52E-120	67.60%	0.119	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
1464	287280_length_872_cvg_9.8_tip_1_4	88	secreted partial	291	1.76E-45	75.60%	0.107	IPR003585 (SMART); IPR027789 (PFAM); PTHR10915:SF1 (PANTHER); IPR001050 (PANTHER); IPR030479 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1465	287308_length_873_cvg_36.8_tip_1_4	488	histone -like	291	3.26E-81	99.20%	0.105	IPR002119 (PRINTS); IPR002119 (SMART); IPR009072 (G3DSA:1.10.20.GENE3D); IPR007125 (PFAM); PTHR23430 (PANTHER); PTHR23430:SF34 (PANTHER); IPR002119 (PROSITE_PATTERNS); IPR009072 (SUPERFAMILY)
1466	287358_length_875_cvg_5.3_tip_1_0	52	probable isocitrate dehydrogenase	292	8.62E-161	87.40%	0.104	IPR024084 (G3DSA:3.40.718.GENE3D); IPR024084 (PFAM); PTHR11835:SF39 (PANTHER); IPR001804 (PANTHER); IPR019818 (PROSITE_PATTERNS); SSF53659 (SUPERFAMILY)
1467	287400_length_876_cvg_6.2_tip_1_4	59	copper chaperone for superoxide dismutase	292	3.46E-80	73.20%	0.169	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); IPR006121 (PFAM); G3DSA:3.30.70.100 (GENE3D); PTHR10003 (PANTHER); IPR006121 (PROSITE_PROFILES); IPR001424 (SUPERFAMILY); IPR006121 (SUPERFAMILY)
1468	287422_length_877_cvg_6.3_tip_1_4	67	macrophage mannose receptor partial	292	8.91E-27	47.50%	0.14	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); PTHR22803:SF16 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
1469	287454_length_878_cvg_54.2_tip_1_5	1064	cathepsin I	292	1.44E-130	79.00%	0.15	IPR000668 (SMART); IPR013201 (SMART); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR013201 (PFAM); IPR013128 (PANTHER); PTHR12411:SF57 (PANTHER); IPR000169 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
1470	287522_length_879_cvg_11.9_tip_1_0	126	protein shifted isoform x1	293	1.11E-80	87.70%	0.143	IPR013309 (PRINTS); IPR003306 (SMART); IPR003306 (PFAM); PTHR24838:SF276 (PANTHER); PTHR24838 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003306 (PRODOM); IPR003306 (PROSITE_PROFILES); TMhelix (TMHMM)
1471	287570_length_881_cvg_13.4_tip_1_1	152	lipophorin receptor isoform e	294	4.71E-13	53.10%	0.786 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY)
1472	287586_length_881_cvg_27.1_tip_1_3	351	polyubiquitin-c-like isoform 2	294	1.82E-107	98.90%	0.181	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY)

1486	288312_length_906_cvg_5.2_tip_1_5	58	leucine-rich repeat-containing protein 15-like isoform x2	302	1.82E-56	59.80%	0.104	Coil (COILS); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1487	288352_length_907_cvg_8.8_tip_1_4	109	---NA---	302			0.123	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1488	288372_length_907_cvg_6.2_tip_1_1	63	collagen alpha-1 chain	302	1.73E-44	55.10%	0.099	IPR008160 (PFAM); PTHR24023:SF397 (PANTHER); PTHR24023 (PANTHER)
1489	288372_length_907_cvg_6.2_tip_1_4	63	mucin-2-like isoform x2	302	2.20E-38	44.40%	0.137	PTHR24023:SF405 (PANTHER); PTHR24023 (PANTHER)
1490	288390_length_908_cvg_79.6_tip_0_4	3230	muscle m-line assembly protein unc-89-like	303	1.20E-80	75.70%	0.101	Coil (COILS); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897:SF148 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1491	288392_length_908_cvg_31.4_tip_1_1	336	cell recognition protein caspr4 isoform 5	303	2.92E-45	52.10%	0.139	IPR001073 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF575 (PANTHER); IPR001073 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); IPR008983 (SUPERFAMILY)
1492	288400_length_908_cvg_12.5_tip_1_3	142	glycosyl-phosphatidylinositol-linked carbonic anhydrase	303	4.63E-54	67.90%	0.11	IPR001148 (SMART); IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); IPR023561 (PANTHER); IPR018338 (PROSITE_PATTERNS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
1493	288416_length_908_cvg_12.8_tip_1_4	149	striatin- partial	303	3.52E-153	82.20%	0.104	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR15653 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1494	288488_length_912_cvg_13.0_tip_1_5	139	cytochrome c oxidase assembly factor 7 homolog	304	3.49E-72	65.80%	0.097	Coil (COILS); IPR006597 (SMART); IPR006597 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR13891:SF1 (PANTHER); PTHR13891 (PANTHER); SSF81901 (SUPERFAMILY)
1495	288508_length_912_cvg_74.6_tip_1_1	9441	trypsinogen 2	304	2.00E-72	62.30%	0.339	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR001254 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009003 (SUPERFAMILY)
1496	288512_length_912_cvg_4.6_tip_1_0	54	isoform cra_a	304	3.65E-14	52.90%	0.203	no IPS match
1497	288512_length_912_cvg_4.6_tip_1_3	54	coagulation factor v	304	1.57E-17	49.00%	0.145	TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1498	288512_length_912_cvg_4.6_tip_1_4	54	coagulation factor v	304	7.65E-19	44.10%	0.167	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1499	288512_length_912_cvg_4.6_tip_1_5	54	coagulation factor v	304	2.51E-10	45.70%	0.506 Y	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-TM (SIGNALP_EUK)
1500	288520_length_913_cvg_27.3_tip_1_5	249	aldo-keto reductase family 1 member b10	304	2.54E-127	76.80%	0.099	IPR020471 (PRINTS); IPR023210 (G3DSA:3.20.20.GENE3D); IPR023210 (PFAM); IPR020471 (PIRSF); PTHR11732:SF202 (PANTHER); IPR001395 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)

1501	288536_length_913_cvg_2.7_tip_1_3	38	very low-density lipoprotein receptor	305	6.24E-18	42.00%	0.114	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1502	288570_length_914_cvg_10.9_tip_1_3	94	adp-ribosylation factor 6	305	7.15E-124	99.60%	0.535 Y	IPR006689 (PRINTS); IPR003579 (SMART); IPR006687 (SMART); IPR024156 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711:SF106 (PANTHER); PTHR11711 (PANTHER); IPR024156 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR027417 (SUPERFAMILY)
1503	288726_length_920_cvg_6.8_tip_1_2	76	fasciclin-2 isoform x6	306	1.34E-14	55.80%	0.113	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PF13895 (PFAM); PTHR19831 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1504	288742_length_920_cvg_12.8_tip_1_2	460	hemagglutinin amebocyte aggregation factor-like	306	1.63E-08	69.20%	0.105	Coil (COILS); PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1505	288746_length_921_cvg_8.4_tip_1_0	87	ion transport peptide-like	307	1.72E-26	69.70%	0.157	IPR001166 (PRINTS); IPR001166 (G3DSA:1.10.2010.GENE3D); IPR001166 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001166 (SUPERFAMILY); TMhelix (TMHMM)
1506	288746_length_921_cvg_8.4_tip_1_2	87	ion transport peptide isoform x2	307	6.99E-06	86.00%	0.357 Y	IPR001166 (PFAM); IPR001166 (G3DSA:1.10.2010.GENE3D); IPR001166 (SUPERFAMILY)
1507	288792_length_921_cvg_6.5_tip_1_5	67	allatostatin precursor	307	1.65E-06	48.00%	0.104	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
1508	288800_length_921_cvg_26.4_tip_1_1	299	gamma-interferon-inducible lysosomal thiol reductase	307	3.42E-50	57.10%	0.282	IPR004911 (PFAM); PTHR13234:SF8 (PANTHER); IPR004911 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS)
1509	288828_length_923_cvg_13.7_tip_1_4	132	serine protease	308	8.64E-106	73.80%	0.114	IPR008758 (PFAM); PTHR11010:SF9 (PANTHER); IPR008758 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1510	288842_length_923_cvg_3.6_tip_1_1	47	n-alpha-acetyltransferase auxiliary subunit	308	5.56E-116	75.40%	0.112	IPR011990 (G3DSA:1.25.40.GENE3D); PTHR22767 (PANTHER); PTHR22767:SF3 (PANTHER); IPR013026 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY)
1511	288876_length_925_cvg_9.2_tip_1_4	103	steroid membrane receptor 25-	308	4.43E-64	81.50%	0.119	IPR001199 (G3DSA:3.10.120.GENE3D); IPR001199 (PFAM); PTHR10281 (PANTHER); PTHR10281:SF25 (PANTHER); IPR001199 (SUPERFAMILY)
1512	288904_length_925_cvg_88.5_tip_1_1	134475	hemocyanin subunit type 1 precursor	308	7.50E-124	69.30%	0.115	IPR005203 (PFAM); IPR005203 (G3DSA:2.60.40.GENE3D); IPR013788 (PANTHER); IPR014756 (SUPERFAMILY)
1513	288958_length_927_cvg_4.0_tip_1_1	52	zinc finger protein 275	309	1.05E-20	57.50%	0.113	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13913 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1514	288990_length_929_cvg_12.6_tip_1_3	115	prolyl 3-hydroxylase 1-like isoform x2	310	3.27E-115	68.70%	0.102	IPR011990 (G3DSA:1.25.40.GENE3D); PTHR13986:SF8 (PANTHER); PTHR13986 (PANTHER)
1515	289056_length_930_cvg_6.1_tip_1_2	51	dipeptidyl aminopeptidase-like protein 6 isoform x1	310	2.00E-83	62.70%	0.104	IPR002469 (G3DSA:2.140.10.GENE3D); IPR002469 (PFAM); PTHR11731 (PANTHER); PTHR11731:SF22 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF82171 (SUPERFAMILY); TMhelix (TMHMM)

1524	289314_length_941_cvg_9.3_tip_1_0	120	macrophage mannose receptor 1	314	9.39E-53	51.60%	0.12	IPR002352 (PRINTS); IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803:SF16 (PANTHER); PTHR22803 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
1525	289320_length_941_cvg_3.9_tip_1_3	44	epidermal growth factor receptor isoform x1	314	5.60E-93	65.00%	0.137	IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24416:SF90 (PANTHER); PTHR24416 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1527	289336_length_942_cvg_25.6_tip_1_4	261	sulfakinin-like peptide	314	1.02E-15	65.70%	0.198	IPR013152 (PROSITE_PATTERNS); IPR013152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1528	289494_length_947_cvg_57.0_tip_1_2	922	mitochondrial manganese superoxide dismutase	315	1.01E-121	86.10%	0.122	Coil (COILS); IPR001189 (PRINTS); G3DSA:1.10.287.990 (GENE3D); IPR019832 (PFAM); IPR019831 (PFAM); PTHR11404:SF6 (PANTHER); IPR001189 (PANTHER); IPR019833 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR019831 (SUPERFAMILY); IPR019832 (SUPERFAMILY); TMhelix (TMHMM)
1529	289548_length_948_cvg_61.0_tip_1_3	843	coagulation factor v	316	2.61E-09	45.00%	0.510 Y	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-TM (SIGNALP_EUK); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1533	289596_length_950_cvg_4.8_tip_1_2	68	membrane glycoprotein lig-	316	1.84E-17	46.60%	0.725 Y	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF52058 (SUPERFAMILY)
1530	289576_length_950_cvg_31.1_tip_1_3	428	aael000271- partial	317	2.81E-71	67.70%	0.111	IPR029062 (G3DSA:3.40.50.GENE3D); IPR011697 (PFAM); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY)
1531	289586_length_950_cvg_4.0_tip_1_4	43	plexin- partial	317	7.98E-100	78.40%	0.116	IPR002909 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR002909 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR22625 (PANTHER); PTHR22625:SF16 (PANTHER); IPR014756 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
1532	289590_length_950_cvg_10.0_tip_1_4	134	prohormone-1-like	317	6.87E-30	83.90%	0.115	no IPS match
1534	289612_length_951_cvg_8.5_tip_1_3	92	low-density lipoprotein receptor-related protein 2	317	2.19E-23	58.80%	0.102	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)

1548	290036_length_969_cvg_4.0_tip_1_1	44	peptidylprolyl isomerase domain and wd repeat-containing protein 1	323	0	88.60%	0.132	IPR002130 (PRINTS); IPR002130 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF228 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); SSF69322 (SUPERFAMILY)
1549	290064_length_970_cvg_3.6_tip_1_1	46	slit homolog 3 protein	323	1.26E-08	47.40%	0.122	IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); PTHR24365:SF265 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1550	290110_length_972_cvg_21.6_tip_1_5	260	plcl_mytga ame: full=perlucin-like protein flags: precursor	324	9.99E-13	44.50%	0.296	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
1551	290130_length_973_cvg_2.7_tip_1_5	42	trypsin-1- partial	324	1.20E-46	54.20%	0.318	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1556	290198_length_974_cvg_3.4_tip_1_2	46	cub domain protein	324	7.82E-11	47.80%	0.102	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
1552	290152_length_973_cvg_4.9_tip_1_3	63	sulfhydryl oxidase 1-like	325	3.25E-65	64.40%	0.135	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR22897 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1553	290168_length_974_cvg_5.5_tip_1_1	62	zinc finger protein zpr1	325	1.28E-128	73.50%	0.113	IPR004457 (SMART); IPR004457 (TIGRFAM); IPR004457 (PFAM); PTHR10876 (PANTHER); PTHR10876:SF0 (PANTHER)
1554	290176_length_974_cvg_70.9_tip_1_1	3207	trypsinogen h2_1g	325	1.15E-58	57.10%	0.934 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1555	290196_length_974_cvg_6.5_tip_1_3	75	serine protease inhibitor	325	8.01E-09	68.00%	0.121	G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); PTHR11461:SF52 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
1557	290236_length_976_cvg_32.7_tip_1_0	415	protein them6	326	2.40E-36	58.40%	0.129	Coil (COILS); IPR029069 (G3DSA:3.10.129.GENE3D); PF13279 (PFAM); PTHR12475 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029069 (SUPERFAMILY); TMhelix (TMHMM)
1558	290312_length_978_cvg_36.7_tip_1_0	465	cytochrome p450 2j2-like	326	9.16E-47	64.90%	0.099	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
1559	290322_length_978_cvg_30.3_tip_1_4	368	thioredoxin-dependent peroxide reductase	326	1.76E-126	84.70%	0.172	IPR000866 (PFAM); IPR019479 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1560	290430_length_982_cvg_5.2_tip_1_0	69	protein phosphatase 1 regulatory subunit 16a	328	1.03E-62	63.20%	0.223	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24186 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1561	290470_length_985_cvg_2.6_tip_1_4	44	vascular endothelial growth factor receptor 1 isoform x1	328	2.32E-18	49.80%	0.287	IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR15360 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1562	290490_length_986_cvg_28.2_tip_1_3	336	mesencephalic astrocyte-derived neurotrophic factor homolog	329	2.64E-77	85.10%	0.794 Y	IPR019345 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR12990 (PANTHER); PTHR12990:SF5 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF68906 (SUPERFAMILY)
1563	290518_length_987_cvg_24.0_tip_1_0	296	venom allergen 3-like	329	1.16E-48	55.00%	0.792 Y	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR014044 (SUPERFAMILY)

1564	290568_length_989_cvg_52.5_tip_0_3	2172	14-3-3 partial	330	1.43E-27	100.00%	0.113	G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); PTHR18860:SF21 (PANTHER); IPR023409 (PROSITE_PATTERNS); IPR023410 (SUPERFAMILY)
1565	290586_length_990_cvg_55.1_tip_1_3	28480	chitinase partial	330	6.46E-51	59.90%	0.104	IPR002557 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); IPR002557 (PFAM); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR017853 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR029070 (SUPERFAMILY)
1566	290588_length_990_cvg_5.0_tip_1_0	52	coiled-coil domain-containing protein 134-like	330	1.02E-53	65.10%	0.148	IPR026321 (PFAM); IPR026321 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1567	290598_length_990_cvg_14.6_tip_0_5	149	nidogen- partial	330	8.40E-109	62.50%	0.104	IPR000742 (SMART); IPR000033 (SMART); IPR024731 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); IPR023413 (G3DSA:2.40.155.GENE3D); PTHR24044 (PANTHER); PTHR24044:SF253 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
1568	290606_length_990_cvg_10.8_tip_1_1	139	collagen alpha-1 chain	330	1.59E-14	58.10%	0.244	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR008160 (PFAM); PTHR24023:SF372 (PANTHER); PTHR24023 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
1569	290606_length_990_cvg_10.8_tip_1_3	139	serine-aspartate repeat protein f	330	2.33E-21	46.50%	0.102	no IPS match
1570	290650_length_992_cvg_58.0_tip_1_1	3075	peptidyl-prolyl cis-trans isomerase	331	1.63E-101	92.50%	0.32	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF116 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1571	290664_length_992_cvg_3.1_tip_1_3	47	peroxidasin extracellular matrix-associated peroxidase	331	6.24E-08	62.70%	0.102	IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
1572	290744_length_996_cvg_8.3_tip_1_0	123	5 -nucleotidase	332	5.96E-120	70.80%	0.11	IPR008334 (G3DSA:3.90.780.GENE3D); IPR008334 (PFAM); IPR006179 (PANTHER); PTHR11575:SF7 (PANTHER); IPR008334 (SUPERFAMILY)
1573	290762_length_996_cvg_4.6_tip_1_4	66	zinc finger protein	332	1.94E-24	52.20%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1574	290862_length_1000_cvg_3.1_tip_1_4	48	atrial natriuretic peptide-converting enzyme-like	333	4.19E-46	61.70%	0.1	Coil (COILS); IPR002172 (SMART); IPR020067 (SMART); IPR020067 (PFAM); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR020067 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR020067 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1575	290870_length_1001_cvg_81.1_tip_1_2	18311	der p 3 allergen	333	4.30E-60	61.00%	0.886 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1576	290874_length_1001_cvg_52.9_tip_1_3	936	scp-like extracellular domain containing protein 1	334	5.99E-45	52.60%	0.854 Y	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR014044 (SUPERFAMILY); TMhelix (TMHMM)

1577	290896_length_1002_cvg_9.5_tip_1_4	130	spondin-1 isoform x3	334	2.10E-110	72.80%	0.132	IPR002861 (PFAM); IPR009465 (PFAM); PTHR11311 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002861 (PROSITE_PROFILES); IPR009465 (PROSITE_PROFILES); TMhelix (TMHMM)
1579	290912_length_1003_cvg_11.8_tip_1_5	125	peptidyl-prolyl cis-trans isomerase a2	334	2.24E-35	54.30%	0.116	IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF202 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1578	290910_length_1003_cvg_6.4_tip_1_3	107	biotinidase isoform x2	335	1.41E-10	45.80%	0.1	PTHR10609:SF14 (PANTHER); IPR012101 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1580	290914_length_1003_cvg_3.7_tip_1_0	59	vascular endothelial growth factor receptor 2	335	8.11E-52	55.90%	0.27	G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416:SF298 (PANTHER); PTHR24416 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1581	290962_length_1005_cvg_3.0_tip_1_0	45	ankyrin repeat domain-containing protein 17	335	0	95.80%	0.12	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PF13637 (PFAM); IPR020683 (PFAM); IPR002110 (PFAM); PTHR23206 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1582	290968_length_1005_cvg_12.9_tip_1_3	191	d-dopachrome decarboxylase-a-like	335	2.36E-24	62.60%	0.112	IPR001398 (PFAM); G3DSA:3.30.429.10 (GENE3D); PTHR11954:SF22 (PANTHER); IPR001398 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001398 (PRODOM); IPR014347 (SUPERFAMILY); TMhelix (TMHMM)
1583	290994_length_1006_cvg_19.2_tip_1_4	217	---NA---	335			0.106	no IPS match
1584	291008_length_1006_cvg_16.6_tip_1_4	183	endoplasmic reticulum resident protein 29	335	1.04E-95	70.80%	0.767 Y	Coil (COILS); IPR011679 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR011679 (G3DSA:1.20.1150.GENE3D); IPR012883 (PFAM); PTHR12211 (PANTHER); PTHR12211:SF0 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR012336 (SUPERFAMILY); IPR011679 (SUPERFAMILY)
1585	291052_length_1008_cvg_59.2_tip_1_5	5006	hemagglutinin amebocyte aggregation factor-like	336	2.24E-41	61.00%	0.252	PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1586	291054_length_1008_cvg_8.9_tip_1_1	118	carbonyl reductase	336	2.71E-128	74.90%	0.144	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF58 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1587	291056_length_1008_cvg_2.0_tip_1_3	32	insulin-like receptor	336	4.88E-105	65.20%	0.116	IPR006212 (SMART); G3DSA:2.10.220.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000494 (PFAM); IPR006211 (PFAM); IPR000494 (G3DSA:3.80.20.GENE3D); IPR000494 (G3DSA:3.80.20.GENE3D); PTHR24416:SF95 (PANTHER); PTHR24416 (PANTHER); IPR009030 (SUPERFAMILY); SSF52058 (SUPERFAMILY)
1609	291966_length_1052_cvg_8.7_tip_1_0	139	aminoacyl trna synthase complex-interacting multifunctional protein 1	338	4.43E-100	68.30%	0.117	Coil (COILS); IPR002547 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); PTHR11586 (PANTHER); PTHR11586:SF1 (PANTHER); IPR002547 (PROSITE_PROFILES); IPR012340 (SUPERFAMILY)
1588	291226_length_1016_cvg_64.0_tip_1_4	11353	snaclec stejaggregin-a subunit beta-1-like isoform x2	339	5.60E-17	48.40%	0.305	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1589	291242_length_1017_cvg_29.2_tip_1_2	429	chorion peroxidase-like	339	5.25E-41	68.70%	0.116	IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)

1590	291274_length_1018_cvg_46.1_tip_1_1	1427	low quality protein: glutathione peroxidase 1-like	339	5.44E-87	79.30%	0.148	IPR000889 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PFAM); PTHR11592:SF21 (PANTHER); IPR000889 (PANTHER); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1591	291302_length_1020_cvg_3.3_tip_1_0	41	ww domain-containing oxidoreductase	340	1.05E-103	72.30%	0.128	IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF115 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1592	291358_length_1023_cvg_6.9_tip_1_2	83	collagen triple helix repeat family protein	341	5.96E-13	53.88%	0.095	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1593	291358_length_1023_cvg_6.9_tip_1_5	83	hypothetical protein	341	4.56E-16	54.50%	0.352 Y	no IPS match
1594	291398_length_1024_cvg_64.1_tip_1_5	20409	glyceraldehyde-3-phosphate dehydrogenase	341	0	90.30%	0.107	IPR020831 (PRINTS); IPR020828 (SMART); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020828 (PFAM); IPR020831 (PIRSF); G3DSA:3.30.360.10 (GENE3D); IPR006424 (TIGRFAM); IPR020829 (PFAM); IPR020831 (PANTHER); IPR020830 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY); SSF55347 (SUPERFAMILY)
1595	291534_length_1030_cvg_2.1_tip_1_0	29	prion-like-(q n-rich) domain-bearing protein 25 isoform x2	344	1.72E-14	42.00%	0.104	no IPS match
1596	291608_length_1033_cvg_3.0_tip_1_1	46	hemocytin	344	3.15E-38	45.40%	0.114	G3DSA:2.10.25.10 (GENE3D); IPR014853 (PFAM); IPR001846 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY)
1597	291614_length_1034_cvg_5.5_tip_1_2	74	von willebrand factor a domain-containing protein 8-like	344	7.95E-130	71.40%	0.103	IPR011042 (G3DSA:2.120.10.GENE3D); PTHR21610:SF9 (PANTHER); PTHR21610 (PANTHER)
1598	291628_length_1034_cvg_62.5_tip_1_4	1449	epidermal retinol dehydrogenase 2-like	345	3.57E-94	72.60%	0.109	Coil (COILS); IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316 (PANTHER); PTHR24316:SF289 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1599	291636_length_1034_cvg_9.1_tip_1_0	94	tissue plasminogen activator	345	5.64E-21	70.60%	0.099	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1600	291638_length_1035_cvg_11.2_tip_1_1	140	i-type lysozyme-like protein 2	345	1.71E-40	66.40%	0.102	IPR008597 (PFAM); PTHR11195:SF13 (PANTHER); IPR008597 (PANTHER); IPR018247 (PROSITE_PATTERNS)
1601	291640_length_1035_cvg_14.2_tip_1_5	219	trypsin 3	345	1.54E-57	60.80%	0.806 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR009003 (SUPERFAMILY)
1602	291790_length_1042_cvg_16.0_tip_1_1	203	brain peptide idl-like protein	347	5.10E-109	87.90%	0.107	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR20967 (PANTHER); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1603	291812_length_1043_cvg_47.6_tip_1_2	637	27 kda hemolymph	347	1.58E-30	49.50%	0.191	IPR009832 (PFAM); PTHR20997 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1604	291856_length_1045_cvg_51.2_tip_1_1	851	zinc metalloproteinase nas-4-like	348	5.31E-43	55.30%	0.907 Y	IPR001506 (PRINTS); IPR006026 (SMART); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_NEGATIVE); SSF55486 (SUPERFAMILY)

1618	292074_length_1058_cvg_4.0_tip_1_4	54	serine-threonine kinase receptor-associated protein	348	0	85.90%	0.13	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19877 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1606	291906_length_1048_cvg_39.8_tip_1_1	595	adiponectin receptor protein	349	3.06E-111	84.20%	0.282	IPR004254 (PFAM); IPR004254 (PANTHER); PTHR20855:SF15 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1608	291914_length_1049_cvg_8.0_tip_1_5	88	macrophage mannose receptor 1-like	349	5.03E-46	49.50%	0.103	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803:SF16 (PANTHER); PTHR22803 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
1605	291890_length_1048_cvg_6.5_tip_1_0	75	dehydrogenase reductase sdr family member 11-like	350	1.62E-97	74.70%	0.165	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR005639 (G3DSA:1.20.190.GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1607	291912_length_1049_cvg_8.2_tip_1_1	109	c-type mannose receptor 2	350	4.69E-16	47.30%	0.178	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802:SF149 (PANTHER); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1610	291988_length_1053_cvg_4.9_tip_1_0	64	low quality protein: hemocytin	351	4.90E-34	48.40%	0.107	IPR025155 (PFAM); SSF57603 (SUPERFAMILY)
1611	291996_length_1053_cvg_23.6_tip_1_4	214	inactive hydroxysteroid dehydrogenase-like protein 1 isoform x1	351	2.85E-97	71.90%	0.104	Coil (COILS); IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF317 (PANTHER); PTHR24316 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
1612	292014_length_1054_cvg_8.0_tip_1_0	102	serine threonine-protein kinase pim-3	352	8.31E-140	77.70%	0.174	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR017348 (PIRSF); PTHR22984 (PANTHER); PTHR22984:SF1 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1613	292018_length_1054_cvg_3.7_tip_1_0	63	probable serine carboxypeptidase cpvl isoform x1	352	8.48E-93	65.30%	0.334	IPR001563 (PRINTS); IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); PTHR11802:SF30 (PANTHER); IPR029058 (SUPERFAMILY)
1614	292032_length_1056_cvg_4.8_tip_1_4	62	laminin a	352	1.93E-53	65.80%	0.097	IPR001791 (SMART); IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10574:SF39 (PANTHER); PTHR10574 (PANTHER); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
1615	292034_length_1056_cvg_3.1_tip_1_2	49	serine protease p153	352	3.67E-08	49.80%	0.102	IPR002172 (PRINTS); IPR003609 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:3.50.4.10 (GENE3D); IPR003014 (PFAM); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); SSF57414 (SUPERFAMILY); SSF57414 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1616	292038_length_1056_cvg_22.4_tip_1_2	338	ovalbumin-related protein x-like isoform x1	352	1.23E-72	61.10%	0.198	IPR023796 (SMART); G3DSA:3.30.497.10 (GENE3D); IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); PTHR11461:SF124 (PANTHER); IPR000215 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023796 (SUPERFAMILY)
1617	292048_length_1056_cvg_7.8_tip_1_1	104	pc3-like endoprotease variant b-like	352	1.72E-30	57.20%	0.187	IPR015500 (PRINTS); IPR000209 (G3DSA:3.40.50.GENE3D); G3DSA:3.30.70.850 (GENE3D); IPR000209 (PFAM); PTHR10795:SF310 (PANTHER); IPR015500 (PANTHER); IPR023827 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009020 (SUPERFAMILY); IPR000209 (SUPERFAMILY)
1619	292084_length_1059_cvg_5.2_tip_1_4	73	5'-nucleotidase	353	1.21E-148	80.40%	0.363 Y	IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11575:SF7 (PANTHER); IPR006179 (PANTHER); IPR029052 (SUPERFAMILY)

1631	292500_length_1078_cvg_35.9_tip_1_0	495	steroid dehydrogenase	360	1.03E-116	68.80%	0.247	Coil (COILS); IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PIRSF); PTHR24316:SF68 (PANTHER); PTHR24316 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1632	292524_length_1080_cvg_54.0_tip_1_0	110785	hemocyanin subunit type 1 precursor	360	0	72.30%	0.202	IPR013788 (PRINTS); IPR000896 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005204 (PFAM); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR013788 (PANTHER); PTHR11511:SF5 (PANTHER); IPR013788 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005204 (SUPERFAMILY); IPR008922 (SUPERFAMILY)
1633	292538_length_1081_cvg_18.5_tip_1_1	231	serine protease snake	360	1.85E-69	61.20%	0.141	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24260:SF46 (PANTHER); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1635	292548_length_1081_cvg_16.6_tip_1_5	215	spondin-1	360	2.22E-82	60.30%	0.141	IPR002223 (PRINTS); IPR002223 (SMART); IPR000884 (SMART); IPR002223 (PFAM); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); G3DSA:2.20.100.10 (GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR11311:SF11 (PANTHER); PTHR11311 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
1634	292546_length_1081_cvg_16.3_tip_1_0	218	superoxide dismutase	361	1.04E-63	68.70%	0.28	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR001424 (SUPERFAMILY); IPR001424 (SUPERFAMILY); TMhelix (TMHMM)
1636	292716_length_1090_cvg_51.0_tip_1_1	732	eukaryotic translation initiation factor 3 subunit i-like	363	0	84.20%	0.121	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19877 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR027525 (HAMAP); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1637	292772_length_1093_cvg_12.8_tip_1_5	167	peroxisomal trans-2-enoyl- reductase-like	364	1.17E-126	74.10%	0.156	IPR002347 (PRINTS); PF13561 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24317 (PANTHER); SSF51735 (SUPERFAMILY)
1638	292808_length_1095_cvg_10.2_tip_1_5	182	acrosin- partial	365	5.64E-55	53.90%	0.395 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1639	292814_length_1095_cvg_9.2_tip_1_4	132	serine threonine-protein phosphatase 6 catalytic subunit	365	0	93.80%	0.102	IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668:SF24 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
1640	292830_length_1095_cvg_75.6_tip_1_3	2404	glycosyl-phosphatidylinositol-linked carbonic anhydrase	365	2.87E-85	63.40%	0.127	IPR001148 (SMART); IPR001148 (G3DSA:3.10.200.GENE3D); IPR001148 (PFAM); IPR023561 (PANTHER); IPR018338 (PROSITE_PATTERNS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
1641	292832_length_1095_cvg_4.0_tip_1_2	51	sco- partial	365	2.71E-41	54.00%	0.107	IPR002919 (PFAM); IPR025155 (PFAM); G3DSA:2.10.25.10 (GENE3D)
1642	292836_length_1096_cvg_62.7_tip_1_2	1505	cytosolic non-specific dipeptidase	365	5.74E-140	82.00%	0.291	IPR011650 (PFAM); IPR011650 (G3DSA:3.30.70.GENE3D); G3DSA:3.40.630.10 (GENE3D); IPR002933 (PFAM); PTHR11014 (PANTHER); PTHR11014:SF51 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); TMhelix (TMHMM)

1643	292872_length_1097_cvg_3.0_tip_1_0	49	u4 u6 small nuclear ribonucleoprotein prp31	366	0	89.50%	0.099	IPR012976 (SMART); IPR002687 (PFAM); IPR019175 (PFAM); IPR012976 (PFAM); IPR027105 (PANTHER); IPR002687 (PROSITE_PROFILES); SSF89124 (SUPERFAMILY)
1644	292882_length_1098_cvg_7.6_tip_1_3	99	beta-n-acetylglucosaminidase-like partial	366	1.28E-95	60.60%	0.827 Y	IPR025705 (PRINTS); IPR029019 (PFAM); IPR015883 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR029018 (G3DSA:3.30.379.GENE3D); PTHR22600 (PANTHER); PTHR22600:SF4 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR029018 (SUPERFAMILY); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1646	292922_length_1100_cvg_66.2_tip_1_5	3789	nuclease-sensitive element-binding protein 1 isoform x4	366	1.30E-59	75.70%	0.112	IPR002059 (PRINTS); IPR011129 (SMART); IPR012340 (G3DSA:2.40.50.GENE3D); IPR002059 (PFAM); PTHR11544 (PANTHER); IPR019844 (PROSITE_PATTERNS); IPR012340 (SUPERFAMILY)
1645	292902_length_1099_cvg_14.8_tip_1_3	184	wd g-beta repeat protein	367	7.35E-111	97.80%	0.133	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR016346 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1647	292936_length_1100_cvg_4.0_tip_1_0	57	---NA---	367			0.097	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS)
1648	292938_length_1100_cvg_27.0_tip_1_4	342	3-hydroxyisobutyrate dehydrogenase	367	1.23E-64	54.90%	0.126	IPR029154 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR013328 (G3DSA:1.10.1040.GENE3D); IPR006115 (PFAM); PTHR22981 (PANTHER); PTHR22981:SF7 (PANTHER); IPR029752 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY); IPR008927 (SUPERFAMILY)
1649	292942_length_1101_cvg_31.8_tip_1_0	462	phospholipase a2-like	367	2.63E-39	61.90%	0.149	IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PFAM); PTHR12253 (PANTHER); IPR013090 (PROSITE_PATTERNS); IPR016090 (SUPERFAMILY)
1650	292946_length_1101_cvg_3.0_tip_1_2	44	vitellogenin fused with superoxide dismutase	367	2.31E-40	47.40%	0.153	IPR011030 (G3DSA:1.25.10.GENE3D); IPR001747 (PFAM); PTHR23345:SF1 (PANTHER); PTHR23345 (PANTHER); IPR001747 (PROSITE_PROFILES); IPR011030 (SUPERFAMILY)
1651	292976_length_1102_cvg_41.7_tip_1_3	683	serine protease1 2	368	1.62E-55	56.90%	0.783 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1652	293034_length_1105_cvg_3.0_tip_1_2	46	isoform b	368	1.15E-95	63.40%	0.103	IPR015812 (PRINTS); G3DSA:2.10.25.10 (GENE3D); IPR014836 (G3DSA:1.20.5.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR012896 (PFAM); IPR014836 (PFAM); G3DSA:1.20.5.100 (GENE3D); IPR015812 (PANTHER); PTHR10082:SF16 (PANTHER); IPR015812 (PROSITE_PATTERNS); IPR015812 (PROSITE_PATTERNS); IPR015812 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF57196 (SUPERFAMILY); IPR012896 (SUPERFAMILY); TMhelix (TMHMM)
1653	293056_length_1105_cvg_8.2_tip_1_5	111	annexin b9-like isoform x3	368	5.56E-128	73.40%	0.107	IPR002391 (PRINTS); IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); SSF47874 (SUPERFAMILY)
1654	293070_length_1106_cvg_6.5_tip_1_5	63	cytoglobin-2-like isoform 1	368	1.81E-45	61.90%	0.137	IPR002336 (PRINTS); IPR000971 (PFAM); IPR012292 (G3DSA:1.10.490.GENE3D); PTHR11442 (PANTHER); PTHR11442:SF36 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000971 (PROSITE_PROFILES); IPR009050 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1655	293090_length_1107_cvg_11.0_tip_1_5	140	acetylcholine receptor subunit alpha-type acr-16	369	1.30E-100	57.90%	0.133	IPR006201 (PRINTS); IPR006029 (PFAM); IPR006202 (G3DSA:2.70.170.GENE3D); IPR027361 (G3DSA:1.20.120.GENE3D); IPR006202 (PFAM); IPR006201 (PANTHER); PTHR18945:SF490 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006029 (SUPERFAMILY); IPR006202 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1656	293134_length_1110_cvg_9.9_tip_1_5	195	pacifastin light chain	370	5.44E-42	41.70%	0.401 Y	IPR006552 (SMART); IPR008037 (PFAM); IPR020862 (PROSITE_PROFILES); IPR001190 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY)
1657	293138_length_1110_cvg_3.0_tip_1_0	47	aael008062- partial	370	7.58E-156	76.10%	0.114	IPR003367 (PFAM); IPR028974 (G3DSA:4.10.1080.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR008859 (PFAM); PTHR10199 (PANTHER); PTHR10199:SF76 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR008859 (PROSITE_PROFILES); IPR028974 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR028974 (SUPERFAMILY); IPR028974 (SUPERFAMILY)
1658	293146_length_1110_cvg_3.0_tip_1_4	59	perlucin-like protein	370	4.37E-19	53.20%	0.313	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1659	293168_length_1112_cvg_43.5_tip_1_5	955	zonadhesin-like isoform x1	370	4.99E-12	45.50%	0.118	IPR001846 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001846 (PROSITE_PROFILES); TMhelix (TMHMM)
1660	293190_length_1113_cvg_8.9_tip_1_3	134	inactive dipeptidyl peptidase 10	371	3.76E-99	58.80%	0.104	IPR002469 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR002469 (G3DSA:2.140.10.GENE3D); PTHR11731 (PANTHER); PTHR11731:SF93 (PANTHER); SSF82171 (SUPERFAMILY)
1661	293208_length_1113_cvg_6.1_tip_1_1	102	titin- partial	371	6.62E-20	57.80%	0.104	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
1662	293218_length_1114_cvg_7.4_tip_1_4	109	26s protease regulatory subunit 8	371	0	97.10%	0.1	Coil (COILS); IPR003593 (SMART); IPR005937 (TIGRFAM); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23073:SF12 (PANTHER); PTHR23073 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
1663	293264_length_1116_cvg_50.3_tip_1_4	814	alpha-n-acetylgalactosaminidase-like isoform x1	372	2.37E-146	87.00%	0.102	IPR002241 (PRINTS); IPR013785 (G3DSA:3.20.20.GENE3D); IPR013780 (G3DSA:2.60.40.GENE3D); PTHR11452:SF23 (PANTHER); PTHR11452 (PANTHER); IPR017853 (SUPERFAMILY); SSF51011 (SUPERFAMILY)
1664	293284_length_1117_cvg_65.3_tip_1_2	1841	epoxide hydrolase 4	372	1.76E-104	62.20%	0.091	IPR000639 (PRINTS); IPR000073 (PRINTS); IPR000073 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR10992 (PANTHER); PTHR10992:SF721 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1665	293326_length_1119_cvg_9.0_tip_1_1	124	acyl- delta desaturase	373	1.73E-159	76.60%	0.204	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351 (PANTHER); PTHR11351:SF28 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1666	293364_length_1121_cvg_27.9_tip_1_2	402	serine protease	373	2.54E-39	52.60%	0.31	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1667	293454_length_1126_cvg_4.2_tip_1_4	73	lipophorin precursor	375	2.29E-68	52.10%	0.209	IPR009454 (PFAM); IPR015255 (PFAM); IPR015817 (G3DSA:2.20.50.GENE3D); IPR015818 (G3DSA:2.20.80.GENE3D); PTHR23345 (PANTHER); IPR015819 (SUPERFAMILY)
1668	293476_length_1127_cvg_5.1_tip_1_3	76	low quality protein: leucine-rich repeat-containing protein ddb_g0290503	376	4.59E-60	59.10%	0.096	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS)
1669	293482_length_1128_cvg_6.1_tip_1_5	86	transcription initiation factor tfiid subunit 5	376	0	84.50%	0.13	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19879 (PANTHER); PTHR19879:SF1 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1671	293522_length_1129_cvg_11.9_tip_1_4	211	low quality protein: selenoprotein h	376	5.14E-20	65.40%	0.107	IPR020478 (PRINTS); IPR017956 (SMART); IPR012336 (G3DSA:3.40.30.GENE3D); IPR011893 (TIGRFAM); IPR011893 (PFAM); IPR017956 (PFAM); IPR012336 (SUPERFAMILY)
1670	293514_length_1129_cvg_5.2_tip_1_0	66	zinc finger protein 467	377	5.94E-17	42.80%	0.096	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57802 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1672	293538_length_1130_cvg_8.0_tip_1_4	106	neuroparsin-like protein	377	1.26E-18	61.30%	0.121	IPR010850 (PFAM); IPR011390 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR010850 (PRODOM); IPR009030 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1673	293556_length_1132_cvg_29.4_tip_1_0	367	dehydrogenase reductase sdr family member 7	378	3.75E-109	67.50%	0.922 Y	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF31 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1674	293566_length_1132_cvg_48.3_tip_1_0	590	low quality protein: galectin-4	378	1.06E-51	50.50%	0.162	IPR001079 (SMART); IPR001079 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001079 (PFAM); PTHR11346 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001079 (PROSITE_PROFILES); IPR001079 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
1675	293572_length_1133_cvg_2.4_tip_1_3	44	ankyrin repeat protein	378	1.34E-18	49.20%	0.107	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PF13637 (PFAM); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1676	293602_length_1134_cvg_28.4_tip_1_1	375	late trypsin	378	5.25E-49	55.70%	0.897 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR009003 (SUPERFAMILY)
1678	293632_length_1135_cvg_2.6_tip_1_4	38	cyclin-h	378	7.46E-158	81.70%	0.103	IPR013763 (SMART); IPR013763 (G3DSA:1.10.472.GENE3D); IPR006671 (PFAM); IPR027081 (TIGRFAM); IPR013763 (G3DSA:1.10.472.GENE3D); IPR027081 (PTHR10026:PANTHER); IPR015429 (PANTHER); IPR013763 (SUPERFAMILY); IPR013763 (SUPERFAMILY)

1677	293622_length_1135_cvg_3.8_tip_1_0	62	ste20-related kinase adapter protein alpha	379	1.99E-142	66.20%	0.1	G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24361:SF273 (PANTHER); PTHR24361 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1679	293646_length_1136_cvg_3.9_tip_1_4	53	protein takeout	379	5.16E-69	57.10%	0.12	IPR010562 (SMART); IPR010562 (PFAM); PTHR11008:SF9 (PANTHER); PTHR11008 (PANTHER)
1680	293660_length_1138_cvg_54.0_tip_1_5	1731	granulins precursor	379	7.73E-45	56.00%	0.152	IPR000118 (SMART); IPR000118 (PFAM); PTHR12274:SF1 (PANTHER); PTHR12274 (PANTHER); IPR000118 (PROSITE_PATTERNS); IPR000118 (PROSITE_PATTERNS); SSF57277 (SUPERFAMILY); SSF57277 (SUPERFAMILY)
1681	293692_length_1140_cvg_15.2_tip_1_2	224	lysosomal acid phosphatase	380	7.10E-118	66.50%	0.585 Y	IPR029033 (G3DSA:3.40.50.GENE3D); IPR000560 (PFAM); PTHR11567 (PANTHER); PTHR11567:SF26 (PANTHER); IPR000560 (PROSITE_PATTERNS); IPR000560 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR029033 (SUPERFAMILY)
1682	293714_length_1141_cvg_2.3_tip_1_3	42	s-antigen partial	381	1.27E-34	62.00%	0.111	Coil (COILS); Coil (COILS); Coil (COILS)
1683	293792_length_1147_cvg_62.0_tip_1_4	4870	transmembrane protease serine 13	382	8.97E-11	47.90%	0.133	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1684	293818_length_1149_cvg_5.0_tip_1_2	87	mam and ldl-receptor class a domain-containing protein c10orf112-like	383	1.93E-07	51.00%	0.111	IPR000998 (SMART); IPR000998 (PFAM); PTHR23282 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
1685	293848_length_1151_cvg_71.6_tip_1_5	1886	zinc metalloproteinase nas-4-like	383	7.18E-50	58.70%	0.21	IPR001506 (PRINTS); IPR002557 (SMART); IPR006026 (SMART); IPR002557 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); IPR002557 (G3DSA:2.170.140.GENE3D); PTHR10127 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1686	293910_length_1154_cvg_6.7_tip_1_2	95	tyrosine-protein kinase src64b	384	2.92E-141	73.70%	0.099	IPR000980 (PRINTS); IPR001452 (PRINTS); IPR020635 (SMART); IPR001452 (SMART); IPR000980 (SMART); IPR001452 (PFAM); G3DSA:3.30.200.20 (GENE3D); IPR000980 (G3DSA:3.30.505.GENE3D); IPR000980 (PFAM); G3DSA:2.30.30.40 (GENE3D); IPR001245 (PFAM); PTHR24418:SF35 (PANTHER); PTHR24418 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR000980 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); IPR000980 (SUPERFAMILY); IPR001452 (SUPERFAMILY)
1687	293930_length_1155_cvg_18.5_tip_1_1	257	multicopper oxidase	385	1.49E-55	63.80%	0.101	IPR008972 (G3DSA:2.60.40.GENE3D); IPR011706 (PFAM); PTHR11709 (PANTHER); PTHR11709:SF33 (PANTHER); IPR002355 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008972 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1688	293960_length_1157_cvg_12.7_tip_1_5	167	thioredoxin-like protein 1	385	5.73E-154	81.30%	0.132	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR010400 (G3DSA:2.60.120.GENE3D); IPR013766 (PFAM); IPR010400 (PFAM); IPR005746 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR010400 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR008979 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1689	293970_length_1158_cvg_7.8_tip_1_3	105	ankyrin repeat protein	386	3.81E-17	44.40%	0.129	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1690	293992_length_1159_cvg_36.3_tip_1_0	552	mite allergen lep d partial	387	4.50E-11	46.50%	0.514 Y	PTHR11008 (PANTHER); PTHR11008:SF13 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM)
1691	294052_length_1163_cvg_5.2_tip_1_1	78	dual specificity mitogen-activated protein kinase kinase 4-like	388	1.41E-154	91.20%	0.114	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24360:SF46 (PANTHER); PTHR24360 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)

1692	294068_length_1164_cvg_5.9_tip_1_4	91	spermatogenesis-associated protein 20	388	7.60E-173	72.20%	0.099	IPR004879 (PFAM); IPR012341 (G3DSA:1.50.10.GENE3D); PTHR12145:SF11 (PANTHER); PTHR12145 (PANTHER); IPR008928 (SUPERFAMILY)
1693	294072_length_1164_cvg_12.4_tip_1_0	149	apolipoprotein d-like	388	6.95E-31	65.20%	0.144	IPR012674 (G3DSA:2.40.128.GENE3D); IPR000566 (PFAM); PTHR10612 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1694	294104_length_1165_cvg_47.2_tip_1_3	745	prophenoloxidase activating factor	389	2.88E-130	67.70%	0.12	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1695	294114_length_1166_cvg_3.6_tip_1_0	87	er membrane protein complex subunit 10	389	2.28E-73	63.10%	0.672 Y	IPR029615 (PTHR21397:PANTHER); PTHR21397 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1696	294130_length_1167_cvg_22.8_tip_1_2	307	dnaj homolog subfamily b member 6-like	389	5.36E-77	67.80%	0.214	Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24077:SF225 (PANTHER); PTHR24077 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1698	294154_length_1168_cvg_70.1_tip_0_1	3947	twitchin isoform x2	389	4.22E-139	76.40%	0.101	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1697	294150_length_1168_cvg_5.0_tip_1_3	75	subtilisin-like protease spc6a	390	1.83E-64	59.60%	0.378 Y	IPR002884 (PFAM); IPR000209 (PFAM); IPR000209 (G3DSA:3.40.50.GENE3D); IPR008979 (G3DSA:2.60.120.GENE3D); IPR015500 (PANTHER); PTHR10795:SF340 (PANTHER); IPR023828 (PROSITE_PATTERNS); IPR000209 (SUPERFAMILY); IPR008979 (SUPERFAMILY)
1699	294174_length_1170_cvg_44.4_tip_1_3	650	meprin a subunit beta	390	6.47E-51	58.20%	0.199	IPR001506 (PRINTS); IPR006026 (SMART); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)
1700	294306_length_1179_cvg_4.9_tip_1_1	60	low quality protein: titin-like	393	2.38E-180	81.00%	0.099	IPR003599 (SMART); IPR003598 (SMART); IPR010939 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF149 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1701	294342_length_1182_cvg_14.8_tip_1_4	207	gpi-anchor transamidase	394	0	85.60%	0.781 Y	IPR001096 (PRINTS); IPR001096 (PIRSF); IPR028361 (PIRSF); IPR001096 (PFAM); IPR001096 (PANTHER); IPR028361 (PTHR12000:PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK)
1702	294350_length_1182_cvg_68.3_tip_1_0	1245	kazal-type serine protease inhibitor 1 serpin	394	4.64E-10	61.00%	0.868 Y	IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); IPR002350 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002350 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1703	294368_length_1183_cvg_37.9_tip_1_3	592	md-2-related lipid-recognition	395	9.15E-17	50.50%	0.401 Y	IPR003172 (SMART); IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014756 (SUPERFAMILY)
1704	294406_length_1187_cvg_3.7_tip_1_1	62	huga_polan ame: full=hyaluronidase short=hya ame: full=hyaluronoglucosaminidase ame: allergen=pol a 2 flags: partial	396	1.73E-72	57.00%	0.407 Y	IPR001329 (PRINTS); IPR018155 (PRINTS); IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PANTHER); PTHR11769:SF8 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY)
1705	294414_length_1188_cvg_5.0_tip_1_3	116	hyaluronidase precursor	396	4.70E-80	60.40%	0.287	IPR001329 (PRINTS); IPR018155 (PRINTS); IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); PTHR11769:SF8 (PANTHER); IPR018155 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1706	294424_length_1188_cvg_12.0_tip_1_2	185	titin isoform x1	396	9.38E-36	45.30%	0.103	Coil (COILS); Coil (COILS); Coil (COILS); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
1707	294510_length_1194_cvg_27.0_tip_1_1	406	26s protease regulatory subunit 10b	398	0	96.70%	0.097	Coil (COILS); IPR003593 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); G3DSA:1.10.8.60 (GENE3D); IPR005937 (TIGRFAM); PTHR23073 (PANTHER); PTHR23073:SF24 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
1708	294540_length_1196_cvg_33.5_tip_1_5	599	hemagglutinin proteinase	398	1.25E-43	48.80%	0.128	IPR023612 (PRINTS); IPR013856 (G3DSA:3.10.170.GENE3D); IPR011096 (PFAM); IPR025711 (PFAM); IPR013856 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY)
1709	294542_length_1196_cvg_30.3_tip_1_1	467	agap005608-pa-like protein	399	1.72E-147	76.40%	0.131	Coil (COILS); Coil (COILS); IPR011992 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR19237 (PANTHER); PTHR19237:SF20 (PANTHER); IPR018247 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); TMhelix (TMHMM)
1710	294602_length_1201_cvg_7.5_tip_1_5	123	3-hydroxyisobutyrate dehydrogenase	400	8.41E-78	57.20%	0.394 Y	IPR013328 (G3DSA:1.10.1040.GENE3D); IPR006115 (PFAM); IPR029154 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22981:SF7 (PANTHER); PTHR22981 (PANTHER); IPR029752 (PROSITE_PATTERNS); IPR008927 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
1711	294622_length_1202_cvg_61.5_tip_1_2	2513	guanine nucleotide-binding protein subunit beta-like protein	400	0	93.10%	0.136	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19868:SF0 (PANTHER); PTHR19868 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1712	294624_length_1202_cvg_41.8_tip_1_5	653	mitochondrial matrix protein p33	400	3.87E-86	67.40%	0.14	IPR003428 (G3DSA:3.10.280.GENE3D); IPR003428 (PFAM); PTHR10826 (PANTHER); PTHR10826:SF1 (PANTHER); IPR003428 (SUPERFAMILY)
1713	294656_length_1204_cvg_2.9_tip_1_1	50	neural cell adhesion molecule 1 isoform x1	401	4.14E-50	52.60%	0.111	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF40 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1721	294834_length_1216_cvg_27.1_tip_1_1	382	serine threonine-protein phosphatase 2a catalytic subunit alpha isoform	401	0	97.60%	0.176	Coil (COILS); IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668:SF216 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
1714	294680_length_1206_cvg_62.6_tip_1_3	1475	hypothetical protein DAPPUDRAFT_250423	402	3.06E-79	49.90%	0.112	IPR005320 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); IPR029062 (SUPERFAMILY)

1744	295324_length_1253_cvg_9.2_tip_1_5	132	atp-dependent rna helicase vasa	417	4.99E-115	78.20%	0.121	IPR001650 (SMART); IPR011545 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR001650 (PFAM); PTHR24031:SF168 (PANTHER); PTHR24031 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR014001 (PROSITE_PROFILES); IPR001650 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1743	295322_length_1253_cvg_24.0_tip_1_0	489	estradiol 17-beta-dehydrogenase 8	418	1.11E-88	72.40%	0.273	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR013968 (SMART); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316 (PANTHER); PTHR24316:SF254 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
1745	295374_length_1256_cvg_52.8_tip_1_0	867	isoform b	419	5.96E-20	41.90%	0.101	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); TMhelix (TMHMM)
1746	295408_length_1259_cvg_20.7_tip_1_5	291	achain structure and binding determinants of the recombinant kringle-2 domain of human plasminogen to an internal peptide from a group a streptococcal surface protein	419	1.15E-28	63.00%	0.101	PR00018 (PRINTS); IPR000001 (SMART); G3DSA:2.40.20.10 (GENE3D); IPR000001 (PFAM); IPR022041 (PFAM); PTHR24259 (PANTHER); IPR018056 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000001 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); TMhelix (TMHMM)
1747	295410_length_1259_cvg_45.2_tip_1_1	799	ves g 5 allergen	420	5.42E-47	52.50%	0.860 Y	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR002172 (SMART); IPR002172 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1748	295466_length_1264_cvg_2.0_tip_1_2	42	zinc finger and btb domain-containing protein 24	421	7.19E-69	57.30%	0.113	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1749	295474_length_1264_cvg_14.3_tip_1_3	245	venom protease-like	422	6.33E-114	58.80%	0.146	IPR001314 (PRINTS); IPR001254 (SMART); IPR006604 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR022700 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF97 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1750	295506_length_1267_cvg_68.2_tip_1_0	2203	serine proteinase stubble	423	9.01E-66	73.30%	0.155	Coil (COILS); IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1751	295510_length_1268_cvg_17.4_tip_1_3	255	low affinity immunoglobulin epsilon fc receptor	423	1.44E-08	51.40%	0.105	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
1752	295550_length_1270_cvg_68.1_tip_0_5	2242	low quality protein: twitchin-like	423	4.69E-178	78.90%	0.124	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF148 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1753	295600_length_1274_cvg_33.3_tip_1_2	570	acid ceramidase	424	1.93E-157	71.60%	0.680 Y	Coil (COILS); IPR016699 (PIRSF); IPR029130 (PFAM); IPR029132 (PFAM); SignalP-noTM (SIGNALP_EUK)
1754	295622_length_1274_cvg_16.8_tip_1_0	344	adp-ribosylation factor-like protein 8b-a	425	3.71E-124	97.70%	0.118	IPR006689 (PRINTS); IPR024156 (SMART); IPR003579 (SMART); IPR006687 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR11711:SF122 (PANTHER); PTHR11711 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)

1767	295932_length_1298_cvg_57.5_tip_1_1	1543	phospholipid-hydroperoxide glutathione peroxidase	433	3.15E-80	80.50%	0.143	IPR000889 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PFAM); IPR000889 (PANTHER); IPR029760 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1768	295984_length_1304_cvg_6.4_tip_1_3	90	27 kda hemolymph	435	4.38E-45	56.10%	0.148	IPR009832 (PFAM); PTHR20997 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1769	296022_length_1306_cvg_8.6_tip_1_2	154	receptor-type tyrosine-protein phosphatase epsilon isoform x1	435	6.82E-87	52.60%	0.175	Coil (COILS); IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); IPR029021 (SUPERFAMILY)
1770	296032_length_1307_cvg_6.1_tip_1_3	139	variant surface antigen e	436	5.28E-20	44.50%	0.108	no IPS match
1771	296142_length_1319_cvg_16.8_tip_1_5	333	epidermal retinol dehydrogenase 2	439	1.38E-105	71.30%	0.153	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF289 (PANTHER); PTHR24316 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1773	296202_length_1322_cvg_11.0_tip_1_5	151	n-acetylglucosamine-1-phosphotransferase subunit gamma-like	440	4.57E-71	59.60%	0.349 Y	Coil (COILS); IPR009011 (G3DSA:2.70.130.GENE3D); PF13015 (PFAM); PTHR12630 (PANTHER); PTHR12630:SF6 (PANTHER); IPR009011 (SUPERFAMILY)
1772	296184_length_1321_cvg_66.3_tip_1_3	3356	apolipoprotein d	441	5.36E-73	62.40%	0.142	IPR003057 (PRINTS); IPR012674 (G3DSA:2.40.128.GENE3D); IPR000566 (PFAM); PTHR10612 (PANTHER); PTHR10612:SF7 (PANTHER); IPR022272 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1774	296220_length_1325_cvg_14.1_tip_1_3	295	gtp-binding protein sar1b	442	1.02E-124	93.20%	0.138	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR005225 (TIGRFAM); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF133 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006687 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1775	296266_length_1328_cvg_5.9_tip_1_0	99	maltase a5	443	1.01E-168	69.40%	0.164	IPR006589 (SMART); IPR006047 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); G3DSA:3.90.400.10 (GENE3D); IPR015902 (PANTHER); PTHR10357:SF76 (PANTHER); IPR017853 (SUPERFAMILY)
1776	296268_length_1328_cvg_58.4_tip_1_4	3867	low quality protein: glutathione peroxidase 3	443	3.87E-59	63.90%	0.21	IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PFAM); IPR000889 (PANTHER); IPR029760 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
1777	296276_length_1329_cvg_55.1_tip_0_0	1151	diphenol oxidase	443	4.38E-20	65.20%	0.1	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1778	296288_length_1330_cvg_11.1_tip_1_1	219	atpase family aaa domain-containing protein 1-b	443	4.49E-166	78.10%	0.121	IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23074:SF20 (PANTHER); PTHR23074 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
1779	296310_length_1332_cvg_65.4_tip_1_4	3284	scp-like extracellular domain containing protein 1	444	4.21E-70	62.10%	0.295	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); PTHR10334:SF174 (PANTHER); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1780	296312_length_1332_cvg_4.8_tip_1_5	94	glutamate-rich wd repeat-containing protein 1	444	1.60E-145	74.50%	0.108	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22850 (PANTHER); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1781	296376_length_1337_cvg_27.6_tip_1_0	456	chymotrypsinogen a	446	2.97E-95	59.30%	0.831 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24260:SF47 (PANTHER); PTHR24260 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1782	296382_length_1338_cvg_84.0_tip_1_4	2771	membrane glycoprotein lig-	446	3.02E-20	47.60%	0.434 Y	IPR003591 (SMART); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF52058 (SUPERFAMILY)
1783	296386_length_1338_cvg_15.4_tip_1_3	308	platelet-activating factor acetylhydrolase	446	4.89E-103	57.20%	0.135	Coil (COILS); IPR016715 (PIRSF); IPR005065 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR005065 (PANTHER); IPR029058 (SUPERFAMILY)
1784	296400_length_1340_cvg_12.1_tip_1_0	204	alpha beta hydrolase domain-containing protein 13	447	2.04E-142	75.00%	0.105	IPR029059 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR12277 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1785	296424_length_1342_cvg_17.6_tip_1_4	305	3-hydroxyisobutyrate dehydrogenase	447	1.35E-65	55.40%	0.16	IPR006115 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); IPR029154 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22981:SF7 (PANTHER); IPR029752 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY); IPR008927 (SUPERFAMILY)
1786	296444_length_1344_cvg_3.4_tip_1_2	73	zinc finger protein glis2-like	448	7.41E-77	75.90%	0.102	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR19818 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1787	296492_length_1349_cvg_9.8_tip_1_4	192	g-protein coupled receptor mth2-like isoform x2	450	1.97E-90	54.50%	0.127	IPR000832 (PFAM); IPR010596 (PFAM); IPR023311 (G3DSA:2.170.180.GENE3D); PTHR12011:SF164 (PANTHER); PTHR12011 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); SSF63877 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1788	296506_length_1351_cvg_5.6_tip_1_5	115	mam and ldl-receptor class a domain-containing protein 1-like	450	9.23E-16	40.00%	0.605 Y	IPR002172 (SMART); IPR000998 (SMART); IPR002172 (PFAM); IPR000998 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR23282 (PANTHER); PTHR23282:SF75 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1789	296512_length_1353_cvg_26.6_tip_1_0	473	annexin a5-like	451	2.40E-18	62.30%	0.102	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)

1790	296548_length_1356_cvg_4.1_tip_1_4	95	latrophilin-3 isoform x10	452	2.57E-41	46.30%	0.109	IPR000832 (PRINTS); IPR000203 (SMART); IPR022624 (PFAM); IPR000203 (PFAM); IPR000832 (PFAM); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000203 (PROSITE_PROFILES); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1791	296556_length_1356_cvg_23.1_tip_1_5	300	mam and ldl-receptor class a domain-containing protein 1	452	5.89E-35	46.40%	0.107	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR23282 (PANTHER); PTHR23282:SF67 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1792	296572_length_1359_cvg_13.3_tip_1_0	224	protein spaetzle	453	7.29E-31	53.20%	0.256	PTHR23199 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029034 (SUPERFAMILY); TMhelix (TMHMM)
1793	296590_length_1360_cvg_49.9_tip_1_5	3900	astakine variant 1	453	3.09E-20	62.00%	0.186	G3DSA:2.10.80.10 (GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002890 (PFAM); PTHR11412 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
1794	296592_length_1360_cvg_7.8_tip_1_0	115	alpha-2-macroglobulin-like protein 1 isoform x2	454	5.32E-119	59.20%	0.649 Y	no IPS match
1795	296596_length_1361_cvg_21.6_tip_1_0	393	f5 8 type c domain protein	454	7.57E-31	38.40%	0.148	IPR008160 (PFAM); PTHR24023 (PANTHER)
1796	296596_length_1361_cvg_21.6_tip_1_3	393	collagen alpha-1 chain	454	4.66E-36	44.10%	0.101	IPR013763 (SMART); IPR013763 (G3DSA:1.10.472.GENE3D); IPR006671 (PFAM); IPR015429 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013763 (SUPERFAMILY); IPR013763 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1797	296612_length_1361_cvg_6.5_tip_1_4	154	cyclin-c	454	9.78E-157	91.20%	0.124	Coil (COILS); IPR001211 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR12253 (PANTHER); IPR016090 (SUPERFAMILY)
1798	296614_length_1362_cvg_59.2_tip_1_5	1535	group 3 secretory phospholipase partial	454	1.52E-87	55.90%	0.14	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24292 (PANTHER); PTHR24292:SF24 (PANTHER); IPR017972 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY)
1799	296634_length_1364_cvg_14.3_tip_1_5	237	cytochrome p450 3a4-like	454	3.24E-70	59.70%	0.164	IPR004104 (PFAM); IPR000683 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); G3DSA:3.30.360.10 (GENE3D); PTHR22604:SF92 (PANTHER); PTHR22604 (PANTHER); SSF51735 (SUPERFAMILY); SSF55347 (SUPERFAMILY)
1800	296638_length_1365_cvg_7.9_tip_1_0	148	uncharacterized oxidoreductase yrbe-like	455	3.52E-142	68.50%	0.106	Coil (COILS); IPR020067 (SMART); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR020067 (PFAM); IPR018933 (PFAM); PTHR11309:SF80 (PANTHER); IPR015526 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020067 (PROSITE_PROFILES); IPR001134 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY); IPR020067 (SUPERFAMILY); TMhelix (TMHMM)
1801	296644_length_1365_cvg_6.0_tip_1_0	156	secreted frizzled-related protein 5	455	1.27E-117	63.80%	0.294	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22844 (PANTHER); PTHR22844:SF166 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
1803	296664_length_1367_cvg_15.8_tip_1_2	282	wd repeat-containing protein 86-like	455	1.31E-78	68.80%	0.11	

1802	296660_length_1366_cvg_30.2_tip_1_3	546	na+ h+ exchange regulatory cofactor nhe-rf2	456	1.22E-08	68.83%	0.109	no IPS match
1804	296690_length_1370_cvg_7.9_tip_1_3	144	dnaj homolog subfamily a member 1	457	0	85.90%	0.156	IPR001623 (PRINTS); IPR001623 (SMART); IPR001305 (G3DSA:2.10.230.GENE3D); IPR001305 (PFAM); G3DSA:2.60.260.20 (GENE3D); IPR001623 (G3DSA:1.10.287.GENE3D); IPR002939 (PFAM); IPR001623 (PFAM); G3DSA:2.60.260.20 (GENE3D); PTHR24076:SF75 (PANTHER); PTHR24076 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR012724 (HAMAP); IPR001623 (PROSITE_PROFILES); IPR001305 (PROSITE_PROFILES); IPR001305 (SUPERFAMILY); IPR008971 (SUPERFAMILY); IPR001623 (SUPERFAMILY); IPR008971 (SUPERFAMILY)
1805	296702_length_1370_cvg_6.9_tip_1_1	119	---NA---	457			0.106	Coil (COILS); Coil (COILS); Coil (COILS)
1806	296710_length_1370_cvg_12.6_tip_1_0	252	lethal giant larvae partial	457	0	76.70%	0.219	IPR000664 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR013577 (PFAM); PTHR10241 (PANTHER); PTHR10241:SF28 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1807	296716_length_1371_cvg_10.9_tip_1_4	159	matrix metalloproteinase-9-like	457	1.27E-09	48.70%	0.149	IPR000562 (SMART); IPR000562 (G3DSA:2.10.10.GENE3D); IPR000562 (PFAM); IPR000562 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY)
1808	296754_length_1375_cvg_30.1_tip_1_0	547	regulatory particle triple-a atpase isoform a	459	0	97.00%	0.105	IPR003593 (SMART); IPR005937 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); PTHR23073 (PANTHER); PTHR23073:SF9 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
1809	296760_length_1375_cvg_5.5_tip_1_0	127	insulin-like growth factor-binding protein complex acid labile subunit	459	1.40E-65	55.90%	0.372 Y	SM00365 (SMART); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1810	296834_length_1384_cvg_45.5_tip_1_5	976	hypothetical protein DAPPUDRAFT_308200	461	8.66E-35	49.70%	0.121	IPR010562 (SMART); IPR010562 (PFAM); PTHR11008:SF9 (PANTHER); PTHR11008 (PANTHER); IPR020234 (PRODOM)
1811	296848_length_1385_cvg_16.4_tip_1_4	297	protein tumorous imaginal mitochondrial-like isoform x2	462	0	79.80%	0.269	IPR001623 (PRINTS); IPR001623 (SMART); IPR001305 (G3DSA:2.10.230.GENE3D); IPR001623 (G3DSA:1.10.287.GENE3D); G3DSA:2.60.260.20 (GENE3D); IPR001623 (PFAM); IPR002939 (PFAM); IPR001305 (PFAM); PTHR24076:SF79 (PANTHER); PTHR24076 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR012724 (HAMAP); IPR001305 (PROSITE_PROFILES); IPR001623 (PROSITE_PROFILES); IPR001305 (SUPERFAMILY); IPR001623 (SUPERFAMILY); IPR008971 (SUPERFAMILY); IPR008971 (SUPERFAMILY)
1812	296912_length_1391_cvg_8.6_tip_1_4	170	carboxypeptidase n subunit 2	464	2.62E-18	41.80%	0.286	IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
1814	296940_length_1394_cvg_7.8_tip_1_2	162	thromboxane a synthase-like protein	464	1.08E-112	58.60%	0.271	IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24292:SF24 (PANTHER); PTHR24292 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
1813	296928_length_1393_cvg_26.2_tip_1_3	397	laccase-5- partial	465	1.68E-131	63.80%	0.253	IPR008972 (G3DSA:2.60.40.GENE3D); IPR011707 (PFAM); IPR008972 (G3DSA:2.60.40.GENE3D); IPR001117 (PFAM); PTHR11709 (PANTHER); PTHR11709:SF33 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR008972 (SUPERFAMILY); IPR008972 (SUPERFAMILY); TMhelix (TMHMM)

1823	297086_length_1412_cvg_3.1_tip_1_5	79	protein turtle	470	5.56E-69	49.90%	0.104	IPR003598 (SMART); IPR003599 (SMART); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF510 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM)
1824	297104_length_1414_cvg_14.4_tip_1_4	235	acyl- delta desaturase	471	1.40E-129	71.50%	0.341 Y	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351:SF28 (PANTHER); PTHR11351 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1825	297114_length_1414_cvg_7.0_tip_1_2	121	sparc-related modular calcium-binding protein 2	471	4.10E-67	66.00%	0.101	IPR000716 (SMART); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); IPR019577 (PFAM); PTHR12352:SF3 (PANTHER); PTHR12352 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000716 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); IPR000716 (SUPERFAMILY)
1827	297122_length_1415_cvg_8.2_tip_1_5	132	casein kinase ii subunit alpha	471	0	94.30%	0.254	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24054 (PANTHER); PTHR24054:SF28 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1826	297118_length_1415_cvg_16.3_tip_1_4	271	#NAME?	472	1.06E-138	78.30%	0.139	IPR002347 (PRINTS); PF13561 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24315:SF2 (PANTHER); PTHR24315 (PANTHER); SSF51735 (SUPERFAMILY)
1828	297132_length_1416_cvg_5.0_tip_1_1	90	protein sda1 homolog isoform x2	472	3.35E-165	72.50%	0.154	IPR007949 (PFAM); IPR027312 (PTHR12730:PANTHER); PTHR12730 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR016024 (SUPERFAMILY)
1829	297186_length_1422_cvg_72.4_tip_1_0	59683	cathepsin partial	474	2.58E-144	75.70%	0.108	IPR000668 (PRINTS); IPR000668 (SMART); IPR013201 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR013201 (PFAM); IPR000668 (PFAM); IPR013128 (PANTHER); PTHR12411:SF57 (PANTHER); IPR025661 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
1830	297194_length_1422_cvg_15.8_tip_1_1	244	hydroxyacyl dehydrogenase	474	4.04E-128	83.50%	0.251	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF251 (PANTHER); IPR020904 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SSF51735 (SUPERFAMILY)
1831	297200_length_1423_cvg_12.7_tip_1_5	203	er degradation-enhancing alpha-mannosidase-like protein 2	474	3.39E-83	74.00%	0.106	IPR001382 (PRINTS); IPR001382 (PFAM); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PANTHER); PTHR11742:SF37 (PANTHER); IPR001382 (SUPERFAMILY)
1832	297202_length_1423_cvg_7.0_tip_1_3	125	vitellogenin fused with superoxide dismutase	475	1.69E-30	48.90%	0.109	IPR001846 (SMART); IPR001846 (PFAM); PTHR23345 (PANTHER); PTHR23345:SF1 (PANTHER); IPR001846 (PROSITE_PROFILES)
1833	297210_length_1425_cvg_7.2_tip_1_5	140	serpin 3	475	1.32E-105	64.90%	0.835 Y	IPR023796 (SMART); IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); G3DSA:3.30.497.10 (GENE3D); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); SignalP-noTM (SIGNALP_EUK); IPR023796 (SUPERFAMILY)

1834	297222_length_1427_cvg_22.4_tip_1_3	470	prophenoloxidase activating factor	476	2.49E-133	65.90%	0.177	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1835	297234_length_1429_cvg_5.5_tip_1_4	118	peroxisomal sarcosine oxidase-like	476	7.15E-103	60.40%	0.244	G3DSA:3.30.9.10 (GENE3D); IPR006076 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR10961:SF7 (PANTHER); PTHR10961 (PANTHER); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY)
1837	297274_length_1435_cvg_33.5_tip_1_2	678	serine threonine-protein phosphatase alpha-2 isoform	478	0	97.40%	0.163	IPR006186 (PRINTS); IPR006186 (SMART); IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); PTHR11668:SF213 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
1836	297272_length_1435_cvg_43.4_tip_1_3	1011	lipase 3	479	4.42E-141	67.70%	0.343 Y	IPR000073 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR006693 (PFAM); PTHR11005 (PANTHER); PTHR11005:SF6 (PANTHER); IPR029058 (SUPERFAMILY)
1838	297308_length_1440_cvg_10.0_tip_1_0	186	ves g 5 allergen	480	4.61E-44	53.20%	0.188	IPR002172 (PRINTS); IPR014044 (SMART); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR014044 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1839	297312_length_1440_cvg_59.0_tip_1_1	1601	von willebrand factor like 1	480	3.79E-19	41.60%	0.107	IPR001007 (PFAM); IPR001007 (PROSITE_PATTERNS); IPR001007 (PROSITE_PROFILES); IPR006207 (PROSITE_PROFILES); SSF57603 (SUPERFAMILY)
1840	297326_length_1442_cvg_17.0_tip_1_1	330	apolipoprotein d	481	9.62E-08	45.60%	0.135	IPR012674 (G3DSA:2.40.128.GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011038 (SUPERFAMILY)
1841	297348_length_1443_cvg_17.4_tip_1_0	279	26s protease regulatory subunit 7	481	0	95.90%	0.186	IPR003593 (SMART); IPR005937 (TIGRFAM); G3DSA:1.10.8.60 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); PTHR23073 (PANTHER); PTHR23073:SF13 (PANTHER); IPR003960 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1842	297358_length_1444_cvg_7.6_tip_1_2	130	tyrosine-protein phosphatase lar	481	0	82.20%	0.124	IPR003961 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19134:SF199 (PANTHER); PTHR19134 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM)
1843	297368_length_1446_cvg_58.0_tip_1_4	1956	aminoacylase-1 isoform x1	482	1.77E-154	69.10%	0.264	IPR002933 (PFAM); IPR011650 (PFAM); IPR010159 (PIRSF); G3DSA:3.40.630.10 (GENE3D); IPR010159 (TIGRFAM); IPR011650 (G3DSA:3.30.70.GENE3D); PTHR11014 (PANTHER); PTHR11014:SF8 (PANTHER); IPR001261 (PROSITE_PATTERNS); IPR001261 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); IPR011650 (SUPERFAMILY)
1844	297380_length_1447_cvg_6.2_tip_1_1	142	ankyrin repeat and kh domain-containing protein 1-like	482	5.86E-40	51.20%	0.112	Coil (COILS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR23206 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1845	297392_length_1448_cvg_17.4_tip_1_3	340	venom carboxylesterase-6	483	2.26E-92	58.40%	0.212	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR019826 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY)

1846	297434_length_1453_cvg_60.9_tip_1_2	2756	lipase 3	484	8.35E-142	67.30%	0.171	IPR006693 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR000073 (PFAM); PTHR11005 (PANTHER); PTHR11005:SF6 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1847	297456_length_1454_cvg_24.3_tip_1_3	302	adiponectin receptor protein	485	3.15E-151	70.70%	0.156	IPR004254 (PFAM); PTHR20855:SF15 (PANTHER); IPR004254 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1848	297474_length_1456_cvg_82.0_tip_1_2	4246	ferritin 2 light chain homologue	485	1.33E-34	53.70%	0.843 Y	IPR012347 (G3DSA:1.20.1260.GENE3D); IPR008331 (PFAM); IPR001519 (PANTHER); PTHR11431:SF28 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR009040 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009078 (SUPERFAMILY)
1849	297562_length_1469_cvg_34.0_tip_1_3	4421	universal minicircle sequence binding protein	490	2.94E-27	53.00%	0.113	Coil (COILS); Coil (COILS); IPR001878 (SMART); IPR001878 (G3DSA:4.10.60.GENE3D); IPR001878 (G3DSA:4.10.60.GENE3D); IPR001878 (PFAM); PTHR23002 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (SUPERFAMILY); IPR001878 (SUPERFAMILY); IPR001878 (SUPERFAMILY); IPR001878 (SUPERFAMILY)
1850	297580_length_1471_cvg_28.1_tip_1_1	770	perlucin-like protein	490	2.47E-19	53.70%	0.864 Y	Coil (COILS); IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1851	297622_length_1475_cvg_8.5_tip_1_4	179	12 kda fk506-binding protein	492	1.23E-61	90.10%	0.166	IPR001179 (PFAM); G3DSA:3.10.50.40 (GENE3D); PTHR10516:SF272 (PANTHER); IPR023566 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY)
1874	297934_length_1523_cvg_56.4_tip_1_1	279613	hemocyanin subunit type 2 precursor	492	0	74.50%	0.101	IPR005203 (G3DSA:2.60.40.GENE3D); IPR005203 (PFAM); IPR000896 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR013788 (PANTHER); IPR002227 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008922 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
1852	297638_length_1478_cvg_3.0_tip_1_3	67	endoplasmic reticulum resident protein 44 isoform x3	493	0	79.10%	0.252	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PF13848 (PFAM); PTHR18929 (PANTHER); PTHR18929:SF49 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1853	297648_length_1478_cvg_8.6_tip_1_4	161	lysosomal alpha-mannosidase	493	5.13E-156	65.70%	0.147	IPR015341 (SMART); G3DSA:1.10.287.530 (GENE3D); IPR015341 (PFAM); IPR011682 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); G3DSA:2.70.98.30 (GENE3D); PTHR11607 (PANTHER); PTHR11607:SF3 (PANTHER); IPR011013 (SUPERFAMILY); IPR028995 (SUPERFAMILY)
1854	297650_length_1479_cvg_37.3_tip_1_3	736	aminoacylase-1	493	0	75.60%	0.101	G3DSA:3.40.630.10 (GENE3D); IPR011650 (G3DSA:3.30.70.GENE3D); IPR002933 (PFAM); IPR011650 (PFAM); IPR010159 (PIRSF); IPR010159 (TIGRFAM); PTHR11014:SF8 (PANTHER); PTHR11014 (PANTHER); IPR001261 (PROSITE_PATTERNS); IPR001261 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011650 (SUPERFAMILY); SSF53187 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1862	297756_length_1494_cvg_5.8_tip_1_4	105	sulfhydryl oxidase 2-like	498	5.70E-80	54.20%	0.108	IPR017905 (PFAM); IPR017905 (G3DSA:1.20.120.GENE3D); PTHR22897:SF8 (PANTHER); PTHR22897 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017905 (PROSITE_PROFILES); IPR017905 (SUPERFAMILY); TMhelix (TMHMM)
1863	297760_length_1496_cvg_5.7_tip_1_2	117	low-density lipoprotein receptor-related protein 2	498	8.47E-32	49.50%	0.108	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1864	297776_length_1498_cvg_55.8_tip_1_0	1417	fk506-binding protein 2 isoform x2	500	2.48E-99	79.00%	0.234	IPR011992 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); IPR023566 (PANTHER); PTHR10516:SF252 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002048 (PROSITE_PROFILES); IPR001179 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); SSF54534 (SUPERFAMILY); TMhelix (TMHMM)
1889	298156_length_1550_cvg_13.0_tip_1_3	264	lissencephaly-1 homolog isoform x1	500	0	91.90%	0.206	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1865	297800_length_1501_cvg_17.9_tip_1_0	333	neurofilament triplet h protein	501	1.43E-28	51.70%	0.108	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1866	297812_length_1503_cvg_8.6_tip_1_5	174	collagen alpha-1 chain-like	501	8.70E-121	81.50%	0.154	IPR001442 (SMART); IPR001442 (G3DSA:2.170.240.GENE3D); IPR001442 (PFAM); PTHR24023:SF381 (PANTHER); PTHR24023 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001442 (PROSITE_PROFILES); IPR001442 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
1867	297838_length_1506_cvg_32.4_tip_1_1	736	torsin- partial	502	1.39E-109	66.80%	0.441 Y	Coil (COILS); IPR027417 (G3DSA:3.40.50.GENE3D); IPR010448 (PFAM); IPR010448 (PANTHER); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1868	297866_length_1511_cvg_6.2_tip_1_2	135	scaffolding protein	503	1.01E-19	64.50%	0.099	Coil (COILS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
1869	297878_length_1514_cvg_3.0_tip_1_0	73	hemicentin-1 isoform x1	505	6.59E-79	58.50%	0.101	IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13927 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11640 (PANTHER); PTHR11640:SF6 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)

1870	297896_length_1516_cvg_60.5_tip_1_5	27199	myosin heavy chain	505	0	88.80%	0.099	Coil (COILS); Coil (COILS); Coil (COILS); IPR000048 (SMART); IPR002928 (PFAM); G3DSA:1.20.5.340 (GENE3D); IPR027401 (G3DSA:4.10.270.GENE3D); PTHR13140 (PANTHER); PTHR13140:SF364 (PANTHER); IPR000048 (PROSITE_PROFILES); IPR001609 (PROSITE_PROFILES); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); IPR027417 (SUPERFAMILY); SSF90257 (SUPERFAMILY)
1871	297900_length_1517_cvg_52.1_tip_1_2	1715	masquerade-like protein	505	1.29E-63	49.40%	0.122	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); PTHR24268:SF95 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1872	297906_length_1517_cvg_21.1_tip_1_2	423	tribbles homolog 2	505	2.99E-123	74.40%	0.134	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR024104 (PANTHER); PTHR22961:SF4 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1873	297922_length_1522_cvg_60.4_tip_1_3	6590	nidogen-2 isoform x5	508	5.80E-20	52.40%	0.735 Y	IPR000716 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PFAM); IPR022339 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY)
1875	297942_length_1524_cvg_25.0_tip_1_2	557	agap007053-pa-like protein	508	9.14E-75	49.90%	0.162	Coil (COILS); IPR000716 (SMART); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); PTHR12352 (PANTHER); PTHR12352:SF9 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY); TMhelix (TMHMM)
1876	297982_length_1528_cvg_16.7_tip_1_3	265	cytochrome p450 monooxygenase	510	1.83E-125	58.70%	0.189	Coil (COILS); IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1877	297990_length_1529_cvg_9.0_tip_1_0	159	dnaj homolog subfamily b member 11	510	0	84.20%	0.860 Y	IPR001623 (PRINTS); IPR001623 (SMART); G3DSA:2.60.260.20 (GENE3D); G3DSA:2.60.260.20 (GENE3D); IPR002939 (PFAM); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24077 (PANTHER); PTHR24077:SF210 (PANTHER); IPR018253 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001623 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR008971 (SUPERFAMILY); IPR001623 (SUPERFAMILY); IPR008971 (SUPERFAMILY); TMhelix (TMHMM)
1878	297996_length_1529_cvg_15.0_tip_1_1	232	chitinase domain-containing protein 1 isoform x1	510	1.74E-149	70.30%	0.165	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF135 (PANTHER); PTHR11177 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1879	297998_length_1529_cvg_6.0_tip_1_0	121	serine threonine-protein kinase warts	510	0	90.20%	0.111	IPR002290 (SMART); IPR000961 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); IPR028741 (PTHR24356:PANTHER); PTHR24356 (PANTHER); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1880	298018_length_1534_cvg_32.6_tip_1_4	723	nidogen- partial	511	1.03E-106	73.40%	0.101	IPR000033 (SMART); IPR000033 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR10529 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY); TMhelix (TMHMM)

1882	298022_length_1534_cvg_4.3_tip_1_5	97	collagen and calcium-binding egf domain-containing protein 1	511	4.46E-100	52.80%	0.307	Coil (COILS); IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR008160 (PFAM); PF14670 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24023 (PANTHER); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
1881	298022_length_1534_cvg_4.3_tip_1_0	97	hypothetical protein CRE_06355	512	7.35E-07	44.00%	0.137	no IPS match
1883	298032_length_1536_cvg_12.9_tip_1_3	236	von willebrand factor like 1	512	1.27E-07	38.75%	0.114	IPR001007 (PROSITE_PATTERNS); PD968187 (PRODOM); IPR001007 (PROSITE_PROFILES)
1884	298056_length_1538_cvg_35.0_tip_1_5	643	scp-like extracellular domain containing protein 1	512	7.00E-37	49.40%	0.417 Y	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR002172 (SMART); IPR014044 (SMART); IPR014044 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR014044 (G3DSA:3.40.33.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR001283 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR014044 (SUPERFAMILY); TMhelix (TMHMM)
1885	298088_length_1541_cvg_5.2_tip_1_0	97	carbohydrate sulfotransferase 11-like	514	9.54E-67	55.00%	0.176	IPR005331 (PFAM); IPR018011 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1886	298092_length_1543_cvg_3.9_tip_1_1	74	dnaj homolog subfamily b member 12	514	1.19E-135	81.60%	0.1	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR015399 (PFAM); IPR001623 (PFAM); PTHR24077:SF239 (PANTHER); PTHR24077 (PANTHER); IPR018253 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM)
1887	298120_length_1546_cvg_20.8_tip_1_5	436	acidic phospholipase a2 pa4 isoform x2	515	9.19E-43	56.90%	0.846 Y	IPR001211 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR12253 (PANTHER); IPR013090 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR016090 (SUPERFAMILY); TMhelix (TMHMM)
1888	298132_length_1547_cvg_9.3_tip_1_3	156	microfibrillar-associated protein 1-like	516	5.18E-177	78.00%	0.1	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR009730 (PFAM); IPR009730 (PANTHER); PTHR15327:SF0 (PANTHER)
1890	298158_length_1550_cvg_6.8_tip_1_0	153	dentin sialophospho	517	5.74E-23	43.10%	0.113	no IPS match
1891	298196_length_1555_cvg_23.1_tip_1_3	360	iron zinc purple acid phosphatase-like protein	519	1.39E-129	78.40%	0.101	IPR029052 (G3DSA:3.60.21.GENE3D); IPR025733 (PFAM); IPR004843 (PFAM); PTHR22953 (PANTHER); PTHR22953:SF9 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1892	298224_length_1557_cvg_6.2_tip_1_5	135	f-box wd repeat-containing protein 7	519	0	87.90%	0.104	IPR020472 (PRINTS); IPR001810 (SMART); IPR001680 (SMART); G3DSA:1.20.1280.50 (GENE3D); IPR001810 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22844 (PANTHER); PTHR22844:SF116 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001810 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR001810 (SUPERFAMILY)
1893	298250_length_1561_cvg_55.2_tip_1_3	2208	beta-hexosaminidase subunit beta isoform x1	521	0	68.80%	0.289	IPR025705 (PRINTS); IPR025705 (PIRSF); IPR029019 (PFAM); IPR015883 (PFAM); IPR029018 (G3DSA:3.30.379.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR22600:SF7 (PANTHER); PTHR22600 (PANTHER); IPR017853 (SUPERFAMILY); IPR029018 (SUPERFAMILY)
1894	298278_length_1565_cvg_60.3_tip_1_4	3928	ferritin 1-like protein a	522	3.93E-45	65.00%	0.499 Y	IPR012347 (G3DSA:1.20.1260.GENE3D); IPR008331 (PFAM); IPR001519 (PANTHER); PTHR11431:SF29 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009040 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009078 (SUPERFAMILY)

1895	298280_length_1566_cvg_11.8_tip_1_1	311	protocadherin fat 4	522	1.17E-68	48.20%	0.112	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); PTHR24027 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); Coil (COILS); Coil (COILS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1896	298282_length_1566_cvg_20.9_tip_1_4	334	---NA---	522			0.109	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR007287 (PFAM); IPR001680 (PFAM); PTHR22851:SF0 (PANTHER); PTHR22851 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1897	298332_length_1573_cvg_19.2_tip_1_1	409	ddb1- and cul4-associated factor 13-like	524	0	80.80%	0.101	IPR000668 (PRINTS); IPR013201 (SMART); IPR000668 (SMART); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR013201 (PFAM); PTHR12411:SF57 (PANTHER); IPR013128 (PANTHER); IPR025661 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
1898	298336_length_1573_cvg_34.2_tip_1_4	664	cathepsin I	524	4.40E-167	77.20%	0.116	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1899	298338_length_1573_cvg_22.4_tip_1_2	508	plasminogen activator spa	524	6.97E-84	64.60%	0.486 Y	IPR004878 (PFAM); IPR004878 (PANTHER); PTHR21522:SF41 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1900	298346_length_1575_cvg_8.0_tip_1_4	189	otopetrin-2-like isoform x3	525	2.40E-123	64.70%	0.102	IPR008930 (G3DSA:1.50.10.GENE3D); IPR002157 (PFAM); IPR002157 (PANTHER); PTHR10559:SF12 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR008930 (SUPERFAMILY); TMhelix (TMHMM)
1903	298356_length_1577_cvg_16.3_tip_1_2	380	hypothetical protein L798_00519	525	5.58E-71	50.80%	0.392 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PFAM); IPR002172 (PFAM); PTHR10529 (PANTHER); PTHR10529:SF222 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1901	298350_length_1576_cvg_7.0_tip_1_0	136	sortilin-related receptor-like	526	4.74E-11	44.00%	0.121	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1902	298354_length_1577_cvg_64.6_tip_0_0	2631	prophenoloxidase activating factor	526	2.85E-26	53.80%	0.604 Y	

1904	298362_length_1577_cvg_13.7_tip_1_3	293	aael014742- partial	526	1.98E-86	56.70%	0.138	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24133 (PANTHER); PTHR24133:SF17 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); IPR020683 (SUPERFAMILY)
1905	298446_length_1589_cvg_18.9_tip_1_0	419	low quality protein: microtubule-associated protein 1a	530	3.19E-08	54.00%	0.106	no IPS match
1906	298450_length_1590_cvg_59.0_tip_1_3	5642	low affinity immunoglobulin epsilon fc receptor	530	1.07E-18	53.80%	0.113	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1907	298452_length_1590_cvg_13.4_tip_1_5	309	flavin-containing monooxygenase fmo gs-ox3	530	2.14E-144	64.80%	0.177	IPR000960 (PRINTS); G3DSA:3.50.50.60 (GENE3D); G3DSA:3.50.50.60 (GENE3D); IPR020946 (PFAM); PTHR23023:SF4 (PANTHER); PTHR23023 (PANTHER); SSF51905 (SUPERFAMILY); SSF51905 (SUPERFAMILY)
1908	298468_length_1593_cvg_9.6_tip_1_4	219	alkaline tissue-nonspecific isozyme-like	531	1.80E-147	63.80%	0.141	IPR001952 (PRINTS); IPR001952 (SMART); IPR001952 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR11596 (PANTHER); IPR018299 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)
1909	298482_length_1594_cvg_5.2_tip_1_2	100	mam and ldl-receptor class a domain-containing protein c10orf112-like	531	4.66E-85	49.80%	0.097	IPR002172 (PRINTS); IPR002172 (SMART); IPR000998 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR23282:SF75 (PANTHER); PTHR23282 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1910	298520_length_1600_cvg_23.2_tip_1_5	491	aael014742- partial	533	2.40E-83	55.80%	0.127	IPR002110 (PRINTS); IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24133:SF17 (PANTHER); PTHR24133 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); IPR020683 (SUPERFAMILY)
1911	298522_length_1600_cvg_2.3_tip_1_1	67	endoplasmic reticulum mannosyl-oligosaccharide - alpha-mannosidase	533	0	80.70%	0.107	IPR001382 (PRINTS); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); PTHR11742:SF7 (PANTHER); IPR001382 (PANTHER); IPR001382 (SUPERFAMILY)
1912	298540_length_1602_cvg_62.4_tip_1_4	3235	phosphoglycerate kinase	534	0	87.40%	0.258	IPR001576 (PRINTS); IPR015824 (G3DSA:3.40.50.GENE3D); IPR015901 (G3DSA:3.40.50.GENE3D); IPR001576 (PFAM); IPR001576 (PANTHER); PTHR11406:SF6 (PANTHER); IPR015911 (PROSITE_PATTERNS); IPR001576 (HAMAP); IPR001576 (SUPERFAMILY)
1913	298546_length_1603_cvg_5.8_tip_1_5	148	15-hydroxyprostaglandin dehydrogenase	534	1.14E-50	60.10%	0.201	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24310 (PANTHER); IPR020904 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY)

1914	298548_length_1604_cvg_41.9_tip_1_2	1238	secreted salivary gland	534	2.03E-31	49.50%	0.470 Y	IPR004991 (PFAM); IPR023307 (G3DSA:2.170.15.GENE3D); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF56973 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1915	298576_length_1610_cvg_10.5_tip_1_3	239	venom metalloproteinase 3 isoform x3	537	5.27E-97	61.80%	0.114	IPR024079 (G3DSA:3.40.390.GENE3D); PTHR13723 (PANTHER); PTHR13723:SF148 (PANTHER); SSF55486 (SUPERFAMILY)
1916	298578_length_1610_cvg_30.9_tip_1_1	560	myosin heavy chain	537	2.03E-12	47.33%	0.118	Coil (COILS); Coil (COILS)
1917	298584_length_1611_cvg_4.0_tip_1_4	95	urokinase-type plasminogen activator	537	1.90E-64	56.20%	0.129	IPR001314 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1918	298608_length_1613_cvg_9.5_tip_1_1	192	cgmp-dependent protein kinase 1-like	538	0	83.10%	0.161	IPR002374 (PRINTS); IPR000595 (SMART); IPR002290 (SMART); IPR000961 (SMART); IPR000595 (PFAM); IPR000719 (PFAM); IPR014710 (G3DSA:2.60.120.GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR014710 (G3DSA:2.60.120.GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24353 (PANTHER); PTHR24353:SF33 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); IPR000595 (PROSITE_PROFILES); IPR000595 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR018490 (SUPERFAMILY); IPR011009 (SUPERFAMILY); IPR018490 (SUPERFAMILY)
1919	298618_length_1615_cvg_7.4_tip_1_5	150	thioredoxin-related transmembrane protein 1-like	538	9.90E-98	71.30%	0.684 Y	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF81 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
1920	298634_length_1616_cvg_5.3_tip_1_0	103	papilin isoform x2	539	7.98E-106	63.20%	0.143	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR010909 (PFAM); PTHR10489 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR010909 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1921	298636_length_1616_cvg_47.0_tip_1_1	1586	d-aspartate oxidase	539	1.91E-98	63.60%	0.13	IPR016040 (G3DSA:3.40.50.GENE3D); IPR006076 (PFAM); IPR023209 (PANTHER); PTHR11530:SF0 (PANTHER); IPR006181 (PROSITE_PATTERNS); SSF51971 (SUPERFAMILY); SSF54373 (SUPERFAMILY)
1922	298642_length_1618_cvg_38.1_tip_1_2	940	ras-related protein rab-10	539	1.71E-116	92.90%	0.207	IPR001806 (PRINTS); IPR024156 (SMART); IPR003579 (SMART); IPR002041 (SMART); IPR020849 (SMART); IPR003578 (SMART); IPR005225 (TIGRFAM); IPR001806 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR24073 (PANTHER); PTHR24073:SF456 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1923	298658_length_1619_cvg_13.6_tip_1_4	251	n-acetylglucosamine-6- partial	540	9.75E-96	55.90%	0.105	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342:SF208 (PANTHER); PTHR10342 (PANTHER); IPR017850 (SUPERFAMILY)
1924	298666_length_1620_cvg_7.6_tip_1_0	152	periodic tryptophan protein 1 homolog	540	1.81E-151	64.20%	0.123	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR14091 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)

1936	298838_length_1648_cvg_24.4_tip_1_2	918	macro domain-containing protein 2	549	2.25E-83	69.40%	0.102	Coil (COILS); IPR002589 (SMART); IPR002589 (PFAM); G3DSA:3.40.220.10 (GENE3D); PTHR11106 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002589 (PROSITE_PROFILES); SSF52949 (SUPERFAMILY); TMhelix (TMHMM)
1937	298840_length_1649_cvg_7.9_tip_1_0	196	bone morphogenetic protein 2-like	550	7.89E-18	51.90%	0.137	IPR001839 (SMART); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001839 (PFAM); PTHR11848:SF126 (PANTHER); IPR015615 (PANTHER); IPR017948 (PROSITE_PATTERNS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)
1938	298846_length_1650_cvg_42.2_tip_1_0	871	cadherin-89d isoform x1	550	3.37E-14	44.90%	0.136	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1939	298864_length_1653_cvg_7.6_tip_1_1	186	vitellogenin receptor	551	1.24E-52	47.50%	0.107	IPR002172 (PRINTS); IPR000033 (SMART); IPR002172 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); PF14670 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); PTHR10529:SF204 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1940	298888_length_1659_cvg_7.3_tip_1_4	156	macrophage mannose receptor 1	553	1.17E-20	36.00%	0.107	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803:SF55 (PANTHER); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
1941	298890_length_1659_cvg_55.9_tip_1_4	2753	retinal dehydrogenase 1-like	553	0	80.40%	0.442 Y	IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699:SF145 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
1942	298910_length_1663_cvg_9.8_tip_1_2	213	leucine-rich repeat and immunoglobulin-like domain-containing nogo receptor-interacting protein 3 isoform x2	554	3.07E-141	64.60%	0.127	Coil (COILS); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24373:SF38 (PANTHER); PTHR24373 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1943	298912_length_1665_cvg_5.6_tip_1_0	163	cysteine-rich motor neuron 1 protein isoform x1	555	2.90E-59	51.70%	0.13	IPR002223 (PRINTS); IPR002223 (SMART); IPR000716 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY); IPR002223 (SUPERFAMILY); TMhelix (TMHMM)

1952	299028_length_1682_cvg_62.0_tip_1_0	22625	hemocytin isoform x1	561	1.01E-20	42.80%	0.101	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); TMhelix (TMHMM)
1953	299042_length_1686_cvg_13.2_tip_1_0	219	angiotensin-converting enzyme-like	562	1.16E-113	78.90%	0.144	IPR001548 (PRINTS); IPR001548 (PFAM); PTHR10514:SF17 (PANTHER); IPR001548 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1954	299064_length_1689_cvg_7.9_tip_1_4	174	chorion peroxidase-like	563	8.28E-126	55.40%	0.136	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
1955	299076_length_1692_cvg_22.1_tip_1_1	517	multiple inositol polyphosphate phosphatase 1	564	5.02E-145	61.10%	0.152	IPR029033 (G3DSA:3.40.50.GENE3D); IPR000560 (PFAM); PTHR20963 (PANTHER); PTHR20963:SF8 (PANTHER); IPR000560 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029033 (SUPERFAMILY)
1956	299084_length_1693_cvg_24.8_tip_1_5	473	neutral and basic amino acid transport protein rbat	564	6.30E-144	57.90%	0.187	IPR006589 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); G3DSA:3.90.400.10 (GENE3D); IPR006047 (PFAM); PTHR10357:SF77 (PANTHER); IPR015902 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1957	299088_length_1693_cvg_6.0_tip_1_4	143	tyrosine-protein kinase csk	564	0	85.70%	0.322	IPR000980 (PRINTS); IPR001245 (PRINTS); IPR000980 (SMART); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000980 (PFAM); IPR000980 (G3DSA:3.30.505.GENE3D); IPR001245 (PFAM); PTHR24418:SF192 (PANTHER); PTHR24418 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR000980 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); IPR000980 (SUPERFAMILY); TMhelix (TMHMM)
1958	299096_length_1697_cvg_20.9_tip_1_3	443	pdgf- and vegf-related factor 1-like precursor	566	7.23E-54	55.50%	0.328	IPR000072 (SMART); IPR000072 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); PTHR11633:SF1 (PANTHER); PTHR11633 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000072 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)
1959	299104_length_1698_cvg_7.2_tip_1_1	182	annexin a4	566	6.31E-94	67.60%	0.113	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); SSF47874 (SUPERFAMILY)
1960	299122_length_1701_cvg_22.7_tip_1_1	390	nucleolar protein 56	567	0	87.50%	0.25	Coil (COILS); IPR012976 (SMART); IPR002687 (PFAM); IPR012976 (PFAM); IPR012974 (PFAM); PTHR10894 (PANTHER); PTHR10894:SF0 (PANTHER); IPR002687 (PROSITE_PROFILES); SSF89124 (SUPERFAMILY)
1962	299150_length_1708_cvg_3.3_tip_1_5	80	collagen alpha-1 chain	569	1.43E-117	63.90%	0.099	IPR008160 (PFAM); PTHR24023 (PANTHER)
1961	299150_length_1708_cvg_3.3_tip_1_0	80	threonine-rich gpi-anchored glycoprotein	570	5.45E-60	43.60%	0.114	PTHR24023 (PANTHER); PTHR24023:SF405 (PANTHER)
1963	299168_length_1713_cvg_14.9_tip_1_1	365	wd40 repeat-containing protein smu1	571	0	93.80%	0.099	IPR020472 (PRINTS); IPR001680 (SMART); IPR006594 (SMART); IPR006595 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22848 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR006595 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR006594 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1964	299172_length_1713_cvg_11.4_tip_1_0	282	estradiol 17-beta-dehydrogenase 2	571	1.09E-71	56.80%	0.123	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF215 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1965	299190_length_1716_cvg_8.7_tip_1_4	178	endothelin-converting enzyme 1	572	8.76E-165	64.60%	0.104	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); IPR008753 (PFAM); IPR000718 (PANTHER); PTHR11733:SF111 (PANTHER); SSF55486 (SUPERFAMILY)
1966	299198_length_1719_cvg_10.0_tip_1_3	234	peptidyl-prolyl cis-trans isomerase fkbp4-like	573	0	73.80%	0.128	Coil (COILS); IPR019734 (SMART); G3DSA:3.10.50.40 (GENE3D); IPR023114 (G3DSA:1.10.150.GENE3D); IPR001440 (PFAM); G3DSA:3.10.50.40 (GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); PF13414 (PFAM); IPR001179 (PFAM); IPR023566 (PANTHER); PTHR10516:SF274 (PANTHER); IPR001179 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY); SSF48452 (SUPERFAMILY); SSF54534 (SUPERFAMILY)
1967	299226_length_1723_cvg_77.9_tip_1_4	7659	inactive pancreatic lipase-related protein 1	574	1.35E-88	56.80%	0.133	IPR002331 (PRINTS); IPR000734 (PRINTS); IPR001024 (G3DSA:2.60.60.GENE3D); IPR013818 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR000734 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); IPR008976 (SUPERFAMILY)
1968	299278_length_1736_cvg_14.3_tip_1_2	330	hydroxysteroid dehydrogenase-like protein 2	578	0	77.00%	0.14	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR003033 (PFAM); IPR003033 (G3DSA:3.30.1050.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF273 (PANTHER); IPR003033 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
1969	299280_length_1736_cvg_8.9_tip_1_4	209	cytochrome p450 2u1-like	579	6.67E-124	57.40%	0.107	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1970	299284_length_1736_cvg_56.0_tip_1_4	1575	leucine-rich repeat neuronal protein 3-like isoform x1	579	3.06E-107	54.90%	0.194	IPR003591 (SMART); IPR000483 (SMART); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PFAM); PTHR24373 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1971	299310_length_1741_cvg_61.7_tip_1_5	1740	heat shock protein 70	580	0	96.30%	0.144	Coil (COILS); IPR013126 (PRINTS); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); G3DSA:3.90.640.10 (GENE3D); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF142 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
1972	299338_length_1749_cvg_6.8_tip_1_5	139	ribonuclease oy	583	1.94E-61	59.30%	0.285	IPR001568 (G3DSA:3.90.730.GENE3D); IPR001568 (PFAM); IPR001568 (PANTHER); IPR018188 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001568 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1973	299348_length_1752_cvg_54.9_tip_1_0	2174	polyketide synthase type i	584	6.23E-27	61.90%	0.115	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1974	299348_length_1752_cvg_54.9_tip_1_1	2174	protein containing tetratricopeptide repeat	584	4.26E-07	76.00%	0.186	Coil (COILS); Coil (COILS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)

1983	299492_length_1778_cvg_8.6_tip_1_5	220	calnexin	592	0	75.20%	0.216	Coil (COILS); IPR001580 (PRINTS); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001580 (PFAM); IPR009033 (G3DSA:2.10.250.GENE3D); IPR009033 (G3DSA:2.10.250.GENE3D); PTHR11073:SF1 (PANTHER); IPR001580 (PANTHER); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013320 (SUPERFAMILY); IPR009033 (SUPERFAMILY); TMhelix (TMHMM)
1982	299490_length_1778_cvg_6.1_tip_1_0	134	von willebrand factor a domain-containing protein 8	593	0	73.10%	0.169	IPR027417 (G3DSA:3.40.50.GENE3D); IPR011704 (PFAM); PTHR21610:SF9 (PANTHER); PTHR21610 (PANTHER); IPR027417 (SUPERFAMILY); IPR027417 (SUPERFAMILY)
1984	299494_length_1778_cvg_6.4_tip_1_4	201	laminin subunit alpha	593	2.29E-153	57.70%	0.137	IPR001791 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10574:SF39 (PANTHER); PTHR10574 (PANTHER); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1986	299498_length_1779_cvg_11.0_tip_1_4	231	dnaj homolog subfamily c member 7	593	0	74.90%	0.104	IPR001623 (PRINTS); IPR001623 (SMART); IPR019734 (SMART); IPR001623 (PFAM); IPR013105 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); PF13414 (PFAM); IPR019734 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF140 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR013026 (PROSITE_PROFILES); IPR001623 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY); IPR001623 (SUPERFAMILY); SSF48452 (SUPERFAMILY); SSF48452 (SUPERFAMILY)
1987	299506_length_1781_cvg_5.8_tip_1_2	187	latrophilin cir1-like isoform x7	593	0	64.20%	0.165	IPR001879 (SMART); IPR000203 (SMART); IPR001879 (PFAM); IPR000922 (PFAM); IPR022624 (PFAM); IPR000832 (PFAM); IPR000203 (PFAM); PTHR12011:SF217 (PANTHER); PTHR12011 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000203 (PROSITE_PROFILES); IPR001879 (PROSITE_PROFILES); IPR000922 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); TMhelix (TMHMM)
1988	299508_length_1781_cvg_3.4_tip_1_2	86	#NAME?	593	0	82.30%	0.135	IPR006589 (SMART); IPR006407 (PIRSF); IPR006047 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR013780 (G3DSA:2.60.40.GENE3D); IPR006048 (PFAM); IPR015902 (PANTHER); PTHR10357:SF110 (PANTHER); IPR017853 (SUPERFAMILY); SSF51011 (SUPERFAMILY)
1989	299512_length_1781_cvg_14.2_tip_1_2	343	af425264_1lysozyme precursor	593	9.74E-37	65.30%	0.102	IPR001916 (PRINTS); IPR000974 (PRINTS); IPR001916 (SMART); G3DSA:1.10.530.10 (GENE3D); IPR001916 (PFAM); PTHR11407 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001916 (PROSITE_PROFILES); IPR023346 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2009	299742_length_1828_cvg_72.7_tip_1_2	8741	retinal dehydrogenase 1-like	593	0	82.10%	0.121	IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF145 (PANTHER); IPR016160 (PROSITE_PATTERNS); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
1990	299518_length_1782_cvg_38.4_tip_1_5	964	5 -nucleotidase-like	594	8.53E-87	56.50%	0.133	IPR006179 (PRINTS); IPR029052 (G3DSA:3.60.21.GENE3D); IPR008334 (G3DSA:3.90.780.GENE3D); IPR008334 (PFAM); IPR006179 (PANTHER); PTHR11575:SF21 (PANTHER); IPR029052 (SUPERFAMILY); IPR008334 (SUPERFAMILY)
1991	299526_length_1784_cvg_36.1_tip_1_0	788	phosphatidylethanolamine-binding protein	595	4.63E-88	79.90%	0.168	IPR008914 (PFAM); IPR008914 (G3DSA:3.90.280.GENE3D); PTHR11362 (PANTHER); IPR008914 (SUPERFAMILY)

1992	299550_length_1788_cvg_6.8_tip_1_5	190	cadherin-like membrane protein	596	1.92E-51	45.70%	0.102	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
1993	299552_length_1788_cvg_35.8_tip_1_5	777	proclotting enzyme	596	6.25E-132	64.00%	0.205	IPR001314 (PRINTS); IPR006604 (SMART); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF81 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1994	299558_length_1789_cvg_6.8_tip_1_1	186	membrane metallo-endopeptidase-like 1-like	596	8.92E-64	47.70%	0.171	IPR018497 (PRINTS); IPR018497 (PFAM); IPR008753 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
2010	299780_length_1832_cvg_30.9_tip_1_1	870	microneme protein mic12	596	7.97E-20	38.80%	0.104	IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR24034 (PANTHER); PTHR24034:SF33 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY); IPR009030 (SUPERFAMILY); TMhelix (TMHMM)
1995	299566_length_1792_cvg_64.5_tip_1_3	2653	preamyase 1	598	0	76.60%	0.274	IPR006046 (PRINTS); IPR006048 (SMART); IPR006589 (SMART); IPR006048 (PFAM); IPR006047 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR013780 (G3DSA:2.60.40.GENE3D); PTHR10357:SF116 (PANTHER); IPR015902 (PANTHER); IPR017853 (SUPERFAMILY); SSF51011 (SUPERFAMILY); TMhelix (TMHMM)
1996	299568_length_1793_cvg_5.1_tip_1_3	119	low quality protein: cubilin	598	2.53E-38	47.10%	0.112	IPR000859 (SMART); IPR002035 (G3DSA:3.40.50.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); IPR002035 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR002035 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR002035 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
1997	299572_length_1794_cvg_57.9_tip_1_3	3474	trypsinogen 2	598	1.54E-66	61.80%	0.117	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1998	299580_length_1795_cvg_19.6_tip_1_1	623	serpin 3	598	2.83E-82	58.90%	0.147	IPR023796 (SMART); G3DSA:3.30.497.10 (GENE3D); G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); PTHR11461:SF52 (PANTHER); IPR023795 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023796 (SUPERFAMILY); TMhelix (TMHMM)
1999	299604_length_1800_cvg_7.9_tip_1_3	172	letm1 and ef-hand domain-containing protein anon-mitochondrial-like	600	2.58E-105	58.30%	0.205	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR011685 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR14009:SF1 (PANTHER); PTHR14009 (PANTHER); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)
2000	299628_length_1806_cvg_9.5_tip_1_4	232	alkaline phosphatase 4-like	602	4.79E-160	64.00%	0.243	IPR001952 (PRINTS); IPR001952 (SMART); IPR001952 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR11596 (PANTHER); IPR018299 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR017850 (SUPERFAMILY); TMhelix (TMHMM)

2001	299636_length_1808_cvg_16.5_tip_0_2	429	fibrinogen-like protein 1	602	2.23E-23	63.00%	0.114	IPR002181 (SMART); IPR002181 (PFAM); IPR014715 (G3DSA:4.10.530.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
2002	299640_length_1809_cvg_9.1_tip_1_2	220	leucine-rich repeat-containing protein 59	603	9.09E-63	65.50%	0.119	Coil (COILS); Coil (COILS); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2003	299642_length_1810_cvg_8.1_tip_1_0	186	tyrosine-protein phosphatase lar-like isoform x6	604	0	93.00%	0.113	IPR000242 (PRINTS); IPR000242 (SMART); IPR003595 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); PTHR19134:SF199 (PANTHER); IPR016130 (PROSITE_PATTERNS); IPR016130 (PROSITE_PATTERNS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); IPR029021 (SUPERFAMILY)
2004	299676_length_1815_cvg_38.1_tip_1_2	1177	peptidyl-prolyl cis-trans isomerase b	605	7.72E-108	86.30%	0.508 Y	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF63 (PANTHER); IPR020892 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002130 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); IPR029000 (SUPERFAMILY)
2005	299692_length_1818_cvg_15.5_tip_1_2	331	rna-binding protein 5-like	606	5.23E-153	64.30%	0.146	Coil (COILS); IPR000467 (SMART); IPR000467 (PFAM); PTHR13948 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000467 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES)
2006	299710_length_1822_cvg_43.2_tip_1_2	834	universal minicircle sequence binding protein	607	8.97E-27	51.50%	0.183	IPR001878 (SMART); IPR001878 (G3DSA:4.10.60.GENE3D); IPR001878 (G3DSA:4.10.60.GENE3D); IPR001878 (PFAM); PTHR23002 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (SUPERFAMILY); IPR001878 (SUPERFAMILY); IPR001878 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2007	299718_length_1823_cvg_15.1_tip_1_1	432	allene oxide synthase-lipoxygenase	608	0	68.80%	0.109	Coil (COILS); IPR013819 (PRINTS); IPR013819 (PFAM); G3DSA:1.20.245.10 (GENE3D); PTHR11771:SF43 (PANTHER); IPR000907 (PANTHER); IPR020834 (PROSITE_PATTERNS); IPR013819 (PROSITE_PROFILES); IPR013819 (SUPERFAMILY)
2016	299824_length_1841_cvg_41.0_tip_1_3	2244	orckinin precursor	609	2.79E-21	77.70%	0.241	no IPS match
2017	299824_length_1841_cvg_41.0_tip_1_4	2244	pedal peptide 2 precursor	609	5.82E-39	59.50%	0.25	no IPS match
2008	299740_length_1828_cvg_9.1_tip_1_0	245	cytochrome p450 3a24-like	610	6.96E-111	58.70%	0.141	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24302 (PANTHER); PTHR24302:SF7 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

2011	299806_length_1839_cvg_6.9_tip_1_3	151	apical endosomal glyco	613	3.60E-14	39.00%	0.107	IPR000998 (SMART); IPR000859 (SMART); IPR002172 (SMART); IPR000998 (PFAM); IPR000859 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR22991 (PANTHER); PTHR22991:SF23 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
2012	299808_length_1839_cvg_9.2_tip_1_4	223	inter-alpha-trypsin inhibitor heavy chain h3-like	613	1.89E-121	62.70%	0.138	Coil (COILS); IPR002035 (SMART); IPR013694 (SMART); IPR002035 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); IPR013694 (PFAM); PTHR10338 (PANTHER); PTHR10338:SF108 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002035 (PROSITE_PROFILES); IPR013694 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY); TMhelix (TMHMM)
2013	299814_length_1840_cvg_5.4_tip_1_2	125	maguk p55 subfamily member 6	613	0	85.80%	0.104	IPR008145 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:3.30.63.10 (GENE3D); G3DSA:2.30.30.40 (GENE3D); IPR001452 (PFAM); IPR008145 (PFAM); PTHR23122 (PANTHER); IPR020590 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001452 (PROSITE_PROFILES); IPR008144 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); IPR027417 (SUPERFAMILY)
2014	299818_length_1841_cvg_19.9_tip_1_1	402	chromodomain-helicase-dna-binding protein mi-2 homolog isoform x5	614	0	76.80%	0.14	Coil (COILS); Coil (COILS); IPR009462 (PFAM); IPR012957 (PFAM); IPR028727 (PTHR10799:PANTHER); PTHR10799 (PANTHER)
2015	299820_length_1841_cvg_9.0_tip_1_1	231	alpha-mannosidase 2	614	7.42E-110	58.20%	0.17	G3DSA:2.70.98.30 (GENE3D); IPR011682 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); PTHR11607 (PANTHER); PTHR11607:SF4 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011013 (SUPERFAMILY); TMhelix (TMHMM)
2033	300028_length_1886_cvg_5.0_tip_1_4	129	n-sulphoglucosamine sulphohydrolase-like	614	0	79.40%	0.101	Coil (COILS); IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); IPR000917 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF76 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017850 (SUPERFAMILY)
2018	299840_length_1843_cvg_8.4_tip_1_0	267	sorbin and sh3 domain-containing protein partial	615	0	77.80%	0.106	Coil (COILS); PR00499 (PRINTS); IPR001452 (PRINTS); IPR001452 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR001452 (PFAM); IPR001452 (PFAM); G3DSA:2.30.30.40 (GENE3D); G3DSA:2.30.30.40 (GENE3D); PTHR10661 (PANTHER); PTHR10661:SF66 (PANTHER); IPR001452 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); IPR001452 (SUPERFAMILY); IPR001452 (SUPERFAMILY)
2019	299856_length_1847_cvg_8.6_tip_1_0	185	ankyrin sam and basic leucine zipper domain-containing protein 1-like	616	1.49E-130	61.00%	0.099	IPR001660 (SMART); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR021129 (PFAM); IPR013761 (G3DSA:1.10.150.GENE3D); PTHR24157 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR001660 (PROSITE_PROFILES); IPR013761 (SUPERFAMILY); IPR020683 (SUPERFAMILY)
2020	299868_length_1850_cvg_12.7_tip_1_2	306	pancreatic lipase-related protein 2-like	616	8.35E-157	64.60%	0.142	IPR002331 (PRINTS); IPR000734 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR013818 (PFAM); IPR001024 (G3DSA:2.60.60.GENE3D); PTHR11610:SF83 (PANTHER); IPR000734 (PANTHER); IPR001024 (PROSITE_PROFILES); IPR029058 (SUPERFAMILY); IPR008976 (SUPERFAMILY)
2021	299874_length_1852_cvg_17.7_tip_1_2	538	cathepsin l-like	617	5.21E-166	79.60%	0.131	IPR000668 (PRINTS); IPR000668 (SMART); IPR013201 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR013201 (PFAM); IPR000668 (PFAM); PTHR12411:SF57 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2022	299898_length_1857_cvg_3.6_tip_1_4	102	mitochondrial import inner membrane translocase subunit tim8 a	619	3.34E-30	82.20%	0.449 Y	IPR004217 (G3DSA:1.10.287.GENE3D); IPR004217 (PFAM); PTHR21535 (PANTHER); IPR004217 (SUPERFAMILY)

2023	299902_length_1857_cvg_10.1_tip_1_1	196	ectonucleotide pyrophosphatase phosphodiesterase family member 6	619	3.86E-108	54.60%	0.106	IPR002591 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); IPR024873 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY)
2024	299918_length_1862_cvg_5.9_tip_1_1	131	neurexin-4 isoform x3	621	0	64.10%	0.129	IPR001791 (SMART); IPR000742 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR000742 (PFAM); IPR001791 (PFAM); PTHR10127:SF346 (PANTHER); PTHR10127 (PANTHER); IPR000742 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
2025	299924_length_1863_cvg_29.1_tip_1_1	862	iron zinc purple acid phosphatase-like protein	621	0	74.40%	0.238	IPR029052 (G3DSA:3.60.21.GENE3D); IPR025733 (PFAM); IPR015914 (G3DSA:2.60.40.GENE3D); IPR004843 (PFAM); PTHR22953 (PANTHER); PTHR22953:SF9 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY); IPR008963 (SUPERFAMILY); TMhelix (TMHMM)
2026	299934_length_1865_cvg_59.4_tip_0_4	3385	kielin chordin-like protein	622	9.00E-58	52.60%	0.117	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR008037 (PFAM); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
2027	299948_length_1868_cvg_27.4_tip_1_2	655	mitochondrial-processing peptidase subunit beta	622	0	85.90%	0.111	IPR011765 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); IPR007863 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); PTHR11851:SF103 (PANTHER); PTHR11851 (PANTHER); IPR001431 (PROSITE_PATTERNS); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY)
2028	299954_length_1868_cvg_53.6_tip_1_5	1840	ectonucleotide pyrophosphatase phosphodiesterase family member 6	622	4.96E-98	54.90%	0.245	IPR017849 (G3DSA:3.40.720.GENE3D); IPR002591 (PFAM); IPR024873 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2031	299994_length_1877_cvg_37.8_tip_1_5	1108	superoxide dismutase	625	1.62E-45	67.20%	0.149	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY)
2032	299996_length_1877_cvg_3.6_tip_1_5	123	homeotic protein spalt-major-like isoform x2	625	1.93E-118	63.60%	0.325	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23233:SF51 (PANTHER); PTHR23233 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2029	299980_length_1876_cvg_21.2_tip_1_3	459	methylmalonate-semialdehyde dehydrogenase	626	0	87.60%	0.127	IPR010061 (TIGRFAM); IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); IPR010061 (PTHR11699:PANTHER); PTHR11699 (PANTHER); IPR016160 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM)

2030	299992_length_1877_cvg_54.7_tip_1_1	1707	ribosome-binding protein partial	626	2.10E-36	49.90%	0.098	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); PTHR18939:SF4 (PANTHER); PTHR18939 (PANTHER)
2034	300056_length_1896_cvg_6.6_tip_1_1	190	sphingomyelin phosphodiesterase	632	3.21E-176	62.50%	0.616 Y	IPR011160 (PIRSF); IPR004843 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR10340:SF13 (PANTHER); PTHR10340 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008139 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR029052 (SUPERFAMILY); IPR011001 (SUPERFAMILY); TMhelix (TMHMM)
2035	300108_length_1908_cvg_7.7_tip_1_2	198	katanin p60 atpase-containing subunit a-like 1	636	0	82.00%	0.14	IPR003593 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR015415 (PFAM); PTHR23074 (PANTHER); PTHR23074:SF65 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR028596 (HAMAP); IPR027417 (SUPERFAMILY)
2036	300128_length_1911_cvg_12.8_tip_1_3	255	wd repeat-containing protein 36	637	0	69.70%	0.111	IPR001680 (SMART); IPR007319 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR13889 (PANTHER); PTHR13889:SF2 (PANTHER); IPR020719 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR011047 (SUPERFAMILY)
2037	300136_length_1912_cvg_21.3_tip_1_5	595	dorsal-ventral patterning protein tolloid	637	0	79.50%	0.177	Coil (COILS); IPR001506 (PRINTS); IPR006026 (SMART); IPR000859 (SMART); IPR001506 (PFAM); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127:SF304 (PANTHER); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
2038	300146_length_1915_cvg_10.9_tip_1_5	286	inter-alpha-trypsin inhibitor heavy chain h3-like	638	4.59E-122	62.80%	0.105	Coil (COILS); IPR002035 (SMART); IPR013694 (SMART); IPR013694 (PFAM); IPR002035 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); PTHR10338 (PANTHER); PTHR10338:SF108 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013694 (PROSITE_PROFILES); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY); TMhelix (TMHMM)
2039	300150_length_1915_cvg_11.4_tip_1_1	257	low-density lipoprotein receptor-related protein 2	638	1.12E-172	70.10%	0.147	IPR000033 (SMART); IPR000033 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10529 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF63825 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2040	300166_length_1918_cvg_10.2_tip_1_2	308	stabilin-1 isoform x1	639	2.90E-127	65.80%	0.204	IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PFAM); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); TMhelix (TMHMM)
2041	300172_length_1919_cvg_5.4_tip_1_2	169	aael001570- partial	639	1.02E-168	55.20%	0.098	IPR005018 (SMART); IPR005018 (PFAM); PTHR22979:SF15 (PANTHER); PTHR22979 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR005018 (PROSITE_PROFILES); IPR005018 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES)

2042	300188_length_1924_cvg_61.8_tip_0_0	2791	twitchin isoform x4	642	0	87.40%	0.098	IPR002290 (SMART); IPR003598 (SMART); IPR003599 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR011009 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2043	300210_length_1931_cvg_17.2_tip_1_5	301	harmonin isoform x2	643	7.57E-52	55.80%	0.12	Coil (COILS); Coil (COILS); IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR23116 (PANTHER); IPR030237 (PTHR23116:PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
2044	300224_length_1935_cvg_6.0_tip_1_2	139	tolloid-like protein 2 isoform x2	645	0	82.60%	0.099	IPR000742 (SMART); IPR000859 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PF14670 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127:SF304 (PANTHER); PTHR10127 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000859 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
2045	300230_length_1937_cvg_14.6_tip_1_3	438	leucine-rich repeat-containing protein partial	646	2.26E-51	47.30%	0.255	IPR000483 (SMART); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR026906 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373 (PANTHER); PTHR24373:SF100 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2050	300352_length_1973_cvg_17.2_tip_1_5	422	transducin beta-like protein 2	648	1.16E-149	69.20%	0.161	Coil (COILS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22847:SF380 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
2046	300260_length_1949_cvg_21.6_tip_1_3	486	mucin- partial	650	2.14E-13	40.90%	0.148	Coil (COILS); Coil (COILS); G3DSA:2.10.70.10 (GENE3D); IPR001846 (PFAM); IPR014853 (PFAM); PTHR11339 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); TMhelix (TMHMM)
2047	300284_length_1957_cvg_22.8_tip_1_4	486	methyltransferase-like protein 23	652	4.11E-93	76.80%	0.11	IPR000582 (PRINTS); IPR002110 (SMART); IPR000504 (SMART); IPR019410 (PFAM); IPR014352 (G3DSA:1.20.80.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR000582 (PFAM); IPR029063 (G3DSA:3.40.50.GENE3D); IPR000504 (PFAM); IPR012677 (G3DSA:3.30.70.GENE3D); IPR020683 (PFAM); PTHR24119 (PANTHER); PTHR24119:SF0 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR000504 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR000582 (PROSITE_PROFILES); IPR029063 (SUPERFAMILY); IPR020683 (SUPERFAMILY); IPR000582 (SUPERFAMILY); SSF54928 (SUPERFAMILY)

2048	300298_length_1959_cvg_4.9_tip_1_0	147	membrane metallo-endopeptidase-like 1-like	653	0	78.40%	0.117	IPR018497 (PRINTS); IPR018497 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR008753 (PFAM); IPR000718 (PANTHER); PTHR11733:SF113 (PANTHER); SSF55486 (SUPERFAMILY)
2049	300318_length_1963_cvg_16.0_tip_1_4	381	coatomer subunit beta	654	0	89.00%	0.104	IPR001680 (SMART); IPR006692 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19876:SF2 (PANTHER); PTHR19876 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR011044 (SUPERFAMILY); IPR017986 (SUPERFAMILY)
2051	300364_length_1975_cvg_13.0_tip_1_4	479	sphingomyelin phosphodiesterase	658	1.48E-177	62.80%	0.221	IPR008139 (SMART); IPR011160 (PIRSF); IPR004843 (PFAM); IPR007856 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR10340:SF13 (PANTHER); PTHR10340 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008139 (PROSITE_PROFILES); IPR011001 (SUPERFAMILY); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
2052	300386_length_1981_cvg_6.6_tip_1_3	136	protein phosphatase 1 regulatory subunit 7	661	9.45E-118	77.00%	0.112	SM00365 (SMART); IPR003591 (SMART); IPR003603 (SMART); IPR025875 (PFAM); PF14580 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR10588 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
2053	300388_length_1981_cvg_11.0_tip_1_0	263	tyrosine--trna cytoplasmic	661	0	80.60%	0.134	IPR002307 (PRINTS); IPR002305 (PFAM); IPR014729 (G3DSA:3.40.50.GENE3D); G3DSA:1.10.240.10 (GENE3D); IPR002547 (PFAM); IPR002307 (TIGRFAM); IPR012340 (G3DSA:2.40.50.GENE3D); PTHR11946 (PANTHER); IPR002547 (PROSITE_PROFILES); SSF52374 (SUPERFAMILY); IPR010987 (SUPERFAMILY); IPR012340 (SUPERFAMILY)
2054	300442_length_1996_cvg_10.8_tip_1_4	267	chorion peroxidase-like	665	2.92E-152	68.20%	0.112	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
2055	300452_length_2001_cvg_61.1_tip_1_4	3823	glycosyl-phosphatidylinositol-linked carbonic anhydrase	667	1.66E-67	57.90%	0.101	IPR001148 (SMART); IPR001148 (G3DSA:3.10.200.GENE3D); IPR001148 (PFAM); IPR023561 (PANTHER); IPR018338 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
2056	300454_length_2001_cvg_72.3_tip_0_2	914092	hemocyanin subunit type 1 precursor	667	0	76.40%	0.096	IPR013788 (PRINTS); IPR005204 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR005203 (G3DSA:2.60.40.GENE3D); IPR000896 (PFAM); IPR005203 (PFAM); IPR013788 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR002227 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); IPR014756 (SUPERFAMILY); IPR008922 (SUPERFAMILY); IPR005204 (SUPERFAMILY)
2057	300464_length_2004_cvg_10.3_tip_1_2	265	scabrous protein	668	8.14E-119	55.30%	0.102	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR002181 (SMART); IPR014715 (G3DSA:4.10.530.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); PTHR19143:SF186 (PANTHER); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
2058	300468_length_2004_cvg_9.9_tip_1_3	264	btb poz domain-containing protein 17	668	0	75.30%	0.138	IPR000210 (SMART); IPR011705 (SMART); IPR011705 (PFAM); IPR013069 (PFAM); G3DSA:3.30.710.10 (GENE3D); PTHR24410:SF9 (PANTHER); PTHR24410 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000210 (PROSITE_PROFILES); IPR011333 (SUPERFAMILY); TMhelix (TMHMM)
2059	300494_length_2010_cvg_8.8_tip_1_3	203	nucleolar protein 58-like	670	1.34E-171	83.50%	0.153	IPR012976 (SMART); IPR002687 (PFAM); IPR012976 (PFAM); PTHR10894:SF1 (PANTHER); PTHR10894 (PANTHER); IPR002687 (PROSITE_PROFILES); SSF89124 (SUPERFAMILY)
2060	300496_length_2010_cvg_5.0_tip_1_4	123	low quality protein: hemocytin-like	670	2.14E-66	43.30%	0.103	IPR001846 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR001846 (PFAM); IPR014853 (PFAM); IPR002919 (PFAM); PTHR11339:SF25 (PANTHER); PTHR11339 (PANTHER); IPR001846 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY); IPR002919 (SUPERFAMILY)
2061	300502_length_2011_cvg_9.4_tip_1_3	290	serine threonine-protein phosphatase 2b catalytic subunit 2-like isoform x1	671	0	95.00%	0.108	IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668:SF186 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)

2062	300504_length_2011_cvg_5.2_tip_1_3	160	phosphatidylinositol -bisphosphate 5-phosphatase a-like	671	4.18E-19	55.50%	0.111	IPR029334 (PFAM)
2063	300506_length_2011_cvg_54.7_tip_1_3	2702	inactive pancreatic lipase-related protein 1	671	1.20E-96	57.30%	0.133	IPR002331 (PRINTS); IPR000734 (PRINTS); IPR001024 (G3DSA:2.60.60.GENE3D); IPR013818 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR000734 (PANTHER); IPR001024 (PROSITE_PROFILES); IPR029058 (SUPERFAMILY); IPR008976 (SUPERFAMILY)
2064	300522_length_2017_cvg_51.3_tip_1_0	2078	adp-ribosylation factor 1	673	3.10E-127	98.50%	0.253	IPR006689 (PRINTS); IPR006687 (SMART); IPR003579 (SMART); IPR024156 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF118 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2065	300532_length_2020_cvg_4.2_tip_1_1	166	twitchin isoform x4	673	0	83.90%	0.113	PR00014 (PRINTS); IPR003961 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2066	300538_length_2022_cvg_14.3_tip_1_2	313	low quality protein: low-density lipoprotein receptor-related protein 2-like	674	1.46E-25	50.00%	0.11	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
2067	300542_length_2023_cvg_3.2_tip_1_5	97	heme utilization protein	674	1.67E-20	46.80%	0.123	no IPS match
2068	300560_length_2030_cvg_7.7_tip_1_1	231	uncharacterized threonine-rich gpi-anchored glyco isoform x5	677	0	90.60%	0.271	Coil (COILS); IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR13902 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2069	300572_length_2032_cvg_26.3_tip_1_2	613	angiotensin-converting enzyme 2	677	2.92E-92	71.70%	0.128	IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2070	300590_length_2039_cvg_35.4_tip_1_0	800	macrophage mannose receptor 1	680	2.37E-81	51.60%	0.105	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803:SF16 (PANTHER); PTHR22803 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR018378 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)

								IPR003591 (SMART); SM00365 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24373 (PANTHER); PTHR24373:SF98 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2071	300592_length_2040_cvg_20.6_tip_1_2	571	slit protein	680	6.92E-94	69.80%	0.112	
2072	300608_length_2046_cvg_36.7_tip_1_2	943	n-acetylgalactosamine-6-sulfatase isoform x1	682	0	77.60%	0.097	G3DSA:3.30.1120.10 (GENE3D); IPR017849 (G3DSA:3.40.720.GENE3D); PF14707 (PFAM); IPR000917 (PFAM); PTHR10342:SF27 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)
2073	300620_length_2048_cvg_6.7_tip_1_0	257	peptidyl-prolyl cis-trans mitochondrial	683	1.94E-141	56.80%	0.175	IPR001841 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR017907 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR001841 (PROSITE_PROFILES); IPR000315 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY); IPR029000 (SUPERFAMILY); SSF57845 (SUPERFAMILY)
2074	300626_length_2049_cvg_45.0_tip_1_0	1505	moxd1 homolog 2	683	6.02E-127	56.20%	0.241	IPR000945 (PRINTS); IPR005018 (SMART); IPR014784 (G3DSA:2.60.120.GENE3D); PF03712 (PFAM); IPR005018 (PFAM); IPR000323 (G3DSA:2.60.120.GENE3D); IPR015920 (G3DSA:2.60.40.GENE3D); IPR000323 (PFAM); IPR000945 (PANTHER); PTHR10157:SF23 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005018 (PROSITE_PROFILES); IPR008977 (SUPERFAMILY); SSF49344 (SUPERFAMILY); IPR008977 (SUPERFAMILY); TMhelix (TMHMM)
2075	300654_length_2056_cvg_6.2_tip_1_1	189	muscle m-line assembly protein unc-89	685	0	67.50%	0.106	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR020675 (PANTHER); PTHR22964:SF45 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2076	300676_length_2063_cvg_10.8_tip_1_2	236	counting factor associated protein d-like	687	0	76.80%	0.288	IPR000668 (PRINTS); IPR000668 (SMART); IPR013201 (SMART); IPR000668 (PFAM); IPR013201 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF284 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
2077	300684_length_2065_cvg_50.9_tip_1_4	1596	spermine oxidase	688	5.41E-117	51.70%	0.531 Y	G3DSA:3.50.50.60 (GENE3D); IPR011032 (G3DSA:3.90.180.GENE3D); G3DSA:3.90.660.10 (GENE3D); IPR002937 (PFAM); PTHR10742:SF255 (PANTHER); PTHR10742 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY); TMhelix (TMHMM)
2079	300690_length_2066_cvg_23.9_tip_1_2	603	prostaglandin g h synthase 2-like isoform x3	688	0	70.20%	0.383 Y	IPR019791 (PRINTS); G3DSA:2.10.25.10 (GENE3D); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11903 (PANTHER); PTHR11903:SF10 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR019791 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF57196 (SUPERFAMILY); IPR010255 (SUPERFAMILY); TMhelix (TMHMM)

2078	300688_length_2066_cvg_6.1_tip_1_1	175	carboxypeptidase d	689	0	63.70%	0.111	IPR000834 (PRINTS); IPR000834 (SMART); G3DSA:3.40.630.10 (GENE3D); G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); IPR014766 (G3DSA:2.60.40.GENE3D); PF13620 (PFAM); IPR015567 (PTHR11532:PANTHER); PTHR11532 (PANTHER); IPR000834 (PROSITE_PATTERNS); IPR000834 (PROSITE_PATTERNS); IPR008969 (SUPERFAMILY); SSF53187 (SUPERFAMILY); IPR008969 (SUPERFAMILY)
2080	300710_length_2071_cvg_5.0_tip_1_1	144	latrophilin- partial	690	2.13E-95	53.90%	0.116	IPR000832 (PRINTS); IPR000203 (SMART); IPR000203 (PFAM); IPR000832 (PFAM); IPR022624 (PFAM); PTHR12011 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000203 (PROSITE_PROFILES); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2081	300714_length_2073_cvg_6.3_tip_1_3	179	extracellular serine threonine protein kinase fam20c isoform x1	691	0	71.70%	0.102	IPR009581 (PFAM); IPR024869 (PANTHER); PTHR12450:SF8 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2082	300722_length_2077_cvg_34.8_tip_1_4	846	probable cytochrome p450 49a1	692	2.58E-143	62.70%	0.153	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24305:SF49 (PANTHER); PTHR24305 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
2083	300736_length_2087_cvg_13.0_tip_1_1	481	probable chitinase 3	696	2.20E-133	56.70%	0.118	IPR002557 (SMART); IPR011583 (SMART); IPR029070 (G3DSA:3.10.50.GENE3D); IPR002557 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR001579 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR029070 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR002557 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2084	300772_length_2099_cvg_6.0_tip_1_2	159	retinol dehydrogenase 13-like	699	5.97E-88	66.70%	0.315	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320 (PANTHER); IPR020904 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
2085	300776_length_2101_cvg_17.6_tip_1_3	621	vitellogenin 2	701	4.66E-106	49.50%	0.576 Y	IPR001747 (SMART); IPR015816 (G3DSA:2.30.230.GENE3D); IPR001747 (PFAM); IPR011030 (G3DSA:1.25.10.GENE3D); PTHR23345 (PANTHER); PTHR23345:SF1 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001747 (PROSITE_PROFILES); SignalIP-TM (SIGNALP_EUK); IPR015819 (SUPERFAMILY); IPR011030 (SUPERFAMILY); TMhelix (TMHMM)
2086	300778_length_2101_cvg_63.1_tip_1_0	3426	aldehyde dehydrogenase 2 family	701	0	83.00%	0.228	IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); PTHR11699:SF145 (PANTHER); PTHR11699 (PANTHER); IPR016160 (PROSITE_PATTERNS); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)

2087	300802_length_2110_cvg_31.9_tip_1_4	1821	---	NA---	703				0.477 Y	IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612 (PANTHER); PTHR10612:SF7 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2088	300806_length_2113_cvg_10.0_tip_1_5	298		lamin dm0-like isoform x1	704	0	75.60%		0.312	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR001322 (G3DSA:2.60.40.GENE3D); G3DSA:1.20.5.170 (GENE3D); IPR001664 (PFAM); IPR001322 (PFAM); IPR001664 (PANTHER); IPR027696 (PTHR23239:PANTHER); IPR018039 (PROSITE_PATTERNS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF64593 (SUPERFAMILY); SSF64593 (SUPERFAMILY); IPR001322 (SUPERFAMILY)
2089	300814_length_2115_cvg_10.6_tip_1_0	253		laminin subunit alpha-like	705	2.79E-83	61.10%		0.111	IPR001791 (SMART); IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10574:SF39 (PANTHER); PTHR10574 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2090	300832_length_2117_cvg_29.3_tip_1_3	907		catalase	706	0	84.60%		0.278	IPR018028 (PRINTS); IPR011614 (SMART); IPR011614 (G3DSA:2.40.180.GENE3D); IPR011614 (PFAM); IPR010582 (PFAM); IPR018028 (PANTHER); IPR002226 (PROSITE_PATTERNS); IPR024708 (PROSITE_PATTERNS); IPR018028 (PROSITE_PROFILES); IPR020835 (SUPERFAMILY)
2091	300846_length_2122_cvg_47.4_tip_1_4	2745		von willebrand factor type egf and pentraxin domain-containing protein 1-like	707	9.85E-14	39.70%		0.707 Y	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); PTHR19325:SF321 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); TMhelix (TMHMM)
2092	300864_length_2132_cvg_8.7_tip_1_0	234		guanine nucleotide exchange	711	0	70.50%		0.102	Coil (COILS); IPR000219 (SMART); IPR001849 (SMART); IPR001452 (SMART); IPR000219 (PFAM); IPR001452 (PFAM); IPR000219 (G3DSA:1.20.900.GENE3D); G3DSA:2.30.30.40 (GENE3D); IPR011993 (G3DSA:2.30.29.GENE3D); PTHR12845 (PANTHER); PTHR12845:SF5 (PANTHER); IPR000219 (PROSITE_PROFILES); IPR001849 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); IPR000219 (SUPERFAMILY); SSF50729 (SUPERFAMILY)
2093	300868_length_2134_cvg_14.0_tip_1_2	416		gels_homam ame: full= cytoplasmic ame: full=actin-depolymerizing factor short=adf	711	0	73.20%		0.138	IPR007122 (PRINTS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY)
2094	300870_length_2135_cvg_9.6_tip_1_2	302		angiotensin-converting enzyme-like	711	0	71.20%		0.507 Y	IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF55486 (SUPERFAMILY)
2095	300878_length_2137_cvg_10.1_tip_1_4	291		cyclin-dependent kinase 12 isoform x1	712	0	82.00%		0.104	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24056:SF125 (PANTHER); PTHR24056 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2096	300886_length_2142_cvg_9.5_tip_1_1	291		adenosine deaminase cecr1	714	2.68E-40	77.10%		0.114	G3DSA:3.20.20.140 (GENE3D); IPR001365 (PFAM); PTHR11409 (PANTHER); PTHR11409:SF39 (PANTHER); SSF51556 (SUPERFAMILY); TMhelix (TMHMM)

2097	300892_length_2143_cvg_9.7_tip_1_0	318	membrane metallo-endopeptidase-like 1-like	715	2.56E-163	62.10%	0.124	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR008753 (PFAM); IPR018497 (PFAM); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR10042:SF24 (PANTHER); PTHR10042 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2098	300896_length_2144_cvg_8.8_tip_1_0	259	early growth response	715	1.09E-120	54.80%	0.106	IPR001506 (PRINTS); IPR006026 (SMART); IPR000859 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR001506 (PFAM); IPR000859 (PFAM); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); SSF55486 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
2099	300912_length_2149_cvg_12.4_tip_1_1	314	meprin a	716	5.34E-55	54.60%	0.112	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559 (PANTHER); IPR019819 (PROSITE_PATTERNS); IPR019826 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY)
2100	300920_length_2152_cvg_9.0_tip_1_1	300	venom carboxylesterase-6 isoform x2	717	9.59E-138	58.20%	0.144	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
2101	300926_length_2153_cvg_25.3_tip_1_5	690	chorion peroxidase-like	717	4.63E-166	59.50%	0.211	IPR002172 (PRINTS); IPR000998 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR000998 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR23282 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
2102	300936_length_2156_cvg_11.1_tip_1_5	231	mam and ldl-receptor class a domain-containing protein 1	718	2.40E-152	54.50%	0.152	IPR000734 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR013818 (PFAM); PTHR11610:SF41 (PANTHER); IPR000734 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY)
2103	300950_length_2165_cvg_27.8_tip_1_0	964	pancreatic lipase-related protein 1	722	4.88E-102	55.40%	0.146	Coil (COILS); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001547 (PFAM); PTHR31308 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY)
2104	300952_length_2166_cvg_9.7_tip_1_1	259	glycoside catalytic core	722	5.33E-94	53.40%	0.282	Coil (COILS); IPR002312 (PRINTS); IPR004364 (PFAM); IPR004523 (TIGRFAM); IPR004365 (PFAM); G3DSA:3.30.930.10 (GENE3D); IPR012340 (G3DSA:2.40.50.GENE3D); IPR018150 (PANTHER); IPR004523 (PTHR22594:PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY); IPR012340 (SUPERFAMILY)
2105	300958_length_2172_cvg_14.7_tip_1_1	404	aspartate--trna cytoplasmic	724	0	85.30%	0.202	PR00421 (PRINTS); IPR005792 (TIGRFAM); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005788 (TIGRFAM); PF13848 (PFAM); PTHR18929 (PANTHER); PTHR18929:SF60 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
2106	300970_length_2176_cvg_57.7_tip_1_2	3229	protein disulfide-isomerase a3	725	0	78.20%	0.361 Y	

2107	301014_length_2199_cvg_27.2_tip_1_4	725	latrophilin cir1-like isoform x1	733	6.32E-175	59.10%	0.232	Coil (COILS); IPR000832 (PRINTS); IPR000832 (PFAM); PTHR12011:SF258 (PANTHER); PTHR12011 (PANTHER); IPR017983 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2119	301180_length_2269_cvg_73.3_tip_1_2	18195	chitinase 1 precursor	735	0	69.50%	0.117	IPR011583 (SMART); IPR002557 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR002557 (PFAM); PTHR11177:SF144 (PANTHER); PTHR11177 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR029070 (SUPERFAMILY)
2108	301068_length_2224_cvg_22.6_tip_1_2	680	lysine--trna ligase isoform x2	741	0	86.20%	0.108	Coil (COILS); IPR018149 (PRINTS); IPR004365 (PFAM); IPR002313 (TIGRFAM); IPR012340 (G3DSA:2.40.50.GENE3D); IPR004364 (PFAM); G3DSA:3.30.930.10 (GENE3D); PTHR22594:SF4 (PANTHER); IPR018150 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006195 (PROSITE_PROFILES); IPR002313 (HAMAP); IPR012340 (SUPERFAMILY); SSF55681 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2109	301072_length_2225_cvg_19.7_tip_1_2	631	delta -sterol reductase	741	0	78.60%	0.151	IPR006094 (PFAM); IPR016169 (G3DSA:3.30.465.GENE3D); PTHR10801 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016166 (PROSITE_PROFILES); IPR016164 (SUPERFAMILY); IPR016166 (SUPERFAMILY); TMhelix (TMHMM)
2110	301076_length_2228_cvg_47.9_tip_0_5	1944	plasma alpha-l-fucosidase	742	0	78.50%	0.102	IPR016286 (PRINTS); IPR000933 (SMART); IPR000933 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR10030:SF26 (PANTHER); IPR000933 (PANTHER); IPR018526 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY)
2111	301078_length_2228_cvg_9.2_tip_1_2	368	PREDICTED: mucin-5AC-like	742	1.26E-07	52.25%	0.169	TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2112	301086_length_2233_cvg_3.8_tip_1_2	145	cd109 antigen	744	0	63.20%	0.187	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR011626 (PFAM); IPR008930 (G3DSA:1.50.10.GENE3D); IPR001599 (PFAM); PTHR11412 (PANTHER); PTHR11412:SF85 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR008930 (SUPERFAMILY)
2113	301098_length_2237_cvg_9.9_tip_1_3	265	trehalase-like isoform x1	746	0	69.40%	0.128	IPR001661 (PRINTS); IPR001661 (PFAM); IPR001661 (PANTHER); PTHR23403:SF1 (PANTHER); IPR018232 (PROSITE_PATTERNS); IPR018232 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008928 (SUPERFAMILY)

2122	301208_length_2285_cvg_27.5_tip_1_0	786	cytochrome p450	762	0	70.00%	0.33	Coil (COILS); IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24290 (PANTHER); PTHR24290:SF0 (PANTHER); IPR017972 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001128 (SUPERFAMILY)
2123	301226_length_2292_cvg_59.1_tip_1_0	4430	heat shock 70 kda protein cognate 4	764	0	94.40%	0.242	Coil (COILS); IPR013126 (PRINTS); IPR029048 (G3DSA:1.20.1270.GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.90.640.10 (GENE3D); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029048 (SUPERFAMILY); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2124	301230_length_2293_cvg_11.9_tip_1_3	377	arylsulfatase b	765	9.74E-173	64.80%	0.223	IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); IPR000917 (PFAM); PTHR10342:SF206 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM)
2125	301238_length_2297_cvg_18.9_tip_1_3	536	utp--glucose-1-phosphate uridylyltransferase-like	766	0	84.40%	0.11	IPR002618 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR002618 (PANTHER); IPR016267 (PTHR11952:PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2126	301244_length_2298_cvg_6.9_tip_1_5	205	phospholipase a-2-activating protein	766	0	66.50%	0.119	IPR001680 (SMART); IPR001680 (PFAM); IPR015155 (PFAM); IPR013535 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19849 (PANTHER); PTHR19849:SF0 (PANTHER); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR013535 (PROSITE_PROFILES); IPR015155 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR016024 (SUPERFAMILY)
2128	301254_length_2300_cvg_44.5_tip_1_5	1880	contactin associated protein 1	766	4.55E-61	50.00%	0.153	Coil (COILS); IPR001073 (SMART); IPR001073 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); IPR008983 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF575 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY); IPR002181 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2127	301248_length_2299_cvg_64.0_tip_1_3	4342	meprin a	767	3.73E-38	48.80%	0.097	IPR000859 (SMART); IPR001506 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); PTHR10127 (PANTHER); PTHR10127:SF580 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

2129	301268_length_2304_cvg_6.9_tip_1_2	191	low density lipoprotein	768	0	64.70%	0.102	IPR000742 (SMART); IPR002223 (SMART); IPR001881 (SMART); IPR006605 (SMART); IPR003886 (SMART); IPR023413 (G3DSA:2.40.155.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR006605 (PFAM); IPR003886 (PFAM); PTHR11339 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR006605 (PROSITE_PROFILES); IPR003886 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR009030 (SUPERFAMILY); IPR009017 (SUPERFAMILY)
2130	301286_length_2313_cvg_16.0_tip_1_1	407	exocyst complex component 6b-like isoform 2	771	0	80.60%	0.098	Coil (COILS); Coil (COILS); Coil (COILS); IPR007225 (PIRSF); IPR007225 (PFAM); IPR007225 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
2131	301300_length_2323_cvg_11.0_tip_1_5	359	phenoloxidase subunit a3-like	774	0	67.40%	0.19	IPR013788 (PRINTS); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR005203 (G3DSA:2.60.40.GENE3D); IPR005204 (PFAM); IPR000896 (PFAM); IPR005203 (PFAM); IPR013788 (PANTHER); PTHR11511:SF24 (PANTHER); IPR002227 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); IPR005204 (SUPERFAMILY); IPR008922 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
2132	301304_length_2324_cvg_38.4_tip_1_4	1036	lim domain-binding protein 3	775	1.25E-107	72.40%	0.327	IPR001781 (SMART); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001781 (PFAM); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001781 (G3DSA:2.10.110.GENE3D); PTHR24214:SF29 (PANTHER); PTHR24214 (PANTHER); IPR001781 (PROSITE_PATTERNS); IPR001781 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001781 (PROSITE_PROFILES); IPR001781 (PROSITE_PROFILES); IPR001781 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SSF57716 (SUPERFAMILY); SSF57716 (SUPERFAMILY); SSF57716 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2135	301410_length_2391_cvg_17.2_tip_1_2	530	14-3-3 protein epsilon	792	9.52E-164	95.40%	0.118	Coil (COILS); IPR000308 (PRINTS); IPR023410 (SMART); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023409 (PROSITE_PATTERNS); IPR023409 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023410 (SUPERFAMILY)
2133	301394_length_2381_cvg_45.2_tip_1_0	1629	superoxide dismutase soluble	794	3.91E-42	55.10%	0.109	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); IPR018152 (PROSITE_PATTERNS); IPR001424 (SUPERFAMILY)
2134	301396_length_2383_cvg_7.3_tip_1_0	276	n-acetylated-alpha-linked acidic dipeptidase	795	0	59.30%	0.21	G3DSA:3.50.30.30 (GENE3D); G3DSA:3.40.630.10 (GENE3D); IPR003137 (PFAM); IPR007365 (G3DSA:1.20.930.GENE3D); IPR007484 (PFAM); IPR007365 (PFAM); PTHR10404 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF52025 (SUPERFAMILY); IPR007365 (SUPERFAMILY); SSF53187 (SUPERFAMILY); TMhelix (TMHMM)
2136	301416_length_2394_cvg_44.8_tip_1_3	1520	chorion peroxidase-like	798	2.88E-133	55.30%	0.103	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

2137	301422_length_2397_cvg_66.7_tip_1_3	123579	myosin heavy chain isoform 3	799	0	91.70%	0.101	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR002928 (PFAM); PTHR13140:SF364 (PANTHER); PTHR13140 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); TMhelix (TMHMM)
2138	301444_length_2425_cvg_52.0_tip_1_0	2386	neutral ceramidase	804	0	66.70%	0.145	IPR006823 (PFAM); IPR006823 (PANTHER); PTHR12670:SF1 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
2139	301468_length_2441_cvg_6.1_tip_1_0	200	sphingomyelin partial	814	0	76.30%	0.119	IPR008139 (SMART); IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR10340:SF13 (PANTHER); PTHR10340 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008139 (PROSITE_PROFILES); IPR029052 (SUPERFAMILY); IPR011001 (SUPERFAMILY); TMhelix (TMHMM)
2140	301494_length_2460_cvg_21.3_tip_1_5	650	low quality protein: mucin-5b-like	820	4.27E-08	56.33%	0.102	no IPS match
2141	301498_length_2461_cvg_43.9_tip_1_3	1459	heat shock 70 kda protein cognate 5	821	0	89.00%	0.158	Coil (COILS); IPR013126 (PRINTS); IPR012725 (TIGRFAM); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.30.30 (GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.90.640.10 (GENE3D); PTHR19375:SF173 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR012725 (HAMAP); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
2142	301512_length_2469_cvg_14.7_tip_1_1	424	sel1l protein	823	0	77.80%	0.298	Coil (COILS); IPR006597 (SMART); IPR011990 (G3DSA:1.25.40.GENE3D); IPR006597 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR11102 (PANTHER); PTHR11102:SF55 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF81901 (SUPERFAMILY); SSF81901 (SUPERFAMILY); SSF81901 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2143	301528_length_2475_cvg_23.6_tip_1_2	609	superoxide dismutase	825	2.56E-61	67.40%	0.184	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY); TMhelix (TMHMM)
2144	301546_length_2486_cvg_36.1_tip_1_4	1031	glucose dehydrogenase	829	0	65.90%	0.131	IPR000172 (PFAM); IPR007867 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR11552:SF77 (PANTHER); PTHR11552 (PANTHER); IPR000172 (PROSITE_PATTERNS); IPR000172 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
2145	301572_length_2497_cvg_29.2_tip_1_1	956	cytochrome p450 6k1-like	832	2.20E-129	59.20%	0.152	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24292 (PANTHER); PTHR24292:SF24 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2146	301582_length_2502_cvg_12.3_tip_1_2	561	hemocyte protein-glutamine gamma- partial	834	0	70.40%	0.461 Y	IPR002931 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR008958 (PFAM); IPR023608 (PIRSF); IPR013783 (G3DSA:2.60.40.GENE3D); IPR001102 (PFAM); IPR002931 (PFAM); IPR002931 (G3DSA:3.90.260.GENE3D); PTHR11590:SF40 (PANTHER); IPR023608 (PANTHER); SignalP-noTM (SIGNALP_EUK); IPR008958 (SUPERFAMILY); IPR008958 (SUPERFAMILY); SSF54001 (SUPERFAMILY); IPR014756 (SUPERFAMILY)

2147	301596_length_2515_cvg_6.2_tip_1_3	224	basement membrane-specific heparan sulfate proteoglycan core protein	839	0	59.70%	0.098	IPR003599 (SMART); IPR003598 (SMART); IPR013106 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013032 (PFAM); IPR002049 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:2.170.300.10 (GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013151 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2148	301606_length_2520_cvg_9.9_tip_1_4	420	arylsulfatase b	840	0	72.00%	0.248	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); PTHR10342 (PANTHER); PTHR10342:SF189 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY)
2149	301610_length_2521_cvg_31.4_tip_1_4	1290	krueppel-like factor 10	840	1.41E-71	63.10%	0.167	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223:SF21 (PANTHER); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2150	301628_length_2531_cvg_7.6_tip_1_0	283	atp-dependent zinc metalloprotease yme1 homolog	844	0	75.30%	0.27	IPR003593 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:1.10.8.60 (GENE3D); IPR005936 (TIGRFAM); IPR003959 (PFAM); IPR000642 (PFAM); PTHR23076 (PANTHER); PTHR23076:SF37 (PANTHER); IPR003960 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR005936 (HAMAP); SSF140990 (SUPERFAMILY); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2151	301634_length_2535_cvg_44.7_tip_1_1	27594	enolase	845	0	89.50%	0.3	IPR000941 (PRINTS); IPR000941 (TIGRFAM); IPR020810 (PFAM); IPR029017 (G3DSA:3.30.390.GENE3D); IPR020811 (PFAM); IPR029065 (G3DSA:3.20.20.GENE3D); IPR000941 (PANTHER); IPR020809 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000941 (HAMAP); IPR029065 (SUPERFAMILY); IPR029017 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

2152	301646_length_2550_cvg_6.2_tip_1_1	185	protein disulfide-isomerase a4-like	850	8.02E-48	70.40%	0.098	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929 (PANTHER); PTHR18929:SF56 (PANTHER); IPR017937 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
2153	301650_length_2551_cvg_19.9_tip_1_2	648	growth differentiation factor 8-like	850	1.07E-109	64.30%	0.449 Y	IPR001839 (SMART); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001111 (PFAM); IPR001839 (PFAM); PTHR11848:SF126 (PANTHER); IPR015615 (PANTHER); IPR017948 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2154	301654_length_2554_cvg_58.0_tip_1_0	3376	heat shock 70 kda protein cognate 3	852	0	93.60%	0.182	Coil (COILS); Coil (COILS); IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); G3DSA:3.90.640.10 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.30.30 (GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF157 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029048 (SUPERFAMILY); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2155	301662_length_2562_cvg_7.0_tip_1_3	288	tensin isoform x11	854	4.83E-143	60.90%	0.117	IPR029021 (G3DSA:3.90.190.GENE3D); G3DSA:2.60.40.1110 (GENE3D); IPR014020 (PFAM); PTHR12583 (PANTHER); PTHR12583:SF7 (PANTHER); IPR014020 (PROSITE_PROFILES); IPR029023 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); IPR000008 (SUPERFAMILY)
2156	301668_length_2567_cvg_58.3_tip_1_2	5939	ubiquitin- isoform a	855	0	99.00%	0.418 Y	IPR019956 (PRINTS); IPR000626 (SMART); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); PTHR10666:SF94 (PANTHER); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); TMhelix (TMHMM)
2157	301682_length_2589_cvg_4.9_tip_1_1	211	sodium calcium exchanger partial	863	0	75.00%	0.103	IPR004836 (PRINTS); IPR003644 (SMART); IPR004837 (PFAM); IPR003644 (PFAM); PTHR11878 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF141072 (SUPERFAMILY); SSF141072 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

2172	301842_length_2715_cvg_41.7_tip_1_0	2102	tissue factor pathway inhibitor 2	905	4.23E-33	62.80%	0.129	Coil (COILS); IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2173	301846_length_2721_cvg_13.3_tip_1_1	498	beta-galactosidase-like isoform x4	907	0	59.70%	0.425 Y	IPR001944 (PRINTS); IPR013781 (G3DSA:3.20.20.GENE3D); IPR008979 (G3DSA:2.60.120.GENE3D); IPR001944 (PFAM); PTHR23421:SF13 (PANTHER); IPR001944 (PANTHER); IPR019801 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008979 (SUPERFAMILY); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
2174	301856_length_2732_cvg_6.5_tip_1_4	272	complement c1s subcomponent	911	3.70E-11	43.75%	0.106	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); TMhelix (TMHMM)
2175	301868_length_2755_cvg_2.8_tip_1_1	171	urokinase-type plasminogen activator	918	2.96E-61	48.00%	0.099	IPR002172 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); IPR003609 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR003014 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR002172 (PFAM); G3DSA:3.50.4.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
2176	301894_length_2783_cvg_7.9_tip_1_0	315	angiotensin-converting enzyme-like	928	1.04E-162	61.70%	0.276	Coil (COILS); IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2177	301900_length_2784_cvg_38.0_tip_1_2	1414	aael014548- partial	928	7.26E-130	88.20%	0.694 Y	IPR012336 (G3DSA:3.40.30.GENE3D); IPR019479 (PFAM); IPR000866 (PFAM); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2178	301902_length_2786_cvg_62.8_tip_1_1	2687	agap011476-pa-like protein	929	4.71E-74	44.80%	0.115	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
2179	301912_length_2792_cvg_40.1_tip_0_0	2385	map kinase-interacting serine threonine-protein kinase 1	931	0	81.40%	0.12	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24349 (PANTHER); IPR008271 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)

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									IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2184	301934_length_2815_cvg_10.6_tip_1_5	387	zinc finger protein 239- partial	938	4.42E-72	55.60%	0.135		Coil (COILS); IPR001747 (SMART); IPR015816 (G3DSA:2.30.230.GENE3D); IPR001747 (PFAM); IPR015255 (PFAM); IPR015817 (G3DSA:2.20.50.GENE3D); IPR011030 (G3DSA:1.25.10.GENE3D); IPR015818 (G3DSA:2.20.80.GENE3D); PTHR23345:SF11 (PANTHER); PTHR23345 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001747 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR011030 (SUPERFAMILY); IPR015819 (SUPERFAMILY); IPR015819 (SUPERFAMILY); TMhelix (TMHMM)
2185	301938_length_2818_cvg_5.5_tip_1_3	246	dip hdl-bgpb precursor	940	0	63.60%	0.727 Y		IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF149 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2186	301942_length_2826_cvg_41.9_tip_1_1	3483	titin isoform x5	942	0	75.50%	0.099		IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); SSF55486 (SUPERFAMILY); SSF55486 (SUPERFAMILY)
2187	301948_length_2836_cvg_7.9_tip_1_1	326	angiotensin-converting enzyme	945	0	63.40%	0.155		IPR014001 (SMART); IPR001650 (SMART); IPR003877 (SMART); IPR011545 (PFAM); IPR001650 (PFAM); IPR003877 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR24031:SF211 (PANTHER); PTHR24031 (PANTHER); IPR014014 (PROSITE_PROFILES); IPR001870 (PROSITE_PROFILES); IPR014001 (PROSITE_PROFILES); IPR001650 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR013320 (SUPERFAMILY) G3DSA:3.40.630.10 (GENE3D); IPR007484 (PFAM); PTHR12053 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53187 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2188	301956_length_2849_cvg_9.3_tip_1_4	364	atp-dependent rna helicase ddx1	950	0	83.50%	0.332		IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR020675 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
2189	301968_length_2860_cvg_30.4_tip_1_1	1296	carboxypeptidase q-like	953	0	75.80%	0.193		
2190	301980_length_2882_cvg_33.8_tip_1_2	1149	muscle m-line assembly protein unc- partial	960	1.70E-45	49.40%	0.105		

2191	301998_length_2905_cvg_74.2_tip_1_0	10688	cathepsin d	969	0	80.50%	0.186	IPR001461 (PRINTS); IPR021109 (G3DSA:2.40.70.GENE3D); IPR021109 (G3DSA:2.40.70.GENE3D); IPR001461 (PFAM); IPR012848 (PFAM); PTHR13683:SF230 (PANTHER); IPR001461 (PANTHER); IPR001969 (PROSITE_PATTERNS); IPR001969 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR021109 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2192	302000_length_2906_cvg_49.4_tip_1_3	2066	low quality protein: mucin-19	969	1.35E-25	41.70%	0.162	TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2193	302028_length_2934_cvg_21.5_tip_1_4	1071	villin-1-like isoform x1	978	0	66.30%	0.114	IPR007122 (PRINTS); IPR003128 (SMART); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR003128 (G3DSA:1.10.950.GENE3D); IPR003128 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR007122 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003128 (PROSITE_PROFILES); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); IPR003128 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY)
2194	302044_length_2946_cvg_27.1_tip_1_1	838	n-acetylated-alpha-linked acidic dipeptidase	982	0	60.00%	0.238	IPR003137 (PFAM); IPR007484 (PFAM); G3DSA:3.50.30.30 (GENE3D); IPR007365 (G3DSA:1.20.930.GENE3D); IPR007365 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR10404 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53187 (SUPERFAMILY); SSF52025 (SUPERFAMILY); IPR007365 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2195	302052_length_2954_cvg_8.0_tip_1_5	299	ferric-chelate reductase 1 homolog	984	2.10E-161	57.80%	0.751 Y	IPR006593 (SMART); IPR005018 (SMART); IPR005018 (PFAM); IPR004877 (PFAM); IPR002861 (PFAM); PTHR23130:SF70 (PANTHER); PTHR23130 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002861 (PROSITE_PROFILES); IPR005018 (PROSITE_PROFILES); IPR006593 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2196	302058_length_2961_cvg_25.6_tip_1_4	1175	beta-lactamase-like protein 2-like	987	1.86E-55	50.40%	0.381 Y	IPR012338 (G3DSA:3.40.710.GENE3D); IPR001466 (PFAM); PTHR22935 (PANTHER); PTHR22935:SF64 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012338 (SUPERFAMILY)
2197	302068_length_2971_cvg_43.0_tip_1_4	2060	hypothetical protein DAPPUDRAFT_200882	990	0	60.50%	0.116	IPR018497 (PRINTS); IPR008753 (PFAM); IPR018497 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR11733:SF111 (PANTHER); IPR000718 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
2201	302086_length_3001_cvg_39.8_tip_1_1	2273	peroxidasin homolog	991	8.66E-119	54.50%	0.418 Y	Coil (COILS); IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)

2198	302074_length_2976_cvg_37.4_tip_1_5	1404	proactivator polypeptide-like	992	0	54.80%	0.307	IPR008373 (PRINTS); IPR008139 (SMART); IPR003119 (SMART); IPR011001 (G3DSA:1.10.225.GENE3D); IPR011001 (G3DSA:1.10.225.GENE3D); IPR003119 (PFAM); IPR007856 (PFAM); IPR008138 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR11480:SF3 (PANTHER); PTHR11480 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003119 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR003119 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); TMhelix (TMHMM)
2199	302076_length_2977_cvg_20.8_tip_1_5	673	sucrase- intestinal-like	992	0	61.70%	0.586 Y	IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF7 (PANTHER); IPR030458 (PROSITE_PATTERNS); IPR030459 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF51011 (SUPERFAMILY); IPR011013 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
2200	302078_length_2981_cvg_44.7_tip_1_2	2064	pdz and lim domain protein zasp-like	993	6.42E-35	53.40%	0.103	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR24214:SF29 (PANTHER); PTHR24214 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
2202	302092_length_3004_cvg_46.0_tip_1_4	1637	meprin a	1001	8.82E-72	50.10%	0.789 Y	IPR001506 (PRINTS); IPR006026 (SMART); IPR000859 (SMART); IPR001506 (PFAM); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF580 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000859 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF55486 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
2203	302114_length_3022_cvg_42.0_tip_1_5	1756	glucose dehydrogenase	1007	0	68.40%	0.141	G3DSA:3.50.50.60 (GENE3D); IPR007867 (PFAM); IPR000172 (PFAM); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); IPR000172 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54373 (SUPERFAMILY); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
2204	302118_length_3030_cvg_15.1_tip_1_1	515	basement membrane-specific heparan sulfate proteoglycan core protein	1010	0	70.20%	0.109	IPR001791 (SMART); IPR001881 (SMART); IPR000742 (SMART); IPR003599 (SMART); IPR003598 (SMART); PF13895 (PFAM); IPR000742 (PFAM); IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001791 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10574:SF247 (PANTHER); PTHR10574 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001791 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

2214	302186_length_3125_cvg_64.6_tip_0_3	36669	e3 ubiquitin-protein ligase partial	1042	0	53.20%	0.104	IPR001841 (SMART); IPR001478 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); PF02176 (PFAM); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PF13920 (PFAM); IPR013323 (G3DSA:3.90.890.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964 (PANTHER); IPR017907 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001293 (PROSITE_PROFILES); IPR001841 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR008974 (SUPERFAMILY); SSF57850 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2215	302196_length_3136_cvg_25.8_tip_1_0	942	a disintegrin and metalloproteinase with thrombospondin motifs 1 isoform x1	1046	4.28E-134	70.50%	0.107	IPR024079 (G3DSA:3.40.390.GENE3D); PF13583 (PFAM); PTHR13723 (PANTHER); PTHR13723:SF148 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001590 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2220	302242_length_3182_cvg_22.2_tip_1_2	1103	transitional endoplasmic reticulum atpase ter94	1046	0	94.80%	0.127	IPR003593 (SMART); IPR004201 (SMART); IPR003338 (SMART); IPR005938 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR029067 (G3DSA:3.10.330.GENE3D); IPR015415 (PFAM); G3DSA:1.10.8.60 (GENE3D); G3DSA:2.40.40.20 (GENE3D); IPR004201 (PFAM); IPR003338 (PFAM); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23077 (PANTHER); PTHR23077:SF69 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR003960 (PROSITE_PATTERNS); IPR029067 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR009010 (SUPERFAMILY)
2216	302204_length_3144_cvg_14.6_tip_1_4	575	a chain structural studies of protein tyrosine phosphatase beta catalytic domain in complex with inhibitors	1048	1.21E-75	57.90%	0.102	IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR003961 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000242 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR029021 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
2217	302216_length_3162_cvg_8.6_tip_1_1	352	serine threonine-protein kinase pim-3	1054	2.50E-128	76.90%	0.107	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR22984:SF1 (PANTHER); PTHR22984 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2218	302228_length_3169_cvg_55.9_tip_1_5	3632	cell surface protein	1056	1.08E-12	44.30%	0.179	TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
2219	302234_length_3171_cvg_6.1_tip_1_4	261	usher syndrome type-1g protein homolog	1057	5.35E-132	62.20%	0.11	Coil (COILS); IPR002110 (SMART); IPR001660 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR013761 (G3DSA:1.10.150.GENE3D); IPR021129 (PFAM); IPR020683 (PFAM); PTHR24161:SF6 (PANTHER); PTHR24161 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR013761 (SUPERFAMILY); IPR020683 (SUPERFAMILY)

2234	302340_length_3374_cvg_18.8_tip_1_4	1079	staphylococcal nuclease domain-containing protein 1-like	1125	0	74.40%	0.147	Coil (COILS); IPR002999 (SMART); IPR016071 (SMART); IPR016071 (PFAM); IPR016071 (G3DSA:2.40.50.GENE3D); G3DSA:2.30.30.140 (GENE3D); IPR002999 (PFAM); IPR016071 (G3DSA:2.40.50.GENE3D); IPR030481 (PTHR12302:PANTHER); PTHR12302 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002999 (PROSITE_PROFILES); IPR016071 (PROSITE_PROFILES); IPR016071 (PROSITE_PROFILES); IPR016071 (PROSITE_PROFILES); IPR016071 (SUPERFAMILY); SSF63748 (SUPERFAMILY); IPR016071 (SUPERFAMILY); IPR016071 (SUPERFAMILY); IPR016071 (SUPERFAMILY); IPR016071 (TMHMM); TMhelix (TMHMM)
2235	302352_length_3406_cvg_12.2_tip_1_2	505	uncharacterized family 31 glucosidase k1a1161 isoform x5	1135	0	62.40%	0.137	IPR013785 (G3DSA:3.20.20.GENE3D); IPR000322 (PFAM); PTHR22762:SF73 (PANTHER); PTHR22762 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51011 (SUPERFAMILY); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
2236	302360_length_3422_cvg_14.6_tip_1_3	575	integrin alpha-8-like	1141	1.71E-153	48.70%	0.105	IPR000413 (PRINTS); IPR013519 (SMART); G3DSA:2.60.40.1530 (GENE3D); G3DSA:2.130.10.130 (GENE3D); IPR013649 (PFAM); PF13517 (PFAM); G3DSA:2.60.40.1510 (GENE3D); G3DSA:1.20.5.930 (GENE3D); G3DSA:2.60.40.1460 (GENE3D); PTHR23220 (PANTHER); PTHR23220:SF71 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); SSF69179 (SUPERFAMILY); SSF69179 (SUPERFAMILY); SSF69179 (SUPERFAMILY); SSF69318 (SUPERFAMILY); TMhelix (TMHMM)
2237	302362_length_3441_cvg_22.6_tip_1_3	1064	hemocyte protein-glutamine gamma-glutamyltransferase-like	1147	0	67.80%	0.101	Coil (COILS); IPR002931 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR008958 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR001102 (PFAM); IPR002931 (G3DSA:3.90.260.GENE3D); IPR002931 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11590:SF40 (PANTHER); IPR023608 (PANTHER); IPR013808 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008958 (SUPERFAMILY); IPR014756 (SUPERFAMILY); SSF54001 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2238	302388_length_3517_cvg_20.7_tip_1_3	1041	cytosolic 10-formyltetrahydrofolate dehydrogenase isoform x1	1173	0	83.50%	0.123	Coil (COILS); Coil (COILS); IPR016163 (G3DSA:3.40.309.GENE3D); IPR005793 (PFAM); IPR015590 (PFAM); IPR009081 (G3DSA:1.10.1200.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); IPR009081 (PFAM); IPR005793 (G3DSA:3.10.25.GENE3D); IPR002376 (PFAM); IPR002376 (G3DSA:3.40.50.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF118 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); IPR001555 (PROSITE_PATTERNS); IPR009081 (PROSITE_PROFILES); IPR009081 (SUPERFAMILY); IPR002376 (SUPERFAMILY); IPR016161 (SUPERFAMILY); IPR011034 (SUPERFAMILY)
2239	302394_length_3529_cvg_18.7_tip_1_4	929	glucose-6-phosphate isomerase	1176	0	87.70%	0.103	IPR001672 (PRINTS); IPR001672 (PFAM); G3DSA:3.40.50.10490 (GENE3D); IPR023096 (G3DSA:1.10.1390.GENE3D); IPR001672 (PANTHER); PTHR11469:SF4 (PANTHER); IPR018189 (PROSITE_PATTERNS); IPR018189 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001672 (PROSITE_PROFILES); IPR001672 (HAMAP); SSF53697 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2240	302398_length_3539_cvg_9.3_tip_1_2	505	puromycin-sensitive aminopeptidase-like	1179	0	78.80%	0.218	Coil (COILS); IPR014782 (PRINTS); IPR024571 (PFAM); IPR014782 (PFAM); G3DSA:1.10.390.10 (GENE3D); IPR001930 (PANTHER); PTHR11533:SF163 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); SSF63737 (SUPERFAMILY)

2241	302408_length_3568_cvg_32.4_tip_1_1	1548	agap005124-pc-like protein	1189	0	78.10%	0.217	Coil (COILS); IPR016162 (G3DSA:3.40.605.GENE3D); IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF15 (PANTHER); IPR029510 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016161 (SUPERFAMILY)
2242	302410_length_3569_cvg_27.6_tip_1_3	1524	lethal giant larvae protein homolog 1-like isoform x3	1190	0	67.10%	0.125	Coil (COILS); Coil (COILS); IPR000664 (PRINTS); IPR013905 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR10241:SF28 (PANTHER); PTHR10241 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2243	302412_length_3574_cvg_56.6_tip_1_4	4320	vitellogenin fused with superoxide dismutase	1191	4.11E-91	43.70%	0.207	IPR001846 (SMART); IPR015818 (G3DSA:2.20.80.GENE3D); IPR001846 (PFAM); IPR011030 (G3DSA:1.25.10.GENE3D); IPR015255 (PFAM); PTHR23345:SF1 (PANTHER); PTHR23345 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001846 (PROSITE_PROFILES); IPR015819 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2244	302422_length_3587_cvg_7.8_tip_1_3	455	sodium calcium exchanger 2 isoform x1	1196	0	77.30%	0.156	IPR004836 (PRINTS); IPR003644 (SMART); IPR004836 (TIGRFAM); IPR004837 (PFAM); IPR003644 (PFAM); PTHR11878 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF141072 (SUPERFAMILY); SSF141072 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2245	302434_length_3619_cvg_12.2_tip_1_5	506	insulin-degrading enzyme	1206	0	76.50%	0.26	Coil (COILS); IPR011237 (G3DSA:3.30.830.GENE3D); IPR007863 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); IPR011765 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); IPR011237 (G3DSA:3.30.830.GENE3D); PTHR11851 (PANTHER); PTHR11851:SF85 (PANTHER); IPR001431 (PROSITE_PATTERNS); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY)
2246	302452_length_3674_cvg_32.4_tip_1_4	1795	titin	1225	0	82.60%	0.117	Coil (COILS); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR010939 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897:SF149 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2247	302456_length_3675_cvg_31.6_tip_1_5	1782	c-1-tetrahydrofolate cytoplasmic	1225	0	83.30%	0.179	Coil (COILS); IPR000672 (PRINTS); G3DSA:3.30.1510.10 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR020630 (PFAM); G3DSA:3.40.192.10 (GENE3D); IPR000559 (PFAM); G3DSA:3.10.410.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020631 (PFAM); PTHR10025 (PANTHER); IPR020867 (PROSITE_PATTERNS); IPR020628 (PROSITE_PATTERNS); IPR020867 (PROSITE_PATTERNS); IPR020628 (PROSITE_PATTERNS); IPR000672 (HAMAP); IPR000559 (HAMAP); SSF51735 (SUPERFAMILY); IPR027417 (SUPERFAMILY); SSF53223 (SUPERFAMILY)
2248	302478_length_3743_cvg_50.9_tip_1_5	3901	sarcolumenin isoform x2	1247	0	79.80%	0.116	IPR027417 (G3DSA:3.40.50.GENE3D); IPR006073 (PFAM); PTHR11216:SF66 (PANTHER); PTHR11216 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR030381 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)

2259	302596_length_4334_cvg_8.3_tip_1_5	506	glutamyl aminopeptidase	1444	0	63.60%	0.111	IPR014782 (PRINTS); G3DSA:1.10.390.10 (GENE3D); IPR014782 (PFAM); IPR024571 (PFAM); IPR001930 (PANTHER); PTHR11533:SF165 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF63737 (SUPERFAMILY); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
2260	302598_length_4353_cvg_17.5_tip_1_2	963	nad mitochondrial	1451	0	83.70%	0.146	IPR007886 (SMART); IPR007698 (SMART); IPR012136 (PFAM); IPR029035 (G3DSA:3.40.50.GENE3D); IPR007886 (PFAM); IPR024605 (PFAM); G3DSA:3.40.50.1770 (GENE3D); IPR026255 (TIGRFAM); IPR007698 (PFAM); G3DSA:3.40.50.1770 (GENE3D); PTHR10160 (PANTHER); PTHR10160:SF19 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF52283 (SUPERFAMILY); IPR029035 (SUPERFAMILY); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2261	302600_length_4384_cvg_5.9_tip_1_1	419	urokinase-type plasminogen activator	1461	7.87E-59	56.00%	0.211	IPR002172 (PRINTS); IPR001254 (SMART); IPR002172 (SMART); IPR003609 (SMART); IPR003014 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:3.50.4.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2262	302602_length_4388_cvg_13.7_tip_1_2	952	angiotensin-converting enzyme	1462	0	59.30%	0.438 Y	Coil (COILS); Coil (COILS); IPR001548 (PRINTS); IPR002000 (PFAM); IPR001548 (PFAM); IPR001548 (PANTHER); PTHR10514:SF17 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF55486 (SUPERFAMILY); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2263	302608_length_4402_cvg_40.4_tip_1_2	3048	inter-alpha-trypsin inhibitor heavy chain h4-like	1467	2.92E-162	53.20%	0.115	Coil (COILS); IPR013694 (SMART); IPR002035 (SMART); IPR006604 (SMART); IPR013694 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); IPR002035 (PFAM); PTHR10338:SF108 (PANTHER); PTHR10338 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002035 (PROSITE_PROFILES); IPR013694 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)

2264	302616_length_4460_cvg_26.7_tip_1_2	1303	epithelial chloride channel partial	1486	0	52.00%	0.185	Coil (COILS); IPR002035 (SMART); IPR003961 (SMART); IPR002035 (G3DSA:3.40.50.GENE3D); IPR015394 (PFAM); IPR013642 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13519 (PFAM); PTHR10579:SF8 (PANTHER); PTHR10579 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2265	302626_length_4503_cvg_28.2_tip_1_1	1987	myosin heavy non-muscle	1501	0	89.00%	0.115	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR001609 (SMART); IPR001609 (PFAM); G3DSA:1.20.5.340 (GENE3D); IPR002928 (PFAM); IPR027401 (G3DSA:4.10.270.GENE3D); PTHR13140 (PANTHER); PTHR13140:SF301 (PANTHER); IPR000048 (PROSITE_PROFILES); IPR001609 (PROSITE_PROFILES); SSF90257 (SUPERFAMILY); SSF57997 (SUPERFAMILY); SSF90257 (SUPERFAMILY); IPR027417 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY)
2266	302628_length_4515_cvg_52.9_tip_0_0	5657	aplp_locmi ame: full=apolipophorins contains: ame: full=apolipophorin-2 ame: full=apolipophorin ii ame: full=apolp-2 contains: ame: full=apolipophorin-1 ame: full=apolipophorin i ame: full=apolp-1 flags: precursor	1505	1.25E-105	49.30%	0.099	Coil (COILS); IPR001846 (SMART); IPR001846 (PFAM); IPR014853 (PFAM); PTHR23361:SF13 (PANTHER); PTHR23361 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001846 (PROSITE_PROFILES); TMhelix (TMHMM)
2267	302632_length_4535_cvg_17.1_tip_1_1	968	Supervillin, partial	1512	0	64.10%	0.099	Coil (COILS); Coil (COILS); IPR007122 (PRINTS); IPR007122 (SMART); IPR003128 (SMART); IPR003128 (PFAM); IPR007123 (PFAM); IPR003128 (G3DSA:1.10.950.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR015628 (PTHR11977:PANTHER); IPR007122 (PANTHER); IPR003128 (PROSITE_PROFILES); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); IPR003128 (SUPERFAMILY)
2268	302644_length_4679_cvg_10.7_tip_1_0	547	neuroglian-like isoform 2	1560	0	77.50%	0.387 Y	IPR003599 (SMART); IPR003961 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR026966 (PFAM); PTHR10489 (PANTHER); PTHR10489:SF553 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2269	302646_length_4684_cvg_60.3_tip_1_1	8752	von willebrand factor a domain-containing protein 7	1561	9.06E-88	44.90%	0.121	PF13519 (PFAM); PTHR14905 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002035 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2270	302650_length_4698_cvg_57.4_tip_1_5	5375	low quality protein: hemocytin-like	1566	1.94E-67	39.50%	0.432 Y	IPR014853 (SMART); IPR001846 (SMART); PTHR11339 (PANTHER); PTHR11339:SF25 (PANTHER); IPR001007 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001846 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY); IPR002919 (SUPERFAMILY)

2276	302692_length_5263_cvg_28.9_tip_1_4	1741	ring finger protein nhl-1	1754	0	74.10%	0.197	Coil (COILS); Coil (COILS); IPR001841 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); IPR018957 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); IPR001258 (PFAM); PTHR24103:SF230 (PANTHER); PTHR24103 (PANTHER); IPR013017 (PROSITE_PROFILES); IPR001841 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR000315 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY); SSF101898 (SUPERFAMILY)
2277	302702_length_5374_cvg_64.8_tip_1_2	259270	vitellogenin fused with superoxide dismutase	1791	0	45.70%	0.196	IPR001747 (SMART); IPR001846 (SMART); IPR015816 (G3DSA:2.30.230.GENE3D); IPR015255 (PFAM); IPR015818 (G3DSA:2.20.80.GENE3D); IPR001846 (PFAM); IPR011030 (G3DSA:1.25.10.GENE3D); IPR001747 (PFAM); PTHR23345:SF1 (PANTHER); PTHR23345 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001846 (PROSITE_PROFILES); IPR001747 (PROSITE_PROFILES); IPR015819 (SUPERFAMILY); IPR015819 (SUPERFAMILY); IPR011030 (SUPERFAMILY); TMhelix (TMHMM)
2278	302706_length_5387_cvg_62.9_tip_1_0	101262	hypothetical protein DAPPUDRAFT_332703	1796	0	51.90%	0.107	Coil (COILS); IPR001846 (SMART); IPR014853 (SMART); IPR014853 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); IPR001846 (PFAM); PTHR23361 (PANTHER); PTHR23361:SF13 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001846 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2279	302718_length_5567_cvg_34.7_tip_1_1	4412	myosin light chain smooth muscle	1856	0	59.20%	0.112	Coil (COILS); IPR003599 (SMART); IPR003598 (SMART); IPR003961 (SMART); IPR013106 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2280	302722_length_5657_cvg_43.2_tip_1_5	3296	von willebrand factor	1885	1.64E-27	41.50%	0.11	IPR001007 (SMART); IPR001007 (PROSITE_PROFILES); IPR006207 (PROSITE_PROFILES)

									CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); COIL (COILS); Coil (COILS); IPR003598 (SMART); IPR001452 (SMART); IPR003599 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR001452 (PFAM); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2281	302740_length_6173_cvg_34.6_tip_1_5	3001	PREDICTED: acrosin-like	2057	8.21E-09	46.00%	0.146		
2282	302760_length_6729_cvg_39.9_tip_1_4	5049	titin- partial	2243	0	60.90%	0.101		
2283	302762_length_7189_cvg_30.7_tip_1_5	2638	hemocytin isoform x4	2396	2.89E-37	43.00%	0.137		
2284	302768_length_7907_cvg_14.8_tip_1_2	1825	multiple ankyrin repeats single kh domain	2635	0	61.80%	0.101		

[illegible]

2286	302784_length_11450_cvg_34.2_tip_1_0	14647	beta- -glucan-binding protein	3817	0	39.40%	0.096	no IPS match
								NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN
2288	302790_length_15619_cvg_32.5_tip_1_2	16248	mucin- partial	5206	2.27E-11	42.29%	0.152	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN

									TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS)
2287	302790_length_15619_cvg_32.5_tip_1_0	16248	coagulation factor v	5207	1.93E-12	41.30%	0.292		NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); COIL (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS);
2289	302790_length_15619_cvg_32.5_tip_1_3	16248	mucin 2	5207	7.39E-66	47.80%	0.102		NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS)

Supplementary Table 7: Whole body tissue transcriptome (Trinity contigs that match against secreted proteins [UniProtSL0243])

Nr.	Contig name	Read Numbers	Blast result (evalue=10 ⁻⁵ , BlastP, Nr database)	Seq. length	min. evalue	mean similarity	SignalP	InterProScan
1	c100101_g1_i1_len_662_path_1_0_661_1	16	tolloid-like protein 2 isoform x1	221	1.41E-75	64.60%	0.118	IPR002172 (SMART); IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:1.20.5.900 (GENE3D); PTHR10127:SF557 (PANTHER); PTHR10127 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000859 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR000859 (SUPERFAMILY); TMhelix (TMHMM)
2	c100109_g1_i1_len_465_path_443_0_464_0	11	leucomyosuppressin precursor	155	6.19E-36	71.40%	0.262	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
3	c100138_g1_i1_len_390_path_1_0_389_0	10	isoform c	130	3.59E-50	79.90%	0.109	IPR000716 (SMART); IPR019577 (PFAM); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR12036 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY)
4	c100142_g1_i1_len_598_path_1_0_597_5	14	cadherin-related tumor suppressor	199	2.52E-72	74.40%	0.102	IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); PTHR24026 (PANTHER); PTHR24026:SF41 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
5	c100151_g1_i1_len_811_path_1_0_810_4	44	ecto-nox disulfide-thiol exchanger 2	270	1.73E-57	74.50%	0.1	Coil (COILS); PTHR16001 (PANTHER)
6	c100167_g1_i1_len_280_path_1_0_279_5	7	notch-regulated ankyrin repeat-containing protein	93	1.56E-32	74.40%	0.104	IPR002110 (SMART); PF13857 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24203 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
7	c100323_g1_i1_len_255_path_1_0_254_2	4	torso-like protein isoform x2	85	3.62E-17	67.60%	0.118	no IPS match
8	c100372_g1_i1_len_234_path_212_0_233_3	2	lactose-binding lectin I-2-like	78	1.46E-08	59.10%	0.102	IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
9	c100512_g1_i1_len_268_path_246_0_267_0	4	serine threonine-protein kinase pak 1	90	4.64E-49	93.00%	0.096	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24361 (PANTHER); PTHR24361:SF245 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
10	c100542_g1_i1_len_897_path_1_0_896_0	28	carbohydrate sulfotransferase 11	299	1.54E-70	65.40%	0.142	IPR005331 (PFAM); IPR018011 (PANTHER); PTHR12137:SF30 (PANTHER); IPR027417 (SUPERFAMILY)
11	c100584_g1_i1_len_303_path_281_0_302_3	6	oocyte zinc finger protein 20	101	4.73E-12	79.60%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
12	c100807_g1_i1_len_324_path_1_0_323_3	11	aqp_aedae ame: full=aquaporin	108	8.34E-20	70.00%	0.21	IPR000425 (PRINTS); IPR023271 (G3DSA:1.20.1080.GENE3D); IPR000425 (PFAM); IPR000425 (PANTHER); PTHR19139:SF45 (PANTHER); IPR022357 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023271 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
13	c100993_g1_i1_len_608_path_586_0_607_0	13	upf0364 protein c6orf211 homolog	203	6.77E-57	64.10%	0.153	IPR002791 (PFAM); PTHR12260:SF1 (PANTHER); PTHR12260 (PANTHER); IPR002791 (SUPERFAMILY)
14	c101109_g1_i1_len_1509_path_1_0_1508_2	64	neuropeptides capa receptor-like	503	3.90E-149	74.20%	0.209	Coil (COILS); IPR000276 (PRINTS); IPR005390 (PRINTS); G3DSA:1.20.1070.10 (GENE3D); IPR000276 (PFAM); PTHR24243 (PANTHER); PTHR24243:SF107 (PANTHER); IPR000276 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017452 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
15	c101175_g1_i1_len_651_path_1_0_650_0	18	h aca ribonucleoprotein complex non-core subunit naf1	217	1.10E-52	76.90%	0.379Y	G3DSA:2.40.10.230 (GENE3D); IPR007504 (PFAM); PTHR31991 (PANTHER); IPR009000 (SUPERFAMILY)

16	c10122_g2_i1_len_364_path_596_0_363_2	6	limbic system-associated membrane protein	121	4.24E-26	57.60%	0.108	IPR013098 (PFAM); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF40 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
17	c101367_g1_i1_len_905_path_1_0_904_2	292	flowering locus t	301	6.11E-24	58.30%	0.189	IPR008914 (G3DSA:3.90.280.GENE3D); IPR008914 (PFAM); PTHR11362 (PANTHER); IPR001858 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008914 (SUPERFAMILY)
18	c101418_g1_i1_len_958_path_936_0_957_1	63	reticulocalbin-2	319	1.11E-97	70.20%	0.410Y	IPR002048 (SMART); IPR011992 (PFAM); IPR002048 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR10827:SF48 (PANTHER); PTHR10827 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)
19	c101553_g1_i1_len_677_path_655_0_676_2	16	transient receptor potential channel pyrexia-like	225	1.79E-26	49.60%	0.168	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24188 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
20	c101573_g1_i1_len_495_path_473_0_494_0	6	scp-like extracellular domain containing protein 1	165	2.37E-23	53.70%	0.117	IPR001283 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR014044 (SUPERFAMILY)
21	c10163_g1_i1_len_340_path_576_0_339_3	6	low quality protein: contactin-like	114	1.77E-27	61.20%	0.212	IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
22	c101875_g1_i1_len_341_path_1_0_340_2	4	kielin chordin-like protein	113	1.04E-18	54.50%	0.152	IPR013320 (SUPERFAMILY)
23	c101907_g1_i1_len_1228_path_1206_0_1227_0	22	aael001549- partial	410	0	95.10%	0.14	IPR000961 (SMART); IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); IPR017892 (PFAM); PTHR24357 (PANTHER); PTHR24357:SF80 (PANTHER); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000961 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
24	c101978_g1_i1_len_685_path_663_0_684_0	20	succinate-semialdehyde mitochondrial	229	6.25E-89	79.70%	0.131	IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); PTHR11699:SF49 (PANTHER); PTHR11699 (PANTHER); IPR016161 (SUPERFAMILY)
25	c101985_g1_i1_len_405_path_1_0_404_0	8	mam and ldl-receptor class a domain-containing protein 2-like	135	1.02E-07	43.50%	0.099	IPR000998 (PFAM); PTHR23282 (PANTHER); PTHR23282:SF75 (PANTHER); IPR013320 (SUPERFAMILY)
26	c102102_g1_i1_len_431_path_409_0_430_5	7	domain and thioredoxin-containing	143	7.65E-49	70.00%	0.111	PR00421 (PRINTS); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF3 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
27	c102112_g1_i1_len_663_path_1_0_662_2	26	enoyl- delta isomerase mitochondrial-like	221	6.95E-58	68.00%	0.164	Coil (COILS); IPR000582 (PRINTS); IPR001753 (PFAM); IPR000582 (PFAM); IPR029045 (G3DSA:3.90.226.GENE3D); IPR014352 (G3DSA:1.20.80.GENE3D); PTHR23310 (PANTHER); PTHR23310:SF55 (PANTHER); IPR022408 (PROSITE_PATTERNS); IPR000582 (PROSITE_PROFILES); IPR000582 (SUPERFAMILY); IPR029045 (SUPERFAMILY)
28	c102211_g1_i1_len_657_path_635_0_656_4	9	leucine-rich repeat-containing protein 15	219	1.05E-44	61.90%	0.11	PR00019 (PRINTS); IPR003591 (SMART); SM00364 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
29	c102279_g1_i1_len_248_path_1_0_247_1	4	collagen alpha chain	83	6.52E-17	71.10%	0.11	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF444 (PANTHER)
30	c102279_g1_i1_len_248_path_1_0_247_5	4	collagen-like protein	82	2.49E-09	50.70%	0.102	no IPS match

31	c102282_g1_i1_len_927_path_1_0_926_3	33	tumor necrosis factor receptor superfamily member 16	309	3.85E-53	50.50%	0.107	IPR001368 (SMART); IPR000488 (SMART); IPR000488 (PFAM); G3DSA:2.10.50.10 (GENE3D); IPR001368 (PFAM); G3DSA:2.10.50.10 (GENE3D); IPR011029 (G3DSA:1.10.533.GENE3D); PTHR23097 (PANTHER); PTHR23097:SF106 (PANTHER); IPR001368 (PROSITE_PATTERNS); IPR001368 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001368 (PROSITE_PROFILES); IPR000488 (PROSITE_PROFILES); IPR001368 (PROSITE_PROFILES); SSF57586 (SUPERFAMILY); IPR011029 (SUPERFAMILY); TMhelix (TMHMM)
32	c102344_g1_i1_len_324_path_1_0_323_4	8	mam and ldl-receptor class a domain-containing protein 1	108	2.18E-20	62.30%	0.405Y	IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PFAM); IPR002172 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
33	c102364_g1_i1_len_533_path_1_0_532_2	14	bcl-6 corepressor	177	3.57E-50	69.10%	0.147	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24117 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
34	c102593_g1_i1_len_364_path_342_0_363_3	14	zinc finger protein 569-like isoform x3	122	6.46E-24	59.60%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
35	c102640_g1_i1_len_536_path_1_0_535_1	13	thromboxane a synthase-like protein	179	4.02E-51	66.60%	0.12	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24292:SF24 (PANTHER); PTHR24292 (PANTHER); IPR001128 (SUPERFAMILY)
36	c102644_g1_i1_len_308_path_1_0_307_1	4	dorsal-ventral patterning protein sog isoform x2	103	4.59E-15	63.60%	0.148	PTHR11339 (PANTHER); PTHR11339:SF223 (PANTHER); IPR010895 (PROSITE_PROFILES); IPR010895 (PROSITE_PROFILES)
37	c102685_g1_i1_len_641_path_619_0_640_5	10	laminin subunit alpha	213	2.50E-68	66.20%	0.141	no IPS match
38	c102689_g1_i1_len_813_path_1_0_812_1	46	calbindin-32 isoform x2	271	2.43E-97	95.20%	0.106	IPR002048 (SMART); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR19972 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)
39	c102837_g1_i1_len_509_path_1_0_508_1	21	reelin-like isoform x4	170	4.31E-58	66.10%	0.114	PTHR11841 (PANTHER)
40	c10284_g1_i1_len_1091_path_1_0_249_251_250_273_2174_274_1090_3	21	gastrula zinc finger	364	5.63E-15	63.30%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
41	c102901_g1_i1_len_293_path_271_0_292_4	10	furin-like protease isoforms 1 1-x 2-like	98	5.46E-50	92.30%	0.288	IPR000209 (G3DSA:3.40.50.GENE3D); IPR000209 (PFAM); IPR015500 (PANTHER); PTHR10795:SF71 (PANTHER); IPR023828 (PROSITE_PATTERNS); IPR000209 (SUPERFAMILY)
42	c103281_g1_i1_len_574_path_1_0_573_3	14	zinc finger protein ozf-like	192	1.02E-32	56.30%	0.099	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

43	c103473_g1_i1_len_339_path_1_0_338_3	4	GH18519	113	5.38E-32	73.50%	0.145	PR00019 (PRINTS); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
44	c103517_g1_i1_len_768_path_1_0_767_2	23	protein lin-7 homolog b	256	1.36E-60	96.00%	0.098	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR14063 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
45	c103519_g1_i1_len_340_path_1_0_339_3	8	transferrin	114	2.97E-22	62.50%	0.1	IPR001156 (PRINTS); G3DSA:3.40.190.10 (GENE3D); IPR001156 (PFAM); G3DSA:3.40.190.10 (GENE3D); PTHR11485:SF18 (PANTHER); PTHR11485 (PANTHER); IPR001156 (PROSITE_PROFILES); SSF53850 (SUPERFAMILY)
46	c103717_g1_i1_len_342_path_320_0_341_4	9	proclotting enzyme	114	2.84E-47	77.50%	0.147	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
47	c103859_g1_i1_len_298_path_276_0_297_1	3	zinc finger protein 235	99	8.82E-18	59.40%	0.115	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
48	c103866_g1_i1_len_619_path_1_0_618_0	15	leucine-rich repeat-containing protein 70 isoform x1	207	8.92E-22	54.50%	0.115	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24367 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
49	c103881_g1_i1_len_481_path_459_0_480_1	15	dnaj homolog subfamily c member 25 homolog	160	8.98E-68	82.50%	0.105	Coil (COILS); Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078:SF125 (PANTHER); PTHR24078 (PANTHER); IPR018253 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM)
50	c103918_g1_i1_len_399_path_1_0_398_0	11	btd_takru ame: full=biotinidase short=biotinase flags: precursor	133	1.36E-13	56.70%	0.113	IPR003010 (G3DSA:3.60.110.GENE3D); IPR003010 (PFAM); IPR012101 (PANTHER); IPR003010 (PROSITE_PROFILES); IPR003010 (SUPERFAMILY)
51	c104026_g1_i1_len_336_path_1_0_335_3	8	chemosensory protein 1 partial	112	1.86E-38	79.20%	0.829Y	IPR005055 (G3DSA:1.10.2080.GENE3D); IPR005055 (PFAM); IPR005055 (PANTHER); PTHR11257:SF4 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR005055 (SUPERFAMILY); TMhelix (TMHMM)
52	c104120_g1_i1_len_404_path_382_0_403_1	6	glucosylceramidase- partial	135	1.58E-52	72.40%	0.1	IPR001139 (PRINTS); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001139 (PFAM); PTHR11069:SF7 (PANTHER); IPR001139 (PANTHER); IPR017853 (SUPERFAMILY)
53	c104363_g1_i1_len_344_path_1_0_343_2	4	vascular endothelial growth factor receptor partial	114	2.08E-19	57.70%	0.115	IPR013783 (G3DSA:2.60.40.GENE3D); PTHR15360 (PANTHER); SSF48726 (SUPERFAMILY)
54	c104536_g1_i1_len_560_path_4_0_559_3	12	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein	187	2.02E-24	60.90%	0.112	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
55	c104577_g1_i1_len_308_path_1_0_307_1	5	protein kinase c-binding protein partial	103	1.78E-30	72.70%	0.11	Coil (COILS); PTHR24042:SF4 (PANTHER); PTHR24042 (PANTHER)
56	c104636_g1_i1_len_619_path_597_0_618_0	22	third variable lymphocyte receptor	207	3.29E-11	51.60%	0.125	IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365:SF241 (PANTHER); PTHR24365 (PANTHER); SSF52058 (SUPERFAMILY)

57	c104743_g1_i1_len_612_path_590_0_611_2	25	zinc finger protein 628 isoform x1	204	6.51E-16	56.10%	0.106	Coil (COILS); IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19863 (PANTHER); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
58	c104990_g1_i1_len_363_path_341_0_362_0	7	wd repeat-containing protein 47 isoform x5	121	6.42E-75	94.30%	0.13	IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24361:SF201 (PANTHER); PTHR24361 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
59	c105120_g1_i1_len_347_path_1_0_346_5	7	serine threonine-protein kinase osr1 isoform x1	115	1.05E-67	94.60%	0.199	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM)
60	c105183_g1_i1_len_948_path_907_0_884_17_92_885_905_1792_906_926_1792_927_947_0	49	ves g 5 allergen	316	7.46E-49	53.00%	0.382Y	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
62	c10534_g1_i1_len_346_path_324_0_345_1	1	zinc finger protein 709-like	115	1.57E-21	63.20%	0.109	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
63	c10534_g2_i1_len_499_path_1123_0_498_2	6	zinc finger protein 850-like isoform x1	166	1.11E-23	55.10%	0.116	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
61	c105340_g1_i1_len_407_path_1_0_406_1	6	upf0454 protein c12orf49 homolog	136	6.78E-34	87.60%	0.132	IPR019352 (PFAM); IPR019352 (PANTHER)
64	c105558_g1_i1_len_279_path_1_0_278_4	4	mam and ldl-receptor class a domain-containing protein 2-like	93	1.96E-10	52.90%	0.103	IPR000998 (PFAM); PTHR23282:SF75 (PANTHER); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
65	c105706_g1_i1_len_327_path_305_0_326_5	4	metallophosphoesterase domain-containing protein 1	109	5.53E-57	92.20%	0.134	IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR12905 (PANTHER); IPR029052 (SUPERFAMILY)
66	c105858_g1_i1_len_413_path_1_0_412_1	7	non-structural protein ns5	138	5.38E-07	52.43%	0.101	IPR029063 (G3DSA:3.40.50.GENE3D)
67	c105886_g1_i1_len_317_path_295_0_316_2	6	cysteine-rich motor neuron 1 protein	105	9.73E-26	59.40%	0.11	G3DSA:2.10.70.10 (GENE3D); SSF57603 (SUPERFAMILY)
68	c10607_g1_i1_len_240_path_218_0_239_2	3	protein fam20c	80	1.01E-44	90.70%	0.131	IPR009581 (PFAM); PTHR12450:SF8 (PANTHER); IPR024869 (PANTHER)
69	c10607_g2_i1_len_179_path_435_0_178_4	2	extracellular serine threonine protein kinase fam20c-like	60	5.64E-26	94.20%	0.098	IPR029207 (PFAM); IPR024869 (PANTHER); PTHR12450:SF8 (PANTHER)
70	c106203_g1_i1_len_378_path_356_0_377_2	6	cyclophilin a	126	7.74E-64	91.90%	0.205	IPR002130 (PRINTS); IPR002130 (PFAM); IPR024936 (PIRSF); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
71	c106240_g1_i1_len_655_path_1_0_654_5	19	ryanodine receptor 44f	218	4.07E-102	83.20%	0.105	IPR003032 (PFAM); IPR003877 (PFAM); IPR015925 (PANTHER); PTHR13715:SF74 (PANTHER); IPR001870 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
72	c106268_g1_i1_len_465_path_1_0_464_1	14	chymotrypsin 1	155	1.34E-14	60.20%	0.203	G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
73	c106414_g1_i1_len_626_path_604_0_625_3	10	receptor-type tyrosine-protein phosphatase kappa	209	1.96E-120	89.90%	0.103	IPR000242 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134:SF227 (PANTHER); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
74	c106462_g1_i1_len_421_path_1_0_420_4	5	glutaminy-peptide cyclotransferase-like isoform x2	140	4.79E-16	58.50%	0.192	G3DSA:3.40.630.10 (GENE3D); PTHR12283 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

75	c10675_g1_i1_len_632_path_610_0_631_2	25	cytochrome p450 3a31	210	9.34E-51	70.00%	0.151	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24292:SF24 (PANTHER); PTHR24292 (PANTHER); IPR001128 (SUPERFAMILY)
76	c106831_g1_i1_len_472_path_450_0_471_0	8	lipoprotein receptor	158	1.34E-21	54.00%	0.113	IPR000203 (SMART); IPR000203 (PFAM); PTHR12011:SF260 (PANTHER); PTHR12011 (PANTHER); IPR000203 (PROSITE_PROFILES)
77	c107555_g1_i1_len_203_path_1_0_202_0	0	carboxypeptidase b-like	68	6.90E-18	69.30%	0.343Y	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
78	c107967_g1_i1_len_278_path_256_0_277_5	4	basement membrane-specific heparan sulfate proteoglycan core protein	92	5.21E-35	78.70%	0.118	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
79	c108345_g1_i1_len_370_path_1_0_369_1	5	lipoprotein receptor	123	4.94E-08	42.33%	0.118	IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
80	c10860_g1_i1_len_771_path_749_0_770_1	53	zinc finger protein 234-like isoform x2	257	2.23E-31	54.60%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
81	c108721_g1_i1_len_290_path_268_0_289_0	4	neural-cadherin isoform x10	97	3.48E-43	83.40%	0.101	IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); PTHR24027 (PANTHER); PTHR24027:SF285 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013320 (SUPERFAMILY)
82	c108786_g1_i1_len_258_path_1_0_257_4	4	thiol peroxiredoxin	86	1.87E-44	97.60%	0.101	IPR012336 (G3DSA:3.40.30.GENE3D); G3DSA:3.30.1020.10 (GENE3D); IPR019479 (PFAM); PTHR10681:SF67 (PANTHER); PTHR10681 (PANTHER); IPR012336 (SUPERFAMILY)
83	c108852_g1_i1_len_694_path_1_0_693_4	17	protein fam3c-like	231	5.92E-59	62.70%	0.455 Y	PTHR14592:SF7 (PANTHER); IPR026101 (PANTHER); SignalP-noTM (SIGNALP_EUK)
84	c108888_g1_i1_len_458_path_436_0_457_0	7	folliculin-related protein 5-like	153	1.06E-83	86.20%	0.103	IPR013783 (G3DSA:2.60.40.GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); IPR013098 (PFAM); IPR011992 (PFAM); PTHR10913:SF14 (PANTHER); PTHR10913 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF47473 (SUPERFAMILY)
85	c10894_g1_i1_len_915_path_1_0_914_5	56	estradiol 17-beta-dehydrogenase 12	305	8.87E-56	67.40%	0.097	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF68 (PANTHER); PTHR24316 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
86	c108980_g1_i1_len_422_path_1_0_421_1	6	protein turtle-like isoform x1	141	1.11E-20	54.80%	0.1	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
87	c109017_g1_i1_len_679_path_657_0_678_2	10	epithelial chloride channel	226	1.84E-68	60.80%	0.821 Y	IPR013642 (PFAM); PTHR10579 (PANTHER); PTHR10579:SF8 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
88	c109030_g1_i1_len_797_path_775_0_796_1	16	zinc finger protein 57-like	266	3.98E-115	76.50%	0.102	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
89	c109113_g1_i1_len_267_path_1_0_266_5	7	aldehyde mitochondrial precursor	89	9.55E-40	86.00%	0.1	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); IPR015657 (PTHR11699:PANTHER); IPR016161 (SUPERFAMILY)

90	c109136_g1_i1_len_347_path_1_0_346_4	8	zinc finger protein 37-like	116	5.24E-19	58.40%	0.102	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
91	c109170_g1_i1_len_142_path_1_0_141_3	1	peptidylglycine alpha-hydroxylating monooxygenase	48	6.90E-14	76.90%	0.119	IPR014784 (G3DSA:2.60.120.GENE3D); PF03712 (PFAM); PTHR10680 (PANTHER); IPR008977 (SUPERFAMILY)
92	c109283_g1_i1_len_365_path_343_0_364_5	6	mam receptor domain-containing partial	121	5.10E-24	56.90%	0.107	IPR000998 (PFAM); G3DSA:4.10.1220.10 (GENE3D); PTHR23282:SF75 (PANTHER); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
93	c10953_g1_i1_len_643_path_1_0_642_4	24	reelin- partial	214	6.75E-54	57.90%	0.255	PTHR11841 (PANTHER)
94	c10953_g2_i1_len_1143_path_1241_0_1142_5	44	reelin-like isoform x1	381	3.32E-82	54.10%	0.132	G3DSA:2.10.25.10 (GENE3D); PTHR11841 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS)
95	c109571_g1_i1_len_253_path_1_0_252_1	4	---NA---	84			0.481 Y	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
96	c10972_g2_i1_len_457_path_435_0_456_1	11	hemacentin- partial	152	7.08E-17	51.60%	0.107	IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR23279 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
97	c109790_g1_i1_len_221_path_199_0_220_5	1	histone-lysine n-methyltransferase prdm9-like	73	3.80E-15	62.20%	0.108	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
98	c110322_g1_i1_len_336_path_314_0_335_3	4	latrophilin and seven transmembrane domain-containing protein 1	112	4.12E-08	55.60%	0.287	IPR00832 (PFAM); PTHR12011 (PANTHER); PTHR12011:SF61 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM)
99	c110452_g1_i1_len_476_path_267_0_55_323_56_265_323_266_475_0	2	repetitive proline-rich cell wall protein 2-like isoform x2	159	7.74E-19	53.70%	0.143	no IPS match
100	c11060_g2_i1_len_637_path_1383_0_636_4	19	homeotic protein spalt-major-like	212	5.58E-97	88.40%	0.108	Coil (COILS); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR23233:SF49 (PANTHER); PTHR23233 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
101	c110796_g1_i1_len_292_path_1_0_291_4	4	tetratricopeptide-like helical domain-containing protein	97	1.57E-16	74.50%	0.157	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
102	c11088_g1_i1_len_445_path_1_0_444_1	6	endothelin-converting enzyme 1-like	148	5.86E-47	60.10%	0.106	IPR008753 (PFAM); G3DSA:1.10.1380.10 (GENE3D); IPR000718 (PANTHER); PTHR11733:SF124 (PANTHER); SSF55486 (SUPERFAMILY)
103	c111081_g1_i1_len_477_path_455_0_476_1	7	down syndrome cell adhesion molecule-like protein dscam2	159	1.97E-81	89.60%	0.108	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR10489 (PANTHER); PTHR10489:SF567 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
104	c111275_g1_i1_len_332_path_1_0_331_4	4	cul o 2 allergen	111	6.56E-21	58.40%	0.105	IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PANTHER); PTHR11769:SF8 (PANTHER); IPR017853 (SUPERFAMILY)
105	c111295_g1_i1_len_267_path_245_0_266_3	5	zinc finger protein 431 isoform x2	89	1.23E-18	67.20%	0.109	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

106	c111625_g1_i1_len_385_path_1_0_384_3	8	zinc finger partial	129	9.95E-20	56.20%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
107	c11163_g2_i1_len_486_path_1042_0_485_3	12	leucine-rich repeat-containing protein 15-like	162	8.65E-39	65.70%	0.1	PR00019 (PRINTS); IPR003591 (SMART); SM00365 (SMART); IPR001611 (PFAM); PF13516 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
108	c111716_g1_i1_len_523_path_501_0_522_4	8	probable isocitrate dehydrogenase	174	1.57E-103	93.40%	0.102	IPR024084 (PFAM); IPR024084 (G3DSA:3.40.718.GENE3D); PTHR11835:SF34 (PANTHER); IPR001804 (PANTHER); SSF53659 (SUPERFAMILY)
109	c112031_g1_i1_len_316_path_26_0_315_3	7	pr domain zinc finger protein 1 isoform x2	106	1.61E-20	65.20%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
110	c112136_g1_i1_len_341_path_1_0_340_1	7	transcription factor e4f1-like	114	1.10E-30	68.00%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13912 (PFAM); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
111	c112223_g1_i1_len_158_path_1_0_157_1	1	paralytic	53	2.09E-23	98.30%	0.288	Coil (COILS); IPR005821 (PFAM); IPR028814 (PTHR10037:PANTHER); PTHR10037 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
112	c112669_g1_i1_len_283_path_261_0_282_3	13	krueppel-like factor 13	95	7.12E-46	85.20%	0.113	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
113	c112937_g1_i1_len_259_path_1_0_258_2	4	fibrillin- partial	86	3.72E-32	81.50%	0.141	IPR017878 (G3DSA:3.90.290.GENE3D); IPR017878 (PFAM); IPR011398 (PANTHER); IPR017878 (PROSITE_PROFILES); IPR017878 (SUPERFAMILY)
114	c113217_g1_i1_len_363_path_1_0_362_3	4	chaperone protein	121	4.91E-34	81.40%	0.118	Coil (COILS); IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); IPR029047 (SUPERFAMILY)
115	c113327_g1_i1_len_195_path_1_0_194_1	3	ferritin hch	65	3.51E-30	87.30%	0.104	IPR008331 (PFAM); IPR012347 (G3DSA:1.20.1260.GENE3D); IPR001519 (PANTHER); PTHR11431:SF29 (PANTHER); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY)
116	c113929_g1_i1_len_518_path_1_0_517_0	9	prolow-density lipoprotein receptor-related protein 1	173	2.73E-52	65.80%	0.114	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
117	c114135_g1_i1_len_302_path_1_0_301_0	4	laminin subunit alpha-2- partial	101	4.75E-36	73.80%	0.112	IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF148 (PANTHER); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
118	c114170_g1_i1_len_268_path_1_0_267_2	3	partial	89	4.21E-55	99.70%	0.119	IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23078 (PANTHER); IPR027417 (SUPERFAMILY)

119	c114694_g1_i1_len_366_path_344_0_365_2	6	peroxisomal multifunctional enzyme type 2-like	122	3.57E-63	91.40%	0.099	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316:SF2 (PANTHER); PTHR24316 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
120	c11473_g1_i1_len_325_path_303_0_324_1	8	serine protease nudel	108	9.65E-59	90.10%	0.113	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
121	c114781_g1_i1_len_351_path_329_0_350_0	6	perlucin-like protein	117	1.69E-11	50.90%	0.117	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802:SF219 (PANTHER); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
122	c114810_g1_i1_len_287_path_1_0_286_0	4	vascular endothelial growth factor receptor 1 isoform x4	96	1.55E-34	84.00%	0.128	IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24416 (PANTHER); PTHR24416:SF298 (PANTHER); IPR001824 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
123	c114822_g1_i1_len_259_path_237_0_258_2	4	female neotenic-specific protein 3	86	8.44E-08	59.33%	0.106	no IPS match
124	c11513_g1_i1_len_1990_path_2066_0_1223_3289_1224_1248_50_1249_1989_1	263	tyrosine--trna cytoplasmic	663	0	80.30%	0.134	IPR002307 (PRINTS); IPR002305 (PFAM); G3DSA:1.10.240.10 (GENE3D); IPR002307 (TIGRFAM); IPR002547 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); IPR014729 (G3DSA:3.40.50.GENE3D); PTHR11946 (PANTHER); IPR002547 (PROSITE_PROFILES); SSF52374 (SUPERFAMILY); IPR010987 (SUPERFAMILY); IPR012340 (SUPERFAMILY)
125	c115373_g1_i1_len_259_path_1_0_258_1	4	enolase	86	6.04E-32	80.80%	0.136	IPR020810 (PFAM); IPR029065 (G3DSA:3.20.20.GENE3D); IPR000941 (PANTHER); IPR029065 (SUPERFAMILY)
126	c115399_g1_i1_len_315_path_293_0_314_2	5	para sodium channel	105	1.68E-51	90.10%	0.263	IPR001696 (PRINTS); IPR005821 (PFAM); IPR028814 (PTHR10037:PANTHER); PTHR10037 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
127	c11588_g1_i1_len_780_path_239_0_779_3	22	xanthine dehydrogenase	260	1.43E-96	71.30%	0.128	IPR002888 (PFAM); IPR012675 (G3DSA:3.10.20.GENE3D); IPR016167 (G3DSA:3.30.43.GENE3D); IPR002888 (G3DSA:1.10.150.GENE3D); IPR002346 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR016166 (SUPERFAMILY); IPR001041 (SUPERFAMILY); IPR002888 (SUPERFAMILY)
128	c116953_g1_i1_len_364_path_1_0_363_3	6	protein toll	122	6.02E-30	63.30%	0.113	G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24369 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
129	c117073_g1_i1_len_345_path_1_0_344_1	4	trehalase 1	115	9.79E-52	82.00%	0.124	IPR001661 (PFAM); IPR001661 (PANTHER); PTHR23403:SF1 (PANTHER); IPR008928 (SUPERFAMILY)
130	c11767_g2_i1_len_336_path_314_0_335_3	4	down syndrome cell adhesion	112	8.86E-57	90.40%	0.119	IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF567 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
131	c118792_g1_i1_len_257_path_1_0_256_1	4	serine threonine-protein kinase nim1	86	3.79E-33	81.20%	0.103	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24343 (PANTHER); PTHR24343:SF106 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
132	c11892_g1_i1_len_449_path_697_0_430_73_431_447_1161_448_448_3	10	zinc finger protein 271-like	150	4.19E-39	68.60%	0.114	IPR015880 (SMART); PF13465 (PFAM); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
133	c119952_g1_i1_len_2075_path_2053_0_2074_1	151	protein disulfide-isomerase a6	692	0	77.20%	0.239	PR00421 (PRINTS); IPR005788 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929:SF38 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)

134	c119979_g1_i1_len_3138_path_1_0_3137_2	379	atp-dependent rna helicase ddx1	1046	0	83.50%	0.332	IPR014001 (SMART); IPR001650 (SMART); IPR003877 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003877 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR011545 (PFAM); IPR001650 (PFAM); PTHR24031 (PANTHER); PTHR24031:SF211 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001650 (PROSITE_PROFILES); IPR014001 (PROSITE_PROFILES); IPR014014 (PROSITE_PROFILES); IPR001870 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
136	c11999_g1_i1_len_816_path_794_0_815_4	44	adp-ribosylation factor-like protein 4a	272	2.70E-95	86.70%	0.119	IPR006689 (PRINTS); IPR006687 (SMART); IPR003579 (SMART); IPR024156 (SMART); IPR005225 (TIGRFAM); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF121 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
135	c119990_g1_i1_len_375_path_353_0_374_2	6	cysteine peptidase c	125	2.08E-33	75.80%	0.098	G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); IPR013128 (PANTHER); SSF54001 (SUPERFAMILY)
137	c120014_g1_i1_len_900_path_878_0_899_3	36	heat shock 70 kda protein cognate 4	300	1.24E-80	81.70%	0.138	Coil (COILS); IPR013126 (PRINTS); G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
138	c120054_g1_i1_len_658_path_1_0_657_3	11	group xv phospholipase a2-like	220	3.84E-74	84.10%	0.361Y	IPR003386 (PFAM); PTHR11440 (PANTHER); PTHR11440:SF47 (PANTHER); TMhelix (TMHMM)
139	c120123_g1_i1_len_344_path_322_0_343_3	5	moxd1 homolog 2	115	6.60E-19	57.10%	0.104	IPR000323 (G3DSA:2.60.120.GENE3D); IPR000323 (PFAM); PTHR10157:SF23 (PANTHER); IPR000945 (PANTHER); IPR008977 (SUPERFAMILY)
140	c120323_g1_i1_len_1235_path_1213_0_1234_4	42	cartilage oligomeric matrix protein	412	2.02E-83	53.80%	0.109	Coil (COILS); IPR024665 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
141	c120340_g1_i1_len_1355_path_1333_0_1354_0	54	low quality protein: prolown-density lipoprotein receptor-related protein 1	452	2.13E-120	59.80%	0.104	IPR000742 (SMART); IPR000033 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000033 (PFAM); PTHR10529 (PANTHER); PTHR10529:SF204 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF63825 (SUPERFAMILY)
142	c12041_g1_i1_len_918_path_1_0_917_4	19	low affinity immunoglobulin epsilon fc receptor isoform x2	306	2.89E-19	54.60%	0.125	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
143	c12041_g1_i1_len_918_path_1_0_917_5	19	macrophage mannose receptor 1-like	306	4.44E-28	55.60%	0.257	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); PTHR22803:SF16 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
144	c120425_g1_i1_len_788_path_1_0_787_5	12	c4b-binding protein beta chain	262	8.43E-49	60.50%	0.166	IPR000436 (SMART); IPR008197 (G3DSA:4.10.75.GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR008197 (PFAM); PTHR19325 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000436 (PROSITE_PROFILES); IPR008197 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
145	c120450_g1_i1_len_626_path_1_0_625_5	16	cyclin-t isoform x6	208	1.53E-128	94.20%	0.103	IPR013763 (SMART); PIRSF028758 (PIRSF); IPR006671 (PFAM); IPR013763 (G3DSA:1.10.472.GENE3D); IPR015430 (PTHR10026:PANTHER); IPR015429 (PANTHER); IPR013763 (SUPERFAMILY); IPR013763 (SUPERFAMILY)
146	c120473_g1_i1_len_449_path_1_0_448_5	8	voltage-gated sodium partial	149	1.92E-79	92.10%	0.106	IPR027359 (G3DSA:1.20.120.GENE3D); IPR005821 (PFAM); PTHR10037 (PANTHER); IPR028814 (PTHR10037:PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF81324 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

179	c121467_g1_i1_len_467_path_445_0_466_4	9	wd sam and u-box domain-containing protein 1-like	156	6.81E-41	69.30%	0.15	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR011047 (SUPERFAMILY)
180	c121607_g1_i1_len_1338_path_1_0_1337_2	95	allatostatin precursor protein	446	1.16E-33	53.40%	0.104	IPR010276 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
181	c121625_g1_i1_len_387_path_365_0_386_1	10	scavenger partial	129	3.61E-58	82.50%	0.113	IPR001695 (PFAM); PTHR19331:SF77 (PANTHER); PTHR19331 (PANTHER); IPR001190 (PROSITE_PROFILES); IPR017448 (SUPERFAMILY)
182	c121685_g1_i1_len_358_path_336_0_357_2	6	Idl receptor protein isoform g	119	2.57E-25	63.40%	0.106	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
183	c121716_g1_i1_len_715_path_693_0_714_1	13	macrophage mannose receptor 1-like	238	1.35E-22	43.00%	0.113	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
184	c121773_g1_i1_len_436_path_414_0_435_5	14	fras1-related extracellular matrix protein 1	145	8.27E-22	54.80%	0.113	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22801 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
185	c121787_g1_i1_len_267_path_245_0_266_3	5	dopamine beta- partial	89	1.96E-15	61.70%	0.118	IPR000945 (PRINTS); IPR000323 (PFAM); IPR000323 (G3DSA:2.60.120.GENE3D); IPR000945 (PANTHER); PTHR10157:SF22 (PANTHER); IPR008977 (SUPERFAMILY)
186	c121827_g1_i1_len_1397_path_1375_0_1396_0	36	retinol dehydrogenase 13-like	466	1.07E-52	64.70%	0.126	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320:SF55 (PANTHER); PTHR24320 (PANTHER); SSF51735 (SUPERFAMILY)
187	c121851_g1_i1_len_1327_path_1305_0_1326_4	49	probable serine carboxypeptidase cpvl isoform x2	442	3.01E-118	62.80%	0.13	IPR001563 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); PTHR11802:SF30 (PANTHER); IPR001563 (PANTHER); IPR018202 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
188	c121856_g1_i1_len_1194_path_1172_0_1193_0	61	26s protease regulatory subunit 6b	398	0	95.10%	0.099	Coil (COILS); IPR001270 (PRINTS); IPR003593 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR005937 (TIGRFAM); PTHR23073 (PANTHER); PTHR23073:SF8 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
219	c122_g1_i1_len_1057_path_1085_0_1056_4	46	plexin- partial	352	1.78E-118	78.40%	0.269	IPR002909 (SMART); G3DSA:3.30.1680.10 (GENE3D); IPR002909 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR22625 (PANTHER); PTHR22625:SF16 (PANTHER); IPR014756 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
189	c122010_g1_i1_len_798_path_1_0_797_5	14	low quality protein: sco-spondin	266	3.63E-23	44.50%	0.114	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
190	c122024_g1_i1_len_307_path_1_0_306_3	10	heat shock protein	103	2.21E-48	89.90%	0.11	IPR029047 (G3DSA:2.60.34.GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); IPR013126 (PFAM); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR029047 (SUPERFAMILY); IPR029048 (SUPERFAMILY)
191	c122041_g1_i1_len_330_path_1_0_329_2	21	peptidyl-prolyl cis-trans isomerase-like	110	2.72E-43	84.90%	0.599Y	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR029000 (SUPERFAMILY)
192	c122114_g1_i1_len_888_path_1_0_887_2	15205	translationally controlled tumor protein	296	4.17E-71	79.20%	0.269	IPR018105 (PRINTS); IPR018105 (PFAM); IPR011323 (G3DSA:2.170.150.GENE3D); IPR018105 (PANTHER); IPR011057 (SUPERFAMILY)

193	c122187_g1_i1_len_1330_path_1_0_1329_3	61	acid sphingomyelinase-like phosphodiesterase 3b	444	1.88E-66	55.00%	0.108	IPR029052 (G3DSA:3.60.21.GENE3D); PTHR10340 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
194	c122188_g1_i1_len_1175_path_1153_0_1174_2	75	Ectodysplasin-A	391	2.08E-57	58.30%	0.106	IPR008983 (G3DSA:2.60.120.GENE3D); IPR006052 (PFAM); PTHR15151:SF4 (PANTHER); PTHR15151 (PANTHER); IPR021184 (PROSITE_PATTERNS); IPR006052 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY)
195	c12224_g1_i1_len_159_path_137_0_158_2	1	thrombospondin type-1 domain-containing protein 4-like	53	1.16E-17	69.20%	0.127	IPR000884 (PFAM); G3DSA:2.20.100.10 (GENE3D); PTHR13723 (PANTHER); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY)
196	c122335_g1_i1_len_1622_path_1650_0_1621_4	146	agap005784-pa-like protein	541	1.70E-47	61.70%	0.114	IPR001258 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR10680 (PANTHER); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); SSF101898 (SUPERFAMILY)
197	c122368_g1_i1_len_952_path_930_0_951_4	31	sh3 and multiple ankyrin repeat domains protein partial	317	4.35E-167	86.60%	0.098	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24135 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
198	c122370_g1_i1_len_389_path_367_0_388_4	5	long form	130	3.66E-74	96.20%	0.109	Coil (COILS); Coil (COILS); Coil (COILS); IPR002928 (PFAM); PTHR13140:SF164 (PANTHER); PTHR13140 (PANTHER)
199	c122372_g1_i1_len_2532_path_1_0_2531_3	283	atp-dependent zinc metalloprotease yme1 homolog	844	0	75.30%	0.27	IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005936 (TIGRFAM); IPR000642 (PFAM); IPR003959 (PFAM); PTHR23076:SF37 (PANTHER); PTHR23076 (PANTHER); IPR003960 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005936 (HAMAP); SSF140990 (SUPERFAMILY); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
200	c122374_g1_i1_len_606_path_1_0_605_2	13	protein cbfa2t1-like isoform x5	202	4.66E-70	77.50%	0.134	Coil (COILS); Coil (COILS); IPR013289 (PRINTS); IPR002893 (PFAM); PTHR10379 (PANTHER); IPR002893 (PROSITE_PATTERNS); IPR002893 (PROSITE_PROFILES); SSF144232 (SUPERFAMILY)
201	c122383_g1_i1_len_583_path_561_0_582_1	24	low quality protein: myosin heavy muscle	194	1.42E-114	98.20%	0.112	Coil (COILS); Coil (COILS); IPR002928 (PFAM); PTHR13140 (PANTHER); PTHR13140:SF364 (PANTHER); SSF57997 (SUPERFAMILY)
202	c122423_g1_i1_len_1203_path_1181_0_1202_2	176	isoform d	401	5.52E-48	60.00%	0.223	IPR003585 (SMART); IPR027789 (PFAM); PTHR10915:SF1 (PANTHER); IPR001050 (PANTHER); IPR030479 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
203	c122429_g1_i1_len_1230_path_1_0_1229_2	112	heat shock protein 40	410	0	82.80%	0.143	IPR001623 (PRINTS); IPR001623 (SMART); IPR002939 (PFAM); G3DSA:2.60.260.20 (GENE3D); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); G3DSA:2.60.260.20 (GENE3D); PTHR24077:SF211 (PANTHER); PTHR24077 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR008971 (SUPERFAMILY); IPR001623 (SUPERFAMILY); IPR008971 (SUPERFAMILY)
204	c122486_g1_i1_len_750_path_728_0_749_1	13	transferrin	250	1.18E-58	57.90%	0.106	Coil (COILS); IPR001156 (PRINTS); IPR001156 (SMART); G3DSA:3.40.190.10 (GENE3D); G3DSA:3.40.190.10 (GENE3D); IPR001156 (PFAM); PTHR11485 (PANTHER); PTHR11485:SF19 (PANTHER); IPR001156 (PROSITE_PROFILES); IPR001156 (PROSITE_PROFILES); SSF53850 (SUPERFAMILY); SSF53850 (SUPERFAMILY)
205	c122547_g1_i1_len_842_path_1_0_841_2	17	peroxisomal sarcosine oxidase	280	7.24E-74	59.70%	0.153	IPR006076 (PFAM); G3DSA:3.50.50.60 (GENE3D); G3DSA:3.30.9.10 (GENE3D); PTHR10961 (PANTHER); PTHR10961:SF7 (PANTHER); SSF51905 (SUPERFAMILY)
206	c122611_g1_i1_len_606_path_584_0_605_2	17	vascular endothelial growth factor receptor 1 isoform x2	202	5.86E-26	47.60%	0.157	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013106 (PFAM); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
207	c122699_g1_i1_len_765_path_743_0_764_0	31	homerin isoform x2	255	3.48E-29	50.50%	0.104	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

208	c122748_g1_i1_len_910_path_1_0_909_1	63	l-xylulose reductase	303	1.96E-114	78.00%	0.12	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR013968 (SMART); PF13561 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24311:SF6 (PANTHER); PTHR24311 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
209	c122754_g1_i1_len_1082_path_1060_0_1081_1	65	probable serine carboxypeptidase cpvl isoform x1	361	7.98E-93	65.30%	0.252	IPR001563 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); PTHR11802:SF30 (PANTHER); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
210	c122755_g1_i1_len_1450_path_1_0_1449_0	280	26s protease regulatory subunit 7	484	0	96.10%	0.186	IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005937 (TIGRFAM); IPR003959 (PFAM); PTHR23073:SF13 (PANTHER); PTHR23073 (PANTHER); IPR003960 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
211	c122781_g1_i1_len_866_path_1_0_865_0	22	chorion peroxidase	289	2.05E-51	61.00%	0.163	IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
212	c12279_g1_i1_len_409_path_387_0_408_5	14	venom serine carboxypeptidase-like	136	2.75E-29	66.00%	0.117	IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); IPR018202 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
213	c122866_g1_i1_len_719_path_697_0_718_0	21	titin- partial	240	4.26E-115	81.90%	0.098	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF149 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
217	c1229_g1_i1_len_197_path_675_0_63_202_64_196_5	2	cadherin-related tumor suppressor- partial	65	3.17E-08	64.00%	0.19	IPR000742 (SMART); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
218	c1229_g1_i2_len_334_path_1_0_200_202_201_333_5	3	agrin- partial	111	5.00E-37	71.50%	0.155	IPR000742 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); PTHR10574:SF227 (PANTHER); PTHR10574 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
214	c122900_g1_i1_len_636_path_614_0_635_3	13	meteorin-like protein	212	3.46E-14	62.20%	0.101	no IPS match
215	c122940_g1_i1_len_600_path_578_0_599_3	13	neutral endopeptidase	200	2.98E-59	70.40%	0.132	IPR008753 (PFAM); G3DSA:1.10.1380.10 (GENE3D); PTHR11733:SF113 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
216	c122990_g1_i1_len_764_path_1_0_763_1	14	adam 17-like protease	255	2.85E-83	82.90%	0.1	PTHR11905 (PANTHER); PTHR11905:SF121 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
220	c123004_g1_i1_len_252_path_230_0_251_0	4	neurexin-3- partial	84	1.32E-13	74.20%	0.23	IPR027789 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
221	c123034_g1_i1_len_1781_path_1_0_1780_1	97	dual specificity mitogen-activated protein kinase kinase 4-like	594	0	89.60%	0.169	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24360:SF46 (PANTHER); PTHR24360 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
222	c123063_g1_i1_len_341_path_1_0_340_2	12	xanthine dehydrogenase	113	3.79E-40	80.20%	0.104	IPR000674 (PFAM); IPR000674 (G3DSA:3.90.1170.GENE3D); IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR008274 (SUPERFAMILY); IPR000674 (SUPERFAMILY)
223	c123088_g1_i1_len_1114_path_1092_0_1113_2	144	aminoacyl trna synthase complex-interacting multifunctional protein 1	371	8.53E-100	68.30%	0.119	Coil (COILS); IPR002547 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); PTHR11586 (PANTHER); PTHR11586:SF1 (PANTHER); IPR002547 (PROSITE_PROFILES); IPR012340 (SUPERFAMILY)
224	c123130_g1_i1_len_1322_path_1_0_1321_3	345	adp-ribosylation factor-like protein 8b-a	441	6.97E-124	97.70%	0.118	IPR006689 (PRINTS); IPR003579 (SMART); IPR006687 (SMART); IPR024156 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF122 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)

225	c123208_g1_i1_len_1203_path_1181_0_1202_4	32	c4b-binding protein beta	401	0	75.50%	0.102	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19325 (PANTHER); PTHR19325:SF230 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
226	c123384_g1_i1_len_409_path_1_0_408_1	6	prolow-density lipoprotein receptor-related protein 1-like isoform x6	136	2.57E-15	52.20%	0.105	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); PTHR10529:SF204 (PANTHER); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
227	c123444_g1_i1_len_392_path_1_0_391_4	10	pr domain zinc finger protein 1	131	2.38E-71	98.00%	0.097	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR016608 (PTHR11389:PANTHER); PTHR11389 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
228	c12348_g1_i1_len_1269_path_1830_0_1195_99_1196_1268_3	114	camp-dependent protein kinase catalytic subunit	423	7.64E-151	94.20%	0.124	Coil (COILS); IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24353 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
229	c12348_g1_i2_len_1597_path_1830_0_1195_3025_1196_1596_4	143	camp-dependent protein kinase catalytic subunit	532	1.58E-147	94.20%	0.368Y	Coil (COILS); IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24353 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
230	c123527_g1_i1_len_411_path_389_0_410_1	15	hemagglutinin amebocyte aggregation factor-like	137	4.57E-13	56.50%	0.16	PF14704 (PFAM); IPR026645 (PANTHER); PTHR15040:SF1 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
231	c123625_g1_i1_len_1122_path_1_0_1121_2	36	low quality protein: de-cadherin	374	4.27E-61	57.30%	0.155	IPR001791 (SMART); IPR027397 (G3DSA:4.10.900.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); IPR000233 (PFAM); PTHR24027:SF276 (PANTHER); PTHR24027 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
232	c123759_g1_i1_len_287_path_265_0_286_5	5	matrix metalloproteinase-17-like	95	1.22E-47	86.40%	0.129	IPR018487 (SMART); IPR000585 (G3DSA:2.110.10.GENE3D); IPR018487 (PFAM); PTHR10201:SF135 (PANTHER); PTHR10201 (PANTHER); IPR018487 (PROSITE_PROFILES); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY)
233	c123824_g1_i1_len_552_path_1_0_551_1	18	cd166 antigen	184	2.08E-35	60.50%	0.104	IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11640:SF52 (PANTHER); PTHR11640 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
234	c123838_g1_i1_len_646_path_624_0_645_2	30	fibronectin type 3 and ankyrin repeat domains protein 1	215	4.25E-42	69.50%	0.455 Y	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR002110 (PFAM); PTHR24183:SF1 (PANTHER); PTHR24183 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR020683 (SUPERFAMILY)
235	c123895_g1_i1_len_372_path_1_0_371_0	5	ovochoymase- partial	124	6.16E-23	55.50%	0.362 Y	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
236	c123902_g1_i1_len_808_path_786_0_807_0	36	hemagglutinin	270	1.42E-26	55.50%	0.175	G3DSA:1.10.390.10 (GENE3D); IPR001570 (PFAM); IPR007280 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

237	c123945_g1_i1_len_743_path_1_0_742_1	14	trehalase-like isoform x1	248	1.77E-68	69.20%	0.129	IPR001661 (PRINTS); IPR001661 (PFAM); IPR001661 (PANTHER); PTHR23403:SF1 (PANTHER); IPR018232 (PROSITE_PATTERNS); IPR008928 (SUPERFAMILY)
238	c123971_g1_i1_len_478_path_1_0_477_4	12	dual specificity testis-specific protein kinase 2	159	2.07E-78	84.90%	0.103	IPR001245 (PRINTS); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR23257:SF324 (PANTHER); PTHR23257 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
239	c123979_g1_i1_len_1227_path_1205_0_1226_1	63	protein twisted gastrulation	409	1.27E-108	76.40%	0.151	IPR006761 (PFAM); IPR006761 (PANTHER); PTHR12312:SF15 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
240	c124050_g1_i1_len_1382_path_1_0_1381_5	132	aael014742- partial	460	3.09E-34	47.20%	0.224	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
241	c12408_g1_i1_len_529_path_1_0_528_1	9	---NA---	176			0.145	IPR000421 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); IPR000421 (PROSITE_PATTERNS); IPR000421 (PROSITE_PROFILES); IPR008979 (SUPERFAMILY)
242	c124175_g1_i1_len_674_path_1_0_673_4	26	heat shock 70 kda protein 14-like	225	1.90E-78	68.40%	0.104	G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.90.640.10 (GENE3D); PTHR19375:SF158 (PANTHER); PTHR19375 (PANTHER); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
243	c124181_g1_i1_len_454_path_1_0_453_0	5	protease inhibitor-like	152	1.29E-15	67.70%	0.585Y	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR002223 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); IPR002223 (SUPERFAMILY); TMhelix (TMHMM)
244	c124343_g1_i1_len_1887_path_1_0_1886_2	179	leukotriene a-4 hydrolase	629	0	73.70%	0.125	IPR014782 (PRINTS); IPR014782 (PFAM); G3DSA:1.10.390.10 (GENE3D); IPR012777 (TIGRFAM); IPR015211 (PFAM); PTHR11533:SF4 (PANTHER); IPR001930 (PANTHER); IPR016024 (SUPERFAMILY); SSF55486 (SUPERFAMILY); SSF63737 (SUPERFAMILY)
245	c124358_g1_i1_len_757_path_1_0_756_1	53	upf0669 protein c6orf120 homolog	252	2.77E-37	64.00%	0.107	PTHR31703 (PANTHER)
246	c124495_g1_i1_len_297_path_1_0_296_3	5	aael002876- partial	99	7.59E-40	79.40%	0.101	IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); PTHR10127:SF557 (PANTHER); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
247	c124561_g1_i1_len_402_path_1_0_200_1_201_401_1	4	ankyrin domain partial	134	1.31E-22	54.70%	0.106	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PF13637 (PFAM); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
248	c124577_g1_i1_len_1118_path_1096_0_1117_1	35	secreted frizzled-related protein 3	373	6.98E-61	57.90%	0.172	Coil (COILS); IPR018933 (SMART); IPR020067 (SMART); G3DSA:2.40.50.120 (GENE3D); IPR020067 (PFAM); IPR018933 (PFAM); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR015526 (PANTHER); PTHR11309:SF83 (PANTHER); IPR020067 (PROSITE_PROFILES); IPR001134 (PROSITE_PROFILES); IPR020067 (SUPERFAMILY); IPR008993 (SUPERFAMILY)
249	c124595_g1_i1_len_598_path_1_0_597_4	18	sco- partial	199	1.41E-08	52.25%	0.105	IPR025155 (PFAM)
250	c12482_g1_i1_len_674_path_652_0_94_747_95_103_756_104_673_2	18	protein unc-45 homolog b	224	1.10E-59	73.10%	0.119	IPR019734 (SMART); IPR013105 (PFAM); PF13414 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR22904:SF302 (PANTHER); PTHR22904 (PANTHER); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY)
251	c12482_g1_i2_len_770_path_652_0_94_1454_95_199_756_200_769_2	14	protein unc-45 homolog b	256	1.88E-59	73.10%	0.113	IPR019734 (SMART); PF13414 (PFAM); IPR013105 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR22904:SF302 (PANTHER); PTHR22904 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY); TMhelix (TMHMM)

252	c124960_g1_i1_len_1131_path_1_0_1130_5	33	matrix metalloproteinase 9	377	7.83E-14	49.10%	0.106	IPR000562 (SMART); IPR000562 (PFAM); IPR000562 (G3DSA:2.10.10.GENE3D); IPR000562 (G3DSA:2.10.10.GENE3D); IPR000562 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY)
253	c124966_g1_i1_len_879_path_857_0_878_0	62	e3 ubiquitin-protein ligase mib2 isoform x1	293	5.65E-141	77.70%	0.1	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24202 (PANTHER); PTHR24202:SF4 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
254	c125282_g1_i1_len_357_path_335_0_356_4	8	egf-like module-containing mucin-like hormone receptor-like partial	119	2.09E-22	60.20%	0.242	IPR000832 (PFAM); PTHR12011:SF235 (PANTHER); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
255	c125283_g1_i1_len_271_path_249_0_270_1	4	macrophage mannose receptor 1-like	90	1.68E-10	55.00%	0.115	IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
256	c125450_g1_i1_len_1093_path_1_0_1092_5	26	attractin-like protein 1 isoform x1	364	3.35E-140	73.60%	0.106	IPR006652 (SMART); IPR000742 (SMART); IPR006652 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PF13418 (PFAM); IPR015916 (G3DSA:2.130.10.GENE3D); G3DSA:2.170.300.10 (GENE3D); IPR013111 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF3 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); SSF117281 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
257	c125508_g1_i1_len_1258_path_1236_0_1257_4	69	carboxypeptidase b-like	419	3.21E-127	62.40%	0.642 Y	IPR000834 (PRINTS); IPR000834 (SMART); IPR003146 (G3DSA:3.30.70.GENE3D); G3DSA:3.40.630.10 (GENE3D); IPR003146 (PFAM); IPR000834 (PFAM); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR009020 (SUPERFAMILY); SSF53187 (SUPERFAMILY)
258	c125515_g1_i1_len_415_path_1_0_414_0	6	phosphoglycerate kinase	139	1.81E-38	66.30%	0.11	IPR001576 (PRINTS); IPR015901 (G3DSA:3.40.50.GENE3D); IPR001576 (PFAM); IPR001576 (PANTHER); PTHR11406:SF6 (PANTHER); IPR001576 (SUPERFAMILY)
259	c125609_g1_i1_len_364_path_342_0_363_1	12	polypeptide n-acetylgalactosaminyltransferase 2-like	121	8.46E-30	58.70%	0.337	PTHR11675:SF24 (PANTHER); PTHR11675 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
260	c12563_g1_i1_len_572_path_825_0_322_114_8_323_433_50_434_571_2	22	calponin homology domain containing	190	9.70E-59	66.20%	0.146	Coil (COILS); IPR025875 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); PTHR23155:SF423 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52075 (SUPERFAMILY)
261	c12563_g1_i2_len_776_path_825_0_322_114_8_323_433_1258_434_637_50_638_775_2	36	leucine-rich repeat and calponin homology domain-containing protein 1	258	1.30E-67	58.80%	0.146	Coil (COILS); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); PTHR23155:SF423 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52075 (SUPERFAMILY)
262	c125789_g1_i1_len_567_path_1_0_566_2	12	growth differentiation factor 8	189	5.14E-31	65.60%	0.124	IPR001111 (PFAM); IPR015616 (PTHR11848:PANTHER); IPR015615 (PANTHER)
263	c126170_g1_i1_len_378_path_383_0_377_2	4553	60s acidic ribosomal protein p1	126	3.65E-31	93.40%	0.131	PF00428 (PFAM); PTHR21141 (PANTHER); IPR027534 (HAMAP)
264	c126295_g1_i1_len_372_path_1_0_371_2	6	polyprotein precursor	124	6.54E-19	54.80%	0.102	IPR000208 (PFAM); SSF56672 (SUPERFAMILY)
265	c126328_g1_i1_len_680_path_1_0_679_4	25	neuroendocrine convertase 2-like	227	6.97E-135	87.70%	0.126	IPR002884 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); IPR000209 (G3DSA:3.40.50.GENE3D); PTHR10795:SF11 (PANTHER); IPR015500 (PANTHER); IPR000209 (SUPERFAMILY); IPR008979 (SUPERFAMILY)
266	c126361_g1_i1_len_343_path_321_0_342_0	10	transmembrane protease serine partial	115	1.06E-19	68.40%	0.147	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF81 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
267	c126565_g1_i1_len_262_path_1_0_261_0	7	matrix metalloproteinase-16 isoform x3	88	1.12E-30	78.30%	0.111	IPR018487 (SMART); IPR018487 (PFAM); IPR000585 (G3DSA:2.110.10.GENE3D); PTHR10201 (PANTHER); PTHR10201:SF131 (PANTHER); IPR018487 (PROSITE_PROFILES); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY)

[illegible]

288	c128120_g1_i1_len_305_path_1_0_304_1	10	isoform e	102	2.37E-07	57.00%	0.238	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
289	c128203_g1_i1_len_281_path_259_0_280_0	4	casin-1 isoform x9	94	1.94E-22	73.00%	0.104	IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR027013 (PANTHER); IPR027001 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
291	c12823_g1_i1_len_1062_path_1337_0_213_2_98_214_1061_2	101	n-acetylglucosamine-1-phosphotransferase subunit gamma-like	354	4.35E-72	60.30%	0.340Y	Coil (COILS); PF13015 (PFAM); IPR009011 (G3DSA:2.70.130.GENE3D); PTHR12630 (PANTHER); PTHR12630:SF6 (PANTHER); IPR009011 (SUPERFAMILY)
292	c12823_g1_i2_len_996_path_150_0_147_298_148_995_2	74	n-acetylglucosamine-1-phosphotransferase subunit partial	332	1.03E-68	61.80%	0.137	Coil (COILS); PF13015 (PFAM); IPR009011 (G3DSA:2.70.130.GENE3D); PTHR12630:SF6 (PANTHER); PTHR12630 (PANTHER); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009011 (SUPERFAMILY)
290	c128233_g1_i1_len_336_path_314_0_335_1	10	transient receptor potential cation channel subfamily a member 1 homolog	112	6.12E-20	60.20%	0.128	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR002110 (PFAM); PTHR24188 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
293	c128407_g1_i1_len_516_path_494_0_515_1	11	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein	172	1.43E-24	59.10%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
294	c128413_g1_i1_len_381_path_1_0_380_2	8	collagen alpha chain cg42342 isoform x1	127	5.78E-22	80.00%	0.114	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF379 (PANTHER)
295	c128413_g1_i1_len_381_path_1_0_380_5	8	collagen-like partial	127	2.82E-17	54.30%	0.136	no IPS match
296	c128425_g1_i1_len_308_path_286_0_307_0	6	PREDICTED: uncharacterized protein C4orf29 homolog isoform X5	103	5.43E-40	81.20%	0.147	IPR019149 (PFAM); PTHR13617 (PANTHER)
297	c128496_g1_i1_len_392_path_370_0_391_1	8	hemiscitin- partial	131	5.54E-11	56.50%	0.191	IPR000884 (SMART); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); PTHR19897 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIOUS); TRANSMEMBRANE (PHOBIOUS); CYTOPLASMIC_DOMAIN (PHOBIOUS); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); TMhelix (TMHMM)
298	c128508_g1_i1_len_1004_path_1_0_1003_5	42	hypothetical protein LOTGIDRAFT_71188, partial	334	5.02E-85	58.50%	0.243	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); PTHR10127 (PANTHER); IPR028876 (PTHR10127:PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
299	c128528_g1_i1_len_323_path_301_0_322_2	4	von willebrand factor type egf and pentraxin domain-containing protein 1	107	1.06E-10	61.50%	0.105	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY)
300	c128649_g1_i1_len_274_path_252_0_273_2	4	very low-density lipoprotein receptor	91	2.01E-21	63.20%	0.106	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); PTHR10529:SF204 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
301	c12871_g1_i1_len_143_path_1_0_142_2	1	rap guanine nucleotide exchange factor 2	47	3.07E-21	95.20%	0.108	IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR23113 (PANTHER); PTHR23113:SF198 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
302	c129003_g1_i1_len_479_path_457_0_478_1	7	tectonic-like protein	160	2.04E-38	63.70%	0.174	PTHR14611 (PANTHER); PTHR14611:SF0 (PANTHER)
303	c129146_g1_i1_len_819_path_1_0_818_5	34	zinc finger protein 676-like	273	3.85E-39	67.60%	0.11	IPR015880 (SMART); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
304	c129363_g1_i1_len_404_path_382_0_403_1	6	very low-density lipoprotein receptor	135	3.35E-09	66.90%	0.112	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
305	c129448_g1_i1_len_312_path_1_0_311_5	6	core histone macro-	104	1.04E-37	85.90%	0.25	IPR002119 (PRINTS); IPR002119 (SMART); IPR009072 (G3DSA:1.10.20.GENE3D); IPR007125 (PFAM); PTHR23430:SF33 (PANTHER); PTHR23430 (PANTHER); IPR009072 (SUPERFAMILY)

306	c129612_g1_i1_len_392_path_1_0_391_5	8	3-ketodihydrosphingosine reductase	130	8.10E-13	70.60%	0.242	IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
307	c129673_g1_i1_len_385_path_1_0_384_5	5	gamma-glutamyltranspeptidase 1	128	3.68E-38	65.00%	0.101	IPR000101 (PRINTS); IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF15 (PANTHER); IPR029055 (SUPERFAMILY)
308	c129682_g1_i1_len_482_path_460_0_481_1	7	lysosomal pro-x carboxypeptidase	161	2.69E-66	72.60%	0.132	IPR008758 (PFAM); IPR008758 (PANTHER); PTHR11010:SF11 (PANTHER)
309	c129762_g1_i1_len_377_path_1_0_376_1	14	basement membrane-specific heparan sulfate proteoglycan core protein	126	1.22E-33	66.00%	0.122	IPR018031 (SMART); IPR000034 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF252 (PANTHER); IPR000034 (PROSITE_PROFILES)
310	c13003_g1_i1_len_396_path_584_0_395_2	9	serine protease easter	132	5.30E-23	60.20%	0.119	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
311	c130255_g1_i1_len_1089_path_1067_0_1088_1	142	prohormone-1-like	363	7.69E-30	77.80%	0.151	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
312	c130283_g1_i1_len_301_path_279_0_300_0	7	protein flightless-1	101	4.46E-46	88.00%	0.165	IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR007122 (PANTHER); IPR029919 (PTHR11977:PANTHER); SSF55753 (SUPERFAMILY)
313	c130460_g1_i1_len_436_path_1_0_435_5	10	trehalase isoform x1	145	7.41E-28	68.40%	0.196	IPR001661 (PFAM); IPR001661 (PANTHER); PTHR23403:SF1 (PANTHER); IPR008928 (SUPERFAMILY)
314	c130728_g1_i1_len_659_path_637_0_658_5	19	leucine-rich repeat protein soc-2 homolog	219	4.40E-130	93.70%	0.111	IPR003591 (SMART); IPR025875 (PFAM); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR027036 (PTHR23155:PANTHER); PTHR23155 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
315	c130729_g1_i1_len_468_path_446_0_467_0	10	kunitz and ntr domain-containing protein 2	156	1.42E-49	89.00%	0.13	IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
316	c130789_g1_i1_len_265_path_1_0_264_4	4	neurotactin	88	4.73E-28	76.20%	0.147	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); PTHR11559:SF140 (PANTHER); IPR029058 (SUPERFAMILY)
317	c130830_g1_i1_len_310_path_1_0_309_5	7	#NAME?	103	9.23E-49	91.60%	0.126	G3DSA:3.40.50.2000 (GENE3D); IPR001830 (PFAM); PTHR10788 (PANTHER); PTHR10788:SF6 (PANTHER); SSF53756 (SUPERFAMILY)
318	c13094_g2_i1_len_146_path_354_0_145_2	1	multiple epidermal growth factor-like domains protein 8	48	3.11E-14	92.30%	0.151	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
319	c130993_g1_i1_len_483_path_1_0_482_3	13	mlrp1_acrmi ame: full=mam and ldl-receptor class a domain-containing protein 1 ame: full=skeletal organic matrix mam and ldl-receptor 1 short=som mam and ldl-receptor partial	161	3.04E-16	64.20%	0.31	IPR000998 (PFAM); PTHR23282:SF75 (PANTHER); PTHR23282 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
320	c131137_g1_i1_len_359_path_337_0_358_5	7	angiopoietin-related protein 1	119	1.46E-26	71.10%	0.125	IPR014715 (G3DSA:4.10.530.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
321	c131300_g1_i1_len_357_path_1_0_356_1	6	insulin-like growth factor-binding protein complex acid labile chain	119	6.83E-30	63.10%	0.102	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24369 (PANTHER); SSF52058 (SUPERFAMILY)
322	c131397_g1_i1_len_311_path_1_0_310_4	7	receptor tyrosine phosphatase type r2a	104	1.51E-38	80.10%	0.115	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19134 (PANTHER); PTHR19134:SF199 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
325	c1314_g1_i1_len_151_path_343_0_150_5	3	isoform b	50	5.36E-21	92.20%	0.097	IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24418:SF0 (PANTHER); PTHR24418 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
323	c131460_g1_i1_len_336_path_1_0_335_2	3	low quality protein: de-cadherin	112	1.42E-22	61.20%	0.205	Coil (COILS); IPR000233 (PFAM); PTHR24027:SF251 (PANTHER); PTHR24027 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
324	c131483_g1_i1_len_582_path_560_0_581_1	9	limbic system-associated membrane protein	194	3.65E-81	81.40%	0.099	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PF13895 (PFAM); PTHR23279 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)

326	c13168_g1_i1_len_638_path_616_0_637_0	49	alpha-mannosidase partial	213	1.55E-110	81.30%	0.102	IPR000602 (PFAM); IPR027291 (G3DSA:3.20.110.GENE3D); IPR015341 (G3DSA:1.20.1270.GENE3D); PTHR11607 (PANTHER); PTHR11607:SF4 (PANTHER); IPR011330 (SUPERFAMILY)
327	c131734_g1_i1_len_781_path_1_0_780_3	18	fasciclin- partial	261	3.56E-30	47.40%	0.102	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
328	c131753_g1_i1_len_343_path_321_0_342_1	3	low quality protein: basement membrane-specific heparan sulfate proteoglycan core	114	2.17E-16	64.90%	0.420Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
329	c131783_g1_i1_len_293_path_271_0_292_1	2	lysosomal pro-x carboxypeptidase	98	1.73E-42	79.40%	0.152	IPR008758 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11010:SF11 (PANTHER); IPR008758 (PANTHER); IPR029058 (SUPERFAMILY)
330	c131936_g1_i1_len_265_path_1_0_264_5	4	sortilin-related receptor	88	3.48E-08	49.90%	0.122	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
331	c131982_g1_i1_len_750_path_728_0_749_4	35	aldehyde dehydrogenase family 9 member a1-b-like	250	1.72E-111	78.80%	0.112	IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF114 (PANTHER); IPR016160 (PROSITE_PATTERNS); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
332	c132012_g1_i1_len_346_path_1_0_345_1	10	discoidin domain-containing receptor partial	115	1.07E-47	79.40%	0.107	IPR020635 (SMART); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24416 (PANTHER); PTHR24416:SF210 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
333	c132014_g1_i1_len_389_path_1_0_388_5	5	four-jointed box protein 1-like	129	4.58E-59	79.40%	0.101	IPR024868 (PRINTS); IPR024868 (PANTHER); PTHR13147:SF5 (PANTHER)
334	c132073_g1_i1_len_285_path_1_0_284_1	4	mucin-19 isoform x2	95	5.04E-08	60.00%	0.146	IPR001846 (PFAM); IPR001846 (PROSITE_PROFILES)
335	c132540_g1_i1_len_353_path_331_0_352_2	4	gastrula zinc finger protein	117	4.30E-15	58.50%	0.105	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
336	c132579_g1_i1_len_295_path_1_0_294_3	2	beta- -galactosyltransferase 1-like	99	8.40E-33	77.00%	0.112	IPR029044 (G3DSA:3.90.550.GENE3D); IPR027995 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
338	c1326_g1_i1_len_881_path_2725_0_880_3	35	peroxidasin homolog	294	2.62E-29	47.40%	0.125	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
337	c132639_g1_i1_len_606_path_584_0_605_3	10	dlp hdl-bgbp precursor	202	9.12E-64	71.80%	0.098	IPR015817 (G3DSA:2.20.50.GENE3D); IPR001747 (PFAM); IPR015255 (PFAM); IPR011030 (G3DSA:1.25.10.GENE3D); PTHR23345:SF11 (PANTHER); PTHR23345 (PANTHER); IPR015819 (SUPERFAMILY); IPR011030 (SUPERFAMILY)
339	c132822_g1_i1_len_355_path_1_0_354_4	7	Agrin, partial	118	2.69E-19	62.10%	0.143	IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); PTHR10574 (PANTHER); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
340	c132862_g1_i1_len_388_path_366_0_387_0	6	neural- partial	130	1.73E-37	61.00%	0.106	G3DSA:2.170.300.10 (GENE3D); IPR000742 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
341	c133015_g1_i1_len_251_path_229_0_250_5	3	low quality protein: coagulation factor vii	83	5.44E-06	54.00%	0.121	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
342	c133040_g1_i1_len_259_path_1_0_258_4	4	glucose dehydrogenase	86	7.34E-22	68.40%	0.112	G3DSA:3.50.50.60 (GENE3D); IPR000172 (PFAM); PTHR11552:SF77 (PANTHER); PTHR11552 (PANTHER); SSF51905 (SUPERFAMILY)
343	c133072_g1_i1_len_372_path_350_0_371_1	8	hypothetical protein L798_10748	124	2.82E-23	60.40%	0.165	IPR007074 (PFAM); PTHR13627:SF24 (PANTHER); PTHR13627 (PANTHER)
344	c133269_g1_i1_len_382_path_360_0_381_1	13	oocyte zinc finger protein 26-like isoform x2	127	1.61E-10	67.40%	0.112	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
345	c133478_g1_i1_len_382_path_1_0_381_5	6	mucin-19 isoform x1	127	4.22E-09	46.20%	0.125	IPR001846 (PFAM); PTHR11339 (PANTHER); IPR001846 (PROSITE_PROFILES)

346	c133538_g1_i1_len_293_path_1_0_292_0	4	fmrfaide-related neuropeptides	98	2.01E-08	70.80%	0.143	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
347	c133563_g1_i1_len_234_path_212_0_233_4	3	glucose dehydrogenase	78	1.92E-18	88.00%	0.127	G3DSA:3.50.50.60 (GENE3D); IPR007867 (PFAM); PTHR11552:SF90 (PANTHER); PTHR11552 (PANTHER); SSF51905 (SUPERFAMILY)
348	c133596_g1_i1_len_257_path_1_0_256_4	4	transforming growth factor-beta-induced protein ig-h3	86	6.64E-28	63.80%	0.104	IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900 (PANTHER); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY)
349	c133652_g1_i1_len_286_path_264_0_285_2	9	alpha- -mannosyl-glycoprotein 4-beta-n-acetylglucosaminyltransferase partial	95	4.38E-24	63.10%	0.149	IPR006759 (PFAM); IPR006759 (PANTHER); PTHR12062:SF0 (PANTHER)
350	c133657_g1_i1_len_744_path_722_0_743_3	11	polypeptide n-acetylgalactosaminyltransferase 14	248	1.47E-97	76.80%	0.105	IPR029044 (G3DSA:3.90.550.GENE3D); IPR001173 (PFAM); PTHR11675 (PANTHER); IPR029044 (SUPERFAMILY)
351	c133671_g1_i1_len_393_path_1_0_392_5	6	serine proteinase stubble-like	131	2.63E-07	71.40%	0.115	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF94 (PANTHER); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
352	c133697_g1_i1_len_333_path_311_0_332_1	4	signal cub and egf-like domain-containing protein 1 isoform x1	111	4.26E-27	81.00%	0.112	PTHR24046:SF4 (PANTHER); PTHR24046 (PANTHER)
353	c134148_g1_i1_len_562_path_540_0_561_0	25	isoform b	188	1.21E-11	62.60%	0.115	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF94 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
354	c134556_g1_i1_len_345_path_323_0_344_1	4	laminin subunit beta-1 isoform x1	115	2.03E-32	71.30%	0.102	Coil (COILS); Coil (COILS); G3DSA:1.20.58.60 (GENE3D); SSF46966 (SUPERFAMILY)
355	c134572_g1_i1_len_479_path_1_0_478_0	8	a disintegrin and metalloproteinase with thrombospondin motifs 14	160	6.56E-15	53.40%	0.096	IPR002870 (PFAM); PTHR13723 (PANTHER); PTHR13723:SF153 (PANTHER)
356	c13471_g2_i1_len_535_path_255_0_534_0	38	cyclin-g-associated kinase	179	2.70E-69	78.80%	0.105	IPR029021 (G3DSA:3.90.190.GENE3D); IPR000340 (PFAM); PTHR23172:SF19 (PANTHER); PTHR23172 (PANTHER); IPR014020 (PROSITE_PROFILES); IPR029023 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
357	c134735_g1_i1_len_383_path_1_0_382_0	10	chloride calcium family member 3	128	1.86E-12	63.60%	0.322	IPR013642 (PFAM); PTHR10579:SF8 (PANTHER); PTHR10579 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
358	c13487_g1_i1_len_2145_path_101_0_2144_5	6588	calreticulin	715	0	84.20%	0.18	Coil (COILS); IPR001580 (PRINTS); IPR001580 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR11073:SF8 (PANTHER); IPR001580 (PANTHER); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009033 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
359	c134888_g1_i1_len_290_path_1_0_289_1	10	zinc finger protein ozf-like	97	1.78E-10	59.50%	0.116	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
360	c134941_g1_i1_len_260_path_238_0_259_1	4	zinc finger protein 649 isoform x1	87	1.71E-09	66.50%	0.151	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
361	c135229_g1_i1_len_401_path_379_0_400_1	17	latrophilin cir1-like isoform x1	134	3.28E-12	54.00%	0.126	IPR000203 (PFAM); PTHR12011 (PANTHER); IPR000203 (PROSITE_PROFILES)
362	c135283_g1_i1_len_261_path_1_0_260_4	5	zinc finger protein 337-like	87	4.56E-19	62.20%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

363	c13540_g2_i1_len_997_path_1173_0_996_5	39	cytoglobin-2-like isoform 1	332	5.92E-46	61.80%	0.137	IPR002336 (PRINTS); IPR000971 (PFAM); IPR012292 (G3DSA:1.10.490.GENE3D); PTHR11442:SF36 (PANTHER); PTHR11442 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000971 (PROSITE_PROFILES); IPR009050 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
364	c135472_g1_i1_len_601_path_1_0_600_1	24	low-density lipoprotein receptor-related protein 2	200	3.63E-96	83.90%	0.1	IPR000742 (SMART); IPR001881 (SMART); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR026823 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10529 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
365	c136024_g1_i1_len_247_path_225_0_246_3	4	insulin-like growth factor-binding protein complex acid labile subunit	83	1.08E-28	77.60%	0.106	SM00365 (SMART); IPR003591 (SMART); PF13516 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
366	c136260_g1_i1_len_456_path_434_0_455_3	8	laminin subunit alpha-like	152	1.34E-65	78.20%	0.102	PR00011 (PRINTS); IPR002049 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); PTHR10574:SF39 (PANTHER); PTHR10574 (PANTHER); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
367	c136411_g1_i1_len_655_path_1_0_654_4	26	ribosomal protein s6 kinase beta-1-like	218	9.75E-98	82.70%	0.366Y	IPR000961 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR017892 (PFAM); IPR000719 (PFAM); PTHR24351 (PANTHER); PTHR24351:SF64 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
368	c136560_g1_i1_len_302_path_1_0_301_2	7	er degradation-enhancing alpha-mannosidase-like 1	100	5.52E-46	86.20%	0.255	IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); IPR001382 (PANTHER); PTHR11742:SF25 (PANTHER); IPR001382 (SUPERFAMILY)
369	c136798_g1_i1_len_247_path_225_0_246_0	2	sortilin-related receptor-like	83	4.53E-12	55.30%	0.102	IPR002172 (SMART); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
370	c136840_g1_i1_len_273_path_251_0_272_5	6	von willebrand factor type egf and pentraxin domain-containing protein 1	91	3.04E-15	57.00%	0.104	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325:SF343 (PANTHER); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
371	c136897_g1_i1_len_313_path_1_0_312_1	9	alpha beta hydrolase domain-containing protein 17c-like	104	1.96E-23	85.50%	0.108	PTHR12277:SF52 (PANTHER); PTHR12277 (PANTHER)
372	c136963_g1_i1_len_301_path_279_0_300_2	6	stress response element binding protein	100	2.15E-14	71.40%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
373	c137000_g1_i1_len_312_path_290_0_311_5	4	threonine synthase-like 2	104	3.01E-39	76.30%	0.114	G3DSA:3.40.50.1100 (GENE3D); PTHR10314 (PANTHER); IPR027457 (PTHR10314:PANTHER); IPR001926 (SUPERFAMILY)
374	c13708_g1_i1_len_1305_path_533_0_1039_2_91_1040_1304_3	549	serine protease1 2	435	1.05E-54	56.90%	0.335	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
375	c13708_g1_i2_len_1180_path_533_0_1039_1_572_1040_1179_4	678	serine protease1 2	393	3.16E-55	56.90%	0.755Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
376	c137305_g1_i1_len_272_path_1_0_271_5	4	neprilysin-2-like isoform x3	90	4.27E-12	63.30%	0.11	IPR008753 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)

377	c137420_g1_i1_len_294_path_1_0_293_3	4	zinc finger protein 502	98	4.07E-21	65.20%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
378	c13753_g1_i1_len_1724_path_1_0_1723_5	1973	leucine rich repeat protein	574	2.54E-29	50.60%	0.593Y	IPR003591 (SMART); SM00364 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF52058 (SUPERFAMILY)
379	c137823_g1_i1_len_286_path_1_0_285_1	4	xanthine dehydrogenase	95	1.54E-21	69.50%	0.103	IPR000674 (SMART); IPR000674 (PFAM); IPR000674 (G3DSA:3.90.1170.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR000674 (SUPERFAMILY)
380	c13812_g2_i1_len_678_path_656_0_677_3	15	low quality protein: von willebrand factor type egf and pentraxin domain-containing protein 1	226	3.17E-41	51.00%	0.104	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
381	c138240_g1_i1_len_348_path_1_0_347_1	6	glucose dehydrogenase	116	3.40E-43	75.80%	0.1	G3DSA:3.50.50.60 (GENE3D); IPR000172 (PFAM); PTHR11552 (PANTHER); PTHR11552:SF90 (PANTHER); IPR000172 (PROSITE_PATTERNS); SSF51905 (SUPERFAMILY)
382	c13827_g1_i1_len_692_path_841_0_598_86_599_691_2	27	lysosomal pro-x carboxypeptidase	230	3.43E-89	70.40%	0.244	IPR008758 (PFAM); PTHR11010:SF11 (PANTHER); IPR008758 (PANTHER)
383	c13827_g1_i2_len_178_path_1_0_84_86_85_177_1	1	lysosomal pro-x carboxypeptidase-like	59	3.05E-12	79.60%	0.107	PTHR11010:SF11 (PANTHER); IPR008758 (PANTHER)
384	c138410_g1_i1_len_385_path_363_0_384_2	6	prenylcysteine oxidase-like	128	1.15E-35	70.10%	0.122	G3DSA:3.50.50.60 (GENE3D); PF13450 (PFAM); IPR017046 (PANTHER); SSF51905 (SUPERFAMILY)
385	c138415_g1_i1_len_406_path_1_0_405_1	9	low-density lipoprotein	135	5.39E-52	69.00%	0.104	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY) IPR013126 (PRINTS); G3DSA:3.30.30.30 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); PTHR19375:SF173 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
386	c138485_g1_i1_len_427_path_1_0_426_3	6	chaperone protein	143	6.22E-41	82.60%	0.102	IPR004911 (PFAM); IPR004911 (PANTHER); PTHR13234:SF8 (PANTHER)
387	c13849_g1_i1_len_905_path_883_0_904_0	90	gamma-interferon-inducible lysosomal thiol reductase	302	1.60E-43	51.30%	0.242	G3DSA:3.40.50.2300 (GENE3D); IPR002455 (PANTHER); PTHR10519:SF3 (PANTHER); IPR028082 (SUPERFAMILY)
388	c13858_g1_i1_len_630_path_1_0_237_1042_238_629_3	9	metabotropic gaba-b receptor subtype isoform b	210	1.33E-26	83.40%	0.108	PR01176 (PRINTS); IPR001828 (PFAM); G3DSA:3.40.50.2300 (GENE3D); IPR002455 (PANTHER); PTHR10519:SF3 (PANTHER); IPR028082 (SUPERFAMILY)
389	c13858_g1_i1_len_630_path_1_0_237_1042_238_629_4	9	gamma-aminobutyric acid type b receptor subunit 1 isoform x3	210	3.24E-74	90.40%	0.11	IPR002456 (PRINTS); IPR001828 (PFAM); G3DSA:3.40.50.2300 (GENE3D); IPR002455 (PANTHER); PTHR10519:SF3 (PANTHER); IPR028082 (SUPERFAMILY)
390	c13858_g1_i2_len_336_path_1_0_237_239_2_38_335_3	12	gamma-aminobutyric acid type b receptor subunit 1-like	112	2.98E-44	81.70%	0.117	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); PTHR11071:SF58 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); TMhelix (TMHMM)
391	c13881_g1_i1_len_494_path_472_0_276_749_277_493_5	22	peptidyl-prolyl cis-trans isomerase h	164	9.07E-57	96.10%	0.1	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); PTHR11071:SF58 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); TMhelix (TMHMM)

392	c13885_g1_i1_len_2216_path_2194_0_2215_1	145	afg3-like protein 2	739	0	92.90%	0.107	IPR003593 (SMART); IPR003959 (PFAM); IPR005936 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR000642 (PFAM); G3DSA:1.10.8.60 (GENE3D); PTHR23076:SF38 (PANTHER); PTHR23076 (PANTHER); IPR003960 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR005936 (HAMAP); SSF140990 (SUPERFAMILY); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
393	c138880_g1_i1_len_346_path_1_0_345_4	16	---NA---	115			0.104	no IPS match
394	c139001_g1_i1_len_267_path_245_0_266_0	4	---NA---	89			0.106	IPR001190 (PFAM); IPR017448 (G3DSA:3.10.250.GENE3D); IPR001190 (PROSITE_PROFILES); IPR017448 (SUPERFAMILY)
395	c13927_g2_i1_len_612_path_590_0_611_5	14	keratin-associated protein 5-	204	2.88E-56	56.10%	0.118	IPR000742 (SMART); G3DSA:2.170.300.10 (GENE3D); IPR013032 (PFAM); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24838 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
396	c139353_g1_i1_len_269_path_1_0_268_2	4	#NAME?	89	4.95E-47	91.50%	0.141	IPR001830 (PFAM); G3DSA:3.40.50.2000 (GENE3D); PTHR10788 (PANTHER); PTHR10788:SF6 (PANTHER); SSF53756 (SUPERFAMILY)
397	c13937_g1_i1_len_879_path_1_0_878_3	52	probable isocitrate dehydrogenase	293	2.95E-162	87.50%	0.104	IPR024084 (G3DSA:3.40.718.GENE3D); IPR024084 (PFAM); IPR004434 (TIGRFAM); PTHR11835:SF39 (PANTHER); IPR001804 (PANTHER); IPR019818 (PROSITE_PATTERNS); SSF53659 (SUPERFAMILY)
398	c139468_g1_i1_len_554_path_532_0_553_5	7	wd repeat domain-containing protein 83	184	9.24E-40	84.60%	0.33	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22842 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
399	c139535_g1_i1_len_314_path_1_0_313_3	4	protease inhibitors-like isoform x2	105	2.29E-11	53.80%	0.104	IPR008037 (PFAM); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY)
400	c13967_g1_i1_len_408_path_1_0_407_5	6	fibrillin-2-like	136	2.41E-61	78.90%	0.101	IPR000742 (SMART); IPR001881 (SMART); IPR017878 (G3DSA:3.90.290.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR017878 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); PTHR24039:SF20 (PANTHER); IPR011398 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR017878 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR017878 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
401	c13967_g2_i1_len_1580_path_2328_0_1579_0	83	fibrillin-2-like	527	1.02E-163	64.40%	0.117	IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); PTHR24039:SF20 (PANTHER); IPR011398 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR009030 (SUPERFAMILY); IPR009030 (SUPERFAMILY)
402	c13970_g1_i1_len_150_path_1_0_149_3	2	b-cell lymphoma leukemia 11a-like	50	8.11E-14	78.60%	0.105	IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)

403	c13972_g1_i1_len_1112_path_1_0_431_433_432_1111_5	39	zinc finger protein 501-like	370	1.82E-21	47.70%	0.1	IPR015880 (SMART); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
404	c140065_g1_i1_len_464_path_1_0_463_3	7	membrane metallo-endopeptidase-like 1-like	155	3.39E-42	68.20%	0.114	IPR008753 (PFAM); G3DSA:1.10.1380.10 (GENE3D); PTHR11733:SF113 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
405	c14022_g1_i1_len_1074_path_1_0_92_94_93_1073_0	56	aael003561- partial	358	1.95E-25	52.80%	0.178	IPR001211 (PRINTS); IPR016090 (SMART); IPR016090 (G3DSA:1.20.90.GENE3D); IPR016090 (PFAM); IPR001211 (PANTHER); PTHR11716:SF45 (PANTHER); IPR013090 (PROSITE_PATTERNS); IPR013090 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016090 (SUPERFAMILY); TMhelix (TMHMM)
406	c14022_g1_i2_len_1059_path_2103_0_77_94_78_1058_0	42	aael003561- partial	353	1.83E-25	52.60%	0.206	IPR001211 (PRINTS); IPR016090 (SMART); IPR016090 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PANTHER); IPR013090 (PROSITE_PATTERNS); IPR013090 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016090 (SUPERFAMILY); TMhelix (TMHMM)
407	c140284_g1_i1_len_141_path_1_0_140_1	0	myosin heavy chain partial	47	2.98E-16	97.40%	0.105	Coil (COILS); IPR002928 (PFAM); PTHR13140:SF364 (PANTHER); PTHR13140 (PANTHER)
408	c140392_g1_i1_len_289_path_1_0_288_1	6	serine proteinase stubble-like	96	7.99E-21	71.20%	0.13	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
409	c14080_g2_i1_len_1186_path_1305_0_1185_5	61	ankyrin repeat domain-containing protein partial	395	1.16E-48	75.60%	0.112	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (PFAM); PTHR24149 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
410	c140921_g1_i1_len_270_path_248_0_269_4	4	cathepsin b	90	2.02E-20	72.20%	0.136	IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF15 (PANTHER); IPR013128 (PANTHER); SSF54001 (SUPERFAMILY)
411	c141015_g1_i1_len_394_path_1_0_393_2	5	low-density lipoprotein receptor-related protein 4	131	2.06E-06	62.80%	0.109	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
412	c14123_g1_i1_len_374_path_470_0_310_962_311_373_4	15	urokinase-type plasminogen activator	125	1.88E-16	72.70%	0.132	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
413	c14123_g1_i2_len_492_path_470_0_310_781_311_491_5	19	urokinase-type plasminogen activator	164	1.84E-12	78.00%	0.167	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
414	c141445_g1_i1_len_180_path_1_0_179_5	3	plexin-b-like isoform x5	60	5.99E-27	91.30%	0.111	IPR002909 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR22625:SF31 (PANTHER); PTHR22625 (PANTHER); IPR014756 (SUPERFAMILY)
415	c141926_g1_i1_len_320_path_298_0_319_0	4	von willebrand factor type egf and pentraxin domain-containing protein 1	107	9.12E-10	56.00%	0.113	G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY)
416	c142041_g1_i1_len_387_path_365_0_386_2	6	protein dachsous-like	129	1.05E-42	72.20%	0.119	IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); PTHR24027:SF256 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
417	c142423_g1_i1_len_336_path_1_0_335_3	5	acid sphingomyelinase-like phosphodiesterase 3a	112	7.63E-20	60.00%	0.257	IPR029052 (G3DSA:3.60.21.GENE3D); PTHR10340 (PANTHER); PTHR10340:SF14 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TMhelix (TMHMM)

418	c14323_g1_i1_len_926_path_1_0_925_4	44	tropinone reductase 2-like	309	8.21E-137	83.50%	0.247	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF111 (PANTHER); IPR020904 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
419	c14329_g1_i1_len_1588_path_1556_0_171_3_134_172_181_1728_182_1587_1	60	ww domain-containing oxidoreductase	529	3.16E-167	74.70%	0.131	Coil (COILS); IPR002347 (PRINTS); IPR001202 (SMART); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); G3DSA:2.20.70.10 (GENE3D); PTHR24316:SF115 (PANTHER); PTHR24316 (PANTHER); IPR001202 (PROSITE_PROFILES); IPR001202 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
420	c143471_g1_i1_len_215_path_1_0_214_0	3	blastula protease 10-like	72	6.98E-25	74.40%	0.102	IPR001506 (PRINTS); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)
421	c14408_g1_i1_len_1064_path_1042_0_268_1_311_269_1063_2	40	arylsulfatase a-like	354	1.43E-114	71.10%	0.294	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF22 (PANTHER); IPR024607 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM)
422	c14408_g1_i2_len_487_path_1042_0_268_21_06_269_486_2	17	arylsulfatase a-like	162	8.42E-11	74.80%	0.294	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342 (PANTHER); PTHR10342:SF27 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
423	c144328_g1_i1_len_147_path_125_0_146_0	2	achain structural basis for dscam isoform specificity	49	5.07E-24	97.00%	0.099	PTHR10489:SF567 (PANTHER); PTHR10489 (PANTHER)
424	c144399_g1_i1_len_165_path_1_0_164_4	1	low-density lipoprotein	55	3.06E-14	73.20%	0.126	IPR001881 (SMART); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR10529 (PANTHER); PTHR10529:SF210 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY)
425	c14479_g1_i1_len_1311_path_1_0_208_210_209_504_506_505_1310_2	210	protein spaetzle	437	2.21E-28	54.20%	0.245	PTHR23199 (PANTHER); IPR029034 (SUPERFAMILY)
426	c14479_g1_i2_len_1015_path_1_0_208_506_209_1014_0	122	spaetzle 1-2 isoform x1	339	1.61E-21	54.40%	0.471Y	PTHR23199 (PANTHER); SignalP-noTM (SIGNALP_EUK); IPR029034 (SUPERFAMILY)
427	c14493_g1_i1_len_837_path_1_0_836_4	43	alpha-mannosidase 2	279	9.21E-139	78.50%	0.102	IPR015341 (SMART); IPR015341 (PFAM); IPR000602 (PFAM); IPR027291 (G3DSA:3.20.110.GENE3D); IPR015341 (G3DSA:1.20.1270.GENE3D); PTHR11607:SF22 (PANTHER); PTHR11607 (PANTHER); IPR011330 (SUPERFAMILY); IPR028995 (SUPERFAMILY)
428	c14493_g2_i1_len_1087_path_1629_0_1086_1	40	alpha-mannosidase 2	362	7.74E-167	73.80%	0.370Y	IPR000602 (PFAM); IPR027291 (G3DSA:3.20.110.GENE3D); PTHR11607 (PANTHER); PTHR11607:SF22 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011330 (SUPERFAMILY); TMhelix (TMHMM)
429	c145096_g1_i1_len_363_path_341_0_362_1	6	zinc finger protein 678-like	121	1.09E-39	69.30%	0.105	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
430	c145103_g1_i1_len_1155_path_1133_0_1154_0	29	85 88 kda calcium-independent phospholipase a2 isoform x1	385	4.92E-137	68.80%	0.178	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002641 (PFAM); IPR020683 (PFAM); G3DSA:3.40.1090.10 (GENE3D); PTHR24139 (PANTHER); PTHR24139:SF33 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); IPR016035 (SUPERFAMILY)
431	c145113_g1_i1_len_2339_path_1_0_2338_5	284	scabrous protein	779	6.61E-118	51.80%	0.096	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR002181 (SMART); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PFAM); IPR014715 (G3DSA:4.10.530.GENE3D); PTHR19143 (PANTHER); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)

432	c145223_g1_i1_len_975_path_953_0_974_2	39	cgmp-dependent protein isozyme 2 forms cd4 t1 t3a t3b-like isoform x3	325	0	91.50%	0.1	IPR002290 (SMART); IPR000961 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24353:SF65 (PANTHER); PTHR24353 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
433	c145247_g1_i1_len_1424_path_1_0_1423_4	63	limulus clotting factor partial	475	1.50E-68	56.90%	0.115	IPR001314 (PRINTS); IPR001881 (SMART); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
434	c145250_g1_i1_len_1684_path_1662_0_1683_0	584	calumenin	562	1.24E-155	79.90%	0.137	IPR002048 (SMART); IPR011992 (PFAM); IPR002048 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR10827 (PANTHER); IPR027239 (PTHR10827:PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); SSF47473 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
435	c14529_g1_i1_len_604_path_582_0_125_708_126_603_5	19	lysosomal pro-x carboxypeptidase-like	201	1.02E-18	77.90%	0.208	IPR008758 (PFAM); IPR008758 (PANTHER); PTHR11010:SF11 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
436	c145309_g1_i1_len_1107_path_1085_0_1106_1	62	adp-ribosylation factor-related protein 1	369	6.82E-125	94.60%	0.103	IPR001806 (PRINTS); IPR003579 (SMART); IPR006687 (SMART); IPR024156 (SMART); IPR006689 (PFAM); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF19 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
437	c145327_g1_i1_len_2269_path_2247_0_2268_0	405	aspartate--trna cytoplasmic	757	0	85.30%	0.231	Coil (COILS); IPR002312 (PRINTS); G3DSA:3.30.930.10 (GENE3D); IPR004523 (TIGRFAM); IPR004364 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); IPR004365 (PFAM); IPR018150 (PANTHER); IPR004523 (PTHR22594:PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY); IPR012340 (SUPERFAMILY)
439	c14541_g2_i1_len_671_path_899_0_670_1	20	26s protease regulatory subunit 6a-b	224	5.31E-155	98.20%	0.16	IPR003593 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); PTHR23073 (PANTHER); PTHR23073:SF7 (PANTHER); IPR027417 (SUPERFAMILY)
438	c145419_g1_i1_len_582_path_560_0_581_0	22	achain structural determinants for improved thermal stability of designed ankyrin repeat proteins with a redesigned c- capping	194	2.49E-22	53.70%	0.11	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
440	c14555_g1_i1_len_642_path_2469_0_15_186_6_16_641_4	20	leucine-rich repeat-containing protein 70 isoform x1	214	1.68E-15	48.20%	0.111	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24369 (PANTHER); SSF52058 (SUPERFAMILY)
441	c14555_g1_i2_len_1257_path_1235_0_630_1_866_631_1256_4	70	leucine-rich repeat-containing protein 70 isoform x1	419	5.82E-15	50.30%	0.111	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24369 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

443	c14560_g1_i1_len_892_path_870_0_751_162_2_752_771_1642_772_891_1	465	pacifastin light chain	297	1.23E-27	44.60%	0.375Y	IPR006552 (SMART); IPR008037 (PFAM); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR012341 (G3DSA:1.50.10.GENE3D); IPR001701 (PFAM); PTHR22298 (PANTHER); PTHR22298:SF17 (PANTHER); IPR008928 (SUPERFAMILY)
442	c145602_g1_i1_len_283_path_1_0_282_5	12	endo-beta- - partial	94	3.24E-28	71.50%	0.115	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19923:SF0 (PANTHER); PTHR19923 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
444	c145625_g1_i1_len_853_path_1_0_852_4	34	pleiotropic regulator 1	284	2.53E-118	73.00%	0.101	IPR002049 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR10574 (PANTHER); PTHR10574:SF39 (PANTHER); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
445	c145638_g1_i1_len_472_path_1_0_471_1	10	laminin subunit alpha	157	6.13E-66	78.50%	0.117	IPR000209 (PFAM); IPR000209 (G3DSA:3.40.50.GENE3D); IPR015500 (PANTHER); PTHR10795:SF71 (PANTHER); IPR000209 (SUPERFAMILY)
446	c145641_g1_i1_len_298_path_276_0_297_2	5	furin-like protease isoform 1-crr isoform x3	99	2.22E-56	96.90%	0.106	IPR000998 (SMART); IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
447	c145728_g1_i1_len_607_path_585_0_606_2	14	mam and ldl-receptor class a domain-containing protein 2-like	202	7.45E-64	66.10%	0.124	IPR022086 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
448	c145755_g1_i1_len_2626_path_2604_0_2625_3	197	membrane skeletal	876	1.04E-37	63.80%	0.162	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); PTHR18937 (PANTHER); IPR027120 (PTHR18937:PANTHER)
449	c145775_g1_i1_len_949_path_927_0_948_3	56	structural maintenance of chromosomes protein 2	317	6.69E-87	71.70%	0.1	IPR000242 (PRINTS); IPR000242 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
450	c145782_g1_i1_len_494_path_472_0_493_0	18	receptor-type tyrosine-protein phosphatase kappa	165	3.50E-42	66.60%	0.106	IPR011682 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); G3DSA:2.70.98.30 (GENE3D); PTHR11607 (PANTHER); PTHR11607:SF22 (PANTHER); IPR011013 (SUPERFAMILY)
451	c145793_g1_i1_len_1492_path_1470_0_1491_1	130	alpha-mannosidase 2	497	0	70.50%	0.125	IPR020472 (PRINTS); IPR001680 (SMART); IPR003613 (SMART); IPR003613 (PFAM); IPR013915 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); PTHR13889 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR003613 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); SSF57850 (SUPERFAMILY)
452	c145872_g1_i1_len_1655_path_1633_0_1654_1	104	pre-mrna-processing factor 19	552	0	90.70%	0.126	IPR000998 (PRINTS); IPR000998 (SMART); IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
453	c145962_g1_i1_len_400_path_378_0_399_4	8	mlrp1_acrmi ame: full=mam and ldl-receptor class a domain-containing protein 1 ame: full=skeletal organic matrix mam and ldl-receptor 1 short=som mam and ldl-receptor partial	133	1.77E-24	59.20%	0.106	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24361:SF208 (PANTHER); PTHR24361 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
454	c145986_g1_i1_len_431_path_1_0_430_4	7	serine threonine-protein kinase mst4 isoform x3	144	2.39E-96	98.80%	0.22	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR009730 (PFAM); PTHR15327:SF0 (PANTHER); IPR009730 (PANTHER)
455	c146014_g1_i1_len_1556_path_1_0_1555_0	157	microfibrillar-associated protein 1-like	519	3.24E-177	77.90%	0.1	

									Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR007148 (PFAM); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19853 (PANTHER); PTHR19853:SF0 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PRO
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470	c14636_g2_i1_len_332_path_514_0_331_3	6	serine threonine-protein kinase 10 isoform x1	111	2.33E-64	96.00%	0.102	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24361:SF249 (PANTHER); PTHR24361 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
469	c146364_g1_i1_len_1278_path_1243_0_1223_2467_1224_1241_2467_1242_1259_2467_1260_1277_2	58	cyclin-g-associated kinase-like	426	1.04E-153	77.00%	0.159	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR23172:SF19 (PANTHER); PTHR23172 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
471	c146396_g1_i1_len_806_path_784_0_805_5	30	omega-amidase nit2-like	268	5.87E-145	83.30%	0.107	IPR003010 (G3DSA:3.60.110.GENE3D); IPR003010 (PFAM); PTHR23088:SF20 (PANTHER); PTHR23088 (PANTHER); IPR003010 (PROSITE_PROFILES); IPR003010 (SUPERFAMILY)
472	c146430_g1_i1_len_233_path_211_0_232_2	5	prolyl 4- beta subunit	77	6.18E-18	70.20%	0.113	IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF74 (PANTHER); PTHR18929 (PANTHER); IPR012336 (SUPERFAMILY)
473	c146452_g1_i1_len_278_path_1_0_277_0	4	transient receptor potential channel pyrexia	93	8.82E-18	68.80%	0.139	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
474	c146457_g1_i1_len_2142_path_2120_0_2141_4	168	alpha-2-macroglobulin-like protein 1 isoform x1	714	5.40E-144	55.20%	0.197	IPR011625 (PFAM); IPR002890 (PFAM); PTHR11412 (PANTHER)
475	c146458_g1_i1_len_303_path_1_0_302_1	5	isoform c	101	8.27E-25	67.60%	0.123	IPR014782 (PRINTS); G3DSA:1.10.390.10 (GENE3D); IPR014782 (PFAM); PTHR11533:SF165 (PANTHER); IPR001930 (PANTHER); SSF55486 (SUPERFAMILY)
477	c14648_g1_i1_len_2505_path_1_0_2504_4	278	n-acetylated-alpha-linked acidic dipeptidase	835	0	59.30%	0.175	IPR007365 (G3DSA:1.20.930.GENE3D); G3DSA:3.50.30.30 (GENE3D); IPR007365 (PFAM); IPR007484 (PFAM); IPR003137 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR10404 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); IPR007365 (SUPERFAMILY); SSF52025 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
476	c146489_g1_i1_len_416_path_394_0_415_3	12	phosphatidylinositol -trisphosphate 3-phosphatase and dual-specificity protein phosphatase pten	139	2.98E-49	86.10%	0.126	IPR029021 (G3DSA:3.90.190.GENE3D); PTHR12305 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029023 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
478	c146509_g1_i1_len_852_path_1_0_851_3	4885	hemagglutinin amebocyte aggregation factor-like	284	9.35E-38	58.00%	0.147	PF14704 (PFAM); IPR026645 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
479	c146512_g1_i1_len_531_path_1_0_530_1	16	ectonucleoside triphosphate diphosphohydrolase 7	177	5.87E-29	75.20%	0.108	IPR000407 (PFAM); IPR000407 (PANTHER); PTHR11782:SF37 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
480	c14678_g1_i1_len_2191_path_2169_0_1289_3459_1290_1383_3553_1384_2190_4	3230	protein disulfide-isomerase a3	730	0	78.20%	0.294	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); PF13848 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR005792 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005788 (TIGRFAM); PTHR18929:SF60 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
481	c146790_g1_i1_len_582_path_560_0_581_0	20	macrophage mannose receptor 1-like	194	7.04E-30	52.00%	0.370Y	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803 (PANTHER); PTHR22803:SF16 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
482	c146818_g1_i1_len_672_path_1_0_671_5	17	cyclin-dependent kinase 2 isoform x2	224	3.05E-89	75.60%	0.139	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24056 (PANTHER); PTHR24056:SF168 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)

483	c146826_g1_i1_len_375_path_353_0_374_3	6	cysteine-rich motor neuron 1 partial	125	8.02E-38	67.40%	0.128	IPR001007 (SMART); IPR001007 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR11339 (PANTHER); IPR001007 (PROSITE_PATTERNS); IPR001007 (PROSITE_PATTERNS); IPR001007 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); SSF57603 (SUPERFAMILY); SSF57603 (SUPERFAMILY)
484	c146839_g1_i1_len_370_path_348_0_369_2	8	slit homolog 2 protein	123	5.13E-57	81.50%	0.123	G3DSA:3.80.10.10 (GENE3D); PTHR24365:SF270 (PANTHER); PTHR24365 (PANTHER); SSF52058 (SUPERFAMILY)
485	c146855_g1_i1_len_267_path_245_0_266_2	4	prolyl 3-hydroxylase 2-like isoform x1	89	7.39E-29	73.50%	0.186	PTHR14049 (PANTHER)
486	c146859_g1_i1_len_1128_path_1_0_1127_1	51	insulin-like growth factor-binding protein complex acid labile chain	376	3.44E-30	54.80%	0.093	G3DSA:3.80.10.10 (GENE3D); PTHR24369 (PANTHER); SSF52058 (SUPERFAMILY)
487	c146925_g1_i1_len_744_path_1_0_743_4	27	adenylate cyclase type 9	248	1.04E-80	86.20%	0.1	IPR001054 (SMART); IPR001054 (PFAM); IPR001054 (G3DSA:3.30.70.GENE3D); PTHR11920:SF272 (PANTHER); PTHR11920 (PANTHER); IPR018297 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001054 (PROSITE_PROFILES); IPR029787 (SUPERFAMILY); TMhelix (TMHMM)
488	c146957_g1_i1_len_645_path_39_0_644_3	54	low quality protein: tenascin	208	2.68E-28	63.50%	0.12	IPR002181 (SMART); IPR014715 (G3DSA:4.10.530.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
489	c14700_g1_i1_len_2244_path_1_0_2243_0	271	wd repeat-containing protein 36	748	0	70.10%	0.192	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR007319 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR13889:SF2 (PANTHER); PTHR13889 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
490	c147019_g1_i1_len_392_path_370_0_391_4	10	protein yellow-like	131	4.80E-22	58.60%	0.11	IPR017996 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D)
491	c147039_g1_i1_len_1585_path_1_0_1584_2	1586	d-aspartate oxidase	528	1.45E-98	63.60%	0.164	IPR016040 (G3DSA:3.40.50.GENE3D); IPR006076 (PFAM); PTHR11530:SF0 (PANTHER); IPR023209 (PANTHER); IPR006181 (PROSITE_PATTERNS); SSF54373 (SUPERFAMILY); SSF51971 (SUPERFAMILY); TMhelix (TMHMM)
492	c147044_g1_i1_len_721_path_1_0_720_5	20	gamma-glutamyltranspeptidase 1-like isoform x2	240	4.18E-75	69.70%	0.103	IPR000101 (PRINTS); IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF15 (PANTHER); IPR029055 (SUPERFAMILY)
493	c14706_g1_i1_len_1999_path_1977_0_1998_5	169	myosin light chain smooth muscle	666	0	79.20%	0.101	Coil (COILS); IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
494	c147164_g1_i1_len_742_path_720_0_741_0	12	zinc finger protein 120-like isoform x1	248	5.36E-70	67.20%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
495	c147180_g1_i1_len_310_path_288_0_309_4	4	membrane metallo-endopeptidase-like 1	103	9.85E-38	83.30%	0.108	IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); PTHR11733:SF111 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)

496	c14719_g1_i1_len_1710_path_1_0_1644_358 3_1645_1709_4	3589	cathepsin b	570	3.64E-164	78.60%	0.174	IPR000668 (PRINTS); IPR000668 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); IPR012599 (PFAM); IPR015643 (PTHR12411:PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
497	c14719_g1_i2_len_1770_path_1_0_1644_164 6_1645_1769_4	3689	cathepsin b	590	6.07E-164	78.60%	0.117	IPR000668 (PRINTS); IPR000668 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR012599 (PFAM); IPR000668 (PFAM); IPR013128 (PANTHER); IPR015643 (PTHR12411:PANTHER); IPR000169 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
498	c147217_g1_i1_len_401_path_379_0_400_2	12	wd repeat and fyve domain-containing protein 2	133	1.90E-69	82.60%	0.143	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR13856:SF7 (PANTHER); PTHR13856 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
499	c14722_g1_i1_len_3082_path_3733_0_2522_25_2523_3081_4	447	exocyst complex component 6b-like isoform 2	1027	0	80.70%	0.141	Coil (COILS); Coil (COILS); Coil (COILS); IPR007225 (PFAM); IPR007225 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
500	c147253_g1_i1_len_667_path_645_0_666_5	24	protein disulfide isomerase family member 4	222	2.59E-69	63.40%	0.126	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PF13848 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF56 (PANTHER); PTHR18929 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
501	c147263_g1_i1_len_285_path_1_0_284_2	4	uncharacterized aarf domain-containing protein kinase 1-like	95	3.18E-35	77.50%	0.162	PTHR10566:SF63 (PANTHER); PTHR10566 (PANTHER)
502	c14731_g1_i1_len_875_path_1_0_874_5	57	oocyte zinc finger protein partial	291	1.55E-08	59.50%	0.1	IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
503	c14739_g1_i1_len_365_path_343_0_364_5	15	vesicle-fusing atpase 1-like	121	3.51E-40	76.90%	0.12	IPR003338 (SMART); G3DSA:2.40.40.20 (GENE3D); IPR003338 (PFAM); PTHR23078 (PANTHER); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009010 (SUPERFAMILY)
504	c147416_g1_i1_len_573_path_551_0_572_4	12	group 3 secretory phospholipase a2-like	191	8.09E-43	71.30%	0.277	IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PFAM); PTHR12253 (PANTHER); PTHR12253:SF8 (PANTHER); IPR013090 (PROSITE_PATTERNS); IPR016090 (SUPERFAMILY)
505	c147494_g1_i1_len_955_path_933_0_954_2	46	dehydrogenase reductase sdr family protein 7-like	318	2.87E-85	83.20%	0.104	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF325 (PANTHER); IPR020904 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY)
506	c147558_g1_i1_len_834_path_1_0_833_3	15	serine threonine-protein kinase dclk2-like isoform x3	278	4.08E-42	75.80%	0.304	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24347:SF49 (PANTHER); IPR020636 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
507	c147561_g1_i1_len_249_path_227_0_248_0	3	matrix metalloproteinase	83	1.58E-17	67.90%	0.491Y	IPR021190 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001818 (PFAM); PTHR10201 (PANTHER); SignalP-noTM (SIGNALP_EUK); SSF55486 (SUPERFAMILY)
508	c147606_g1_i1_len_1008_path_1_0_1007_4	21	low affinity immunoglobulin epsilon fc receptor-like	336	1.05E-18	48.80%	0.11	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
509	c147773_g1_i1_len_242_path_220_0_241_1	6	esterase e4-like	81	9.76E-29	77.20%	0.201	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559 (PANTHER); IPR029058 (SUPERFAMILY)

510	c14789_g1_i1_len_818_path_1_0_817_1	96	glutathione peroxidase 7	273	7.88E-76	70.60%	0.531Y	IPR000889 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PFAM); IPR000889 (PANTHER); PTHR11592:SF10 (PANTHER); IPR029759 (PROSITE_PATTERNS); IPR029760 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000889 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
511	c147928_g1_i1_len_693_path_671_0_692_2	14	integrin alpha-ps1 isoform x2	231	1.04E-96	74.30%	0.111	IPR000413 (PRINTS); IPR013519 (SMART); G3DSA:2.130.10.130 (GENE3D); PF13517 (PFAM); IPR013517 (PFAM); G3DSA:2.60.40.1460 (GENE3D); PTHR23220 (PANTHER); PTHR23220:SF77 (PANTHER); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); SSF69318 (SUPERFAMILY)
512	c147969_g1_i1_len_276_path_254_0_275_3	12	titin isoform x1	92	2.37E-33	77.80%	0.111	IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF149 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
513	c148104_g1_i1_len_353_path_1_0_352_0	5	low-density lipoprotein receptor-related protein 4	118	1.98E-15	57.90%	0.106	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
514	c148132_g1_i1_len_507_path_1_0_278_280_279_392_280_393_506_2	13	sortilin-related receptor-like	169	6.74E-10	47.40%	0.099	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
515	c148179_g1_i1_len_247_path_1_0_246_1	4	c-type lectin domain family 4 member d	82	3.70E-09	55.90%	0.112	IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
516	c148194_g1_i1_len_310_path_288_0_309_4	6	hormone-sensitive lipase	103	1.08E-42	76.10%	0.182	IPR013094 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR23025 (PANTHER); PTHR23025:SF3 (PANTHER); IPR029058 (SUPERFAMILY)
521	c1482_g1_i1_len_375_path_125_0_374_4	8	down syndrome cell adhesion molecule isoform x101	125	1.38E-65	93.00%	0.121	PR00014 (PRINTS); IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF567 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
517	c148222_g1_i1_len_1616_path_1_0_1615_2	150	thioredoxin-related transmembrane protein 1-like	538	1.08E-97	71.30%	0.684Y	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929 (PANTHER); PTHR18929:SF81 (PANTHER); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
518	c148260_g1_i1_len_594_path_1_0_296_1_297_593_0	15	titin-like isoform x26	198	9.38E-12	45.40%	0.107	IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
519	c148265_g1_i1_len_639_path_1_0_638_2	42	aldehyde dehydrogenase family 9 member a1-a-like	213	1.95E-54	81.40%	0.112	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699:SF114 (PANTHER); PTHR11699 (PANTHER); IPR016161 (SUPERFAMILY)
520	c148274_g1_i1_len_705_path_1_0_704_0	14	acyl- delta desaturase	235	5.33E-83	73.70%	0.1	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351 (PANTHER); PTHR11351:SF28 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
522	c148374_g1_i1_len_363_path_341_0_362_4	6	glucosylceramidase- partial	121	3.60E-37	68.20%	0.144	IPR013780 (G3DSA:2.60.40.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001139 (PFAM); PTHR11069:SF7 (PANTHER); IPR001139 (PANTHER); IPR017853 (SUPERFAMILY)
523	c148388_g1_i1_len_1220_path_1198_0_1219_3	51	peptidylprolyl isomerase domain and wd repeat-containing protein 1	407	0	88.40%	0.105	IPR002130 (PRINTS); IPR015943 (G3DSA:2.130.10.GENE3D); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); PTHR11071:SF228 (PANTHER); IPR002130 (PROSITE_PROFILES); SSF69322 (SUPERFAMILY); IPR029000 (SUPERFAMILY)

524	c148496_g1_i1_len_738_path_716_0_737_1	34	contactin associated protein 1	246	6.40E-31	50.30%	0.104	IPR001073 (PRINTS); IPR001073 (SMART); IPR008983 (G3DSA:2.60.120.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); IPR001073 (PFAM); PTHR10127 (PANTHER); PTHR10127:SF575 (PANTHER); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY); IPR002181 (SUPERFAMILY)
525	c148521_g1_i1_len_1110_path_1_0_1109_4	57	iduronate 2-sulfatase-like	370	1.20E-88	59.70%	0.115	IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); IPR000917 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF185 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY) G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023409 (PROSITE_PATTERNS); IPR023410 (SUPERFAMILY)
526	c148556_g1_i1_len_260_path_1_0_259_2	8	dna damage checkpoint protein	86	1.12E-15	93.50%	0.109	IPR001623 (PRINTS); IPR001623 (SMART); G3DSA:3.90.10.10 (GENE3D); PF14901 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF141 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
527	c14856_g1_i1_len_645_path_463_0_644_0	28	dnaj homolog dnj-5	215	2.99E-95	84.00%	0.11	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
528	c148607_g1_i1_len_738_path_716_0_737_0	59	peptidyl-prolyl cis-trans isomerase-like 1	234	1.90E-86	92.30%	0.115	IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24166 (PANTHER); PTHR24166:SF8 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
529	c148690_g1_i1_len_963_path_1_0_962_5	86	protein tanc2 isoform x2	321	1.52E-121	78.40%	0.133	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
530	c148730_g1_i1_len_310_path_1_0_309_0	10	ankyrin repeat	104	2.21E-22	60.30%	0.113	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
531	c148787_g1_i1_len_381_path_359_0_380_2	6	d chain coupling of remote alternating-access transport mechanisms for protons and substrates in the multidrug efflux pump acrb	127	6.01E-18	68.60%	0.104	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24182 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
532	c148867_g1_i1_len_323_path_1_0_322_3	4	peptidylprolyl isomerase	108	2.22E-39	68.70%	0.11	IPR001179 (PFAM); G3DSA:3.10.50.40 (GENE3D); IPR023566 (PANTHER); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY)
533	c148874_g1_i1_len_1820_path_1_0_1819_3	38	protein jagged-1-like	607	4.13E-14	38.10%	0.107	no IPS match
534	c148924_g1_i1_len_318_path_296_0_317_1	12	proclotting enzyme	106	2.55E-19	59.50%	0.133	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260:SF3 (PANTHER); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
535	c148990_g1_i1_len_423_path_401_0_422_0	6	protogenin a-like	141	6.19E-26	65.00%	0.111	IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF20 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
536	c149035_g1_i1_len_396_path_374_0_395_1	22	ankyrin repeat domain-containing protein 16-like	132	7.57E-30	63.50%	0.241	IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24181:SF20 (PANTHER); PTHR24181 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
537	c149055_g1_i1_len_728_path_706_0_727_5	11	endothelin-converting enzyme 1 isoform x2	242	1.73E-41	73.60%	0.146	IPR000718 (PANTHER); IPR029734 (PTHR11733:PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

538	c149086_g1_i1_len_382_path_360_0_381_4	4	zinc finger protein 214 isoform x3	127	1.09E-31	68.00%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
539	c149118_g1_i1_len_1347_path_1_0_1346_5	71	low quality protein: hemocytin	449	4.38E-37	48.40%	0.1	IPR025155 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); IPR000421 (PFAM); PTHR24543 (PANTHER); IPR000421 (PROSITE_PROFILES); IPR008979 (SUPERFAMILY)
540	c149154_g1_i1_len_944_path_945_0_747_16_93_748_943_2	52	zinc finger protein 275	314	1.03E-20	57.50%	0.112	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13913 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
541	c149176_g1_i1_len_1191_path_1169_0_1190_5	35	amyloid beta a4 protein	397	8.92E-145	70.00%	0.1	IPR008197 (PRINTS); IPR002223 (PRINTS); IPR002223 (SMART); IPR006150 (SMART); IPR008197 (SMART); IPR000716 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR004094 (PFAM); IPR000716 (PFAM); IPR028150 (PFAM); IPR008197 (G3DSA:4.10.75.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR004094 (G3DSA:2.10.22.GENE3D); IPR008197 (PFAM); PTHR19441:SF10 (PANTHER); PTHR19441 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR004094 (PROSITE_PROFILES); IPR008197 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR011061 (SUPERFAMILY); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY); IPR008197 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
542	c149210_g1_i1_len_455_path_433_0_454_4	8	leucine-rich repeat and calponin homology domain-containing protein 1 isoform x2	152	1.67E-59	79.50%	0.112	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR23155 (PANTHER); PTHR23155:SF423 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
543	c149380_g1_i1_len_647_path_625_0_646_5	22	leukocyte-antigen-related- isoform b	215	3.56E-83	78.30%	0.188	PR00014 (PRINTS); IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19134:SF199 (PANTHER); PTHR19134 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
544	c14940_g2_i1_len_509_path_527_0_508_1	15	alpha-mannosidase 2x	170	3.86E-53	74.40%	0.103	IPR027291 (G3DSA:3.20.110.GENE3D); IPR000602 (PFAM); PTHR11607:SF4 (PANTHER); PTHR11607 (PANTHER); IPR011330 (SUPERFAMILY)
545	c149430_g1_i1_len_1191_path_1169_0_1190_1	78	low quality protein: thioredoxin domain-containing protein 11-like	397	1.84E-69	54.50%	0.105	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929:SF61 (PANTHER); PTHR18929 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
546	c149551_g1_i1_len_749_path_727_0_748_5	12	receptor-type tyrosine-protein phosphatase f-like isoform x2	249	8.45E-19	54.70%	0.12	IPR000242 (PFAM); G3DSA:2.170.300.10 (GENE3D); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000242 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)
547	c149674_g1_i1_len_356_path_1_0_355_3	7	low quality protein: myosin heavy muscle	119	1.71E-64	92.70%	0.103	Coil (COILS); Coil (COILS); IPR002928 (PFAM); PTHR13140 (PANTHER); PTHR13140:SF332 (PANTHER); SSF90257 (SUPERFAMILY)
548	c149677_g1_i1_len_373_path_1_0_372_1	4	reelin- partial	124	6.55E-26	59.70%	0.105	PTHR11841 (PANTHER)
549	c149808_g1_i1_len_1530_path_1508_0_1529_0	60	ga-binding protein subunit beta-2	510	8.15E-99	56.70%	0.538Y	Coil (COILS); IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24193:SF73 (PANTHER); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR020683 (SUPERFAMILY)

550	c14985_g1_i1_len_1031_path_1009_0_629_1_639_630_1030_5	49	n-alpha-acetyltransferase auxiliary subunit	343	6.94E-123	68.10%	0.112	IPR011990 (G3DSA:1.25.40.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR22767:SF3 (PANTHER); PTHR22767 (PANTHER); IPR013026 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY)
551	c149861_g1_i1_len_373_path_1_0_372_4	39	alpha-carbonic anhydrase	124	5.21E-35	65.20%	0.143	IPR001148 (SMART); IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); IPR023561 (PANTHER); PTHR18952:SF92 (PANTHER); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
552	c149863_g1_i1_len_591_path_32_0_590_5	30	homeotic protein spalt-major-like isoform x2	197	1.32E-59	60.10%	0.325	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR23233:SF51 (PANTHER); PTHR23233 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
553	c149870_g1_i1_len_869_path_1_0_868_1	17	gastrula zinc finger	290	4.23E-148	66.00%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
554	c149954_g1_i1_len_543_path_521_0_542_2	22	arylsulfatase b	181	6.30E-39	56.90%	0.098	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); PTHR10342:SF196 (PANTHER); PTHR10342 (PANTHER); IPR017850 (SUPERFAMILY)
555	c150145_g1_i1_len_471_path_1_0_470_1	12	probable flavin-containing monoamine oxidase a	157	5.16E-51	71.60%	0.17	G3DSA:1.10.405.10 (GENE3D); G3DSA:3.50.50.60 (GENE3D); PF13450 (PFAM); PTHR10742 (PANTHER); PTHR10742:SF217 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
556	c15023_g1_i1_len_169_path_1_0_168_0	2	type-2 ice-structuring isoform x2	57	4.19E-07	57.50%	0.103	IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
557	c150262_g1_i1_len_308_path_1_0_307_3	4	upf0454 protein c12orf49 homolog	103	6.09E-34	68.80%	0.517Y	IPR019352 (PFAM); IPR019352 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-TM (SIGNALP_EUK); TMhelix (TMHMM)
558	c150386_g1_i1_len_385_path_363_0_384_5	6	zinc finger protein 225	128	3.27E-31	61.20%	0.111	IPR015880 (SMART); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
559	c150418_g1_i1_len_361_path_1_0_360_3	7	von willebrand factor type egf and pentraxin domain-containing protein 1 isoform x1	121	4.59E-40	72.00%	0.116	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); PTHR19325:SF340 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
560	c150530_g1_i1_len_462_path_1_0_461_1	10	lysosomal pro-x carboxypeptidase	154	2.07E-69	78.00%	0.101	IPR029058 (G3DSA:3.40.50.GENE3D); IPR008758 (PFAM); IPR008758 (PANTHER); PTHR11010:SF11 (PANTHER); IPR029058 (SUPERFAMILY)
561	c150632_g1_i1_len_534_path_1_0_77_79_78_305_79_306_533_4	10	ubiquitin (ribosomal protein l40)	178	5.88E-100	90.60%	0.128	IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666 (PANTHER); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY)

562	c15064_g1_i1_len_497_path_607_0_496_4	15	aael017480- partial	166	2.02E-27	56.40%	0.27	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
563	c150793_g1_i1_len_776_path_754_0_775_1	18	glycoprotein-n-acetylgalactosamine 3-beta-galactosyltransferase 1	259	8.70E-93	75.10%	0.1	IPR003378 (PFAM); PTHR23033 (PANTHER)
566	c1508_g1_i1_len_913_path_891_0_912_2	48	sortilin-related receptor-like	304	2.55E-115	71.30%	0.121	IPR006581 (SMART); G3DSA:2.130.10.140 (GENE3D); IPR002860 (PFAM); PTHR12106:SF7 (PANTHER); PTHR12106 (PANTHER); SSF110296 (SUPERFAMILY)
564	c150868_g1_i1_len_492_path_470_0_491_4	11	receptor-type tyrosine-protein phosphatase v-like	164	1.32E-09	64.70%	0.203	IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)
565	c150892_g1_i1_len_850_path_864_0_849_1	24	xanthine dehydrogenase isoform x1	283	1.54E-119	76.30%	0.106	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR008274 (SUPERFAMILY)
567	c150943_g1_i1_len_584_path_562_0_583_3	10	gamma-glutamyltransferase 7	195	5.69E-32	67.00%	0.201	IPR000101 (PRINTS); IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF18 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029055 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
568	c150946_g1_i1_len_914_path_892_0_913_1	18	vascular endothelial growth factor receptor 1	305	4.51E-33	46.40%	0.113	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR10489:SF518 (PANTHER); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
569	c15106_g2_i1_len_580_path_558_0_579_0	9	zinc finger protein 729- partial	194	2.58E-24	57.20%	0.098	IPR015880 (SMART); PF13912 (PFAM); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
570	c151081_g1_i1_len_826_path_804_0_825_2	66	insulin-like growth factor-binding protein 7 precursor	275	4.97E-74	58.90%	0.544Y	IPR000867 (SMART); IPR003598 (SMART); IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR013098 (PFAM); IPR000867 (PFAM); IPR002350 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR011390 (PANTHER); PTHR14186:SF9 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR002350 (PROSITE_PROFILES); IPR000867 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); SSF100895 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR009030 (SUPERFAMILY)
571	c15117_g3_i1_len_639_path_617_0_638_4	25	---NA---	213			0.149	TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
572	c151198_g1_i1_len_945_path_1_0_944_1	38	lachesin	315	6.82E-139	81.00%	0.374Y	IPR013106 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR016243 (PIRSF); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR19831:SF43 (PANTHER); PTHR19831 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
573	c151330_g1_i1_len_385_path_1_0_384_1	9	collagen alpha-5 chain	128	9.60E-18	58.20%	0.099	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF379 (PANTHER)
574	c151391_g1_i1_len_806_path_1_0_805_1	33	folistatin-related protein 5-like	269	1.32E-160	88.30%	0.121	PTHR10913 (PANTHER); PTHR10913:SF14 (PANTHER)

575	c151443_g1_i1_len_477_path_455_0_476_0	24	heat shock 70 kda protein 14	159	1.95E-31	54.90%	0.125	IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF158 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
576	c151594_g1_i1_len_510_path_1_0_509_3	12	zinc finger protein 777- partial	170	1.25E-13	73.90%	0.122	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
577	c151693_g1_i1_len_1188_path_1166_0_1187_1	22	protein flightless-1	396	0	86.20%	0.102	Coil (COILS); IPR007122 (PRINTS); IPR007122 (SMART); IPR001611 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029919 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF52058 (SUPERFAMILY)
578	c151706_g1_i1_len_260_path_1_0_259_2	7	carboxypeptidase b-like	86	8.08E-28	76.20%	0.125	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
579	c151866_g1_i1_len_761_path_12_0_760_0	19	apolipophorin precursor	254	5.73E-41	51.60%	0.111	IPR014853 (SMART); IPR001846 (PFAM); IPR014853 (PFAM); PTHR23361 (PANTHER); PTHR23361:SF13 (PANTHER); IPR001846 (PROSITE_PROFILES)
580	c151873_g1_i1_len_261_path_1_0_260_4	6	adamts-like protein 4 isoform x1	87	4.05E-31	57.20%	0.119	IPR000884 (SMART); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); PTHR13723 (PANTHER); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
581	c15193_g1_i1_len_393_path_371_0_392_5	9	serine threonine-protein kinase 17b-like	131	2.78E-39	82.20%	0.411Y	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24342 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
582	c15193_g2_i1_len_177_path_895_0_176_4	2	serine threonine-protein kinase 17a-like	59	2.18E-28	94.00%	0.101	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24342 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
583	c151946_g1_i1_len_572_path_1_0_571_4	9	low quality protein: zinc finger protein 233	191	5.90E-47	69.20%	0.165	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
584	c151970_g1_i1_len_449_path_1_0_448_3	8	cytokine receptor	150	7.49E-39	69.60%	0.113	IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
585	c151998_g1_i1_len_442_path_1_0_441_1	12	crustacean cardioactive peptide	147	1.67E-14	64.80%	0.102	IPR024276 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024276 (PRODOM); TMhelix (TMHMM)
586	c152186_g1_i1_len_603_path_581_0_602_5	27	gastrula zinc finger isoform x1	201	2.05E-64	68.20%	0.105	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
587	c15222_g1_i1_len_3156_path_3184_0_3155_2	356	agap000560-pa-like protein	1052	0	77.80%	0.166	IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); IPR005936 (TIGRFAM); IPR000642 (PFAM); PTHR23076 (PANTHER); PTHR23076:SF47 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005936 (HAMAP); IPR027417 (SUPERFAMILY); SSF140990 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

588	c152413_g1_i1_len_643_path_621_0_642_1	23	beta- -n-acetylgalactosaminyltransferase bre-4	214	1.78E-17	63.70%	0.099	Coil (COILS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027995 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
589	c152413_g1_i1_len_643_path_621_0_642_2	23	beta- -n-acetylgalactosaminyltransferase bre- partial	214	5.41E-16	62.00%	0.14	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
590	c15251_g2_i1_len_439_path_915_0_438_1	6	basement membrane-specific heparan sulfate proteoglycan core protein	146	4.33E-12	64.40%	0.201	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529:SF3 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
591	c152604_g1_i1_len_371_path_1_0_370_4	6	transforming growth factor-beta-induced protein ig-h3-like	124	1.07E-10	60.40%	0.581Y	IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900 (PANTHER); IPR000782 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR000782 (SUPERFAMILY)
592	c15261_g1_i1_len_157_path_135_0_156_3	3	laminin subunit alpha	53	1.58E-16	78.40%	0.102	IPR002049 (SMART); IPR002049 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR10574 (PANTHER); PTHR10574:SF39 (PANTHER); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
593	c152630_g1_i1_len_378_path_1_0_377_0	34	blastula protease 10-like	126	3.03E-16	50.10%	0.104	IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
594	c152663_g1_i1_len_248_path_1_0_247_1	2	oocyte zinc finger protein xlcof22	83	6.48E-17	60.90%	0.097	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
595	c152721_g1_i1_len_302_path_280_0_301_0	13	xanthine dehydrogenase isoform x1	101	2.28E-26	74.30%	0.098	IPR000674 (PFAM); IPR000674 (G3DSA:3.90.1170.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR000674 (SUPERFAMILY)
596	c152800_g1_i1_len_630_path_608_0_629_0	12	ring finger and spry domain-containing protein 1-like	210	2.61E-108	82.30%	0.127	PTHR13363 (PANTHER); IPR016024 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
597	c152840_g1_i1_len_327_path_1_0_326_5	6	xdh protein	109	6.80E-21	61.60%	0.103	IPR000674 (SMART); IPR000674 (PFAM); IPR000674 (G3DSA:3.90.1170.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF65 (PANTHER); IPR000674 (SUPERFAMILY)
598	c152885_g1_i1_len_468_path_446_0_467_5	11	#NAME?	156	3.61E-74	83.90%	0.131	G3DSA:3.40.50.2000 (GENE3D); IPR001830 (PFAM); PTHR10788 (PANTHER); PTHR10788:SF6 (PANTHER); SSF53756 (SUPERFAMILY)
599	c152888_g1_i1_len_366_path_344_0_365_1	6	zinc finger protein 850-like	122	2.41E-18	55.00%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
600	c15291_g1_i1_len_794_path_628_0_627_155_1_628_793_4	24	sortilin-related I(dlr class) a repeats-containing-like isoform x2	265	2.16E-17	55.40%	0.278	Coil (COILS); Coil (COILS); IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
601	c152964_g1_i1_len_429_path_1_0_428_3	9	alpha platelet-derived growth factor receptor	143	2.84E-19	46.60%	0.111	PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); SSF48726 (SUPERFAMILY)
602	c153145_g1_i1_len_648_path_626_0_647_3	11	glyceraldehyde-3-phosphate dehydrogenase	216	2.97E-137	92.60%	0.102	IPR020831 (PRINTS); IPR020828 (SMART); IPR020828 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020829 (PFAM); G3DSA:3.30.360.10 (GENE3D); IPR020831 (PANTHER); IPR020830 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY); SSF55347 (SUPERFAMILY)
603	c153149_g1_i1_len_276_path_1_0_275_3	6	---NA---	92			0.576Y	IPR012674 (G3DSA:2.40.128.GENE3D); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-TM (SIGNALP_EUK); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)

604	c153194_g1_i1_len_461_path_51_0_460_4	8	zinc finger protein 420-like	154	3.02E-30	61.20%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
605	c153235_g1_i1_len_470_path_1_0_469_4	7	a disintegrin and metalloproteinase with thrombospondin motifs 3-like	157	6.49E-65	69.00%	0.126	PR01705 (PRINTS); IPR000884 (SMART); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); PTHR13723 (PANTHER); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY)
606	c153266_g1_i1_len_397_path_375_0_396_1	5	cysteine-rich motor neuron 1 protein	132	1.76E-09	54.90%	0.157	SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TMhelix (TMHMM)
607	c153609_g1_i1_len_629_path_607_0_628_4	22	basement membrane-specific heparan sulfate proteoglycan core isoform x2	210	3.30E-93	78.50%	0.102	IPR013106 (SMART); IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013106 (PFAM); PF13895 (PFAM); PTHR23279 (PANTHER); PTHR23279:SF6 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
608	c153785_g1_i1_len_492_path_470_0_491_2	12	group xv phospholipase a2-like	164	2.20E-59	70.20%	0.119	IPR003386 (PFAM); PTHR11440 (PANTHER); PTHR11440:SF47 (PANTHER); IPR029058 (SUPERFAMILY)
609	c153924_g1_i1_len_552_path_600_0_551_4	10	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	184	5.00E-23	55.60%	0.121	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
611	c15396_g1_i1_len_991_path_1_0_990_1	262	sulfakinin-like peptide	330	8.48E-16	65.70%	0.205	IPR013152 (PROSITE_PATTERNS); IPR013152 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
610	c153960_g1_i1_len_509_path_1_0_508_2	19	serine beta-lactamase-like protein mitochondrial isoform x2	169	1.01E-57	74.40%	0.107	Coil (COILS); IPR001466 (PFAM); IPR012338 (G3DSA:3.40.710.GENE3D); PTHR22935 (PANTHER); PTHR22935:SF64 (PANTHER); IPR012338 (SUPERFAMILY)
612	c154126_g1_i1_len_400_path_378_0_399_1	19	collagen alpha-5 chain	133	9.03E-12	66.10%	0.131	IPR008160 (PFAM); PTHR24023:SF381 (PANTHER); PTHR24023 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
613	c154126_g1_i1_len_400_path_378_0_399_4	19	signal recognition protein	133	1.19E-07	54.00%	0.122	no IPS match
615	c1543_g1_i1_len_923_path_45_0_278_323_2_79_548_44_549_922_4	17	protein partial	308	8.80E-68	77.10%	0.106	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); IPR016313 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
616	c1543_g1_i2_len_653_path_45_0_278_44_27_9_652_4	11	low quality protein: protein lap4-like	218	5.86E-39	79.80%	0.106	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); IPR016313 (PANTHER); PTHR23119:SF28 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
614	c154383_g1_i1_len_347_path_1_0_346_2	6	collagen alpha-1 chain	115	4.32E-07	52.90%	0.103	IPR008160 (PFAM); PTHR24023 (PANTHER)
617	c154455_g1_i1_len_410_path_1_0_409_5	12	granzyme c	136	1.26E-23	61.10%	0.105	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
618	c154766_g1_i1_len_289_path_1_0_288_4	4	beta- -n-acetylgalactosaminyltransferase bre-4	96	3.66E-40	78.60%	0.104	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
619	c154852_g1_i1_len_421_path_399_0_420_3	7	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	141	5.34E-18	63.20%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

620	c155425_g1_i1_len_352_path_330_0_351_2	5	zinc finger protein 431 isoform x2	117	4.88E-13	64.50%	0.126	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
621	c155528_g1_i1_len_591_path_569_0_590_1	9	epidermal growth factor receptor isoform x1	197	9.42E-105	87.40%	0.121	IPR006212 (SMART); IPR006211 (PFAM); G3DSA:2.10.220.10 (GENE3D); G3DSA:2.10.220.10 (GENE3D); IPR000494 (G3DSA:3.80.20.GENE3D); IPR000494 (PFAM); PTHR24416:SF95 (PANTHER); PTHR24416 (PANTHER); IPR009030 (SUPERFAMILY); SSF52058 (SUPERFAMILY)
622	c155529_g1_i1_len_587_path_565_0_586_1	10	serine protease snake	196	7.01E-26	52.50%	0.459 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
623	c155596_g1_i1_len_568_path_1_0_567_4	7	zinc finger protein 629- partial	189	2.33E-13	62.40%	0.096	IPR015880 (SMART); PF13912 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
624	c155823_g1_i1_len_542_path_1_0_541_1	12	zinc finger protein 699-like	181	2.73E-31	56.70%	0.103	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
625	c155929_g1_i1_len_510_path_488_0_509_2	17	carboxypeptidase pm20d1	170	1.19E-11	80.30%	0.108	G3DSA:3.40.630.10 (GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
626	c155979_g1_i1_len_481_path_459_0_480_0	9	tyramine beta-hydroxylase	161	2.64E-66	75.30%	0.164	IPR014784 (G3DSA:2.60.120.GENE3D); PF03712 (PFAM); IPR000945 (PANTHER); IPR028460 (PTHR10157:PANTHER); IPR008977 (SUPERFAMILY)
627	c155999_g1_i1_len_263_path_241_0_262_1	10	5 -nucleotidase-like	88	4.26E-21	70.20%	0.162	IPR029052 (G3DSA:3.60.21.GENE3D); IPR006179 (PANTHER); PTHR11575:SF21 (PANTHER); IPR006146 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
628	c156237_g1_i1_len_434_path_1_0_433_1	7	a disintegrin and metalloproteinase with thrombospondin motifs partial	145	3.04E-22	59.40%	0.137	IPR024079 (G3DSA:3.40.390.GENE3D); PTHR13723:SF160 (PANTHER); PTHR13723 (PANTHER); IPR001590 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY)
629	c156465_g1_i1_len_324_path_302_0_323_4	7	arylsulfatase d	108	1.72E-20	58.60%	0.124	PF14707 (PFAM); G3DSA:3.30.1120.10 (GENE3D); PTHR10342 (PANTHER); PTHR10342:SF200 (PANTHER); IPR017850 (SUPERFAMILY)
630	c1565_g1_i1_len_1380_path_1_0_46_48_47_1379_2	88	zinc finger protein zpr1	460	2.35E-177	73.70%	0.185	IPR004457 (SMART); IPR004457 (TIGRFAM); IPR004457 (PFAM); PTHR10876:SF0 (PANTHER); PTHR10876 (PANTHER)
631	c1565_g1_i2_len_1372_path_1445_0_38_48_39_1371_0	91	zinc finger protein zpr1	458	1.25E-177	73.80%	0.126	IPR004457 (SMART); IPR004457 (TIGRFAM); IPR004457 (PFAM); PTHR10876 (PANTHER); PTHR10876:SF0 (PANTHER)
632	c1566_g1_i1_len_2494_path_3057_0_532_35_89_533_2493_0	171	von willebrand factor a domain-containing protein partial	832	0	65.50%	0.117	PTHR21610 (PANTHER); PTHR21610:SF9 (PANTHER)
633	c1566_g1_i2_len_825_path_3057_0_532_25_533_824_0	47	von willebrand factor a domain-containing protein 8-like	275	2.71E-84	86.00%	0.117	PTHR21610:SF9 (PANTHER); PTHR21610 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
634	c156720_g1_i1_len_641_path_1_0_640_3	10	fibroblast growth factor receptor-like 1	214	1.34E-40	59.70%	0.098	IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19890 (PANTHER); PTHR19890:SF5 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
635	c156724_g1_i1_len_280_path_258_0_279_2	4	hemocentin-1-like	93	3.32E-14	59.10%	0.128	IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)

636	c156732_g1_i1_len_537_path_515_0_536_2	16	complement c1q tumor necrosis factor-related protein 2	179	1.44E-27	61.50%	0.624Y	IPR001073 (PRINTS); IPR001073 (SMART); IPR001073 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); PTHR22923 (PANTHER); PTHR22923:SF51 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001073 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR008983 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
637	c156886_g1_i1_len_321_path_1_0_320_3	7	guanine nucleotide-binding protein subunit beta-5	107	1.56E-62	93.70%	0.123	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19850:SF12 (PANTHER); IPR016346 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
638	c156990_g1_i1_len_249_path_1_0_248_4	4	tsa family protein	83	4.89E-27	78.10%	0.137	IPR000866 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10681:SF101 (PANTHER); PTHR10681 (PANTHER); IPR012336 (SUPERFAMILY)
639	c157041_g1_i1_len_371_path_349_0_370_1	27	14-3-3 protein	124	1.39E-58	85.90%	0.103	IPR000308 (PRINTS); IPR023410 (SMART); IPR023410 (PFAM); G3DSA:1.20.190.20 (GENE3D); IPR000308 (PANTHER); IPR023410 (SUPERFAMILY)
640	c157058_g1_i1_len_474_path_1_0_473_3	6	protein disulfide-isomerase a6-like	158	9.49E-22	52.70%	0.101	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
641	c15706_g1_i1_len_2510_path_2587_0_2509_0	543265	hemocyanin subunit type 2 precursor	837	0	73.10%	0.332	IPR013788 (PRINTS); IPR000896 (PFAM); IPR005203 (PFAM); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005204 (PFAM); IPR005203 (G3DSA:2.60.40.GENE3D); IPR013788 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR002227 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005204 (SUPERFAMILY); IPR008922 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
642	c157101_g1_i1_len_322_path_1_0_321_0	8	enolase 2-like	108	4.26E-43	81.20%	0.108	IPR000941 (PRINTS); IPR020810 (PFAM); IPR029065 (G3DSA:3.20.20.GENE3D); IPR000941 (PANTHER); IPR029065 (SUPERFAMILY)
643	c157129_g1_i1_len_717_path_695_0_716_3	46	low-density lipoprotein receptor-related protein 2	239	1.87E-39	57.10%	0.104	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
644	c157258_g1_i1_len_440_path_418_0_439_4	12	gastrula zinc finger	147	3.61E-52	69.10%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
645	c157272_g1_i1_len_413_path_1_0_412_1	6	zinc finger protein 705a-like isoform x1	138	1.03E-17	51.20%	0.099	IPR015880 (SMART); G3DSA:3.30.60.20 (GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
646	c157401_g1_i1_len_269_path_1_0_268_3	4	semaphorin-1a	90	3.17E-41	87.00%	0.111	IPR001627 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR11036:SF66 (PANTHER); IPR027231 (PANTHER); IPR001627 (PROSITE_PROFILES); IPR001627 (SUPERFAMILY)
647	c157484_g1_i1_len_260_path_1_0_259_0	5	iron zinc purple acid phosphatase-like isoform x1	87	1.21E-32	75.80%	0.099	IPR015914 (G3DSA:2.60.40.GENE3D); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); IPR008963 (SUPERFAMILY)

648	c157751_g1_i1_len_511_path_489_0_510_1	8	cell division protein kinase 5	170	9.75E-119	99.10%	0.101	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24056 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
649	c157968_g1_i1_len_511_path_489_0_510_1	12	tyrosine-protein phosphatase 69d	170	5.52E-82	84.80%	0.102	IPR000242 (PRINTS); IPR000242 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134:SF277 (PANTHER); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
650	c158058_g1_i1_len_262_path_240_0_261_1	6	wd repeat-containing protein 33	87	8.03E-47	92.10%	0.102	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22836 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
651	c158154_g1_i1_len_587_path_569_0_586_2	20	myostatin	195	2.54E-76	84.70%	0.464Y	IPR001839 (SMART); IPR001839 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); IPR015615 (PANTHER); IPR015616 (PTHR11848:PANTHER); IPR017948 (PROSITE_PATTERNS); IPR001839 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR029034 (SUPERFAMILY)
652	c158168_g1_i1_len_260_path_238_0_259_0	4	low quality protein: matrilin-4	87	1.28E-06	61.33%	0.104	IPR001881 (SMART); PF14670 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY)
653	c158233_g1_i1_len_201_path_179_0_200_1	1	---NA---	67			0.411Y	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
654	c158245_g1_i1_len_386_path_1_0_385_5	3	cyclin-dependent kinase-like partial	128	5.63E-40	90.20%	0.125	IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24056:SF153 (PANTHER); PTHR24056 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
655	c158358_g1_i1_len_688_path_666_0_687_0	18	adam 17-like protease	230	2.34E-67	70.20%	0.214	IPR002870 (PFAM); PTHR11905:SF121 (PANTHER); PTHR11905 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
656	c158504_g1_i1_len_402_path_1_0_401_0	5	proclotting enzyme	134	2.16E-08	77.30%	0.184	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
657	c158730_g1_i1_len_638_path_616_0_637_2	21	venom protease-like	212	3.12E-54	61.40%	0.147	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
658	c158838_g1_i1_len_373_path_1_0_372_1	9	microtubule-associated serine threonine-protein kinase 3 isoform x1	124	4.66E-78	95.50%	0.126	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24356 (PANTHER); PTHR24356:SF36 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
659	c15885_g1_i1_len_1404_path_333_0_859_11_92_860_964_332_965_1403_4	70	serine proteinase	468	2.79E-71	56.70%	0.278	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF81 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
660	c15885_g1_i2_len_1440_path_333_0_859_19_1_860_1000_332_1001_1439_4	76	venom protease-like	480	7.01E-71	55.40%	0.278	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
661	c158907_g1_i1_len_313_path_1_0_312_0	4	endonuclease mitochondrial	105	6.06E-52	84.10%	0.1	IPR020821 (SMART); IPR020821 (G3DSA:3.40.570.GENE3D); IPR001604 (PFAM); PTHR13966 (PANTHER); SSF54060 (SUPERFAMILY)
662	c158913_g1_i1_len_278_path_1_0_277_4	8	hemacentin-1-like protein	93	1.12E-25	66.00%	0.11	G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR026823 (PFAM); PTHR24034:SF33 (PANTHER); PTHR24034 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY)
663	c158919_g1_i1_len_332_path_1_0_331_4	4	fat-like cadherin-related tumor suppressor-like protein	111	1.90E-44	82.50%	0.142	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24026:SF39 (PANTHER); PTHR24026 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY)
664	c15893_g2_i1_len_138_path_312_0_137_1	0	t-cell immunomodulatory protein	46	5.99E-06	67.00%	0.105	no IPS match

665	c158946_g1_i1_len_243_path_221_0_242_3	7	neutral endopeptidase	81	1.02E-23	72.00%	0.113	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); PTHR11733:SF113 (PANTHER); IPR000718 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
666	c159006_g1_i1_len_523_path_1_0_522_2	8	serine threonine-protein kinase partial	174	5.49E-81	83.10%	0.113	IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR23257:SF63 (PANTHER); PTHR23257 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
667	c159461_g1_i1_len_519_path_1_0_518_2	11	gastrula zinc finger	173	1.71E-35	59.50%	0.099	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
668	c159700_g1_i1_len_150_path_128_0_149_3	3	blastula protease 10-like	50	2.99E-11	70.80%	0.106	IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); PTHR10127:SF580 (PANTHER); SSF55486 (SUPERFAMILY)
669	c159989_g1_i1_len_422_path_1_0_421_2	8	fibrillin-2 isoform x3	140	1.82E-49	73.90%	0.099	IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR026823 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); PF14670 (PFAM); PTHR24034 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
670	c160259_g1_i1_len_746_path_1_0_745_3	15	ras-responsive element-binding protein 1	249	1.79E-55	57.60%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR23233:SF42 (PANTHER); PTHR23233 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
671	c160268_g1_i1_len_482_path_1_0_481_3	14	wd sam and u-box domain-containing protein 1-like isoform x2	161	5.25E-35	63.60%	0.119	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
672	c160415_g1_i1_len_357_path_1_0_356_3	8	zinc finger protein 160-like	119	1.09E-24	64.60%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
673	c160718_g1_i1_len_152_path_1_0_151_1	20	cathepsin I	51	1.99E-20	92.20%	0.099	IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF57 (PANTHER); IPR013128 (PANTHER); SSF54001 (SUPERFAMILY)
674	c160855_g1_i1_len_139_path_1_0_138_4	0	pdz domain-containing protein 2	46	7.72E-17	88.20%	0.136	IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964 (PANTHER); PTHR19964:SF22 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
675	c161216_g1_i1_len_276_path_1_0_275_4	4	carbonyl reductase	92	7.46E-33	79.60%	0.1	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF58 (PANTHER); SSF51735 (SUPERFAMILY)
676	c161385_g1_i1_len_542_path_1_0_541_2	21	gilt-like protein	180	1.40E-30	63.50%	0.133	IPR004911 (PFAM); PTHR13234:SF8 (PANTHER); IPR004911 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
677	c161429_g1_i1_len_341_path_319_0_340_0	4	transposase	114	2.11E-12	53.00%	0.108	no IPS match

678	c1616_g1_i1_len_1652_path_1_0_1651_3	224	di-n-acetylchitobiase	551	2.82E-114	63.00%	0.881Y	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF146 (PANTHER); PTHR11177 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
679	c1618_g1_i1_len_1780_path_1_0_1779_4	187	secreted frizzled-related protein 5	593	2.47E-116	63.80%	0.105	Coil (COILS); IPR020067 (SMART); IPR018933 (PFAM); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR020067 (PFAM); IPR015526 (PANTHER); PTHR11309:SF80 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020067 (PROSITE_PROFILES); IPR001134 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY); IPR020067 (SUPERFAMILY); TMhelix (TMHMM)
680	c162416_g1_i1_len_283_path_261_0_282_1	4	nadph--cytochrome p450 reductase	94	7.36E-56	96.50%	0.103	IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24305:SF21 (PANTHER); PTHR24305 (PANTHER); IPR001128 (SUPERFAMILY)
681	c162748_g1_i1_len_472_path_1_0_471_3	7	thrombospondin type-1 domain-containing protein 4-like	158	7.49E-16	60.40%	0.112	IPR000884 (SUPERFAMILY)
682	c162826_g1_i1_len_277_path_1_0_276_0	2	collagen alpha-1 chain	93	3.79E-12	61.50%	0.1	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF372 (PANTHER)
683	c162898_g1_i1_len_280_path_258_0_279_0	4	nad h-hydrate epimerase isoform x1	94	1.00E-41	82.20%	0.164	IPR004443 (G3DSA:3.40.50.GENE3D); IPR004443 (PFAM); PTHR13232:SF11 (PANTHER); PTHR13232 (PANTHER); IPR004443 (PROSITE_PROFILES); IPR004443 (SUPERFAMILY)
684	c163161_g1_i1_len_257_path_235_0_256_2	4	moxd1 homolog 1-like	85	1.97E-06	68.00%	0.155	PF03712 (PFAM); IPR014784 (G3DSA:2.60.120.GENE3D); IPR008977 (SUPERFAMILY)
685	c1636_g1_i1_len_540_path_1_0_539_3	10	tyrosine-protein phosphatase non-receptor type 9 isoform x6	180	3.87E-77	81.70%	0.106	IPR000242 (PRINTS); IPR000242 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134:SF232 (PANTHER); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
686	c164763_g1_i1_len_392_path_1_0_391_0	17	maguk p55 subfamily member 5	131	4.98E-72	92.00%	0.107	Coil (COILS); Coil (COILS); IPR008145 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR008145 (PFAM); PTHR23122 (PANTHER); PTHR23122:SF32 (PANTHER); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
687	c164825_g1_i1_len_436_path_414_0_435_2	6	von willebrand factor type egf and pentraxin domain-containing protein 1- partial	145	3.07E-69	83.80%	0.119	IPR003410 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR24049:SF6 (PANTHER); PTHR24049 (PANTHER); IPR003410 (PROSITE_PROFILES)
688	c165078_g1_i1_len_370_path_1_0_369_2	10	#NAME?	123	6.61E-25	83.40%	0.177	Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24077 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
689	c165124_g1_i1_len_268_path_246_0_267_4	4	zinc finger protein 567 isoform x2	89	1.44E-46	87.50%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR23228 (PANTHER); PTHR23228:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
690	c16540_g1_i1_len_2213_path_43_0_173_21_174_2212_2	183	extracellular serine threonine protein kinase fam20c isoform x1	737	0	71.70%	0.15	IPR009581 (PFAM); PTHR12450:SF8 (PANTHER); IPR024869 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
691	c16589_g1_i1_len_1362_path_1390_0_1361_5	58	isoform b	454	2.12E-107	64.90%	0.101	IPR015812 (PRINTS); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR014836 (G3DSA:1.20.5.GENE3D); IPR014836 (PFAM); G3DSA:1.20.5.100 (GENE3D); IPR015812 (PANTHER); PTHR10082:SF16 (PANTHER); IPR015812 (PROSITE_PATTERNS); IPR015812 (PROSITE_PATTERNS); IPR015812 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF57196 (SUPERFAMILY); IPR012896 (SUPERFAMILY); TMhelix (TMHMM)
692	c166729_g1_i1_len_248_path_1_0_247_0	6	carboxypeptidase n subunit 2	83	1.19E-11	62.50%	0.106	IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); SSF52058 (SUPERFAMILY)
693	c166983_g1_i1_len_253_path_231_0_252_5	4	chaperone protein	84	2.88E-25	86.10%	0.154	IPR013126 (PRINTS); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF173 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)

694	c16699_g1_i1_len_2273_path_2301_0_2272_2	297	serine threonine-protein kinase grp-like	757	0	74.50%	0.173	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24344 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
695	c167229_g1_i1_len_380_path_358_0_379_4	5	kinase d-interacting substrate of 220 kda isoform x7	127	1.34E-63	87.70%	0.105	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24139 (PANTHER); PTHR24139:SF10 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
696	c16754_g1_i1_len_2135_path_2163_0_2134_4	146	leucine rich repeat protein	712	5.73E-36	53.10%	0.505 Y	PR00019 (PRINTS); IPR003591 (SMART); SM00364 (SMART); SM00365 (SMART); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF52058 (SUPERFAMILY); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
697	c167603_g1_i1_len_189_path_1_0_188_3	0	zinc finger protein 717-like	63	8.92E-11	66.20%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
698	c169380_g1_i1_len_278_path_256_0_277_1	2	vitellogenin-1-like isoform x2	93	1.10E-09	56.75%	0.311	IPR001747 (PFAM); IPR015816 (G3DSA:2.30.230.GENE3D); IPR015819 (SUPERFAMILY)
699	c170238_g1_i1_len_890_path_1_0_889_2	22	variable lymphocyte receptor a	296	1.01E-09	51.00%	0.114	SM00364 (SMART); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
700	c170248_g1_i1_len_1471_path_1_0_1470_4	84	transducin beta-like protein 3	490	6.78E-107	76.10%	0.209	Coil (COILS); Coil (COILS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR013934 (PFAM); PTHR19854 (PANTHER); PTHR19854:SF15 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
701	c170250_g1_i1_len_1648_path_1_0_1647_2	941	ras-related protein rab-10	549	3.99E-116	92.90%	0.173	IPR001806 (PRINTS); IPR003579 (SMART); IPR003578 (SMART); IPR002041 (SMART); IPR024156 (SMART); IPR020849 (SMART); IPR001806 (PFAM); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR24073:SF456 (PANTHER); PTHR24073 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
702	c170269_g1_i1_len_693_path_671_0_692_5	36	vitellogenic-like precursor	231	6.80E-67	67.00%	0.16	IPR001563 (PRINTS); IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
703	c170278_g1_i1_len_1317_path_1_0_1316_1	56	dual specificity mitogen-activated protein kinase kinase dsor1	439	0	85.60%	0.104	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24360:SF15 (PANTHER); PTHR24360 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
704	c170303_g1_i1_len_467_path_1_0_466_3	7	fras1-related extracellular matrix protein 1-like	156	2.15E-07	57.00%	0.126	SSF141072 (SUPERFAMILY)

[illegible]

716	c170789_g1_i1_len_1683_path_987_0_288_1_276_289_985_1276_986_1682_4	128	protein phosphatase 1 regulatory subunit 16a	561	8.47E-61	60.30%	0.196	Coil (COILS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24186 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
717	c170826_g1_i1_len_522_path_500_0_521_4	10	fat-like cadherin-related tumor suppressor homolog	174	1.87E-66	73.30%	0.128	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); PTHR24027:SF260 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
718	c170831_g1_i1_len_455_path_1_0_454_5	14	glutamyl aminopeptidase	151	5.99E-14	53.40%	0.164	IPR024571 (PFAM); PTHR11533:SF165 (PANTHER); IPR001930 (PANTHER) IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
719	c170849_g1_i1_len_931_path_1_0_930_1	23	zinc finger protein 850-like	310	2.27E-38	57.90%	0.1	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM) IPR000998 (SMART); IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000998 (PFAM); PTHR22991 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR000859 (SUPERFAMILY); TMhelix (TMHMM)
720	c170862_g1_i1_len_471_path_1_0_470_2	8	---NA---	157			0.104	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351:SF28 (PANTHER); PTHR11351 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
721	c170906_g1_i1_len_1364_path_1342_0_1363_5	59	mam and ldl-receptor class a domain-containing protein 1-like	454	4.03E-11	42.70%	0.466 Y	IPR001548 (PRINTS); IPR001548 (PFAM); PTHR10514:SF17 (PANTHER); IPR001548 (PANTHER); SSF55486 (SUPERFAMILY)
722	c170908_g1_i1_len_1168_path_1_0_1167_3	126	acyl- delta desaturase	390	2.03E-163	76.30%	0.500Y	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24369 (PANTHER); SSF52058 (SUPERFAMILY)
723	c170910_g1_i1_len_292_path_270_0_291_1	4	angiotensin-converting enzyme-like	97	2.18E-39	81.30%	0.131	G3DSA:2.10.70.10 (GENE3D); IPR001007 (PFAM); SSF57603 (SUPERFAMILY); SSF57603 (SUPERFAMILY)
724	c170929_g1_i1_len_1119_path_1_0_1118_1	24	connectin isoform x1	373	4.19E-45	65.70%	0.127	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR017348 (PIRSF); PTHR22984 (PANTHER); PTHR22984:SF1 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
725	c170934_g1_i1_len_293_path_271_0_292_4	4	kielin chordin-like protein	98	7.87E-16	55.70%	0.111	IPR002172 (SMART); IPR002172 (PFAM); IPR000998 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR23282:SF75 (PANTHER); PTHR23282 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
726	c171102_g1_i1_len_1075_path_1_0_1074_4	103	serine threonine-protein kinase pim-3	358	1.08E-139	77.80%	0.132	
727	c171176_g1_i1_len_431_path_1_0_430_5	12	mam and ldl-receptor class a domain-containing protein 2-like	143	8.73E-30	58.90%	0.108	

728	c171277_g1_i1_len_557_path_1_0_556_3	9	slit protein	186	4.08E-92	85.60%	0.111	PR00019 (PRINTS); IPR000742 (SMART); IPR000483 (SMART); IPR003591 (SMART); IPR001611 (PFAM); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); PTHR24373 (PANTHER); PTHR24373:SF110 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR001611 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF52058 (SUPERFAMILY) IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300 (PANTHER); IPR001128 (SUPERFAMILY)
729	c171288_g1_i1_len_1299_path_1_0_1298_5	44	cytochrome p450 monooxygenase	433	3.36E-116	59.90%	0.099	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM)
730	c171314_g1_i1_len_1872_path_1_0_1871_2	114	serine threonine-protein phosphatase 6 regulatory ankyrin repeat subunit c-like	624	4.63E-96	55.00%	0.102	IPR003593 (SMART); IPR003959 (PFAM); IPR005937 (TIGRFAM); G3DSA:1.10.8.60 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23073:SF9 (PANTHER); PTHR23073 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
731	c171386_g1_i1_len_1445_path_1_0_1444_3	548	26s protease regulatory subunit 4	482	0	97.10%	0.105	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
732	c171397_g1_i1_len_693_path_671_0_692_3	25	hemagglutinin amebocyte aggregation factor-like	231	3.32E-42	61.10%	0.302	IPR001791 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR24026 (PANTHER); PTHR24026:SF39 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR001791 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
733	c171420_g1_i1_len_698_path_1_0_697_0	28	fat-like cadherin-related tumor suppressor homolog isoform x5	233	6.52E-97	77.60%	0.104	IPR002035 (G3DSA:3.40.50.GENE3D); IPR013642 (PFAM); PTHR10579 (PANTHER); PTHR10579:SF8 (PANTHER); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
734	c17148_g1_i1_len_822_path_1064_0_821_0	33	calcium-activated chloride channel regulator 2	274	2.77E-29	47.00%	0.118	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24419:SF19 (PANTHER); PTHR24419 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
735	c171613_g1_i1_len_1823_path_1_0_1822_2	68	partial	607	3.26E-116	76.80%	0.105	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325:SF340 (PANTHER); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
736	c171626_g1_i1_len_858_path_836_0_857_1	21	von willebrand factor type egf and pentraxin domain-containing protein 1	286	1.96E-95	69.90%	0.106	Coil (COILS); IPR002456 (PRINTS); PRO1176 (PRINTS); IPR017978 (PFAM); IPR002455 (PANTHER); PTHR10519:SF3 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017978 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
737	c171713_g1_i1_len_1068_path_1046_0_1067_2	38	gamma-aminobutyric acid type b receptor subunit 1	356	1.11E-164	81.60%	0.165	IPR000889 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PANTHER); IPR029760 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
738	c171731_g1_i1_len_1330_path_1308_0_1329_1	3867	low quality protein: glutathione peroxidase 3	443	3.99E-59	63.90%	0.21	no IPS match
739	c17175_g2_i1_len_238_path_466_0_237_1	2	preprotachykinin b	79	1.15E-19	62.50%	0.107	

740	c171806_g1_i1_len_979_path_1_0_978_1	415	protein them6	326	2.64E-36	58.40%	0.129	Coil (COILS); PF13279 (PFAM); IPR029069 (G3DSA:3.10.129.GENE3D); PTHR12475 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029069 (SUPERFAMILY); TMhelix (TMHMM)
741	c171832_g1_i1_len_559_path_537_0_558_5	23	short neuropeptide f	186	2.17E-22	68.60%	0.175	no IPS match
742	c171932_g1_i1_len_471_path_449_0_470_0	13	protocadherin fat 2	157	2.84E-74	83.50%	0.098	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); PTHR24026 (PANTHER); PTHR24026:SF39 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
743	c171933_g1_i1_len_350_path_328_0_349_3	6	cubilin isoform x1	117	3.26E-40	68.20%	0.11	IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
744	c172043_g1_i1_len_396_path_374_0_395_0	10	low-density lipoprotein receptor-related protein 2	132	1.37E-15	57.40%	0.115	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
745	c172057_g1_i1_len_310_path_1_0_309_4	23	heat shock cognate 71 kda	103	1.43E-49	98.00%	0.155	IPR013126 (PRINTS); G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
746	c172141_g1_i1_len_289_path_267_0_288_0	20	iron zinc purple acid phosphatase-like protein isoform x2	97	2.69E-47	89.30%	0.1	IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); IPR029052 (SUPERFAMILY)
747	c172300_g1_i1_len_569_path_534_0_520_10_55_521_532_1055_533_544_1055_545_556_1055_557_568_4	49	protoporphyrin ix magnesium chelatase	190	5.70E-11	67.50%	0.12	TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
748	c172320_g1_i1_len_700_path_1_0_699_1	183	diuretic hormone class 2-like	233	1.36E-29	73.30%	0.155	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
749	c172410_g1_i1_len_430_path_1_0_429_4	22	adp-ribosylation factor-like protein 16	143	1.62E-27	73.10%	0.26	IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF42 (PANTHER); PTHR11711 (PANTHER); IPR027417 (SUPERFAMILY)
750	c172437_g1_i1_len_1333_path_1_0_1332_2	48	eukaryotic translation initiation factor 2-alpha kinase	444	1.95E-88	67.00%	0.101	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR11042 (PANTHER); PTHR11042:SF86 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
751	c172496_g1_i1_len_701_path_1_0_700_1	25	zinc finger protein ozf-like	234	1.56E-27	56.50%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
755	c1725_g2_i1_len_1000_path_978_0_999_4	36	laccase- partial	333	1.99E-75	67.50%	0.116	IPR008972 (G3DSA:2.60.40.GENE3D); IPR008972 (G3DSA:2.60.40.GENE3D); IPR011707 (PFAM); PTHR11709:SF33 (PANTHER); PTHR11709 (PANTHER); IPR008972 (SUPERFAMILY)
752	c172505_g1_i1_len_2031_path_2009_0_2030_3	74	big brain	677	8.98E-136	61.60%	0.236	IPR000425 (PRINTS); IPR000425 (TIGRFAM); IPR023271 (G3DSA:1.20.1080.GENE3D); IPR000425 (PFAM); PTHR19139:SF85 (PANTHER); IPR000425 (PANTHER); IPR022357 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023271 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

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763	c172890_g1_i1_len_161_path_139_0_160_0	2	stromal cell-derived factor 2	54	3.04E-21	83.50%	0.099	G3DSA:2.80.10.50 (GENE3D); IPR027005 (PANTHER); IPR016093 (SUPERFAMILY)
764	c172981_g1_i1_len_1019_path_997_0_1018_2	37	nedd4 family-interacting protein 1-like	339	2.46E-82	62.20%	0.214	IPR019325 (PFAM); PTHR13396 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
765	c172999_g1_i1_len_763_path_741_0_762_2	17	spermatogenesis-associated protein partial	254	2.12E-06	72.00%	0.101	no IPS match
766	c173056_g1_i1_len_515_path_493_0_514_0	6	ankyrin repeat	172	6.46E-23	59.30%	0.231	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
767	c173088_g1_i1_len_593_path_571_0_592_1	13	ankyrin-2-like isoform x2	198	6.23E-17	54.80%	0.142	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
768	c173092_g1_i1_len_381_path_359_0_380_5	5	adenosine monophosphate-protein transferase fidd homolog	127	6.97E-61	85.80%	0.107	IPR003812 (G3DSA:1.10.3290.GENE3D); IPR003812 (PFAM); PTHR13504:SF12 (PANTHER); PTHR13504 (PANTHER); IPR003812 (PROSITE_PROFILES); IPR003812 (SUPERFAMILY)
769	c173102_g1_i1_len_694_path_672_0_693_0	18	chorion peroxidase	232	2.63E-45	74.60%	0.157	IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
770	c173186_g1_i1_len_327_path_1_0_326_0	6	serine threonine-protein kinase 17b-like	109	1.44E-52	86.10%	0.109	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24342 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
771	c173195_g1_i1_len_351_path_329_0_350_2	10	prostaglandin f synthase-like	117	3.31E-38	71.20%	0.108	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); IPR001395 (PANTHER); PTHR11732:SF133 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
772	c173214_g1_i1_len_1052_path_1_0_1051_2	40	hemicentin-1 isoform x2	350	3.92E-86	57.20%	0.105	PR01832 (PRINTS); IPR013162 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR11640:SF6 (PANTHER); PTHR11640 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
773	c173227_g1_i1_len_432_path_1_0_431_0	6	deleted in malignant brain tumors 1	144	5.48E-13	44.80%	0.103	IPR017448 (G3DSA:3.10.250.GENE3D); IPR001190 (PFAM); PTHR19331:SF253 (PANTHER); PTHR19331 (PANTHER); IPR001190 (PROSITE_PROFILES); IPR001190 (PROSITE_PROFILES); IPR017448 (SUPERFAMILY); IPR017448 (SUPERFAMILY)
774	c173280_g1_i1_len_682_path_1_0_681_1	16	hexamerin 1	227	1.47E-70	81.20%	0.101	IPR005203 (PFAM); IPR005203 (G3DSA:2.60.40.GENE3D); IPR013788 (PANTHER); PTHR11511:SF5 (PANTHER); IPR014756 (SUPERFAMILY)
775	c173288_g1_i1_len_1049_path_1_0_1048_0	36	latrophilin-3 isoform x2	350	1.86E-61	67.20%	0.411 Y	IPR000832 (PRINTS); IPR000832 (PFAM); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
776	c173362_g1_i1_len_1136_path_1114_0_1135_0	39	dbh-like monooxygenase protein partial	379	4.74E-14	50.10%	0.107	IPR014784 (G3DSA:2.60.120.GENE3D); PF03712 (PFAM); IPR000945 (PANTHER); IPR008977 (SUPERFAMILY)
779	c1735_g1_i1_len_1231_path_1209_0_1230_1	41	very low-density lipoprotein partial	410	1.94E-23	48.60%	0.205	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

780	c1735_g1_i1_len_1231_path_1209_0_1230_2	41	very low-density lipoprotein receptor-like isoform x2	410	1.13E-21	43.60%	0.102	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:4.10.1220.10 (GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
777	c17356_g1_i1_len_1327_path_1355_0_1326_3	80	lipophorin receptor	443	2.28E-98	56.60%	0.304	IPR002172 (PRINTS); IPR000742 (SMART); IPR000033 (SMART); IPR002172 (SMART); IPR001881 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000033 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009030 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
778	c173595_g1_i1_len_3140_path_1_0_3139_4	202	macrophage mannose receptor 1	1047	9.20E-20	38.50%	0.14	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803:SF55 (PANTHER); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
782	c17366_g1_i1_len_251_path_121_0_70_30_7_1_130_30_131_190_30_191_250_3	5	hypothetical protein KLMA_20728	84	7.59E-06	50.50%	0.101	no IPS match
781	c173662_g1_i1_len_270_path_248_0_269_2	4	disease resistance family protein lrr family	90	2.76E-06	60.50%	0.096	IPR025875 (PFAM); G3DSA:3.80.10.10 (GENE3D); SSF52058 (SUPERFAMILY)
783	c173689_g1_i1_len_300_path_1_0_299_4	6	beta- -n-acetylgalactosaminyltransferase bre-4	100	8.10E-56	88.40%	0.105	IPR003859 (PRINTS); IPR027791 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); PTHR19300:SF30 (PANTHER); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
784	c173820_g1_i1_len_577_path_555_0_576_0	7	achain crystal structure of engineered northeast structural genomics consortium target	193	6.31E-17	55.10%	0.121	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
785	c17401_g2_i1_len_1411_path_835_0_1410_4	61	neuropilin and tolloid-like protein 2-like	470	1.11E-126	61.00%	0.109	IPR000859 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF572 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000859 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); TMhelix (TMHMM)
786	c174047_g1_i1_len_279_path_257_0_278_0	4	transient receptor potential cation channel subfamily a member 1 homolog	93	1.57E-28	66.80%	0.103	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
787	c174091_g1_i1_len_372_path_1_0_371_2	8	c-type mbl-2 protein	124	2.08E-11	54.00%	0.137	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
788	c174119_g1_i1_len_271_path_1_0_270_5	5	tyrosine-protein phosphatase lar isoform x1	90	7.03E-34	80.70%	0.105	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19134 (PANTHER); PTHR19134:SF199 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
789	c174164_g1_i1_len_922_path_900_0_921_2	31	ankyrin repeat domain-containing protein 39	307	2.15E-53	66.80%	0.292	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24148 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)

790	c174184_g1_i1_len_764_path_742_0_763_0	24		cytokine receptor	255	4.03E-40	57.50%	0.134	IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
791	c174196_g1_i1_len_412_path_1_0_411_3	9		papain family cysteine protease	138	6.61E-45	69.10%	0.245	IPR000668 (SMART); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF15 (PANTHER); IPR013128 (PANTHER); SSF54001 (SUPERFAMILY)
792	c174268_g1_i1_len_665_path_1_0_664_2	18		centaurin-gamma 1a	221	3.76E-77	71.20%	0.164	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR001164 (PFAM); IPR020683 (PFAM); PTHR23180 (PANTHER); PTHR23180:SF229 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); SSF57863 (SUPERFAMILY)
793	c174298_g1_i1_len_1112_path_1090_0_1111_1	505		histone -like	371	2.20E-81	99.20%	0.105	IPR002119 (PRINTS); IPR002119 (SMART); IPR007125 (PFAM); IPR009072 (G3DSA:1.10.20.GENE3D); PTHR23430:SF34 (PANTHER); PTHR23430 (PANTHER); IPR002119 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009072 (SUPERFAMILY)
794	c174348_g1_i1_len_826_path_1_0_825_0	12		prophenoxidase activating factor	276	1.05E-60	62.30%	0.099	IPR001314 (PRINTS); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); PTHR24268:SF95 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
795	c174371_g1_i1_len_790_path_1_0_789_5	12		gastrula zinc finger	263	1.96E-43	57.00%	0.098	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
796	c174385_g1_i1_len_482_path_460_0_481_1	12		dnaj homolog subfamily c member 17	161	9.87E-57	77.50%	0.105	Coil (COILS); Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078:SF153 (PANTHER); PTHR24078 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
797	c174551_g1_i1_len_322_path_1_0_321_3	5		pdz domain protein	108	2.57E-41	83.10%	0.138	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR19964 (PANTHER); PTHR19964:SF22 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
798	c174674_g1_i1_len_1282_path_1260_0_1281_5	39		endo-beta- -glucanase	427	3.88E-51	49.10%	0.911Y	IPR012341 (G3DSA:1.50.10.GENE3D); IPR001701 (PFAM); PTHR22298 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR008928 (SUPERFAMILY); IPR008965 (SUPERFAMILY)
800	c17468_g1_i1_len_611_path_339_0_442_25_443_610_2	11		tequila, partial	203	3.49E-70	70.30%	0.111	IPR001190 (PRINTS); IPR017448 (SMART); IPR002172 (SMART); IPR001190 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR017448 (G3DSA:3.10.250.GENE3D); PTHR19331 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR001190 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001190 (PROSITE_PROFILES); IPR017448 (SUPERFAMILY); IPR017448 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
799	c174686_g1_i1_len_646_path_7_0_645_3	1663		protein bv8	216	2.74E-20	59.10%	0.177	G3DSA:2.10.80.10 (GENE3D)
801	c174770_g1_i1_len_3316_path_3294_0_3315_4	948		14-3-3 protein epsilon	1105	2.31E-161	95.20%	0.165	Coil (COILS); IPR000308 (PRINTS); IPR023410 (SMART); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023409 (PROSITE_PATTERNS); IPR023409 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
802	c174808_g1_i1_len_312_path_290_0_311_0	9		cytochrome p450 mitochondrial-like	104	1.79E-30	63.30%	0.133	IPR002397 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24291 (PANTHER); IPR001128 (SUPERFAMILY)

803	c174811_g1_i1_len_971_path_949_0_970_5	30	cysteine-rich with egf-like domain protein 2	323	1.91E-106	67.40%	0.289	IPR021852 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); PTHR24838:SF13 (PANTHER); PTHR24838 (PANTHER); IPR002049 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); TMhelix (TMHMM)
804	c174858_g1_i1_len_560_path_538_0_559_3	16	thrombospondin type-1 domain-containing protein 4-like	187	6.53E-40	77.10%	0.104	IPR010294 (PFAM); PTHR13723 (PANTHER)
805	c174881_g1_i1_len_155_path_133_0_154_3	1	hemicentin- partial	52	1.55E-14	73.10%	0.126	IPR023413 (G3DSA:2.40.155.GENE3D); PTHR19897:SF158 (PANTHER); PTHR19897 (PANTHER); IPR006605 (PROSITE_PROFILES); IPR009017 (SUPERFAMILY)
806	c175170_g1_i1_len_906_path_884_0_905_0	27	low quality protein: papilin-like	302	3.99E-144	81.80%	0.1	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
808	c1753_g1_i1_len_3051_path_53_0_3050_0	326	otopetrin-2-like isoform x3	1017	0	70.20%	0.139	IPR004878 (PFAM); PTHR21522:SF41 (PANTHER); IPR004878 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
807	c175323_g1_i1_len_414_path_392_0_413_2	8	zinc finger protein	138	2.93E-27	56.00%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
809	c175454_g1_i1_len_844_path_1_0_843_0	41	adp-ribosylation factor-like protein 1	272	2.63E-90	95.60%	0.104	IPR006689 (PRINTS); IPR024156 (SMART); IPR006687 (SMART); IPR005225 (TIGRFAM); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF41 (PANTHER); PTHR11711 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
810	c175481_g1_i1_len_355_path_1_0_354_0	8	fat-like cadherin-related tumor suppressor-like protein	119	6.45E-50	86.40%	0.12	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24026:SF39 (PANTHER); PTHR24026 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY)
811	c175494_g1_i1_len_1087_path_1_0_1086_0	34	phosphodiesterase i	363	7.65E-17	61.20%	0.171	IPR017849 (G3DSA:3.40.720.GENE3D); IPR002591 (PFAM); IPR024873 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY)
812	c175494_g1_i1_len_1087_path_1_0_1086_2	34	ectonucleotide pyrophosphatase phosphodiesterase family member 6	362	1.64E-60	57.00%	0.169	IPR017849 (G3DSA:3.40.720.GENE3D); IPR002591 (PFAM); IPR024873 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY)

813	c175585_g1_i1_len_534_path_1_0_533_3	10	phenoloxidase subunit a3	178	1.64E-52	66.50%	0.102	IPR013788 (PRINTS); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR000896 (PFAM); IPR013788 (PANTHER); PTHR11511:SF24 (PANTHER); IPR013788 (PROSITE PATTERNS); IPR008922 (SUPERFAMILY)
814	c175748_g1_i1_len_862_path_840_0_861_3	29	tripartite motif-containing protein 2-like isoform x5	288	2.35E-148	84.80%	0.114	IPR001258 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR24103:SF1 (PANTHER); PTHR24103 (PANTHER); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); SSF101898 (SUPERFAMILY)
815	c17588_g1_i1_len_2247_path_53_0_2246_0	120	conserved hypothetical protein	749	9.96E-139	53.70%	0.493 Y	Coil (COILS); IPR002223 (PRINTS); IPR001791 (SMART); IPR002223 (SMART); IPR002223 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10574 (PANTHER); PTHR10574:SF39 (PANTHER); IPR020901 (PROSITE PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR013320 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
816	c175929_g1_i1_len_664_path_1_0_663_4	14	protein vein	221	1.71E-57	61.40%	0.139	IPR003598 (SMART); IPR003599 (SMART); IPR000742 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR013098 (PFAM); PTHR11100 (PANTHER); IPR013032 (PROSITE PATTERNS); IPR013032 (PROSITE PATTERNS); IPR000742 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
817	c175993_g1_i1_len_902_path_880_0_901_4	32	5 -nucleotidase-like	301	9.47E-86	64.40%	0.098	IPR006179 (PRINTS); IPR008334 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); IPR008334 (G3DSA:3.90.780.GENE3D); PTHR11575:SF21 (PANTHER); IPR006179 (PANTHER); IPR008334 (SUPERFAMILY); IPR029052 (SUPERFAMILY)
818	c176038_g1_i1_len_670_path_1_0_669_2	10	zinc finger protein 121 isoform x2	223	4.42E-21	73.50%	0.2	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
819	c176069_g1_i1_len_1324_path_1_0_1323_0	71	trans- -dihydrobenzene- -diol dehydrogenase-like	442	4.87E-139	70.80%	0.206	IPR016040 (G3DSA:3.40.50.GENE3D); IPR000683 (PFAM); G3DSA:3.30.360.10 (GENE3D); IPR004104 (PFAM); PTHR22604:SF96 (PANTHER); PTHR22604 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55347 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
820	c176089_g1_i1_len_485_path_463_0_484_1	25	zinc finger protein 64	162	2.65E-59	77.80%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
821	c176113_g1_i1_len_322_path_300_0_321_0	5	low-density lipoprotein receptor-related protein 1b-like	108	1.40E-06	67.10%	0.105	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
822	c176610_g1_i1_len_416_path_394_0_415_4	12	dappu_318553-like protein	139	8.22E-32	69.30%	0.145	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
823	c176746_g1_i1_len_549_path_527_0_548_4	11	---NA---	183			0.136	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24264 (PANTHER); PTHR24264:SF9 (PANTHER); IPR009003 (SUPERFAMILY)
824	c176794_g1_i1_len_430_path_1_0_15_17_16_222_17_223_429_1	4	peptidyl-alpha-hydroxyglycine alpha-amidating lyase 1	143	3.36E-14	57.30%	0.129	IPR011042 (G3DSA:2.120.10.GENE3D); IPR001258 (PFAM); PTHR10680 (PANTHER); SSF63825 (SUPERFAMILY)
825	c177022_g1_i1_len_182_path_160_0_181_1	3	protein tanc2	61	3.92E-09	62.90%	0.098	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24181 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
826	c177338_g1_i1_len_413_path_391_0_412_2	19	calbindin isoform a	137	4.69E-87	93.20%	0.107	IPR002048 (SMART); IPR011992 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR19972 (PANTHER); IPR018247 (PROSITE PATTERNS); IPR018247 (PROSITE PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)

827	c177440_g1_i1_len_1489_path_1467_0_1488_2	81	aael005189- partial	496	7.00E-118	69.90%	0.104	IPR003112 (SMART); IPR003112 (PFAM); PTHR23192 (PANTHER); PTHR23192:SF33 (PANTHER); IPR003112 (PROSITE_PROFILES)
828	c177455_g1_i1_len_258_path_236_0_257_0	4	fibroblast growth factor receptor-like protein 1	86	1.72E-42	89.40%	0.107	IPR020635 (SMART); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24416:SF291 (PANTHER); PTHR24416 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
829	c17751_g1_i1_len_498_path_143_0_140_284_141_497_4	14	lachesin isoform x2	166	7.57E-66	75.70%	0.121	IPR003598 (SMART); IPR003599 (SMART); IPR013106 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831:SF43 (PANTHER); PTHR19831 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
830	c177703_g1_i1_len_596_path_336_0_73_410_74_334_410_335_595_3	8	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein	199	8.14E-38	57.40%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
831	c177712_g1_i1_len_350_path_1_0_349_4	8	st14a protein	117	2.12E-10	54.60%	0.163	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY) IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); PTHR24027:SF45 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
832	c177815_g1_i1_len_490_path_468_0_489_1	6	cadherin- partial	163	3.79E-55	69.50%	0.132	IPR001599 (PFAM); IPR011625 (PFAM); IPR019565 (PFAM); IPR008930 (G3DSA:1.50.10.GENE3D); PTHR11412 (PANTHER); IPR019742 (PROSITE_PATTERNS); IPR014756 (SUPERFAMILY); IPR008930 (SUPERFAMILY)
833	c178059_g1_i1_len_1423_path_1_0_1422_2	116	alpha-2-macroglobulin-like protein 1	474	2.33E-131	59.10%	0.164	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847 (PANTHER); PTHR22847:SF319 (PANTHER); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
834	c178076_g1_i1_len_313_path_291_0_312_2	4	poc1 centriolar protein homolog partial	104	1.76E-45	81.00%	0.096	IPR006101 (PRINTS); IPR013781 (G3DSA:3.20.20.GENE3D); IPR006103 (PFAM); PTHR10066:SF51 (PANTHER); PTHR10066 (PANTHER); IPR023232 (PROSITE_PATTERNS); IPR023230 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
835	c178154_g1_i1_len_532_path_510_0_531_3	18	beta-glucuronidase- partial	178	1.02E-74	75.60%	0.127	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR009003 (SUPERFAMILY)
836	c178180_g1_i1_len_344_path_322_0_343_0	5	serine protease partial	115	2.00E-06	74.00%	0.196	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529:SF204 (PANTHER); PTHR10529 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
837	c178339_g1_i1_len_405_path_383_0_404_3	10	low quality protein: sco-spondin	135	6.09E-12	54.90%	0.208	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24179 (PANTHER); PTHR24179:SF23 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
838	c178424_g1_i1_len_721_path_1_0_720_1	37	protein phosphatase 1 regulatory subunit 27	240	2.58E-61	70.60%	0.191	no IPS match
839	c17854_g1_i1_len_163_path_1_0_162_3	1	PREDICTED: uncharacterized protein CG3556	55	1.82E-17	77.40%	0.314	IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); PTHR20910 (PANTHER); IPR001424 (SUPERFAMILY)
840	c178604_g1_i1_len_527_path_1_0_526_2	10	hypothetical protein DAPPUDRAFT_192774	175	1.79E-49	63.50%	0.191	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
841	c178966_g1_i1_len_257_path_1_0_256_2	4	cubilin- partial	85	4.58E-16	65.80%	0.121	IPR001007 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR24042:SF4 (PANTHER); PTHR24042 (PANTHER); IPR001007 (PROSITE_PROFILES); SSF57603 (SUPERFAMILY)
842	c179017_g1_i1_len_263_path_1_0_262_0	2	protein kinase c-binding protein nell1-like	88	2.09E-17	61.00%	0.115	

843	c179089_g1_i1_len_464_path_471_0_463_5	28	interstitial collagenase	154	2.17E-54	70.00%	0.134	IPR021190 (PRINTS); IPR018487 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018487 (PFAM); IPR000585 (G3DSA:2.110.10.GENE3D); IPR001818 (PFAM); PTHR10201 (PANTHER); IPR018486 (PROSITE_PATTERNS); IPR018487 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); IPR000585 (SUPERFAMILY) IPR022049 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR32073 (PANTHER); PTHR32073:SF7 (PANTHER); IPR011009 (SUPERFAMILY)
844	c179206_g1_i1_len_635_path_1_0_634_1	10	upf0672 protein c3orf58 homolog	212	3.81E-30	55.90%	0.106	IPR001863 (PFAM); IPR001863 (PANTHER); IPR019803 (PROSITE_PATTERNS)
845	c179369_g1_i1_len_392_path_1_0_391_5	6	glypican- partial	130	4.42E-66	81.80%	0.101	IPR002413 (PRINTS); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (SUPERFAMILY)
846	c179430_g1_i1_len_286_path_1_0_285_5	8	allergen 5	95	2.91E-12	59.80%	0.099	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
847	c179803_g1_i1_len_398_path_20_0_397_5	8	low-density lipoprotein receptor-related protein partial	132	1.74E-08	46.60%	0.102	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24416:SF309 (PANTHER); PTHR24416 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR002011 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
848	c179814_g1_i1_len_603_path_1_0_602_4	8	tyrosine-protein kinase transmembrane receptor ror	201	7.94E-122	90.50%	0.107	IPR000772 (SMART); G3DSA:2.80.10.50 (GENE3D); IPR000772 (PFAM); PTHR11675:SF24 (PANTHER); PTHR11675 (PANTHER); IPR000772 (PROSITE_PROFILES); IPR000772 (SUPERFAMILY)
849	c180065_g1_i1_len_550_path_528_0_549_5	15	polypeptide n-acetylgalactosaminyltransferase 2	183	1.21E-21	52.30%	0.102	IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); PTHR24033:SF36 (PANTHER); PTHR24033 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
850	c18027_g2_i1_len_145_path_203_0_144_0	4	notch protein	49	1.97E-16	87.00%	0.11	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24193 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
851	c180292_g1_i1_len_256_path_1_0_255_1	6	achain 3ank: a designed ankyrin repeat protein with three identical consensus repeats	85	7.92E-13	65.60%	0.112	IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
852	c180413_g1_i1_len_252_path_230_0_251_3	3	PREDICTED: cubilin	84	2.77E-06	52.50%	0.1	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF150 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
853	c180560_g1_i1_len_303_path_281_0_302_0	16	dnaj homolog subfamily c member 21-like	101	2.20E-36	86.40%	0.136	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
855	c1807_g1_i1_len_667_path_695_0_666_4	15	cadherin egf lag seven-pass g-type receptor 3	222	2.52E-58	64.20%	0.1	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF130 (PANTHER); IPR018253 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM)
854	c180753_g1_i1_len_333_path_1_0_332_0	6	dnaj homolog subfamily c member 1-like	111	7.88E-49	85.00%	0.117	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
856	c181160_g1_i1_len_150_path_128_0_149_2	0	zinc finger protein 891 isoform x8	50	1.15E-14	81.00%	0.101	IPR001660 (SMART); IPR013761 (G3DSA:1.10.150.GENE3D); IPR011510 (PFAM); IPR001660 (PROSITE_PROFILES); IPR013761 (SUPERFAMILY)
857	c181229_g1_i1_len_295_path_273_0_294_0	3	transcription factor 20-like	99	5.61E-15	71.25%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
858	c181233_g1_i1_len_347_path_1_0_346_4	6	zinc finger and scan domain-containing protein 2-like	116	1.22E-53	82.50%	0.11	

859	c18125_g2_i1_len_388_path_366_0_387_0	4	actin-interacting protein 1	130	1.38E-73	92.40%	0.099	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19856 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
860	c181909_g1_i1_len_464_path_442_0_463_0	14	polypeptide n-acetylgalactosaminyltransferase 5 isoform x2	155	1.63E-47	72.10%	0.116	PTHR11675 (PANTHER); PTHR11675:SF21 (PANTHER); IPR029044 (SUPERFAMILY)
861	c181987_g1_i1_len_261_path_1_0_260_5	4	protein partial	87	8.72E-29	71.10%	0.1	IPR002126 (PRINTS); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
862	c182316_g1_i1_len_388_path_366_0_387_0	6	fad-linked sulfhydryl oxidase partial	130	6.25E-46	80.90%	0.105	IPR017905 (G3DSA:1.20.120.GENE3D); IPR017905 (PFAM); PTHR12645 (PANTHER); PTHR12645:SF0 (PANTHER); IPR017905 (PROSITE_PROFILES); IPR017905 (SUPERFAMILY)
863	c182503_g1_i1_len_338_path_1_0_337_5	8	wd repeat-containing protein 37-like	112	4.18E-47	92.80%	0.121	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19855 (PANTHER); PTHR19855:SF12 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
864	c182574_g1_i1_len_261_path_1_0_260_1	6	pban-type neuropeptide	87	9.14E-08	51.00%	0.114	no IPS match
865	c182775_g1_i1_len_431_path_1_0_430_0	10	low quality protein: hemocytin	144	2.84E-27	66.70%	0.107	G3DSA:2.10.25.10 (GENE3D); IPR002919 (PFAM); PTHR11339:SF25 (PANTHER); PTHR11339 (PANTHER); IPR002919 (SUPERFAMILY)
867	c1828_g1_i1_len_828_path_53_0_827_0	32	isoamyl acetate-hydrolyzing esterase 1 homolog	276	1.58E-74	65.70%	0.11	IPR013830 (G3DSA:3.40.50.GENE3D); IPR001087 (PFAM); PTHR14209 (PANTHER); IPR013830 (SUPERFAMILY)
866	c182887_g1_i1_len_315_path_1_0_314_5	4	serine protease like protein	105	2.42E-12	73.60%	0.126	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF94 (PANTHER); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
868	c183126_g1_i1_len_150_path_128_0_149_4	1	cubilin isoform x2	50	2.67E-08	70.00%	0.106	IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
869	c183232_g1_i1_len_338_path_316_0_337_2	8	zinc finger protein 665-like isoform x1	112	3.40E-16	61.30%	0.12	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF57667 (SUPERFAMILY)
870	c183385_g1_i1_len_334_path_312_0_333_0	5	c-type mannose receptor 2	112	6.94E-15	52.60%	0.14	IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
871	c183692_g1_i1_len_838_path_816_0_837_2	14	convoluted-like protein	279	2.70E-65	64.30%	0.109	PR00019 (PRINTS); IPR000483 (SMART); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR001611 (PFAM); IPR001611 (PFAM); PTHR24365:SF83 (PANTHER); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
872	c18394_g1_i1_len_1680_path_1_0_1679_5	143	bmp-binding endothelial regulator protein	560	4.84E-22	36.50%	0.631Y	IPR001846 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR001846 (PFAM); PTHR11339 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001846 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK)
873	c184094_g1_i1_len_312_path_290_0_311_1	7	extracellular serine threonine protein kinase fam20c	104	1.42E-17	70.90%	0.102	IPR024869 (PANTHER); PTHR12450:SF8 (PANTHER)
874	c18420_g1_i1_len_1053_path_327_0_440_17 2_441_554_286_555_563_326_564_884_109 5_885_968_1095_969_1052_2	41	serine carboxypeptidase cpvl	351	9.48E-24	57.30%	0.195	IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
875	c184530_g1_i1_len_278_path_256_0_277_4	4	transferrin receptor family dimerization domain containing protein	93	1.53E-26	71.30%	0.111	IPR003137 (PFAM); G3DSA:3.50.30.30 (GENE3D); PTHR10404 (PANTHER); SSF52025 (SUPERFAMILY)
876	c184548_g1_i1_len_268_path_1_0_267_5	6	protein giant-lens	89	2.20E-25	75.20%	0.719 Y	IPR021633 (PFAM); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM)
877	c184615_g1_i1_len_523_path_1_0_522_1	15	matrix metalloproteinase 2	174	1.52E-42	53.10%	0.109	IPR021190 (PRINTS); IPR018487 (SMART); IPR001818 (PFAM); IPR018487 (PFAM); IPR000585 (G3DSA:2.110.10.GENE3D); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10201 (PANTHER); PTHR10201:SF135 (PANTHER); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY); SSF55486 (SUPERFAMILY)

878	c184706_g1_i1_len_306_path_284_0_305_3	5	zinc finger protein 729- partial	102	1.49E-14	56.40%	0.116	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
879	c184734_g1_i1_len_279_path_257_0_278_0	3	peptidase partial	93	3.03E-07	65.00%	0.175	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY) IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); PTHR19325 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR000436 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR000436 (SUPERFAMILY)
880	c184823_g1_i1_len_261_path_1_0_260_0	3	von willebrand factor type egf and pentraxin domain-containing protein 1-like	87	4.70E-19	70.40%	0.751 Y	G3DSA:2.10.25.10 (GENE3D); IPR013111 (PFAM); PTHR11841 (PANTHER); SSF57196 (SUPERFAMILY)
881	c184929_g1_i1_len_235_path_213_0_234_4	3	reelin-like isoform x4	78	1.10E-24	68.30%	0.129	IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
882	c18500_g1_i1_len_411_path_1_0_410_4	5	cubilin	137	2.14E-24	58.20%	0.138	IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
883	c18500_g2_i1_len_225_path_979_0_224_5	2	hypothetical protein D918_02869	75	9.84E-06	54.00%	0.105	no IPS match
884	c185084_g1_i1_len_506_path_1_0_445_447_446_475_447_476_505_4	9	ppmp i antigen cs34	169	1.42E-20	44.60%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
885	c185162_g1_i1_len_263_path_241_0_262_2	6	zinc finger protein 525-like	87	6.51E-20	64.00%	0.169	G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR009003 (SUPERFAMILY)
886	c185179_g1_i1_len_319_path_297_0_318_0	2	prostasin isoform x2	107	1.45E-07	58.50%	0.115	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
887	c185219_g1_i1_len_279_path_257_0_278_0	6	low-density lipoprotein receptor-related protein 2	93	4.27E-46	87.20%	0.107	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342 (PANTHER); PTHR10342:SF183 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)
888	c185221_g1_i1_len_373_path_351_0_372_5	4	extracellular sulfatase sulf-1-like partial	124	2.59E-45	85.10%	0.101	IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); PTHR10334:SF189 (PANTHER); IPR014044 (SUPERFAMILY)
889	c185465_g1_i1_len_286_path_264_0_285_0	5	golgi-associated plant pathogenesis-related protein 1	96	2.68E-35	63.60%	0.103	IPR014853 (SMART); IPR014853 (PFAM); PTHR11339:SF224 (PANTHER); PTHR11339 (PANTHER)
890	c185478_g1_i1_len_271_path_249_0_270_3	8	kielin chordin-like protein	91	6.20E-37	78.30%	0.142	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
891	c185856_g1_i1_len_319_path_1_0_318_5	6	zinc finger protein 37-like	106	3.09E-19	61.00%	0.102	IPR029034 (G3DSA:2.10.90.GENE3D); IPR001839 (PFAM); PTHR11848:SF131 (PANTHER); IPR015615 (PANTHER); IPR001839 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR029034 (SUPERFAMILY)
892	c186210_g1_i1_len_156_path_134_0_155_1	3	bone morphogenetic protein 7-like	52	5.01E-13	85.60%	0.481 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PROFILES); IPR023415 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
895	c1870_g1_i1_len_604_path_632_0_603_5	21	vitellogenin receptor	201	7.34E-20	47.90%	0.142	

893	c187058_g1_i1_len_315_path_1_0_44_46_45_93_95_94_117_119_118_168_95_169_192_119_193_243_95_244_267_1	6	repetitive proline-rich cell wall protein 2-like	105	2.70E-14	58.40%	0.149	no IPS match
894	c187068_g1_i1_len_313_path_1_0_312_5	4	protein turtle homolog a isoform x2	104	9.24E-07	52.40%	0.121	IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
896	c187141_g1_i1_len_256_path_234_0_255_0	4	short gastrulation	86	1.96E-19	57.40%	0.099	IPR001007 (SMART); IPR001007 (PFAM); G3DSA:2.10.70.10 (GENE3D); SSF57603 (SUPERFAMILY)
897	c18742_g2_i1_len_411_path_201_0_410_5	6	serine threonine-protein kinase 17a-like	137	1.33E-49	74.90%	0.105	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24342 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
898	c187431_g1_i1_len_268_path_1_0_267_5	8	class c metabotropic glutamate-like g-protein coupled receptor	89	1.79E-13	77.40%	0.315	G3DSA:3.40.50.2300 (GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR028082 (SUPERFAMILY); TMhelix (TMHMM)
899	c187504_g1_i1_len_187_path_165_0_186_1	3	zinc finger protein	62	5.88E-11	64.50%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
900	c187653_g1_i1_len_425_path_1_0_424_1	9	down syndrome cell adhesion molecule	142	1.28E-37	66.40%	0.163	IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR10489 (PANTHER); PTHR10489:SF580 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); TMhelix (TMHMM)
901	c187797_g1_i1_len_336_path_1_0_335_5	4	---NA---	112			0.167	IPR014853 (PFAM)
902	c187925_g1_i1_len_275_path_253_0_274_4	4	vitellogenin	92	9.23E-30	74.30%	0.098	IPR001846 (PFAM); IPR001846 (PROSITE_PROFILES)
903	c188142_g1_i1_len_267_path_1_0_266_2	4	zinc finger protein partial	89	2.07E-15	60.10%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
904	c188173_g1_i1_len_221_path_1_0_220_3	2	serine protease	74	6.70E-12	74.10%	0.117	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF94 (PANTHER); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
905	c188718_g1_i1_len_266_path_1_0_265_0	4	zinc finger protein 69	89	1.83E-18	63.20%	0.321	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
906	c18878_g1_i1_len_622_path_1_0_421_1170_422_621_4	9	fukutin isoform 2	207	1.68E-48	65.70%	0.391 Y	IPR007074 (PFAM); IPR009644 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TMhelix (TMHMM)
907	c18878_g1_i2_len_596_path_1_0_421_423_4_22_595_5	6	fukutin isoform 2	198	8.30E-49	67.70%	0.12	IPR007074 (PFAM); IPR009644 (PANTHER)
908	c189076_g1_i1_len_198_path_1_0_197_1	0	zinc c2h2 type domain-containing protein	66	2.92E-12	62.40%	0.111	IPR015880 (SMART); IPR008598 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
909	c18927_g1_i1_len_363_path_701_0_362_4	6	dehydrogenase reductase sdr family member on chromosome partial	121	4.39E-23	65.30%	0.119	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320:SF55 (PANTHER); PTHR24320 (PANTHER); SSF51735 (SUPERFAMILY)
910	c189465_g1_i1_len_270_path_248_0_269_5	7	insulin-like growth factor-binding protein complex acid labile chain	90	9.50E-13	60.20%	0.158	PR00019 (PRINTS); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
911	c189532_g1_i1_len_501_path_1_0_500_0	12	15-hydroxyprostaglandin dehydrogenase	167	1.86E-82	76.00%	0.117	IPR002198 (PRINTS); IPR002424 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24310 (PANTHER); SSF51735 (SUPERFAMILY)
912	c1896_g1_i1_len_340_path_1_0_339_1	23	cytochrome p450 partial	113	1.07E-36	72.20%	0.116	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24292 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)

913	c19129_g1_i1_len_369_path_347_0_368_4	10	moxd1 homolog 1	123	1.12E-29	66.30%	0.098	PF03712 (PFAM); IPR014784 (G3DSA:2.60.120.GENE3D); IPR000945 (PANTHER); IPR008977 (SUPERFAMILY)
914	c191633_g1_i1_len_151_path_129_0_150_4	1	beta- -n-acetylgalactosaminyltransferase bre-4	50	7.16E-16	78.60%	0.102	IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
915	c19193_g1_i1_len_544_path_75_0_543_1	70	anti-lipopolysaccharide partial	181	5.91E-20	68.70%	0.796 Y	IPR024509 (PFAM); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024716 (PRODOM); SignalP-noTM (SIGNALP_EUK)
916	c192165_g1_i1_len_292_path_16_0_291_4	3	zinc finger protein rotund-like isoform x1	97	2.51E-43	96.00%	0.141	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR11389:SF431 (PANTHER); PTHR11389 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
917	c19356_g1_i1_len_1588_path_1566_0_1587_0	829	ves g 5 allergen	530	2.17E-46	52.50%	0.754 Y	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR002172 (SMART); IPR014044 (SMART); IPR002172 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001283 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR002172 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR014044 (SUPERFAMILY); TMhelix (TMHMM)
918	c193640_g1_i1_len_319_path_1_0_318_0	7	zinc finger and scan domain-containing protein 22	107	2.18E-28	69.50%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
919	c194713_g1_i1_len_205_path_126_0_53_126_54_107_126_108_161_179_162_204_0	0	---NA---	69			0.109	no IPS match
920	c19568_g1_i1_len_290_path_29_0_75_105_7_6_108_138_109_289_0	5	histone h2b-like	97	9.23E-47	97.40%	0.142	IPR000558 (PRINTS); IPR000558 (SMART); IPR007125 (PFAM); IPR009072 (G3DSA:1.10.20.GENE3D); IPR000558 (PANTHER); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009072 (SUPERFAMILY)
921	c19658_g1_i1_len_3178_path_49_0_431_480_432_433_48_434_3177_3	261	usher syndrome type-1g protein homolog	1060	4.48E-132	62.20%	0.112	Coil (COILS); IPR002110 (SMART); IPR001660 (SMART); IPR013761 (G3DSA:1.10.150.GENE3D); IPR020683 (PFAM); IPR021129 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24161 (PANTHER); PTHR24161:SF6 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); IPR013761 (SUPERFAMILY)
922	c19670_g1_i1_len_1506_path_1484_0_1505_3	460	chymotrypsinogen a	502	6.19E-95	58.40%	0.261	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24260 (PANTHER); PTHR24260:SF47 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
923	c1979_g1_i1_len_1537_path_1_0_1536_4	232	chitinase domain-containing protein 1 isoform x1	512	2.10E-149	70.30%	0.142	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF135 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
924	c19813_g1_i1_len_341_path_1_0_340_1	4	fibroblast growth factor receptor-like partial	114	1.02E-23	64.40%	0.104	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19890 (PANTHER); PTHR19890:SF5 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)

925	c19821_g1_i1_len_760_path_1_0_759_0	31	e3 ubiquitin-protein ligase rnf185-like isoform x2	254	1.87E-88	81.00%	0.103	IPR001841 (SMART); PF13923 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); PTHR12313 (PANTHER); PTHR12313:SF3 (PANTHER); IPR017907 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001841 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
926	c19831_g1_i1_len_1557_path_1535_0_370_1_906_371_1556_0	45	---NA---	519			0.1	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS)
927	c20132_g1_i1_len_1969_path_53_0_1968_1	194	cytochrome p450 partial	642	8.86E-113	55.30%	0.186	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24292 (PANTHER); PTHR24292:SF24 (PANTHER); IPR017972 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
928	c20175_g2_i1_len_636_path_539_0_635_5	30	hyaluronan and proteoglycan link protein 1-like isoform x1	212	1.06E-20	56.30%	0.101	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
929	c20209_g1_i1_len_855_path_833_0_695_152_9_696_854_5	23	ankyrin repeat and sam domain-containing protein 6-like	285	2.39E-72	60.10%	0.609Y	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR10627:SF2 (PANTHER); PTHR10627 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR020683 (SUPERFAMILY)
930	c20209_g1_i2_len_733_path_833_0_695_168_8_696_732_3	18	ankyrin repeat and sam domain-containing protein 6	245	2.33E-64	61.50%	0.101	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR10627:SF2 (PANTHER); PTHR10627 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
931	c2026_g1_i1_len_1403_path_1_0_1402_1	149	uncharacterized oxidoreductase yrbe-like	468	5.78E-142	68.50%	0.127	IPR000683 (PFAM); IPR004104 (PFAM); G3DSA:3.30.360.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22604 (PANTHER); PTHR22604:SF92 (PANTHER); SSF55347 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
932	c20281_g1_i1_len_817_path_53_0_816_5	22	spermatogenesis-associated protein 5	272	2.63E-59	79.40%	0.143	Coil (COILS); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23077 (PANTHER); PTHR23077:SF27 (PANTHER); IPR003960 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
933	c20322_g1_i1_len_803_path_814_0_409_161_1_410_802_2	28	hypothetical protein YQE_04199, partial	267	1.43E-54	59.70%	0.358 Y	IPR004947 (PFAM); IPR004947 (PANTHER)
934	c20322_g1_i2_len_409_path_1609_0_15_161_1_16_408_1	6	deoxyribonuclease- partial	136	3.42E-16	66.80%	0.106	IPR004947 (PFAM); IPR004947 (PANTHER)
935	c20395_g1_i1_len_615_path_755_0_192_111_0_193_614_0	57	peptidyl-prolyl cis-trans isomerase-like 3	205	3.72E-46	59.60%	0.144	IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
936	c20395_g1_i2_len_777_path_755_0_192_948_193_354_1110_355_776_0	91	peptidyl-prolyl cis-trans isomerase-like 3	259	2.44E-97	91.00%	0.145	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
937	c20460_g1_i1_len_2117_path_2197_0_1840_52_1841_2116_1	287	lamin dm0-like isoform x1	706	0	75.60%	0.325	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR001322 (G3DSA:2.60.40.GENE3D); IPR001322 (PFAM); G3DSA:1.20.5.170 (GENE3D); IPR001664 (PFAM); IPR027696 (PTHR23239:PANTHER); IPR001664 (PANTHER); IPR018039 (PROSITE_PATTERNS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF64593 (SUPERFAMILY); IPR001322 (SUPERFAMILY); SSF64593 (SUPERFAMILY)

938	c20460_g1_i2_len_2147_path_2197_0_1840_22_1841_1870_52_1871_2146_1	265	lamin dm0-like isoform x1	716	0	74.60%	0.325	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); G3DSA:1.20.5.170 (GENE3D); IPR001322 (G3DSA:2.60.40.GENE3D); IPR001322 (PFAM); IPR001664 (PFAM); IPR027696 (PTHR23239:PANTHER); IPR001664 (PANTHER); IPR018039 (PROSITE_PATTERNS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF64593 (SUPERFAMILY); SSF64593 (SUPERFAMILY); IPR001322 (SUPERFAMILY)
939	c20479_g1_i1_len_1314_path_1292_0_257_1_550_258_1313_1	230	inactive hydroxysteroid dehydrogenase-like protein 1	438	6.92E-110	68.10%	0.179	Coil (COILS); IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF317 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
940	c20479_g1_i2_len_1078_path_2605_0_21_15_50_22_1077_2	212	inactive hydroxysteroid dehydrogenase-like protein 1	359	2.71E-97	72.00%	0.116	Coil (COILS); IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF317 (PANTHER); PTHR24316 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
941	c20493_g1_i1_len_962_path_940_0_961_5	72	insulin-like growth factor binding protein 7-like protein	320	7.92E-09	51.00%	0.494Y	IPR000867 (SMART); IPR000867 (PFAM); IPR011390 (PANTHER); PTHR14186:SF8 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000867 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009030 (SUPERFAMILY); TMhelix (TMHMM)
942	c20515_g1_i1_len_635_path_1581_0_634_1	15	laminin subunit gamma-1	212	1.87E-94	76.20%	0.115	IPR018031 (SMART); IPR000034 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR10574 (PANTHER); PTHR10574:SF231 (PANTHER); IPR002049 (PROSITE_PATTERNS); IPR000034 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
943	c20515_g2_i1_len_507_path_485_0_506_2	10	lanb2	169	5.47E-88	82.80%	0.106	IPR002049 (SMART); IPR000742 (SMART); IPR002049 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10574:SF231 (PANTHER); PTHR10574 (PANTHER); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR009030 (SUPERFAMILY)
944	c20591_g2_i1_len_328_path_306_0_327_4	5	peripheral plasma membrane protein cask-like	109	2.76E-59	96.50%	0.101	G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR23122:SF40 (PANTHER); PTHR23122 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
945	c20647_g1_i1_len_565_path_1_0_246_248_2_47_308_310_309_564_0	19	lysosomal pro-x carboxypeptidase-like	189	3.06E-54	75.40%	0.142	IPR008758 (PFAM); PTHR11010:SF11 (PANTHER); IPR008758 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY)
946	c20701_g1_i1_len_787_path_104_0_93_923_94_786_3	30	astacin- partial	263	6.48E-42	59.90%	0.124	IPR001506 (PRINTS); IPR006026 (SMART); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)
947	c20914_g1_i1_len_372_path_1_0_371_3	6	leucine-rich repeat-containing protein 47-like	124	1.81E-30	67.90%	0.113	IPR003591 (SMART); SM00364 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR10947:SF2 (PANTHER); PTHR10947 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
948	c2095_g1_i1_len_357_path_1_0_356_5	4	zinc finger protein 431-like isoform x1	119	3.57E-39	72.80%	0.116	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
949	c2095_g2_i1_len_164_path_669_0_163_1	3	zinc finger protein 596-like	55	9.14E-15	74.30%	0.113	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
950	c20998_g1_i1_len_1177_path_1155_0_1176_1	44	ankyrin repeat protein	392	2.98E-18	49.80%	0.103	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)

962	c21662_g1_i1_len_1292_path_1270_0_1291_2	37	hemacentin- partial	430	5.10E-142	62.40%	0.129	IPR001881 (SMART); IPR000742 (SMART); IPR001881 (PFAM); IPR026823 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR19897:SF158 (PANTHER); PTHR19897 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR009030 (SUPERFAMILY)
963	c21665_g1_i1_len_578_path_1_0_577_5	26	vascular cell adhesion protein 1	192	3.62E-65	66.30%	0.128	IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR11640:SF6 (PANTHER); PTHR11640 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
964	c21702_g1_i1_len_388_path_1_0_387_2	4	polypeptide n-acetylgalactosaminyltransferase 5 isoform x1	129	4.11E-77	94.20%	0.223	IPR001173 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); PTHR11675 (PANTHER); PTHR11675:SF19 (PANTHER); IPR029044 (SUPERFAMILY)
965	c21702_g2_i1_len_167_path_875_0_166_1	2	polypeptide n-acetylgalactosaminyltransferase 5 isoform x2	56	1.62E-29	94.40%	0.19	PTHR11675 (PANTHER); PTHR11675:SF21 (PANTHER); IPR029044 (SUPERFAMILY)
966	c21745_g1_i1_len_1940_path_53_0_1939_4	82	vascular endothelial growth factor receptor 1-like isoform x1	647	1.19E-149	59.40%	0.168	Coil (COILS); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416:SF298 (PANTHER); PTHR24416 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
967	c21765_g1_i1_len_2008_path_1986_0_2007_1	104	serine-threonine kinase receptor-associated protein	669	0	85.50%	0.114	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19877 (PANTHER); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
968	c21792_g1_i1_len_552_path_1_0_551_0	12	matrix metalloproteinase-9	184	2.17E-10	45.30%	0.108	IPR000562 (SMART); IPR000562 (PFAM); IPR000562 (G3DSA:2.10.10.GENE3D); IPR000562 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY)
969	c21915_g1_i1_len_957_path_935_0_956_3	68	membrane glycoprotein lig-	319	1.64E-17	46.00%	0.797Y	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF52058 (SUPERFAMILY)
970	c21992_g1_i1_len_1425_path_51_0_1424_0	236	acyl- delta desaturase	475	1.80E-129	71.50%	0.355Y	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351:SF28 (PANTHER); PTHR11351 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
971	c22000_g1_i1_len_355_path_383_0_354_2	66	nidogen-2- partial	118	6.03E-08	71.10%	0.116	IPR000716 (SMART); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY)

972	c22032_g1_i1_len_4008_path_31_0_4007_3	45688	ligand of numb protein x 2 isoform x1	1336	1.41E-177	53.00%	0.106	IPR001841 (SMART); IPR001478 (SMART); PF02176 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR013323 (G3DSA:3.90.890.GENE3D); IPR001478 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); PF13920 (PFAM); PTHR19964 (PANTHER); IPR017907 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001841 (PROSITE_PROFILES); IPR001293 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR008974 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); SSF57850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
973	c22068_g1_i1_len_622_path_1_0_621_2	25	maguk p55 subfamily member 7 isoform x4	207	1.55E-99	86.60%	0.1	IPR008145 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR008145 (PFAM); G3DSA:3.30.63.10 (GENE3D); PTHR23122 (PANTHER); PTHR23122:SF14 (PANTHER); IPR020590 (PROSITE_PATTERNS); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
974	c22073_g1_i1_len_1334_path_2921_0_17_15_9_18_1333_5	37	camp-dependent protein kinase catalytic	444	0	90.60%	0.1	Coil (COILS); IPR000239 (PRINTS); IPR000961 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24355 (PANTHER); PTHR24355:SF24 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR000961 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR016137 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); IPR016137 (SUPERFAMILY)
975	c22073_g1_i2_len_1474_path_1_0_157_159_158_1473_5	40	camp-dependent protein kinase catalytic	491	0	90.20%	0.1	Coil (COILS); IPR000239 (PRINTS); IPR000961 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24355 (PANTHER); PTHR24355:SF24 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR016137 (PROSITE_PROFILES); IPR016137 (SUPERFAMILY); IPR011009 (SUPERFAMILY)
976	c22403_g1_i1_len_795_path_1509_0_794_2	30	mucin 17-like partial	265	3.05E-27	45.50%	0.123	PTHR24023 (PANTHER); PTHR24023:SF405 (PANTHER)
977	c22403_g1_i1_len_795_path_1509_0_794_5	30	collagen alpha-1 chain	265	1.71E-67	68.90%	0.106	IPR008160 (PFAM); PTHR24023:SF164 (PANTHER); PTHR24023 (PANTHER)
978	c22472_g1_i1_len_334_path_1_0_333_2	3	zinc finger protein 177-like	111	3.14E-31	76.50%	0.204	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
979	c22472_g2_i1_len_150_path_623_0_149_5	2	zinc finger protein	50	1.97E-25	95.20%	0.13	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
980	c22477_g2_i1_len_268_path_1_0_179_181_1_80_203_1506_204_267_3	5	zinc finger protein	90	2.00E-15	58.80%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
981	c22546_g1_i1_len_231_path_687_0_230_3	6	---NA---	77			0.102	G3DSA:2.60.40.1110 (GENE3D); IPR014020 (PFAM); IPR000008 (SUPERFAMILY)
982	c22546_g2_i1_len_262_path_1_0_261_5	2	phosphatidylinositol -trisphosphate 3-phosphatase and dual-specificity protein phosphatase pten isoform x4	87	2.74E-13	73.80%	0.135	G3DSA:2.60.40.1110 (GENE3D); IPR014020 (PFAM); IPR014020 (PROSITE_PROFILES); IPR000008 (SUPERFAMILY)
983	c22590_g1_i1_len_867_path_1_0_866_5	24	zinc finger protein 665 isoform x2	289	1.79E-11	64.10%	0.098	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
984	c22591_g1_i1_len_263_path_209_0_262_2	3	collagen alpha-1 partial	87	6.90E-16	65.80%	0.099	IPR008160 (PFAM); PTHR24023:SF379 (PANTHER); PTHR24023 (PANTHER)

985	c22634_g1_i1_len_2549_path_1_0_2548_0	171	sulfhydryl oxidase 1-like	850	5.62E-156	54.70%	0.415Y	IPR017905 (G3DSA:1.20.120.GENE3D); IPR017905 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR22897:SF8 (PANTHER); PTHR22897 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR017905 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR017905 (SUPERFAMILY); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
986	c22664_g1_i1_len_1787_path_2163_0_1786_1	112	exocyst complex component 7	596	0	70.60%	0.102	IPR004140 (PFAM); PTHR12542:SF7 (PANTHER); IPR004140 (PANTHER); IPR016159 (SUPERFAMILY)
987	c22727_g1_i1_len_947_path_925_0_946_2	29	zinc finger and scan domain-containing protein 2-like isoform x1	315	8.26E-48	51.80%	0.12	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
988	c22740_g1_i1_len_2472_path_3405_0_1277_532_1278_2471_5	272	hydroxysteroid dehydrogenase-like protein 2	824	2.11E-163	76.40%	0.131	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF273 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
989	c22740_g1_i2_len_1717_path_9_0_522_532_523_1716_5	314	hydroxysteroid dehydrogenase-like protein 2	572	0	77.00%	0.131	IPR002347 (PRINTS); IPR003033 (PFAM); IPR003033 (G3DSA:3.30.1050.GENE3D); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF273 (PANTHER); PTHR24322 (PANTHER); IPR003033 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
990	c22757_g1_i1_len_850_path_828_0_849_0	30	syntaxin-1a isoform x2	284	0	93.10%	0.104	Coil (COILS); Coil (COILS); IPR000727 (SMART); IPR006011 (SMART); G3DSA:1.20.58.70 (GENE3D); G3DSA:1.20.5.110 (GENE3D); IPR000727 (PFAM); IPR006011 (PFAM); PTHR19957 (PANTHER); IPR028669 (PTHR19957:PANTHER); IPR006012 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000727 (PROSITE_PROFILES); IPR010989 (SUPERFAMILY); TMhelix (TMHMM)
991	c22820_g1_i1_len_151_path_479_0_150_1	1	endothelin-converting enzyme 1 isoform x1	50	2.68E-18	86.90%	0.156	G3DSA:1.10.1380.10 (GENE3D); IPR008753 (PFAM); IPR000718 (PANTHER); IPR029734 (PTHR11733:PANTHER); SSF55486 (SUPERFAMILY)
992	c22820_g2_i1_len_198_path_176_0_197_1	1	endothelin-converting enzyme 1 isoform x2	66	2.08E-23	87.80%	0.105	IPR000718 (PANTHER); IPR029733 (PTHR11733:PANTHER); SSF55486 (SUPERFAMILY)
993	c22877_g1_i1_len_925_path_903_0_756_166_0_757_924_3	93	adp-ribosylation factor 6	309	8.47E-124	99.30%	0.535Y	IPR006689 (PRINTS); IPR006687 (SMART); IPR003579 (SMART); IPR024156 (SMART); IPR005225 (TIGRFAM); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF106 (PANTHER); IPR024156 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR027417 (SUPERFAMILY)
994	c22888_g1_i1_len_742_path_720_0_741_5	22	achain crystal structure of engineered northeast structural genomics consortium target	247	4.45E-15	58.40%	0.097	IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
995	c22888_g2_i1_len_534_path_1439_0_533_1	8	ankyrin neuronal	178	1.25E-16	54.20%	0.115	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM)
996	c22973_g1_i1_len_430_path_408_0_429_5	13	basement membrane-specific heparan sulfate proteoglycan core protein	143	2.52E-48	70.40%	0.12	IPR002049 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR10574:SF252 (PANTHER); PTHR10574 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
997	c22973_g2_i1_len_633_path_815_0_632_3	28	basement membrane-specific heparan sulfate proteoglycan core protein	211	1.45E-76	72.00%	0.108	IPR018031 (SMART); IPR000034 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF252 (PANTHER); IPR000034 (PROSITE_PROFILES)

998	c23003_g1_i1_len_1161_path_1309_0_1075_2555_1076_1160_4	446	peptidyl-prolyl cis-trans isomerase e	387	2.48E-122	81.30%	0.105	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF242 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
999	c23003_g1_i2_len_1331_path_1309_0_1075_2385_1076_1245_2555_1246_1330_3	704	peptidyl-prolyl cis-trans isomerase e	444	1.06E-168	84.30%	0.108	IPR002130 (PRINTS); IPR000504 (SMART); IPR000504 (PFAM); IPR012677 (G3DSA:3.30.70.GENE3D); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF242 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR000504 (PROSITE_PROFILES); SSF54928 (SUPERFAMILY); IPR029000 (SUPERFAMILY)
1000	c23023_g1_i1_len_603_path_1_0_115_117_1_16_602_1	19	adrenodoxin-like mitochondrial	201	7.65E-73	87.80%	0.096	IPR001055 (PRINTS); IPR001041 (PFAM); IPR012675 (G3DSA:3.10.20.GENE3D); PTHR23426:SF1 (PANTHER); PTHR23426 (PANTHER); IPR018298 (PROSITE_PATTERNS); IPR001041 (PROSITE_PROFILES); IPR001041 (SUPERFAMILY)
1001	c23023_g1_i2_len_655_path_866_0_167_117_168_654_2	28	adrenodoxin-like mitochondrial	218	8.21E-77	84.70%	0.191	IPR001055 (PRINTS); IPR001041 (PFAM); IPR012675 (G3DSA:3.10.20.GENE3D); PTHR23426 (PANTHER); PTHR23426:SF1 (PANTHER); IPR018298 (PROSITE_PATTERNS); IPR001041 (PROSITE_PROFILES); IPR001041 (SUPERFAMILY)
1002	c23044_g1_i1_len_643_path_1_0_642_4	34	carboxypeptidase d-like	214	4.45E-37	52.30%	0.148	IPR014766 (G3DSA:2.60.40.GENE3D); PF13620 (PFAM); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11532 (PANTHER); PTHR11532:SF50 (PANTHER); IPR008969 (SUPERFAMILY); SSF53187 (SUPERFAMILY)
1003	c23044_g2_i1_len_341_path_1241_0_340_3	6	carboxypeptidase d-like	114	2.59E-19	73.50%	0.123	IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); SSF53187 (SUPERFAMILY)
1004	c23063_g1_i1_len_732_path_789_0_477_44_478_731_3	25	low affinity immunoglobulin epsilon fc receptor-like	244	9.36E-14	44.30%	0.127	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
1005	c23063_g1_i2_len_769_path_789_0_477_126_6_478_514_44_515_768_4	41	low affinity immunoglobulin epsilon fc receptor-like	256	2.78E-17	46.60%	0.19	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1006	c23067_g2_i1_len_2574_path_3998_0_2573_2	186	serine threonine-protein kinase warts	858	0	78.70%	0.127	IPR000961 (SMART); IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:3.90.1200.10 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); IPR028741 (PTHR24356:PANTHER); PTHR24356 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000961 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1007	c23104_g1_i1_len_317_path_1_0_316_3	10	gamma-glutamyltranspeptidase 1	106	1.39E-39	76.90%	0.098	IPR000101 (PRINTS); IPR000101 (PFAM); PTHR11686:SF15 (PANTHER); IPR000101 (PANTHER); IPR029055 (SUPERFAMILY)
1008	c23186_g2_i1_len_163_path_363_0_162_1	4	peptidyl-prolyl cis-trans isomerase	54	8.19E-23	88.20%	0.139	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1009	c23266_g1_i1_len_1186_path_1164_0_1185_2	168	thioredoxin-like protein 1	395	1.41E-153	81.30%	0.18	PR00421 (PRINTS); IPR013766 (PFAM); IPR010400 (PFAM); IPR010400 (G3DSA:2.60.120.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005746 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR010400 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR008979 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1010	c23341_g1_i1_len_529_path_1_0_528_2	14	bifunctional protein ncoat isoform x2	176	4.73E-82	92.00%	0.201	IPR011496 (PFAM); PTHR13170 (PANTHER); PTHR13170:SF17 (PANTHER); IPR017853 (SUPERFAMILY)
1012	c2357_g2_i1_len_558_path_536_0_557_1	16	zinc finger protein 77-like	186	1.55E-30	58.70%	0.119	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1011	c23576_g1_i1_len_1423_path_53_0_1422_4	114	hypothetical protein LOTGIDRAFT_228404	474	4.46E-06	53.00%	0.119	IPR000998 (SMART); IPR000998 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)

1013	c23600_g1_i1_len_245_path_1_0_97_99_98_244_2	1	beta- -n-acetylgalactosaminyltransferase bre-4	81	4.33E-27	70.00%	0.103	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027995 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
1014	c23600_g1_i2_len_345_path_643_0_197_99_198_344_0	4	beta- -n-acetylgalactosaminyltransferase bre-4	115	4.83E-38	69.60%	0.229	IPR003859 (PRINTS); IPR027995 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
1015	c23661_g1_i1_len_984_path_1012_0_983_2	87837	ferritin 2	328	1.24E-73	80.40%	0.202	IPR008331 (PFAM); IPR012347 (G3DSA:1.20.1260.GENE3D); IPR001519 (PANTHER); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY)
1016	c23690_g1_i1_len_252_path_1_0_251_4	4	serine threonine-protein kinase tao1 isoform x1	84	1.46E-49	97.00%	0.121	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24361 (PANTHER); PTHR24361:SF259 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1017	c23727_g2_i1_len_319_path_231_0_318_4	5	myosin heavy chain	106	4.05E-61	99.00%	0.119	Coil (COILS); IPR002928 (PFAM); PTHR13140 (PANTHER); PTHR13140:SF332 (PANTHER)
1018	c23980_g1_i1_len_514_path_1_0_513_4	13	bone morphogenetic protein 4-like	171	1.32E-17	62.00%	0.139	IPR001111 (PFAM); PTHR11848:SF146 (PANTHER); IPR015615 (PANTHER)
1019	c23980_g2_i1_len_144_path_983_0_143_1	1	bone morphogenetic protein 2-like	48	1.04E-21	89.60%	0.109	IPR001839 (SMART); IPR001839 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); PTHR11848:SF131 (PANTHER); IPR015615 (PANTHER); IPR017948 (PROSITE_PATTERNS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)
1020	c23997_g2_i1_len_271_path_249_0_270_5	4	adenylate cyclase type 8 isoform x1	90	9.57E-41	87.80%	0.129	IPR001054 (G3DSA:3.30.70.GENE3D); IPR001054 (PFAM); PTHR11920:SF236 (PANTHER); PTHR11920 (PANTHER); IPR018297 (PROSITE_PATTERNS); IPR001054 (PROSITE_PROFILES); IPR029787 (SUPERFAMILY)
1021	c24022_g1_i1_len_2078_path_1_0_2077_4	104	inactivation-no-after-potential d	693	9.96E-171	62.50%	0.153	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964:SF34 (PANTHER); PTHR19964 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
1022	c24022_g2_i1_len_139_path_4111_0_138_4	0	inactivation-no-after-potential d	46	1.83E-15	84.90%	0.112	IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR19964:SF11 (PANTHER); PTHR19964 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
1023	c24090_g1_i1_len_3661_path_3689_0_214_3_903_215_217_52_218_3660_1	302	guanine nucleotide exchange	1220	0	70.20%	0.105	Coil (COILS); IPR001849 (SMART); IPR001452 (SMART); IPR000219 (SMART); IPR000219 (PFAM); IPR000219 (G3DSA:1.20.900.GENE3D); IPR011993 (G3DSA:2.30.29.GENE3D); IPR001452 (PFAM); G3DSA:2.30.30.40 (GENE3D); PTHR12845:SF5 (PANTHER); PTHR12845 (PANTHER); IPR000219 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR001849 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); IPR000219 (SUPERFAMILY); SSF50729 (SUPERFAMILY)
1024	c24162_g1_i1_len_276_path_510_0_275_1	6	spermatogenesis-associated protein 5	92	8.59E-49	92.80%	0.112	IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); PTHR23077 (PANTHER); PTHR23077:SF27 (PANTHER); IPR027417 (SUPERFAMILY)
1025	c24300_g1_i1_len_1505_path_1_0_1504_3	1012	lipase 3	502	2.03E-140	67.70%	0.343Y	IPR029058 (G3DSA:3.40.50.GENE3D); IPR006693 (PFAM); IPR000073 (PFAM); PTHR11005 (PANTHER); PTHR11005:SF6 (PANTHER); IPR029058 (SUPERFAMILY)
1026	c24308_g1_i1_len_150_path_1_0_149_3	1	optix-binding protein	50	5.85E-10	66.40%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1027	c24308_g2_i1_len_584_path_255_0_583_0	8	histone-lysine n-methyltransferase prdm9-like	195	1.93E-47	60.10%	0.104	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1028	c24594_g1_i1_len_2189_path_53_0_2188_2	105	dnaj homolog subfamily b member 12	729	5.20E-158	74.50%	0.103	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR015399 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24077 (PANTHER); PTHR24077:SF239 (PANTHER); IPR018253 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)

1029	c24607_g2_i1_len_196_path_438_0_195_4	1	krueppel-like factor partial	65	4.42E-26	98.10%	0.11	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); PTHR23223:SF80 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1030	c24665_g1_i1_len_1026_path_1004_0_1025_5	1428	low quality protein: glutathione peroxidase 1-like	342	5.95E-87	79.30%	0.129	IPR000889 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PFAM); PTHR11592:SF23 (PANTHER); IPR000889 (PANTHER); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1031	c25120_g1_i1_len_864_path_53_0_863_1	44	anti-lipopolysaccharide factor like protein	288	8.25E-15	57.30%	0.156	IPR024509 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024716 (PRODOM); TMhelix (TMHMM); TMhelix (TMHMM)
1032	c25130_g1_i1_len_445_path_423_0_444_0	5	laminin subunit alpha	149	1.77E-61	79.90%	0.139	PR00011 (PRINTS); IPR002049 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); PTHR10574 (PANTHER); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
1033	c25130_g2_i1_len_171_path_845_0_170_1	1	laminin subunit alpha	57	8.71E-21	84.10%	0.112	no IPS match
1034	c25269_g2_i1_len_307_path_539_0_306_5	9	zinc finger protein	102	2.65E-60	95.10%	0.103	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23228:SF26 (PANTHER); PTHR23228 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1035	c25325_g1_i1_len_1651_path_1679_0_1650_2	91	serine protease mitochondrial	550	1.43E-130	69.10%	0.212	IPR001940 (PRINTS); IPR001478 (SMART); G3DSA:2.40.10.10 (GENE3D); PF13365 (PFAM); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR22939 (PANTHER); PTHR22939:SF69 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
1036	c25608_g1_i1_len_512_path_540_0_511_5	24	serine protease easter	170	1.11E-15	52.00%	0.198	IPR022700 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
1037	c25667_g1_i1_len_965_path_943_0_964_5	29	fizzy-related protein homolog	321	0	95.00%	0.254	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19918 (PANTHER); PTHR19918:SF6 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1038	c25679_g1_i1_len_1196_path_1224_0_1195_1	67	transmembrane protease serine 11d isoform x1	399	3.05E-136	64.90%	0.105	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); IPR012224 (PIRSF); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.20.100.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265:SF76 (PANTHER); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR000884 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1039	c25802_g1_i1_len_349_path_53_0_348_1	10	lactase-phlorizin partial	116	7.04E-30	76.70%	0.101	IPR001360 (PRINTS); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001360 (PFAM); IPR001360 (PANTHER); IPR017853 (SUPERFAMILY)
1040	c25887_g1_i1_len_153_path_219_0_152_1	1	tectonic-1 isoform x2	51	3.11E-07	68.00%	0.1	IPR011677 (PFAM)
1041	c25912_g1_i1_len_1046_path_1074_0_1045_3	145	cytochrome c oxidase assembly factor 7 homolog	349	1.56E-71	65.70%	0.099	Coil (COILS); IPR006597 (SMART); IPR006597 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR13891 (PANTHER); PTHR13891:SF1 (PANTHER); SSF81901 (SUPERFAMILY)
1042	c25953_g2_i1_len_146_path_227_0_145_2	2	low quality protein: hemicentin-2	48	4.16E-12	63.50%	0.125	IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR018097 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY)
1043	c26108_g2_i1_len_147_path_163_0_146_0	2	thrombospondin-type laminin g domain and ear repeat-containing isoform x1	49	1.15E-12	75.70%	0.115	IPR005492 (PFAM); IPR009039 (PROSITE_PROFILES)

1055	c27007_g1_i1_len_1851_path_1879_0_1850_1	285	estradiol 17-beta-dehydrogenase 2	617	3.16E-71	56.70%	0.114	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316:SF215 (PANTHER); PTHR24316 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1056	c27115_g2_i1_len_939_path_1199_0_141_21_32_142_146_1345_147_938_0	53	ribonuclease oy	313	9.41E-64	59.40%	0.124	IPR001568 (G3DSA:3.90.730.GENE3D); IPR001568 (PFAM); IPR001568 (PANTHER); IPR018188 (PROSITE_PATTERNS); IPR001568 (SUPERFAMILY) IPR006689 (PRINTS); IPR003579 (SMART); IPR024156 (SMART); IPR006687 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF118 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1057	c27123_g1_i1_len_1918_path_53_0_1917_2	2092	adp-ribosylation factor 1	639	1.84E-127	98.50%	0.11	IPR017849 (G3DSA:3.40.720.GENE3D); IPR002591 (PFAM); IPR024873 (PANTHER); IPR017850 (SUPERFAMILY)
1058	c27128_g1_i1_len_566_path_544_0_565_3	22	ectonucleotide pyrophosphatase phosphodiesterase family member partial	189	3.44E-31	65.80%	0.11	IPR003172 (SMART); IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014756 (SUPERFAMILY)
1059	c27142_g1_i1_len_1243_path_53_0_72_126_73_1210_1262_1211_1242_1	605	md-2-related lipid-recognition	414	1.37E-16	50.50%	0.281	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1060	c27166_g1_i1_len_1619_path_1697_0_1618_2	509	plasminogen activator spa	539	8.86E-84	64.60%	0.406Y	IPR002290 (SMART); IPR016253 (PIRSF); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR22988 (PANTHER); PTHR22988:SF2 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1061	c27254_g1_i1_len_724_path_587_0_69_44_7_0_723_3	24	serine threonine-protein kinase genghis khan isoform x1	242	3.79E-144	98.90%	0.133	IPR001747 (PFAM); IPR015816 (G3DSA:2.30.230.GENE3D); PTHR23345 (PANTHER); PTHR23345:SF1 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR015819 (SUPERFAMILY); TMhelix (TMHMM)
1062	c27271_g1_i2_len_570_path_1_0_245_247_2_46_569_4	29	beta- -glucan-binding protein precursor	190	3.38E-17	51.70%	0.907Y	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF237 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1063	c27333_g1_i1_len_730_path_1665_0_21_980_22_729_0	66	uncharacterized oxidoreductase	244	1.12E-62	69.00%	0.097	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1064	c27333_g1_i2_len_855_path_833_0_146_980_147_854_2	83	uncharacterized oxidoreductase	285	1.34E-81	68.00%	0.103	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF237 (PANTHER); SSF51735 (SUPERFAMILY)
1065	c27336_g1_i1_len_1332_path_1_0_337_720_338_412_339_413_1331_5	84	glypican- partial	444	2.27E-67	58.20%	0.151	IPR001863 (PFAM); IPR001863 (PANTHER); IPR019803 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1066	c27336_g1_i2_len_1063_path_721_0_68_720_69_143_339_144_1062_5	67	glypican- partial	354	2.68E-68	58.90%	0.151	IPR001863 (PFAM); IPR001863 (PANTHER); IPR019803 (PROSITE_PATTERNS)
1067	c27336_g1_i3_len_1257_path_1_0_337_339_338_1256_5	82	glypican- partial	419	3.38E-68	56.60%	0.151	IPR001863 (PFAM); IPR001863 (PANTHER); IPR019803 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1068	c27340_g1_i1_len_764_path_53_0_763_2	166	von willebrand factor like 2	254	2.21E-11	40.30%	0.102	no IPS match

1069	c27340_g2_i1_len_355_path_1863_0_354_1	91	phosphatidylinositol phosphatase ptrq-like protein	118	7.67E-06	52.00%	0.11	no IPS match IPR000118 (SMART); IPR000118 (PFAM); PTHR12274 (PANTHER); PTHR12274:SF1 (PANTHER); IPR000118 (PROSITE_PATTERNS); IPR000118 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF57277 (SUPERFAMILY); SSF57277 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1070	c2735_g1_i1_len_3616_path_1_0_3615_2	5292	granulins- partial	1205	2.28E-50	52.10%	0.124	IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); PTHR19134:SF252 (PANTHER); IPR016130 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)
1071	c27442_g2_i1_len_1413_path_1391_0_1412_1	68	tyrosine-protein phosphatase non-receptor	471	5.72E-155	72.60%	0.102	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1072	c27460_g1_i1_len_1064_path_105_0_1063_5	78	von willebrand factor type egf and pentraxin domain-containing protein 1	354	3.67E-30	43.70%	0.118	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24357:SF70 (PANTHER); PTHR24357 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1073	c27507_g1_i1_len_1403_path_1289_0_1024_2312_1025_1213_2312_1214_1402_3	78	protein kinase 3-like	468	7.33E-84	80.90%	0.102	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013151 (PFAM); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
1074	c2769_g2_i1_len_346_path_287_0_345_5	6	protein sidekick-1-like isoform x5	115	1.48E-13	50.90%	0.148	IPR010795 (PFAM); IPR017046 (PANTHER)
1075	c27762_g1_i1_len_818_path_896_0_817_1	30	prenylcysteine oxidase-like	273	2.42E-51	61.10%	0.117	IPR003172 (SMART); IPR003172 (G3DSA:2.60.40.GENE3D); IPR003172 (PFAM); PTHR11306 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR014756 (SUPERFAMILY); TMhelix (TMHMM)
1076	c27800_g1_i1_len_679_path_1_0_678_1	530	epididymal secretory protein e1	226	9.52E-31	57.80%	0.396Y	PTHR22901 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1077	c2783_g1_i2_len_496_path_1_0_237_239_238_495_5	9	sialate o-acetyltransferase-like	165	1.61E-15	57.10%	0.205	IPR013788 (PRINTS); IPR005203 (G3DSA:2.60.40.GENE3D); IPR005203 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR000896 (PFAM); IPR005204 (PFAM); PTHR11511:SF5 (PANTHER); IPR013788 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR002227 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR005204 (SUPERFAMILY); IPR014756 (SUPERFAMILY); IPR008922 (SUPERFAMILY)
1078	c27866_g2_i1_len_2377_path_4616_0_2376_0	949079	hemocyanin subunit type 1 precursor	793	0	75.70%	0.811 Y	IPR004172 (SMART); IPR014775 (PFAM); PTHR23122 (PANTHER); IPR004172 (PROSITE_PROFILES); IPR004172 (PROSITE_PROFILES); SSF101288 (SUPERFAMILY)
1079	c28043_g1_i1_len_523_path_1_0_303_305_304_522_0	19	maguk p55 subfamily member 6	175	9.69E-52	69.80%	0.106	IPR004172 (SMART); IPR014775 (PFAM); PTHR23122 (PANTHER); IPR004172 (PROSITE_PROFILES); SSF101288 (SUPERFAMILY)
1080	c28043_g1_i2_len_486_path_5746_0_266_305_267_485_2	13	calcium calmodulin-dependent serine protein kinase	162	1.31E-16	65.10%	0.123	IPR004172 (SMART); IPR014775 (PFAM); PTHR23122 (PANTHER); IPR004172 (PROSITE_PROFILES); SSF101288 (SUPERFAMILY)

1081	c28043_g2_i1_len_2262_path_1001_0_2261_5	150	calcium calmodulin-dependent serine protein kinase	754	0	81.10%	0.105	IPR001452 (SMART); IPR001478 (SMART); IPR008145 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); G3DSA:2.30.30.40 (GENE3D); G3DSA:3.30.63.10 (GENE3D); IPR008145 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR001478 (PFAM); IPR011511 (PFAM); PTHR23122 (PANTHER); IPR020590 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008144 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001452 (SUPERFAMILY)
1082	c28145_g1_i1_len_1531_path_1689_0_680_8_62_681_1530_5	66	pancreatic triacylglycerol lipase	510	4.11E-70	58.00%	0.28	IPR000734 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR013818 (PFAM); IPR000734 (PANTHER); IPR029058 (SUPERFAMILY)
1083	c28240_g1_i1_len_1144_path_1241_0_702_8_6_703_714_98_715_893_31_894_1143_1	47	coiled-coil domain-containing protein 134-like	381	7.57E-51	63.80%	0.420Y	IPR026321 (PFAM); IPR026321 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1084	c28240_g1_i2_len_1132_path_1241_0_702_9_8_703_881_31_882_1131_1	55	coiled-coil domain-containing protein 134-like	377	4.74E-53	65.10%	0.420 Y	IPR026321 (PFAM); IPR026321 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
1085	c28264_g2_i1_len_358_path_959_0_356_140_4_357_357_1	11	ecdysteroid-regulated 16 kda	119	7.59E-26	74.20%	0.162	IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306 (PANTHER); PTHR11306:SF0 (PANTHER); IPR014756 (SUPERFAMILY)
1086	c28274_g1_i1_len_1094_path_1072_0_1093_1	105	pc3-like endoprotease variant b-like	365	4.17E-39	61.10%	0.187	IPR015500 (PRINTS); IPR000209 (G3DSA:3.40.50.GENE3D); IPR000209 (PFAM); G3DSA:3.30.70.850 (GENE3D); PTHR10795:SF340 (PANTHER); IPR015500 (PANTHER); IPR023827 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009020 (SUPERFAMILY); IPR000209 (SUPERFAMILY)
1087	c28274_g2_i1_len_153_path_2273_0_152_1	2	cre-bli-4 protein	51	2.50E-10	74.70%	0.101	IPR000209 (G3DSA:3.40.50.GENE3D); IPR000209 (SUPERFAMILY)
1088	c28289_g1_i1_len_440_path_1_0_236_238_2_37_263_238_264_290_265_291_304_279_30_5_326_809_327_434_784_4_1	13	flocculation protein flo11-like	147	2.38E-08	41.00%	0.116	no IPS match
1089	c28330_g1_i1_len_1549_path_832_0_385_17_34_386_1548_0	166	arylsulfatase b	517	1.18E-97	68.10%	0.199	G3DSA:3.30.1120.10 (GENE3D); IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342:SF189 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY)
1090	c28330_g1_i2_len_854_path_832_0_385_121_8_386_853_0	91	arylsulfatase b	285	1.10E-107	77.80%	0.199	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342 (PANTHER); PTHR10342:SF189 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY)
1091	c28338_g2_i1_len_390_path_710_0_228_439_229_252_463_253_389_2	15	zinc finger protein 358	130	3.45E-14	61.80%	0.13	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1092	c28358_g1_i1_len_766_path_541_0_162_704_163_211_25_212_456_270_457_765_4	40	upf0764 protein c16orf89 homolog	255	2.61E-29	47.70%	0.105	no IPS match
1093	c28358_g1_i2_len_922_path_869_0_327_704_328_376_1244_377_612_270_613_921_4	48	upf0764 protein c16orf89 homolog	307	1.35E-28	48.60%	0.105	no IPS match
1094	c28379_g1_i1_len_221_path_941_0_220_1	1	ensangg00000017398 protein	74	1.01E-41	99.40%	0.1	IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
1095	c28379_g2_i1_len_255_path_233_0_254_1	6	heat shock protein 70 cognate	85	8.10E-52	99.20%	0.1	G3DSA:3.90.640.10 (GENE3D); IPR013126 (PFAM); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); SSF53067 (SUPERFAMILY)
1096	c28379_g3_i1_len_162_path_465_0_161_2	1	heat shock cognate partial	54	2.15E-27	98.60%	0.106	IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
1097	c28383_g1_i1_len_513_path_1_0_512_0	19	protein flightless-1-like	171	5.89E-52	94.70%	0.102	IPR007122 (PRINTS); IPR007122 (SMART); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029919 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY)

1098	c28470_g1_i1_len_17166_path_105_0_17165_5	116346	hypothetical protein DAPPUDRAFT_332703	5722	0	50.70%	0.113	Coil (COILS); IPR014853 (SMART); IPR001846 (SMART); IPR014853 (PFAM); IPR001846 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); PTHR23361:SF13 (PANTHER); PTHR23361 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001846 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1099	c28486_g1_i1_len_1098_path_1_0_1097_2	1517	plasminogen activator spa	366	1.03E-67	57.70%	0.381 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1100	c28548_g1_i1_len_750_path_728_0_749_4	1079	af425264_1lysozyme precursor	250	3.42E-46	63.90%	0.126	IPR001916 (PRINTS); IPR000974 (PRINTS); IPR001916 (SMART); G3DSA:1.10.530.10 (GENE3D); IPR001916 (PFAM); PTHR11407 (PANTHER); IPR019799 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001916 (PROSITE_PROFILES); IPR023346 (SUPERFAMILY); TMhelix (TMHMM)
1101	c28603_g1_i2_len_1515_path_53_0_451_503_452_1514_4	100	protein partial	505	7.85E-97	56.10%	0.095	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR029605 (PANTHER)
1102	c28610_g1_i1_len_2494_path_105_0_2389_2_491_2390_2441_2491_2442_2493_4	305	chorion peroxidase-like	831	8.51E-136	55.00%	0.129	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
1103	c28630_g1_i1_len_945_path_969_0_545_151_4_546_560_48_561_944_0	54	calcium-activated chloride channel regulator 1-like	315	9.63E-25	54.40%	0.103	PTHR10579 (PANTHER); PTHR10579:SF8 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1104	c28630_g1_i2_len_930_path_969_0_545_48_546_929_0	36	calcium-activated chloride channel regulator 1-like	310	1.57E-23	54.70%	0.103	PTHR10579:SF8 (PANTHER); PTHR10579 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1105	c28639_g1_i1_len_541_path_519_0_431_951_432_444_964_445_540_1	42	protein disulfide-isomerase a4-like	180	5.23E-60	68.10%	0.902 Y	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005788 (TIGRFAM); IPR013766 (PFAM); PTHR18929 (PANTHER); PTHR18929:SF56 (PANTHER); IPR017937 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY)
1106	c28676_g1_i1_len_2181_path_1261_0_1573_625_1574_2180_1	108	endothelin-converting enzyme 1 isoform x2	727	0	65.10%	0.1	IPR018497 (PRINTS); G3DSA:1.10.1380.10 (GENE3D); IPR008753 (PFAM); IPR018497 (PFAM); IPR000718 (PANTHER); IPR029733 (PTHR11733:PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)

1107	c28738_g1_i1_len_1607_path_1585_0_1606_2	194	acetylcholine receptor subunit alpha-type acr-16	535	7.59E-112	59.90%	0.175	IPR006201 (PRINTS); IPR027361 (G3DSA:1.20.120.GENE3D); IPR006029 (PFAM); IPR006202 (PFAM); IPR006202 (G3DSA:2.70.170.GENE3D); IPR006201 (PANTHER); PTHR18945:SF490 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006202 (SUPERFAMILY); IPR006029 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1108	c2879_g1_i1_len_1213_path_1_0_588_590_589_1212_2	291	protein enhancer of sevenless 2b	404	4.02E-139	96.00%	0.152	IPR000980 (PRINTS); IPR001452 (PRINTS); PR00499 (PRINTS); IPR001452 (SMART); IPR000980 (SMART); IPR000980 (PFAM); IPR000980 (G3DSA:3.30.505.GENE3D); IPR001452 (PFAM); G3DSA:2.30.30.40 (GENE3D); G3DSA:2.30.30.40 (GENE3D); IPR001452 (PFAM); PTHR22820 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001452 (PROSITE_PROFILES); IPR000980 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); IPR001452 (SUPERFAMILY); IPR000980 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1109	c28820_g1_i1_len_264_path_53_0_105_619_106_147_201_148_263_1	9	venom protein a3ym10cm1	88	1.32E-08	65.20%	0.321	IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1110	c28863_g1_i1_len_366_path_555_0_322_25_323_365_3	10	prostaglandin f synthase-like	122	2.88E-35	74.50%	0.115	IPR020471 (PRINTS); IPR023210 (G3DSA:3.20.20.GENE3D); IPR023210 (PFAM); PTHR11732:SF133 (PANTHER); IPR001395 (PANTHER); IPR023210 (SUPERFAMILY)
1111	c28863_g1_i2_len_490_path_555_0_322_877_323_489_4	16	aldo-keto reductase	163	9.05E-42	73.30%	0.185	IPR020471 (PRINTS); IPR023210 (G3DSA:3.20.20.GENE3D); IPR023210 (PFAM); IPR001395 (PANTHER); PTHR11732:SF133 (PANTHER); IPR023210 (SUPERFAMILY)
1112	c28908_g1_i1_len_1511_path_1_0_1510_2	61	alcohol dehydrogenase	503	1.40E-103	66.70%	0.104	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); IPR001395 (PANTHER); PTHR11732:SF183 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023210 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1113	c28969_g1_i1_len_589_path_649_0_565_125_1_566_588_4	121	fatty acid binding protein	196	3.87E-54	75.10%	0.157	IPR000463 (PRINTS); IPR000566 (PFAM); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR11955 (PANTHER); IPR000463 (PROSITE_PATTERNS); IPR011038 (SUPERFAMILY)
1114	c28974_g1_i1_len_630_path_1_0_629_5	33	gamma-glutamyl hydrolase a-like isoform x3	210	3.05E-42	60.50%	0.108	IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY)
1115	c28974_g2_i1_len_284_path_1663_0_283_5	1	gamma-glutamyl hydrolase	94	3.13E-30	71.30%	0.115	IPR011697 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); PTHR11315:SF2 (PANTHER); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY)
1116	c28988_g2_i1_len_329_path_1075_0_328_5	7	inversin- partial	109	8.84E-31	71.10%	0.133	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24178 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1117	c28994_g1_i1_len_598_path_576_0_597_3	29	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein	200	7.81E-18	55.60%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1118	c28994_g2_i1_len_283_path_1199_0_282_2	2	zinc finger protein partial	94	6.71E-16	61.00%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1119	c29051_g1_i1_len_551_path_375_0_15_374_16_518_115_519_521_761_522_526_767_527_534_767_535_542_767_5_0	153	possible rna polymerase sigma factor	184	7.47E-14	51.33%	0.356Y	SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TMhelix (TMHMM)
1120	c29088_g1_i1_len_1990_path_1968_0_1989_2	156	protein unc-13 homolog c	663	1.24E-16	54.30%	0.111	IPR029334 (PFAM)
1121	c29116_g1_i1_len_1744_path_8_0_1743_2	151	15-hydroxyprostaglandin dehydrogenase	581	2.85E-50	60.10%	0.783 Y	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24310 (PANTHER); IPR020904 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); SSF51735 (SUPERFAMILY)
1122	c29139_g1_i1_len_1023_path_1001_0_1022_4	74	carbonic anhydrase	341	1.84E-59	71.70%	0.106	IPR001148 (SMART); IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); IPR023561 (PANTHER); IPR018338 (PROSITE_PATTERNS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
1123	c29139_g2_i1_len_924_path_2902_0_923_0	44	carbonic anhydrase 1	308	9.31E-35	68.20%	0.136	IPR001148 (SMART); IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); IPR023561 (PANTHER); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
1124	c29140_g1_i1_len_370_path_1_0_369_3	10	limbic system-associated membrane protein	124	1.63E-35	68.70%	0.098	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF47 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1125	c29140_g2_i1_len_880_path_1600_0_879_0	36	limbic system-associated membrane protein	294	6.67E-81	66.90%	0.111	IPR003599 (SMART); IPR003598 (SMART); IPR003961 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF45 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1127	c2915_g1_i1_len_643_path_51_0_39_25_40_642_1	33	von willebrand factor a domain-containing protein 8-like	214	7.73E-54	79.00%	0.113	IPR011704 (PFAM); PTHR21610:SF9 (PANTHER); PTHR21610 (PANTHER)
1128	c2915_g1_i2_len_679_path_51_0_39_90_40_75_25_76_678_1	59	von willebrand factor a domain-containing protein 8-like	226	9.46E-54	79.00%	0.122	IPR011704 (PFAM); PTHR21610:SF9 (PANTHER); PTHR21610 (PANTHER)
1126	c29152_g1_i1_len_1203_path_1181_0_1202_4	87	mam and ldl-receptor class a domain-containing protein c10orf112-like	401	1.87E-07	51.00%	0.108	IPR000998 (SMART); IPR000998 (PFAM); PTHR23282 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
1129	c29185_g1_i1_len_657_path_53_0_157_211_158_656_4	22	zinc finger protein 431-like isoform x2	219	3.96E-38	62.60%	0.106	IPR015880 (SMART); PF13465 (PFAM); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1130	c29185_g1_i2_len_890_path_371_0_390_211_391_889_4	43	zinc finger protein	297	6.59E-48	57.30%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1131	c29219_g1_i1_len_1473_path_47_0_235_46_236_1472_2	129	insulin-like growth factor-binding protein complex acid labile subunit	491	4.95E-74	56.30%	0.14	SM00365 (SMART); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1132	c29308_g1_i1_len_1110_path_1088_0_1109_3	497	steroid dehydrogenase	370	1.46E-116	68.80%	0.181	Coil (COILS); IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PIRSF); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316:SF68 (PANTHER); PTHR24316 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1133	c29342_g1_i1_len_2569_path_1_0_153_155_154_2568_1	26451	enolase isoform x2	856	0	89.70%	0.27	IPR000941 (PRINTS); IPR000941 (TIGRFAM); IPR029065 (G3DSA:3.20.20.GENE3D); IPR020811 (PFAM); IPR029017 (G3DSA:3.30.390.GENE3D); IPR020810 (PFAM); IPR000941 (PANTHER); IPR020809 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000941 (HAMAP); IPR029017 (SUPERFAMILY); IPR029065 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1134	c29342_g1_i2_len_2505_path_2842_0_89_155_90_2504_0	27238	enolase isoform x2	835	0	89.70%	0.105	IPR000941 (PRINTS); IPR020811 (PFAM); IPR029017 (G3DSA:3.30.390.GENE3D); IPR000941 (TIGRFAM); IPR020810 (PFAM); IPR029065 (G3DSA:3.20.20.GENE3D); IPR000941 (PANTHER); IPR020809 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000941 (HAMAP); IPR029065 (SUPERFAMILY); IPR029017 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1135	c29374_g2_i1_len_1398_path_1376_0_890_2267_891_1397_2	48	b-cell lymphoma 3-encoded protein	466	4.57E-44	55.40%	0.134	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1136	c29394_g1_i1_len_1365_path_1267_0_469_1735_470_472_1738_473_1066_2332_1067_1215_2332_1216_1364_1	201	follistatin-related protein 1	455	2.85E-86	57.40%	0.839Y	IPR002350 (SMART); IPR011992 (G3DSA:1.10.238.GENE3D); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR011992 (PFAM); PTHR10913 (PANTHER); PTHR10913:SF38 (PANTHER); IPR018247 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR002048 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF100895 (SUPERFAMILY); SSF47473 (SUPERFAMILY); SSF57603 (SUPERFAMILY)
1137	c29492_g3_i1_len_863_path_841_0_862_4	31	periostin- partial	288	8.26E-24	50.40%	0.135	IPR000782 (SMART); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900 (PANTHER); PTHR10900:SF72 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY)
1138	c29503_g1_i1_len_366_path_53_0_365_0	10	Aap	122	2.42E-14	54.20%	0.134	no IPS match
1139	c29503_g1_i1_len_366_path_53_0_365_4	10	collagen alpha-2 chain	122	1.47E-14	60.10%	0.103	PTHR24023 (PANTHER); PTHR24023:SF379 (PANTHER)
1140	c29503_g2_i1_len_312_path_739_0_311_2	14	collagen alpha-4 chain	104	2.80E-11	58.80%	0.098	IPR008160 (PFAM); PTHR24023:SF379 (PANTHER); PTHR24023 (PANTHER)
1141	c29503_g2_i1_len_312_path_739_0_311_5	14	hypothetical protein, partial	104	4.64E-09	45.60%	0.129	no IPS match
1142	c29516_g1_i1_len_800_path_1313_0_799_1	51	laminin subunit gamma- partial	267	7.78E-64	63.40%	0.104	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); SSF58104 (SUPERFAMILY)

1143	c29516_g2_i1_len_679_path_657_0_678_1	27	laminin a	226	1.61E-86	73.60%	0.101	Coil (COILS); Coil (COILS); PR00011 (PRINTS); IPR002049 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); PTHR10574:SF231 (PANTHER); PTHR10574 (PANTHER); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
1144	c29549_g2_i1_len_1958_path_1653_0_1957_2	122	bone morphogenetic protein receptor type-1b-like	652	0	76.00%	0.598Y	IPR003605 (SMART); IPR002290 (SMART); IPR000719 (PFAM); IPR000472 (PFAM); G3DSA:2.10.60.10 (GENE3D); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR003605 (PFAM); PTHR23255:SF53 (PANTHER); IPR000333 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR003605 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF57302 (SUPERFAMILY); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1145	c29556_g1_i1_len_1253_path_53_0_1252_2	69	apolipoprotein partial	417	7.05E-86	55.00%	0.186	PR00018 (PRINTS); IPR000001 (SMART); G3DSA:2.40.20.10 (GENE3D); IPR000001 (PFAM); PTHR24259 (PANTHER); PTHR24259:SF70 (PANTHER); IPR018056 (PROSITE_PATTERNS); IPR018056 (PROSITE_PATTERNS); IPR018056 (PROSITE_PATTERNS); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY)
1146	c29581_g1_i1_len_192_path_516_0_191_3	2	endothelin-converting enzyme 1 isoform x2	64	6.63E-23	81.20%	0.266	IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); IPR000718 (PANTHER); IPR029733 (PTHR11733:PANTHER); SSF55486 (SUPERFAMILY)
1147	c29581_g3_i1_len_408_path_1070_0_407_0	7	endothelin-converting enzyme	136	8.50E-76	90.60%	0.118	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); IPR000718 (PANTHER); IPR029733 (PTHR11733:PANTHER); SSF55486 (SUPERFAMILY)
1148	c29585_g1_i1_len_832_path_1080_0_831_4	54	carboxypeptidase m isoform x2	277	1.19E-44	69.90%	0.201	IPR014766 (G3DSA:2.60.40.GENE3D); PF13620 (PFAM); PTHR11532 (PANTHER); IPR027062 (PTHR11532:PANTHER); IPR008969 (SUPERFAMILY)
1149	c2959_g2_i1_len_393_path_371_0_392_0	8	tyrosine kinase receptor cad96ca	131	1.78E-66	89.00%	0.171	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416 (PANTHER); PTHR24416:SF268 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1150	c29615_g1_i1_len_1946_path_1_0_1331_339_0_1332_1571_1333_1572_1945_4	125	isoform cra_d	649	3.31E-39	49.10%	0.121	PR00018 (PRINTS); IPR000001 (SMART); G3DSA:2.40.20.10 (GENE3D); IPR000001 (PFAM); PTHR24259 (PANTHER); IPR018056 (PROSITE_PATTERNS); IPR018056 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY); TMhelix (TMHMM)
1151	c29615_g1_i2_len_1706_path_1_0_1331_133_3_1332_1705_4	131	hypothetical protein BRAFLDRAFT_239152	569	7.60E-17	69.40%	0.121	PR00018 (PRINTS); IPR000001 (SMART); G3DSA:2.40.20.10 (GENE3D); IPR000001 (PFAM); PTHR24259 (PANTHER); IPR018056 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000001 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); TMhelix (TMHMM)
1152	c29661_g1_i1_len_3116_path_53_0_3115_2	695	collagen alpha-1 chain isoform x3	1038	1.08E-107	49.80%	0.159	IPR002172 (SMART); IPR008160 (PFAM); IPR010515 (PFAM); IPR002172 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24023 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1153	c29661_g1_i1_len_3116_path_53_0_3115_4	695	collagen alpha-2 chain-like isoform x3	1039	1.00E-35	41.90%	0.099	PTHR24023:SF405 (PANTHER); PTHR24023 (PANTHER)
1154	c29687_g2_i1_len_1003_path_317_0_44_362_45_1002_4	28	serine proteinase	334	9.81E-29	53.90%	0.136	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF81 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR009003 (SUPERFAMILY)

1155	c29688_g1_i1_len_1639_path_89_0_641_53_642_671_53_672_701_53_702_731_2265_73_2_735_28_736_762_28_763_4	140	glutamine-rich protein 2	546	5.64E-23	44.60%	0.099	no IPS match	
1156	c29688_g1_i3_len_1612_path_89_0_641_53_642_671_53_672_701_53_702_731_2265_73_2_735_28_736_762_28_763_4	152	glutamine-rich protein 2	537	1.44E-21	44.70%	0.099	no IPS match	
1157	c29740_g1_i1_len_1819_path_53_0_1818_1	107	thioredoxin domain-containing protein 5	606	9.21E-168	72.20%	0.292		PR00421 (PRINTS); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005788 (TIGRFAM); PTHR18929:SF52 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1158	c29872_g2_i1_len_620_path_715_0_619_1	19	fibrillin-2 isoform x3	207	4.81E-33	61.50%	0.102		IPR003410 (PFAM); PTHR24273:SF29 (PANTHER); PTHR24273 (PANTHER); IPR003410 (PROSITE_PROFILES)
1159	c29878_g1_i1_len_2946_path_1_0_49_51_50_2945_0	711	beta-mannosidase	982	0	63.30%	0.203		IPR006103 (PFAM); IPR006102 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR008979 (G3DSA:2.60.120.GENE3D); IPR013812 (G3DSA:2.60.40.GENE3D); IPR006104 (PFAM); PTHR10066 (PANTHER); IPR028369 (PTHR10066:PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006102 (SUPERFAMILY); IPR006102 (SUPERFAMILY); IPR006102 (SUPERFAMILY); IPR008979 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1160	c29878_g1_i2_len_2931_path_155_0_34_51_35_2930_0	714	beta-mannosidase	977	0	63.30%	0.223		IPR006104 (PFAM); IPR006102 (PFAM); IPR006103 (PFAM); IPR013812 (G3DSA:2.60.40.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR008979 (G3DSA:2.60.120.GENE3D); PTHR10066 (PANTHER); IPR028369 (PTHR10066:PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006102 (SUPERFAMILY); IPR006102 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR008979 (SUPERFAMILY); IPR006102 (SUPERFAMILY)
1161	c29879_g1_i1_len_1522_path_1_0_1260_126_2_1261_1305_3256_1306_1327_1329_1328_1521_4	6271	serine protease 56	507	6.74E-11	43.90%	0.103		IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1162	c29881_g1_i1_len_1101_path_1079_0_20_11_00_21_298_1378_299_300_1380_301_1100_2	626	meprin a subunit beta	367	4.72E-51	58.20%	0.368	Y	IPR001506 (PRINTS); IPR006026 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1163	c29881_g1_i2_len_1245_path_2322_0_164_1_100_165_442_1378_443_444_1380_445_12_44_2	622	meprin a subunit beta	415	1.25E-50	58.20%	0.177		IPR001506 (PRINTS); IPR006026 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)
1164	c29900_g1_i1_len_2348_path_2326_0_2347_2	575	pdgf- and vegf-related factor 1-like precursor	782	7.02E-53	55.80%	0.157		IPR000072 (SMART); IPR000072 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); PTHR11633 (PANTHER); PTHR11633:SF1 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000072 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1165	c29953_g1_i1_len_1228_path_1_0_1227_1	51	vascular endothelial growth factor receptor partial	409	1.13E-27	47.20%	0.125		PR01832 (PRINTS); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR15360 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)

1171	c30008_g3_i1_len_3002_path_771_0_289_73_8_290_322_3763_323_3001_3	303	low-density lipoprotein receptor-related protein 2	1001	0	71.70%	0.113	IPR002172 (PRINTS); IPR001881 (SMART); IPR000033 (SMART); IPR002172 (SMART); IPR000742 (SMART); IPR000033 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1172	c3003_g1_i1_len_541_path_1589_0_540_3	14	zinc finger protein ozf-like	181	5.05E-26	62.20%	0.103	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1173	c30068_g1_i1_len_1880_path_1_0_352_352_353_1136_1136_1137_1879_0	84	tbc domain-containing protein kinase-like protein	627	3.63E-73	69.00%	0.14	G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24362 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1174	c30068_g1_i2_len_2332_path_1_0_352_352_353_1136_4209_1137_1588_1136_1589_23_31_0	104	tbc domain-containing protein kinase-like protein	778	0	68.50%	0.14	G3DSA:1.10.8.270 (GENE3D); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); IPR000195 (PFAM); PTHR22957:SF22 (PANTHER); PTHR22957 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000195 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); IPR000195 (SUPERFAMILY)
1175	c30140_g1_i1_len_1483_path_1511_0_1318_2830_1319_1482_5	186	ves g 5 allergen	494	3.93E-44	53.20%	0.167	IPR002172 (PRINTS); IPR014044 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001283 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1176	c30140_g1_i2_len_1371_path_1511_0_1318_3044_1319_1370_4	139	ves g 5 allergen	457	6.35E-44	53.20%	0.278	IPR002172 (PRINTS); IPR002172 (SMART); IPR014044 (SMART); IPR014044 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

1177	c30156_g1_i1_len_1323_path_1334_0_570_370_571_578_1912_579_1322_1	285	neurofilament triplet h protein	441	3.51E-09	52.20%	0.107	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1178	c30180_g1_i1_len_1591_path_53_0_538_592_539_1590_1	410	ddb1- and cul4-associated factor 13-like	530	0	80.80%	0.099	IPR001680 (SMART); IPR007287 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22851:SF0 (PANTHER); PTHR22851 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1179	c30199_g1_i1_len_935_path_51_0_652_25_6_53_934_4	48	peptidoglycan recognition protein 2 short class	312	2.06E-17	64.30%	0.874 Y	IPR006619 (SMART); IPR002502 (G3DSA:3.40.80.GENE3D); IPR015510 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR002502 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1180	c30199_g1_i1_len_935_path_51_0_652_25_6_53_934_5	48	peptidoglycan recognition protein 1	311	3.46E-12	65.70%	0.768 Y	IPR002502 (G3DSA:3.40.80.GENE3D); IPR015510 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR002502 (SUPERFAMILY)
1181	c30199_g1_i2_len_1054_path_51_0_652_703_653_771_25_772_1053_4	84	peptidoglycan recognition protein 3 short class	351	1.21E-57	64.50%	0.874 Y	IPR006619 (SMART); IPR002502 (SMART); IPR002502 (PFAM); IPR002502 (G3DSA:3.40.80.GENE3D); IPR015510 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR002502 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1182	c30201_g1_i1_len_1655_path_3455_0_19_92_20_187_260_188_1654_2	336	wd40 repeat-containing protein partial	551	0	94.20%	0.098	IPR020472 (PRINTS); IPR006595 (SMART); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22848 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR006595 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1183	c30201_g1_i2_len_1726_path_1_0_90_92_91_258_260_259_1725_1	364	wd40 repeat-containing protein smu1	575	0	93.80%	0.099	IPR020472 (PRINTS); IPR006595 (SMART); IPR001680 (SMART); IPR006594 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22848 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR006594 (PROSITE_PROFILES); IPR006595 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1184	c30216_g1_i1_len_1365_path_1343_0_1364_2	83	ubx domain-containing protein 1	455	6.32E-127	67.30%	0.467 Y	Coil (COILS); Coil (COILS); IPR001012 (SMART); IPR015940 (SMART); IPR000449 (PFAM); G3DSA:3.10.20.90 (GENE3D); IPR001012 (PFAM); G3DSA:1.10.8.10 (GENE3D); PTHR13020 (PANTHER); PTHR13020:SF25 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR001012 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR015940 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR029071 (SUPERFAMILY); IPR009060 (SUPERFAMILY)
1185	c30221_g1_i1_len_1070_path_16023_0_1069_2	47	hemocytin	356	1.45E-38	45.10%	0.107	G3DSA:2.10.25.10 (GENE3D); IPR014853 (PFAM); IPR001846 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY)
1186	c30221_g2_i1_len_8017_path_37_0_8016_4	3637	von willebrand factor	2672	3.50E-30	41.70%	0.108	IPR001007 (SMART); PTHR11339 (PANTHER); IPR001007 (PROSITE_PATTERNS); IPR001007 (PROSITE_PATTERNS); PD968187 (PRODOM); IPR001007 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); IPR006207 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES)

1187	c30244_g1_i1_len_3069_path_3097_0_2035_5131_2036_2204_5300_2205_3068_0	2585	neutral ceramidase	1023	0	66.70%	0.256	IPR006823 (PFAM); PTHR12670:SF1 (PANTHER); IPR006823 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1188	c30244_g1_i2_len_2900_path_3097_0_2035_5300_2036_2899_0	2107	neutral ceramidase isoform x2	967	0	67.60%	0.256	IPR006823 (PFAM); IPR006823 (PANTHER); PTHR12670:SF1 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1189	c30275_g1_i1_len_1100_path_1306_0_695_2_178_696_1099_5	224	dehydrogenase reductase sdr family member 4-like isoform x4	366	7.11E-69	75.70%	0.15	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PF13561 (PFAM); PTHR24322:SF239 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
1190	c30275_g1_i2_len_1278_path_1306_0_695_2_000_696_873_2178_874_1277_3	503	dehydrogenase reductase sdr family member 4-like isoform x1	426	1.40E-106	74.40%	0.136	IPR002198 (PRINTS); IPR002347 (PRINTS); PF13561 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF239 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
1191	c30508_g1_i1_len_933_path_911_0_932_4	46	calcium calmodulin-dependent protein kinase	311	3.49E-124	92.10%	0.117	IPR008145 (SMART); IPR008145 (PFAM); G3DSA:3.30.63.10 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23122 (PANTHER); PTHR23122:SF7 (PANTHER); IPR020590 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1192	c30508_g2_i1_len_1068_path_1821_0_1067_1	26	peripheral plasma membrane protein cask-like	356	1.27E-168	80.80%	0.236	IPR004172 (SMART); IPR000719 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); G3DSA:1.10.287.650 (GENE3D); IPR014775 (PFAM); IPR001478 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR23122:SF40 (PANTHER); PTHR23122 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR004172 (PROSITE_PROFILES); IPR004172 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR011009 (SUPERFAMILY); SSF101288 (SUPERFAMILY); SSF101288 (SUPERFAMILY)
1193	c30508_g3_i1_len_428_path_4161_0_427_4	12	peripheral plasma membrane protein cask isoform x2	143	1.49E-86	94.50%	0.107	IPR001452 (PRINTS); IPR001452 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR011511 (PFAM); PTHR23122:SF7 (PANTHER); PTHR23122 (PANTHER); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY)
1194	c30512_g1_i1_len_1261_path_1_0_133_1579_134_135_456_136_1260_1	38	cyclin-dependent kinase 9-like	420	0	93.50%	0.135	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24056 (PANTHER); PTHR24056:SF158 (PANTHER); IPR008271 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1195	c30515_g1_i1_len_1395_path_41_0_903_20_904_1394_2	170	carboxypeptidase n subunit 2	465	1.94E-18	41.80%	0.286	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
1196	c30553_g1_i1_len_1007_path_1_0_161_1963_162_281_163_282_729_611_730_742_624_743_1006_4	43	neuroendocrine protein 7b2	336	7.71E-91	62.80%	0.26	Coil (COILS); IPR007945 (PFAM); PTHR12738:SF0 (PANTHER); IPR007945 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1197	c30553_g1_i2_len_887_path_1_0_161_163_162_609_611_610_622_624_623_886_4	55	neuroendocrine protein 7b2	296	7.02E-85	64.60%	0.26	IPR007945 (PFAM); PTHR12738:SF0 (PANTHER); IPR007945 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1198	c30706_g1_i1_len_1293_path_53_0_9_63_10_1292_4	85	protein disulfide-isomerase a4-like	431	1.06E-54	70.10%	0.098	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF56 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1199	c30799_g1_i1_len_1409_path_1563_0_1408_1	68	periodic tryptophan protein 2 homolog	470	0	79.00%	0.18	IPR001680 (SMART); IPR007148 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR027145 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)

1200	c30832_g1_i1_len_1867_path_1895_0_1866_0	113	carboxylesterase 4a	623	6.99E-148	57.40%	0.136	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR019819 (PROSITE_PATTERNS); IPR019826 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY)
1201	c30882_g1_i1_len_1647_path_1625_0_1010_3396_1011_1646_2	91	laccase-1 isoform x1	549	4.15E-88	62.00%	0.246	IPR008972 (G3DSA:2.60.40.GENE3D); IPR011706 (PFAM); IPR008972 (G3DSA:2.60.40.GENE3D); PTHR11709 (PANTHER); PTHR11709:SF33 (PANTHER); IPR002355 (PROSITE_PATTERNS); IPR002355 (PROSITE_PATTERNS); IPR008972 (SUPERFAMILY)
1202	c30981_g1_i1_len_1348_path_1326_0_1347_4	61	serine threonine-protein kinase 16	449	8.39E-144	76.90%	0.457Y	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR22967 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR011009 (SUPERFAMILY)
1203	c31027_g1_i1_len_329_path_1625_0_328_1	5	spondin-1	110	9.63E-11	61.30%	0.109	IPR000884 (SMART); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); PTHR11311:SF11 (PANTHER); PTHR11311 (PANTHER); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY)
1204	c31027_g3_i1_len_534_path_750_0_533_0	11	spondin-1	178	2.81E-50	61.80%	0.11	IPR002223 (PRINTS); IPR000884 (SMART); IPR002223 (SMART); G3DSA:2.20.100.10 (GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR000884 (PFAM); PTHR11311:SF11 (PANTHER); PTHR11311 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR000884 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
1205	c31054_g1_i1_len_161_path_885_0_160_4	1	allatostatin precursor protein	54	1.63E-06	84.00%	0.108	no IPS match
1206	c31054_g2_i1_len_532_path_61_0_411_47_4_12_441_47_442_471_47_472_501_47_502_531_1	27	allatostatin precursor protein	177	1.93E-32	59.80%	0.099	IPR010276 (PFAM)
1207	c31056_g1_i1_len_1109_path_1087_0_73_11_61_74_75_1163_76_1108_2	733	eukaryotic translation initiation factor 3 subunit i-like	369	1.11E-180	84.20%	0.113	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19877 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR027525 (HAMAP); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1208	c31075_g1_i1_len_785_path_787_0_8_796_9_784_3	88	cysteine string protein	262	6.43E-100	76.10%	0.271	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF5 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1209	c31097_g1_i1_len_1707_path_53_0_1637_34_65_1638_1641_1692_1642_1706_0	96	protein sda1 homolog isoform x2	569	0	71.50%	0.209	IPR007949 (PFAM); IPR027312 (PTHR12730:PANTHER); PTHR12730 (PANTHER); IPR016024 (SUPERFAMILY)
1210	c31104_g1_i2_len_2116_path_2437_0_207_2_645_208_1508_311_1509_1532_3968_1533_1543_346_1544_2115_2	573	agap005124-pc-like protein	705	0	78.00%	0.118	Coil (COILS); IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); PTHR11699:SF15 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM)
1211	c31104_g1_i3_len_2030_path_4527_0_121_2_645_122_1422_311_1423_1446_3968_1447_1457_346_1458_2029_0	567	agap005124-pc-like protein	677	0	78.00%	0.11	Coil (COILS); IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF15 (PANTHER); IPR029510 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM)
1212	c31149_g1_i1_len_2212_path_2190_0_2211_0	132	tl5a_tactr ame: full=techylectin-5a flags: precursor	738	2.34E-53	60.50%	0.828Y	Coil (COILS); Coil (COILS); IPR002181 (SMART); IPR002181 (PFAM); IPR014715 (G3DSA:4.10.530.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR002181 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002181 (SUPERFAMILY)

1213	c31222_g1_i1_len_684_path_1_0_451_453_452_459_461_460_683_2	27	tight junction protein zo-3	228	1.87E-17	74.70%	0.109	Coil (COILS); IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964 (PANTHER); PTHR19964:SF22 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY) IPR001199 (PFAM); IPR001199 (G3DSA:3.10.120.GENE3D); PTHR10281:SF25 (PANTHER); PTHR10281 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001199 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1214	c31224_g1_i1_len_1074_path_1083_0_296_16_297_1073_2	106	membrane-associated progesterone receptor component 1-like	358	6.86E-74	77.20%	0.155	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); PTHR10342:SF206 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM)
1215	c31305_g2_i2_len_2325_path_3008_0_2129_5138_2130_2324_1	378	arylsulfatase b	775	1.46E-172	64.80%	0.158	IPR002126 (SMART); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24026 (PANTHER); PTHR24026:SF39 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY) IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24028 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY)
1216	c31334_g2_i1_len_237_path_497_0_236_2	0	fat-like cadherin-related tumor suppressor homolog isoform x1	79	1.95E-21	77.10%	0.101	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); PTHR22802:SF219 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
1217	c31334_g3_i1_len_263_path_711_0_262_3	5	fat-like cadherin-related tumor suppressor homolog isoform x1	88	1.47E-17	67.40%	0.106	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); SSF47874 (SUPERFAMILY)
1218	c31371_g1_i1_len_417_path_1_0_416_2	15	isoform a	139	7.24E-14	56.90%	0.118	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); SSF47874 (SUPERFAMILY)
1219	c31561_g1_i1_len_2005_path_389_0_519_4882_520_521_3401_522_2004_2	186	annexin a4	668	6.41E-92	67.60%	0.102	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); SSF47874 (SUPERFAMILY)
1220	c31561_g1_i3_len_1740_path_3145_0_254_4882_255_256_3401_257_1739_1	182	annexin partial	580	1.05E-93	67.70%	0.108	IPR002591 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); IPR024873 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1221	c31578_g1_i1_len_1846_path_1_0_1845_0	1691	ectonucleotide pyrophosphatase phosphodiesterase family member 6	616	3.17E-98	54.80%	0.234	Coil (COILS); IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24056 (PANTHER); PTHR24056:SF45 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); SSF101447 (SUPERFAMILY)
1222	c31626_g1_i1_len_2651_path_1_0_2328_2330_2329_2334_2336_2335_2491_5086_2492_2493_2336_2494_2650_4	342	serine threonine-protein kinase prp4 homolog	884	0	74.80%	0.128	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24054:SF28 (PANTHER); PTHR24054 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1223	c31647_g1_i1_len_1451_path_1596_0_154_1751_155_1277_2873_1278_1450_5	126	casein kinase ii subunit alpha	483	0	95.00%	0.155	

1224	c31647_g1_i2_len_1597_path_1596_0_154_3_045_155_300_1751_301_1423_2873_1424_1596_5	118	casein kinase ii subunit alpha	532	0	95.50%	0.155	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24054 (PANTHER); PTHR24054:SF28 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1225	c31647_g1_i3_len_1361_path_1596_0_154_1_751_155_1277_25_1278_1360_5	110	casein kinase ii subunit alpha	453	0	94.90%	0.102	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24054 (PANTHER); PTHR24054:SF28 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1226	c31704_g1_i1_len_1198_path_1_0_1197_0	46	complement c1q tumor necrosis factor-related protein 4	400	2.85E-09	43.90%	0.108	Coil (COILS); Coil (COILS); IPR001073 (SMART); IPR001073 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); PTHR22923 (PANTHER); PTHR22923:SF53 (PANTHER); IPR001073 (PROSITE_PROFILES); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY); IPR008983 (SUPERFAMILY); IPR008983 (SUPERFAMILY)
1227	c31725_g1_i1_len_2810_path_2788_0_2809_4	316	angiotensin-converting enzyme-like	937	1.12E-162	61.70%	0.247	Coil (COILS); IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1228	c31738_g2_i1_len_287_path_5748_0_198_59_46_199_211_5486_212_223_344_224_247_5_993_248_286_2	9	macrophage mannose receptor 1-like	95	5.62E-14	57.40%	0.103	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
1229	c31738_g3_i1_len_2581_path_5275_0_210_5_486_211_222_344_223_246_368_247_2580_1	178	macrophage mannose receptor 1-like	860	9.34E-132	49.50%	0.102	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); PTHR22803:SF16 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR018378 (PROSITE_PATTERNS); IPR018378 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1230	c31798_g1_i1_len_4051_path_4029_0_4050_5	1773	low-density lipoprotein receptor-related protein 6	1350	5.77E-13	46.20%	0.278	IPR002172 (PRINTS); IPR000859 (SMART); IPR000998 (SMART); IPR002172 (SMART); IPR000998 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
1231	c31858_g1_i1_len_972_path_53_0_971_5	60	leucine-rich repeat-containing protein 15-like isoform x2	324	9.16E-58	60.00%	0.101	Coil (COILS); Coil (COILS); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24373 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)

1232	c31931_g1_i1_len_1546_path_1624_0_1545_5	119	er membrane protein complex subunit 10	515	4.07E-72	63.60%	0.672	Y	IPR029615 (PTHR21397:PANTHER); PTHR21397 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1233	c31947_g1_i1_len_1492_path_409_0_147_55_6_148_1491_2	472	prophenoloxidase activating factor	497	4.12E-133	66.00%	0.116		IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); PTHR24268:SF95 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1234	c3195_g1_i1_len_146_path_255_0_145_2	1	thioredoxin-like protein	48	1.82E-21	96.70%	0.104		IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005746 (PANTHER); IPR012336 (SUPERFAMILY)
1235	c31967_g2_i1_len_1211_path_1943_0_1210_4	119	hyaluronidase precursor	404	1.41E-79	60.10%	0.216		IPR018155 (PRINTS); IPR001329 (PRINTS); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); IPR018155 (PANTHER); PTHR11769:SF8 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1236	c32030_g4_i1_len_1867_path_4222_0_230_7_19_231_254_743_255_644_1132_645_1866_5	421	26s protease regulatory subunit 10b	622	0	96.70%	0.097		Coil (COILS); IPR003593 (SMART); IPR005937 (TIGRFAM); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23073:SF24 (PANTHER); PTHR23073 (PANTHER); IPR003960 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR027417 (SUPERFAMILY)
1237	c32040_g1_i1_len_1612_path_1806_0_567_7_1_568_1611_4	160	serine protease	537	1.03E-57	75.40%	0.198		IPR008758 (PFAM); IPR008758 (PANTHER)
1238	c32040_g1_i1_len_1612_path_1806_0_567_7_1_568_1611_5	160	serine protease	537	9.53E-125	71.10%	0.171		IPR008758 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR008758 (PANTHER); PTHR11010:SF9 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1239	c32040_g1_i2_len_1700_path_1806_0_567_2_371_568_655_71_656_1699_5	220	serine protease	566	0	72.20%	0.171		IPR029058 (G3DSA:3.40.50.GENE3D); IPR008758 (PFAM); IPR008758 (PANTHER); PTHR11010:SF9 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1240	c32110_g1_i1_len_810_path_888_0_809_0	712	peptidase	270	8.36E-10	48.20%	0.132		IPR025711 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1241	c32126_g1_i1_len_1186_path_1164_0_717_1_882_718_924_2449_925_1185_4	71	trypsinogen 1	395	1.24E-77	63.00%	0.176		IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1242	c32126_g1_i2_len_255_path_2327_0_47_188_2_48_254_4	3	female reproductive tract protease partial	85	3.80E-14	66.30%	0.115		G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

1243	c32133_g1_i1_len_4456_path_93_0_3009_92_3010_4455_3	409	receptor-type tyrosine-protein phosphatase f	1486	0	85.00%	0.103	IPR000242 (PRINTS); IPR003961 (SMART); IPR000242 (SMART); IPR003595 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19134 (PANTHER); PTHR19134:SF199 (PANTHER); IPR016130 (PROSITE_PATTERNS); IPR016130 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000242 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR029021 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)
1244	c32152_g1_i1_len_407_path_287_0_404_92_405_406_1	7	hypothetical protein DAPPUDRAFT_246507	136	4.03E-16	59.60%	0.098	IPR025714 (PFAM); PTHR32026 (PANTHER)
1245	c32184_g1_i1_len_1158_path_53_0_941_993_942_943_995_944_1157_2	48	isoform j	386	8.06E-128	69.00%	0.109	IPR000742 (SMART); IPR013032 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF90148 (SUPERFAMILY)
1246	c32295_g1_i2_len_249_path_1955_0_68_202_4_69_248_0	2	suppressor of tumorigenicity 14 isoform x1	83	9.84E-07	63.50%	0.113	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
1247	c32315_g1_i1_len_1014_path_105_0_906_10_4_907_1013_0	106	lipophorin receptor	338	4.62E-50	64.10%	0.132	IPR000033 (SMART); PF14670 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); IPR000033 (PFAM); PTHR10529 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF63825 (SUPERFAMILY)
1248	c32324_g1_i1_len_1171_path_2639_0_704_3_368_705_732_27_733_807_2183_808_1063_2439_1064_1170_0	64	inhibitor of apoptosis	391	1.91E-53	51.50%	0.113	IPR001370 (SMART); IPR001841 (SMART); PF13920 (PFAM); G3DSA:1.10.8.10 (GENE3D); IPR001370 (G3DSA:1.10.1170.GENE3D); IPR001370 (PFAM); PTHR10044:SF86 (PANTHER); PTHR10044 (PANTHER); IPR001370 (PROSITE_PROFILES); IPR015940 (PROSITE_PROFILES); IPR001841 (PROSITE_PROFILES); SSF57924 (SUPERFAMILY); IPR009060 (SUPERFAMILY)
1249	c32324_g1_i2_len_1628_path_2639_0_704_3_368_705_732_27_733_807_102_808_1627_0	75	inhibitor of apoptosis	543	9.18E-52	51.50%	0.113	IPR001370 (SMART); IPR001841 (SMART); PF13920 (PFAM); IPR001370 (G3DSA:1.10.1170.GENE3D); G3DSA:1.10.8.10 (GENE3D); IPR013083 (G3DSA:3.30.40.GENE3D); IPR001370 (PFAM); PTHR10044:SF86 (PANTHER); PTHR10044 (PANTHER); IPR001841 (PROSITE_PROFILES); IPR001370 (PROSITE_PROFILES); IPR015940 (PROSITE_PROFILES); IPR009060 (SUPERFAMILY); SSF57924 (SUPERFAMILY)
1250	c32331_g1_i1_len_1417_path_129_0_1416_4	448	otogelin	472	7.37E-11	41.30%	0.106	no IPS match
1251	c32349_g1_i1_len_417_path_961_0_416_5	13	c-type lectin domain family member a	139	2.05E-24	57.50%	0.147	PR01504 (PRINTS); IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
1252	c32380_g1_i1_len_1318_path_1482_0_846_1_9_847_1317_2	103	flavin-containing monooxygenase fmo gs-ox-like 4	439	1.85E-129	63.40%	0.098	IPR000960 (PRINTS); G3DSA:3.50.50.60 (GENE3D); G3DSA:3.50.50.60 (GENE3D); IPR020946 (PFAM); PTHR23023 (PANTHER); PTHR23023:SF4 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51905 (SUPERFAMILY); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
1253	c32477_g1_i1_len_4022_path_53_0_4021_1	290	cd109 antigen	1341	0	60.10%	0.103	IPR002172 (SMART); IPR009048 (G3DSA:2.60.40.GENE3D); IPR001599 (PFAM); IPR011626 (PFAM); IPR011625 (PFAM); IPR008930 (G3DSA:1.50.10.GENE3D); IPR009048 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR11412 (PANTHER); PTHR11412:SF85 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR008930 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009048 (SUPERFAMILY); TMhelix (TMHMM)

1254	c32493_g1_i1_len_540_path_755_0_274_662_275_298_1051_299_416_1168_417_539_2	39	sortilin-related receptor	180	1.29E-10	41.10%	0.1	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1255	c32494_g1_i1_len_1820_path_1882_0_1605_3485_1606_1606_18_1607_1819_1	219	serine threonine-protein phosphatase 6 catalytic subunit	607	0	93.80%	0.102	IPR006186 (PRINTS); IPR006186 (SMART); IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); PTHR11668 (PANTHER); PTHR11668:SF24 (PANTHER); IPR006186 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
1256	c32501_g1_i1_len_408_path_1_0_407_0	24	low quality protein: mam and ldl-receptor class a domain-containing protein 1-like	136	8.66E-23	55.80%	0.177	IPR000998 (PFAM); PTHR23282:SF75 (PANTHER); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
1257	c32501_g2_i1_len_1300_path_823_0_1299_1	47	apical endosomal glycoprotein	433	1.95E-31	46.50%	0.103	IPR000998 (SMART); IPR000998 (PFAM); PTHR23282 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
1258	c32539_g3_i1_len_434_path_311_0_433_2	6	zinc finger protein ozf-like	144	3.03E-27	58.30%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1259	c32545_g1_i1_len_1438_path_53_0_202_256_203_1437_2	113	torsin-1b-like isoform x2	479	4.42E-25	53.00%	0.269	IPR027417 (G3DSA:3.40.50.GENE3D); IPR010448 (PFAM); IPR010448 (PANTHER); IPR030553 (PTHR10760:PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1260	c32545_g1_i2_len_1366_path_3010_0_130_2_56_131_1365_2	115	torsin-1b-like isoform x1	455	2.81E-25	52.60%	0.107	IPR010448 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR010448 (PANTHER); IPR030553 (PTHR10760:PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1261	c32640_g1_i1_len_1260_path_97_0_1138_96_1139_1259_0	140	matrix metalloproteinase-9-like	420	1.50E-09	48.90%	0.131	IPR000562 (SMART); IPR000562 (PFAM); IPR000562 (G3DSA:2.10.10.GENE3D); IPR000562 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY)
1262	c32677_g1_i1_len_2050_path_1_0_647_4108_648_680_649_681_2049_5	271	serine threonine-protein phosphatase 2b catalytic subunit 2-like isoform x1	683	0	93.50%	0.405Y	IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668:SF186 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
1263	c32677_g1_i2_len_2017_path_1_0_647_649_648_2016_5	283	serine threonine-protein phosphatase 2b catalytic subunit 2-like isoform x2	672	0	94.90%	0.405 Y	IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668:SF186 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
1264	c32716_g1_i1_len_1207_path_199_0_98_23_99_100_122_101_1206_1	43	probable histone-binding protein caf1 isoform x2	402	0	98.80%	0.249	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR022052 (PFAM); PTHR22850 (PANTHER); PTHR22850:SF82 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1265	c32716_g1_i2_len_1182_path_47_0_55_102_56_75_122_76_1181_0	30	probable histone-binding protein caf1	394	0	99.00%	0.15	IPR020472 (PRINTS); IPR001680 (SMART); IPR022052 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22850:SF82 (PANTHER); PTHR22850 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)

1266	c32716_g1_i3_len_1164_path_47_0_55_23_5_6_57_122_58_1163_0	32	probable histone-binding protein caf1 isoform x2	388	0	99.00%	0.123	IPR020472 (PRINTS); IPR001680 (SMART); IPR022052 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22850:SF82 (PANTHER); PTHR22850 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1267	c32786_g2_i1_len_1745_path_1943_0_1544_3707_1545_1744_4	209	cytochrome p450 2u1-like	582	8.27E-126	57.40%	0.105	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1268	c32828_g1_i1_len_1789_path_1867_0_1788_3	379	guanine nucleotide-binding protein g g subunit beta-1	597	0	97.80%	0.14	Coil (COILS); IPR001632 (PRINTS); IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR016346 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1269	c32835_g1_i1_len_521_path_241_0_224_466_225_520_2	12	serine protease	173	1.44E-08	64.00%	0.115	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
1270	c32835_g1_i2_len_444_path_1113_0_147_46_6_148_443_0	26	serine protease	148	6.80E-09	64.60%	0.129	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR009003 (SUPERFAMILY)
1271	c32911_g1_i1_len_152_path_3612_0_151_2	1	attractin-like protein 1	50	9.33E-11	73.20%	0.103	no IPS match
1272	c32911_g2_i1_len_845_path_1_0_786_3764_787_844_3	31	attractin-like protein 1 isoform x2	282	1.10E-125	81.80%	0.262	IPR002049 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR10574:SF3 (PANTHER); PTHR10574 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)
1273	c32911_g2_i2_len_1764_path_1_0_786_788_787_1763_4	83	attractin-like protein 1 isoform x2	588	0	69.10%	0.122	IPR016201 (SMART); IPR002049 (SMART); IPR015915 (G3DSA:2.120.10.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); IPR002165 (PFAM); PF13854 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR10574 (PANTHER); PTHR10574:SF3 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF117281 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)
1274	c32960_g1_i1_len_882_path_1_0_881_1	58	zinc finger protein ozf-like	294	3.42E-62	61.20%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1275	c32999_g1_i1_len_830_path_917_0_748_25_749_829_5	68	virulence metalloprotease	266	5.71E-19	54.40%	0.173	IPR011096 (PFAM); IPR025711 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)

1276	c32999_g1_i2_len_881_path_917_0_748_166_6_749_799_25_800_880_5	73	virulence metalloprotease	283	1.79E-18	54.40%	0.136	IPR025711 (PFAM); IPR011096 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1277	c32999_g1_i3_len_890_path_917_0_748_166_6_749_799_1716_800_889_5	73	virulence metalloprotease	286	2.48E-18	54.40%	0.138	IPR025711 (PFAM); IPR011096 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1278	c33008_g1_i1_len_1460_path_1488_0_1459_3	115	vitellogenin fused with superoxide dismutase	487	7.13E-32	48.90%	0.273	IPR001846 (SMART); IPR001846 (PFAM); PTHR23345 (PANTHER); PTHR23345:SF1 (PANTHER); IPR001846 (PROSITE_PROFILES)
1279	c33012_g1_i2_len_562_path_1025_0_36_106_1_37_561_5	24	dehydrogenase reductase sdr family member 11-like	187	4.41E-59	73.30%	0.191	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF310 (PANTHER); SSF51735 (SUPERFAMILY)
1280	c33017_g1_i1_len_1951_path_103_0_1204_2_051_1205_1950_3	101	insulin-like receptor	651	4.31E-139	82.00%	0.102	IPR001245 (PRINTS); IPR020635 (SMART); IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24416 (PANTHER); PTHR24416:SF254 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR002011 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1281	c3302_g1_i1_len_926_path_1_0_185_187_18_6_925_2	26	phospholipase a2-like	308	4.46E-54	65.30%	0.114	IPR001211 (PRINTS); IPR016090 (SMART); IPR016090 (G3DSA:1.20.90.GENE3D); IPR016090 (PFAM); IPR001211 (PANTHER); PTHR11716:SF45 (PANTHER); IPR013090 (PROSITE_PATTERNS); IPR013090 (PROSITE_PATTERNS); IPR016090 (SUPERFAMILY)
1282	c3302_g1_i2_len_926_path_1993_0_185_187_186_925_2	22	phospholipase a2-like	308	4.83E-54	65.10%	0.252	IPR001211 (PRINTS); IPR016090 (SMART); IPR016090 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR11716:SF45 (PANTHER); IPR001211 (PANTHER); IPR013090 (PROSITE_PATTERNS); IPR013090 (PROSITE_PATTERNS); IPR016090 (SUPERFAMILY)
1283	c3306_g1_i1_len_1020_path_998_0_1019_3	11353	snaclec stejaggregin-a subunit beta-1-like isoform x2	340	5.55E-17	48.40%	0.295	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1284	c33081_g1_i1_len_4058_path_4090_0_4057_5	18173	long form-like	1352	0	86.30%	0.134	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR002928 (PFAM); PTHR13140 (PANTHER); PTHR13140:SF164 (PANTHER); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY)
1285	c33162_g1_i1_len_442_path_610_0_273_883_274_295_147_296_366_25_367_391_50_39_2_441_3	30	chemosensory protein	148	2.25E-55	81.80%	0.846Y	IPR005055 (PFAM); IPR005055 (G3DSA:1.10.2080.GENE3D); IPR005055 (PANTHER); PTHR11257:SF2 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR005055 (SUPERFAMILY)
1286	c33201_g1_i1_len_1860_path_53_0_1297_13_49_1298_1578_1349_1579_1859_1	253	alpha beta hydrolase domain-containing protein 13	620	2.56E-140	75.10%	0.099	IPR029059 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR12277 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)

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1298	c33878_g1_i1_len_616_path_678_0_254_932_255_272_43_273_615_1	32	apolipoprotein d	205	1.36E-08	43.00%	0.356Y	IPR012674 (G3DSA:2.40.128.GENE3D); IPR000566 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)
1299	c33884_g1_i1_len_1899_path_53_0_325_377_326_452_504_453_476_528_477_560_612_561_1898_0	6806	low affinity immunoglobulin epsilon fc receptor	633	4.67E-20	53.20%	0.510Y	Coil (COILS); IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001304 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1300	c33919_g1_i1_len_990_path_108_0_225_274_8_226_227_2600_228_354_734_355_375_75_5_376_989_1	158	dnaj homolog subfamily b member 6-b isoform x1	330	2.69E-85	65.20%	0.1	Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24077 (PANTHER); PTHR24077:SF225 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1301	c33919_g1_i2_len_1153_path_217_0_291_10_8_292_517_734_518_538_755_539_1152_2	303	dnaj homolog subfamily b member 6-like	384	3.83E-77	67.90%	0.214	Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24077 (PANTHER); PTHR24077:SF225 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1302	c33934_g1_i1_len_2060_path_2108_0_2059_0	18169	chitinase 1 precursor	687	0	69.60%	0.316	IPR002557 (SMART); IPR011583 (SMART); IPR002557 (PFAM); IPR001223 (PFAM); IPR029070 (G3DSA:3.10.50.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF144 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR029070 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1303	c34022_g1_i1_len_1243_path_1_0_1242_4	108	neurogenic locus notch partial	414	5.41E-161	81.10%	0.102	IPR001507 (SMART); IPR001507 (PFAM); PTHR22907 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001507 (PROSITE_PROFILES); TMhelix (TMHMM)
1304	c34025_g1_i1_len_1422_path_495_0_496_99_1_497_498_417_499_826_219_827_999_39_2_1000_1421_3	269	probable nuclear transport factor 2 isoform x1	474	4.80E-60	79.10%	0.225	IPR002075 (PFAM); G3DSA:3.10.450.50 (GENE3D); PTHR12612 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR018222 (PROSITE_PROFILES); SSF54427 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1305	c34025_g1_i2_len_1249_path_495_0_496_99_1_497_498_417_499_826_392_827_1248_3	457	probable nuclear transport factor 2 isoform x1	417	1.47E-61	81.80%	0.225	G3DSA:3.10.450.50 (GENE3D); IPR002075 (PFAM); PTHR12612 (PANTHER); IPR018222 (PROSITE_PROFILES); SSF54427 (SUPERFAMILY)
1306	c34049_g1_i2_len_3517_path_245_0_31_276_32_53_144_54_1441_1684_1442_2501_50_2502_3516_0	1041	cytosolic 10-formyltetrahydrofolate dehydrogenase isoform x1	1173	0	83.50%	0.123	Coil (COILS); Coil (COILS); IPR016162 (G3DSA:3.40.605.GENE3D); IPR005793 (G3DSA:3.10.25.GENE3D); IPR002376 (PFAM); IPR009081 (PFAM); IPR009081 (G3DSA:1.10.1200.GENE3D); IPR005793 (PFAM); IPR002376 (G3DSA:3.40.50.GENE3D); IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF118 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR001555 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); IPR009081 (PROSITE_PROFILES); IPR011034 (SUPERFAMILY); IPR009081 (SUPERFAMILY); IPR002376 (SUPERFAMILY); IPR016161 (SUPERFAMILY)
1307	c34059_g2_i1_len_236_path_214_0_187_780_188_194_787_195_235_2	96	hemagglutinin amebocyte aggregation factor-like	78	3.55E-09	63.00%	0.677Y	PF14704 (PFAM); IPR026645 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK)

1308	c34073_g1_i1_len_7197_path_1_0_906_908_907_907_909_908_3304_3306_3305_3380_3382_3381_7196_4	234020	myosin heavy chain isoform 3	2399	0	89.30%	0.18	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR001609 (PRINTS); IPR000048 (SMART); IPR001609 (SMART); IPR027401 (G3DSA:4.10.270.GENE3D); IPR001609 (PFAM); IPR004009 (PFAM); IPR002928 (PFAM); G3DSA:1.20.5.340 (GENE3D); PTHR13140:SF364 (PANTHER); PTHR13140 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001609 (PROSITE_PROFILES); IPR000048 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); TMhelix (TMHMM)
1309	c34073_g1_i2_len_7197_path_1_0_906_908_907_907_909_908_3304_14505_3305_3380_3382_3381_7196_4	226524	myosin heavy chain isoform 1	2399	0	89.40%	0.18	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR001609 (PRINTS); IPR001609 (SMART); IPR000048 (SMART); IPR027401 (G3DSA:4.10.270.GENE3D); IPR004009 (PFAM); IPR002928 (PFAM); G3DSA:1.20.5.340 (GENE3D); IPR001609 (PFAM); PTHR13140 (PANTHER); PTHR13140:SF364 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000048 (PROSITE_PROFILES); IPR001609 (PROSITE_PROFILES); SSF90257 (SUPERFAMILY); IPR027417 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); TMhelix (TMHMM)
1310	c34088_g1_i1_len_2904_path_5980_0_180_3_099_181_2671_5590_2672_2681_5600_2682_2903_2	507	beta-galactosidase-like isoform x2	968	0	59.70%	0.127	IPR001944 (PRINTS); IPR008979 (G3DSA:2.60.120.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001944 (PFAM); IPR001944 (PANTHER); PTHR23421:SF13 (PANTHER); IPR019801 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008979 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1311	c34088_g1_i2_len_2922_path_2900_0_198_3_099_199_2689_5590_2690_2699_5600_2700_2921_2	502	beta-galactosidase-like isoform x4	974	0	59.90%	0.273	IPR001944 (PRINTS); IPR001944 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR008979 (G3DSA:2.60.120.GENE3D); IPR001944 (PANTHER); PTHR23421:SF13 (PANTHER); IPR019801 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); IPR008979 (SUPERFAMILY)
1312	c34132_g1_i1_len_1301_path_105_0_1300_1	235	ribosome biogenesis protein wdr12 homolog	434	0	74.50%	0.103	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR012972 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19855 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR028599 (HAMAP); IPR017986 (SUPERFAMILY)
1313	c34145_g1_i1_len_2120_path_1_0_779_928_780_2119_0	370	pancreatic lipase-related protein 2-like	707	2.05E-129	56.50%	0.137	IPR000734 (PRINTS); IPR001024 (G3DSA:2.60.60.GENE3D); IPR013818 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR000734 (PANTHER); PTHR11610:SF83 (PANTHER); IPR008976 (SUPERFAMILY); IPR029058 (SUPERFAMILY)
1314	c34145_g1_i2_len_2267_path_1_0_779_781_780_926_928_927_2266_0	433	pancreatic lipase-related protein 2-like	756	3.08E-157	63.90%	0.137	IPR002331 (PRINTS); IPR000734 (PRINTS); IPR013818 (PFAM); IPR001024 (G3DSA:2.60.60.GENE3D); IPR029058 (G3DSA:3.40.50.GENE3D); IPR000734 (PANTHER); PTHR11610:SF83 (PANTHER); IPR029058 (SUPERFAMILY); IPR008976 (SUPERFAMILY)
1315	c34150_g1_i1_len_1340_path_1_0_954_2918_955_1136_2115_1137_1138_2094_1139_1339_0	275	prostatic acid phosphatase-like	447	1.11E-122	63.60%	0.582Y	IPR000560 (PFAM); IPR029033 (G3DSA:3.40.50.GENE3D); PTHR11567 (PANTHER); PTHR11567:SF26 (PANTHER); IPR000560 (PROSITE_PATTERNS); IPR000560 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR029033 (SUPERFAMILY); TMhelix (TMHMM)
1316	c34150_g1_i2_len_1156_path_1_0_954_2094_955_1155_0	176	lysosomal acid phosphatase	386	9.72E-101	67.00%	0.582Y	IPR000560 (PFAM); IPR029033 (G3DSA:3.40.50.GENE3D); PTHR11567 (PANTHER); PTHR11567:SF26 (PANTHER); IPR000560 (PROSITE_PATTERNS); IPR000560 (PROSITE_PATTERNS); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR029033 (SUPERFAMILY)

1317	c34169_g1_i1_len_914_path_1600_0_550_44_8_551_626_275_627_716_365_717_740_389_741_766_415_767_799_95_5	95	perlucin-like protein	304	1.01E-21	53.70%	0.499 Y	Coil (COILS); IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1318	c34187_g1_i1_len_1265_path_1_0_1264_0	1146	ferritin	422	6.73E-83	84.70%	0.183	Coil (COILS); IPR012347 (G3DSA:1.20.1260.GENE3D); IPR008331 (PFAM); IPR001519 (PANTHER); IPR014034 (PROSITE_PATTERNS); IPR014034 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1319	c34221_g4_i1_len_886_path_1911_0_885_3	58	collagen alpha 1 chain	296	7.22E-50	69.30%	0.106	IPR010515 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR026917 (PTHR24023:PANTHER); PTHR24023 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016187 (SUPERFAMILY)
1320	c34299_g1_i1_len_2140_path_679_0_108_46_109_180_859_181_2139_3	146	n-sulphoglucosamine partial	699	0	78.30%	0.824 Y	Coil (COILS); G3DSA:3.30.1120.10 (GENE3D); IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF76 (PANTHER); IPR024607 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017850 (SUPERFAMILY)
1321	c34308_g2_i1_len_965_path_105_0_964_1	30	ankyrin repeat domain-containing protein 6	322	6.92E-92	68.00%	0.109	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1322	c34327_g1_i1_len_2267_path_5255_0_213_1_428_214_753_1990_754_2266_1	114	microtubule-associated protein futsch isoform x1	756	0	76.60%	0.127	Coil (COILS); IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24343:SF26 (PANTHER); PTHR24343 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1323	c34327_g1_i2_len_1006_path_984_0_443_14_28_444_983_5514_984_1005_0	45	nuak family snf1-like kinase 1	336	1.07E-96	95.00%	0.13	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24343 (PANTHER); PTHR24343:SF26 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1324	c34327_g1_i3_len_2497_path_984_0_443_14_28_444_983_1990_984_2496_0	143	microtubule-associated protein futsch isoform x1	833	0	75.60%	0.13	Coil (COILS); IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24343 (PANTHER); PTHR24343:SF26 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1325	c34378_g1_i1_len_2025_path_1_0_206_208_207_2024_0	432	adp-ribosylation factor 5	675	4.25E-112	93.20%	0.264	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR003579 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF153 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1326	c34378_g1_i2_len_2031_path_4053_0_212_208_213_2030_0	411	adp-ribosylation factor 2	677	1.02E-116	95.70%	0.133	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR003579 (SMART); IPR005225 (TIGRFAM); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF153 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1327	c34397_g1_i1_len_3421_path_3541_0_747_4288_748_3420_1	1080	staphylococcal nuclease domain-containing protein 1-like	1140	0	74.40%	0.147	Coil (COILS); IPR016071 (SMART); IPR002999 (SMART); G3DSA:2.30.30.140 (GENE3D); IPR016071 (G3DSA:2.40.50.GENE3D); IPR016071 (PFAM); IPR002999 (PFAM); IPR016071 (G3DSA:2.40.50.GENE3D); IPR030481 (PTHR12302:PANTHER); PTHR12302 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002999 (PROSITE_PROFILES); IPR016071 (PROSITE_PROFILES); IPR016071 (PROSITE_PROFILES); IPR016071 (PROSITE_PROFILES); IPR016071 (SUPERFAMILY); SSF63748 (SUPERFAMILY); IPR016071 (SUPERFAMILY); IPR016071 (SUPERFAMILY); IPR016071 (SUPERFAMILY); IPR016071 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1328	c34424_g1_i1_len_1911_path_1988_0_1910_2	8805	retinal dehydrogenase 1-like	637	0	82.10%	0.117	IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF145 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016161 (SUPERFAMILY)
1329	c34447_g1_i1_len_937_path_1_0_936_5	41	endochitinase isoform x1	312	5.45E-150	80.40%	0.103	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF144 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
1330	c34447_g2_i1_len_661_path_2345_0_660_3	56	chitinase 5 isoform x1	221	5.86E-58	56.90%	0.105	IPR002557 (SMART); IPR001223 (PFAM); IPR029070 (G3DSA:3.10.50.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002557 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF144 (PANTHER); PTHR11177 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR029070 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1331	c34459_g1_i1_len_3233_path_6336_0_1380_5865_1381_1851_6336_1852_3232_5	788	chromodomain-helicase-dna-binding protein 7	1077	1.27E-46	50.60%	0.208	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); PTHR10799 (PANTHER); PTHR10799:SF536 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1332	c34483_g1_i1_len_958_path_986_0_957_4	172	plasminogen activator spa	319	2.28E-58	57.10%	0.313	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1333	c34489_g1_i1_len_2376_path_2354_0_861_3216_862_883_3238_884_2375_2	212	laminin subunit gamma-1-like	792	8.84E-60	67.20%	0.105	Coil (COILS); Coil (COILS); Coil (COILS); PTHR10574 (PANTHER); PTHR10574:SF228 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1334	c34517_g1_i1_len_1254_path_1232_0_1253_3	250	low quality protein: selenoprotein h	418	6.03E-20	65.30%	0.362Y	IPR020478 (PRINTS); IPR017956 (SMART); IPR017956 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR011893 (TIGRFAM); IPR011893 (PFAM); IPR012336 (SUPERFAMILY)

1335	c34530_g1_i1_len_5084_path_53_0_3149_32_01_3150_3173_3201_3174_3197_6453_3198_5083_2	3383	inter-alpha-trypsin inhibitor heavy chain h3 isoform x2	1694	1.28E-171	54.30%	0.14	Coil (COILS); IPR013694 (SMART); IPR006604 (SMART); IPR002035 (SMART); IPR002035 (PFAM); IPR013694 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); PTHR10338:SF108 (PANTHER); PTHR10338 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013694 (PROSITE_PROFILES); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
1336	c34541_g1_i1_len_3348_path_3426_0_3347_0	374	adenosine deaminase cecr1-like	1116	1.69E-163	65.40%	0.267	G3DSA:3.20.20.140 (GENE3D); IPR006331 (TIGRFAM); IPR001365 (PFAM); IPR013659 (PFAM); PTHR11409:SF39 (PANTHER); PTHR11409 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51556 (SUPERFAMILY); TMhelix (TMHMM)
1337	c34571_g1_i1_len_1671_path_1853_0_773_7_8_774_1145_3577_1146_1670_0	144	very low-density lipoprotein receptor isoform x2	557	8.89E-29	44.30%	0.109	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1338	c34571_g1_i2_len_543_path_3575_0_17_357_7_18_542_0	28	sortilin-related receptor	181	1.03E-12	59.70%	0.101	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1339	c34571_g1_i3_len_1728_path_1853_0_773_2_1_774_830_78_831_1202_3577_1203_1727_0	150	very low-density lipoprotein receptor isoform x2	576	3.02E-30	43.00%	0.109	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1340	c34594_g1_i1_len_4440_path_4666_0_4439_0	963	angiotensin-converting enzyme	1480	0	59.40%	0.275	Coil (COILS); Coil (COILS); IPR001548 (PRINTS); IPR001548 (PFAM); IPR002000 (PFAM); PTHR10514:SF17 (PANTHER); IPR001548 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1341	c34611_g2_i1_len_1953_path_457_0_118_48_99_119_1952_5	250	early growth response	651	3.95E-122	54.90%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR10042 (PANTHER); PTHR10042:SF24 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1342	c34645_g1_i1_len_762_path_1_0_761_3	50	mam and ldl-receptor class a domain-containing protein 1-like	254	1.30E-43	64.20%	0.114	IPR000998 (SMART); IPR000998 (PFAM); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
1343	c34721_g2_i1_len_2211_path_2515_0_2210_2	250	alpha-mannosidase 2	737	7.81E-162	58.80%	0.098	G3DSA:2.70.98.30 (GENE3D); G3DSA:1.10.287.530 (GENE3D); IPR015341 (PFAM); IPR011682 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); PTHR11607 (PANTHER); PTHR11607:SF4 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011013 (SUPERFAMILY); IPR028995 (SUPERFAMILY); TMhelix (TMHMM)
1344	c34737_g1_i1_len_1358_path_1513_0_468_1_44_469_516_192_517_1164_230_1165_1357_2	63	cuticlin- partial	452	0	72.80%	0.163	IPR001507 (SMART); IPR001507 (PFAM); PTHR22907 (PANTHER); PTHR22907:SF1 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001507 (PROSITE_PROFILES); TMhelix (TMHMM)
1345	c34737_g1_i2_len_1310_path_1513_0_468_1_92_469_1116_230_1117_1309_2	75	cuticlin- partial	436	0	75.00%	0.163	IPR001507 (SMART); IPR001507 (PFAM); PTHR22907 (PANTHER); PTHR22907:SF1 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001507 (PROSITE_PROFILES); TMhelix (TMHMM)
1346	c34760_g1_i1_len_3566_path_6155_0_509_3_074_510_3565_4	345	cgmp-dependent protein kinase 1-like	1189	0	76.90%	0.101	Coil (COILS); IPR002374 (PRINTS); IPR002290 (SMART); IPR000595 (SMART); IPR000961 (SMART); IPR014710 (G3DSA:2.60.120.GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); IPR000595 (PFAM); IPR014710 (G3DSA:2.60.120.GENE3D); PTHR24353 (PANTHER); PTHR24353:SF33 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000595 (PROSITE_PROFILES); IPR000595 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR018490 (SUPERFAMILY); IPR018490 (SUPERFAMILY); IPR011009 (SUPERFAMILY)
1347	c34764_g1_i1_len_1119_path_3195_0_1118_2	101	nf-kappa-b inhibitor	373	1.69E-68	67.30%	0.137	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24139:SF26 (PANTHER); PTHR24139 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1348	c34780_g1_i1_len_1298_path_151_0_1111_5_0_1112_1297_4	333	mite allergen lep d partial	433	7.89E-11	46.00%	0.259	PTHR11008:SF13 (PANTHER); PTHR11008 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1349	c34780_g1_i2_len_1421_path_151_0_1111_1_259_1112_1234_50_1235_1420_4	553	mite allergen lep d partial	474	1.02E-10	46.33%	0.199	PTHR11008 (PANTHER); PTHR11008:SF13 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1350	c34791_g1_i1_len_682_path_6373_0_160_58_29_161_681_1	20	sh3 domain-containing ring finger protein 3 isoform x1	227	1.88E-43	65.40%	0.115	IPR001452 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR001452 (PFAM); PTHR10661:SF7 (PANTHER); PTHR10661 (PANTHER); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY)
1351	c34817_g1_i1_len_444_path_1135_0_391_56_6_392_443_0	11	achain crystal structure of engineered northeast structural genomics consortium target	148	1.03E-24	60.10%	0.137	IPR002110 (SMART); PF13637 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1352	c34830_g1_i1_len_1215_path_1_0_1214_3	52	leucine-rich repeat neuronal protein 1-like	405	7.68E-90	49.20%	0.129	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1353	c34850_g1_i1_len_1290_path_1377_0_232_2_1_233_805_2181_806_815_77_816_1289_4	52	ankyrin repeat and socs box-containing protein 2 isoform x1	430	4.83E-20	40.90%	0.176	IPR002110 (SMART); IPR001496 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR001496 (PFAM); PTHR24188 (PANTHER); PTHR24188:SF32 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020683 (PROSITE_PROFILES); IPR001496 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); SSF158235 (SUPERFAMILY); IPR020683 (SUPERFAMILY)

1354	c34850_g1_i2_len_1077_path_1_0_19_21__2_0_592_2181_593_602_77_603_1076_4	38	ankyrin repeat and socs box protein 3	359	7.33E-18	45.20%	0.176	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1355	c34863_g1_i2_len_3109_path_3087_0_2898_5986_2899_2905_5993_2906_2961_6049_29_62_2966_6054_2967_2983_0	229	carboxypeptidase d-like	1037	0	64.20%	0.294	Coil (COILS); IPR000834 (PRINTS); IPR000834 (SMART); G3DSA:3.40.630.10 (GENE3D); IPR014766 (G3DSA:2.60.40.GENE3D); PF13620 (PFAM); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11532 (PANTHER); IPR015567 (PTHR11532:PANTHER); IPR000834 (PROSITE_PATTERNS); IPR000834 (PROSITE_PATTERNS); IPR000834 (PROSITE_PATTERNS); IPR000834 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); PS51257 (PROSITE_PROFILES); IPR008969 (SUPERFAMILY); IPR008969 (SUPERFAMILY); SSF53187 (SUPERFAMILY); SSF53187 (SUPERFAMILY)
1356	c34865_g1_i1_len_2391_path_1_0_2390_1	120	Pro-interleukin-16	797	3.36E-97	65.20%	0.107	Coil (COILS); IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR11324 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
1357	c34883_g1_i1_len_994_path_1_0_900_902_9_01_903_905_904_993_5	13011	trypsinogen 2	331	1.30E-72	62.40%	0.811Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1358	c34910_g1_i1_len_3007_path_49_0_1679_17_28_1680_1681_24_1682_3006_1	1300	carboxypeptidase q-like	1002	0	75.80%	0.242	IPR007484 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR12053 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1359	c34924_g1_i1_len_3369_path_1995_0_803_2_799_804_2016_3998_2017_2040_3998_2041_2064_3998_2065_2088_53_0	2457	zinc finger protein on ecdysone puffs	1123	6.68E-57	60.30%	0.153	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); G3DSA:1.10.601.10 (GENE3D); PF12874 (PFAM); PTHR15491 (PANTHER); IPR026811 (PTHR15491:PANTHER); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1360	c34924_g1_i2_len_2747_path_6669_0_205_2_799_206_1418_3998_1419_1442_3998_1443_1466_5364_1467_2746_2	1944	zinc finger protein on ecdysone puffs	915	4.44E-56	62.50%	0.273	Coil (COILS); Coil (COILS); Coil (COILS); PF12874 (PFAM); G3DSA:1.10.601.10 (GENE3D); PTHR15491 (PANTHER); IPR026811 (PTHR15491:PANTHER); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1361	c34924_g1_i3_len_3345_path_1995_0_803_2_799_804_2016_3998_2017_2040_3998_2041_2064_5364_2065_3344_0	2583	zinc finger protein on ecdysone puffs	1115	1.66E-55	63.50%	0.153	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); PF12874 (PFAM); G3DSA:1.10.601.10 (GENE3D); IPR026811 (PTHR15491:PANTHER); PTHR15491 (PANTHER); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)

1362	c34985_g1_i1_len_2475_path_4994_0_291_2_5_292_733_467_734_2474_5	473	stabilin-1 isoform x1	825	1.59E-126	65.90%	0.204	IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PFAM); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); TMhelix (TMHMM)
1363	c34996_g1_i1_len_2751_path_2879_0_2750_2	489	phenoloxidase subunit a3-like	917	0	67.40%	0.19	IPR013788 (PRINTS); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005203 (G3DSA:2.60.40.GENE3D); IPR005204 (PFAM); IPR000896 (PFAM); IPR005203 (PFAM); IPR005204 (G3DSA:1.20.1370.GENE3D); PTHR11511:SF24 (PANTHER); IPR013788 (PANTHER); IPR002227 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); IPR008922 (SUPERFAMILY); IPR014756 (SUPERFAMILY); IPR005204 (SUPERFAMILY)
1364	c35008_g1_i1_len_1905_path_163_0_57_22_58_73_38_74_428_573_429_434_162_435_1904_0	5438	universal minicircle sequence binding protein	635	2.32E-29	51.90%	0.173	Coil (COILS); Coil (COILS); IPR001878 (SMART); IPR001878 (G3DSA:4.10.60.GENE3D); IPR001878 (PFAM); IPR001878 (G3DSA:4.10.60.GENE3D); PTHR23002 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (SUPERFAMILY); IPR001878 (SUPERFAMILY)
1365	c35008_g1_i2_len_1889_path_163_0_57_38_58_412_573_413_418_162_419_1888_2	5763	universal minicircle sequence binding protein	629	7.73E-30	51.90%	0.121	Coil (COILS); Coil (COILS); IPR001878 (SMART); IPR001878 (G3DSA:4.10.60.GENE3D); IPR001878 (PFAM); IPR001878 (G3DSA:4.10.60.GENE3D); PTHR23002 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (SUPERFAMILY); IPR001878 (SUPERFAMILY)
1366	c35041_g1_i1_len_1856_path_1984_0_1855_1	186	serine-aspartate repeat protein f	619	4.50E-16	47.90%	0.1	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1367	c35041_g1_i1_len_1856_path_1984_0_1855_5	186	collagen alpha- chain	618	6.46E-132	71.80%	0.104	IPR001442 (SMART); IPR001442 (G3DSA:2.170.240.GENE3D); IPR008160 (PFAM); IPR001442 (PFAM); PTHR24023:SF381 (PANTHER); PTHR24023 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001442 (PROSITE_PROFILES); IPR001442 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1368	c35056_g1_i1_len_833_path_449_0_446_896_447_832_4	55	ankyrin repeat and socs box protein 3-like isoform x1	278	3.89E-38	58.90%	0.118	IPR002110 (PRINTS); IPR002110 (SMART); PF13637 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24188:SF24 (PANTHER); PTHR24188 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1369	c35057_g1_i1_len_494_path_93_0_336_430_337_349_443_350_381_71_382_402_92_403_493_5	14	zinc finger protein	164	4.32E-20	60.70%	0.103	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1382	c35206_g1_i1_len_2102_path_3443_0_1050_746_1051_2101_5	25071	glyceraldehyde-3-phosphate dehydrogenase	700	0	90.30%	0.14	IPR020831 (PRINTS); IPR020828 (SMART); IPR006424 (TIGRFAM); G3DSA:3.30.360.10 (GENE3D); IPR020829 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020828 (PFAM); IPR020831 (PANTHER); IPR020830 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); SSF55347 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1383	c35206_g1_i2_len_1696_path_105_0_644_74_6_645_1695_5	31033	glyceraldehyde-3-phosphate dehydrogenase	565	0	89.90%	0.14	IPR020831 (PRINTS); IPR020828 (SMART); IPR020828 (PFAM); G3DSA:3.30.360.10 (GENE3D); IPR020829 (PFAM); IPR006424 (TIGRFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020831 (PANTHER); IPR020830 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55347 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
1384	c35217_g1_i1_len_1712_path_1690_0_53_17_44_54_405_2096_406_1177_5036_1178_11_78_2869_1179_1711_2	92	zinc finger protein glis2 homolog	570	5.39E-76	74.10%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR19818 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1385	c35217_g1_i3_len_1677_path_1690_0_53_17_44_54_405_2096_406_1177_5036_1178_11_78_4976_1179_1193_436_2	80	zinc finger protein glis2-like	559	4.17E-75	73.30%	0.103	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR19818 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1386	c35219_g1_i1_len_2317_path_2395_0_2316_5	1041	n-acetylgalactosamine-6-sulfatase isoform x1	772	0	77.60%	0.104	IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); IPR000917 (PFAM); PF14707 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF27 (PANTHER); IPR024607 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1387	c35234_g1_i1_len_3365_path_157_0_3232_3384_3233_3276_3384_3277_3320_3384_3321_3364_1	446	arylsulfatase b	1122	0	72.00%	0.229	IPR000917 (PFAM); G3DSA:3.30.1120.10 (GENE3D); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342 (PANTHER); PTHR10342:SF189 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1388	c35242_g1_i1_len_2699_path_2777_0_2698_1	428	sel1l protein	900	0	77.70%	0.288	Coil (COILS); IPR006597 (SMART); IPR006597 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR11102:SF55 (PANTHER); PTHR11102 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF81901 (SUPERFAMILY); SSF81901 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1389	c35262_g1_i1_len_1476_path_109_0_1475_4	175	reelin- partial	492	3.71E-94	62.30%	0.104	G3DSA:2.10.25.10 (GENE3D); IPR013111 (PFAM); PTHR11841 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1390	c35265_g3_i1_len_424_path_2618_0_423_4	8	apical endosomal glycoprotein	141	3.22E-38	60.00%	0.112	IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1391	c35270_g1_i1_len_2507_path_1_0_220_222_221_221_223_222_439_441_440_2506_0	288	trehalase-like isoform x1	836	0	69.40%	0.163	IPR001661 (PRINTS); IPR001661 (PFAM); PTHR23403:SF1 (PANTHER); IPR001661 (PANTHER); IPR018232 (PROSITE_PATTERNS); IPR018232 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008928 (SUPERFAMILY)
1392	c35275_g1_i1_len_1550_path_1584_0_1361_29_1362_1549_3	186	cyclin-c	517	2.27E-164	90.90%	0.102	IPR013763 (SMART); IPR013763 (G3DSA:1.10.472.GENE3D); IPR006671 (PFAM); IPR015429 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013763 (SUPERFAMILY); IPR013763 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1393	c35329_g1_i1_len_1544_path_1572_0_17_15_90_18_1204_2775_1205_1205_2776_1206_1543_2	457	serine threonine-protein phosphatase 2a catalytic subunit alpha isoform	514	0	97.70%	0.176	Coil (COILS); IPR006186 (PRINTS); IPR006186 (SMART); IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); PTHR11668 (PANTHER); PTHR11668:SF216 (PANTHER); IPR006186 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
1394	c35347_g1_i1_len_981_path_1034_0_980_2	17078	der p 3 allergen	327	4.14E-60	60.80%	0.886Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1395	c35351_g1_i1_len_967_path_105_0_966_3	290	venom allergen 3-like	323	1.49E-48	55.00%	0.785 Y	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR014044 (SUPERFAMILY); TMhelix (TMHMM)
1396	c35354_g1_i1_len_1720_path_1_0_1719_0	272	atpase family aaa domain-containing protein 1-b	574	7.38E-165	77.60%	0.121	IPR003593 (SMART); IPR003959 (PFAM); G3DSA:1.10.8.60 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23074 (PANTHER); PTHR23074:SF20 (PANTHER); IPR003960 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY)

1397	c35361_g1_i1_len_1896_path_1_0_1170_1172_1171_1759_4856_1760_1895_3	132	sparc-related modular calcium-binding protein 1-like	632	8.24E-68	62.00%	0.177	IPR000716 (SMART); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); IPR019577 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR12352 (PANTHER); PTHR12352:SF3 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY); SSF47473 (SUPERFAMILY); TMhelix (TMHMM)
1398	c35361_g1_i2_len_2439_path_1_0_1170_1172_1171_1759_1761_1760_2438_3	154	sparc-related modular calcium-binding protein 1-like isoform x2	813	2.99E-119	56.20%	0.107	IPR000716 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR019577 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); IPR000716 (PFAM); PTHR12352:SF3 (PANTHER); PTHR12352 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); IPR000716 (SUPERFAMILY); SSF47473 (SUPERFAMILY); IPR000716 (SUPERFAMILY)
1399	c35366_g1_i1_len_545_path_1064_0_363_23_31_364_544_5	53	beta- -n-acetylgalactosaminyltransferase bre-4-like	181	8.23E-21	57.40%	0.257	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); PTHR19300:SF30 (PANTHER); IPR003859 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM)
1400	c35366_g1_i2_len_1086_path_1064_0_363_1_428_364_550_1615_551_1085_3	103	beta- -n-acetylgalactosaminyltransferase bre-4-like	362	1.12E-47	56.80%	0.13	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027995 (PFAM); IPR027791 (PFAM); PTHR19300:SF30 (PANTHER); IPR003859 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1401	c35366_g1_i3_len_1665_path_1064_0_363_1_428_364_550_3108_551_1129_1615_1130_1_664_3	137	beta- -n-acetylgalactosaminyltransferase bre-4	555	4.96E-66	58.10%	0.13	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR027995 (PFAM); IPR003859 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1402	c3538_g1_i1_len_700_path_1_0_74_76_75_6_99_5	15	5 -nucleotidase-like	233	4.71E-32	67.10%	0.14	IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11575:SF21 (PANTHER); IPR006179 (PANTHER); IPR006146 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
1403	c35392_g1_i1_len_1122_path_1150_0_675_1_824_676_696_1845_697_1121_1	54	neural ectodermal development factor imp-12	374	1.88E-44	51.60%	0.11	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR10489 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1404	c35397_g1_i1_len_2045_path_1_0_1287_760_7_1288_1309_1311_1310_2044_4	246	receptor-type tyrosine-protein phosphatase kappa	682	1.10E-150	57.10%	0.13	Coil (COILS); IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)

1405	c35397_g2_i1_len_1770_path_4045_0_1769_0	107	cre-let-805 protein	590	3.28E-18	42.20%	0.176	IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR022041 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
1406	c3542_g1_i1_len_2351_path_1_0_2350_0	238	sortilin-related receptor-like	784	8.74E-12	43.50%	0.121	IPR002172 (PRINTS); IPR000998 (SMART); IPR002172 (SMART); IPR002172 (PFAM); IPR000998 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR23282 (PANTHER); PTHR23282:SF75 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1407	c35485_g2_i1_len_1535_path_1759_0_1454_24_1455_1534_4	98	protein o-linked-mannose beta- -n-acetylglucosaminyltransferase 1	512	0	84.10%	0.111	IPR004139 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR004139 (PANTHER); PTHR10468:SF4 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM)
1408	c35485_g2_i2_len_1685_path_1759_0_1454_3211_1455_1604_24_1605_1684_4	104	protein o-linked-mannose beta- -n-acetylglucosaminyltransferase 1	562	0	84.10%	0.112	IPR004139 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); PTHR10468:SF4 (PANTHER); IPR004139 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM)
1409	c35534_g1_i1_len_712_path_886_0_532_141_6_533_581_74_582_711_2	39	integrin alpha-8	237	4.66E-42	55.10%	0.141	IPR000413 (PRINTS); IPR013519 (SMART); G3DSA:2.60.40.1460 (GENE3D); IPR013649 (PFAM); G3DSA:2.130.10.130 (GENE3D); IPR013517 (PFAM); PTHR23220 (PANTHER); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); SSF69179 (SUPERFAMILY); SSF69318 (SUPERFAMILY)
1410	c35554_g1_i2_len_2114_path_481_0_1714_2_40_1715_2113_5	141	protein	704	2.42E-140	49.80%	0.129	IPR007074 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); PTHR13627:SF24 (PANTHER); PTHR13627 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM)
1411	c35602_g1_i1_len_630_path_608_0_629_5	30	spermatogenesis-associated protein 20	210	2.62E-62	81.30%	0.128	IPR012336 (G3DSA:3.40.30.GENE3D); IPR004879 (PFAM); PTHR12145:SF11 (PANTHER); PTHR12145 (PANTHER); IPR012336 (SUPERFAMILY)
1412	c35602_g2_i1_len_2049_path_1215_0_119_1_335_120_2048_2	179	spermatogenesis-associated protein 20	683	0	71.30%	0.11	IPR024705 (PIRSF); IPR012341 (G3DSA:1.50.10.GENE3D); IPR004879 (PFAM); PTHR12145:SF11 (PANTHER); PTHR12145 (PANTHER); IPR008928 (SUPERFAMILY)
1413	c35609_g1_i1_len_772_path_1617_0_683_23_01_684_727_2301_728_771_0	26	serine protease 45 isoform x2	258	2.57E-09	78.00%	0.174	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1414	c35609_g2_i1_len_595_path_1103_0_245_13_49_246_256_788_257_594_4	25	urokinase-type plasminogen activator	198	1.75E-46	56.10%	0.127	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1415	c35609_g2_i2_len_501_path_1103_0_245_33_51_246_500_3	12	urokinase-type plasminogen activator	167	3.26E-36	56.30%	0.161	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1416	c35609_g2_i3_len_574_path_552_0_235_788_236_573_4	17	trypsin-1- partial	191	7.30E-42	55.90%	0.127	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1417	c35635_g1_i1_len_470_path_1017_0_57_86_58_182_938_183_210_239_211_228_29_229_268_536_269_469_5	12	ubiquitin isoform cra_e	156	9.77E-69	99.10%	0.211	IPR019956 (PRINTS); IPR000626 (SMART); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); G3DSA:3.10.20.90 (GENE3D); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY)

1418	c35638_g1_i1_len_1896_path_1_0_22_24_23_1895_2	469	methyltransferase-like protein 23	632	3.82E-85	80.30%	0.18	IPR000582 (PRINTS); IPR002110 (SMART); IPR000504 (SMART); IPR012677 (G3DSA:3.30.70.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR000582 (PFAM); IPR000504 (PFAM); IPR014352 (G3DSA:1.20.80.GENE3D); IPR029063 (G3DSA:3.40.50.GENE3D); IPR019410 (PFAM); IPR020683 (PFAM); PTHR24119 (PANTHER); PTHR24119:SF0 (PANTHER); IPR000504 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR000582 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR000582 (SUPERFAMILY); IPR029063 (SUPERFAMILY); SSF54928 (SUPERFAMILY); IPR020683 (SUPERFAMILY)
1419	c35638_g1_i2_len_1974_path_1999_0_100_24_101_1973_2	491	methyltransferase-like protein 23	658	3.57E-93	76.80%	0.109	IPR000582 (PRINTS); IPR000504 (SMART); IPR002110 (SMART); IPR019410 (PFAM); IPR029063 (G3DSA:3.40.50.GENE3D); IPR012677 (G3DSA:3.30.70.GENE3D); IPR000504 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR000582 (PFAM); IPR014352 (G3DSA:1.20.80.GENE3D); PTHR24119 (PANTHER); PTHR24119:SF0 (PANTHER); IPR000504 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR000582 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); IPR000582 (SUPERFAMILY); SSF54928 (SUPERFAMILY); IPR029063 (SUPERFAMILY)
1420	c35657_g1_i1_len_1077_path_157_0_884_1036_885_932_1036_933_980_1036_981_1028_1036_1029_1076_3	103	low-density lipoprotein receptor-related protein 2	359	6.01E-24	58.10%	0.096	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1421	c35657_g1_i1_len_1077_path_157_0_884_1036_885_932_1036_933_980_1036_981_1028_1036_1029_1076_5	103	---NA---	359			0.106	no IPS match
1422	c35681_g1_i1_len_993_path_53_0_992_4	102	dipeptidyl peptidase 1 isoform x1	331	1.15E-83	83.90%	0.101	IPR000668 (SMART); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); G3DSA:2.40.50.170 (GENE3D); IPR013128 (PANTHER); PTHR12411:SF314 (PANTHER); IPR025661 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
1423	c35681_g2_i1_len_898_path_2964_0_897_2	64	cathepsin c	299	8.26E-96	66.30%	0.253	G3DSA:3.90.70.10 (GENE3D); IPR014882 (PFAM); IPR000668 (PFAM); IPR014882 (G3DSA:2.40.128.GENE3D); PTHR12411:SF314 (PANTHER); IPR013128 (PANTHER); IPR000169 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014882 (SUPERFAMILY); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
1424	c35695_g1_i1_len_1871_path_143_0_239_382_240_259_142_260_1748_1888_1749_1809_1888_1810_1870_0	153	retinol dehydrogenase 13-like	624	4.20E-89	66.70%	0.179	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); IPR020904 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1425	c35719_g1_i1_len_3237_path_105_0_251_35_7_252_3236_5	355	serine threonine-protein kinase pim-3	1079	2.94E-128	76.90%	0.115	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR22984:SF1 (PANTHER); PTHR22984 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1426	c35733_g1_i1_len_2862_path_157_0_2861_5	455	leucine-rich repeat and immunoglobulin-like domain-containing nogo receptor-interacting protein 3 isoform x2	954	1.16E-136	64.70%	0.117	Coil (COILS); IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR013098 (PFAM); PTHR24373:SF38 (PANTHER); PTHR24373 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1427	c35769_g1_i1_len_1347_path_185_0_899_10_80_900_917_80_918_1346_5	770	projectin short variant	449	5.01E-40	49.60%	0.101	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1428	c35775_g1_i1_len_797_path_207_0_796_3	6163	epididymal secretory protein e1	266	1.32E-28	59.00%	0.111	IPR003172 (SMART); IPR003172 (G3DSA:2.60.40.GENE3D); IPR003172 (PFAM); PTHR11306 (PANTHER); IPR014756 (SUPERFAMILY)
1429	c35843_g1_i1_len_697_path_1007_0_29_103_7_30_34_1042_35_498_1505_499_565_1571_566_597_1505_598_664_1_2	284	thioredoxin 1	232	4.53E-50	83.30%	0.375 Y	PR00421 (PRINTS); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005746 (TIGRFAM); IPR005746 (PANTHER); IPR017937 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1430	c35892_g1_i1_len_1290_path_157_0_21_179_22_1289_0	238	leucine-rich repeat-containing protein partial	430	4.69E-53	47.20%	0.228	IPR003591 (SMART); IPR000483 (SMART); IPR026906 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24373 (PANTHER); PTHR24373:SF100 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1431	c35892_g1_i2_len_1974_path_2173_0_229_1_79_230_1497_3667_1498_1524_104_1525_1_973_1	408	leucine-rich repeat-containing protein partial	658	2.35E-51	48.80%	0.117	IPR000483 (SMART); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR026906 (PFAM); PTHR24373:SF100 (PANTHER); PTHR24373 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1432	c35900_g3_i1_len_2217_path_3879_0_2216_2	144	midnolin-b-like isoform x1	739	3.15E-59	68.10%	0.338	PTHR23010 (PANTHER); PTHR23010:SF0 (PANTHER)
1433	c35952_g2_i1_len_1610_path_433_0_1003_1_436_1004_1408_272_1409_1409_432_1410_1609_3	94	multiple inositol polyphosphate phosphatase 1	537	3.48E-119	59.40%	0.636Y	IPR000560 (PFAM); IPR029033 (G3DSA:3.40.50.GENE3D); PTHR20963:SF8 (PANTHER); PTHR20963 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR029033 (SUPERFAMILY)
1434	c35952_g2_i3_len_1205_path_433_0_1003_2_72_1004_1004_432_1005_1204_3	78	multiple inositol polyphosphate phosphatase 1	402	1.75E-89	59.70%	0.628Y	IPR000560 (PFAM); IPR029033 (G3DSA:3.40.50.GENE3D); PTHR20963 (PANTHER); PTHR20963:SF8 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR029033 (SUPERFAMILY)
1435	c35962_g1_i1_len_1860_path_2261_0_939_3_199_940_975_3235_976_1121_245_1122_18_59_5	341	protein shifted isoform x1	620	0	81.40%	0.143	IPR013309 (PRINTS); IPR003306 (SMART); IPR000742 (SMART); IPR013032 (PFAM); IPR003306 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR24838 (PANTHER); PTHR24838:SF276 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003306 (PRODOM); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR003306 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
1436	c35962_g1_i2_len_1824_path_2261_0_939_3_235_940_1085_245_1086_1823_5	330	wnt inhibitory factor 1	608	0	83.00%	0.143	IPR013309 (PRINTS); IPR003306 (SMART); IPR000742 (SMART); IPR003306 (PFAM); IPR013032 (PFAM); G3DSA:2.170.300.10 (GENE3D); PTHR24838 (PANTHER); PTHR24838:SF276 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003306 (PRODOM); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR003306 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
1437	c35962_g1_i3_len_918_path_65_0_179_245_180_917_5	108	protein shifted	306	1.83E-47	87.30%	0.143	IPR003306 (SMART); IPR003306 (PFAM); PTHR24838:SF276 (PANTHER); PTHR24838 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003306 (PRODOM); IPR003306 (PROSITE_PROFILES)
1438	c36001_g1_i1_len_1266_path_53_0_963_244_0_964_1265_3	257	epidermal retinol dehydrogenase 2-like	422	1.01E-75	70.20%	0.216	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF289 (PANTHER); PTHR24316 (PANTHER); SSF51735 (SUPERFAMILY)
1439	c36001_g1_i2_len_1345_path_53_0_963_101_7_964_1344_4	334	epidermal retinol dehydrogenase 2	448	1.90E-105	71.30%	0.215	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316:SF289 (PANTHER); PTHR24316 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)

1440	c36017_g1_i1_len_4740_path_4868_0_4739_2	562	sodium calcium exchanger 3-like isoform x1	1580	0	76.90%	0.123	IPR004836 (PRINTS); IPR003644 (SMART); IPR004837 (PFAM); IPR003644 (PFAM); IPR004836 (TIGRFAM); PTHR11878 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF141072 (SUPERFAMILY); SSF141072 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1441	c36049_g1_i1_len_1864_path_105_0_1863_5	186	ankyrin sam and basic leucine zipper domain-containing protein 1-like	621	1.49E-130	61.10%	0.099	IPR002110 (SMART); IPR001660 (SMART); IPR021129 (PFAM); IPR013761 (G3DSA:1.10.150.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24157 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR001660 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); IPR013761 (SUPERFAMILY)
1442	c36090_g1_i1_len_625_path_153_0_301_455_302_393_546_394_396_127_397_624_3	81	bola-like protein 3	209	4.69E-32	75.40%	0.183	IPR002634 (PFAM); G3DSA:3.30.70.1500 (GENE3D); PTHR12735:SF4 (PANTHER); PTHR12735 (PANTHER); IPR002634 (SUPERFAMILY)
1443	c36112_g1_i1_len_2451_path_105_0_2450_4	258	cytochrome p450 partial	817	1.24E-108	58.80%	0.122	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24302:SF7 (PANTHER); PTHR24302 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1444	c36123_g1_i1_len_662_path_3323_0_113_89_7_114_174_958_175_661_1	51	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	221	2.77E-21	53.40%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1445	c36129_g1_i1_len_2154_path_3323_0_1746_5070_1747_1777_402_1778_2153_1	300	venom carboxylesterase-6 isoform x2	718	9.88E-138	58.20%	0.144	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559 (PANTHER); IPR019819 (PROSITE_PATTERNS); IPR019826 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY)
1446	c36129_g2_i1_len_1196_path_6342_0_604_5_070_605_635_5100_636_1195_2	81	venom carboxylesterase-6	398	4.12E-40	53.20%	0.101	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR029058 (SUPERFAMILY)
1447	c36146_g1_i1_len_3784_path_557_0_513_53_1_514_3783_3	524	uncharacterized family 31 glucosidase k1a1161 isoform x5	1262	0	62.10%	0.122	IPR000322 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); PTHR22762 (PANTHER); PTHR22762:SF73 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); SSF51011 (SUPERFAMILY); TMhelix (TMHMM)

1448	c36169_g1_i1_len_1422_path_53_0_770_824_771_783_2956_784_1421_0	16211	trypsin-like serine proteinase 2	474	9.15E-61	56.70%	0.103	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1452	c3617_g1_i1_len_1141_path_1144_0_1140_0	79	dehydrogenase reductase sdr family member 11-like	381	8.71E-105	74.50%	0.285	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1449	c36173_g1_i1_len_2071_path_2099_0_2070_0	148	glutamate-rich wd repeat-containing protein 1	691	0	72.40%	0.107	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR022052 (PFAM); PTHR22850:SF6 (PANTHER); PTHR22850 (PANTHER); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1450	c36178_g1_i2_len_1592_path_211_0_644_85_6_645_1396_4619_1397_1591_2	114	tolloid-like protein 2 isoform x2	530	0	83.50%	0.099	IPR000742 (SMART); IPR000859 (SMART); IPR001881 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); PF14670 (PFAM); IPR000859 (PFAM); IPR015446 (PIRSF); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10127 (PANTHER); PTHR10127:SF304 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR000859 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
1451	c36178_g1_i3_len_2119_path_211_0_644_85_6_645_1396_1608_1397_1950_210_1951_2_118_2	146	tolloid-like protein 2 isoform x2	706	0	82.60%	0.099	IPR001881 (SMART); IPR000859 (SMART); IPR000742 (SMART); IPR001881 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); PF14670 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR000859 (PFAM); PTHR10127 (PANTHER); PTHR10127:SF304 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
1453	c36194_g1_i1_len_958_path_1_0_154_156_1_55_178_180_179_249_251_250_252_254_25_3_957_2	754	aael003561- partial	319	9.72E-26	49.90%	0.641 Y	IPR001211 (PRINTS); IPR016090 (SMART); IPR016090 (G3DSA:1.20.90.GENE3D); IPR016090 (PFAM); IPR001211 (PANTHER); IPR013090 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR016090 (SUPERFAMILY)
1454	c36210_g1_i1_len_4027_path_53_0_671_812_2_672_692_725_693_4026_1	1271	coatomer subunit alpha	1342	0	87.60%	0.128	IPR020472 (PRINTS); IPR001680 (SMART); IPR016391 (PIRSF); IPR010714 (PFAM); IPR006692 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19876 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); SSF82171 (SUPERFAMILY); IPR017986 (SUPERFAMILY)

1455	c36210_g1_i2_len_4006_path_53_0_671_725_672_4005_1	1267		coatomer subunit alpha	1335	0	87.50%	0.128	IPR020472 (PRINTS); IPR001680 (SMART); IPR010714 (PFAM); IPR006692 (PFAM); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR016391 (PIRSF); PTHR19876 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); SSF82171 (SUPERFAMILY); IPR017986 (SUPERFAMILY)
1456	c36228_g1_i1_len_2239_path_77_0_129_460_4_130_130_4605_131_150_4625_151_162_4_579_163_170_246_171_223_4	99		calcium activated chlorine	746	3.95E-49	45.20%	0.101	IPR013783 (G3DSA:2.60.40.GENE3D); IPR015394 (PFAM); PTHR10579:SF43 (PANTHER); PTHR10579 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1457	c36265_g1_i1_len_822_path_1_0_278_280_2_79_279_281_280_821_0	9372		unnamed protein product	274	1.85E-09	73.90%	0.128	no IPS match
1458	c36352_g1_i1_len_1063_path_1001_0_609_5_2_610_634_1920_635_967_1794_968_1062_3	39		zinc finger protein 420-like isoform x1	355	8.43E-62	58.10%	0.111	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1459	c36352_g1_i2_len_330_path_1_0_50_52_51_75_1635_76_234_1794_235_329_3	8		gastrula zinc finger protein	110	2.52E-22	64.40%	0.109	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1460	c36356_g1_i1_len_1919_path_1897_0_1918_2	183		integrin-linked protein kinase	639	0	86.90%	0.182	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); IPR002110 (PFAM); G3DSA:3.30.200.20 (GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR23257:SF30 (PANTHER); PTHR23257 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); IPR020683 (SUPERFAMILY); TMhelix (TMHMM)
1461	c36358_g1_i1_len_927_path_905_0_926_0	329		neuferricin -like protein	309	1.28E-74	66.50%	0.163	IPR001199 (G3DSA:3.10.120.GENE3D); IPR001199 (PFAM); PTHR10281:SF4 (PANTHER); PTHR10281 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001199 (SUPERFAMILY); TMhelix (TMHMM)
1462	c36384_g1_i1_len_899_path_233_0_622_70_623_674_232_675_898_2	206		micos complex subunit mic27	299	5.07E-27	54.70%	0.181	IPR019166 (PFAM); PTHR14564 (PANTHER); PTHR14564:SF1 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1463	c36384_g1_i2_len_944_path_233_0_622_25_623_667_70_668_719_232_720_943_2	180		micos complex subunit mic27	314	6.93E-28	52.90%	0.181	IPR019166 (PFAM); PTHR14564 (PANTHER); PTHR14564:SF1 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)

1464	c36411_g1_i1_len_360_path_111_0_122_880_123_167_279_168_192_304_193_205_317_206_359_3	3459	cathepsin partial	120	1.39E-38	67.40%	0.111	IPR013201 (SMART); IPR013201 (PFAM); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR013128 (PANTHER); IPR000169 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
1465	c36418_g2_i1_len_922_path_495_0_492_988_493_520_2517_521_921_1	47	von willebrand factor type egf and pentraxin domain-containing protein 1	307	2.71E-06	45.00%	0.111	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR000436 (SUPERFAMILY)
1466	c36418_g3_i1_len_1113_path_1942_0_547_9_88_548_575_4404_576_1112_2	68	von willebrand factor type egf and pentraxin domain-containing protein 1	371	5.08E-09	42.50%	0.224	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325:SF331 (PANTHER); PTHR19325 (PANTHER); IPR001368 (PROSITE_PATTERNS); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1467	c36441_g1_i1_len_1361_path_1556_0_607_2_160_608_642_120_643_1360_2	224	protein spaetzle	453	7.29E-31	53.20%	0.256	PTHR23199 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029034 (SUPERFAMILY); TMhelix (TMHMM)
1468	c36552_g1_i1_len_3381_path_3471_0_281_7_764_282_282_3820_283_1873_5410_1874_1874_24_1875_3380_2	529	basement membrane-specific heparan sulfate proteoglycan core protein	1127	0	68.60%	0.161	IPR003599 (SMART); IPR000742 (SMART); IPR003598 (SMART); IPR001791 (SMART); IPR001881 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR001791 (PFAM); IPR001791 (PFAM); PF13895 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR10574:SF247 (PANTHER); PTHR10574 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR013320 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR013320 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
1469	c36552_g1_i2_len_3447_path_3471_0_281_3_753_282_348_3820_349_1939_5410_1940_1940_24_1941_3446_2	552	basement membrane-specific heparan sulfate proteoglycan core protein	1149	0	68.20%	0.161	IPR001881 (SMART); IPR003599 (SMART); IPR001791 (SMART); IPR000742 (SMART); IPR003598 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); PF13895 (PFAM); IPR001791 (PFAM); PTHR10574:SF247 (PANTHER); PTHR10574 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR013320 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);

1470	c36552_g1_i3_len_3580_path_6893_0_414_3_753_415_481_3820_482_2072_5410_2073_2073_24_2074_3579_0	542	basement membrane-specific heparan sulfate proteoglycan core protein	1194	0	70.10%	0.15	IPR000742 (SMART); IPR001791 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR001881 (SMART); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000742 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR001791 (PFAM); G3DSA:2.170.300.10 (GENE3D); PTHR10574 (PANTHER); PTHR10574:SF247 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR013320 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR013320 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1471	c36558_g1_i1_len_2550_path_2563_0_686_1_8_687_2549_0	165	protein turtle	850	2.92E-67	49.80%	0.103	IPR003598 (SMART); IPR003961 (SMART); IPR003599 (SMART); IPR013098 (PFAM); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489:SF510 (PANTHER); PTHR10489 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1472	c36600_g1_i1_len_621_path_91_0_246_1049_247_273_1049_274_300_1076_301_307_34_2_308_485_519_486_512_5_1	193	keratin-associated protein 5-4-like isoform x1	207	5.86E-24	46.50%	0.101	no IPS match
1473	c36609_g2_i1_len_1422_path_587_0_1421_4	127	g-protein coupled receptor mth2	474	3.06E-44	64.40%	0.198	IPR000832 (PFAM); PTHR12011 (PANTHER); PTHR12011:SF164 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1474	c36625_g1_i1_len_621_path_649_0_620_3	280	mucin- partial	207	7.44E-06	37.00%	0.153	TMhelix (TMHMM); TMhelix (TMHMM)
1475	c36625_g2_i1_len_987_path_1386_0_25_340_7_26_29_1485_30_976_3397_977_986_1	661	---NA---	329			0.186	TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1476	c36638_g1_i1_len_373_path_1_0_372_4	132	zinc metalloproteinase dpy-31	124	7.22E-11	52.90%	0.837Y	IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF55486 (SUPERFAMILY)
1477	c36638_g2_i1_len_672_path_1480_0_671_0	596	zinc metalloproteinase nas-13	224	5.12E-28	61.80%	0.3	IPR001506 (PRINTS); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)
1478	c36647_g1_i1_len_1175_path_187_0_1135_4_0_1136_1174_0	901	kcp_halai ame: full=bpti kunitz domain-containing partial	392	2.12E-27	60.20%	0.122	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)

1479	c36656_g1_i1_len_2228_path_2356_0_237_1_238_238_130_239_262_26_263_2227_2	270	bone morphogenetic protein 2-like	742	1.09E-17	51.90%	0.118	IPR001839 (SMART); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001839 (PFAM); PTHR11848:SF126 (PANTHER); IPR015615 (PANTHER); IPR017948 (PROSITE_PATTERNS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)
1480	c36662_g1_i1_len_1271_path_1299_0_1270_5	156	3-hydroxybutyrate dehydrogenase type 2	423	1.36E-119	81.00%	0.117	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24321:SF3 (PANTHER); PTHR24321 (PANTHER); IPR020904 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1481	c36667_g1_i1_len_1652_path_1681_0_257_1_940_258_1651_5	298	isocitrate dehydrogenase	550	1.41E-180	82.60%	0.113	Coil (COILS); IPR004434 (TIGRFAM); IPR024084 (PFAM); IPR024084 (G3DSA:3.40.718.GENE3D); IPR001804 (PANTHER); PTHR11835:SF42 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53659 (SUPERFAMILY)
1482	c36673_g1_i1_len_2595_path_53_0_2594_1	1549	chorion peroxidase-like	865	2.18E-132	55.20%	0.814Y	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR019791 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR010255 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1483	c36696_g1_i1_len_1533_path_1598_0_467_3_101_468_494_2066_495_572_2144_573_967_2538_968_1000_58_10_4	946	scp-like extracellular domain containing protein 1	511	3.13E-43	52.90%	0.652 Y	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR002172 (SMART); IPR014044 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1484	c36696_g1_i2_len_597_path_1598_0_467_31_01_468_494_2066_495_572_3245_573_583_3440_584_596_4	124	low-density lipoprotein receptor-related protein partial	199	4.60E-07	63.67%	0.101	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
1485	c36696_g1_i3_len_570_path_1598_0_467_20_66_468_545_3245_546_556_3440_557_569_4	141	low-density lipoprotein receptor-related protein partial	190	3.76E-07	62.00%	0.104	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
1486	c36696_g1_i4_len_1506_path_1598_0_467_2_066_468_545_2144_546_940_2538_941_973_58_974_1505_4	1228	scp-like extracellular domain containing protein 1	502	2.47E-43	52.90%	0.652 Y	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR014044 (SMART); IPR002172 (SMART); IPR014044 (PFAM); IPR002172 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001283 (PANTHER); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR014044 (SUPERFAMILY)
1487	c36702_g1_i1_len_1253_path_509_0_168_12_9_169_347_306_348_1252_3	697	annexin b10-like	418	8.71E-117	71.10%	0.145	Coil (COILS); IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF47874 (SUPERFAMILY)
1488	c36702_g1_i2_len_1253_path_509_0_168_67_7_169_347_306_348_1252_3	746	annexin b10-like	418	5.37E-118	70.90%	0.145	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF47874 (SUPERFAMILY)

1489	c36771_g1_i1_len_2751_path_157_0_2390_2542_2391_2417_2542_2418_2444_5290_2445_2750_3	219	hypothetical protein DAPPUDRAFT_304103	917	0	60.20%	0.164	Coil (COILS); IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); IPR008753 (PFAM); IPR000718 (PANTHER); PTHR11733:SF111 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1490	c36781_g1_i1_len_717_path_1063_0_98_1162_99_166_25_167_278_137_279_319_348_320_343_372_344_716_4	27	coagulation factor x	239	4.56E-22	58.60%	0.147	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1491	c36784_g1_i1_len_1325_path_331_0_74_40675_75_142_76_223_3462_224_316_1295_317_317_236_318_502_1479_0	177	tropinone reductase 2-like	442	1.38E-121	76.40%	0.482Y	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR013968 (SMART); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF111 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF51735 (SUPERFAMILY)
1492	c36784_g1_i3_len_1083_path_331_0_74_1295_75_75_236_76_260_1479_261_353_1272_354_1082_1	174	tropinone reductase 2-like	361	3.72E-122	76.50%	0.34	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR013968 (SMART); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF111 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1493	c36784_g1_i4_len_1100_path_143_0_92_23693_277_1479_278_370_1272_371_1099_0	154	tropinone reductase 2-like	367	1.30E-122	76.40%	0.335	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR013968 (SMART); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF111 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1494	c36784_g1_i5_len_990_path_331_0_74_129575_75_236_76_260_1272_261_989_1	116	tropinone reductase 2-like	330	1.97E-102	69.40%	0.34	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); PF13561 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF111 (PANTHER); IPR020904 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1495	c36790_g1_i1_len_1301_path_1479_0_1300_1	173	d-aspartate oxidase	434	3.82E-142	74.10%	0.19	G3DSA:3.30.9.10 (GENE3D); IPR006076 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR11530:SF2 (PANTHER); IPR023209 (PANTHER); SSF54373 (SUPERFAMILY); SSF51971 (SUPERFAMILY)
1496	c36798_g1_i1_len_1337_path_1465_0_1336_3	2591	guanine nucleotide-binding protein subunit beta-like protein	446	0	93.20%	0.172	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19868 (PANTHER); PTHR19868:SF0 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1497	c36808_g1_i1_len_3164_path_3142_0_3163_4	1102	transitional endoplasmic reticulum atpase ter94	1048	0	94.80%	0.126	IPR003593 (SMART); IPR004201 (SMART); IPR003338 (SMART); G3DSA:1.10.8.60 (GENE3D); G3DSA:2.40.40.20 (GENE3D); IPR005938 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR004201 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003338 (PFAM); IPR029067 (G3DSA:3.10.330.GENE3D); IPR015415 (PFAM); IPR003959 (PFAM); PTHR23077 (PANTHER); PTHR23077:SF69 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR003960 (PROSITE_PATTERNS); IPR029067 (SUPERFAMILY); IPR009010 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR027417 (SUPERFAMILY)

1498	c36810_g1_i1_len_3306_path_162_0_3305_4	2322	transforming growth factor-beta-induced protein ig-h3	1102	0	55.80%	0.182	Coil (COILS); IPR000782 (SMART); IPR000782 (PFAM); IPR000782 (G3DSA:2.30.180.GENE3D); PTHR10900:SF73 (PANTHER); PTHR10900 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY)
1499	c36824_g1_i1_len_1601_path_3115_0_1600_3	72	laccase 1	534	0	68.70%	0.303	IPR01117 (PFAM); IPR011707 (PFAM); IPR008972 (G3DSA:2.60.40.GENE3D); IPR008972 (G3DSA:2.60.40.GENE3D); PTHR11709:SF33 (PANTHER); PTHR11709 (PANTHER); IPR008972 (SUPERFAMILY); IPR008972 (SUPERFAMILY)
1500	c36824_g2_i1_len_766_path_744_0_765_2	29	low quality protein: laccase-1-like	255	2.51E-46	74.90%	0.124	IPR008972 (G3DSA:2.60.40.GENE3D); IPR011706 (PFAM); PTHR11709 (PANTHER); PTHR11709:SF33 (PANTHER); IPR002355 (PROSITE_PATTERNS); IPR008972 (SUPERFAMILY)
1501	c36830_g2_i1_len_1820_path_2204_0_1819_1	1177	peptidyl-prolyl cis-trans isomerase b	607	8.16E-108	86.30%	0.489Y	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF63 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1502	c36842_g1_i1_len_476_path_2336_0_475_1	91	low quality protein: hemocytin-like	159	7.10E-14	49.50%	0.126	IPR01846 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR01846 (PROSITE_PROFILES)
1503	c36848_g1_i1_len_1312_path_1290_0_1311_2	1021	membrane glycoprotein lig-	437	1.98E-18	47.00%	0.137	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1504	c36849_g1_i1_len_1095_path_143_0_502_64_3_503_522_2464_523_1094_0	2404	glycosyl-phosphatidylinositol-linked carbonic anhydrase	365	2.87E-85	63.40%	0.127	IPR001148 (SMART); IPR001148 (G3DSA:3.10.200.GENE3D); IPR001148 (PFAM); IPR023561 (PANTHER); IPR018338 (PROSITE_PATTERNS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
1505	c36850_g1_i1_len_1750_path_1928_0_1749_1	2289	von willebrand factor type egf and pentraxin domain-containing protein 1-like	583	2.72E-10	41.80%	0.098	Coil (COILS); IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1506	c36861_g1_i1_len_1942_path_1_0_1941_0	199	katanin p60 atpase-containing subunit a-like 1-like isoform x2	648	0	82.10%	0.383 Y	IPR003593 (SMART); IPR015415 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); PTHR23074 (PANTHER); PTHR23074:SF65 (PANTHER); IPR003960 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR028596 (HAMAP); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1507	c36875_g1_i1_len_679_path_890_0_56_947_57_92_983_93_408_1299_409_409_1300_4_10_516_1405_517_554_1_4	105	lipophorin receptor isoform e	226	2.73E-12	58.00%	0.106	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

1508	c36882_g2_i1_len_1589_path_4786_0_347_1 490_348_366_5152_367_539_2521_540_158 8_5	749	adiponectin receptor protein	529	5.29E-170	84.10%	0.282	IPR004254 (PFAM); PTHR20855:SF15 (PANTHER); IPR004254 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1509	c36882_g2_i2_len_1618_path_1113_0_376_1 490_377_395_5152_396_568_2521_569_161 7_5	631	adiponectin receptor protein	539	2.79E-150	84.00%	0.282	IPR004254 (PFAM); IPR004254 (PANTHER); PTHR20855:SF15 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1510	c36882_g2_i3_len_1879_path_6347_0_21_51 52_22_194_1888_195_803_2496_804_804_1 089_805_829_2521_830_18_4	650	adiponectin receptor protein	626	1.50E-19	77.70%	0.122	IPR004254 (PFAM); PTHR20855:SF15 (PANTHER); IPR004254 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1511	c36882_g2_i3_len_1879_path_6347_0_21_51 52_22_194_1888_195_803_2496_804_804_1 089_805_829_2521_830_18_5	650	adiponectin receptor protein	626	1.90E-108	84.20%	0.282	IPR004254 (PFAM); PTHR20855:SF15 (PANTHER); IPR004254 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1512	c36907_g1_i1_len_1662_path_1_0_39_41_40 _40_42_41_1661_5	177	deoxyribonuclease-1	554	5.27E-81	61.60%	0.743Y	IPR016202 (PRINTS); IPR016202 (SMART); IPR005135 (PFAM); IPR005135 (G3DSA:3.60.10.GENE3D); IPR016202 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR005135 (SUPERFAMILY)
1513	c36911_g1_i1_len_3284_path_3298_0_2768_ 6736_2769_2779_6079_2780_2781_36_2782 _3283_2	720	retinoid-inducible serine carboxypeptidase	1087	1.59E-141	67.10%	0.15	IPR001563 (PRINTS); IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); PTHR11802:SF3 (PANTHER); IPR018202 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1514	c36914_g1_i1_len_1631_path_925_0_755_16_81_756_785_1862_786_802_2002_803_1630_1	191	af425264_1lysozyme precursor	544	3.07E-37	65.30%	0.108	IPR000974 (PRINTS); IPR001916 (PRINTS); IPR001916 (SMART); IPR001916 (PFAM); G3DSA:1.10.530.10 (GENE3D); PTHR11407 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001916 (PROSITE_PROFILES); IPR023346 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1515	c36914_g1_i2_len_872_path_925_0_755_168_1_756_785_1711_786_856_2941_857_871_1	217	af425264_1lysozyme precursor	291	1.76E-35	65.40%	0.108	IPR001916 (PRINTS); IPR000974 (PRINTS); IPR001916 (SMART); G3DSA:1.10.530.10 (GENE3D); IPR001916 (PFAM); PTHR11407 (PANTHER); IPR001916 (PROSITE_PROFILES); IPR023346 (SUPERFAMILY)
1516	c36922_g1_i1_len_1306_path_53_0_599_651_600_618_670_619_1305_5	1348	macrophage migration inhibitory factor	435	3.90E-37	69.80%	0.126	G3DSA:3.30.429.10 (GENE3D); IPR001398 (PFAM); PTHR11954:SF6 (PANTHER); IPR001398 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001398 (PRODOM); IPR014347 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1517	c36932_g1_i1_len_1849_path_129_0_268_63_269_281_76_282_1848_1	123	low quality protein: cubilin	616	2.56E-38	47.20%	0.116	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); IPR002035 (PFAM); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
1518	c36953_g1_i2_len_1446_path_1524_0_932_2_455_933_1445_0	375	3-hydroxyisobutyrate dehydrogenase	482	2.49E-63	54.90%	0.14	IPR006115 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); IPR029154 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22981:SF7 (PANTHER); PTHR22981 (PANTHER); IPR029752 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY); IPR008927 (SUPERFAMILY)
1519	c36957_g1_i1_len_3282_path_1_0_2099_210_1_2100_3281_1	569	methylmalonate-semialdehyde dehydrogenase	1094	0	87.60%	0.127	IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); IPR010061 (TIGRFAM); IPR010061 (PTHR11699:PANTHER); PTHR11699 (PANTHER); IPR016160 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1520	c36967_g1_i1_len_3095_path_3622_0_3094_4	911	26s proteasome non-atpase regulatory subunit 10	1032	6.57E-75	71.30%	0.142	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24199 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1529	c37085_g1_i1_len_2337_path_209_0_2336_0	389	aquaporin 1	779	3.99E-103	72.70%	0.119	IPR000425 (PRINTS); IPR000425 (PFAM); IPR000425 (TIGRFAM); IPR023271 (G3DSA:1.20.1080.GENE3D); IPR000425 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023271 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1530	c37090_g1_i1_len_838_path_816_0_755_157_2_756_756_1573_757_837_4	54	dnaj homolog subfamily c member 30-like	279	6.53E-26	54.20%	0.134	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF171 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1531	c37109_g1_i2_len_2559_path_2537_0_863_3_401_864_884_3422_885_2200_4738_2201_2_558_3	206	amyloid beta a4 protein	853	4.02E-78	53.60%	0.102	IPR002223 (PRINTS); IPR002223 (SMART); IPR000716 (SMART); IPR002223 (PFAM); IPR000716 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR000716 (G3DSA:4.10.800.GENE3D); PTHR10083 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY); TMhelix (TMHMM)
1532	c37137_g1_i1_len_3014_path_6082_0_1799_7881_1800_1808_3612_1809_1854_7934_18_55_2006_509_2007_2068_1_0	239	agap000815-pa-like protein	1005	5.69E-98	59.50%	0.131	IPR015812 (PRINTS); G3DSA:1.20.5.100 (GENE3D); IPR014836 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR012896 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR015812 (PANTHER); PTHR10082:SF16 (PANTHER); IPR015812 (PROSITE_PATTERNS); IPR015812 (PROSITE_PATTERNS); IPR015812 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012896 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1533	c37137_g1_i2_len_2496_path_6082_0_1799_3603_1800_1808_3612_1809_1854_325_185_5_2038_509_2039_2100_81_0	147	agap000815-pa-like protein	832	2.12E-98	59.50%	0.131	IPR015812 (PRINTS); G3DSA:1.20.5.100 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR012896 (PFAM); IPR014836 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR015812 (PANTHER); PTHR10082:SF16 (PANTHER); IPR015812 (PROSITE_PATTERNS); IPR015812 (PROSITE_PATTERNS); IPR015812 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF57196 (SUPERFAMILY); IPR012896 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1534	c37192_g1_i1_len_900_path_1191_0_118_10_8_119_180_1370_181_899_2	136	u8-agatoxin-ao1a-like isoform x2	300	4.22E-35	73.00%	0.672Y	IPR004169 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_EUK); SSF57059 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1535	c37192_g1_i2_len_927_path_1191_0_118_10_8_119_180_2083_181_207_1370_208_926_2	116	u8-agatoxin-ao1a-like isoform x1	309	2.72E-41	75.90%	0.648Y	IPR004169 (PFAM); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_NEGATIVE); SSF57059 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1536	c37192_g1_i3_len_1011_path_1191_0_118_2_4_119_202_108_203_264_2083_265_291_13_70_292_1010_2	110	u8-agatoxin-ao1a-like isoform x1	337	9.80E-38	69.70%	0.594Y	IPR004169 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_EUK); SSF57059 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1537	c37192_g1_i4_len_984_path_1191_0_118_24_119_202_108_203_264_1370_265_983_2	124	u16-lycotoxin-ls1b-like isoform x2	328	1.59E-31	67.30%	0.594Y	IPR004169 (PFAM); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_EUK); SSF57059 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1538	c37208_g1_i1_len_1978_path_53_0_33_87_3_4_1977_5	479	sphingomyelin phosphodiesterase	659	1.53E-177	62.80%	0.221	IPR008139 (SMART); IPR029052 (G3DSA:3.60.21.GENE3D); IPR011160 (PIRSF); IPR004843 (PFAM); IPR007856 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR10340:SF13 (PANTHER); PTHR10340 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008139 (PROSITE_PROFILES); IPR011001 (SUPERFAMILY); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
1539	c37267_g1_i1_len_3154_path_3132_0_716_3_849_717_743_3876_744_1209_4342_1210_3_153_3	357	dipeptidyl aminopeptidase-like protein 6 isoform x1	1052	0	62.10%	0.106	IPR001375 (PFAM); IPR002469 (G3DSA:2.140.10.GENE3D); IPR002469 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11731:SF22 (PANTHER); PTHR11731 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF82171 (SUPERFAMILY); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1540	c37267_g1_i2_len_3127_path_3132_0_716_3_876_717_1182_4342_1183_3126_3	322	dipeptidyl aminopeptidase-like protein 6 isoform x1	1043	0	61.20%	0.106	IPR001375 (PFAM); IPR002469 (G3DSA:2.140.10.GENE3D); IPR002469 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11731:SF22 (PANTHER); PTHR11731 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF82171 (SUPERFAMILY); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1541	c37305_g1_i1_len_2060_path_117_0_1410_1_528_1411_1568_1686_1569_1992_4555_199_3_1993_4466_1994_2059_3	335	lissencephaly-1 homolog	687	0	90.70%	0.1	Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR006594 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR006594 (PFAM); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR006594 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017252 (HAMAP); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); SSF109925 (SUPERFAMILY)
1542	c37305_g1_i3_len_2077_path_117_0_1410_1_528_1411_1568_1686_1569_1992_4555_199_3_1993_2110_1994_2076_5	352	lissencephaly-1 homolog	692	0	90.90%	0.174	Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR006594 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR006594 (PFAM); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017252 (HAMAP); SSF109925 (SUPERFAMILY); IPR017986 (SUPERFAMILY)

1543	c37321_g3_i1_len_619_path_2095_0_618_0	22	ankyrin repeat and socs box protein 16-like isoform x2	207	1.97E-89	84.10%	0.101	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24133 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1544	c37334_g2_i1_len_1025_path_6237_0_917_8_419_918_1024_5	165	endoplasmic reticulum resident protein 29	341	3.67E-83	72.60%	0.184	Coil (COILS); IPR012883 (PFAM); IPR011679 (G3DSA:1.20.1150.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR011679 (PFAM); PTHR12211 (PANTHER); PTHR12211:SF0 (PANTHER); IPR012336 (SUPERFAMILY); IPR011679 (SUPERFAMILY)
1545	c37334_g2_i2_len_1049_path_6237_0_917_7_155_918_1048_5	181	endoplasmic reticulum resident protein 29	349	1.42E-95	70.80%	0.767 Y	Coil (COILS); IPR011679 (PFAM); IPR012883 (PFAM); IPR011679 (G3DSA:1.20.1150.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR12211:SF0 (PANTHER); PTHR12211 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); IPR011679 (SUPERFAMILY)
1546	c37376_g3_i1_len_1680_path_4335_0_157_2_040_158_950_69_951_1679_0	34	diuretic hormone 44 receptor	560	1.58E-126	68.30%	0.202	IPR002001 (PRINTS); IPR000832 (PRINTS); IPR001879 (SMART); IPR001879 (PFAM); IPR000832 (PFAM); PTHR12011 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); IPR001879 (PROSITE_PROFILES); SSF111418 (SUPERFAMILY); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1547	c37376_g3_i2_len_1878_path_4335_0_157_2_040_158_950_2832_951_1022_2904_1023_1031_2913_1032_1148_6_0	55	diuretic hormone receptor-like isoform x1	626	1.75E-152	69.30%	0.202	IPR002001 (PRINTS); IPR000832 (PRINTS); IPR001879 (SMART); IPR000832 (PFAM); IPR001879 (PFAM); PTHR12011 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001879 (PROSITE_PROFILES); IPR017981 (PROSITE_PROFILES); SSF111418 (SUPERFAMILY); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1548	c37391_g1_i1_len_2514_path_53_0_2513_4	671	laccase 2	838	0	62.10%	0.17	IPR001117 (PFAM); IPR008972 (G3DSA:2.60.40.GENE3D); IPR011707 (PFAM); IPR008972 (G3DSA:2.60.40.GENE3D); IPR011706 (PFAM); IPR008972 (G3DSA:2.60.40.GENE3D); PTHR11709:SF33 (PANTHER); PTHR11709 (PANTHER); IPR002355 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008972 (SUPERFAMILY); IPR008972 (SUPERFAMILY); IPR008972 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1549	c37395_g1_i1_len_2866_path_2819_0_2151_4971_2152_2793_5613_2794_2817_5613_2818_2841_5613_2842_2865_1	619	hypoxia up-regulated protein 1 isoform x1	955	0	71.00%	0.221	Coil (COILS); Coil (COILS); IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.30.30 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.90.640.10 (GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); PTHR19375 (PANTHER); PTHR19375:SF90 (PANTHER); IPR029048 (SUPERFAMILY); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY)

1550	c37433_g1_i1_len_2025_path_201_0_118_39_84_119_119_320_120_1631_1830_1632_18_84_114_1885_1912_114_0	4666	phosphoglycerate kinase	675	0	87.40%	0.111	IPR001576 (PRINTS); IPR015824 (G3DSA:3.40.50.GENE3D); IPR015901 (G3DSA:3.40.50.GENE3D); IPR001576 (PFAM); IPR001576 (PANTHER); PTHR11406:SF6 (PANTHER); IPR015911 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001576 (HAMAP); IPR001576 (SUPERFAMILY)
1551	c37490_g1_i1_len_1662_path_1640_0_176_1_817_177_1027_2668_1028_1661_0	154	fasciclin-2 isoform x3	554	1.48E-28	46.20%	0.106	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1552	c37495_g1_i1_len_380_path_335_0_247_205_248_262_205_263_277_596_278_292_220_293_304_622_305_328_107_1	20	transmembrane protease serine partial	127	1.97E-06	76.90%	0.103	G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
1553	c37495_g2_i1_len_389_path_16_0_21_38_22_38_58_39_388_0	17	serine protease snake	130	2.25E-10	58.70%	0.16	G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
1554	c37504_g1_i1_len_725_path_2757_0_125_54_6_126_127_548_128_724_0	66	neuroparsin 1 precursor	242	6.01E-19	60.60%	0.252	IPR010850 (PFAM); IPR011390 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR010850 (PRODOM); IPR009030 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1555	c37504_g1_i2_len_1144_path_1_0_543_545_544_544_546_545_546_548_547_1143_2	99	neuroparsin 1 precursor	381	1.29E-18	61.20%	0.112	IPR010850 (PFAM); IPR011390 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR010850 (PRODOM); IPR009030 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1556	c37504_g1_i3_len_737_path_2243_0_139_54_8_140_736_0	44	neuroparsin 1 precursor	246	4.41E-19	62.40%	0.123	IPR010850 (PFAM); IPR011390 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR010850 (PRODOM); IPR009030 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1557	c37507_g2_i1_len_2162_path_4773_0_2135_95_2136_2149_109_2150_2161_4	201	PREDICTED: uncharacterized protein LOC105267282 isoform X1	721	0	61.60%	0.111	IPR005018 (SMART); IPR005018 (PFAM); PTHR22979:SF15 (PANTHER); PTHR22979 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005018 (PROSITE_PROFILES); IPR005018 (PROSITE_PROFILES); TMhelix (TMHMM)
1558	c37522_g2_i1_len_637_path_1859_0_290_21_49_291_311_1200_312_636_5	288	hemagglutinin amebocyte aggregation factor-like	212	6.03E-38	60.00%	0.162	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1559	c37523_g1_i2_len_549_path_424_0_285_710_286_296_721_297_422_721_423_548_3	25	---NA---	183			0.105	PR01217 (PRINTS)
1560	c37534_g1_i1_len_633_path_875_0_399_127_4_400_408_654_409_460_831_461_503_874_504_632_4	22	zinc finger protein 648	211	1.40E-13	63.40%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1561	c37534_g2_i1_len_307_path_285_0_306_2	3	zinc finger protein	102	6.82E-17	59.00%	0.104	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1562	c37552_g1_i1_len_1743_path_1821_0_126_1948_127_1742_2	408	iron zinc purple acid phosphatase-like protein	576	0	73.90%	0.208	IPR004843 (PFAM); IPR015914 (G3DSA:2.60.40.GENE3D); IPR029052 (G3DSA:3.60.21.GENE3D); IPR025733 (PFAM); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); IPR008963 (SUPERFAMILY); IPR029052 (SUPERFAMILY)
1563	c37552_g1_i2_len_1646_path_3683_0_29_1948_30_1645_1	322	purple acid phosphatase	544	0	73.60%	0.848Y	IPR015914 (G3DSA:2.60.40.GENE3D); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); IPR025733 (PFAM); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); SignalP-noTM (SIGNALP_EUK); IPR008963 (SUPERFAMILY); IPR029052 (SUPERFAMILY)
								IPR001713 (PRINTS); IPR000010 (SMART); IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); G3DSA:3.10.450.10 (GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR000010 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR018073 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF54403 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1564	c37574_g1_i1_len_2700_path_1_0_128_130_129_2699_1	1065	gastrula zinc finger	900	8.02E-52	51.80%	0.102	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1565	c37580_g1_i1_len_1411_path_206_0_27_234_28_91_298_92_94_298_95_97_298_98_100_298_101_103_298_104_10_4	1124	von willebrand factor type egf and pentraxin domain-containing protein 1-like isoform x1	470	1.60E-12	42.80%	0.101	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1566	c37580_g1_i2_len_1454_path_1_0_204_206_205_232_1560_233_267_1186_268_297_1216_298_311_1230_312_351_4	1382	von willebrand factor type egf and pentraxin domain-containing protein 1-like	485	2.29E-13	40.00%	0.101	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1567	c37585_g1_i2_len_1534_path_807_0_45_118_46_286_2215_287_1153_3081_1154_1171_990_1172_1533_0	549	sparc	512	2.26E-114	77.30%	0.287	Coil (COILS); Coil (COILS); IPR003645 (SMART); IPR019577 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR13866 (PANTHER); PTHR13866:SF14 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR001999 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF100895 (SUPERFAMILY); SSF47473 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1568	c37626_g4_i1_len_2798_path_4489_0_555_5043_556_2797_1	338	thromboxane a synthase-like protein	933	5.22E-139	59.60%	0.192	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24292:SF24 (PANTHER); PTHR24292 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)

1569	c37654_g1_i1_len_1824_path_4433_0_158_4_592_159_1688_6122_1689_1713_6296_1714_1823_1	118	sodium calcium exchanger partial	608	1.70E-173	78.30%	0.104	IPR004836 (PRINTS); IPR003644 (SMART); IPR004837 (PFAM); IPR003644 (PFAM); PTHR11878 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF141072 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1570	c37654_g1_i2_len_1817_path_4433_0_158_4_592_159_1688_6122_1689_1713_6147_1714_1791_6122_1792_1816_1	158	sodium calcium exchanger partial	606	4.75E-173	78.30%	0.104	IPR004836 (PRINTS); IPR003644 (SMART); IPR004837 (PFAM); IPR003644 (PFAM); PTHR11878 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF141072 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1571	c37665_g1_i1_len_1388_path_129_0_249_37_7_250_1387_1	1693	cphe_pseag ame: full=cyanophycinase ame: full=extracellular cgpase short=cphepa ame: full=extracellular cyanophycinase flags: precursor	463	1.82E-85	51.10%	0.246	IPR005320 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); IPR029062 (SUPERFAMILY); TMhelix (TMHMM)
1572	c37665_g1_i2_len_1415_path_129_0_249_29_10_250_276_377_277_1414_1	1336	cphe_pseag ame: full=cyanophycinase ame: full=extracellular cgpase short=cphepa ame: full=extracellular cyanophycinase flags: precursor	472	6.24E-83	50.40%	0.246	IPR029062 (G3DSA:3.40.50.GENE3D); IPR005320 (PFAM); IPR029062 (SUPERFAMILY); TMhelix (TMHMM)
1573	c37670_g1_i1_len_227_path_166_0_13_180_14_24_287_25_40_303_41_76_303_77_112_1045_113_192_72_193_226_4	27	3d domain protein	76	8.96E-09	60.80%	0.105	no IPS match
1574	c37670_g1_i2_len_263_path_166_0_13_180_14_24_287_25_40_303_41_76_303_77_112_303_113_148_1045_149_22_4	213	carbohydrate-binding module family 48 protein	88	9.32E-12	60.70%	0.105	no IPS match
1575	c37681_g2_i1_len_1354_path_1_0_1190_119_2_1191_1271_3973_1272_1274_3977_1275_1353_1	179	prolyl 3-hydroxylase partial	451	6.67E-122	66.30%	0.255	IPR011990 (G3DSA:1.25.40.GENE3D); PTHR13986 (PANTHER); PTHR13986:SF8 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
1576	c37681_g2_i2_len_1463_path_1_0_1190_362_6_1191_1462_1	155	prolyl 3-hydroxylase partial	488	4.61E-127	65.40%	0.255	Coil (COILS); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR13986:SF8 (PANTHER); PTHR13986 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1577	c37684_g2_i1_len_1784_path_3448_0_1783_5	110	wd repeat-containing protein 61	594	3.32E-172	81.70%	0.104	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22841 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1578	c37720_g1_i1_len_598_path_1731_0_597_5	116	serine protease hepsin	199	4.46E-09	66.40%	0.11	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR009003 (SUPERFAMILY)
1579	c37720_g3_i1_len_861_path_2331_0_189_10_58_190_860_4	115	transmembrane protease serine partial	287	6.22E-34	51.00%	0.323	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1580	c37720_g3_i2_len_1131_path_2331_0_189_7_88_190_459_1058_460_1130_4	116	transmembrane protease serine 2-like	377	2.86E-18	52.80%	0.323	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

1581	c37725_g1_i1_len_2184_path_105_0_405_51_1_406_2183_1	484	probable chitinase 3	728	4.68E-133	57.40%	0.112	IPR011583 (SMART); IPR002557 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR002557 (PFAM); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR001579 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR017853 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR029070 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1582	c37726_g1_i1_len_1490_path_1617_0_99_32_0_100_224_448_225_536_760_537_1489_0	260	venom protease-like	497	8.39E-113	58.70%	0.163	IPR001314 (PRINTS); IPR001254 (SMART); IPR006604 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR022700 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF97 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1583	c37726_g1_i2_len_1660_path_53_0_266_320_267_391_445_392_394_448_395_706_760_707_1659_2	286	venom protease-like	553	1.45E-111	58.70%	0.129	IPR001314 (PRINTS); IPR001254 (SMART); IPR006604 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR022700 (PFAM); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF97 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1584	c37727_g1_i1_len_1657_path_1734_0_1039_2774_1040_1048_2783_1049_1174_3523_11_75_1656_2	458	46 kda fk506-binding nuclear protein	552	6.42E-47	73.40%	0.454 Y	Coil (COILS); G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); IPR023566 (PANTHER); IPR001179 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR024057 (SUPERFAMILY); SSF54534 (SUPERFAMILY)
1585	c37781_g2_i1_len_8422_path_8225_0_1783_5822_1784_4331_5822_4332_6879_1564_68_80_8421_3	1169	centrosomin-like protein	2808	2.26E-86	51.40%	0.226	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR012943 (PFAM); PTHR13895:SF14 (PANTHER); PTHR13895 (PANTHER)
1586	c37803_g1_i1_len_9545_path_1_0_9544_3	43640	low quality protein: hemocytin-like	3182	3.07E-65	39.70%	0.415 Y	IPR001846 (SMART); IPR014853 (SMART); PTHR11339 (PANTHER); PTHR11339:SF25 (PANTHER); IPR001007 (PROSITE_PATTERNS); IPR001007 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY); TMhelix (TMHMM)
1587	c37804_g2_i1_len_3488_path_3818_0_1638_5455_1639_3487_2	565	cadherin egf lag seven-pass g-type receptor partial	1162	5.00E-107	42.60%	0.303	IPR000203 (SMART); IPR000203 (PFAM); IPR000832 (PFAM); IPR022624 (PFAM); PTHR12011:SF74 (PANTHER); PTHR12011 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF81321 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1588	c37815_g1_i1_len_2027_path_105_0_2026_4	266	btb poz domain-containing protein 17	676	0	75.30%	0.28	IPR000210 (SMART); IPR011705 (SMART); IPR013069 (PFAM); IPR011705 (PFAM); G3DSA:3.30.710.10 (GENE3D); PTHR24410:SF9 (PANTHER); PTHR24410 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000210 (PROSITE_PROFILES); IPR011333 (SUPERFAMILY); TMhelix (TMHMM)
1589	c37821_g1_i1_len_2827_path_3361_0_222_4_42_223_2207_5568_2208_2216_6971_2217_2231_6986_2232_2241_635_0	3341	plasma alpha-l-fucosidase	943	0	78.10%	0.705 Y	IPR016286 (PRINTS); IPR000933 (SMART); IPR000933 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR000933 (PANTHER); PTHR10030:SF26 (PANTHER); IPR018526 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017853 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1590	c37821_g1_i2_len_2824_path_222_0_219_44_2_220_2204_5568_2205_2213_6971_2214_2_228_6986_2229_2238_6355_0	3046	plasma alpha-l-fucosidase	942	0	78.80%	0.414 Y	IPR016286 (PRINTS); IPR000933 (SMART); IPR000933 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR013780 (G3DSA:2.60.40.GENE3D); IPR000933 (PANTHER); PTHR10030:SF26 (PANTHER); IPR018526 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR017853 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1591	c37827_g1_i1_len_1768_path_1846_0_1767_2	1992	cytosolic non-specific dipeptidase	589	0	81.50%	0.142	IPR011650 (PFAM); G3DSA:3.40.630.10 (GENE3D); IPR011650 (G3DSA:3.30.70.GENE3D); IPR002933 (PFAM); PTHR11014:SF51 (PANTHER); PTHR11014 (PANTHER); IPR001261 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53187 (SUPERFAMILY); TMhelix (TMHMM)
1592	c37858_g1_i1_len_1286_path_53_0_756_810_757_793_4658_794_1285_5	968	contactin associated protein	428	1.94E-19	50.30%	0.189	Coil (COILS); IPR014716 (G3DSA:3.90.215.GENE3D); IPR001073 (PFAM); IPR002181 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); PTHR22923 (PANTHER); PTHR22923:SF49 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001073 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); IPR008983 (SUPERFAMILY); TMhelix (TMHMM)
1593	c37861_g1_i1_len_1081_path_1349_0_994_7_1_995_1080_4	144	superoxide dismutase	360	4.40E-63	67.80%	0.113	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); IPR001424 (SUPERFAMILY); IPR001424 (SUPERFAMILY)
1594	c37861_g1_i2_len_1154_path_1349_0_994_2_342_995_1077_23_1078_1153_5	224	superoxide dismutase	384	1.21E-63	68.70%	0.189	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR001424 (SUPERFAMILY); IPR001424 (SUPERFAMILY); TMhelix (TMHMM)

1595	c37876_g1_i1_len_3999_path_1_0_94_96_95_113_115_114_1884_1886_1885_2072_2074_2073_3998_0	839	sucrase- intestinal-like	1333	0	61.60%	0.122	IPR000322 (PFAM); PTHR22762:SF7 (PANTHER); PTHR22762 (PANTHER); IPR030458 (PROSITE_PATTERNS); IPR030459 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); SSF51011 (SUPERFAMILY); IPR011013 (SUPERFAMILY); TMhelix (TMHMM)
1596	c37880_g1_i1_len_600_path_1047_0_2_1050_3_42_1787_43_160_1208_161_314_205_315_469_360_470_599_4	17	zinc finger protein 420-like	200	9.95E-29	57.40%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007527 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1597	c37880_g1_i2_len_560_path_1090_0_117_1208_118_271_1359_272_429_360_430_559_4	21	zinc finger protein 420-like	187	7.64E-30	58.80%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13912 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007527 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1600	c3794_g1_i1_len_414_path_1_0_413_0	47	dnaja4 protein	138	1.57E-36	95.10%	0.148	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24076 (PANTHER); PTHR24076:SF75 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1598	c37942_g1_i1_len_159_path_1082_0_158_2	41	hemagglutinin amebocyte aggregation factor-like	53	5.84E-09	63.10%	0.189	PF14704 (PFAM); IPR026645 (PANTHER)
1599	c37942_g2_i1_len_450_path_1220_0_449_1	815	hemagglutinin amebocyte aggregation factor-like	150	6.20E-17	66.80%	0.129	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1601	c37955_g1_i1_len_1490_path_1518_0_1489_2	2253	epidermal retinol dehydrogenase 2-like isoform x2	496	1.38E-111	71.70%	0.123	Coil (COILS); IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF289 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1602	c37995_g1_i1_len_977_path_1_0_49_53_50_862_866_863_976_4	359	thioredoxin-dependent peroxide reductase	326	5.30E-127	84.70%	0.172	IPR019479 (PFAM); IPR000866 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1603	c38024_g1_i1_len_3260_path_3288_0_3259_1	2308	peroxidasin homolog	1087	8.64E-118	54.50%	0.418Y	Coil (COILS); IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1604	c38034_g1_i2_len_903_path_207_0_199_406_200_382_129_383_546_750_547_548_104_549_902_1	7367	snaclec stejaggregin-a subunit beta-1-like isoform x2	301	1.83E-13	47.10%	0.285	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)

1605	c38039_g1_i1_len_731_path_3458_0_199_36 58_200_240_3697_241_256_154_257_298_3 752_299_730_2	19104	nidogen-2 isoform x5	243	1.07E-22	54.70%	0.266	IPR000716 (SMART); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); IPR022339 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY)
1606	c38039_g1_i2_len_1498_path_4161_0_161_3 658_162_202_138_203_218_154_219_260_1 541_261_590_1871_591_14_0	6564	nidogen-2 isoform x3	500	5.71E-20	52.60%	0.735 Y	IPR000716 (SMART); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); IPR022339 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY)
1607	c38055_g2_i1_len_859_path_1_0_620_1532_621_858_4	48	protein bowel	286	2.56E-106	80.60%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR14196 (PANTHER); PTHR14196:SF0 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1608	c38096_g1_i2_len_2020_path_1455_0_130_1 586_131_154_3129_155_424_3399_425_426 3401_427_901_3876_9_0	319	flavin-containing monooxygenase fmo gs-ox3	674	1.03E-142	64.80%	0.183	IPR000960 (PRINTS); IPR020946 (PFAM); G3DSA:3.50.50.60 (GENE3D); G3DSA:3.50.50.60 (GENE3D); PTHR23023:SF4 (PANTHER); PTHR23023 (PANTHER); SSF51905 (SUPERFAMILY); SSF51905 (SUPERFAMILY)
1609	c38096_g1_i3_len_1111_path_1455_0_130_1 586_131_154_3129_155_424_3399_425_426 3401_427_901_7265_9_0	170	flavin-containing monooxygenase fmo gs-ox4-like isoform x1	371	1.57E-89	66.20%	0.183	IPR000960 (PRINTS); G3DSA:3.50.50.60 (GENE3D); IPR020946 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR23023:SF4 (PANTHER); PTHR23023 (PANTHER); SSF51905 (SUPERFAMILY)
1610	c38096_g2_i1_len_1543_path_2909_0_196_1 586_197_220_1610_221_1542_0	150	flavin-containing monooxygenase fmo gs-ox4-like isoform x1	515	5.92E-134	62.90%	0.424 Y	IPR000960 (PRINTS); IPR020946 (PFAM); G3DSA:3.50.50.60 (GENE3D); G3DSA:3.50.50.60 (GENE3D); PTHR23023:SF4 (PANTHER); PTHR23023 (PANTHER); SSF51905 (SUPERFAMILY); SSF51905 (SUPERFAMILY)
1611	c38101_g2_i1_len_2160_path_2238_0_2159_5	303	angiotensin-converting enzyme-like	720	0	71.20%	0.499Y	IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF55486 (SUPERFAMILY)
1612	c38113_g1_i1_len_2012_path_4194_0_316_5 23_317_687_892_688_723_4913_724_785_1 027_786_1393_5581_13_0	263	mam and ldl-receptor class a domain-containing protein 2-like	671	3.87E-13	40.80%	0.357 Y	IPR002172 (PRINTS); IPR000998 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR000998 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR23282:SF75 (PANTHER); PTHR23282 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1613	c38125_g1_i1_len_632_path_3135_0_73_320 9_74_146_2573_147_631_4	47	complement c1q tumor necrosis factor-related protein 4	211	1.47E-11	47.60%	0.139	IPR001073 (SMART); IPR008983 (G3DSA:2.60.120.GENE3D); IPR001073 (PFAM); PTHR22923 (PANTHER); PTHR22923:SF49 (PANTHER); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY)
1614	c38125_g2_i1_len_1228_path_3535_0_1227_0	80	contactin associated protein 1	410	1.60E-64	55.70%	0.653 Y	Coil (COILS); IPR000885 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF575 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR002181 (SUPERFAMILY)
1615	c38146_g1_i1_len_1810_path_245_0_679_36 _680_1809_2	220	leucine-rich repeat-containing protein 59	603	9.09E-63	65.50%	0.119	Coil (COILS); Coil (COILS); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1616	c38149_g1_i1_len_1001_path_243_0_278_52_2_279_303_547_304_405_648_406_406_219_407_867_1103_868_91_3	1409	kazal-type serine protease inhibitor 1 serpin	334	1.38E-08	62.20%	0.262	IPR002350 (SMART); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1617	c38149_g1_i2_len_957_path_243_0_278_522_279_303_547_304_405_648_406_406_219_407_867_144_868_956_4	833	kazal-type serine protease inhibitor 1 serpin	319	7.23E-09	61.83%	0.301	IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); IPR002350 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1618	c38156_g1_i1_len_2165_path_2256_0_807_2_4_808_955_3288_956_1135_3468_1136_119_6_3468_1197_1257_3529_1_5	297	cyclin-dependent kinase 11b-like isoform x4	721	1.36E-132	91.50%	0.097	Coil (COILS); Coil (COILS); IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24056 (PANTHER); PTHR24056:SF107 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1619	c38156_g1_i2_len_2243_path_2256_0_807_3_063_808_882_24_883_1030_3285_1031_103_3_3288_1034_1213_3468_1_5	310	cyclin-dependent kinase 11b-like isoform x4	747	1.00E-132	92.10%	0.097	Coil (COILS); Coil (COILS); IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24056:SF107 (PANTHER); PTHR24056 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1620	c38177_g1_i1_len_2014_path_1_0_1876_187_8_1877_2013_1	204	5 -nucleotidase	671	0	76.30%	0.289	IPR006179 (PRINTS); IPR008334 (G3DSA:3.90.780.GENE3D); IPR004843 (PFAM); IPR008334 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11575:SF7 (PANTHER); IPR006179 (PANTHER); IPR008334 (SUPERFAMILY); IPR029052 (SUPERFAMILY)
1621	c38177_g1_i2_len_2116_path_1_0_1876_405_2_1877_1978_1878_1979_2115_1	172	5 -nucleotidase	705	0	76.40%	0.289	IPR006179 (PRINTS); IPR008334 (PFAM); IPR008334 (G3DSA:3.90.780.GENE3D); IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); PTHR11575:SF7 (PANTHER); IPR006179 (PANTHER); IPR008334 (SUPERFAMILY); IPR029052 (SUPERFAMILY)
1622	c38185_g2_i1_len_3141_path_905_0_1188_9_05_1189_2377_3598_2378_3140_5	496	harmonin isoform x2	1047	8.31E-42	59.40%	0.097	Coil (COILS); Coil (COILS); Coil (COILS); IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR23116 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
1623	c38192_g1_i1_len_2134_path_2292_0_1889_4179_1890_1905_186_1906_2133_0	131	blastula protease 10-like	712	4.44E-48	50.00%	0.12	IPR001506 (PRINTS); IPR000859 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR001506 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127:SF580 (PANTHER); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
1624	c38196_g1_i1_len_2470_path_2685_0_1607_4288_1608_1626_148_1627_2469_5	333	n-acetylglucosamine-6-sulfatase-like isoform x1	823	9.88E-171	59.50%	0.13	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF208 (PANTHER); IPR024607 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM)
1625	c38200_g1_i1_len_5308_path_1_0_5307_4	1741	ring finger protein nhl-1	1769	0	74.10%	0.238	Coil (COILS); Coil (COILS); IPR001841 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); IPR001258 (PFAM); IPR018957 (PFAM); PTHR24103 (PANTHER); PTHR24103:SF230 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001841 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR000315 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); SSF101898 (SUPERFAMILY); SSF57850 (SUPERFAMILY)

1626	c38204_g1_i1_len_1756_path_1734_0_1217_3746_1218_1218_3747_1219_1225_2960_12_26_1234_2969_1235_14_0	1781	phospholipid-hydroperoxide glutathione peroxidase	586	2.78E-81	80.70%	0.163	IPR000889 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PFAM); IPR000889 (PANTHER); IPR029760 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1627	c38204_g1_i2_len_1742_path_1734_0_1217_3746_1218_1218_3747_1219_1225_2960_12_26_1234_2969_1235_14_0	1781	phospholipid-hydroperoxide glutathione peroxidase	581	2.47E-81	80.70%	0.163	IPR000889 (PRINTS); IPR000889 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PANTHER); IPR029760 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1628	c38209_g1_i1_len_766_path_2681_0_14_300_0_15_29_628_30_509_1108_510_653_1252_654_765_4	48	aael012165- partial	255	8.77E-86	73.40%	0.559Y	IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF15 (PANTHER); IPR029510 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR016161 (SUPERFAMILY)
1629	c38209_g1_i2_len_1307_path_2735_0_23_81_24_555_3000_556_570_628_571_1050_110_8_1051_1194_1252_1195_1_4	94	aldehyde dimeric nadp-preferring isoform x2	436	2.40E-176	76.90%	0.559 Y	IPR012394 (PIRSF); IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF116 (PANTHER); IPR029510 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR016161 (SUPERFAMILY)
1630	c38209_g1_i3_len_1363_path_1_0_79_81_80_611_3000_612_626_628_627_1106_1108_1_107_1250_1252_1251_1362_4	116	aldehyde dimeric nadp-preferring isoform x3	454	0	77.80%	0.559 Y	IPR012394 (PIRSF); IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF15 (PANTHER); IPR029510 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR016161 (SUPERFAMILY)
1631	c38209_g1_i4_len_1219_path_1_0_79_81_80_611_3000_612_626_628_627_1106_1252_1_107_1218_4	84	aldehyde dimeric nadp-preferring isoform x3	406	2.43E-172	80.00%	0.568 Y	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); IPR012394 (PIRSF); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699:SF15 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR016161 (SUPERFAMILY)
1632	c38209_g1_i5_len_745_path_1_0_79_81_80_611_3000_612_626_2874_627_744_4	48	aldehyde dimeric nadp-preferring isoform x4	248	1.00E-98	83.50%	0.143	IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699:SF15 (PANTHER); PTHR11699 (PANTHER); IPR016161 (SUPERFAMILY)
1633	c38211_g1_i1_len_2566_path_559_0_2565_1	288	tensin isoform x11	855	5.17E-143	61.20%	0.121	IPR029021 (G3DSA:3.90.190.GENE3D); IPR014020 (PFAM); G3DSA:2.60.40.1110 (GENE3D); PTHR12583:SF7 (PANTHER); PTHR12583 (PANTHER); IPR029023 (PROSITE_PROFILES); IPR014020 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); IPR000008 (SUPERFAMILY)
1634	c38245_g1_i1_len_1518_path_1_0_377_379_378_390_392_391_749_751_750_774_776_775_1098_3086_1099_2	1950	zinc metalloproteinase nas-14-like	506	1.18E-48	58.40%	0.183	IPR001506 (PRINTS); IPR006026 (SMART); IPR002557 (SMART); IPR002557 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1635	c38274_g2_i1_len_973_path_1830_0_319_15_4_320_353_2854_354_483_2319_484_507_3_069_508_525_2361_526_97_1	387	cathepsin I-like	324	5.13E-136	76.60%	0.12	IPR000668 (PRINTS); IPR013201 (SMART); IPR000668 (SMART); IPR000668 (PFAM); IPR013201 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR013128 (PANTHER); PTHR12411:SF57 (PANTHER); IPR000169 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)

1636	c38283_g1_i1_len_1959_path_1937_0_1958_3	199	biotinidase	653	1.30E-75	50.40%	0.209	IPR003010 (G3DSA:3.60.110.GENE3D); IPR003010 (PFAM); IPR012101 (PANTHER); PTHR10609:SF14 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003010 (PROSITE_PROFILES); IPR003010 (SUPERFAMILY); TMhelix (TMHMM)
1637	c38285_g1_i1_len_1897_path_1875_0_1896_2	92	c-type mannose receptor 2-like	632	1.33E-12	51.50%	0.263	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1638	c38299_g1_i1_len_610_path_687_0_21_709_22_514_3461_515_609_4	165	acidic phospholipase a2 pa4 isoform x2	203	9.03E-28	54.70%	0.193	IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PFAM); PTHR12253:SF13 (PANTHER); PTHR12253 (PANTHER); IPR013090 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016090 (SUPERFAMILY); TMhelix (TMHMM)
1639	c38299_g1_i2_len_1238_path_598_0_27_235_1_28_649_709_650_1142_3461_1143_1237_4	408	acidic phospholipase a2 pa4 isoform x2	413	2.62E-43	56.90%	0.193	IPR001211 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR12253 (PANTHER); IPR013090 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016090 (SUPERFAMILY); TMhelix (TMHMM)
1640	c38331_g1_i1_len_2189_path_2167_0_1153_3321_1154_1384_3552_1385_2188_5	948	pancreatic lipase-related protein partial	729	5.67E-102	55.30%	0.129	IPR000734 (PRINTS); IPR013818 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11610:SF41 (PANTHER); IPR000734 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1641	c38331_g1_i2_len_1958_path_2167_0_1153_3552_1154_1957_5	771	pancreatic lipase-related protein partial	652	2.18E-63	47.30%	0.129	IPR000734 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR013818 (PFAM); IPR000734 (PANTHER); PTHR11610:SF41 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1642	c38338_g1_i1_len_531_path_263_0_156_420_157_530_4	54	platelet-activating factor acetylhydrolase	177	2.50E-06	68.80%	0.123	IPR005065 (PFAM)
1643	c38338_g1_i2_len_1486_path_1979_0_1111_420_1112_1485_4	348	platelet-activating factor acetylhydrolase	495	3.61E-102	57.20%	0.123	Coil (COILS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR005065 (PFAM); IPR005065 (PANTHER); IPR029058 (SUPERFAMILY)
1644	c38381_g2_i1_len_3331_path_7073_0_2581_9655_2582_2604_9678_2605_3330_0	322	glutamyl aminopeptidase	1111	0	63.50%	0.297	IPR014782 (PRINTS); G3DSA:1.10.390.10 (GENE3D); IPR024571 (PFAM); IPR014782 (PFAM); IPR001930 (PANTHER); PTHR11533:SF165 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF63737 (SUPERFAMILY); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1645	c38385_g1_i1_len_2155_path_2245_0_1039_6919_1040_2154_5	304	venom carboxylesterase-6	718	1.17E-37	52.40%	0.247	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); PTHR11559:SF153 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY)
1646	c38385_g1_i3_len_2267_path_2245_0_1039_3285_1040_1722_3968_1723_1917_5768_1918_1930_4176_1931_2266_3	402	esterase fe4	756	1.79E-145	58.10%	0.208	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR019819 (PROSITE_PATTERNS); IPR019826 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY)

1647	c38470_g1_i1_len_3338_path_140_0_23_164_24_47_315_48_1003_86_1004_3337_4	663	12 kda fk506-binding protein	1113	8.10E-59	90.10%	0.313	G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); PTHR10516:SF272 (PANTHER); IPR023566 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1648	c38483_g1_i1_len_2448_path_53_0_14_68_1_5_550_604_551_2402_2454_2403_2417_245_4_2418_2432_2454_2433_2_4	1628	superoxide dismutase soluble	816	1.14E-42	54.60%	0.105	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001424 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1649	c38483_g1_i2_len_2521_path_4933_0_87_68_88_623_604_624_2475_2454_2476_2490_2_454_2491_2505_2454_2506_4	1634	superoxide dismutase soluble	840	1.54E-42	54.60%	0.105	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001424 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1650	c38485_g1_i1_len_1739_path_2871_0_1144_4834_1145_1325_587_1326_1738_1	175	delta-1-pyrroline-5-carboxylate mitochondrial isoform x1	580	0	79.70%	0.344 Y	IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF18 (PANTHER); IPR016160 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR016161 (SUPERFAMILY)
1651	c38485_g1_i2_len_1883_path_2871_0_1144_4834_1145_1325_4193_1326_1818_4683_18_19_1837_22_1838_1882_1	254	delta-1-pyrroline-5-carboxylate mitochondrial	628	0	80.30%	0.344 Y	IPR016162 (G3DSA:3.40.605.GENE3D); IPR016163 (G3DSA:3.40.309.GENE3D); IPR005931 (TIGRFAM); IPR015590 (PFAM); PTHR11699:SF18 (PANTHER); PTHR11699 (PANTHER); IPR016160 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR016161 (SUPERFAMILY)
1652	c38485_g1_i3_len_1864_path_2871_0_1144_4834_1145_1325_4193_1326_1818_22_1819_1863_1	248	pyrroline-5-carboxylate dehydrogenase	621	0	80.50%	0.344 Y	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); IPR005931 (TIGRFAM); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF18 (PANTHER); IPR016160 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR016161 (SUPERFAMILY)
1653	c38487_g1_i1_len_1503_path_91_0_794_71_795_1502_4	590	acid ceramidase	501	1.90E-158	71.90%	0.209	Coil (COILS); IPR029130 (PFAM); IPR029132 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1654	c38494_g2_i1_len_1410_path_1678_0_276_1_954_277_549_2225_550_560_2236_561_584_2260_585_990_2666_991_1	202	peptidyl-prolyl cis-trans isomerase-like isoform x1	470	1.35E-50	53.90%	0.218	IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF209 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1655	c38494_g2_i2_len_1035_path_1678_0_276_1_954_277_549_7532_550_560_2236_561_584_7566_585_1034_1	134	peptidyl-prolyl cis-trans isomerase a2	345	1.01E-45	53.20%	0.218	IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF202 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1656	c38500_g1_i1_len_1375_path_157_0_1185_4_106_1186_1374_2	250	serpin 3	458	2.15E-84	59.70%	0.115	IPR023796 (SMART); IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); G3DSA:3.30.497.10 (GENE3D); IPR000215 (PANTHER); PTHR11461:SF52 (PANTHER); IPR023795 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023796 (SUPERFAMILY); TMhelix (TMHMM)

1657	c38500_g1_i2_len_1835_path_157_0_1185_1 337_1186_1834_2	618	serpin 3	611	3.68E-82	58.90%	0.115	IPR023796 (SMART); G3DSA:3.30.497.10 (GENE3D); G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); PTHR11461:SF52 (PANTHER); IPR023795 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023796 (SUPERFAMILY); TMhelix (TMHMM)
1658	c38530_g1_i1_len_2213_path_6927_0_1075_ 8001_1076_2212_2	727	latrophilin cirl-like isoform x1	737	2.49E-178	59.50%	0.351 Y	Coil (COILS); IPR000832 (PFAM); PTHR12011:SF258 (PANTHER); PTHR12011 (PANTHER); IPR017983 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1659	c38530_g2_i1_len_2001_path_2192_0_1735_ 3928_1736_1759_4639_1760_1860_4740_18 61_2000_5	185	latrophilin cirl-like isoform x1	667	0	67.20%	0.127	IPR000203 (SMART); IPR001879 (SMART); IPR000203 (PFAM); IPR000922 (PFAM); IPR022624 (PFAM); IPR001879 (PFAM); IPR000832 (PFAM); PTHR12011 (PANTHER); PTHR12011:SF217 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000922 (PROSITE_PROFILES); IPR017981 (PROSITE_PROFILES); IPR000203 (PROSITE_PROFILES); IPR001879 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1660	c38530_g2_i2_len_2214_path_2192_0_1735_ 3928_1736_1759_9849_1760_1760_3953_17 61_2213_5	198	latrophilin cirl-like isoform x1	738	0	64.70%	0.102	IPR000203 (SMART); IPR001879 (SMART); IPR000832 (PFAM); IPR001879 (PFAM); IPR000203 (PFAM); IPR022624 (PFAM); PTHR12011:SF217 (PANTHER); PTHR12011 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); IPR001879 (PROSITE_PROFILES); IPR000203 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1661	c38535_g1_i1_len_1146_path_1224_0_373_1 594_374_387_1608_388_1028_2249_1029_ 1054_2275_1055_1145_5	84	i-type lysozyme	382	1.93E-35	64.50%	0.12	IPR008597 (PFAM); IPR008597 (PANTHER); IPR018247 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1662	c38535_g1_i2_len_1120_path_1224_0_373_1 594_374_387_1608_388_1028_2275_1029_ 1119_3	70	i-type lysozyme	374	1.69E-35	65.30%	0.183	IPR008597 (PFAM); IPR008597 (PANTHER); IPR018247 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1663	c38544_g1_i1_len_2797_path_3016_0_543_3 557_544_545_171_546_1980_4990_1981_2 004_70_2005_2672_48_2_3	731	leucine-rich repeat-containing protein let-4	933	2.36E-150	69.30%	0.161	IPR003591 (SMART); SM00365 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373:SF98 (PANTHER); PTHR24373 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1664	c38544_g1_i3_len_2773_path_3016_0_543_3 557_544_545_171__546_1980_70_1981_264 8_48_2649_2772_3	695	leucine-rich repeat-containing protein 70 isoform x1	925	1.44E-152	69.90%	0.161	IPR003591 (SMART); SM00365 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373 (PANTHER); PTHR24373:SF98 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1665	c38559_g1_i1_len_3628_path_105_0_200_30 4_201_224_328_225_3627_1	506	insulin-degrading enzyme	1209	0	76.50%	0.254	Coil (COILS); IPR007863 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); IPR011237 (G3DSA:3.30.830.GENE3D); IPR011237 (G3DSA:3.30.830.GENE3D); PTHR11851 (PANTHER); PTHR11851:SF85 (PANTHER); IPR001431 (PROSITE_PATTERNS); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY)
1666	c38580_g1_i1_len_1567_path_1595_0_685_2 279_686_1120_2714_1121_1122_2716__11 23_1513_3107_1514_1_0	2454	epoxide hydrolase 4	523	2.90E-102	62.10%	0.098	IPR000639 (PRINTS); IPR000073 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR10992:SF721 (PANTHER); PTHR10992 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1667	c38587_g1_i1_len_859_path_105_0_858_3	834	cre-nas-7 protein	287	7.58E-34	53.90%	0.891 Y	IPR001506 (PRINTS); IPR006026 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1669	c3859_g1_i1_len_1279_path_1_0_329_331_3 30_1278_5	7814	hemagglutinin amebocyte aggregation factor-like	426	1.74E-40	60.30%	0.217	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1668	c38597_g1_i1_len_2272_path_209_0_2271_1	1567	von willebrand factor like 1	757	5.51E-21	40.50%	0.101	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001007 (PROSITE_PROFILES); IPR006207 (PROSITE_PROFILES); TMhelix (TMHMM)
1670	c38613_g1_i1_len_2514_path_305_0_11_317 12_28_5627_29_30_5629_31_34_5633_35_ 36_3027_37_2513_5	162	hemicentin-1 isoform x2	838	4.93E-81	58.60%	0.249	IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13927 (PFAM); PTHR11640:SF6 (PANTHER); PTHR11640 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1671	c38616_g1_i1_len_1686_path_203_0_60_263 61_63_202_64_1685_2	618	alpha-aminoadipic semialdehyde dehydrogenase	562	0	83.70%	0.129	IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF144 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)

1672	c38634_g1_i1_len_2109_path_22_0_1407_1430_1408_1489_1512_1490_2108_2	7489	protein disulfide-isomerase	696	0	80.70%	0.668Y	PR00421 (PRINTS); IPR013766 (PFAM); IPR005788 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005792 (TIGRFAM); PF13848 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929 (PANTHER); PTHR18929:SF48 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1673	c38634_g1_i2_len_2166_path_22_0_1407_6940_1408_1473_7006_1474_1497_10648_1498_1546_1512_1547_2165_2	7180	disulfide isomerase	715	0	80.20%	0.668Y	PR00421 (PRINTS); IPR005792 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PF13848 (PFAM); IPR005788 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929 (PANTHER); PTHR18929:SF48 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1674	c38687_g1_i1_len_4629_path_1_0_2056_2058_2057_2362_2397_2363_4284_4319_4285_4287_4322_4288_4628_3	812	fasciclin-2 isoform x2	1543	0	58.70%	0.166	IPR009138 (PRINTS); IPR003599 (SMART); IPR003598 (SMART); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13927 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR003961 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF556 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1675	c38687_g1_i2_len_2716_path_9279_0_415_9695_416_416_2364_417_448_2396_449_449_2397_450_2371_4319_3	481	fascilin 2-like protein	906	0	59.70%	0.166	IPR009138 (PRINTS); IPR003599 (SMART); IPR003961 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR003961 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13927 (PFAM); PTHR10489:SF556 (PANTHER); PTHR10489 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)

1676	c38687_g1_i3_len_4662_path_1_0_2056_2058_2057_2362_2364_2363_2394_2396_2395_2395_2397_2396_4317_3	837	fasciclin- partial	1554	0	58.10%	0.166	IPR009138 (PRINTS); IPR003598 (SMART); IPR003961 (SMART); IPR003599 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13927 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489:SF556 (PANTHER); PTHR10489 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1677	c38687_g1_i4_len_2683_path_9279_0_415_2396_416_416_2397_417_2338_4319_2339_2341_4322_2342_2682_3	466	fascilin 2-like protein	895	0	59.40%	0.166	IPR009138 (PRINTS); IPR003961 (SMART); IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13927 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF556 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1678	c38706_g1_i1_len_2137_path_2052_0_1967_4210_1968_2030_4020_2031_2136_5	250	peptidyl-prolyl cis-trans isomerase fkbp4-like	712	0	73.80%	0.107	Coil (COILS); IPR019734 (SMART); G3DSA:3.10.50.40 (GENE3D); IPR023114 (G3DSA:1.10.150.GENE3D); IPR001440 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); IPR001179 (PFAM); G3DSA:3.10.50.40 (GENE3D); PF13414 (PFAM); IPR023566 (PANTHER); PTHR10516:SF274 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR001179 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY); SSF54534 (SUPERFAMILY); SSF48452 (SUPERFAMILY); TMhelix (TMHMM)
1679	c38706_g1_i2_len_2074_path_2052_0_1967_4020_1968_2073_5	250	peptidyl-prolyl cis-trans isomerase fkbp4-like	691	0	73.80%	0.11	Coil (COILS); IPR019734 (SMART); IPR011990 (G3DSA:1.25.40.GENE3D); IPR001440 (PFAM); G3DSA:3.10.50.40 (GENE3D); IPR023114 (G3DSA:1.10.150.GENE3D); IPR001179 (PFAM); G3DSA:3.10.50.40 (GENE3D); PF13414 (PFAM); IPR023566 (PANTHER); PTHR10516:SF274 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR001179 (PROSITE_PROFILES); IPR001179 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF54534 (SUPERFAMILY); SSF48452 (SUPERFAMILY); SSF54534 (SUPERFAMILY); TMhelix (TMHMM)
1680	c38707_g1_i1_len_1444_path_1_0_1443_5	1457	thioredoxin peroxidase	481	1.90E-117	88.20%	0.104	IPR019479 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000866 (PFAM); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)

1681	c38806_g1_i2_len_6682_path_9297_0_867_1 5778_868_897_10165_898_6293_15558_629 4_6483_1609_6484_6491_1_1	2169	myosin heavy non-muscle-like	2227	0	89.10%	0.187	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR001609 (PRINTS); IPR001609 (SMART); IPR027401 (G3DSA:4.10.270.GENE3D); IPR004009 (PFAM); IPR001609 (PFAM); G3DSA:1.20.5.340 (GENE3D); IPR002928 (PFAM); PTHR13140 (PANTHER); PTHR13140:SF301 (PANTHER); IPR000048 (PROSITE_PROFILES); IPR001609 (PROSITE_PROFILES); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF57997 (SUPERFAMILY); IPR027417 (SUPERFAMILY); SSF90257 (SUPERFAMILY)
1682	c38806_g1_i3_len_6652_path_9297_0_867_1 0165_868_6263_15558_6264_6453_1609_64 54_6461_15558_6462_6651_1	2157	myosin heavy non-muscle-like isoform 2	2217	0	89.60%	0.187	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR001609 (PRINTS); IPR001609 (SMART); IPR002928 (PFAM); IPR001609 (PFAM); IPR004009 (PFAM); IPR027401 (G3DSA:4.10.270.GENE3D); G3DSA:1.20.5.340 (GENE3D); PTHR13140 (PANTHER); PTHR13140:SF301 (PANTHER); IPR000048 (PROSITE_PROFILES); IPR001609 (PROSITE_PROFILES); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); IPR027417 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF57997 (SUPERFAMILY)
1683	c38809_g1_i1_len_747_path_4711_0_746_2	129	membrane metallo-endopeptidase-like 1-like	249	2.06E-28	54.70%	0.133	IPR008753 (PFAM); G3DSA:1.10.1380.10 (GENE3D); IPR000718 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY)
1684	c38809_g2_i1_len_2276_path_53_0_684_738 685_2275_1	320	membrane metallo-endopeptidase-like 1-like	759	9.70E-163	62.20%	0.123	IPR018497 (PRINTS); IPR018497 (PFAM); IPR008753 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
1685	c38812_g2_i1_len_3652_path_206_0_557_76 2_558_599_804_600_1255_1459_1256_125 8_98_1259_1913_211_5	434	membrane metallo-endopeptidase-like 1	1217	1.02E-99	47.50%	0.098	IPR018497 (PRINTS); IPR018497 (PFAM); IPR008753 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
1686	c38819_g1_i1_len_1853_path_103_0_1852_4	11265	cre-nas-15 protein	618	1.06E-60	57.90%	0.229	IPR001506 (PRINTS); IPR006026 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1687	c38843_g1_i2_len_1756_path_53_0_853_905 854_1018_1070_1019_1374_1426_1375_17 55_0	226	abhydrolase domain-containing protein 16a	586	0	68.90%	0.118	IPR029059 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR12277 (PANTHER); PTHR12277:SF44 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1688	c38846_g1_i1_len_2915_path_53_0_2914_0	10690	cathepsin d	972	0	80.50%	0.164	IPR001461 (PRINTS); IPR021109 (G3DSA:2.40.70.GENE3D); IPR012848 (PFAM); IPR021109 (G3DSA:2.40.70.GENE3D); IPR001461 (PFAM); IPR001461 (PANTHER); PTHR13683:SF230 (PANTHER); IPR001969 (PROSITE_PATTERNS); IPR001969 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR021109 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1689	c38867_g1_i1_len_3690_path_3902_0_1154_5057_1155_1157_5060__1158_3505_134_35_06_3689_2	331		zinc finger protein 676-like	1230	2.13E-75	60.70%	0.146	Coil (COILS); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1690	c38876_g1_i1_len_2885_path_225_0_2459_2_678_2460_2468_68_2469_2741_5996_2742_2758_2976_2759_2884_4	1695		moxd1 homolog 2	962	1.42E-124	56.20%	0.239	IPR000945 (PRINTS); IPR005018 (SMART); IPR000323 (G3DSA:2.60.120.GENE3D); PF03712 (PFAM); IPR015920 (G3DSA:2.60.40.GENE3D); IPR005018 (PFAM); IPR014784 (G3DSA:2.60.120.GENE3D); IPR000323 (PFAM); IPR000945 (PANTHER); PTHR10157-SF23 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005018 (PROSITE_PROFILES); IPR008977 (SUPERFAMILY); SSF49344 (SUPERFAMILY); IPR008977 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1691	c38902_g1_i1_len_1516_path_1494_0_574_2_069_575_1515_2	411		late trypsin	505	6.58E-48	55.70%	0.304	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1692	c38905_g4_i1_len_2359_path_1785_0_1342_3128_1343_2358_4	286		striatin- partial	773	0	75.40%	0.1	Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR013258 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR15653 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
1693	c38905_g4_i2_len_2476_path_1785_0_1342_9176_1343_1459_3128_1460_2475_4	296		striatin-3-like isoform x1	812	0	73.40%	0.1	Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR013258 (PFAM); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR15653 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)

1694	c38933_g1_i1_len_3472_path_121_0_1196_1_317_1197_1205_34_1206_3471_1	6313	ferritin 1-like protein a	1157	4.13E-43	65.40%	0.167	IPR012347 (G3DSA:1.20.1260.GENE3D); IPR008331 (PFAM); PTHR11431:SF29 (PANTHER); IPR001519 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
1695	c38943_g1_i1_len_3300_path_5335_0_2690_8024_2691_3087_77_3088_3299_3	907	a disintegrin and metalloproteinase with thrombospondin motifs 18 isoform x1	1100	1.74E-101	66.80%	0.128	IPR024079 (G3DSA:3.40.390.GENE3D); PTHR13723:SF148 (PANTHER); PTHR13723 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001590 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1696	c38943_g1_i2_len_4894_path_5335_0_2690_10214_2691_2702_8024_2703_3099_8420_3100_3227_8548_3228_3_4	1149	a disintegrin and metalloproteinase with thrombospondin motifs 16-like isoform x3	1631	0	65.20%	0.114	IPR024079 (G3DSA:3.40.390.GENE3D); PF13582 (PFAM); PTHR13723 (PANTHER); PTHR13723:SF148 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001590 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1697	c38943_g1_i3_len_4882_path_5335_0_2690_8024_2691_3087_8420_3088_3215_8548_3_216_3270_8603_3271_36_4	1201	a disintegrin and metalloproteinase with thrombospondin motifs 16-like isoform x3	1627	0	65.70%	0.114	PF13582 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR13723 (PANTHER); PTHR13723:SF148 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001590 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1698	c38949_g1_i1_len_1486_path_1_0_498_500_499_503_505_504_1485_2	932	trypsinogen 2	495	4.14E-68	59.00%	0.882 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1699	c38958_g1_i2_len_1698_path_1676_0_211_1_888_212_1264_2941_1265_1288_2965_1289_1377_3054_1378_1697_2	284	bola-like protein 2-like	566	1.16E-33	83.20%	0.237	IPR002634 (G3DSA:3.30.300.GENE3D); IPR002634 (PFAM); PTHR12735 (PANTHER); PTHR12735:SF2 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002634 (SUPERFAMILY)
1700	c38987_g1_i1_len_1434_path_1412_0_1433_1	274	#NAME?	478	1.19E-138	77.90%	0.16	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PF13561 (PFAM); PTHR24315 (PANTHER); PTHR24315:SF2 (PANTHER); SSF51735 (SUPERFAMILY)
1701	c38994_g1_i1_len_8051_path_139_0_5837_5_975_5838_6085_6223_6086_6874_7012_68_75_7403_86_7404_8050_2	1969	muscle m-line assembly protein unc- partial	2683	1.64E-71	43.80%	0.1	Coil (COILS); Coil (COILS); IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR020675 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
1702	c39004_g1_i1_len_735_path_1015_0_144_11_58_145_734_1	1629	carboxypeptidase b-like	245	1.11E-71	66.70%	0.146	IPR000834 (SMART); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53187 (SUPERFAMILY); TMhelix (TMHMM)

1703	c39004_g1_i2_len_1365_path_1717_0_774_158_775_1364_1	2573	carboxypeptidase b-like	455	3.33E-120	64.20%	0.25	IPR000834 (PRINTS); IPR000834 (SMART); G3DSA:3.40.630.10 (GENE3D); IPR003146 (PFAM); IPR000834 (PFAM); IPR003146 (G3DSA:3.30.70.GENE3D); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY); IPR009020 (SUPERFAMILY)
1704	c39022_g1_i1_len_2028_path_275_0_415_68_8_416_423_222_424_2027_1	1365	kielin chordin-like protein	676	2.20E-27	39.20%	0.784Y	IPR001846 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR001846 (PFAM); PTHR11339 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001846 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); TMhelix (TMHMM); TMhelix (TMHMM)
1705	c39025_g1_i1_len_4391_path_255_0_3581_3_828_3582_3584_46_3585_4291_4537_4292_4324_4537_4325_4357_453_1	8431	von willebrand factor a domain-containing protein 7	1464	4.19E-88	44.90%	0.11	PF13519 (PFAM); PTHR14905 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002035 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1706	c39028_g1_i1_len_1208_path_1256_0_730_1_987_731_752_2009_753_1055_2624_1056_1207_0	1213	granulins- partial	403	3.58E-38	51.30%	0.552Y	IPR000118 (SMART); IPR000118 (PFAM); PTHR12274:SF1 (PANTHER); PTHR12274 (PANTHER); IPR000118 (PROSITE_PATTERNS); IPR000118 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF57277 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1707	c39028_g1_i2_len_1278_path_1256_0_730_1_987_731_752_2009_753_1055_2312_1056_1277_0	1239	granulins- partial	426	3.74E-38	51.80%	0.552 Y	IPR000118 (SMART); IPR000118 (PFAM); PTHR12274:SF1 (PANTHER); PTHR12274 (PANTHER); IPR000118 (PROSITE_PATTERNS); IPR000118 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF57277 (SUPERFAMILY); TMhelix (TMHMM)
1708	c39031_g1_i1_len_680_path_658_0_62_2082_63_113_2125_114_120_2132_121_144_803_145_184_2219_185_212_8_5	30	zinc finger protein gfi-1	226	1.85E-35	57.00%	0.152	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1709	c39036_g3_i1_len_2446_path_6815_0_2264_9076_2265_2266_9078_2267_2445_1	304	er degradation-enhancing alpha-mannosidase-like protein 2	815	0	76.70%	0.098	IPR001382 (PRINTS); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); PTHR11742:SF37 (PANTHER); IPR001382 (PANTHER); IPR001382 (SUPERFAMILY)
1710	c39039_g1_i2_len_1754_path_852_0_402_54_82_403_405_3007_406_1586_4187_1587_17_53_1	482	cytochrome p450 2j2	585	3.96E-104	58.60%	0.122	Coil (COILS); IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY)
1711	c39039_g1_i3_len_1767_path_852_0_402_54_69_403_414_5481_415_415_5482_416_418_3007_419_1599_4187_1600_2	479	cytochrome p450 2j2-like	589	1.42E-104	58.60%	0.133	Coil (COILS); IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24300 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1712	c39042_g1_i1_len_1091_path_1819_0_105_3_05_106_127_696_128_467_368_468_746_2_560_747_1090_5	491	peroxiredoxin partial	363	2.40E-115	83.50%	0.189	IPR000866 (PFAM); G3DSA:3.30.1020.10 (GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR019479 (PFAM); PTHR10681:SF77 (PANTHER); PTHR10681 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)

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1717	c39048_g1_i3_len_5023_path_209_0_1307_1 1116_1308_1309_1518_1310_1623_11139_1 624_1624_11140_1625_162_3	555	neuroglian-like isoform 2	1675	0	77.50%	0.292	IPR003961 (SMART); IPR003598 (SMART); IPR003599 (SMART); PF13895 (PFAM); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR026966 (PFAM); PTHR10489 (PANTHER); PTHR10489:SF553 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM)
1718	c39048_g1_i4_len_5130_path_209_0_1307_1 1116_1308_1309_1518_1310_1623_11139_1 624_1624_11140_1625_162_5	588	neuroglian-like isoform 2	1710	0	77.50%	0.148	IPR003598 (SMART); IPR003599 (SMART); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR026966 (PFAM); PTHR10489:SF553 (PANTHER); PTHR10489 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1719	c39048_g1_i5_len_3584_path_51_0_77_1113 9_78_78_11140_79_79_25_80_3437_5190_3438_3583_5	412	neuroglian isoform x3	1194	0	78.00%	0.148	IPR003961 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489:SF553 (PANTHER); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)

1720	c39048_g1_i6_len_4812_path_209_0_1307_25__1308_4665_5190_4666_4811_5	544	neuroglian isoform x1	1604	0	77.80%	0.148	IPR003961 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR10489 (PANTHER); PTHR10489:SF553 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY);
1721	c39061_g3_i1_len_619_path_60_0_20_2841_21_21_82_22_618_5	2507	vp302_lycmc ame: full=venom protein 302 flags: precursor	206	2.42E-14	56.20%	0.779Y	PTHR14186:SF8 (PANTHER); IPR011390 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR000867 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009030 (SUPERFAMILY)
1722	c39063_g2_i2_len_1070_path_1895_0_1044_6329_1045_1045_6330_1046_1046_6331_1047_1069_0	525	aminoacylase-1	357	6.94E-153	75.30%	0.101	IPR010159 (TIGRFAM); G3DSA:3.40.630.10 (GENE3D); IPR010159 (PIRSF); IPR011650 (G3DSA:3.30.70.GENE3D); IPR011650 (PFAM); IPR002933 (PFAM); PTHR11014 (PANTHER); PTHR11014:SF8 (PANTHER); IPR001261 (PROSITE_PATTERNS); IPR001261 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY); IPR011650 (SUPERFAMILY)
1723	c39063_g2_i3_len_1483_path_1895_0_1044_6329_1045_1045_6330_1046_1046_2938_1047_1482_0	735	aminoacylase-1	495	0	75.60%	0.101	IPR011650 (PFAM); G3DSA:3.40.630.10 (GENE3D); IPR010159 (TIGRFAM); IPR010159 (PIRSF); IPR002933 (PFAM); IPR011650 (G3DSA:3.30.70.GENE3D); PTHR11014 (PANTHER); PTHR11014:SF8 (PANTHER); IPR001261 (PROSITE_PATTERNS); IPR001261 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53187 (SUPERFAMILY); IPR011650 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1724	c39076_g1_i1_len_744_path_1018_0_147_1166_148_157_1176_158_208_1227_209_253_1272_254_443_1462_444_4_1	84	spindolin-related protein	248	6.70E-40	56.60%	0.103	G3DSA:2.70.50.50 (GENE3D); IPR004302 (PFAM); IPR009030 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
1725	c39079_g1_i1_len_1754_path_2229_0_902_3132_903_1594_4528_1595_1753_0	278	24-dehydrocholesterol reductase	585	0	78.80%	0.11	IPR016169 (G3DSA:3.30.465.GENE3D); IPR006094 (PFAM); PTHR10801 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016166 (PROSITE_PROFILES); IPR016166 (SUPERFAMILY); TMhelix (TMHMM)
1726	c39079_g1_i2_len_2251_path_2229_0_902_3132_903_1594_3824_1595_2250_0	633	delta -sterol reductase	751	0	78.60%	0.11	IPR006094 (PFAM); IPR016169 (G3DSA:3.30.465.GENE3D); PTHR10801 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016166 (PROSITE_PROFILES); IPR016166 (SUPERFAMILY); IPR016164 (SUPERFAMILY); TMhelix (TMHMM)
1727	c39087_g1_i1_len_1009_path_327_0_118_445_119_127_292_128_176_2455_177_1008_0	3208	trypsinogen h2_1g	337	1.85E-58	57.10%	0.420Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)

1728	c39099_g1_i1_len_1196_path_1424_0_1195_4	118	membrane glycoprotein lig-	399	1.34E-21	44.00%	0.327	G3DSA:3.80.10.10 (GENE3D); PTHR24367 (PANTHER); PTHR24367:SF251 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1765	c391_g1_i1_len_3638_path_3666_0_3637_0	637	transducin beta-like protein 2	1213	9.15E-143	69.20%	0.15	Coil (COILS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22847:SF380 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1729	c39100_g1_i1_len_1783_path_75_0_1113_1188_1114_1125_74_1126_1782_5	13718	dermatopontin 2	594	9.11E-38	59.10%	0.161	PF14704 (PFAM); IPR026645 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TMhelix (TMHMM)
1730	c39105_g1_i1_len_2913_path_9784_0_93_9877_94_2763_6516_2764_2912_5	670	cd109 antigen-like isoform x2	971	0	75.40%	0.103	IPR009048 (G3DSA:2.60.40.GENE3D); IPR001599 (PFAM); IPR011626 (PFAM); IPR008930 (G3DSA:1.50.10.GENE3D); IPR009048 (PFAM); IPR019565 (PFAM); PTHR11412 (PANTHER); PTHR11412:SF84 (PANTHER); IPR019742 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009048 (SUPERFAMILY); IPR008930 (SUPERFAMILY); IPR014756 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1731	c39105_g2_i1_len_2609_path_6089_0_211_2921_212_2189_4899_2190_2285_4995_2286_2286_4996_2287_2359_5	194	cd109 antigen-like isoform x2	869	0	70.20%	0.732Y	IPR002890 (PFAM); IPR011625 (PFAM); PTHR11412 (PANTHER); PTHR11412:SF84 (PANTHER); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM); TMhelix (TMHMM)
1732	c39105_g2_i2_len_2439_path_6089_0_211_2921_212_2189_5069_2190_2282_5162_2283_2438_3	185	cd109 antigen-like isoform x2	813	0	70.20%	0.463 Y	IPR011625 (PFAM); IPR002890 (PFAM); PTHR11412 (PANTHER); PTHR11412:SF84 (PANTHER); SignalP-noTM (SIGNALP_EUK)
1733	c39105_g2_i3_len_2442_path_6089_0_211_2921_212_2189_4899_2190_2285_5162_2286_2441_3	187	cd109 antigen-like isoform x2	814	0	70.10%	0.452 Y	IPR002890 (PFAM); IPR011625 (PFAM); PTHR11412 (PANTHER); PTHR11412:SF84 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM)
1734	c39105_g2_i5_len_2263_path_6089_0_211_2921_212_2189_4996_2190_2262_4	172	cd109 antigen-like isoform x2	754	0	70.10%	0.278	IPR002890 (PFAM); IPR011625 (PFAM); PTHR11412:SF84 (PANTHER); PTHR11412 (PANTHER)
1735	c39106_g1_i1_len_3094_path_53_0_3093_0	545	neutral alpha-glucosidase ab-like	1032	0	71.60%	0.179	IPR025887 (PFAM); IPR000322 (PFAM); PTHR22762:SF54 (PANTHER); PTHR22762 (PANTHER); SSF51011 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR011013 (SUPERFAMILY)

1736	c39109_g1_i1_len_1977_path_2022_0_1598_3621_1599_1742_3765_1743_1934_4096_1935_1976_3	560	prostaglandin g h synthase 2-like isoform x3	659	0	70.20%	0.689 Y	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR019791 (PFAM); PTHR11903 (PANTHER); PTHR11903:SF10 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR019791 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF57196 (SUPERFAMILY); IPR010255 (SUPERFAMILY); TMhelix (TMHMM)
1737	c39109_g1_i2_len_1833_path_2022_0_1598_3765_1599_1790_4096_1791_1832_3	478	prostaglandin g h synthase 2-like isoform x3	611	0	65.30%	0.689 Y	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR11903 (PANTHER); PTHR11903:SF10 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR019791 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR010255 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)
1738	c39109_g1_i3_len_1888_path_2022_0_1598_3765_1599_1790_3957_1791_1887_4	504	prostaglandin g h synthase 2-like isoform x3	629	0	65.30%	0.369 Y	IPR019791 (PRINTS); G3DSA:2.10.25.10 (GENE3D); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11903:SF10 (PANTHER); PTHR11903 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR019791 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF57196 (SUPERFAMILY); IPR010255 (SUPERFAMILY); TMhelix (TMHMM)
1739	c39109_g1_i4_len_2032_path_2022_0_1598_3621_1599_1742_3765_1743_1934_3957_1935_2031_4	588	prostaglandin g h synthase 2-like isoform x3	677	0	70.20%	0.369 Y	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR11903 (PANTHER); PTHR11903:SF10 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR019791 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF57196 (SUPERFAMILY); IPR010255 (SUPERFAMILY); TMhelix (TMHMM)
1740	c39112_g1_i1_len_3458_path_1_0_303_7038_304_323_325_324_3457_3	306	complement c1s subcomponent	1153	4.16E-10	43.40%	0.106	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1741	c39113_g1_i1_len_2099_path_3166_0_445_3_612_446_764_3931_765_765_3932_766_113_7_4304_1138_1314_4481_1_0	562	peptidyl-prolyl cis-trans isomerase cyp11 isoform x1	700	1.38E-147	72.40%	0.133	Coil (COILS); Coil (COILS); IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF229 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1742	c39113_g1_i2_len_1687_path_3166_0_445_3_612_446_764_3931_765_765_3932_766_113_7_4304_1138_1314_3932_1_0	565	peptidyl-prolyl cis-trans isomerase cyp11 isoform x1	563	4.51E-146	72.10%	0.133	Coil (COILS); IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF229 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1743	c39113_g1_i3_len_2215_path_3166_0_445_6_396_446_561_3612_562_880_3931_881_881_3932_882_1253_4304_125_0	525	peptidyl-prolyl cis-trans isomerase cyp11-like isoform x2	739	2.00E-68	88.60%	0.133	Coil (COILS); Coil (COILS); Coil (COILS); IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF229 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1744	c39113_g1_i3_len_2215_path_3166_0_445_6_396_446_561_3612_562_880_3931_881_881_3932_882_1253_4304_125_2	525	peptidyl-prolyl cis-trans isomerase g isoform x3	738	2.19E-61	62.40%	0.135	Coil (COILS); Coil (COILS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF229 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)

1745	c39128_g1_i1_len_2799_path_213_0_417_63_0_418_420_212_421_1789_1998_1790_1816_104_1817_2401_2609_4	5379	meprin a	933	2.22E-78	52.00%	0.17	IPR001506 (PRINTS); IPR000859 (SMART); IPR006026 (SMART); IPR001506 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000859 (PFAM); PTHR10127:SF580 (PANTHER); PTHR10127 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000859 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
1746	c39131_g1_i1_len_805_path_1_0_41_43_42_396_1892_397_409_411_410_653_655_654_657_659_658_663_2_1	64	galectin partial	268	2.21E-59	69.30%	0.108	IPR001079 (SMART); IPR001079 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001079 (PFAM); PTHR11346 (PANTHER); IPR001079 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
1747	c39145_g1_i1_len_251_path_2723_0_22_274_8_23_121_295_122_154_328_155_227_175_228_250_4	669	ubiquitin family protein	84	3.07E-51	100.00%	0.201	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY)
1748	c39145_g1_i2_len_894_path_779_0_785_767_786_797_328_798_870_175_871_893_4	348	polyubiquitin-c-like isoform 2	298	1.34E-110	98.90%	0.201	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY)
1749	c39153_g1_i1_len_1241_path_7174_0_1083_264_1084_1108_157_1109_1215_264_1216_1240_5	343	bile salt-activated lipase isoform x4	413	5.16E-11	40.50%	0.104	no IPS match
1750	c39153_g2_i1_len_4395_path_264_0_24_828_1_25_3284_384_3285_3395_11650_3396_43_22_1121_4323_4349_1112_4	1149	bile salt-activated lipase isoform x1	1465	6.99E-19	45.17%	0.119	TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1751	c39170_g2_i1_len_2337_path_4217_0_659_3_6_660_1220_7059_1221_1222_3108_1223_1404_62_1405_1405_328_4	6350	nuclease-sensitive element-binding protein 1 isoform x4	779	7.49E-57	77.00%	0.102	IPR002059 (PRINTS); IPR011129 (SMART); IPR002059 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); PTHR11544 (PANTHER); IPR019844 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012340 (SUPERFAMILY); TMhelix (TMHMM)
1752	c39170_g2_i2_len_2493_path_4217_0_659_3_6_660_1220_7059_1221_1222_6803_1223_1227_2957_1228_1251_2_4	6335	nuclease-sensitive element-binding protein 1 isoform x4	831	6.54E-57	77.00%	0.102	IPR002059 (PRINTS); IPR011129 (SMART); IPR002059 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); PTHR11544 (PANTHER); IPR019844 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012340 (SUPERFAMILY); TMhelix (TMHMM)
1753	c39170_g2_i3_len_2376_path_4217_0_659_3_6_660_1220_3067_1221_1261_3108_1262_1443_62_1444_1444_328_4	7081	nuclease-sensitive element-binding protein 1 isoform x4	792	9.60E-57	75.40%	0.102	IPR002059 (PRINTS); IPR011129 (SMART); IPR002059 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); PTHR11544 (PANTHER); IPR019844 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012340 (SUPERFAMILY); TMhelix (TMHMM)
1754	c39170_g2_i4_len_1979_path_2243_0_713_2_957_714_737_2981_738_823_3067_824_864_3108_865_1046_62_1047_4	3648	nuclease-sensitive element-binding protein 1 isoform x4	660	3.52E-57	75.40%	0.102	IPR002059 (PRINTS); IPR011129 (SMART); IPR012340 (G3DSA:2.40.50.GENE3D); IPR002059 (PFAM); PTHR11544 (PANTHER); IPR019844 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012340 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1755	c39170_g2_i5_len_2394_path_4217_0_659_3 6_660_1220_3067_1221_1261_3108_1262_1443_44_1444_1461_62_4	6437	nuclease-sensitive element-binding protein 1 isoform x4	798	8.84E-57	75.40%	0.102	IPR002059 (PRINTS); IPR011129 (SMART); IPR002059 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); PTHR11544 (PANTHER); IPR019844 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012340 (SUPERFAMILY); TMhelix (TMHMM)
1756	c39170_g2_i6_len_2394_path_4217_0_659_3 6_660_1220_3067_1221_1261_3108_1262_1443_62_1444_1444_328_4	6431	nuclease-sensitive element-binding protein 1 isoform x4	798	9.01E-57	75.40%	0.102	IPR002059 (PRINTS); IPR011129 (SMART); IPR012340 (G3DSA:2.40.50.GENE3D); IPR002059 (PFAM); PTHR11544 (PANTHER); IPR019844 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012340 (SUPERFAMILY); TMhelix (TMHMM)
1757	c39170_g2_i7_len_2412_path_4217_0_659_3 6_660_1220_3067_1221_1261_3108_1262_1443_44_1444_1461_62_4	6437	nuclease-sensitive element-binding protein 1 isoform x3	804	9.69E-57	75.40%	0.102	IPR002059 (PRINTS); IPR011129 (SMART); IPR012340 (G3DSA:2.40.50.GENE3D); IPR002059 (PFAM); PTHR11544 (PANTHER); IPR019844 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012340 (SUPERFAMILY); TMhelix (TMHMM)
1758	c39170_g2_i8_len_2355_path_4217_0_659_3 6_660_1220_7059_1221_1222_3108_1223_1404_44_1405_1422_62_4	5798	nuclease-sensitive element-binding protein 1 isoform x4	785	7.52E-57	77.00%	0.102	IPR002059 (PRINTS); IPR011129 (SMART); IPR012340 (G3DSA:2.40.50.GENE3D); IPR002059 (PFAM); PTHR11544 (PANTHER); IPR019844 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012340 (SUPERFAMILY); TMhelix (TMHMM)
1759	c39184_g1_i1_len_1346_path_1220_0_522_1 743_523_527_1748_528_726_252_727_746_272_747_756_252_757_776_1	582	extensin-1-like isoform x1	449	2.65E-08	50.00%	0.121	no IPS match
1760	c39184_g1_i2_len_1399_path_1220_0_522_1 743_523_527_1748_528_726_252_727_746_272_747_756_252_757_776_1	759	extensin-1-like isoform x1	466	3.32E-08	49.30%	0.121	no IPS match
1761	c39190_g1_i1_len_2165_path_4078_0_408_1 519_409_485_1574_486_2140_1502_2141_2164_3	1337	serine threonine-protein phosphatase alpha-2 isoform	722	0	98.00%	0.099	IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668 (PANTHER); PTHR11668:SF213 (PANTHER); IPR006186 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029052 (SUPERFAMILY)
1762	c39190_g1_i2_len_2483_path_4078_0_408_1 519_409_485_1574_486_2140_6214_2141_2482_3	1492	serine threonine-protein phosphatase alpha-2 isoform	828	0	97.30%	0.116	IPR006186 (PRINTS); IPR006186 (SMART); IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); PTHR11668:SF213 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY)
1763	c39196_g1_i1_len_2316_path_697_0_116_49 3_117_319_696_320_841_1333_842_925_2_46_926_2315_1	1177	alpha-n-acetylgalactosaminidase isoform x4	772	0	85.80%	0.107	Coil (COILS); IPR002241 (PRINTS); IPR013785 (G3DSA:3.20.20.GENE3D); IPR000111 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); PTHR11452:SF23 (PANTHER); PTHR11452 (PANTHER); IPR000111 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51011 (SUPERFAMILY); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1764	c39196_g1_i2_len_2113_path_697_0_116_69 6_117_638_1333_639_722_246_723_2112_2	1169	alpha-n-acetylgalactosaminidase isoform x4	704	0	85.80%	0.143	IPR002241 (PRINTS); IPR013780 (G3DSA:2.60.40.GENE3D); IPR013785 (G3DSA:3.20.20.GENE3D); IPR000111 (PFAM); PTHR11452 (PANTHER); PTHR11452:SF23 (PANTHER); IPR000111 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); SSF51011 (SUPERFAMILY); TMhelix (TMHMM)
1766	c39205_g2_i1_len_1002_path_1140_0_1001_1	149	mam and ldl-receptor class a domain-containing protein c10orf112-like	334	3.88E-08	51.50%	0.138	IPR000998 (SMART); IPR000998 (PFAM); PTHR23282 (PANTHER); PTHR23282:SF75 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)

1767	c39209_g1_i1_len_1159_path_473_0_105_57_8_106_950_1419_951_1055_1523_1056_1057_23_1058_1158_0	443	mesencephalic astrocyte-derived neurotrophic factor homolog	387	1.20E-76	84.80%	0.144	IPR019345 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR12990 (PANTHER); PTHR12990:SF5 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF68906 (SUPERFAMILY); TMhelix (TMHMM)
1768	c39243_g1_i1_len_2305_path_207_0_275_48_3_276_629_837_630_1732_1935_1733_2018_1935_2019_2304_1	238	dnaj homolog subfamily c member 7	768	0	74.80%	0.104	IPR001623 (PRINTS); IPR001623 (SMART); IPR019734 (SMART); IPR011990 (G3DSA:1.25.40.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); IPR013105 (PFAM); IPR019734 (PFAM); IPR001623 (PFAM); PF13414 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF140 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR019734 (PROSITE_PROFILES); IPR001623 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY); SSF48452 (SUPERFAMILY); IPR001623 (SUPERFAMILY); SSF48452 (SUPERFAMILY)
1769	c39243_g1_i2_len_2128_path_4279_0_98_48_3_99_452_837_453_1555_1935_1556_1841_1935_1842_2127_1	238	dnaj homolog subfamily c member 7	709	0	73.60%	0.104	IPR001623 (PRINTS); IPR019734 (SMART); IPR001623 (SMART); IPR019734 (PFAM); PF13414 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); IPR013105 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); IPR001623 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF140 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY); SSF48452 (SUPERFAMILY); IPR001623 (SUPERFAMILY); SSF48452 (SUPERFAMILY)
1770	c39248_g2_i2_len_597_path_1084_0_39_112_4_40_83_25_84_205_147_206_229_3668_23_0_232_174_233_251_193_2_2	33	cre-ptr-16 protein	199	6.39E-17	62.00%	0.137	PTHR11660:SF46 (PANTHER); PTHR11660 (PANTHER)
1771	c39255_g1_i1_len_2051_path_2187_0_1345_4245_1346_1471_3525_1472_1670_3723_1_671_1690_147_1691_205_0	347	protein tumorous imaginal mitochondrial-like isoform x2	684	0	75.00%	0.23	IPR001623 (PRINTS); IPR001623 (SMART); IPR002939 (PFAM); IPR001305 (PFAM); IPR001305 (G3DSA:2.10.230.GENE3D); G3DSA:2.60.260.20 (GENE3D); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF79 (PANTHER); IPR018253 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012724 (HAMAP); IPR001305 (PROSITE_PROFILES); IPR001623 (PROSITE_PROFILES); IPR008971 (SUPERFAMILY); IPR001305 (SUPERFAMILY); IPR001623 (SUPERFAMILY); IPR008971 (SUPERFAMILY); TMhelix (TMHMM)
1772	c39255_g1_i2_len_1925_path_2187_0_1345_3525_1346_1544_3723_1545_1564_147_15_65_1924_0	370	protein tumorous imaginal mitochondrial-like isoform x2	642	0	74.90%	0.23	IPR001623 (PRINTS); IPR001623 (SMART); IPR002939 (PFAM); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); G3DSA:2.60.260.20 (GENE3D); IPR001305 (PFAM); IPR001305 (G3DSA:2.10.230.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF79 (PANTHER); IPR018253 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR012724 (HAMAP); IPR001305 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); IPR008971 (SUPERFAMILY); IPR008971 (SUPERFAMILY); IPR001305 (SUPERFAMILY); TMhelix (TMHMM)
1773	c39275_g1_i1_len_2244_path_2295_0_2243_4	1000	catalase	748	0	84.60%	0.153	IPR018028 (PRINTS); IPR011614 (SMART); IPR010582 (PFAM); IPR011614 (PFAM); IPR011614 (G3DSA:2.40.180.GENE3D); IPR018028 (PANTHER); IPR002226 (PROSITE_PATTERNS); IPR024708 (PROSITE_PATTERNS); IPR018028 (PROSITE_PROFILES); IPR020835 (SUPERFAMILY)
1774	c39300_g1_i1_len_2180_path_2258_0_1603_4746_1604_2179_2	268	alkaline phosphatase	726	5.72E-172	64.40%	0.116	IPR001952 (PRINTS); IPR001952 (SMART); IPR001952 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR11596 (PANTHER); IPR018299 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)
1775	c39302_g1_i1_len_3137_path_4862_0_1087_8248_1088_1088_5946_1089_3136_3	386	peptidyl-prolyl cis-trans mitochondrial	1046	2.40E-137	56.40%	0.175	IPR001841 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR017907 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000315 (PROSITE_PROFILES); IPR001841 (PROSITE_PROFILES); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); SSF57850 (SUPERFAMILY); SSF57845 (SUPERFAMILY)

1776	c39309_g1_i1_len_554_path_2199_0_84_175_5_85_553_4	63	cationic trypsin-3-like	185	5.66E-17	60.60%	0.335	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1777	c39309_g1_i2_len_1098_path_1126_0_628_1_755_629_1097_4	230	trypsin 3	366	4.11E-57	61.00%	0.335	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1778	c39316_g1_i1_len_2531_path_2609_0_1294_3900_1295_2530_4	7693	scp-like extracellular domain containing protein 1	844	1.65E-67	61.60%	0.295	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); PTHR10334:SF174 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR014044 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1779	c39335_g1_i1_len_1254_path_1381_0_1051_2826_1052_1253_4	396	aldose reductase	418	2.92E-153	77.60%	0.2	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); PTHR11732:SF202 (PANTHER); IPR001395 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
1780	c39336_g3_i1_len_5750_path_6686_0_2168_374_2169_3412_727_3413_3580_12894_3_581_5690_12200_5691_4	1937	lethal giant larvae protein homolog 1-like isoform x4	1917	0	67.80%	0.175	Coil (COILS); Coil (COILS); IPR000664 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR013905 (PFAM); IPR013577 (PFAM); PTHR10241 (PANTHER); PTHR10241:SF28 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1781	c39336_g3_i2_len_5582_path_6686_0_2168_374_2169_3412_12894_3413_5522_12200_5523_5543_420_5544_4	2001	lethal giant larvae protein homolog 1-like isoform x5	1861	0	71.00%	0.175	Coil (COILS); Coil (COILS); IPR000664 (PRINTS); IPR001680 (SMART); IPR013577 (PFAM); IPR013905 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR10241 (PANTHER); PTHR10241:SF28 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1782	c39348_g1_i1_len_2722_path_155_0_1483_1_639_1484_2393_2544_2394_2395_154_239_6_2721_0	352	dnaj homolog subfamily b member 11	908	0	84.10%	0.231	IPR001623 (PRINTS); IPR001623 (SMART); IPR002939 (PFAM); IPR001623 (PFAM); G3DSA:2.60.260.20 (GENE3D); IPR001623 (G3DSA:1.10.287.GENE3D); G3DSA:2.60.260.20 (GENE3D); PTHR24077 (PANTHER); PTHR24077:SF210 (PANTHER); IPR018253 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001623 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR008971 (SUPERFAMILY); IPR008971 (SUPERFAMILY); IPR001623 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1783	c39359_g1_i1_len_2332_path_2825_0_2031_30_2032_2063_30_2064_2095_5106_2096_2_100_399_2101_2331_0	977	iron zinc purple acid phosphatase-like protein	778	0	74.90%	0.22	IPR015914 (G3DSA:2.60.40.GENE3D); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); IPR025733 (PFAM); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008963 (SUPERFAMILY); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
1784	c39359_g1_i2_len_2364_path_2825_0_2031_30_2032_2063_30_2064_2095_30_2096_212_7_5106_2128_2132_399_21_0	1035	iron zinc purple acid phosphatase-like protein	788	0	74.70%	0.22	IPR025733 (PFAM); IPR015914 (G3DSA:2.60.40.GENE3D); IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); PTHR22953 (PANTHER); PTHR22953:SF9 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY); IPR008963 (SUPERFAMILY); TMhelix (TMHMM)
1785	c39376_g1_i1_len_1552_path_53_0_121_175_122_140_194_141_372_3425_373_525_57_7_526_1551_0	341	3-hydroxyisobutyrate dehydrogenase	518	9.18E-65	55.40%	0.434Y	IPR029154 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); IPR006115 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22981 (PANTHER); PTHR22981:SF7 (PANTHER); IPR029752 (PROSITE_PATTERNS); IPR008927 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
1786	c39376_g1_i2_len_1399_path_53_0_121_175_122_140_194_141_372_577_373_1398_0	252	3-hydroxyisobutyrate dehydrogenase	467	1.38E-56	55.10%	0.434 Y	IPR029154 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR006115 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); PTHR22981 (PANTHER); PTHR22981:SF7 (PANTHER); IPR008927 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
1787	c39389_g1_i1_len_219_path_269_0_27_297_28_87_938_88_91_942_92_94_361_95_97_3_64_98_121_154_122_218_0	7	ankyrin repeat domain-containing protein 2	73	1.02E-13	61.00%	0.118	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1788	c39398_g1_i1_len_1300_path_2991_0_190_1_911_191_369_2087_370_414_298_415_478_2195_479_521_2238_522_5_3	78	phospholipase b-like 2	434	2.30E-160	72.50%	0.101	IPR007000 (PFAM); IPR007000 (PANTHER); PTHR12370:SF3 (PANTHER)
1789	c39398_g1_i2_len_1341_path_1680_0_19_21_20_231_1911_232_410_253_411_455_298_456_519_3396_520_562_22_3	86	phospholipase b-like 2	447	1.10E-159	72.80%	0.101	IPR007000 (PFAM); PTHR12370:SF3 (PANTHER); IPR007000 (PANTHER)
1790	c39401_g1_i1_len_1232_path_1842_0_529_1_30_530_638_2804_639_666_53_667_1231_5	469	calponin transgelin	410	1.94E-89	86.40%	0.464 Y	IPR003096 (PRINTS); IPR001997 (PRINTS); IPR001715 (SMART); IPR001715 (PFAM); IPR000557 (PFAM); IPR001715 (G3DSA:1.10.418.GENE3D); PTHR18959 (PANTHER); PTHR18959:SF51 (PANTHER); IPR001715 (PROSITE_PROFILES); IPR000557 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR001715 (SUPERFAMILY)
1791	c39401_g1_i2_len_1564_path_1842_0_529_2_367_530_861_130_862_970_2804_971_998_53_999_1563_5	819	calponin transgelin	521	6.28E-88	86.40%	0.464 Y	IPR001997 (PRINTS); IPR003096 (PRINTS); IPR001715 (SMART); IPR001715 (PFAM); IPR001715 (G3DSA:1.10.418.GENE3D); IPR000557 (PFAM); PTHR18959:SF51 (PANTHER); PTHR18959 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001715 (PROSITE_PROFILES); IPR000557 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR001715 (SUPERFAMILY)
1792	c39403_g1_i1_len_2553_path_2177_0_1552_2022_1553_1588_964_1589_2114_1490_211_5_2138_4274_2139_2552_3	319	alkaline phosphatase 4-like	851	7.26E-156	64.20%	0.519Y	IPR001952 (PRINTS); IPR001952 (SMART); IPR017849 (G3DSA:3.40.720.GENE3D); IPR001952 (PFAM); PTHR11596 (PANTHER); IPR018299 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-TM (SIGNALP_EUK); IPR017850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1793	c39403_g2_i1_len_1035_path_1921_0_100_2_022_101_136_3761_137_626_1490_627_650_1514_651_1034_3	51	alkaline tissue-nonspecific isozyme-like	345	1.62E-96	64.40%	0.167	IPR001952 (PRINTS); IPR001952 (SMART); IPR001952 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR11596 (PANTHER); IPR018299 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)

1794	c39418_g1_i1_len_2875_path_3257_0_1680_5054_1681_2065_5436_2066_2083_95_2084_2874_0	1249	proactivator polypeptide	959	0	52.20%	0.207	IPR008373 (PRINTS); IPR003119 (SMART); IPR008139 (SMART); IPR007856 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); IPR011001 (G3DSA:1.10.225.GENE3D); IPR008138 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); IPR003119 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR11480 (PANTHER); PTHR11480:SF3 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008139 (PROSITE_PROFILES); IPR003119 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR003119 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY)
1795	c39418_g1_i2_len_2995_path_3257_0_1680_4934_1681_1800_5054_1801_2185_5436_2186_2203_95_2204_2994_0	1401	proactivator polypeptide-like	999	0	54.80%	0.207	IPR008373 (PRINTS); IPR003119 (SMART); IPR008139 (SMART); IPR011001 (G3DSA:1.10.225.GENE3D); IPR011001 (G3DSA:1.10.225.GENE3D); IPR007856 (PFAM); IPR008138 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); IPR003119 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR11480 (PANTHER); PTHR11480:SF3 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008139 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR003119 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR003119 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY)
1796	c39420_g1_i1_len_2009_path_2501_0_1252_23_1253_1425_196_1426_2008_5	1494	fk506-binding protein 2 isoform x2	669	9.26E-94	78.50%	0.234	G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); PTHR10516:SF252 (PANTHER); IPR023566 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002048 (PROSITE_PROFILES); IPR001179 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); SSF54534 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1797	c39420_g1_i2_len_1836_path_2501_0_1252_196_1253_1835_5	1749	fk506-binding protein 2 isoform x2	612	8.41E-98	79.60%	0.234	IPR001179 (PFAM); G3DSA:3.10.50.40 (GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); PTHR10516:SF252 (PANTHER); IPR023566 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001179 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); SSF54534 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1798	c39421_g1_i1_len_848_path_276_0_36_313_37_70_2307_71_88_682_89_250_455_251_271_476_272_797_2463_798_5	202	translocase of inner mitochondrial membrane 8 homolog b	282	7.06E-32	78.30%	0.103	IPR004217 (PFAM); IPR004217 (G3DSA:1.10.287.GENE3D); PTHR21535:SF25 (PANTHER); PTHR21535 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR004217 (SUPERFAMILY); TMhelix (TMHMM)

1799	c39438_g4_i2_len_3687_path_4310_0_990_1_4316_991_1636_10412_1637_1777_5947_1778_2129_6299_2130_4	509	serine threonine-protein kinase mark2-like isoform x10	1229	0	72.40%	0.184	IPR015940 (SMART); IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.8.10 (GENE3D); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR028375 (G3DSA:3.30.310.GENE3D); PTHR24346 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR015940 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); IPR028375 (SUPERFAMILY)
1800	c39438_g4_i3_len_1804_path_321_0_231_55_3_232_246_6299_247_404_6457_405_1714_7767_1715_1803_4	175	serine threonine-protein kinase mark2-like isoform x10	601	0	87.70%	0.184	IPR002290 (SMART); IPR015940 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.8.10 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24346 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR015940 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1801	c39438_g4_i4_len_3561_path_4310_0_990_1_4316_991_1636_5947_1637_1988_553_19_89_2003_6299_2004_2_4	552	serine threonine-protein kinase mark2-like isoform x10	1187	0	74.80%	0.184	IPR015940 (SMART); IPR002290 (SMART); IPR028375 (G3DSA:3.30.310.GENE3D); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.8.10 (GENE3D); IPR000719 (PFAM); PTHR24346 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR015940 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR028375 (SUPERFAMILY); IPR011009 (SUPERFAMILY)
1802	c39438_g4_i5_len_3546_path_4310_0_990_1_4316_991_1636_5947_1637_1988_6299_1_989_2146_6457_2147_4	558	serine threonine-protein kinase mark2-like isoform x10	1182	0	74.10%	0.184	IPR015940 (SMART); IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR028375 (G3DSA:3.30.310.GENE3D); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.8.10 (GENE3D); IPR000719 (PFAM); PTHR24346 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR015940 (PROSITE_PROFILES); IPR028375 (SUPERFAMILY); IPR011009 (SUPERFAMILY)
1803	c39451_g1_i1_len_1341_path_1269_0_637_2_523_638_813_1905_814_1022_2111_1023_1_028_118_1029_1340_2	5361	secreted salivary gland	447	1.63E-28	46.40%	0.706 Y	IPR004991 (PFAM); IPR023307 (G3DSA:2.170.15.GENE3D); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF56973 (SUPERFAMILY)
1804	c39452_g1_i1_len_395_path_5496_0_11_948_12_70_5202_71_100_7796_101_115_7723_116_128_7960_129_140_79_3	8	zinc finger and btb domain-containing protein	132	2.74E-14	55.10%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1805	c39452_g1_i2_len_360_path_7298_0_8_716_9_32_740_33_110_818_111_359_3	2	zinc c2h2 type	120	1.45E-11	59.10%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13909 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1806	c39452_g1_i3_len_1004_path_410_0_5_416_6_29_440_30_305_716_306_329_7330_330_359_7359_360_438_3908_4_3	41	zinc finger protein	335	1.26E-30	53.60%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1807	c39452_g1_i4_len_805_path_4721_0_480_52_02_481_510_5595_511_538_7960_539_550_7990_551_555_818_556_80_3	33	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfpheX133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	269	1.30E-44	57.90%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1808	c39452_g3_i1_len_592_path_819_0_31_851_32_192_2145_193_216_2379_217_591_4	11	mds1 and evi1 complex locus protein evi1	197	7.20E-16	51.80%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1809	c39452_g7_i1_len_214_path_7072_0_213_3	1	zinc finger protein	72	4.22E-11	64.70%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1810	c39460_g1_i1_len_2588_path_2655_0_1945_4599_1946_1947_4601_1948_2587_1	314	nicotinamide phosphoribosyltransferase-like	863	0	81.60%	0.177	G3DSA:3.20.140.10 (GENE3D); IPR007229 (PFAM); IPR016471 (PTHR11098:PANTHER); IPR007229 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002638 (SUPERFAMILY); TMhelix (TMHMM)
1811	c39462_g1_i1_len_2409_path_2912_0_567_2_5_568_782_240_783_2065_4971_2066_208_2_4988_2083_2408_0	1035	nicotinic acetylcholine receptor subunit alpha10	803	1.22E-105	59.90%	0.166	IPR006201 (PRINTS); IPR027361 (G3DSA:1.20.120.GENE3D); IPR006029 (PFAM); IPR006202 (PFAM); IPR006202 (G3DSA:2.70.170.GENE3D); PTHR18945:SF490 (PANTHER); IPR006201 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006029 (SUPERFAMILY); IPR006202 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1812	c39462_g1_i2_len_2406_path_2912_0_567_3_479_568_779_240_780_2062_4971_2063_2_079_4988_2080_2405_0	1038	nicotinic acetylcholine receptor subunit alpha10	802	1.08E-104	59.10%	0.166	IPR006201 (PRINTS); IPR027361 (G3DSA:1.20.120.GENE3D); IPR006202 (PFAM); IPR006029 (PFAM); IPR006202 (G3DSA:2.70.170.GENE3D); IPR006201 (PANTHER); PTHR18945:SF490 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006029 (SUPERFAMILY); IPR006202 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1813	c39468_g2_i1_len_1199_path_535_0_78_297_7_79_79_397_80_216_534_217_250_646_25_1_255_651_256_1171_3068_0	550	low quality protein: galectin-4	400	1.78E-51	50.50%	0.117	IPR001079 (SMART); IPR001079 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR11346 (PANTHER); IPR001079 (PROSITE_PROFILES); IPR001079 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY)

1822	c39513_g1_i1_len_1743_path_2112_0_1017_193_1018_1160_336_1161_1742_0	147	ves g 5 allergen	581	1.78E-42	49.30%	0.239	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1823	c39513_g1_i2_len_1600_path_2112_0_1017_336_1018_1599_0	155	ves g 5 allergen	534	3.02E-42	49.20%	0.239	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1824	c39521_g1_i1_len_2045_path_169_0_1821_1_991_1822_1823_1993_1824_1863_2032_1864_1866_147_1867_1896_20_5	12412	vitelline membrane outer layer protein 1 homolog	681	1.69E-38	55.10%	0.158	IPR000742 (SMART); IPR020864 (SMART); IPR020864 (PFAM); IPR005515 (PFAM); IPR005515 (G3DSA:2.100.10.GENE3D); IPR023413 (G3DSA:2.40.155.GENE3D); IPR005515 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR020864 (PROSITE_PROFILES); IPR005515 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
1825	c39534_g1_i1_len_5007_path_105_0_2155_1_0343_2156_5006_4	951	calnexin	1669	0	73.50%	0.185	Coil (COILS); IPR001580 (PRINTS); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001580 (PFAM); IPR009033 (G3DSA:2.10.250.GENE3D); PTHR11073:SF1 (PANTHER); IPR001580 (PANTHER); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR013320 (SUPERFAMILY); IPR009033 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1826	c39536_g2_i1_len_1105_path_2191_0_14_18_04_15_633_2823_634_658_2112_659_797_906_798_831_940_832_8_2	71	alcohol dehydrogenase	368	4.62E-111	67.70%	0.205	IPR020471 (PRINTS); IPR020471 (PIRSF); IPR023210 (G3DSA:3.20.20.GENE3D); IPR023210 (PFAM); IPR001395 (PANTHER); PTHR11732:SF183 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
1827	c39556_g2_i2_len_881_path_1209_0_47_125_7_48_49_1259_50_389_1599_390_603_181_3_604_880_4	1665	apolipoprotein d-like	294	6.60E-14	45.70%	0.125	IPR012674 (G3DSA:2.40.128.GENE3D); IPR000566 (PFAM); PTHR10612:SF10 (PANTHER); PTHR10612 (PANTHER); IPR011038 (SUPERFAMILY)
1828	c39559_g3_i1_len_3216_path_5941_0_8_597_3_9_56_17915_57_61_17920_62_77_6042_7_8_3215_0	3290	sarcalumenin isoform x2	1072	0	81.30%	0.104	IPR027417 (G3DSA:3.40.50.GENE3D); IPR006073 (PFAM); PTHR11216:SF66 (PANTHER); PTHR11216 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR030381 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1829	c39564_g1_i1_len_1962_path_1_0_207_209_208_208_210_209_1961_4	47087	probable chitinase 3-like	654	1.89E-169	64.30%	0.289	IPR011583 (SMART); IPR002557 (SMART); IPR029070 (G3DSA:3.10.50.GENE3D); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002557 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR029070 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR017853 (SUPERFAMILY)

1830	c39578_g1_i1_len_2747_path_1_0_222_224_223_959_961_960_969_971_970_2746_5	1476	heat shock 70 kda protein cognate 5	915	0	89.00%	0.164	Coil (COILS); IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); G3DSA:3.90.640.10 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); IPR012725 (TIGRFAM); G3DSA:3.30.30.30 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF173 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR012725 (HAMAP); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
1831	c39582_g1_i1_len_815_path_927_0_178_110_6_179_181_1109_182_563_1491_564_621_1_548_622_633_101_634_673_0	86	protein creg1	272	2.65E-72	75.70%	0.17	IPR012349 (G3DSA:2.30.110.GENE3D); PF13883 (PFAM); PTHR13343 (PANTHER); PTHR13343:SF12 (PANTHER); IPR012349 (SUPERFAMILY)
1832	c39587_g1_i1_len_2512_path_3216_0_231_3_447_232_434_713_435_1047_198_1048_20_09_5217_2010_2029_688_0	1037	glucose dehydrogenase	838	0	65.90%	0.135	IPR000172 (PFAM); G3DSA:3.50.50.60 (GENE3D); IPR007867 (PFAM); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); IPR000172 (PROSITE_PATTERNS); IPR000172 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY); TMhelix (TMHMM)
1833	c39587_g1_i2_len_1543_path_119_0_78_198_79_1040_5217_1041_1060_688_1061_154_2_0	584	glucose dehydrogenase	515	3.52E-78	63.50%	0.192	IPR007867 (PFAM); G3DSA:3.30.560.10 (GENE3D); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY)
1834	c39587_g1_i3_len_2309_path_3216_0_231_7_13_232_844_198_845_1806_5217_1807_18_26_688_1827_2308_1	915	glucose dehydrogenase	770	7.87E-161	65.80%	0.289	G3DSA:3.50.50.60 (GENE3D); IPR007867 (PFAM); IPR000172 (PFAM); PTHR11552:SF77 (PANTHER); PTHR11552 (PANTHER); IPR000172 (PROSITE_PATTERNS); IPR000172 (PROSITE_PATTERNS); SSF54373 (SUPERFAMILY); SSF51905 (SUPERFAMILY)
1835	c39596_g1_i1_len_2347_path_2582_0_2167_4955_2168_2346_5	441	serine protease	782	1.61E-27	64.10%	0.287	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1836	c39596_g1_i2_len_2554_path_2582_0_2167_4748_2168_2374_4955_2375_2553_5	596	anionic trypsin-like	851	8.85E-40	53.30%	0.298	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1837	c39624_g1_i1_len_5386_path_1721_0_1593_1672_1594_1683_3404_1684_1704_3425_1_705_2119_3840_2120_21_5	546	laminin subunit alpha	1795	0	57.00%	0.111	Coil (COILS); Coil (COILS); Coil (COILS); IPR001791 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR010307 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR009254 (PFAM); PTHR10574:SF39 (PANTHER); PTHR10574 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); PD936484 (PRODOM); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1838	c39624_g1_i2_len_4627_path_837_0_834_16_72_835_924_12646_925_945_3425_946_13_60_3840_1361_1383_386_5	389	laminin subunit alpha	1542	0	57.00%	0.111	Coil (COILS); Coil (COILS); Coil (COILS); IPR001791 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); IPR010307 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR009254 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); PTHR10574:SF39 (PANTHER); PTHR10574 (PANTHER); PD936484 (PRODOM); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY)

1839	c39626_g1_i1_len_1482_path_1963_0_977_1_68_978_1481_4	261	low affinity immunoglobulin epsilon fc receptor	494	6.69E-17	51.00%	0.891 Y	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR016187 (SUPERFAMILY)
1840	c39626_g1_i2_len_567_path_105_0_62_168_63_566_4	15	low affinity immunoglobulin epsilon fc receptor	189	6.27E-18	50.70%	0.891 Y	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001304 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR016187 (SUPERFAMILY)
1841	c39626_g1_i3_len_567_path_285_0_62_168_63_566_4	19	low affinity immunoglobulin epsilon fc receptor	189	6.08E-18	50.70%	0.891 Y	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR016187 (SUPERFAMILY)
1842	c39642_g1_i2_len_1093_path_1303_0_154_2_572_155_175_144_176_591_1888_592_664_166_665_667_1963_668_3	285	protein spaetzle	365	6.31E-28	51.90%	0.152	PTHR23199 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029034 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1843	c39642_g1_i3_len_1020_path_1303_0_154_2_572_155_175_144_176_591_166_592_594_1963_595_1019_5	223	protein spaetzle	340	3.18E-22	56.60%	0.109	PTHR23199 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029034 (SUPERFAMILY); TMhelix (TMHMM)
1844	c39648_g1_i1_len_1398_path_387_0_267_65_4_268_311_317_312_361_746_362_382_202_383_1397_2	8621	venom allergen 3-like	466	3.47E-44	52.20%	0.326	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1845	c39660_g1_i1_len_4786_path_5148_0_107_5_256_108_4745_12176_4746_4755_12220_4_756_4785_0	788	dystroglycan isoform x1	1596	0	61.20%	0.492 Y	IPR006644 (SMART); IPR027468 (G3DSA:3.30.70.GENE3D); IPR008465 (PFAM); IPR008009 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR21559:SF16 (PANTHER); PTHR21559 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR030398 (PROSITE_PROFILES); IPR030398 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR027468 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1846	c39660_g1_i2_len_5591_path_10855_0_496_12187_497_912_5256_913_5550_12176_55_51_5560_12220_5561_55_1	889	dystroglycan isoform x1	1864	0	61.30%	0.13	IPR006644 (SMART); IPR008009 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR008465 (PFAM); IPR027468 (G3DSA:3.30.70.GENE3D); PTHR21559 (PANTHER); PTHR21559:SF16 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR030398 (PROSITE_PROFILES); IPR030398 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR027468 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1847	c39662_g1_i1_len_829_path_1147_0_290_20_11_291_311_46_312_828_3	492	hemagglutinin amebocyte aggregation factor-like	277	7.65E-10	74.10%	0.115	PF14704 (PFAM); IPR026645 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)

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1855	c39736_g1_i1_len_2724_path_2702_0_2723_0	2103	tissue factor pathway inhibitor 2	908	4.20E-33	62.80%	0.124	Coil (COILS); IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1857	c39750_g1_i1_len_6586_path_8171_0_366_1_82_367_6585_3	1460	cyclin-dependent kinase 12 isoform x1	2196	0	76.80%	0.133	Coil (COILS); IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24056 (PANTHER); PTHR24056:SF125 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1858	c39750_g1_i2_len_6348_path_53_0_128_182_129_6347_3	1424	cyclin-dependent kinase 12 isoform x1	2116	0	76.90%	0.133	Coil (COILS); IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24056:SF125 (PANTHER); PTHR24056 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1859	c39753_g1_i2_len_1034_path_1555_0_186_2_20_187_289_1843_290_309_371_310_764_4_59_765_836_29_837_1033_2	115	protein them6	344	6.25E-32	55.60%	0.101	PF13279 (PFAM); IPR029069 (G3DSA:3.10.129.GENE3D); PTHR12475 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029069 (SUPERFAMILY); TMhelix (TMHMM)
1860	c39769_g1_i1_len_3123_path_261_0_2365_6_771_2366_2389_2641_2390_3122_2	793	gels_homam ame: full= cytoplasmic ame: full=actin-depolymerizing factor short=adf	1041	0	73.50%	0.138	Coil (COILS); IPR007122 (PRINTS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR007122 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1861	c39769_g1_i2_len_3179_path_261_0_2365_6_771_2366_2389_6591_2390_2445_2641_244_6_3178_2	799	gels_homam ame: full= cytoplasmic ame: full=actin-depolymerizing factor short=adf	1059	0	73.50%	0.138	IPR007122 (PRINTS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007122 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1862	c39786_g1_i1_len_276_path_647_0_2_650_3_45_914_46_51_5953_52_60_3557_61_89_4_822_90_243_6164_244_262_4	285	---NA---	92			0.321	TMhelix (TMHMM)
1863	c39786_g3_i2_len_338_path_703_0_167_871_168_210_914_211_216_5953_217_225_355_7_226_254_3586_255_260_3	16	muc19_human ame: full=mucin-19 short=muc-19 flags: partial	113	8.77E-06	47.00%	0.153	TMhelix (TMHMM); TMhelix (TMHMM)
1864	c39786_g3_i4_len_720_path_703_0_167_871_168_210_914_211_216_5953_217_225_355_7_226_254_3586_255_260_4	595	low quality protein: mucin-19	240	5.45E-14	44.90%	0.207	SSF141571 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1865	c39792_g1_i1_len_3494_path_3522_0_1030_4553_1031_2054_5575_2055_2072_5593_2073_3493_2	3283	beta-hexosaminidase subunit beta isoform x1	1164	0	69.80%	0.360Y	IPR025705 (PRINTS); IPR029019 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR015883 (PFAM); IPR029018 (G3DSA:3.30.379.GENE3D); PTHR22600 (PANTHER); PTHR22600:SF7 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029018 (SUPERFAMILY); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1866	c39806_g1_i1_len_1804_path_2097_0_181_2299_182_373_253_374_374_254_375_1803_3	1273	superoxide dismutase	595	2.30E-79	84.90%	0.165	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); PTHR10003:SF33 (PANTHER); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY)
1867	c39806_g1_i2_len_1825_path_2097_0_181_2277_182_203_2299_204_395_254_396_1824_3	1377	superoxide dismutase	602	2.71E-79	84.90%	0.165	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003:SF33 (PANTHER); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001424 (SUPERFAMILY)
1868	c39828_g1_i1_len_4563_path_3827_0_4562_4	4393	low quality protein: hemocytin-like	1521	0	54.00%	0.106	IPR001846 (SMART); IPR006207 (SMART); IPR014853 (SMART); IPR001007 (SMART); IPR002919 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR001846 (PFAM); IPR014853 (PFAM); PTHR11339:SF25 (PANTHER); PTHR11339 (PANTHER); IPR001007 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY); IPR002919 (SUPERFAMILY); SSF57603 (SUPERFAMILY)
1869	c39828_g2_i1_len_1083_path_2368_0_26_2395_27_120_2489_121_144_2513_145_216_2585_217_251_13207_252_3_3	118	low quality protein: hemocytin-like	361	2.82E-62	59.30%	0.106	IPR000421 (SMART); IPR000421 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24543 (PANTHER); IPR000421 (PROSITE_PATTERNS); IPR000421 (PROSITE_PATTERNS); IPR000421 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR008979 (SUPERFAMILY)
1870	c39828_g2_i2_len_1702_path_1752_0_615_2368_616_642_13573_643_736_2489_737_760_13690_761_835_2585_83_3	527	low quality protein: hemocytin-like	568	2.57E-102	55.80%	0.106	IPR002172 (SMART); IPR000421 (SMART); IPR008979 (G3DSA:2.60.120.GENE3D); IPR000421 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24543 (PANTHER); IPR000421 (PROSITE_PATTERNS); IPR000421 (PROSITE_PATTERNS); IPR000421 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR008979 (SUPERFAMILY)
1871	c39831_g1_i1_len_3132_path_3260_0_1277_4536_1278_3131_4	248	protein canopy 4	1044	3.04E-83	79.60%	0.179	IPR021852 (PFAM); PTHR15382 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1872	c39845_g1_i1_len_2103_path_53_0_46_140_47_2102_5	243	maltase 2-like	701	0	65.60%	0.19	IPR006589 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR006047 (PFAM); G3DSA:3.90.400.10 (GENE3D); PTHR10357:SF76 (PANTHER); IPR015902 (PANTHER); IPR017853 (SUPERFAMILY)
1873	c39845_g1_i2_len_2143_path_53_0_46_100_47_86_140_87_2142_5	263	maltase 2-like	714	0	65.60%	0.19	IPR006589 (SMART); G3DSA:3.90.400.10 (GENE3D); IPR006047 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR10357:SF76 (PANTHER); IPR015902 (PANTHER); IPR017853 (SUPERFAMILY)
1874	c39867_g1_i1_len_6456_path_209_0_6455_0	1532	titin- partial	2152	5.65E-25	59.80%	0.098	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)

1875	c39869_g2_i1_len_3883_path_11256_0_3_10 670_4_47_11277_48_91_11277_92_135_680 9_136_518_7192_519_5_3	645	integrin alpha-8-like	1295	9.03E-165	48.80%	0.135	IPR000413 (PRINTS); IPR013519 (SMART); G3DSA:2.60.40.1510 (GENE3D); G3DSA:1.20.5.930 (GENE3D); PF13517 (PFAM); G3DSA:2.130.10.130 (GENE3D); G3DSA:2.60.40.1460 (GENE3D); IPR013649 (PFAM); G3DSA:2.60.40.1530 (GENE3D); PTHR23220:SF71 (PANTHER); PTHR23220 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); SSF69179 (SUPERFAMILY); SSF69318 (SUPERFAMILY); SSF69179 (SUPERFAMILY); SSF69179 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1876	c39869_g2_i3_len_3927_path_11256_0_3_10 670_4_47_11277_48_91_11277_92_135_112 77_136_179_6809__180_3	633	integrin alpha-8-like	1309	9.31E-165	48.80%	0.135	IPR000413 (PRINTS); IPR013519 (SMART); IPR013649 (PFAM); PF13517 (PFAM); G3DSA:2.60.40.1510 (GENE3D); G3DSA:2.60.40.1530 (GENE3D); G3DSA:2.60.40.1460 (GENE3D); G3DSA:1.20.5.930 (GENE3D); G3DSA:2.130.10.130 (GENE3D); PTHR23220 (PANTHER); PTHR23220:SF71 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); IPR013519 (PROSITE_PROFILES); SSF69179 (SUPERFAMILY); SSF69318 (SUPERFAMILY); SSF69179 (SUPERFAMILY); SSF69179 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1877	c39874_g1_i1_len_1755_path_2031_0_270_2 301_271_287_2030_288_1154_3184_1155_1 184_505_1185_1354_324_1_0	361	cytochrome p450 2j6	585	7.37E-116	59.20%	0.115	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
1878	c39874_g2_i1_len_2390_path_8426_0_920_3 184_921_950_3213_951_2117_36_2118_238 9_0	436	aael002067- partial	797	1.51E-123	58.50%	0.421 Y	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY)
1879	c39879_g2_i1_len_2238_path_4351_0_54_44 06_55_886_5236_887_1664_6014__1665_2 058_6408_2059_2059_2	674	lysine--trna ligase isoform x2	746	0	86.20%	0.108	Coil (COILS); IPR018149 (PRINTS); G3DSA:3.30.930.10 (GENE3D); IPR004364 (PFAM); IPR002313 (TIGRFAM); IPR004365 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); PTHR22594:SF4 (PANTHER); IPR018150 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006195 (PROSITE_PROFILES); IPR002313 (HAMAP); SSF55681 (SUPERFAMILY); IPR012340 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1880	c39879_g2_i2_len_2222_path_9159_0_38_44 06_39_870_5236_871_1648_6014__1649_2 042_6408_2043_2043_1	574	lysine--trna ligase isoform x1	741	0	86.30%	0.115	Coil (COILS); IPR018149 (PRINTS); G3DSA:3.30.930.10 (GENE3D); IPR002313 (TIGRFAM); IPR004364 (PFAM); IPR004365 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); PTHR22594:SF4 (PANTHER); IPR018150 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006195 (PROSITE_PROFILES); IPR002313 (HAMAP); SSF55681 (SUPERFAMILY); IPR012340 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1881	c39879_g2_i3_len_998_path_4351_0_54_440 6_55_886_11730_887_997_2	277	lysyl-trna synthetase	332	6.38E-146	83.20%	0.108	Coil (COILS); IPR018149 (PRINTS); IPR004364 (PFAM); G3DSA:3.30.930.10 (GENE3D); IPR012340 (G3DSA:2.40.50.GENE3D); IPR004365 (PFAM); PTHR22594:SF4 (PANTHER); IPR018150 (PANTHER); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY); IPR012340 (SUPERFAMILY)

1882	c39881_g3_i2_len_2305_path_441_0_203_64_5_204_413_853_414_609_1048_610_667_11_05_668_676_68_677_2304_2	257	vitellogenin receptor	768	1.50E-70	48.60%	0.116	IPR002172 (PRINTS); IPR002172 (SMART); IPR000033 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PF14670 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); PTHR10529:SF222 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)
1883	c39884_g1_i1_len_1022_path_6065_0_1021_1	160	pacifastin light chain	341	1.54E-35	42.90%	0.859Y	IPR006552 (SMART); IPR008037 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR001190 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY)
1884	c39884_g2_i1_len_2615_path_629_0_708_59_44_709_733_1363_734_1291_278_1292_131_6_1944_1317_1815_2443_1_2	942	pacifastin light chain	871	2.93E-32	46.70%	0.134	IPR001007 (SMART); IPR002223 (SMART); IPR008037 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); PTHR10083 (PANTHER); IPR020862 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR001190 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY)
1885	c39884_g3_i1_len_302_path_1_0_276_278_2_77_301_1	56	pacifastin light chain	101	2.92E-13	48.30%	0.219	IPR008037 (PFAM); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY)
1886	c39901_g1_i1_len_3065_path_4585_0_1023_5608_1024_1033_2760_1034_1277_5858_12_78_1300_254_1301_1543_6_2	1633	meprin a	1021	1.21E-71	50.10%	0.785 Y	IPR001506 (PRINTS); IPR000859 (SMART); IPR006026 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127:SF580 (PANTHER); PTHR10127 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000859 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR000859 (SUPERFAMILY); SSF55486 (SUPERFAMILY)
1887	c39912_g1_i1_len_2709_path_1_0_2086_208_8_2087_2087_2089_2088_2398_2400_2399_2415_2417_2416_2708_2	1131	integral membrane protein 2c	903	1.56E-117	67.30%	0.137	IPR007084 (SMART); IPR007084 (PFAM); PTHR10962:SF1 (PANTHER); PTHR10962 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007084 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1888	c39921_g1_i1_len_2452_path_3813_0_845_2_82_846_1747_1182_1748_1762_1197_1763_1975_1410_1976_1998_1	654	golgi-associated plant pathogenesis-related protein 1	817	1.48E-155	62.20%	0.151	IPR001283 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); PTHR10334:SF189 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); IPR014044 (SUPERFAMILY); IPR014044 (SUPERFAMILY)
1889	c39925_g2_i1_len_12677_path_13128_0_249_11372_250_1166_14293_1167_1169_1429_6_1170_1662_3289_1663_0	6262	phd and ring finger domain-containing protein 1	4226	3.79E-99	54.20%	0.131	Coil (COILS); Coil (COILS); IPR001841 (SMART); IPR001965 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); IPR013083 (G3DSA:3.30.40.GENE3D); IPR019787 (PFAM); IPR001841 (PFAM); PTHR15242 (PANTHER); PTHR15242:SF1 (PANTHER); IPR017907 (PROSITE_PATTERNS); IPR019786 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001841 (PROSITE_PROFILES); IPR019787 (PROSITE_PROFILES); IPR011011 (SUPERFAMILY); SSF57850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1890	c39925_g2_i1_len_12677_path_13128_0_249_11372_250_1166_14293_1167_1169_1429_6_1170_1662_3289_1663_2	6262	ring and phd-finger domain-containing protein kiaa1542	4225	1.05E-20	42.50%	0.176	Coil (COILS); Coil (COILS); Coil (COILS)
1891	c39932_g3_i1_len_3594_path_5465_0_171_5_637_172_195_10554_196_1186_4268_1187_3593_5	1139	agap007053-pa-like protein	1198	2.19E-70	50.30%	0.162	Coil (COILS); IPR000716 (SMART); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); PTHR12352 (PANTHER); PTHR12352:SF9 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1892	c39944_g1_i1_len_2044_path_1_0_246_4751_247_1247_1249_1248_1258_1260_1259_1_410_4613_1411_1422_14_1	999	hemolymph juvenile hormone binding protein	681	2.93E-40	51.10%	0.389Y	IPR010562 (SMART); IPR010562 (PFAM); PTHR11008 (PANTHER); PTHR11008:SF9 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020234 (PRODOM); TMhelix (TMHMM)
1893	c39944_g1_i2_len_1971_path_4381_0_173_4_751_174_1174_1249_1175_1185_1260_118_6_1337_1412_1338_1349_0	1146	hemolymph juvenile hormone binding protein	657	1.56E-40	51.00%	0.316	IPR010562 (SMART); IPR010562 (PFAM); PTHR11008 (PANTHER); PTHR11008:SF9 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020234 (PRODOM)
1894	c39950_g3_i1_len_980_path_6855_0_191_15_91_192_196_7144_197_217_1617_218_979_2	268	apolipoprotein d-like	326	2.74E-42	60.40%	0.346Y	IPR003057 (PRINTS); IPR000566 (PFAM); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612 (PANTHER); PTHR10612:SF7 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)

1895	c39950_g4_i1_len_2120_path_1387_0_180_1_568_181_203_1591_204_208_7144_209_229_4805_230_333_4908_334_2	314	apolipoprotein d-like	706	1.11E-56	62.20%	0.322	IPR003057 (PRINTS); IPR000566 (PFAM); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612 (PANTHER); PTHR10612:SF7 (PANTHER); IPR022272 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1896	c39951_g1_i1_len_2306_path_287_0_48_336_49_71_359_72_76_364_77_1286_5323_12_87_2237_2516_2238_223_1	1781	5 -nucleotidase-like	769	3.42E-96	54.20%	0.115	IPR006179 (PRINTS); IPR029052 (G3DSA:3.60.21.GENE3D); IPR008334 (PFAM); IPR008334 (G3DSA:3.90.780.GENE3D); PTHR11575:SF21 (PANTHER); IPR006179 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008334 (SUPERFAMILY); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
1897	c39956_g1_i1_len_6397_path_8371_0_3206_667_3207_4885_21734_4886_4887_2532_4_888_4936_2581_4937_61_5	7441	titin- partial	2132	0	58.50%	0.101	Coil (COILS); PR00014 (PRINTS); IPR003961 (SMART); IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF146 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1898	c39956_g1_i2_len_3492_path_8371_0_3206_517_3207_3491_4	4086	titin- partial	1164	0	69.70%	0.11	PR00014 (PRINTS); IPR003599 (SMART); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF142 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1899	c39956_g1_i3_len_6346_path_8371_0_3206_667_3207_4885_2581_4886_6139_14786_6_140_6165_14811_6166_6_5	7434	titin- partial	2115	0	58.50%	0.101	Coil (COILS); PR00014 (PRINTS); IPR003961 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF146 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1900	c39956_g1_i4_len_8215_path_8371_0_3206_667_3207_4885_21734_4886_4887_714_4888_6705_2532_6706_675_5	8038	titin- partial	2738	0	60.40%	0.101	Coil (COILS); PR00014 (PRINTS); IPR003599 (SMART); IPR001452 (SMART); IPR003961 (SMART); IPR003598 (SMART); IPR013098 (PFAM); G3DSA:2.30.30.40 (GENE3D); IPR001452 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001452 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR001452 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1901	c39956_g1_i5_len_6682_path_8371_0_3206_466_3207_3257_517_3258_3542_667_3543_5221_2581_5222_6475_5	7648	titin- partial	2227	0	69.00%	0.101	Coil (COILS); PR00014 (PRINTS); IPR003599 (SMART); IPR003961 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF146 (PANTHER); PTHR19897 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1902	c39980_g1_i1_len_1313_path_1747_0_501_2_241_502_505_320_506_763_2500_764_788_2525_789_956_104_957_10_0	4190	mite allergen lep d partial	438	3.86E-18	49.60%	0.567Y	PTHR11008:SF13 (PANTHER); PTHR11008 (PANTHER); IPR020234 (PRODOM); SignalP-noTM (SIGNALP_EUK)
1903	c39980_g1_i2_len_1260_path_1747_0_501_2_241_502_505_320_506_763_3040_764_788_2525_789_956_2690_957_9_0	4271	mite allergen lep d partial	420	2.19E-18	49.60%	0.567 Y	PTHR11008 (PANTHER); PTHR11008:SF13 (PANTHER); IPR020234 (PRODOM); SignalP-noTM (SIGNALP_EUK)
1904	c39990_g1_i1_len_1266_path_251_0_82_334_83_84_229_85_978_1417_979_1265_1	166	adiponectin receptor protein	422	1.26E-90	67.00%	0.168	IPR004254 (PFAM); PTHR20855:SF15 (PANTHER); IPR004254 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1905	c39990_g1_i2_len_1389_path_3107_0_11_33_4_12_13_229_14_907_1225_908_1101_1417_1102_1388_2	294	adiponectin receptor protein	463	1.07E-151	70.80%	0.097	IPR004254 (PFAM); IPR004254 (PANTHER); PTHR20855:SF15 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1906	c39990_g1_i3_len_1460_path_251_0_82_334_83_84_229_85_978_1225_979_1172_1417_1173_1459_1	295	adiponectin receptor protein	487	1.98E-151	70.70%	0.168	IPR004254 (PFAM); IPR004254 (PANTHER); PTHR20855:SF15 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1907	c40007_g1_i1_len_5313_path_1_0_2034_2036_2035_2141_2143_2142_5312_4	994	angiotensin-converting enzyme	1771	0	63.80%	0.145	IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); PTHR10514:SF17 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
1908	c40015_g1_i2_len_1308_path_395_0_38_307_39_261_656_262_276_671_277_316_711_317_333_728_334_464_858_0	2606	hemagglutinin amebocyte aggregation factor-like	436	5.58E-39	62.20%	0.227	PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1909	c40015_g2_i1_len_1487_path_3359_0_49_34_08_50_53_126_54_187_3542_188_201_3271_202_479_104_480_1486_2	8917	dermatopontin 2	495	2.13E-36	58.90%	0.189	Coil (COILS); PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1910	c40018_g1_i1_len_1954_path_317_0_662_976_663_689_1003_690_1011_1322_1012_1016_30_1017_1953_4	3872	membrane glycoprotein lig-	651	1.08E-19	47.80%	0.434 Y	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF52058 (SUPERFAMILY)

1911	c40021_g1_i1_len_5279_path_5458_0_1364_6820_1365_5278_3	894	puromycin-sensitive aminopeptidase-like	1760	0	78.80%	0.235	Coil (COILS); IPR014782 (PRINTS); G3DSA:1.10.390.10 (GENE3D); IPR024571 (PFAM); IPR014782 (PFAM); IPR001930 (PANTHER); PTHR11533:SF163 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF63737 (SUPERFAMILY); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1912	c40030_g1_i1_len_2174_path_2574_0_82_26_57_83_295_2870_296_1267_3841_1268_12_78_420_1279_1398_3970_2	225	3-hydroxyisobutyrate dehydrogenase	724	4.09E-74	57.10%	0.133	IPR013328 (G3DSA:1.10.1040.GENE3D); IPR029154 (PFAM); IPR006115 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22981:SF7 (PANTHER); PTHR22981 (PANTHER); IPR029752 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008927 (SUPERFAMILY); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1913	c40032_g1_i1_len_368_path_6619_0_125_38_11_126_153_6355_154_165_3851_166_367_0	36	glucose dehydrogenase	123	1.86E-30	75.30%	0.212	IPR000172 (PFAM); G3DSA:3.30.560.10 (GENE3D); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); IPR000172 (PROSITE_PATTERNS); SSF51905 (SUPERFAMILY)
1914	c40032_g1_i2_len_3148_path_3149_0_133_3_306_134_134_3307_135_638_3811_639_666_3839_667_678_3851_679_0	1695	glucose dehydrogenase	1050	0	68.40%	0.363Y	IPR000172 (PFAM); G3DSA:3.50.50.60 (GENE3D); IPR007867 (PFAM); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); IPR000172 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY); TMhelix (TMHMM)
1915	c40032_g1_i3_len_3171_path_3149_0_133_7_660_134_150_3300_151_156_3306_157_157_3307_158_661_3811_662_2	1779	glucose dehydrogenase	1057	0	68.40%	0.204	G3DSA:3.50.50.60 (GENE3D); IPR007867 (PFAM); IPR000172 (PFAM); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); IPR000172 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY); TMhelix (TMHMM)
1916	c40042_g1_i1_len_3058_path_383_0_26_206_27_1874_50_1875_2724_3101_2725_2741_290_2742_2837_3212_2_0	840	n-acetylated-alpha-linked acidic dipeptidase	1020	0	60.00%	0.255	G3DSA:3.40.630.10 (GENE3D); G3DSA:3.50.30.30 (GENE3D); IPR003137 (PFAM); IPR007365 (G3DSA:1.20.930.GENE3D); IPR007484 (PFAM); IPR007365 (PFAM); PTHR10404 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53187 (SUPERFAMILY); SSF52025 (SUPERFAMILY); IPR007365 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1917	c40059_g1_i1_len_10188_path_365_0_10187_2	2258	multiple ankyrin repeats single kh domain	3396	0	61.80%	0.245	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR002110 (PRINTS); IPR004087 (SMART); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR004088 (PFAM); IPR004088 (G3DSA:3.30.1370.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR23206 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR004088 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); IPR004088 (SUPERFAMILY); IPR020683 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1918	c4006_g1_i1_len_142_path_255_0_141_0	1	papilin- partial	48	1.48E-09	69.20%	0.123	PTHR13723 (PANTHER) IPR002352 (PRINTS); IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803:SF16 (PANTHER); PTHR22803 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR018378 (PROSITE_PATTERNS); IPR018378 (PROSITE_PATTERNS); IPR018378 (PROSITE_PATTERNS); IPR018378 (PROSITE_PATTERNS); IPR018378 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1919	c40088_g1_i1_len_4640_path_4917_0_329_9_724_330_4639_3	1049	macrophage mannose receptor 1	1547	7.61E-171	49.90%	0.107	IPR029154 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR013328 (G3DSA:1.10.1040.GENE3D); PTHR22981 (PANTHER); PTHR22981:SF7 (PANTHER); IPR008927 (SUPERFAMILY) IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR22961:SF4 (PANTHER); IPR024104 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1920	c40112_g5_i2_len_1078_path_1819_0_958_2_778_959_1077_0	40	3-hydroxyisobutyrate dehydrogenase	360	1.70E-46	58.60%	0.142	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); PTHR23223:SF21 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1921	c40113_g2_i1_len_3255_path_4435_0_992_5_424_993_1412_9954_1413_1436_567_1437_3254_5	769	tribbles homolog 2	1085	6.57E-121	72.20%	0.134	
1922	c40121_g2_i1_len_2500_path_6961_0_118_7_974_119_125_6306_126_504_596_505_528_620_529_2499_3	1288	krueppel-like factor 10	834	2.05E-71	63.10%	0.158	

1923	c40137_g1_i1_len_1650_path_5096_0_3_530 2_4_6_3269_7_11_5894_12_29_3292_30_41 4_5958_415_428_39_429_1_4	98	low-density lipoprotein receptor-related protein 2	550	2.50E-33	49.80%	0.143	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1924	c40138_g1_i1_len_3814_path_3191_0_284_1 528_285_359_10952_360_425_3613_426_56 6_3138_567_2287_11073_2_4	600	contactin-associated 4 isoform x1	1271	0	61.10%	0.360Y	IPR000742 (SMART); IPR001791 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10127:SF346 (PANTHER); PTHR10127 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
1925	c40151_g1_i1_len_1738_path_724_0_17_76 18_60_785_61_84_809_85_630_1355_631_ 668_1393_669_1135_3	510	serpin b8	580	1.51E-107	60.50%	0.179	IPR023796 (SMART); IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); G3DSA:3.30.497.10 (GENE3D); PTHR11461:SF124 (PANTHER); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023796 (SUPERFAMILY)
1926	c40158_g2_i1_len_6583_path_195_0_356_55 2_357_1069_1264_1070_1078_150_1079_ 2261_14788_2262_226_1	1653	chromodomain-helicase-dna-binding protein mi-2 homolog isoform x2	2194	0	84.00%	0.466Y	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR001650 (SMART); IPR014001 (SMART); IPR001650 (PFAM); IPR009463 (PFAM); IPR000330 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR009462 (PFAM); IPR012957 (PFAM); PTHR10799 (PANTHER); PTHR10799:SF460 (PANTHER); IPR002464 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001650 (PROSITE_PROFILES); IPR014001 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR027417 (SUPERFAMILY); IPR027417 (SUPERFAMILY)
1927	c40158_g2_i2_len_6619_path_195_0_356_55 2_357_1069_1264_1070_1078_150_1079_ 2261_2455_2262_6_0	1675	chromodomain-helicase-dna-binding protein mi-2 homolog isoform x5	2207	0	79.70%	0.133	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR001965 (SMART); IPR000953 (SMART); IPR001650 (SMART); IPR014001 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR013083 (G3DSA:3.30.40.GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR023780 (PFAM); IPR012958 (PFAM); IPR009463 (PFAM); IPR001650 (PFAM); G3DSA:2.40.50.40 (GENE3D); IPR019787 (PFAM); IPR000330 (PFAM); IPR012957 (PFAM); IPR009462 (PFAM); PTHR10799 (PANTHER); PTHR10799:SF460 (PANTHER); IPR002464 (PROSITE_PATTERNS); IPR019787 (PROSITE_PROFILES); IPR014001 (PROSITE_PROFILES); IPR019787 (PROSITE_PROFILES); IPR001650 (PROSITE_PROFILES); IPR000953 (PROSITE_PROFILES); IPR011011 (SUPERFAMILY); IPR011011 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR016197 (SUPERFAMILY); IPR016197 (SUPERFAMILY)

1928	c40158_g2_i3_len_6650_path_195_0_356_55 2_357_1069_1264_1070_1078_150_1079_2261_2455_2262_6_0	1663	chromodomain-helicase-dna-binding protein mi-2 homolog isoform x5	2217	0	79.50%	0.133	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR000953 (SMART); IPR014001 (SMART); IPR001650 (SMART); IPR001965 (SMART); G3DSA:2.40.50.40 (GENE3D); IPR023780 (PFAM); IPR001650 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); IPR012957 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR009462 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR019787 (PFAM); IPR012958 (PFAM); IPR009463 (PFAM); IPR000330 (PFAM); PTHR10799 (PANTHER); PTHR10799:SF460 (PANTHER); IPR002464 (PROSITE_PATTERNS); IPR019787 (PROSITE_PROFILES); IPR000953 (PROSITE_PROFILES); IPR001650 (PROSITE_PROFILES); IPR014001 (PROSITE_PROFILES); IPR019787 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); IPR011011 (SUPERFAMILY); IPR016197 (SUPERFAMILY); IPR016197 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR011011 (SUPERFAMILY)
1929	c40158_g2_i4_len_6689_path_195_0_356_55 2_357_1069_1264_1070_1078_150_1079_2261_2455_2262_6_0	1704	chromodomain-helicase-dna-binding protein mi-2 homolog isoform x5	2230	0	79.50%	0.133	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR014001 (SMART); IPR001965 (SMART); IPR001650 (SMART); IPR000953 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR000330 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); IPR023780 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR012958 (PFAM); IPR009463 (PFAM); IPR012957 (PFAM); IPR009462 (PFAM); IPR001650 (PFAM); IPR019787 (PFAM); G3DSA:2.40.50.40 (GENE3D); PTHR10799 (PANTHER); PTHR10799:SF460 (PANTHER); IPR002464 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014001 (PROSITE_PROFILES); IPR019787 (PROSITE_PROFILES); IPR000953 (PROSITE_PROFILES); IPR001650 (PROSITE_PROFILES); IPR019787 (PROSITE_PROFILES); IPR011011 (SUPERFAMILY); IPR016197 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR011011 (SUPERFAMILY); IPR016197 (SUPERFAMILY); IPR027417 (SUPERFAMILY)
1930	c40158_g2_i5_len_6726_path_195_0_356_55 2_357_1069_1264_1070_1078_150_1079_2261_2455_2262_6_0	1704	chromodomain-helicase-dna-binding protein mi-2 homolog isoform x5	2242	0	79.50%	0.133	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR000953 (SMART); IPR014001 (SMART); IPR001965 (SMART); IPR001650 (SMART); G3DSA:2.40.50.40 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR001650 (PFAM); IPR023780 (PFAM); IPR009463 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); IPR000330 (PFAM); IPR009462 (PFAM); IPR012958 (PFAM); IPR012957 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR019787 (PFAM); PTHR10799 (PANTHER); PTHR10799:SF460 (PANTHER); IPR002464 (PROSITE_PATTERNS); IPR019787 (PROSITE_PROFILES); IPR019787 (PROSITE_PROFILES); IPR000953 (PROSITE_PROFILES); IPR014001 (PROSITE_PROFILES); IPR001650 (PROSITE_PROFILES); IPR016197 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR011011 (SUPERFAMILY); IPR016197 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR011011 (SUPERFAMILY)
1931	c40174_g1_i1_len_3531_path_4461_0_77_91 0_78_2850_266_2851_2871_408_2872_353_0_1	1745	c-1-tetrahydrofolate cytoplasmic	1177	0	83.30%	0.202	Coil (COILS); IPR000672 (PRINTS); IPR020631 (PFAM); G3DSA:3.30.1510.10 (GENE3D); G3DSA:3.10.410.10 (GENE3D); G3DSA:3.40.192.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR000559 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR020630 (PFAM); PTHR10025 (PANTHER); IPR020867 (PROSITE_PATTERNS); IPR020867 (PROSITE_PATTERNS); IPR020628 (PROSITE_PATTERNS); IPR020628 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000559 (HAMAP); IPR000672 (HAMAP); SSF51735 (SUPERFAMILY); SSF53223 (SUPERFAMILY); IPR027417 (SUPERFAMILY)
1932	c40174_g1_i2_len_3639_path_4461_0_77_91 0_78_2850_158_2851_2958_266_2959_297_9_408_2980_3638_1	1709	c-1-tetrahydrofolate cytoplasmic	1213	0	80.00%	0.202	Coil (COILS); IPR000672 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020631 (PFAM); IPR020630 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:3.40.192.10 (GENE3D); G3DSA:3.10.410.10 (GENE3D); G3DSA:3.30.1510.10 (GENE3D); IPR000559 (PFAM); PTHR10025 (PANTHER); IPR020628 (PROSITE_PATTERNS); IPR020867 (PROSITE_PATTERNS); IPR020867 (PROSITE_PATTERNS); IPR020628 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000559 (HAMAP); IPR000672 (HAMAP); SSF53223 (SUPERFAMILY); IPR027417 (SUPERFAMILY); SSF51735 (SUPERFAMILY)

1933	c40174_g1_i3_len_3702_path_661_0_248_91_0_249_3021_387_3022_3042_408_3043_3701_1	1660	c-1-tetrahydrofolate cytoplasmic	1234	0	83.30%	0.198	Coil (COILS); IPR000672 (PRINTS); G3DSA:3.30.1510.10 (GENE3D); G3DSA:3.10.410.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020631 (PFAM); IPR020630 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR000559 (PFAM); G3DSA:3.40.192.10 (GENE3D); PTHR10025 (PANTHER); IPR020867 (PROSITE_PATTERNS); IPR020628 (PROSITE_PATTERNS); IPR020628 (PROSITE_PATTERNS); IPR020867 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000672 (HAMAP); IPR000559 (HAMAP); IPR027417 (SUPERFAMILY); SSF51735 (SUPERFAMILY); SSF53223 (SUPERFAMILY)
1934	c40176_g1_i2_len_2341_path_4818_0_189_8004_190_246_5063_247_328_5145_329_362_8172_363_364_5180_365_5	140	PREDICTED: uncharacterized protein LOC103578371 isoform X4	780	3.48E-10	51.20%	0.496Y	IPR002172 (PRINTS); IPR003609 (SMART); IPR002172 (SMART); IPR002172 (PFAM); G3DSA:3.50.4.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:3.50.4.10 (GENE3D); IPR003014 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); SSF57414 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1935	c40176_g2_i1_len_902_path_7297_0_99_7396_100_116_6840_117_319_5145_320_353_8172_354_355_7821_356_51_3	39	serine protease p153	301	2.89E-09	50.10%	0.111	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR003014 (PFAM); G3DSA:3.50.4.10 (GENE3D); IPR002172 (PFAM); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
1936	c40176_g3_i1_len_153_path_3681_0_102_8186_103_113_5324_114_126_5337_127_138_8206_139_152_3	1	---NA---	51			0.104	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
1937	c40179_g1_i1_len_2459_path_2905_0_121_3027_122_219_3125_220_270_3175_271_566_3466_567_816_275_81_5	225	ectonucleotide pyrophosphatase phosphodiesterase family member 6	819	1.34E-105	54.80%	0.355 Y	Coil (COILS); IPR002591 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); IPR024873 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY)
1938	c40179_g1_i2_len_2454_path_2905_0_121_8748_122_122_3027_123_220_3125_221_271_3175_272_567_3466_568_5	211	ectonucleotide pyrophosphatase phosphodiesterase family member 6	818	7.05E-106	54.60%	0.355 Y	IPR017849 (G3DSA:3.40.720.GENE3D); IPR002591 (PFAM); IPR024873 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY)
1939	c40179_g2_i1_len_954_path_5600_0_144_3125_145_195_575_196_953_5	36	ectonucleotide pyrophosphatase phosphodiesterase family member 6	318	2.75E-71	54.50%	0.128	IPR002591 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); IPR024873 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017850 (SUPERFAMILY)
1940	c40181_g1_i1_len_302_path_2634_0_33_2667_34_68_2203_69_81_2714_82_116_503_117_181_568_182_301_2	73	hypothetical protein LOTGIDRAFT_133595	100	5.74E-06	72.00%	0.096	PF14704 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
1941	c40181_g2_i1_len_548_path_259_0_59_31960_111_1355_112_140_3685_141_165_415_166_179_429_180_233_205_3	93	hemagglutinin amebocyte aggregation factor-like	183	2.91E-26	58.80%	0.393 Y	PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TMhelix (TMHMM)
1942	c40181_g2_i2_len_410_path_1264_0_8_12739_39_319_40_91_1355_92_120_3685_121_145_1408_146_159_429_16_5	105	hemagglutinin amebocyte aggregation factor-like	136	3.63E-24	59.80%	0.213	PF14704 (PFAM); IPR026645 (PANTHER)
1943	c40207_g1_i1_len_2079_path_2375_0_153_2528_154_204_202_205_849_91_850_1004_3376_1005_1016_3388_1017_3	848	probable cytochrome p450 49a1	693	2.50E-143	62.70%	0.14	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24305 (PANTHER); PTHR24305:SF49 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)

1944	c40209_g1_i1_len_2111_path_2089_0_756_2_846_757_758_2848_759_2110_4	1686	leucine-rich repeat neuronal protein 3-like isoform x1	704	1.48E-105	54.80%	0.194	IPR000483 (SMART); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1945	c40211_g1_i1_len_3204_path_173_0_206_38_0_207_207_381_208_1839_2010_1840_184_9_147_1850_3203_3	423	peroxinectin	1068	0	62.00%	0.16	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY); TMhelix (TMHMM)
1946	c40216_g2_i1_len_1607_path_2095_0_1558_3646_1559_1598_7603_1599_1606_1	466	di-n-acetylchitobiase	536	5.71E-94	59.40%	0.341 Y	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF146 (PANTHER); IPR001579 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1947	c40218_g1_i1_len_1138_path_1456_0_111_1_567_112_118_84_119_952_2883_953_964_2417_965_1054_3103_10_4	143	marginal zone b- and b1-cell-specific	379	1.37E-43	56.20%	0.202	PTHR15881:SF1 (PANTHER); PTHR15881 (PANTHER)
1948	c40218_g1_i2_len_1131_path_1456_0_111_1_567_112_118_84_119_952_2883_953_964_2417_965_1054_2696_10_3	145	marginal zone b- and b1-cell-specific protein	377	1.13E-43	55.90%	0.237	PTHR15881 (PANTHER); PTHR15881:SF1 (PANTHER)
1949	c40218_g1_i3_len_1151_path_1456_0_111_1_567_112_118_84_119_952_2405_953_964_2417_965_1054_3103_10_5	161	marginal zone b- and b1-cell-specific	383	9.75E-43	56.40%	0.182	PTHR15881 (PANTHER); PTHR15881:SF1 (PANTHER)
1950	c40222_g1_i1_len_1743_path_259_0_1041_4_652_1042_1042_1299_1043_1239_1495_124_0_1251_141_1252_1742_0	1189	hypothetical protein CHLREDRAFT_179663	581	8.60E-18	39.33%	0.371 Y	Coil (COILS); IPR006796 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); PD936484 (PRODOM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1951	c40224_g1_i1_len_2314_path_3630_0_2313_1	801	chitinase 2	771	5.19E-130	57.20%	0.106	IPR011583 (SMART); IPR002557 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR002557 (PFAM); IPR029070 (G3DSA:3.10.50.GENE3D); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR001579 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR029070 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR002557 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1952	c40229_g1_i1_len_3064_path_102_0_45_148_46_2235_6654_2236_3063_0	1703	protein ambp	1022	7.47E-27	55.20%	0.128	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); TMhelix (TMHMM)

1953	c40229_g1_i2_len_3071_path_149_0_52_148_53_2242_6654_2243_3070_1	1798	protein ambp	1024	7.44E-27	55.30%	0.146	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); TMhelix (TMHMM)
1954	c40230_g1_i1_len_2981_path_6288_0_14_67_09_15_33_6728_34_2766_2754_2767_2780_6842_2781_2801_6578_280_5	951	hemocyte protein-glutamine gamma-glutamyltransferase-like	993	0	67.80%	0.101	Coil (COILS); IPR002931 (SMART); IPR002931 (PFAM); IPR002931 (G3DSA:3.90.260.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR001102 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR008958 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11590:SF40 (PANTHER); IPR023608 (PANTHER); IPR013808 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54001 (SUPERFAMILY); IPR008958 (SUPERFAMILY); IPR008958 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
1955	c40233_g1_i1_len_1357_path_827_0_160_98_7_161_253_224_254_278_1101_279_280_54_281_373_1193_374_378_0	152	squamous cell carcinoma antigen 2	453	7.94E-77	53.40%	0.335	IPR023796 (SMART); G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); G3DSA:3.30.497.10 (GENE3D); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
1956	c40233_g1_i2_len_1217_path_827_0_160_98_7_161_253_224_254_278_1101_279_280_54_281_373_1193_374_378_0	140	serine proteinase inhibitor b3	406	5.24E-76	53.60%	0.335	IPR023796 (SMART); G3DSA:3.30.497.10 (GENE3D); IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
1957	c40236_g1_i1_len_1698_path_6046_0_32_98_13_33_34_27_35_69_9842_70_132_7803_13_3_156_7827_157_168_6208_1	1860	factor d-like protein	566	2.56E-79	50.80%	0.112	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1958	c40237_g1_i12_len_1589_path_4829_0_625_5455_626_816_4828_817_912_9661_913_91_5_5742_916_1077_5904_10_3	756	aspartyl asparaginyl beta-hydroxylase	530	1.02E-13	69.80%	0.222	Coil (COILS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1959	c40237_g1_i7_len_1436_path_4829_0_625_5455_626_816_4828_817_912_9661_913_915_5742_916_1077_6057_107_3	570	glutamic acid-rich protein	479	2.58E-07	61.00%	0.222	Coil (COILS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1960	c40238_g1_i2_len_924_path_869_0_188_105_8_189_232_1102_233_248_851_249_257_11_26_258_263_5963_264_274_4	683	---NA---	308			0.620 Y	IPR008197 (PRINTS); IPR008197 (SMART); IPR008197 (G3DSA:4.10.75.GENE3D); IPR008197 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR008197 (PROSITE_PROFILES); IPR008197 (PROSITE_PROFILES); SignalIP-TM (SIGNALP_EUK); IPR008197 (SUPERFAMILY); TMhelix (TMHMM)
1961	c40238_g1_i4_len_1095_path_5072_0_366_5436_367_389_558_390_541_1058_542_585_5935_586_619_5963_620_6_5	333	hypothetical protein LOTGIDRAFT_159529	365	2.03E-07	68.00%	0.259	IPR008197 (PRINTS); IPR008197 (SMART); IPR008197 (G3DSA:4.10.75.GENE3D); IPR008197 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008197 (PROSITE_PROFILES); IPR008197 (SUPERFAMILY); TMhelix (TMHMM)
1962	c40256_g2_i1_len_2522_path_561_0_2521_2	951	beta-galactosidase-1-like protein 2	840	0	61.10%	0.151	IPR001944 (PRINTS); IPR001944 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR23421:SF66 (PANTHER); IPR001944 (PANTHER); IPR019801 (PROSITE_PATTERNS); IPR008979 (SUPERFAMILY); IPR017853 (SUPERFAMILY)

1963	c40260_g1_i1_len_4835_path_5572_0_1205_516_1206_4834_2	2080	I-aminoadipate-semialdehyde dehydrogenase-like	1611	0	67.70%	0.106	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR013968 (SMART); IPR013120 (PFAM); G3DSA:3.40.50.980 (GENE3D); IPR010080 (TIGRFAM); IPR010071 (TIGRFAM); IPR000873 (PFAM); G3DSA:3.30.300.30 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR025110 (PFAM); G3DSA:3.40.50.980 (GENE3D); IPR002198 (PFAM); IPR009081 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); G3DSA:2.30.38.10 (GENE3D); IPR009081 (G3DSA:1.10.1200.GENE3D); PTHR24095:SF141 (PANTHER); PTHR24095 (PANTHER); IPR020904 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009081 (PROSITE_PROFILES); SSF51735 (SUPERFAMILY); SSF56801 (SUPERFAMILY); IPR009081 (SUPERFAMILY); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1964	c40260_g1_i2_len_3808_path_337_0_178_516_179_3807_1	1740	I-aminoadipate-semialdehyde dehydrogenase-like	1269	0	67.30%	0.125	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR013968 (SMART); G3DSA:2.30.38.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); G3DSA:3.30.300.30 (GENE3D); IPR013120 (PFAM); IPR009081 (G3DSA:1.10.1200.GENE3D); IPR010080 (TIGRFAM); IPR025110 (PFAM); IPR002198 (PFAM); IPR009081 (PFAM); IPR000873 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24095 (PANTHER); PTHR24095:SF141 (PANTHER); IPR020904 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009081 (PROSITE_PROFILES); SSF56801 (SUPERFAMILY); SSF51735 (SUPERFAMILY); SSF51735 (SUPERFAMILY); IPR009081 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1965	c40268_g1_i1_len_1028_path_1_0_22_6057_23_47_49_48_97_99_98_342_344_343_741_5472_742_1027_2	259	growth differentiation factor 8-like	342	4.17E-36	57.40%	0.419Y	IPR001111 (PFAM); IPR015615 (PANTHER); PTHR11848:SF126 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1966	c40268_g1_i2_len_2521_path_1_0_22_6057_23_47_49_48_97_99_98_342_344_343_741_743_742_2520_2	640	growth differentiation factor 8-like	840	7.07E-110	64.30%	0.419Y	IPR001839 (SMART); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001111 (PFAM); IPR001839 (PFAM); IPR015615 (PANTHER); PTHR11848:SF126 (PANTHER); IPR017948 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1967	c40296_g3_i1_len_1193_path_7883_0_1192_1	3231	cathepsin I precursor	398	2.80E-24	87.90%	0.106	G3DSA:2.40.50.170 (GENE3D); IPR000668 (PFAM); PTHR12411:SF265 (PANTHER); IPR013128 (PANTHER); IPR025661 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
1968	c40298_g2_i1_len_862_path_1979_0_16_1996_17_861_3	170	gtp-binding protein sar1	288	2.78E-126	93.10%	0.132	IPR006689 (PRINTS); IPR024156 (SMART); IPR006687 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); IPR005225 (TIGRFAM); PTHR11711 (PANTHER); PTHR11711:SF133 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006687 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)

1969	c40298_g2_i2_len_2450_path_1041_0_909_1_951_910_933_7467_934_1342_7875_1343_1348_2031_1349_1466_2558_3	421	gtp-binding protein sar1	817	3.28E-128	93.40%	0.132	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR006689 (PFAM); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF133 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006687 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1970	c40299_g1_i1_len_4155_path_1_0_3541_3543_3542_4154_4	6275	map kinase-interacting serine threonine-protein kinase 1	1385	0	78.30%	0.302	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24349 (PANTHER); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1971	c40308_g1_i1_len_2898_path_257_0_1742_1_998_1743_1758_2014_1759_2559_232_256_0_2773_6445_2774_2777_2	869	hemocyte protein-glutamine gamma- partial	966	0	70.40%	0.335	IPR002931 (SMART); IPR001102 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR002931 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR002931 (G3DSA:3.90.260.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR008958 (PFAM); PTHR11590:SF40 (PANTHER); IPR023608 (PANTHER); IPR008958 (SUPERFAMILY); IPR008958 (SUPERFAMILY); SSF54001 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
1972	c40310_g1_i3_len_438_path_1807_0_28_132_0_29_59_2687_60_65_1357_66_76_1368_77_113_1405_114_230_1520_3	23	zinc finger	146	3.30E-30	57.80%	0.136	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1973	c40325_g1_i1_len_3007_path_1_0_502_504_503_1923_1925_1924_2276_2278_2277_22_77_2279_2278_2939_2	2058	pdz and lim domain protein zasp-like	1002	6.22E-35	53.40%	0.108	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR24214:SF29 (PANTHER); PTHR24214 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
1974	c40325_g1_i2_len_3049_path_1_0_502_6249_503_544_504_545_1965_1925_1966_2318_2278_2319_2319_2279_2	1938	pdz and lim domain protein zasp-like	1016	7.84E-35	54.00%	0.108	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR24214 (PANTHER); PTHR24214:SF29 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
1975	c40328_g1_i1_len_3855_path_2574_0_1770_4359_1771_1890_9738_1891_1911_4502_1912_1937_5986_1938_1938_5	710	ectonucleoside triphosphate diphosphohydrolase 5 isoform x2	1285	1.04E-154	67.10%	0.134	IPR000407 (PFAM); PTHR11782:SF30 (PANTHER); IPR000407 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1976	c40328_g1_i2_len_3873_path_2574_0_1770_4343_1771_1786_4359_1787_1906_9738_1907_1927_4500_1928_1929_5	789	ectonucleoside triphosphate diphosphohydrolase 5 isoform x2	1291	1.91E-154	67.10%	0.134	IPR000407 (PFAM); IPR000407 (PANTHER); PTHR11782:SF30 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1977	c40329_g3_i1_len_1839_path_8793_0_474_9_268_475_1170_20156_1171_1172_11742_1173_1838_4	92	maltase- partial	613	4.57E-138	55.70%	0.109	IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF7 (PANTHER); IPR011013 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1978	c40329_g3_i3_len_3326_path_10938_0_108_9268_109_804_20156_805_806_1427_807_1379_20204_1380_3115_202_3	387	maltase- partial	1109	4.44E-63	64.80%	0.412 Y	IPR000322 (PFAM); PTHR22762:SF7 (PANTHER); PTHR22762 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY); IPR011013 (SUPERFAMILY)
1979	c40329_g3_i4_len_3692_path_8793_0_474_9_268_475_1170_20156_1171_1172_1427_1173_1745_20204_1746_3481_3	418	maltase- partial	1231	2.52E-101	59.50%	0.412Y	IPR000322 (PFAM); PTHR22762:SF7 (PANTHER); PTHR22762 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY); IPR011013 (SUPERFAMILY)
1980	c40333_g1_i4_len_686_path_335_0_56_2782_57_60_2742_61_77_667_78_85_47_86_95_973_96_685_4	772	pacifastin light chain	229	8.54E-16	51.60%	0.474Y	IPR008197 (PRINTS); IPR008197 (SMART); IPR008037 (PFAM); IPR008197 (G3DSA:4.10.75.GENE3D); IPR008197 (PFAM); IPR020862 (PROSITE_PROFILES); IPR008197 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008197 (SUPERFAMILY); IPR008037 (SUPERFAMILY); TMhelix (TMHMM)
1981	c40338_g1_i1_len_1352_path_4233_0_53_17_39_54_88_1774_89_146_1832_147_185_328_8_186_239_1925_240_271_5	4409	mite allergen lep d partial	450	9.29E-13	47.70%	0.105	PTHR11008:SF13 (PANTHER); PTHR11008 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020234 (PRODOM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1982	c40347_g1_i3_len_1960_path_2755_0_1717_4472_1718_1815_189_1816_1890_4644_1891_1920_6450_1921_1929_4_1	98	sco- partial	653	8.71E-85	49.30%	0.103	IPR000421 (SMART); IPR008979 (G3DSA:2.60.120.GENE3D); IPR002919 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR025155 (PFAM); IPR000421 (PFAM); PTHR24543 (PANTHER); IPR000421 (PROSITE_PATTERNS); IPR000421 (PROSITE_PROFILES); IPR008979 (SUPERFAMILY)
1983	c40347_g1_i5_len_1902_path_2755_0_1717_391_1718_1901_1	75	sco- partial	634	6.96E-89	50.60%	0.103	IPR000421 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000421 (PFAM); IPR025155 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); IPR002919 (PFAM); PTHR24543:SF244 (PANTHER); PTHR24543 (PANTHER); IPR000421 (PROSITE_PATTERNS); IPR000421 (PROSITE_PROFILES); IPR008979 (SUPERFAMILY)
1984	c40348_g1_i1_len_3417_path_127_0_217_34_5_218_249_377_250_319_446_320_331_37_332_2122_7034_2123_2_0	4145	aldehyde dehydrogenase 2 family	1139	0	83.10%	0.121	IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF145 (PANTHER); IPR016160 (PROSITE_PATTERNS); IPR029510 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1985	c40352_g1_i1_len_931_path_1_0_164_166_1_65_930_5	1101	aminoacylase-1 isoform x2	310	7.97E-69	69.40%	0.251	IPR002933 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11014 (PANTHER); PTHR11014:SF8 (PANTHER); IPR001261 (PROSITE_PATTERNS); IPR001261 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY)

1986	c40352_g1_i2_len_1792_path_5047_0_185_5 233_186_212_5260_213_236_5284_237_252_5300_253_293_5341_294_5	1957	aminoacylase-1 isoform x1	597	1.60E-152	69.30%	0.251	IPR002933 (PFAM); IPR010159 (TIGRFAM); IPR011650 (PFAM); G3DSA:3.40.630.10 (GENE3D); IPR011650 (G3DSA:3.30.70.GENE3D); PTHR11014 (PANTHER); PTHR11014:SF8 (PANTHER); IPR001261 (PROSITE_PATTERNS); IPR001261 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53187 (SUPERFAMILY); IPR011650 (SUPERFAMILY)
1987	c40352_g1_i3_len_2163_path_2714_0_683_3 398_684_725_6240_726_762_3477_763_109_5_3806_1096_1108_3819_1_5	2058	aminoacylase-1 isoform x1	721	2.65E-151	68.90%	0.251	IPR010159 (TIGRFAM); G3DSA:3.40.630.10 (GENE3D); IPR002933 (PFAM); IPR011650 (G3DSA:3.30.70.GENE3D); IPR011650 (PFAM); PTHR11014 (PANTHER); PTHR11014:SF8 (PANTHER); IPR001261 (PROSITE_PATTERNS); IPR001261 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011650 (SUPERFAMILY); SSF53187 (SUPERFAMILY); TMhelix (TMHMM)
1988	c40357_g1_i1_len_1305_path_3671_0_741_4 411_742_890_4560_891_928_4597_929_104_9_2129_1050_1090_4758_1_0	1513	cathepsin I	435	0	80.90%	0.124	IPR000668 (PRINTS); IPR013201 (SMART); IPR000668 (SMART); IPR013201 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); IPR013128 (PANTHER); PTHR12411:SF57 (PANTHER); IPR000169 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
1989	c40357_g1_i2_len_1868_path_3671_0_741_8 942_742_890_4560_891_928_129_929_980_181_981_1867_0	1064	cathepsin I	623	3.79E-171	79.50%	0.124	IPR000668 (PRINTS); IPR000668 (SMART); IPR013201 (SMART); IPR013201 (PFAM); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF57 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1990	c40357_g2_i1_len_1969_path_129_0_51_206 0_52_120_2129_121_161_5216_162_586_56_39_587_1139_6189_114_1	1029	cathepsin I	656	2.53E-25	86.50%	0.148	IPR000668 (PFAM); G3DSA:2.40.50.170 (GENE3D); PTHR12411:SF54 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY)
1991	c40357_g2_i2_len_1999_path_129_0_51_206 0_52_120_2129_121_161_5216_162_586_91_60_587_616_5639_617_1	1027	cathepsin I	666	2.67E-25	86.50%	0.148	IPR000668 (PFAM); G3DSA:2.40.50.170 (GENE3D); PTHR12411:SF54 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54001 (SUPERFAMILY)
1992	c40379_g1_i1_len_1284_path_3249_0_331_3 37_332_370_2697_371_554_558_555_704_7_08_705_841_4200_842_128_3	102	huga_polan ame: full=hyaluronidase short=hya ame: full=hyaluronoglucosaminidase ame: allergen=pol a 2 flags: partial	428	1.84E-70	56.30%	0.341 Y	IPR018155 (PRINTS); IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PANTHER); PTHR11769:SF8 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1993	c40379_g1_i2_len_1184_path_105_0_231_33 7_232_270_376_271_454_558_455_604_311_3_605_741_4200_742_1183_3	151	hyaluronidase-like	395	3.81E-74	56.90%	0.341 Y	IPR018155 (PRINTS); IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); PTHR11769:SF8 (PANTHER); IPR018155 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1994	c40385_g1_i1_len_1983_path_1_0_781_783_782_817_819_818_848_13343_849_877_879_878_1727_13282_1728_17_4	19078	pancreatic triacylglycerol lipase-like	661	6.53E-106	58.30%	0.374 Y	IPR000734 (PRINTS); IPR002331 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001024 (G3DSA:2.60.60.GENE3D); IPR013818 (PFAM); IPR000734 (PANTHER); IPR008976 (SUPERFAMILY); IPR029058 (SUPERFAMILY)
1995	c40385_g1_i2_len_2267_path_10048_0_11_1 0060_12_1065_783_1066_1101_12893_1102_1132_13343_1133_1161_4_4	3306	inactive pancreatic lipase-related protein 1	756	7.76E-104	57.70%	0.368 Y	IPR002331 (PRINTS); IPR000734 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001024 (G3DSA:2.60.60.GENE3D); IPR013818 (PFAM); IPR000734 (PANTHER); IPR001024 (PROSITE_PROFILES); IPR029058 (SUPERFAMILY); IPR008976 (SUPERFAMILY)

1996	c40385_g2_i1_len_2073_path_5751_0_1611_5345_1612_1635_7384_1636_1864_13255_1_865_1900_13282_1901_190_5	8567	pancreatic triacylglycerol lipase-like	691	4.23E-99	56.90%	0.837 Y	IPR002331 (PRINTS); IPR000734 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001024 (G3DSA:2.60.60.GENE3D); IPR013818 (PFAM); IPR000734 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR008976 (SUPERFAMILY); IPR029058 (SUPERFAMILY)
1997	c40396_g1_i1_len_2037_path_53_0_1205_12_59_1206_1218_1272_1219_1435_1489_1436_1464_4773_1465_1565_16_3	9337	sjchgc02838 protein	679	1.97E-124	51.40%	0.426 Y	IPR001547 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR31308 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1998	c40399_g1_i1_len_3829_path_4458_0_493_4_952_494_1301_5759_1302_1326_50_1327_2173_9055_2174_3828_2	735	cytosolic phospholipase a2-like isoform x5	1276	0	60.10%	0.101	Coil (COILS); IPR000008 (SMART); IPR002642 (SMART); IPR002642 (PFAM); IPR000008 (G3DSA:2.60.40.GENE3D); IPR000008 (PFAM); G3DSA:3.40.1090.10 (GENE3D); PTHR10728 (PANTHER); PTHR10728:SF13 (PANTHER); IPR000008 (PROSITE_PROFILES); IPR002642 (PROSITE_PROFILES); IPR000008 (SUPERFAMILY); IPR016035 (SUPERFAMILY); IPR016035 (SUPERFAMILY)
1999	c40411_g1_i1_len_2677_path_157_0_2670_2_826_2671_2676_2	516	allene oxide synthase-lipoxygenase	892	0	65.60%	0.132	Coil (COILS); IPR013819 (PRINTS); IPR001024 (SMART); IPR013819 (PFAM); IPR001024 (G3DSA:2.60.60.GENE3D); IPR001024 (PFAM); G3DSA:1.20.245.10 (GENE3D); PTHR11771:SF43 (PANTHER); IPR000907 (PANTHER); IPR020834 (PROSITE_PATTERNS); IPR001024 (PROSITE_PROFILES); IPR013819 (PROSITE_PROFILES); IPR008976 (SUPERFAMILY); IPR013819 (SUPERFAMILY)
2000	c40412_g1_i1_len_2874_path_2419_0_1954_8682_1955_1959_77_1960_2395_513_2396_2873_1	807	von willebrand domain-containing protein	958	0	56.80%	0.109	Coil (COILS); IPR002035 (SMART); IPR013694 (SMART); IPR002035 (G3DSA:3.40.50.GENE3D); IPR013694 (PFAM); PF13768 (PFAM); PTHR10338:SF95 (PANTHER); PTHR10338 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013694 (PROSITE_PROFILES); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
2001	c40412_g1_i2_len_3088_path_2419_0_1954_8682_1955_1959_4370_1960_3087_1	986	von willebrand domain-containing protein	1029	0	57.40%	0.109	Coil (COILS); IPR013694 (SMART); IPR002035 (SMART); IPR002035 (G3DSA:3.40.50.GENE3D); PF13768 (PFAM); IPR013694 (PFAM); PTHR10338 (PANTHER); PTHR10338:SF95 (PANTHER); IPR013694 (PROSITE_PROFILES); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
2002	c40412_g1_i3_len_2433_path_2419_0_1954_513_1955_2432_1	732	von willebrand domain-containing protein	811	0	59.80%	0.109	Coil (COILS); IPR013694 (SMART); IPR002035 (SMART); IPR002035 (G3DSA:3.40.50.GENE3D); PF13768 (PFAM); IPR013694 (PFAM); PTHR10338:SF95 (PANTHER); PTHR10338 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013694 (PROSITE_PROFILES); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
2003	c40415_g1_i1_len_761_path_3743_0_59_380_2_60_193_5402_194_195_3937_196_760_3	174	na(+) h(+) exchange regulatory cofactor nhe-rf2	254	1.87E-56	73.60%	0.161	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR14191 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
2004	c40415_g1_i3_len_2002_path_1_0_384_386_385_1219_3074_1220_1434_5402_1435_143_6_3937_1437_2001_3	499	na(+) h(+) exchange regulatory cofactor nhe-rf2-like	668	2.24E-61	60.60%	0.161	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR14191 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
2005	c40415_g1_i4_len_1724_path_1_0_384_386_385_1219_3074_1220_1434_5402_1435_143_6_3290_1437_1663_3517_1_4	655	na+ h+ exchange regulatory cofactor nhe-rf2	575	1.50E-08	65.00%	0.108	no IPS match
2006	c40422_g1_i1_len_1269_path_1192_0_524_4_535_525_1112_4427_1113_1190_4427_1191_1268_4	490	hypothetical protein CHLREDRAFT_179663	423	1.02E-14	36.00%	0.101	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); PD936484 (PRODOM); TMhelix (TMHMM)
2007	c40438_g1_i1_len_850_path_2600_0_198_17_77_199_225_3016_226_394_1978_395_431_399_432_486_454_487_513_4	1053	u24-ctenitoxin- partial	283	2.16E-14	47.40%	0.268	IPR000716 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PFAM); IPR000716 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY)

2008	c40438_g1_i2_len_957_path_1478_0_298_17_77_299_325_3479_326_501_1978_502_538_2014_539_593_454_594_62_4	2498	u24-ctenitoxin- partial	319	2.45E-14	46.50%	0.268	IPR000716 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); PTHR12352 (PANTHER); IPR000716 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY)
2009	c40460_g1_i1_len_1178_path_2642_0_1177_1	57	zinc finger protein 431-like isoform x2	393	1.88E-33	54.80%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2010	c40476_g2_i1_len_1795_path_9032_0_1794_2	2797	retinal dehydrogenase 1-like	598	0	80.00%	0.27	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF145 (PANTHER); IPR016160 (PROSITE_PATTERNS); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
2011	c40478_g1_i1_len_2104_path_3984_0_1530_5511_1531_2035_6740_2036_2036_6741_2_037_2103_3	486	iron zinc purple acid phosphatase-like protein	702	0	75.50%	0.217	IPR029052 (G3DSA:3.60.21.GENE3D); IPR004843 (PFAM); IPR025733 (PFAM); IPR015914 (G3DSA:2.60.40.GENE3D); PTHR22953 (PANTHER); PTHR22953:SF9 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008963 (SUPERFAMILY); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
2012	c40478_g1_i2_len_595_path_6057_0_21_551_1_22_526_6740_527_527_6741_528_594_3	85	iron zinc purple acid phosphatase-like partial	199	3.67E-59	70.70%	0.217	IPR015914 (G3DSA:2.60.40.GENE3D); IPR018946 (PFAM); IPR003961 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); IPR008963 (SUPERFAMILY)
2013	c40478_g1_i3_len_2105_path_3984_0_1530_5511_1531_2035_1181_2036_2104_4	456	iron zinc purple acid phosphatase-like protein	702	0	75.30%	0.243	IPR029052 (G3DSA:3.60.21.GENE3D); IPR025733 (PFAM); IPR004843 (PFAM); IPR015914 (G3DSA:2.60.40.GENE3D); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008963 (SUPERFAMILY); IPR029052 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2014	c40484_g1_i1_len_3629_path_5927_0_194_6_122_195_789_9035_790_1922_10168_1923_1924_10170_1925_3628_2	639	supervillin-like isoform x1	1209	0	64.00%	0.118	Coil (COILS); IPR007122 (PRINTS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR015628 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY)
2015	c40484_g1_i2_len_5456_path_6175_0_1278_7700_1279_2021_6122_2022_2616_9035_2_617_3749_10168_3750_3_2	760	supervillin-like isoform x1	1818	0	63.10%	0.107	Coil (COILS); Coil (COILS); IPR007122 (SMART); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007122 (PANTHER); IPR015628 (PTHR11977:PANTHER); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY)
2016	c40484_g1_i3_len_3568_path_20700_0_728_9035_729_1861_10168_1862_1863_10170_1864_3567_1	611	supervillin-like isoform x1	1189	0	66.30%	0.098	Coil (COILS); IPR007122 (PRINTS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR015628 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY)
2017	c40484_g1_i4_len_5702_path_6175_0_1278_7454_1279_1524_7700_1525_2267_6122_22_68_2862_9035_2863_39_2	784	supervillin-like isoform x1	1900	0	63.40%	0.107	Coil (COILS); Coil (COILS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR015628 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY)

2018	c40485_g1_i1_len_2566_path_4325_0_90_71 20_91_101_4426_102_187_4511_188_200_9 0_201_277_4599_278_292_1	166	latrophilin- partial	855	9.00E-62	49.10%	0.098	IPR001879 (SMART); IPR000203 (SMART); IPR001879 (PFAM); IPR000203 (PFAM); IPR000832 (PFAM); IPR022624 (PFAM); PTHR12011 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001879 (PROSITE_PROFILES); IPR017981 (PROSITE_PROFILES); IPR000203 (PROSITE_PROFILES); SSF111418 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2019	c40485_g1_i1_len_2566_path_4325_0_90_71 20_91_101_4426_102_187_4511_188_200_9 0_201_277_4599_278_292_2	166	latrophilin-3-like isoform x1	855	2.32E-19	61.30%	0.12	IPR000832 (PFAM); PTHR12011 (PANTHER); PTHR12011:SF222 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2020	c40485_g1_i2_len_2688_path_4325_0_90_71 20_91_101_4426_102_187_4511_188_200_9 0_201_277_4599_278_292_1	186	latrophilin- partial	896	7.73E-100	52.00%	0.098	IPR000832 (PRINTS); IPR000203 (SMART); IPR001879 (SMART); IPR001879 (PFAM); IPR022624 (PFAM); IPR000203 (PFAM); IPR000832 (PFAM); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001879 (PROSITE_PROFILES); IPR017981 (PROSITE_PROFILES); IPR000203 (PROSITE_PROFILES); SSF111418 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2021	c40485_g1_i3_len_3315_path_3596_0_379_3 976_380_406_4003_407_675_7154_676_68 2_4279_683_717_4314_7_1	233	latrophilin- partial	1105	1.79E-98	52.20%	0.147	IPR000832 (PRINTS); IPR000203 (SMART); IPR001879 (SMART); IPR001879 (PFAM); IPR000203 (PFAM); IPR000832 (PFAM); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000203 (PROSITE_PROFILES); IPR001879 (PROSITE_PROFILES); IPR017981 (PROSITE_PROFILES); SSF111418 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

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									TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS);
2024	c40493_g2_i4_len_7556_path_11261_0_125_11386_126_522_6042_523_607_11866_608_620_26682_621_632_11890_4	6008	PREDICTED: acrosin-like	2519	3.59E-09	43.75%	0.355Y		
2025	c40494_g2_i1_len_1329_path_16986_0_1016_18003_1017_1019_18006_1020_1220_1820_7_1221_1274_18207_1275_0	287	tpa: low quality protein: transglutaminase	443	9.30E-07	45.00%	0.119	no IPS match	
2026	c40495_g1_i1_len_1461_path_1405_0_620_2_026_621_623_2029_624_653_5517_654_655_3026_656_1460_3	330	low-density lipoprotein receptor-related protein 4 isoform x2	487	7.02E-16	57.20%	0.207	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)	
2027	c40495_g1_i2_len_1427_path_1405_0_620_2_026_621_623_2029_624_653_5517_654_655_2061_656_1426_5	609	scp-like extracellular domain containing protein 1	475	6.76E-37	49.60%	0.1	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR014044 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)	
2028	c40495_g1_i3_len_929_path_5237_0_155_55_17_156_157_2061_158_928_5	171	scp-like extracellular domain containing protein 1	309	5.08E-38	49.10%	0.1	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR014044 (SUPERFAMILY)	

									Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR003108 (SMART); IPR002048 (SMART); IPR018159 (SMART); IPR002017 (PFAM); IPR003108 (PFAM); IPR003108 (G3DSA:3.30.920.GENE3D); IPR011992 (PFAM); G3DSA:1.20.58.60 (GENE3D); G3DSA:1.20.58.60 (GENE3D); G3DSA:1.20.58.60 (GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); G3DSA:1.20.58.60 (GENE3D); G3DSA:1.20.58.60 (GENE3D); PTHR11915 (PANTHER); PTHR11915:SF212 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR003108 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF46966 (SUPERFAMILY); IPR003108 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF47473 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY)
2036	c40548_g1_i8_len_9989_path_11401_0_6447_17848_6448_6516_1841_6517_6618_18016__6619_7142_18540__1	5511	microtubule-actin cross-linking factor 1-like	3330	0	74.80%	0.1		
2037	c40557_g1_i1_len_2018_path_2877_0_81_18_1_82_208_464_209_2017_2	647	cytochrome p450 partial	672	1.83E-131	59.50%	0.104		IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24292:SF24 (PANTHER); PTHR24292 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
2038	c40557_g1_i2_len_2174_path_2877_0_81_18_1_82_208_308_209_269_369_270_276_376_277_364_464_365_2173_2	677	cytochrome p450 partial	724	8.46E-131	59.70%	0.104		IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24292 (PANTHER); PTHR24292:SF24 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
2039	c40557_g1_i3_len_1891_path_2877_0_81_46_4_82_1890_1	673	cytochrome p450 partial	630	5.12E-132	59.60%	0.267		IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24292 (PANTHER); PTHR24292:SF24 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
2040	c40567_g1_i2_len_1510_path_1605_0_488_2_094_489_491_2097_492_561_2167_562_564_2170_565_1093_2699_109_4	1493	protein kiaa1199-like	503	4.96E-20	44.30%	0.134		IPR025155 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2041	c40567_g2_i1_len_1668_path_5333_0_469_5_798_470_470_3708_471_1095_2699_1096_1_138_4240_1139_1374_3833_4	1069	cartilage intermediate layer protein 2-like	556	5.65E-18	43.60%	0.28		IPR025155 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
2042	c40575_g1_i1_len_2074_path_2102_0_169_2_272_170_197_2300__198_703_5320_704_70_6_2809_707_1447_35_1	1477	spermine oxidase	691	3.69E-116	51.60%	0.388Y		G3DSA:3.50.50.60 (GENE3D); IPR002937 (PFAM); IPR011032 (G3DSA:3.90.180.GENE3D); G3DSA:3.90.660.10 (GENE3D); PTHR10742 (PANTHER); PTHR10742:SF255 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY); TMhelix (TMHMM)
2043	c40575_g1_i2_len_2111_path_2102_0_169_2_272_170_197_2300__198_703_2806_704_70_6_2809_707_1447_55_1	1244	spermine oxidase	704	6.17E-74	49.80%	0.388Y		IPR002937 (PFAM); IPR011032 (G3DSA:3.90.180.GENE3D); G3DSA:3.50.50.60 (GENE3D); PTHR10742 (PANTHER); PTHR10742:SF255 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
2044	c40575_g1_i3_len_1992_path_4723_0_87_22_72_88_115_2300__116_621_2806_622_624_2809_625_1365_3548_0	1491	spermine oxidase	664	2.23E-117	51.50%	0.105		IPR002937 (PFAM); G3DSA:3.90.660.10 (GENE3D); G3DSA:3.50.50.60 (GENE3D); PTHR10742:SF255 (PANTHER); PTHR10742 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY); TMhelix (TMHMM)

2045	c40578_g1_i1_len_1726_path_6447_0_517_6 960_518_652_1052_653_1053_654_757 _8357_758_762_7196_763_0	66705	cathepsin partial	576	2.69E-143	74.50%	0.105	IPR000668 (PRINTS); IPR000668 (SMART); IPR013201 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); IPR013201 (PFAM); PTHR12411:SF57 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY)
2046	c40578_g1_i2_len_2364_path_6447_0_517_6 960_518_652_1052_653_1053_654_757 _4509_758_800_4552_801_0	63087	cathepsin partial	788	2.42E-138	73.30%	0.105	IPR000668 (PRINTS); IPR000668 (SMART); IPR013201 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR013201 (PFAM); IPR000668 (PFAM); PTHR12411:SF57 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY)
2047	c40583_g1_i1_len_2771_path_10171_0_1081 _9094_1082_1107_7434_1108_1512_1454_1 513_1536_7862_1537_1543_4	3909	chitin-binding protein	924	6.16E-69	41.10%	0.098	IPR002557 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002557 (PFAM); PTHR23301 (PANTHER); PTHR23301:SF0 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR002557 (SUPERFAMILY)
2048	c40598_g1_i1_len_1928_path_2235_0_1157_3392_1158_1169_172_1170_1452_4560_14_53_1526_3754_1527_153_1	421	hypothetical protein L798_00519	643	1.08E-69	50.80%	0.248	IPR008930 (G3DSA:1.50.10.GENE3D); IPR002157 (PFAM); IPR002157 (PANTHER); PTHR10559:SF12 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008930 (SUPERFAMILY); TMhelix (TMHMM)
2049	c40598_g1_i2_len_1941_path_2235_0_1157_3392_1158_1169_172_1170_1452_4560_14_53_1526_3754_1527_153_1	457	hypothetical protein L798_00519	647	1.01E-69	50.80%	0.248	IPR002157 (PFAM); IPR008930 (G3DSA:1.50.10.GENE3D); IPR002157 (PANTHER); PTHR10559:SF12 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008930 (SUPERFAMILY); TMhelix (TMHMM)
2050	c40600_g1_i1_len_3335_path_3769_0_3334_1	5274	serine proteinase stubble	1112	2.03E-103	61.90%	0.233	Coil (COILS); IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); PTHR24268:SF95 (PANTHER); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2051	c40606_g1_i2_len_1803_path_2171_0_288_2 459_289_297_1892_298_565_1383_566_680 _2847_681_839_3006_840_4	583	fasciclin-3 isoform x2	601	9.29E-41	47.80%	0.256	IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013162 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11640:SF52 (PANTHER); PTHR11640 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
2052	c40606_g1_i3_len_1599_path_1021_0_361_1 383_362_476_2847_477_635_3006_636_759 _8386_760_760_5076_761_4	295	fasciclin-3 isoform x1	533	1.67E-55	48.10%	0.256	Coil (COILS); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013162 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11640:SF52 (PANTHER); PTHR11640 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
2053	c40608_g1_i1_len_3572_path_53_0_187_241 _188_191_245_192_3571_2	6550	preamylyase 1	1183	0	76.60%	0.1	Coil (COILS); IPR006046 (PRINTS); IPR006048 (SMART); IPR006589 (SMART); IPR006048 (PFAM); IPR006047 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR10357:SF116 (PANTHER); IPR015902 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY); SSF51011 (SUPERFAMILY); TMhelix (TMHMM)

2054	c40616_g1_i1_len_545_path_201_0_178_380_179_213_4307_214_226_4320_227_342_44_36_343_374_4468_375_402_2	96	plasminogen precursor	181	5.27E-22	58.60%	0.179	PR00018 (PRINTS); IPR000001 (SMART); G3DSA:2.40.20.10 (GENE3D); IPR000001 (PFAM); PTHR24272 (PANTHER); IPR018056 (PROSITE_PATTERNS); IPR000001 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY)
2055	c40616_g2_i1_len_3206_path_4320_0_115_7_640_116_147_4468_148_175_4495_176_984_5301_985_1044_74_10_0	628	plasminogen-like isoform x1	1069	3.41E-95	49.50%	0.112	PR00018 (PRINTS); IPR000001 (SMART); IPR000001 (PFAM); G3DSA:2.40.20.10 (GENE3D); IPR022041 (PFAM); PTHR24259 (PANTHER); PTHR24259:SF70 (PANTHER); IPR018056 (PROSITE_PATTERNS); IPR018056 (PROSITE_PATTERNS); IPR018056 (PROSITE_PATTERNS); IPR018056 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2056	c40616_g2_i2_len_3146_path_4320_0_115_7_640_116_147_4468_148_175_4495_176_984_74_985_1737_6112_17_0	618	plasminogen-like isoform x1	1049	6.31E-98	51.70%	0.112	PR00018 (PRINTS); IPR000001 (SMART); IPR022041 (PFAM); IPR000001 (PFAM); G3DSA:2.40.20.10 (GENE3D); PTHR24259 (PANTHER); PTHR24259:SF70 (PANTHER); IPR018056 (PROSITE_PATTERNS); IPR018056 (PROSITE_PATTERNS); IPR018056 (PROSITE_PATTERNS); IPR018056 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR000001 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2057	c40627_g1_i1_len_2002_path_1982_0_153_2_136_154_177_2160_178_470_2451_471_47_4_2455_475_1756_3735_4	3777	glycosyl-phosphatidylinositol-linked carbonic anhydrase	667	1.71E-67	57.90%	0.122	IPR001148 (SMART); IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); IPR023561 (PANTHER); IPR018338 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
2058	c40674_g1_i1_len_546_path_1797_0_97_123_2_98_167_902_168_218_953_219_222_957_223_243_978_244_287_276_1	2965	serine protease inhibitor dipetalogastin-like	182	8.40E-16	51.30%	0.299	IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); PTHR10913:SF46 (PANTHER); PTHR10913 (PANTHER); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
2059	c40682_g1_i1_len_3471_path_105_0_387_49_3_388_393_499_394_539_645_540_548_654_549_911_1017_912_91_3	3451	agap011476-pa-like protein	1157	5.22E-73	44.80%	0.21	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2060	c40689_g1_i1_len_3510_path_151_0_91_783_2_92_148_150_149_3509_1	3248	heat shock 70 kda protein cognate 4	1170	0	93.90%	0.155	Coil (COILS); IPR013126 (PRINTS); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.30.30 (GENE3D); G3DSA:3.90.640.10 (GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53067 (SUPERFAMILY); IPR029048 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

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2065	c40722_g1_i1_len_1521_path_1441_0_217_1_659_218_219_1661_220_314_7006_315_326_7018_327_361_1800_362_2	3116	techylectin-5b isoform	507	1.20E-61	64.90%	0.103	IPR002181 (SMART); IPR014716 (G3DSA:3.90.215.GENE3D); IPR014715 (G3DSA:4.10.530.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); TMhelix (TMHMM)
2066	c40722_g1_i2_len_1777_path_159_0_458_61_8_459_486_6658_487_501_1951_502_569_9_3_570_576_100_577_631_2_1	2643	tl5a_tactr ame: full=techylectin-5a flags: precursor	592	1.50E-61	64.90%	0.187	Coil (COILS); IPR002181 (SMART); IPR002181 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); IPR014715 (G3DSA:4.10.530.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2067	c40722_g1_i3_len_1793_path_1441_0_217_6_745_218_219_1661_220_314_6877_315_326_7018_327_361_1431_362_2	2359	techylectin-5b isoform	597	1.92E-60	64.30%	0.11	Coil (COILS); IPR002181 (SMART); IPR014715 (G3DSA:4.10.530.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2068	c40730_g1_i2_len_4337_path_3438_0_2277_5716_2278_2295_5734_2296_2344_5783_23_45_2354_5793_2355_2505_3	1704	agap005608-pa-like protein	1446	1.49E-138	75.30%	0.13	Coil (COILS); Coil (COILS); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); PTHR19237:SF20 (PANTHER); PTHR19237 (PANTHER); IPR018247 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2069	c40730_g1_i3_len_1330_path_6923_0_98_10_524_99_100_7599_101_1329_3	473	ef-hand protein nucb1	444	5.85E-150	74.20%	0.13	Coil (COILS); Coil (COILS); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); PTHR19237 (PANTHER); PTHR19237:SF20 (PANTHER); IPR018247 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)
2070	c40753_g1_i9_len_7459_path_17798_0_2366_13395_2367_3151_21078_3152_4019_156_21_4020_4020_21946_40_3	5415	protein disulfide-isomerase	2487	0	77.10%	0.127	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR010893 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR19991 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

2071	c40772_g2_i1_len_2111_path_6657_0_48_63_38_49_50_4194_51_89_6744_90_2110_5	767	cytochrome p450	703	0	69.50%	0.134	Coil (COILS); IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24290 (PANTHER); PTHR24290:SF0 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
2072	c40783_g1_i1_len_3133_path_635_0_148_78_3_149_154_399_155_759_7127_760_967_1_604_968_1358_1994_2	5149	group 3 secretory phospholipase partial	1044	2.19E-76	54.80%	0.14	Coil (COILS); IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PFAM); PTHR12253 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016090 (SUPERFAMILY)
2073	c40783_g1_i2_len_3136_path_635_0_148_78_3_149_154_399_155_759_1393_760_970_1_604_971_1361_1994_2	5734	group 3 secretory phospholipase partial	1045	1.17E-82	56.30%	0.14	Coil (COILS); IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PFAM); PTHR12253 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016090 (SUPERFAMILY)
2074	c40789_g1_i1_len_2516_path_2789_0_514_5_533_515_556_3304_557_1548_4294_1549_1553_4299_1554_1718_4_2	1698	prophenoloxidase activating factor	838	7.35E-125	67.70%	0.211	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2075	c40789_g1_i2_len_2474_path_2789_0_514_3_304_515_1506_4294_1507_1511_4299_151_2_1676_4459_1677_1677_2	1759	prophenoloxidase activating factor	824	4.83E-125	67.70%	0.211	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF95 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2076	c40794_g1_i1_len_3446_path_1_0_162_164_163_2665_2667_2666_2666_2668_2667_34_45_1	1176	chorion peroxidase-like	1149	0	61.20%	0.175	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
2077	c40794_g1_i2_len_3330_path_6991_0_46_16_4_47_2549_2667_2550_2550_2668_2551_3_329_2	1138	chorion peroxidase-like	1110	0	61.20%	0.366 Y	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
2078	c40817_g3_i1_len_383_path_395_0_297_693_298_382_1	29	cda2 isoform a	128	4.00E-60	85.30%	0.196	IPR002172 (SMART); IPR002557 (PFAM); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR11177:SF106 (PANTHER); PTHR11177 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002557 (SUPERFAMILY)
2079	c40821_g1_i1_len_1790_path_28_0_1_779_2_10_7674_11_31_944_32_61_974_62_1288_6736_1289_1295_6743_3	4056	meprin a	597	8.81E-78	53.70%	0.630 Y	IPR001506 (PRINTS); IPR000859 (SMART); IPR006026 (SMART); IPR001506 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000859 (PFAM); PTHR10127 (PANTHER); PTHR10127:SF580 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR000859 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR000859 (SUPERFAMILY); SSF55486 (SUPERFAMILY)

2080	c40821_g1_i2_len_1829_path_28_0_1_779_2_10_7674_11_31_974_32_1258_6736_1259_1265_6743_1266_16_3	4281	meprin a	610	9.38E-78	53.90%	0.638	Y	IPR001506 (PRINTS); IPR006026 (SMART); IPR000859 (SMART); IPR000859 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF580 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR000859 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR000859 (SUPERFAMILY); SSF55486 (SUPERFAMILY)
2081	c40821_g1_i3_len_1859_path_28_0_1_779_2_10_7674_11_31_944_32_61_974_62_1288_6736_1289_1295_6743_3	4370	meprin a	620	2.02E-77	53.70%	0.638	Y	IPR001506 (PRINTS); IPR000859 (SMART); IPR006026 (SMART); IPR000859 (PFAM); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127:SF580 (PANTHER); PTHR10127 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR000859 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR000859 (SUPERFAMILY); SSF55486 (SUPERFAMILY)
2082	c40821_g2_i1_len_1333_path_7523_0_0_752_4_1_23_4243_24_43_631_44_45_633_46_96_684_97_101_4268_102_12_0	4621	---NA---	445			0.112		no IPS match
2083	c40821_g2_i2_len_1281_path_177_0_22_200_23_42_631_43_44_684_45_49_4268_50_12_33_5445_1234_1280_2	4589	---NA---	427			0.129		no IPS match
2084	c40822_g1_i1_len_1956_path_1127_0_176_1_304_177_272_1400_273_347_1475_348_441_1569_442_482_1610_483_1	1165	heat shock protein 70	652	0	90.30%	0.102		Coil (COILS); IPR013126 (PRINTS); G3DSA:3.30.30.30 (GENE3D); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.90.640.10 (GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); IPR029048 (SUPERFAMILY)
2085	c40822_g2_i1_len_363_path_497_0_362_3	70	heat shock cognate 71 kda protein	121	2.07E-23	93.80%	0.179		IPR013126 (PRINTS); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF155 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
2086	c40825_g1_i1_len_3004_path_6912_0_74_64_6_75_2143_2714_2144_2150_104_2151_2_843_26_2844_2859_34_0	1075	villin-1-like isoform x1	1002	0	66.30%	0.168		IPR007122 (PRINTS); IPR007122 (SMART); IPR003128 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR003128 (PFAM); IPR003128 (G3DSA:1.10.950.GENE3D); IPR007122 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003128 (PROSITE_PROFILES); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); IPR003128 (SUPERFAMILY); TMhelix (TMHMM)
2087	c40825_g1_i2_len_3082_path_493_0_152_64_6_153_2221_2714_2222_2228_104_2229_2921_26_2922_2937_3_0	1095	villin-1-like isoform x1	1028	0	66.30%	0.209		IPR007122 (PRINTS); IPR007122 (SMART); IPR003128 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR003128 (G3DSA:1.10.950.GENE3D); IPR003128 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007122 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003128 (PROSITE_PROFILES); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); IPR003128 (SUPERFAMILY); TMhelix (TMHMM)
2088	c40827_g1_i1_len_3258_path_7645_0_157_3_12_158_2183_2338_2184_2200_2355_2201_2827_2982_2828_2833_1	585	a chain structural studies of protein tyrosine phosphatase beta catalytic domain in complex with inhibitors	1086	1.07E-75	57.90%	0.105		IPR000242 (PRINTS); IPR003961 (SMART); IPR003595 (SMART); IPR000242 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR029021 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY)

2089	c40831_g2_i1_len_3132_path_3669_0_661_4 76_662_697_4364_698_713_4380_714_787_ 4453_788_1292_4958_1293_1	1173	microneme protein partial	1035	4.83E-28	38.40%	0.450Y	IPR000742 (SMART); IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR024731 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24034 (PANTHER); PTHR24034:SF36 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); PD968187 (PRODOM); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR009030 (SUPERFAMILY); IPR009030 (SUPERFAMILY); TMhelix (TMHMM)
2090	c40834_g1_i1_len_333_path_2486_0_65_366 6_66_186_2667_187_196_4566_197_224_38 9_225_289_454_290_332_1	5	cytolysin src-1-like isoform x2	111	1.64E-17	56.60%	0.201	IPR015926 (G3DSA:2.60.270.GENE3D); IPR015926 (SUPERFAMILY)
2091	c40834_g2_i1_len_1079_path_2297_0_72_23 70_73_75_2373_76_158_2456_159_160_245 8_161_188_4427_189_333_1	96	cytolysin src-1-like isoform x2	360	4.89E-25	51.30%	0.11	IPR009104 (PFAM); IPR015926 (G3DSA:2.60.270.GENE3D); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR015926 (SUPERFAMILY); TMhelix (TMHMM)
2092	c40834_g2_i2_len_672_path_3229_0_149_24 56_150_151_2458_152_179_2486_180_245_ 2552_246_300_1417_301_3_1	71	cytolysin src-1-like isoform x2	224	1.31E-23	52.80%	0.101	IPR015926 (G3DSA:2.60.270.GENE3D); IPR015926 (SUPERFAMILY)
2093	c40838_g1_i1_len_3240_path_12569_0_49_2 36_50_81_268_82_135_322_136_137_324_1 38_162_12849_163_179_36_2	1002	nidogen-2 isoform x1	1080	0	61.90%	0.135	IPR002223 (PRINTS); IPR000033 (SMART); IPR000742 (SMART); IPR002223 (SMART); IPR011042 (G3DSA:2.120.10.GENE3D); IPR024731 (PFAM); IPR000033 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR023413 (G3DSA:2.40.155.GENE3D); PTHR10529 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR009030 (SUPERFAMILY); SSF63825 (SUPERFAMILY)

2094	c40838_g1_i2_len_3230_path_25_0_46_72_4 7_86_112_87_101_127_102_137_163_138_2 10_236_211_242_268_243_1	1016	nidogen-2 isoform x1	1077	0	61.20%	0.1	IPR002223 (PRINTS); IPR000742 (SMART); IPR002223 (SMART); IPR000033 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR024731 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR000033 (PFAM); IPR023413 (G3DSA:2.40.155.GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR10529 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR009030 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
2095	c40838_g1_i3_len_2827_path_12690_0_20_7 56_21_886_1622_887_909_1645_910_237 0_3106_2371_2373_31_1	997	nidogen- partial	942	0	65.80%	0.111	IPR000742 (SMART); IPR000033 (SMART); IPR000033 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); IPR024731 (PFAM); IPR023413 (G3DSA:2.40.155.GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10529 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY)
2096	c40840_g1_i1_len_3911_path_4393_0_1317_ 5703_1318_1340_516_1341_2204_6586_22 05_2211_6593_2212_5	1416	neutral and basic amino acid transport protein rbat	1303	2.09E-160	56.50%	0.182	IPR006589 (SMART); IPR013780 (G3DSA:2.60.40.GENE3D); IPR006047 (PFAM); G3DSA:3.90.400.10 (GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR10357:SF77 (PANTHER); IPR015902 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
2097	c40841_g1_i1_len_652_path_6206_0_12_622 9_13_13_6220_14_210_3883_211_213_3886 _214_308_3645_309_335_5_3	5084	brasiliensin precursor	218	1.49E-26	50.10%	0.106	IPR002350 (SMART); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); PTHR10913:SF46 (PANTHER); PTHR10913 (PANTHER); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
2098	c40841_g2_i1_len_1681_path_1991_0_1325_ 3317_1326_1336_3328_1337_1358_6112_13 59_1359_3351_1360_1362_5	12103	kazal-type protease inhibitor	560	3.25E-10	53.80%	0.115	IPR002350 (SMART); IPR002350 (PFAM); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
2099	c40856_g1_i1_len_4997_path_8043_0_1631_ 23818_1632_2746_10784_2747_4319_1234 6_4320_4443_298_44_1	1465	annu_scham ame: full=annulin ame: full=protein-glutamine gamma-glutamyltransferase ame: full=transglutaminase	1666	0	74.00%	0.107	IPR002931 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR001102 (PFAM); IPR002931 (G3DSA:3.90.260.GENE3D); IPR002931 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR008958 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR023608 (PANTHER); PTHR11590:SF16 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008958 (SUPERFAMILY); IPR008958 (SUPERFAMILY); IPR014756 (SUPERFAMILY); SSF54001 (SUPERFAMILY)

2100	c40856_g6_i1_len_1320_path_801_0_204_10_06_205_232_5058_233_1319_3	395	gamma-interferon-inducible lysosomal thiol reductase	440	1.50E-48	57.20%	0.197	IPR004911 (PFAM); IPR004911 (PANTHER); PTHR13234:SF8 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2101	c40858_g1_i1_len_1866_path_1947_0_17_19_65_18_616_5384_617_683_7265_684_685_7267_686_1842_7481_2	507	cytochrome p450	622	9.56E-165	73.60%	0.164	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24290 (PANTHER); PTHR24290:SF0 (PANTHER); IPR017972 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY)
2102	c40858_g1_i2_len_2024_path_844_0_841_72_65_842_843_7267_844_2000_7481_2001_2_023_1	358	cytochrome p450	675	5.97E-64	76.50%	0.125	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24290 (PANTHER); PTHR24290:SF0 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2103	c40858_g1_i3_len_2426_path_4376_0_279_4_656_280_300_4677_301_409_1965_410_10_08_5384_1009_1075_726_1	658	cytochrome p450	800	0	70.90%	0.198	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24290 (PANTHER); PTHR24290:SF0 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
2104	c40858_g1_i4_len_2189_path_4376_0_279_4_656_280_300_4677_301_409_1965_410_10_08_7267_1009_2165_1	562	cytochrome p450	730	0	67.30%	0.198	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24290 (PANTHER); PTHR24290:SF0 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
2105	c40861_g1_i1_len_2866_path_8242_0_158_2_5_159_444_311_445_469_8695_470_548_87_74_549_595_1655_596_994_4	628	epithelial chloride channel partial	955	0	52.50%	0.114	IPR002035 (SMART); IPR015394 (PFAM); IPR013642 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13519 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); PTHR10579 (PANTHER); PTHR10579:SF8 (PANTHER); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM)
2106	c40861_g1_i2_len_724_path_12477_0_28_12_506_29_43_964_44_142_1063_143_187_105_61_188_528_14246_529_53_4	113	calcium-activated chloride channel regulator 4-like	241	6.00E-30	62.10%	0.138	IPR013642 (PFAM); PTHR10579 (PANTHER); PTHR10579:SF8 (PANTHER)
2107	c40861_g1_i3_len_2753_path_8242_0_158_2_5_159_444_311_445_469_8695_470_548_87_74_549_595_1655_596_994_5	630	epithelial chloride channel partial	917	0	52.50%	0.149	IPR002035 (SMART); IPR002035 (G3DSA:3.40.50.GENE3D); PF13519 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR015394 (PFAM); IPR013642 (PFAM); PTHR10579:SF8 (PANTHER); PTHR10579 (PANTHER); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM)
2108	c40861_g1_i4_len_2884_path_8242_0_158_2_5_159_444_311_445_469_8695_470_548_87_74_549_595_1655_596_994_4	655	epithelial chloride channel partial	961	0	52.50%	0.138	IPR002035 (SMART); IPR013642 (PFAM); PF13519 (PFAM); IPR015394 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10579:SF8 (PANTHER); PTHR10579 (PANTHER); IPR002035 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR002035 (SUPERFAMILY)

2109	c40861_g2_i1_len_3852_path_7153_0_1088_8242_1089_1247_8400_1248_1518_311_1519_1543_13056_1544_1622_3	1051	calcium-activated chloride channel regulator 4-like	1284	0	53.60%	0.128	IPR002035 (SMART); IPR003961 (SMART); IPR015394 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13519 (PFAM); IPR013642 (PFAM); PTHR10579 (PANTHER); PTHR10579:SF8 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002035 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR002035 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2110	c40865_g1_i1_len_351_path_5759_0_67_137_0_68_220_236_221_238_1756_239_273_782_7_274_313_5087_314_325_2	139	ubiquitin isoform cra_e	117	1.19E-56	100.00%	0.245	IPR019956 (PRINTS); IPR000626 (SMART); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); G3DSA:3.10.20.90 (GENE3D); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY)
2111	c40865_g1_i2_len_594_path_5759_0_67_137_0_68_220_236_221_238_8569_239_241_857_2_242_249_264_250_593_2	2645	ubiquitin-40s ribosomal protein s27a-like	198	2.54E-94	96.10%	0.245	IPR019956 (PRINTS); IPR000626 (SMART); IPR002906 (PFAM); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666:SF99 (PANTHER); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR011332 (SUPERFAMILY)
2112	c40865_g4_i1_len_306_path_5046_0_40_508_7_41_52_3912_53_196_30_197_202_8339_2_03_208_42_209_248_82_24_2	381	polyubiquitin-b- partial	102	7.85E-64	100.00%	0.214	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY)
2113	c40865_g6_i1_len_780_path_3380_0_56_236_57_74_1756_75_109_4398_110_212_2833_213_241_2862_242_779_0	1195	ubiquitin c	260	1.20E-82	99.40%	0.113	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2114	c40865_g7_i1_len_321_path_2657_0_175_28_33_176_204_4952_205_274_8339_275_280_42_281_320_2	132	ubiquitin-40s ribosomal protein partial	107	5.30E-44	96.80%	0.418Y	IPR019956 (PRINTS); IPR000626 (SMART); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY)
2115	c40871_g8_i1_len_1672_path_29264_0_872_42099_873_873_30137_874_874_24327_875_1049_30308_1050_1074_2_2	1227	thioredoxin peroxidase	557	5.78E-134	87.40%	0.694 Y	IPR019479 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000866 (PFAM); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2116	c40871_g8_i2_len_1476_path_29264_0_872_42099_873_873_30137_874_874_24327_875_1049_23874_1050_1383_2_2	1085	thioredoxin peroxidase	492	4.97E-136	87.40%	0.694Y	IPR019479 (PFAM); IPR000866 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY)
2117	c40872_g1_i1_len_1768_path_661_0_953_25_954_957_29_958_1105_489_1106_1127_51_1_1128_1160_4425_1161_1_4	13508	anti-lipopolysaccharide factor isoform 7	589	1.35E-28	64.00%	0.11	IPR024509 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024716 (PRODOM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

2118	c40873_g1_i1_len_5679_path_7989_0_5678_4	260520	vitellogenin fused with superoxide dismutase	1893	0	45.70%	0.177	IPR001747 (SMART); IPR001846 (SMART); IPR015816 (G3DSA:2.30.230.GENE3D); IPR001747 (PFAM); IPR001846 (PFAM); IPR015818 (G3DSA:2.20.80.GENE3D); IPR011030 (G3DSA:1.25.10.GENE3D); IPR015255 (PFAM); PTHR23345:SF1 (PANTHER); PTHR23345 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001747 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR015819 (SUPERFAMILY); IPR015819 (SUPERFAMILY); IPR011030 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2119	c40883_g1_i1_len_3576_path_443_0_759_35_2_760_1156_1591_1157_1177_8515__1178_2229_2661_2230_228_1	741	hypothetical protein DAPPUDRAFT_321105	1192	0	64.70%	0.144	IPR002223 (PRINTS); IPR002223 (SMART); IPR000884 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR000884 (PFAM); IPR002223 (PFAM); IPR002861 (PFAM); G3DSA:2.20.100.10 (GENE3D); G3DSA:2.20.100.10 (GENE3D); IPR009465 (PFAM); PTHR11311 (PANTHER); IPR020901 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR009465 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR002861 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
2120	c40883_g1_i2_len_3520_path_443_0_759_35_2_760_1156_1591_1157_1177_8515__1178_2229_423_2230_3519_1	670	spondin-1 isoform x1	1173	0	66.30%	0.144	IPR002223 (PRINTS); IPR002223 (SMART); IPR000884 (SMART); G3DSA:2.20.100.10 (GENE3D); IPR009465 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002861 (PFAM); IPR002223 (PFAM); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); PTHR11311 (PANTHER); IPR020901 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR009465 (PROSITE_PROFILES); IPR002861 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
2121	c40883_g1_i2_len_3520_path_443_0_759_35_2_760_1156_1591_1157_1177_8515__1178_2229_423_2230_3519_2	670	perq amino acid-rich with gyf domain-containing protein 2-like	1173	2.88E-23	60.60%	0.262	IPR000884 (SMART); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY)
2122	c40886_g2_i1_len_5092_path_9769_0_283_2_8_284_2899_2644_2900_2903_2648__2904_3883_3628__3884_0	839	tyrosine-protein phosphatase non-receptor type 13-like isoform x3	1698	3.14E-140	52.50%	0.114	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964 (PANTHER); PTHR19964:SF32 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)

2123	c40886_g2_i2_len_4836_path_1_0_26_28_2_7_2642_2644_2643_2646_2648_2647_3626_11122_3627_3627_3_1	828	tyrosine-protein phosphatase non-receptor type 13-like isoform x3	1612	2.84E-141	52.70%	0.17	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR19964:SF32 (PANTHER); PTHR19964 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2124	c40895_g2_i3_len_2862_path_4_0_167_172_168_254_10096_255_436_441_437_471_101_62_472_490_10181_491_50_4	693	von willebrand factor-like	954	8.65E-17	42.20%	0.11	Coil (COILS); Coil (COILS); PR01217 (PRINTS); IPR001846 (SMART); IPR001846 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR014853 (PFAM); PTHR11339 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000436 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR000436 (SUPERFAMILY); TMhelix (TMHMM)
2127	c40906_g1_i1_len_3867_path_11569_0_1475_6276_1476_1833_3092_1834_2059_3318_2060_2082_3341_208_5	8464	cellulosome anchoring protein cohesin region	1289	4.57E-10	46.40%	0.114	Coil (COILS); Coil (COILS); Coil (COILS); PR01217 (PRINTS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2125	c40906_g1_i11_len_4029_path_11569_0_147_5_6276_1476_1833_3092_1834_2059_3318_2060_2082_3341_20_5	8854	cellulosome anchoring protein cohesin region	1343	3.53E-10	45.60%	0.114	Coil (COILS); Coil (COILS); Coil (COILS); PR01217 (PRINTS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2126	c40906_g1_i12_len_4032_path_11569_0_147_5_6276_1476_1833_3092_1834_2059_3318_2060_2082_3341_20_5	8502	cellulosome anchoring protein cohesin region	1344	3.94E-10	45.60%	0.114	Coil (COILS); Coil (COILS); Coil (COILS); PR01217 (PRINTS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2128	c40906_g1_i2_len_4632_path_11569_0_1475_6276_1476_1833_3092_1834_2059_3318_2060_2082_3341_208_5	8669	cellulosome anchoring protein cohesin region	1544	9.60E-12	45.20%	0.11	Coil (COILS); Coil (COILS); PR01217 (PRINTS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2129	c40906_g1_i3_len_4098_path_11569_0_1475_6276_1476_1833_3092_1834_2059_3318_2060_2082_3341_208_5	8535	cellulosome anchoring protein cohesin region	1366	3.21E-10	45.60%	0.114	Coil (COILS); Coil (COILS); PR01217 (PRINTS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

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2135	c40906_g1_i9_len_4521_path_11569_0_1475_6276_1476_1833_3092_1834_2059_3318_2060_2082_3341_208_5	8716	cellulosome anchoring protein cohesin region	1507	2.36E-11	45.00%	0.11	Coil (COILS); Coil (COILS); Coil (COILS); PR01217 (PRINTS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2136	c40913_g3_i1_len_3085_path_1048_0_82_10_73_83_161_1152_162_198_7504_199_519_1_287_520_1011_8315_10_5	755	kielin chordin-like protein isoform x1	1028	9.64E-42	50.30%	0.102	IPR002223 (PRINTS); IPR002223 (SMART); IPR003961 (SMART); IPR002350 (SMART); IPR003645 (SMART); IPR000742 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); G3DSA:2.170.300.10 (GENE3D); IPR002350 (PFAM); IPR003961 (PFAM); PTHR10083 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF100895 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
2137	c40913_g3_i2_len_2595_path_1257_0_29_12_87_30_521_8315_522_2594_5	509	kunitz bovine pancreatic trypsin inhibitor domain protein	865	4.11E-38	41.00%	0.102	IPR002223 (PRINTS); IPR003645 (SMART); IPR002223 (SMART); IPR003961 (SMART); IPR002350 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF100895 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
2138	c40913_g3_i3_len_1161_path_1048_0_82_10_73_83_161_1152_162_198_7504_199_519_1_287_520_1011_25_1012_4	317	kielin chordin-like protein isoform x1	387	5.60E-44	51.60%	0.224	IPR000742 (SMART); IPR002350 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10913 (PANTHER); PTHR10913:SF45 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002350 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
2139	c40920_g1_i1_len_3184_path_313_0_3069_3_373_3070_3096_7782_3097_3156_3373_315_7_3183_0	1212	beta-lactamase-like protein 2-like	1062	3.26E-55	50.50%	0.367 Y	IPR001466 (PFAM); IPR012338 (G3DSA:3.40.710.GENE3D); PTHR22935 (PANTHER); PTHR22935:SF64 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012338 (SUPERFAMILY)

2140	c40928_g3_i1_len_2641_path_7718_0_535_2 1590_536_548_8266_549_606_8324_607_63 8_8356_639_693_8411_694_1	6572	14-3-3 protein zeta isoform x1	880	6.55E-165	96.40%	0.131	Coil (COILS); Coil (COILS); IPR000308 (PRINTS); IPR023410 (SMART); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023409 (PROSITE_PATTERNS); IPR023409 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023410 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2141	c40941_g3_i1_len_3871_path_2241_0_48_22 90_49_72_23997_73_589_29692_590_590_2 9631_591_604_29645_605_3	2596	hypothetical protein DAPPUDRAFT_200882	1291	0	60.50%	0.107	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR008753 (PFAM); IPR018497 (PFAM); IPR000718 (PANTHER); PTHR11733:SF111 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2142	c40943_g1_i1_len_1482_path_5599_0_633_3 684_634_938_1589_939_1052_1702_1053_1 099_956_1100_1124_1773_4	2594	pacifastin light chain	494	4.42E-16	51.50%	0.125	IPR008037 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2143	c40943_g1_i2_len_1462_path_5599_0_633_3 684_634_938_1589_939_1052_1702_1053_1 099_956_1100_1124_1773_5	2532	pacifastin light chain	487	4.18E-16	50.90%	0.226	IPR008037 (PFAM); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2144	c40943_g2_i1_len_1173_path_1009_0_370_7 555_371_376_1384_377_378_1386_379_414 _7584_415_431_42_432_58_5	1512	pacifastin light chain	391	7.04E-16	51.10%	0.425Y	IPR008037 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); TMhelix (TMHMM)
2145	c40947_g1_i1_len_908_path_3739_0_31_377 0_32_36_230_37_80_3818_81_103_3841_10 4_344_5872_345_350_1135_3	26544	trypsinogen 2	303	3.39E-101	70.50%	0.803 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24264 (PANTHER); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR009003 (SUPERFAMILY)
2146	c40947_g1_i2_len_916_path_3739_0_31_377 0_32_36_230_37_80_3818_81_103_3841_10 4_344_3219_345_363_5941_5	20101	trypsin 3	305	1.84E-105	71.90%	0.753Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)

2147	c40947_g1_i3_len_1324_path_2469_0_752_3_219_753_771_5941_772_777_3243_778_784_364_785_817_4785_818_1_5	17711	trypsinogen 2	441	3.09E-105	72.30%	0.753 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
2148	c40953_g3_i1_len_1971_path_1822_0_250_2_073_251_342_6737_343_361_6105_362_371_6115_372_374_6788_375_5	855	apolipoprotein d	657	1.05E-08	45.00%	0.099	IPR012674 (G3DSA:2.40.128.GENE3D); IPR000566 (PFAM); PTHR10612 (PANTHER); PTHR10612:SF7 (PANTHER); IPR022272 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011038 (SUPERFAMILY)
2149	c40964_g1_i1_len_3530_path_150_0_32_77_33_81_4906_82_343_5168_344_3529_3	930	glucose-6-phosphate isomerase	1177	0	87.70%	0.105	IPR001672 (PRINTS); G3DSA:3.40.50.10490 (GENE3D); IPR001672 (PFAM); IPR023096 (G3DSA:1.10.1390.GENE3D); PTHR11469:SF4 (PANTHER); IPR001672 (PANTHER); IPR018189 (PROSITE_PATTERNS); IPR018189 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001672 (PROSITE_PROFILES); IPR001672 (HAMAP); SSF53697 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2150	c40972_g16_i1_len_2015_path_6245_0_80_6_326_81_83_6329_84_1811_8057_1812_185_0_5793_1851_1861_3891_0	896	phosphatidylethanolamine-binding protein	672	1.17E-90	79.90%	0.125	IPR008914 (G3DSA:3.90.280.GENE3D); IPR008914 (PFAM); PTHR11362 (PANTHER); IPR008914 (SUPERFAMILY)
2151	c40973_g1_i1_len_2249_path_8887_0_323_2_583_324_625_2885_626_630_2890_631_67_9_2939_680_707_2967_7_4	1296	cell recognition protein caspr4 isoform 5	750	2.17E-69	52.00%	0.127	Coil (COILS); IPR001073 (SMART); IPR000885 (PFAM); IPR001073 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); IPR008983 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF575 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001073 (PROSITE_PROFILES); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); IPR002181 (SUPERFAMILY); IPR008983 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2152	c40973_g1_i2_len_2082_path_17592_0_36_2_461_37_99_2524_100_105_2530_106_132_2_557_133_158_2583_159_5	1224	contactin associated protein 1	694	7.92E-69	51.90%	0.255	Coil (COILS); IPR001073 (SMART); IPR014716 (G3DSA:3.90.215.GENE3D); IPR008983 (G3DSA:2.60.120.GENE3D); IPR000885 (PFAM); IPR001073 (PFAM); PTHR10127:SF575 (PANTHER); PTHR10127 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR001073 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); IPR002181 (SUPERFAMILY); IPR008983 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2153	c40973_g1_i3_len_2084_path_17592_0_36_2_461_37_99_2524_100_105_2530_106_132_2_557_133_158_2583_159_4	1280	cell recognition protein caspr4 isoform 5	695	1.22E-69	52.20%	0.127	Coil (COILS); IPR001073 (SMART); IPR000885 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); IPR001073 (PFAM); PTHR10127 (PANTHER); PTHR10127:SF575 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR001073 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); IPR002181 (SUPERFAMILY); IPR008983 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

2154	c40981_g1_i1_len_1043_path_821_0_56_878_57_116_2465_117_133_2482_134_176_396_177_264_484_265_552_5	39	zinc finger protein 699-like isoform x1	347	1.61E-22	62.00%	0.102	IPR015880 (SMART); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR026590 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2155	c40981_g1_i4_len_900_path_1196_0_205_87_8_206_265_5380_266_282_2482_283_325_2_523_326_413_484_414_4	21	zinc finger protein 77 isoform x1	300	2.86E-31	59.90%	0.596 Y	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2156	c40981_g2_i1_len_418_path_1871_0_231_21_03_232_256_1035_257_417_4	11	zinc finger protein 699-like	139	1.52E-23	62.30%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

	c40983_g1_i1_len_12655_path_2321_0_1055 1_28820__10552_12309_14604_12310_1231 1_711_12312_12359_146_2	17356	twitchin isoform x4	4218	0	80.90%	0.101	(SMART); IPR002290 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897-SF155 (PANTHER); PTHR19897 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR011009 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
	c40983_g1_i2_len_2405_path_28171_0_301_ 28820__302_2059_14604_2060_2061_711_2 062_2109_14651_2110_2_0	11442	twitchin isoform x2	802	7.56E-133	76.20%	0.125	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
	c40984_g1_i4_len_630_path_3268_0_45_761 9_46_58_179_59_177_298_178_201_2687_2 02_286_2770_287_314_800_0	42	carboxyl cholinesterase 5as	210	7.77E-10	72.30%	0.251	IPR023612 (PRINTS); IPR013856 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); G3DSA:1.10.390.10 (GENE3D); IPR011096 (PFAM); IPR025711 (PFAM); IPR001570 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
	c41001_g1_i1_len_564_path_1238_0_210_47 93_211_278_1517_279_322_3731_323_563_ 0	51	hemagglutinin	188	2.58E-42	67.60%	0.098	IPR001570 (PFAM); G3DSA:1.10.390.10 (GENE3D); SSF55486 (SUPERFAMILY)
	c41001_g1_i2_len_1756_path_1_0_252_254_ 253_408_410__409_648_650_649_660_662_ 661_795_797_796_820_8_1	887	hemagglutinin proteinase	585	1.24E-101	54.70%	0.125	IPR023612 (PRINTS); IPR013856 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); G3DSA:1.10.390.10 (GENE3D); IPR011096 (PFAM); IPR025711 (PFAM); IPR001570 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)

[illegible]

2166	c41047_g1_i2_len_5318_path_207_0_150_35 8_151_2000_102_2001_3354_206__3355_40 29_23028_4030_4031_2_1	5435	muscle m-line assembly protein unc-89	1773	0	75.60%	0.291	IPR003599 (SMART); IPR003598 (SMART); IPR003961 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR003961 (PFAM); G3DSA:3.30.200.20 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR020675 (PANTHER); PTHR22964:SF45 (PANTHER); IPR017441 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR011009 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR011009 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2167	c41057_g1_i1_len_17457_path_48298_0_40_49592_41_42_6455_43_4679_11092_4680_14322_20735_14323_174_3	16841	nesprin-1 isoform x4	5819	0	69.60%	0.111	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR018159 (SMART); G3DSA:1.20.58.60 (GENE3D); G3DSA:1.20.58.60 (GENE3D); G3DSA:1.20.58.60 (GENE3D); G3DSA:1.20.58.60 (GENE3D); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY)
2168	c41057_g1_i3_len_20799_path_1_0_1905_19_07_1906_3567_3569_3568_3683_3685_3684_3687_3689_3688_3721_37_3	24783	nesprin-1 isoform x3	6933	6.36E-166	73.40%	0.142	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR018159 (SMART); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY)
2169	c41057_g1_i4_len_14388_path_48298_0_40_49592_41_42_6455_43_4679_11092_4680_14322_48157_14323_143_3	16479	nesprin-1 isoform x3	4796	4.08E-166	73.20%	0.142	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR018159 (SMART); SSF46966 (SUPERFAMILY); SSF46966 (SUPERFAMILY)
2170	c41070_g2_i1_len_1696_path_731_0_29_760_30_371_13458_372_1670_8548_1671_169_5_0	571	nac-alpha domain-containing protein 1	566	7.93E-09	43.56%	0.106	Coil (COILS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
2171	c41070_g2_i3_len_2093_path_11260_0_121_13322_122_125_11386_126_323_11584_324_324_6621_325_512_2440_1	1631	von willebrand factor type a domain protein	698	1.39E-16	47.30%	0.196	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
2172	c41070_g2_i4_len_1932_path_6458_0_29_17_3_30_163_6621_164_351_2440_352_353_69_99_354_607_13458_608_2	2056	von willebrand factor type a domain protein	644	1.23E-16	47.30%	0.14	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
2173	c41070_g2_i5_len_4057_path_6458_0_29_17_3_30_163_6621_164_351_6808_352_543_24_40_544_545_6999_546_799_2	3823	neurofilament heavy polypeptide	1352	1.93E-33	44.90%	0.14	Coil (COILS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
2174	c41070_g2_i6_len_945_path_12998_0_216_6_999_217_470_11873_471_914_731_915_944_0	400	lpxtg-motif cell wall anchor domain protein	315	9.78E-10	42.60%	0.196	no IPS match
2175	c41078_g1_i1_len_2243_path_2583_0_257_2_841_258_277_2861_278_305_7154_306_329_8234_330_382_2966_383_1	268	thromboxane a synthase-like protein	748	1.49E-116	56.20%	0.11	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24292 (PANTHER); PTHR24292:SF24 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2176	c41078_g1_i2_len_2240_path_2583_0_257_4_915_258_277_2861_278_305_2889_306_382_2966_383_400_2984_401_1	244	cytochrome p450 partial	747	1.93E-109	56.80%	0.11	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24292 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

Supplementary Table 7

2181	c41079_g1_i6_len_2680_path_33_0_27_60_2 8_147_180_148_512_11717_513_523_686_ _524_1002_2400_1003_3	6125	projectin short variant	894	0	75.10%	0.276	Coil (COILS); IPR003598 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2182	c41079_g1_i7_len_2809_path_33_0_27_60_2 8_147_435_148_273_11353_274_276_180_ 277_641_11717_642_652_3	6123	muscle m-line assembly protein unc-89-like	937	0	75.30%	0.276	Coil (COILS); Coil (COILS); IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2183	c41079_g1_i8_len_2698_path_33_0_27_60_2 8_147_180_148_512_11717_513_523_686_ _524_1002_2400_1003_3	6021	projectin short variant	900	0	73.60%	0.276	Coil (COILS); IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2184	c41089_g1_i1_len_2262_path_3267_0_134_3 401_135_165_2662_166_219_3485_220_240 _3506_241_268_3534_269_1	2921	cytochrome p450 2j6-like	754	2.66E-105	55.80%	0.114	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2185	c41089_g1_i2_len_2262_path_3267_0_134_2 631_135_165_2662_166_219_8768_220_240 _3506_241_268_8024_269_1	1848	cytochrome p450 2j6-like	754	5.66E-108	56.80%	0.107	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2186	c41099_g3_i1_len_928_path_3576_0_57_363 4_58_376_10181_377_378_728_379_413_10 210_414_414_10211_415_4_0	70	mariner mos1 transposase	310	7.64E-26	58.30%	0.171	PTHR23345 (PANTHER); PTHR23345:SF1 (PANTHER); IPR001846 (PROSITE_PROFILES)
2187	c41101_g1_i1_len_4153_path_6091_0_113_5 186_114_892_6981_893_894_4626_895_3 286_1368_3287_3287_2	15211	ferritin 2 light chain homologue	1384	9.29E-33	54.10%	0.352 Y	IPR008331 (PFAM); IPR012347 (G3DSA:1.20.1260.GENE3D); IPR001519 (PANTHER); PTHR11431:SF28 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY); TMhelix (TMHMM)

2188	c41101_g1_i2_len_4395_path_4831_0_355_5 186_356_1134_6981_1135_1136_4626__11 37_3528_1368_3529_3_1	15083	ferritin 2 light chain homologue	1465	1.36E-32	54.20%	0.470Y	IPR008331 (PFAM); IPR012347 (G3DSA:1.20.1260.GENE3D); PTHR11431:SF28 (PANTHER); IPR001519 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009040 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009078 (SUPERFAMILY)
2189	c41104_g1_i1_len_9451_path_9778_0_3319_ 13096_3320_3344_13121_3345_9450_1	4119	low quality protein: hemocytin-like	3150	4.86E-69	42.20%	0.267	IPR001846 (SMART); IPR001007 (SMART); PTHR11339 (PANTHER); IPR001007 (PROSITE_PATTERNS); IPR001007 (PROSITE_PATTERNS); PD968187 (PRODOM); IPR006207 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY); IPR002919 (SUPERFAMILY)
2190	c41111_g2_i1_len_1336_path_1124_0_1121_ 2246_1122_1239_18022_1240_1257_18022_ 1258_1275_18022_1276_12_3	1906	alpha-l-fucosidase	446	7.26E-08	55.10%	0.104	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2191	c41111_g2_i1_len_1336_path_1124_0_1121_ 2246_1122_1239_18022_1240_1257_18022_ 1258_1275_18022_1276_12_4	1906	hypothetical protein	445	2.73E-08	51.25%	0.107	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
2192	c41111_g2_i2_len_1318_path_1124_0_1121_ 2246_1122_1239_18022_1240_1257_18022_ 1258_1275_18038_1276_12_3	1922	---NA---	440			0.105	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2193	c41111_g2_i2_len_1318_path_1124_0_1121_ 2246_1122_1239_18022_1240_1257_18022_ 1258_1275_18038_1276_12_4	1922	hypothetical protein	439	1.25E-06	54.00%	0.105	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
2194	c41113_g1_i1_len_5501_path_5479_0_1972_ 7452_1973_1984_7464_1985_3143_8623_3 144_3146_8626_3147_32_1	4943	vitellogenin 2	1834	0	44.90%	0.138	IPR001747 (SMART); IPR001846 (SMART); IPR015816 (G3DSA:2.30.230.GENE3D); IPR001846 (PFAM); IPR001747 (PFAM); IPR015255 (PFAM); IPR011030 (G3DSA:1.25.10.GENE3D); PTHR23345:SF1 (PANTHER); PTHR23345 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001846 (PROSITE_PROFILES); IPR001747 (PROSITE_PROFILES); IPR011030 (SUPERFAMILY); IPR015819 (SUPERFAMILY); IPR015819 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2195	c41113_g1_i2_len_5285_path_5479_0_1972_ 7452_1973_1984_7464_1985_3143_8623_3 144_3146_8626_3147_32_1	3335	vitellogenin 2	1762	0	44.90%	0.138	IPR001846 (SMART); IPR001747 (SMART); IPR015816 (G3DSA:2.30.230.GENE3D); IPR015255 (PFAM); IPR001747 (PFAM); IPR001846 (PFAM); IPR011030 (G3DSA:1.25.10.GENE3D); PTHR23345 (PANTHER); PTHR23345:SF1 (PANTHER); IPR001846 (PROSITE_PROFILES); IPR001747 (PROSITE_PROFILES); IPR011030 (SUPERFAMILY); IPR015819 (SUPERFAMILY); IPR015819 (SUPERFAMILY)

	c41124_g3_i1_len_9227_path_30602_0_2144 _10445_2145_2258_10559_2259_4373_126 74_4374_4386_12687_43_0	5328	myosin light chain smooth muscle	3076	0	58.50%	0.114	Coil (COILS); IPR003599 (SMART); IPR002290 (SMART); IPR003961 (SMART); IPR003598 (SMART); IPR013106 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); IPR003961 (PFAM); IPR020675 (PANTHER); PTHR22964:SF56 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR011009 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
	c41124_g3_i2_len_8912_path_30602_0_2144 _10559_2145_4259_12674_4260_4272_126 87_4273_4296_12711_42_0	5183	muscle m-line assembly protein unc-89 isoform x2	2971	0	57.30%	0.114	Coil (COILS); IPR003961 (SMART); IPR003598 (SMART); IPR002290 (SMART); IPR013106 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000719 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR020675 (PANTHER); PTHR22964:SF56 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR011009 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

	c41124_g3_i3_len_8996_path_30602_0_2144 _10445_2145_2258_10559_2259_4373_126 74_4374_4386_12687_43_0	5245	muscle m-line assembly protein unc-89 isoform x2	2999	0	56.30%	0.114	Coil (COILS); IPR003599 (SMART); IPR013106 (SMART); IPR003961 (SMART); IPR003598 (SMART); IPR002290 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR020675 (PANTHER); PTHR22964:SF56 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR011009 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
	c41124_g3_i4_len_9026_path_30602_0_2144 _10445_2145_2258_10559_2259_4373_126 74_4374_4386_12687_43_0	5346	muscle m-line assembly protein unc-89 isoform x1	3009	0	56.50%	0.114	Coil (COILS); IPR003599 (SMART); IPR003961 (SMART); IPR013106 (SMART); IPR003598 (SMART); IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR000719 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR020675 (PANTHER); PTHR22964:SF56 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR011009 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)

	c41124_g3_i5_len_9627_path_30602_0_2144_10445_2145_2258_10559_2259_4373_12674_4374_4386_12687_43_0	5214	muscle m-line assembly protein unc-89 isoform x2	3209	0	56.00%	0.114		Coil (COILS); IPR002290 (SMART); IPR003599 (SMART); IPR013106 (SMART); IPR003961 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000719 (PFAM); IPR013098 (PFAM); G3DSA:1.10.510.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR22964:SF56 (PANTHER); IPR020675 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR011009 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
	c41126_g1_i1_len_6399_path_239_0_3382_3618_3383_5179_5413_5180_5180_5414_5181_5562_14950_5563_5771_0	3152	protein mesh isoform x2	2133	0	70.70%	0.341	Y	IPR005533 (SMART); IPR000436 (SMART); IPR001846 (SMART); IPR003886 (SMART); IPR005533 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR001846 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000436 (PFAM); IPR003886 (PFAM); IPR002909 (PFAM); PTHR13802:SF41 (PANTHER); PTHR13802 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005533 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR014756 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
	c41126_g1_i2_len_3770_path_239_0_3382_13629_3383_3769_0	1335	protein mesh isoform x1	1257	0	69.70%	0.341	Y	IPR001846 (SMART); IPR000436 (SMART); IPR005533 (SMART); IPR003886 (SMART); IPR001846 (PFAM); IPR005533 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR002909 (PFAM); IPR000436 (PFAM); IPR003886 (PFAM); PTHR13802:SF41 (PANTHER); PTHR13802 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000436 (PROSITE_PROFILES); IPR005533 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR003886 (PROSITE_PROFILES); IPR014756 (SUPERFAMILY); IPR000436 (SUPERFAMILY); TMhelix (TMHMM)

[illegible]

2205	c41130_g1_i6_len_6103_path_6838_0_705_1 3048_706_802_22_803_928_14222_929_929 _14223_930_931_13146_93_1	3105	lim domain-binding protein 3	2034	4.62E-104	70.00%	0.144	IPR006643 (SMART); IPR001781 (SMART); IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001781 (PFAM); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001478 (PFAM); PTHR24214 (PANTHER); PTHR24214:SF29 (PANTHER); IPR001781 (PROSITE_PATTERNS); IPR001781 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001781 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001781 (PROSITE_PROFILES); SSF57716 (SUPERFAMILY); SSF57716 (SUPERFAMILY); SSF57716 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2206	c41130_g1_i7_len_5770_path_6838_0_705_7 544_706_866_14223_867_868_7706_869_10 10_7848_1011_1161_596_1_1	3249	lim domain-binding protein 3	1923	5.52E-103	74.50%	0.144	IPR001478 (SMART); IPR006643 (SMART); IPR001781 (SMART); IPR001478 (PFAM); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001781 (PFAM); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR24214 (PANTHER); PTHR24214:SF29 (PANTHER); IPR001781 (PROSITE_PATTERNS); IPR001781 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001781 (PROSITE_PROFILES); IPR001781 (PROSITE_PROFILES); SSF57716 (SUPERFAMILY); SSF57716 (SUPERFAMILY); IPR001478 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

	c41130_g1_i8_len_5842_path_6838_0_705_7 544_706_866_14223_867_868_7706_869_10 10_7848_1011_1161_596_1_1	3220	lim domain-binding protein 3	1947	6.23E-103	74.50%	0.144	IPR006643 (SMART); IPR001478 (SMART); IPR001781 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001478 (PFAM); IPR001781 (PFAM); PTHR24214:SF29 (PANTHER); PTHR24214 (PANTHER); IPR001781 (PROSITE_PATTERNS); IPR001781 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001781 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); SSF57716 (SUPERFAMILY); IPR001478 (SUPERFAMILY); SSF57716 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
	c41130_g1_i9_len_5733_path_6838_0_705_7 544_706_866_14223_867_868_7706_869_10 10_7848_1011_1161_596_1_1	3002	lim domain-binding protein 3	1911	2.94E-102	72.40%	0.144	IPR001781 (SMART); IPR001478 (SMART); IPR006643 (SMART); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001781 (G3DSA:2.10.110.GENE3D); IPR001781 (PFAM); IPR001478 (PFAM); PTHR24214 (PANTHER); PTHR24214:SF29 (PANTHER); IPR001781 (PROSITE_PATTERNS); IPR001781 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001781 (PROSITE_PROFILES); IPR001781 (PROSITE_PROFILES); IPR001781 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); SSF57716 (SUPERFAMILY); SSF57716 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
	c41135_g1_i1_len_555_path_32257_0_2_753 55_3_8_75361_9_15_75368_16_20_75373_2 1_25_75378_26_30_75388_0	25	---NA---	185			0.1	no IPS match

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[illegible]

2229	c41222_g1_i3_len_8758_path_9512_0_189_9 701_190_211_411_212_285_9796_286_759_ _10268__760_1368_6_5	6095		centromeric protein	2919	0	56.00%	0.102	Coil (COILS); IPR027881 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
2230	c41222_g1_i4_len_8614_path_9512_0_189_9 701_190_211_411_212_285_9796_286_759_ _10268__760_1368_6_5	5952		centromeric protein	2871	0	56.20%	0.102	Coil (COILS); IPR027881 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
2231	c41222_g1_i5_len_8755_path_9512_0_189_9 701_190_211_411_212_285_9796_286_759_ _10268__760_1368_63_5	6143		centromeric protein	2918	0	56.20%	0.102	Coil (COILS); IPR027881 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
2232	c41231_g1_i1_len_1461_path_781_0_461_12 43_462_550_4219_551_575_4244_576_609_ 4013_610_636_4040_637_8_3	315	tlf5a_tactr	ame: full=techylectin-5a flags: precursor	487	2.44E-63	63.80%	0.127	IPR002181 (SMART); IPR014716 (G3DSA:3.90.215.GENE3D); IPR014715 (G3DSA:4.10.530.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); TMhelix (TMHMM)
2233	c41231_g1_i3_len_2404_path_8813_0_75_14 658_76_162_8972_163_194_9003_195_198_ 8262_199_1188_1243_1189_3	519	tlf5a_tactr	ame: full=techylectin-5a flags: precursor	802	7.31E-63	62.90%	0.127	IPR002181 (SMART); IPR002181 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); IPR014715 (G3DSA:4.10.530.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); TMhelix (TMHMM)
2234	c41231_g1_i4_len_2191_path_8813_0_75_14 658_76_162_8972_163_194_9003_195_198_ 8262_199_1188_1243_1189_3	535	tlf5a_tactr	ame: full=techylectin-5a flags: precursor	731	5.23E-63	63.20%	0.127	IPR002181 (SMART); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PFAM); IPR014715 (G3DSA:4.10.530.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); TMhelix (TMHMM)
2235	c41238_g4_i1_len_3372_path_10962_0_316_ 11279_317_2875_13904_2876_3218_6186_ 1_3219_3371_5	3521		low quality protein: titin-like	1124	0	72.20%	0.166	Coil (COILS); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF149 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

Supplementary Table 7

2240	c41246_g5_i1_len_675_path_22060_0_13_22 074_14_17_22078_18_23_22084_24_25_220 86_26_29_22090_30_32_96_3	31	zinc finger protein	225	1.39E-17	55.90%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2241	c41246_g5_i2_len_639_path_22060_0_13_22 074_14_17_22078_18_23_22093_24_25_137 1_26_37_1383_38_45_1182_3	37	zinc c2h2 type domain-containing protein	213	3.34E-16	54.50%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2242	c41251_g5_i9_len_1896_path_16911_0_72_1 6984_73_1823_8148_1824_1824_18735_182 5_1825_9152_1826_1837_1_1	665	mitochondrial-processing peptidase subunit beta	632	0	84.60%	0.179	IPR007863 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); IPR011765 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); PTHR11851:SF103 (PANTHER); PTHR11851 (PANTHER); IPR001431 (PROSITE_PATTERNS); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY)
2243	c41267_g3_i1_len_1702_path_6274_0_306_6 581_307_1373_4136_1374_1397_4160_1398 1531_4294_1532_1557_33_2	390	nucleolar protein 56	567	0	87.50%	0.25	Coil (COILS); IPR012976 (SMART); IPR012974 (PFAM); IPR002687 (PFAM); IPR012976 (PFAM); PTHR10894:SF0 (PANTHER); PTHR10894 (PANTHER); IPR002687 (PROSITE_PROFILES); SSF89124 (SUPERFAMILY)
2244	c41269_g2_i1_len_1066_path_6263_0_935_2 706_936_1065_0	441	phospholipase a2-like	356	1.42E-39	62.00%	0.149	IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PFAM); PTHR12253 (PANTHER); IPR013090 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016090 (SUPERFAMILY)
2245	c41271_g1_i1_len_2199_path_5779_0_453_2 425_454_545_2517_546_606_6383_607_620 _2361_621_682_6458_683_0	188	probable cytochrome p450 49a1	733	7.30E-133	61.30%	0.129	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24305:SF49 (PANTHER); PTHR24305 (PANTHER); IPR017972 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
2246	c41271_g1_i2_len_2224_path_5779_0_453_6 232_454_545_2517_546_606_2347_607_620 _2361_621_682_8193_683_0	260	probable cytochrome p450 49a1-like	742	2.29E-137	61.30%	0.129	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24305:SF49 (PANTHER); PTHR24305 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
2247	c41271_g1_i4_len_587_path_1006_0_221_12 28_222_262_7343_263_300_9411_301_311_ 7389_312_351_2815_352_4_0	36	cytochrome p450 partial	196	2.01E-35	66.90%	0.145	IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24305 (PANTHER); PTHR24305:SF49 (PANTHER); IPR001128 (SUPERFAMILY)
2248	c41272_g1_i1_len_967_path_7695_0_24_401 3_25_90_4079_91_130_4119_131_340_107 56_341_353_4339_354_3_4	159	g-protein coupled receptor mth2 isoform x1	322	1.41E-41	57.50%	0.159	IPR000832 (PFAM); PTHR12011 (PANTHER); PTHR12011:SF164 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

2249	c41272_g1_i2_len_3737_path_7695_0_24_40 13_25_90_4079_91_130_4119__131_340_10 756_341_353_4339_354_5	449	g-protein coupled receptor mth2-like isoform x2	1245	2.22E-88	54.00%	0.14	IPR023311 (G3DSA:2.170.180.GENE3D); IPR000832 (PFAM); IPR010596 (PFAM); PTHR12011:SF164 (PANTHER); PTHR12011 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017981 (PROSITE_PROFILES); SSF63877 (SUPERFAMILY); SSF63877 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
2250	c41290_g1_i1_len_452_path_15739_0_85_32 694_86_109_17539_110_419_15538_420_42 7_8970_428_451_4	20	enteropeptidase isoform 2 precursor	151	2.70E-32	64.60%	0.126	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2251	c41290_g2_i1_len_2407_path_1_0_1148_115 0_1149_1176_15278_1177_1411_1404_1412 _1435_1428_1436_1447_14_3	246	urokinase-type plasminogen activator	803	6.12E-61	56.70%	0.117	IPR001314 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
2252	c41290_g2_i2_len_2656_path_11643_0_358 12002_359_433_12076_434_459_8487_460 513_32463_514_1829_1347_4	212	urokinase-type plasminogen activator	885	8.52E-57	55.10%	0.108	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2253	c41290_g2_i3_len_2285_path_1_0_1148_115 0_1149_1176_15278_1177_1411_1404_1412 _1435_1428_1436_1447_14_4	252	urokinase-type plasminogen activator	762	1.68E-53	53.90%	0.108	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
2254	c41290_g2_i5_len_4402_path_1_0_1148_115 0_1149_1176_15278_1177_1411_1404_1412 _1435_1428_1436_1447_14_3	420	urokinase-type plasminogen activator	1468	8.15E-59	56.00%	0.172	IPR002172 (PRINTS); IPR003609 (SMART); IPR001254 (SMART); IPR002172 (SMART); IPR003014 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001254 (PFAM); G3DSA:3.50.4.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

2255	c41290_g2_i7_len_1986_path_1_0_1148_115_0_1149_1176_15278_1177_1411_1404_1412_1435_1428_1436_1447_14_5	174	urokinase-type plasminogen activator	662	1.88E-56	55.00%	0.105	IPR001314 (PRINTS); IPR001254 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
2256	c41290_g3_i1_len_2939_path_24287_0_59_1_5982_60_185_24469_186_201_8710_202_5_25_24801_526_539_2481_5	670	urokinase-type plasminogen activator	979	1.07E-58	48.20%	0.1	IPR002172 (PRINTS); IPR003609 (SMART); IPR001254 (SMART); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001254 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24265 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2257	c41290_g3_i2_len_3125_path_24287_0_59_1_5982_60_185_24469_186_201_8710_202_5_25_24801_526_539_2481_5	642	urokinase-type plasminogen activator	1041	2.36E-58	46.30%	0.1	IPR002172 (PRINTS); IPR002172 (SMART); IPR003609 (SMART); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24265 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2258	c41290_g3_i3_len_711_path_30431_0_23_25_438_24_389_25801_390_448_21094_449_4_57_20894_458_544_3321_3	161	complement component factor i	237	4.09E-21	53.30%	0.114	IPR001314 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); PTHR24265:SF76 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR003609 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
2259	c41290_g4_i1_len_1130_path_19551_0_875_1150_876_903_1178_904_1129_4	102	adhesive serine protease	377	5.55E-21	62.90%	0.279	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)

2260	c41306_g9_i1_len_3450_path_6053_0_2341_1704_2342_3167_32093_3168_3177_32103_3178_3181_32107_3182_31_5	1897	torsin- partial	1150	4.40E-104	66.80%	0.212	Coil (COILS); IPR010448 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR010448 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2261	c41306_g9_i3_len_1111_path_1684_0_19_17_04_20_845_32093_846_855_32103_856_859_32107_860_861_32109_86_3	393	torsin-1b-like isoform x1	371	1.47E-77	66.90%	0.2	IPR001270 (PRINTS); IPR010448 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR010448 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY)
2262	c41306_g9_i5_len_3433_path_6053_0_2341_1704_2342_3167_32093_3168_3177_32103_3178_3181_32107_3182_31_3	1897	torsin- partial	1145	7.02E-104	66.80%	0.2	Coil (COILS); IPR027417 (G3DSA:3.40.50.GENE3D); IPR010448 (PFAM); IPR010448 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2263	c41328_g1_i1_len_2313_path_4288_0_384_4_673_385_413_4702_414_478_4766_479_494_1390_495_556_4843_557_4	1180	amine oxidase	771	7.40E-167	65.00%	0.118	IPR001613 (PRINTS); G3DSA:3.90.660.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002937 (PFAM); PF13450 (PFAM); G3DSA:1.10.405.10 (GENE3D); PTHR10742:SF253 (PANTHER); PTHR10742 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY)
2264	c41328_g1_i2_len_2604_path_4288_0_384_4_673_385_413_4702_414_478_4766_479_494_1390_495_556_4843_557_4	1010	amine oxidase	868	5.17E-166	65.10%	0.103	IPR001613 (PRINTS); PF13450 (PFAM); G3DSA:3.90.660.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); G3DSA:1.10.405.10 (GENE3D); IPR002937 (PFAM); PTHR10742:SF253 (PANTHER); PTHR10742 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54373 (SUPERFAMILY); SSF51905 (SUPERFAMILY)
2265	c41328_g1_i3_len_2326_path_4288_0_384_8_381_385_426_4702_427_491_1374_492_507_1390_508_569_4843_570_4	1184	amine oxidase	775	8.92E-167	65.10%	0.118	IPR001613 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PF13450 (PFAM); G3DSA:3.90.660.10 (GENE3D); IPR002937 (PFAM); G3DSA:1.10.405.10 (GENE3D); PTHR10742:SF253 (PANTHER); PTHR10742 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54373 (SUPERFAMILY); SSF51905 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2266	c41335_g1_i1_len_2793_path_27212_0_504_29462_505_567_27778_568_640_27850_641_650_17224_651_2052_220_1	294	cadherin egf lag seven-pass g-type receptor 2	931	7.68E-18	41.00%	0.285	IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); TMhelix (TMHMM)
2267	c41335_g2_i1_len_2638_path_22083_0_61_2_2144_62_808_22891_809_811_22894_812_1_556_16558_1557_2369_169_0	1324	protocadherin fat partial	880	9.11E-14	45.00%	0.303	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

2276	c41368_g19_i1_len_2321_path_23295_0_255_23546_256_258_17316_259_440_23725__4_41_2294_43102_2295_22_0	793	cathepsin I-associated protein	774	1.96E-78	60.90%	0.298	IPR000782 (SMART); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); IPR000782 (G3DSA:2.30.180.GENE3D); PTHR10900 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2277	c41381_g1_i2_len_2480_path_598_0_352_95_1_353_366_965_367_367_966_368_595_235_95_596_606_23606_607_61_5	3839	trypsinogen 2	826	1.82E-69	61.70%	0.111	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
2278	c41381_g1_i6_len_2521_path_7891_0_212_8_104_213_228_23318_229_236_8128_237_26_4_23328_265_285_23350_2_5	3764	trypsinogen 2	840	3.38E-65	61.80%	0.111	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
2279	c41381_g1_i9_len_2484_path_7891_0_212_8_104_213_228_23318_229_236_8128_237_26_4_23328_265_285_19468_2_5	3685	trypsinogen 2	828	4.10E-69	61.70%	0.111	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2280	c41392_g2_i1_len_1334_path_17723_0_1274_2376_1275_1333_3	539	gamma-glutamyl hydrolase	445	9.27E-100	65.80%	0.183	IPR029062 (G3DSA:3.40.50.GENE3D); IPR011697 (PFAM); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY)
2281	c41392_g2_i2_len_1498_path_17723_0_1274_24682_1275_1279_10622_1280_1497_5	503	gamma-glutamyl hydrolase	499	2.56E-99	66.10%	0.203	IPR011697 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY)
2282	c41392_g2_i3_len_1377_path_17723_0_1274_24682_1275_1279_2338_1280_1317_2376_1318_1376_4	485	gamma-glutamyl hydrolase	459	1.45E-99	66.10%	0.128	IPR029062 (G3DSA:3.40.50.GENE3D); IPR011697 (PFAM); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY)

	c41394_g2_i1_len_6022_path_2077_0_296_1 9816_297_399_19861_400_400_19862_401_ 401_19863_402_411_19873_4	13902	pacifastin light chain	2007	5.30E-58	45.00%	0.269	IPR002223 (PRINTS); IPR003645 (SMART); IPR006552 (SMART); IPR002223 (SMART); IPR008037 (PFAM); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR001190 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (TMhelix (TMHMM)); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
	c41421_g5_i2_len_2744_path_3018_0_140_3 159_141_143_3162_144_190_18135_191_22 4_18163_225_246_18185_2_4	14360	perlucin 6	915	3.64E-12	44.50%	0.429Y	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY) Coil (COILS); IPR003593 (SMART); IPR005937 (TIGRFAM); IPR003959 (PFAM); G3DSA:1.10.8.60 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23073.SF12 (PANTHER); PTHR23073 (PANTHER); IPR003960 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY)
	c41452_g3_i1_len_1404_path_7135_0_1403_ 4	147	26s protease regulatory subunit 8	468	0	97.10%	0.1	IPR023796 (SMART); G3DSA:3.30.497.10 (GENE3D); G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023796 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
	c41454_g5_i1_len_1657_path_3717_0_221_4 115_222_1293_35855_1294_1295_35857_12 96_1296_5190_1297_1656_2	127	serpin 3	552	3.62E-104	65.10%	0.14	IPR023796 (SMART); G3DSA:3.30.497.10 (GENE3D); G3DSA:2.30.39.10 (GENE3D); IPR023795 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023796 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
	c41454_g5_i2_len_1838_path_3717_0_221_3 939_222_397_4115_398_1469_35855_1470_ 1471_35857_1472_1472_75_1	131	serpin 3	613	1.70E-97	63.60%	0.181	G3DSA:2.30.39.10 (GENE3D); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
	c41454_g5_i3_len_1833_path_3717_0_221_3 939_222_397_4115_398_1469_35855_1470_ 1471_35857_1472_1472_51_1	142	serpin 3	611	1.82E-104	64.40%	0.181	IPR023796 (SMART); G3DSA:3.30.497.10 (GENE3D); IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
	c41454_g5_i4_len_1761_path_3717_0_221_3 939_222_397_4115_398_1469_35855_1470_ 1471_21297_1472_1760_1	125	serpin 3	587	1.07E-98	63.70%	0.181	IPR023796 (SMART); IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); G3DSA:3.30.497.10 (GENE3D); IPR000215 (PANTHER); PTHR11461.SF52 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)

2290	c41471_g8_i1_len_9865_path_34383_0_1_17_617_2_143_17759_144_9864_3	7231	lipophorin precursor	3289	0	44.30%	0.124	Coil (COILS); IPR001846 (SMART); IPR009454 (PFAM); IPR011030 (G3DSA:1.25.10.GENE3D); IPR001747 (PFAM); IPR015817 (G3DSA:2.20.50.GENE3D); IPR015255 (PFAM); IPR001846 (PFAM); IPR015818 (G3DSA:2.20.80.GENE3D); IPR014853 (PFAM); PTHR23345 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001747 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR011030 (SUPERFAMILY); IPR015819 (SUPERFAMILY)
2291	c41473_g1_i1_len_9142_path_12739_0_87_1_2827_88_170_12910_171_264_13003_265_3_36_3170_337_470_13207_4_1	91294	low quality protein: hemocytin-like	3047	5.80E-45	38.90%	0.154	PTHR11339 (PANTHER); PTHR11339:SF25 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR006207 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY); TMhelix (TMHMM)
2292	c41504_g1_i1_len_2910_path_2128_0_21_18_842_22_45_2174_46_62_2191_63_121_2250_122_125_2254_126_282_2_4	1510	gag-like protein	970	2.36E-14	45.40%	0.143	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR001878 (SMART); IPR001878 (G3DSA:4.10.60.GENE3D); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
2293	c41586_g1_i1_len_1355_path_1333_0_1354_5	48	rna polymerase ii-associated protein 3	451	6.14E-70	61.30%	0.103	Coil (COILS); Coil (COILS); IPR019734 (SMART); IPR001440 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PF13414 (PFAM); PTHR22904 (PANTHER); PTHR22904:SF292 (PANTHER); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY)
2294	c41669_g1_i1_len_1665_path_1643_0_1664_1	238	macrophage mannose receptor 1-like	555	1.20E-52	46.50%	0.101	IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803:SF16 (PANTHER); PTHR22803 (PANTHER); IPR018378 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2295	c41688_g1_i1_len_383_path_361_0_382_3	27	folistatin-related protein 5-like	128	3.93E-60	85.10%	0.099	PTHR10913 (PANTHER); PTHR10913:SF14 (PANTHER)
2296	c41720_g1_i1_len_881_path_859_0_880_0	41	plexin domain-containing protein 2-like	294	9.37E-44	48.50%	0.144	IPR016201 (SMART); G3DSA:3.30.1680.10 (GENE3D); PTHR13055:SF12 (PANTHER); PTHR13055 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2297	c41721_g1_i1_len_266_path_244_0_265_2	4	receptor-type tyrosine-protein phosphatase beta-partial	88	3.37E-14	75.30%	0.107	IPR000242 (PRINTS); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134:SF251 (PANTHER); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
2298	c41729_g1_i1_len_458_path_1_0_457_0	12	xanthine dehydrogenase oxidase	153	5.73E-71	82.30%	0.108	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR022407 (PROSITE_PATTERNS); IPR008274 (SUPERFAMILY)
2299	c41764_g1_i1_len_2028_path_2006_0_2027_0	133	isoform e	676	0	90.50%	0.135	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR013543 (PFAM); G3DSA:3.10.450.50 (GENE3D); IPR020636 (PANTHER); PTHR24347:SF108 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); SSF54427 (SUPERFAMILY)
2300	c41788_g1_i1_len_945_path_923_0_944_2	48	isoform b	315	8.43E-42	52.90%	0.149	IPR000483 (SMART); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); PTHR24365:SF269 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF52058 (SUPERFAMILY); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
2301	c41862_g1_i1_len_2315_path_2319_0_2314_4	301	alpha-2-macroglobulin-like protein 1	772	2.05E-145	60.50%	0.189	IPR011626 (PFAM); IPR009048 (G3DSA:2.60.40.GENE3D); IPR009048 (PFAM); IPR008930 (G3DSA:1.50.10.GENE3D); PTHR11412 (PANTHER); IPR009048 (SUPERFAMILY); IPR008930 (SUPERFAMILY)
2302	c41895_g1_i1_len_505_path_483_0_504_3	13	preproneuropeptide f i	169	2.46E-17	64.13%	0.299	IPR020392 (PROSITE_PATTERNS); IPR001955 (PROSITE_PROFILES)

2303	c41904_g1_i1_len_1459_path_1_0_1458_3	2756	lipase 3	487	1.08E-141	67.30%	0.164	IPR029058 (G3DSA:3.40.50.GENE3D); IPR000073 (PFAM); IPR006693 (PFAM); PTHR11005 (PANTHER); PTHR11005:SF6 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
2304	c41924_g1_i1_len_816_path_1_0_815_3	16	e3 ubiquitin-protein ligase mib1	272	7.09E-166	92.90%	0.135	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (PFAM); PTHR24202:SF52 (PANTHER); PTHR24202 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2305	c41946_g1_i1_len_273_path_251_0_272_2	2203	cytotoxic t lymphocyte-associated protein 2 alpha precursor	91	2.37E-09	58.50%	0.311	G3DSA:3.90.70.10 (GENE3D); IPR013201 (PFAM); PTHR12411:SF289 (PANTHER); IPR013128 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
2306	c41950_g1_i1_len_306_path_284_0_305_1	4	gastrula zinc finger	102	6.15E-28	68.90%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2307	c42008_g1_i1_len_2433_path_2411_0_2432_1	148	protein kinase c isoform x1	811	0	78.60%	0.149	IPR020454 (PRINTS); IPR002219 (SMART); IPR002290 (SMART); IPR000008 (SMART); IPR000961 (SMART); IPR000008 (PFAM); IPR014376 (PIRSF); IPR017892 (PFAM); G3DSA:3.30.60.20 (GENE3D); IPR002219 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); IPR000008 (G3DSA:2.60.40.GENE3D); PTHR24357 (PANTHER); PTHR24357:SF52 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR002219 (PROSITE_PATTERNS); IPR002219 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000961 (PROSITE_PROFILES); IPR002219 (PROSITE_PROFILES); IPR000008 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR002219 (PROSITE_PROFILES); IPR000008 (SUPERFAMILY); SSF57889 (SUPERFAMILY); SSF57889 (SUPERFAMILY); IPR011009 (SUPERFAMILY)
2308	c42064_g1_i1_len_371_path_1_0_370_0	10	zinc c2h2 type domain-containing protein	124	2.69E-22	61.30%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2309	c42066_g1_i1_len_341_path_1_0_166_168_167_253_168_254_340_0	4	zinc finger protein 501-like	114	4.86E-21	69.90%	0.126	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2310	c42077_g1_i1_len_516_path_1_0_515_2	14	peroxisomal biogenesis aaa atpase pex1	172	1.35E-95	88.90%	0.114	IPR003593 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); PTHR23077 (PANTHER); IPR025653 (PTHR23077:PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
2311	c42116_g1_i1_len_377_path_1_0_376_0	7	thioredoxin-related transmembrane protein 2 homolog	126	3.31E-54	81.70%	0.261	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR15853 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
2312	c42252_g1_i1_len_762_path_740_0_761_1	20	tyrosine-protein kinase btk29a isoform x3	254	2.18E-157	93.00%	0.11	IPR001245 (PRINTS); IPR020635 (SMART); IPR016253 (PIRSF); G3DSA:3.30.200.20 (GENE3D); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418:SF162 (PANTHER); PTHR24418 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)

2313	c42331_g1_i1_len_2029_path_2007_0_2028_5	196	sphingomyelin phosphodiesterase	676	1.13E-175	62.40%	0.568Y	IPR004843 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); IPR029052 (G3DSA:3.60.21.GENE3D); IPR011160 (PIRSF); PTHR10340 (PANTHER); PTHR10340:SF13 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR008139 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR011001 (SUPERFAMILY); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
2314	c42337_g1_i1_len_322_path_300_0_321_3	6	protein lap1-like	108	1.38E-35	78.10%	0.099	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR025875 (PFAM); PTHR23155:SF466 (PANTHER); PTHR23155 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52075 (SUPERFAMILY)
2315	c42477_g1_i1_len_877_path_1_0_876_0	28	irregular chiasm c-roughest protein isoform x1	293	8.00E-129	78.10%	0.099	IPR003598 (SMART); IPR013162 (PFAM); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11640:SF54 (PANTHER); PTHR11640 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2316	c42528_g1_i1_len_954_path_932_0_953_3	41	zinc finger protein 350-like isoform x1	318	2.12E-56	80.00%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2317	c42536_g1_i1_len_602_path_580_0_601_4	18	eph receptor tyrosine	201	3.53E-135	93.60%	0.141	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR013761 (G3DSA:1.1.10.150.GENE3D); IPR001245 (PFAM); PTHR24416:SF263 (PANTHER); PTHR24416 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR001660 (PROSITE_PROFILES); IPR013761 (SUPERFAMILY); IPR011009 (SUPERFAMILY)
2318	c42556_g1_i1_len_976_path_1_0_975_1	47	zinc finger protein partial	325	2.11E-115	73.20%	0.335	IPR015880 (SMART); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2319	c42764_g1_i1_len_394_path_1_0_393_5	4	melanotransferrin isoform x2	131	3.69E-31	63.10%	0.114	IPR001156 (SMART); G3DSA:3.40.190.10 (GENE3D); IPR001156 (PFAM); PTHR11485 (PANTHER); IPR018195 (PROSITE_PATTERNS); IPR001156 (PROSITE_PROFILES); SSF53850 (SUPERFAMILY)
2320	c42813_g1_i1_len_1305_path_1_0_1304_0	47	c4b-binding protein beta	435	6.52E-159	62.50%	0.122	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR19325 (PANTHER); PTHR19325:SF230 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)

2321	c42819_g1_i1_len_987_path_1_0_986_5	28	g-protein coupled receptor mth2	329	4.32E-93	65.50%	0.207	IPR000832 (PRINTS); IPR000832 (PFAM); PTHR12011:SF244 (PANTHER); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2322	c42862_g1_i1_len_312_path_1_0_311_4	6	syntaxin-binding protein 5-like	104	1.19E-50	88.30%	0.126	IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR10241:SF22 (PANTHER); PTHR10241 (PANTHER); IPR019775 (PROSITE_PATTERNS)
2323	c42872_g1_i1_len_1098_path_1076_0_1097_2	47	interleukin-1 receptor-associated kinase 4	366	3.12E-109	67.20%	0.102	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24419:SF0 (PANTHER); PTHR24419 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2324	c42952_g1_i1_len_318_path_1_0_317_5	6	vitellogenin partial	106	2.85E-24	64.70%	0.105	no IPS match
2325	c42986_g1_i1_len_315_path_293_0_314_1	6	laminin a	105	2.25E-47	87.60%	0.1	IPR008211 (SMART); IPR008211 (PFAM); PTHR10574:SF39 (PANTHER); PTHR10574 (PANTHER); IPR008211 (PROSITE_PROFILES)
2326	c43000_g1_i1_len_989_path_967_0_988_2	73	probable cytosolic iron-sulfur protein assembly protein ciao1 isoform x1	329	9.13E-154	82.60%	0.135	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19920:SF0 (PANTHER); PTHR19920 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR028608 (HAMAP); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2327	c43022_g1_i1_len_399_path_1_0_398_1	19	senseless- isoform a	133	5.10E-20	53.00%	0.101	IPR015880 (SMART); PF13465 (PFAM); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2328	c43024_g1_i1_len_748_path_726_0_747_1	11	taf5-like rna polymerase ii p300 cbp-associated factor-associated factor 65 kda subunit partial	249	8.39E-71	73.80%	0.101	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19879:SF3 (PANTHER); PTHR19879 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2329	c43157_g1_i1_len_732_path_710_0_731_1	20	basement membrane-specific heparan sulfate proteoglycan core protein isoform x13	244	1.43E-67	65.10%	0.114	IPR018031 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000034 (PFAM); PTHR10574:SF252 (PANTHER); PTHR10574 (PANTHER); IPR000034 (PROSITE_PROFILES)
2330	c43182_g2_i1_len_565_path_829_0_564_0	11	krueppel-like factor 13	189	1.37E-12	62.70%	0.101	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2331	c43200_g1_i1_len_659_path_1_0_658_4	59	apolipoprotein d-like	220	4.52E-34	56.60%	0.21	IPR000566 (PFAM); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612:SF7 (PANTHER); PTHR10612 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011038 (SUPERFAMILY)
2332	c43208_g1_i1_len_414_path_1_0_413_0	8	dorsal-ventral patterning protein partial	138	3.25E-31	62.20%	0.21	IPR001007 (SMART); IPR001007 (PFAM); PTHR11339 (PANTHER); PTHR11339:SF223 (PANTHER); SSF57603 (SUPERFAMILY)

2333	c43222_g1_i1_len_400_path_23_0_399_5	6	hyaluronidase-1 isoform x2	133	2.60E-12	61.90%	0.1	IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); PTHR11769:SF8 (PANTHER); IPR018155 (PANTHER); IPR017853 (SUPERFAMILY)
2334	c43248_g1_i1_len_1603_path_1_0_1602_1	67	acyl- -binding domain-containing protein 5 isoform x2	534	2.76E-49	44.10%	0.171	Coil (COILS); IPR000582 (PRINTS); IPR000582 (PFAM); IPR014352 (G3DSA:1.20.80.GENE3D); PTHR23310:SF14 (PANTHER); PTHR23310 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000582 (PROSITE_PROFILES); IPR000582 (SUPERFAMILY); TMhelix (TMHMM)
2335	c43297_g1_i1_len_639_path_617_0_638_5	19	sortilin-related receptor-like	213	6.25E-12	45.60%	0.109	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
2336	c43299_g1_i1_len_501_path_1_0_500_3	10	achain crystal structure of engineered northeast structural genomics consortium target	167	7.06E-12	61.20%	0.106	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24193 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2337	c43331_g1_i1_len_279_path_1_0_278_4	4	transmembrane protein 2	93	2.36E-07	72.00%	0.111	PTHR12277 (PANTHER); PTHR12277:SF48 (PANTHER)
2338	c43371_g1_i1_len_694_path_1_0_693_3	14	ecto-nox disulfide-thiol exchanger 2-like isoform x4	232	5.54E-06	53.00%	0.1	PTHR16001 (PANTHER)
2339	c43384_g1_i1_len_355_path_333_0_354_0	10	retinol dehydrogenase 14	119	2.94E-25	78.20%	0.157	IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320 (PANTHER); PTHR24320:SF36 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
2341	c4350_g1_i1_len_1025_path_1003_0_1024_4	58	copper chaperone for superoxide dismutase	342	3.07E-113	77.00%	0.111	IPR001424 (PRINTS); G3DSA:3.30.70.100 (GENE3D); IPR001424 (G3DSA:2.60.40.GENE3D); IPR006121 (PFAM); IPR001424 (PFAM); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006121 (PROSITE_PROFILES); IPR001424 (SUPERFAMILY); IPR006121 (SUPERFAMILY)
2340	c43503_g1_i1_len_293_path_271_0_292_3	4	insulin-like growth factor-binding protein complex acid labile subunit	98	1.99E-37	73.70%	0.115	IPR000483 (SMART); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); SSF52058 (SUPERFAMILY)
2342	c43522_g1_i1_len_344_path_1_0_343_0	6	carboxypeptidase b-like	115	1.45E-27	66.30%	0.102	IPR000834 (PRINTS); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY)
2343	c43546_g1_i1_len_511_path_1_0_510_3	9	laminin a	171	3.24E-76	80.30%	0.105	PR00011 (PRINTS); IPR002049 (SMART); IPR002049 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10574:SF231 (PANTHER); PTHR10574 (PANTHER); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PATTERNS); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
2344	c43555_g1_i1_len_388_path_366_0_387_5	7	dehydrogenase reductase sdr family protein 7-like isoform x1	129	3.32E-23	68.90%	0.262	IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF308 (PANTHER); PTHR24322 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
2345	c43556_g1_i1_len_901_path_1_0_900_1	63	twitchin isoform x4	300	2.07E-141	82.60%	0.108	PR00014 (PRINTS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF155 (PANTHER); PTHR19897 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
2346	c43665_g1_i1_len_1374_path_1352_0_1373_1	54	map kinase-activated protein kinase 2	458	0	85.80%	0.115	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR027442 (G3DSA:4.10.1170.GENE3D); IPR000719 (PFAM); PTHR24349:SF64 (PANTHER); PTHR24349 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)

2347	c43688_g1_i1_len_1297_path_1_0_1296_4	43	papilin isoform x2	432	3.82E-138	65.10%	0.119	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
2348	c43701_g1_i1_len_306_path_1_0_305_5	4	leucine-rich repeat-containing protein partial	102	6.92E-28	72.00%	0.096	IPR003591 (SMART); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155:SF424 (PANTHER); PTHR23155 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52075 (SUPERFAMILY)
2349	c43720_g1_i1_len_325_path_1_0_324_0	10	slit homolog 2	109	1.79E-39	77.50%	0.102	IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365:SF249 (PANTHER); PTHR24365 (PANTHER); SSF52075 (SUPERFAMILY)
2350	c43725_g1_i1_len_378_path_1_0_377_4	6	dbh-like monooxygenase protein 1	126	1.81E-16	66.30%	0.860Y	IPR005018 (PFAM); PTHR10157:SF23 (PANTHER); IPR000945 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005018 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM)
2351	c43795_g1_i1_len_1185_path_1163_0_1184_1	34	leucine-rich transmembrane	395	3.41E-53	52.00%	0.113	Coil (COILS); IPR000483 (SMART); G3DSA:3.80.10.10 (GENE3D); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
2352	c43844_g1_i1_len_563_path_541_0_562_2	17	endo-b- -glucanase	187	3.16E-62	76.50%	0.163	IPR001701 (PFAM); IPR012341 (G3DSA:1.50.10.GENE3D); PTHR22298:SF17 (PANTHER); PTHR22298 (PANTHER); IPR018221 (PROSITE_PATTERNS); IPR008928 (SUPERFAMILY)
2353	c43910_g1_i1_len_2072_path_10_0_2071_5	155	ankyrin repeat and mynd domain-containing protein 2	690	7.14E-139	68.20%	0.099	Coil (COILS); Coil (COILS); IPR002110 (SMART); IPR002893 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24150 (PANTHER); IPR002893 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR002893 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); SSF144232 (SUPERFAMILY); IPR020683 (SUPERFAMILY); TMhelix (TMHMM)
2354	c43929_g1_i1_len_292_path_270_0_291_0	4	zinc finger protein 345	98	1.39E-15	58.60%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2355	c43994_g1_i1_len_466_path_1_0_465_3	6	wd repeat and socs box-containing protein partial	156	2.03E-55	71.00%	0.152	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR15622:SF2 (PANTHER); PTHR15622 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2356	c44071_g1_i1_len_303_path_281_0_302_4	25	zinc finger protein 235-like	101	2.49E-22	66.90%	0.101	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2357	c44099_g1_i1_len_1651_path_1629_0_1650_2	69	tyrosine-protein kinase abl	550	1.98E-133	59.30%	0.148	IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418 (PANTHER); PTHR24418:SF87 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)

2358	c44114_g1_i1_len_1258_path_1236_0_1257_1	146	glutaminy-peptide cyclotransferase-like	414	6.44E-116	68.90%	0.188	G3DSA:3.40.630.10 (GENE3D); IPR007484 (PFAM); PTHR12283 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY)
2359	c44135_g1_i1_len_649_path_1_0_648_3	29	acid sphingomyelinase-like phosphodiesterase 3b	217	3.88E-37	61.80%	0.125	IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR10340:SF14 (PANTHER); PTHR10340 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY); TMhelix (TMHMM)
2360	c44167_g1_i1_len_616_path_594_0_615_0	10	lymphokine-activated killer t-cell-originated protein kinase	206	5.36E-21	61.60%	0.13	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR26266 (PANTHER); PTHR26266:SF76 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2361	c44238_g1_i1_len_2719_path_2697_0_2718_2	230	epithelial chloride channel	906	7.69E-33	44.80%	0.11	IPR015394 (PFAM); PTHR10579:SF8 (PANTHER); PTHR10579 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
2362	c44309_g1_i1_len_589_path_567_0_588_0	23	group xiaa secretory phospholipase a2	197	1.36E-53	62.40%	0.411 Y	IPR010711 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); IPR010711 (PANTHER); PTHR12824:SF8 (PANTHER); IPR013090 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR016090 (SUPERFAMILY); TMhelix (TMHMM)
2363	c44331_g1_i1_len_1352_path_1_0_1263_1265_1264_1307_1265_1308_1351_4	36	leucine-rich repeat-containing protein 15	451	4.34E-22	47.30%	0.336	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373 (PANTHER); PTHR24373:SF112 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF52058 (SUPERFAMILY)
2364	c44336_g1_i1_len_375_path_1_0_374_5	12	heat shock protein partial	125	9.35E-57	85.90%	0.26	IPR013126 (PRINTS); IPR013126 (PFAM); IPR029047 (G3DSA:2.60.34.GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR029047 (SUPERFAMILY)
2365	c44343_g1_i1_len_339_path_317_0_338_2	7	signal cub and egf-like domain-containing protein partial	113	4.63E-22	60.30%	0.111	IPR000742 (SMART); IPR001881 (SMART); IPR026823 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PF14670 (PFAM); PTHR24034 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
2366	c44359_g1_i1_len_269_path_247_0_268_4	4	serine threonine-protein kinase plk1-like	90	2.79E-36	76.80%	0.267	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24345 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2367	c44400_g1_i1_len_288_path_119_0_287_0	21	zinc finger protein 431-like isoform x5	96	2.63E-24	68.10%	0.104	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2368	c44412_g1_i1_len_687_path_665_0_686_1	27	macrophage mannose receptor 1-like	229	8.86E-47	54.90%	0.125	IPR002352 (PRINTS); IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22803 (PANTHER); PTHR22803:SF16 (PANTHER); IPR018378 (PROSITE_PATTERNS); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
2369	c44477_g1_i1_len_201_path_275_0_200_1	4	cd4-specific ankyrin repeat protein	67	3.57E-11	66.20%	0.146	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24182 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2370	c44537_g1_i1_len_836_path_814_0_835_3	23	trypsin- partial	279	1.29E-90	67.20%	0.119	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24258 (PANTHER); PTHR24258:SF4 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2371	c44550_g1_i1_len_168_path_6_0_167_3	0	70-kda heat shock partial	56	8.68E-25	89.90%	0.199	IPR013126 (PFAM); IPR029047 (G3DSA:2.60.34.GENE3D); PTHR19375 (PANTHER); PTHR19375:SF156 (PANTHER); IPR029047 (SUPERFAMILY)
2372	c44579_g1_i1_len_242_path_220_0_241_0	4	bone morphogenetic protein 10	81	1.93E-23	73.00%	0.106	IPR001839 (SMART); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001839 (PFAM); IPR015615 (PANTHER); PTHR11848:SF146 (PANTHER); IPR017948 (PROSITE_PATTERNS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)

2373	c44675_g1_i1_len_559_path_537_0_558_3	18	peroxisomal biogenesis factor 7	187	7.77E-83	74.00%	0.102	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22850 (PANTHER); PTHR22850:SF98 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2374	c44759_g1_i1_len_531_path_509_0_530_4	18	peptidyl-prolyl cis-trans isomerase cwc27 homolog	177	3.19E-91	90.70%	0.113	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF152 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
2375	c44800_g1_i1_len_338_path_1_0_337_4	3	zinc finger protein 227	113	1.75E-34	70.90%	0.114	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2376	c4482_g1_i1_len_1055_path_1033_0_429_14_63_430_1054_1	31	plexin b	352	1.39E-127	85.30%	0.103	IPR013548 (PFAM); PTHR22625 (PANTHER); PTHR22625:SF31 (PANTHER); IPR008936 (SUPERFAMILY)
2377	c44863_g1_i1_len_183_path_1_0_182_0	1	plexin b	61	9.35E-33	95.10%	0.125	IPR013548 (PFAM); PTHR22625 (PANTHER); IPR008936 (SUPERFAMILY)
2378	c44907_g1_i1_len_824_path_802_0_823_5	33	urokinase-type plasminogen activator	274	4.12E-49	55.20%	0.203	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2379	c4498_g1_i1_len_996_path_25_0_22_48_23_995_5	55	syntaxin-12	332	2.15E-97	72.50%	0.224	IPR006011 (SMART); IPR000727 (SMART); PF14523 (PFAM); IPR000727 (PFAM); G3DSA:1.20.58.70 (GENE3D); PTHR19957:SF87 (PANTHER); PTHR19957 (PANTHER); IPR006012 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000727 (PROSITE_PROFILES); IPR010989 (SUPERFAMILY); TMhelix (TMHMM)
2380	c4498_g1_i2_len_1334_path_49_0_360_48_3_61_1333_5	88	syntaxin-12	444	4.34E-96	72.40%	0.224	IPR000727 (SMART); IPR006011 (SMART); G3DSA:1.20.58.70 (GENE3D); IPR000727 (PFAM); PF14523 (PFAM); PTHR19957 (PANTHER); PTHR19957:SF87 (PANTHER); IPR006012 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000727 (PROSITE_PROFILES); IPR010989 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2381	c45032_g1_i1_len_480_path_458_0_479_0	10	wnt-receptor frizzled-like protein variant 2	160	1.36E-76	87.20%	0.460 Y	IPR020067 (SMART); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR020067 (PFAM); IPR015526 (PANTHER); IPR026561 (PTHR11309:PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR020067 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR020067 (SUPERFAMILY)
2382	c45124_g1_i1_len_1417_path_1_0_1416_2	45	receptor-type tyrosine-protein phosphatase beta-like	472	1.31E-70	56.00%	0.14	IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)
2383	c4522_g1_i1_len_1903_path_5623_0_125_38_69_126_1902_3	178	beta- -glucan-binding protein precursor	635	3.14E-176	60.90%	0.727 Y	IPR001747 (SMART); IPR001747 (PFAM); IPR015816 (G3DSA:2.30.230.GENE3D); IPR011030 (G3DSA:1.25.10.GENE3D); PTHR23345:SF11 (PANTHER); PTHR23345 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001747 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR015819 (SUPERFAMILY); IPR011030 (SUPERFAMILY); TMhelix (TMHMM)

2384	c4522_g1_i2_len_2834_path_2812_0_1056_3 869_1057_2833_3	243	dlp hdl-bgbp precursor	945	0	63.60%	0.727Y	Coil (COILS); IPR001747 (SMART); IPR015816 (G3DSA:2.30.230.GENE3D); IPR015818 (G3DSA:2.20.80.GENE3D); IPR001747 (PFAM); IPR015255 (PFAM); IPR011030 (G3DSA:1.25.10.GENE3D); IPR015817 (G3DSA:2.20.50.GENE3D); PTHR23345 (PANTHER); PTHR23345:SF11 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001747 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR015819 (SUPERFAMILY); IPR015819 (SUPERFAMILY); IPR011030 (SUPERFAMILY); TMhelix (TMHMM)
2385	c45244_g1_i1_len_337_path_315_0_336_1	6	hemacentin- partial	112	5.88E-39	75.50%	0.255	IPR023413 (G3DSA:2.40.155.GENE3D); IPR006605 (PFAM); PTHR19897:SF158 (PANTHER); PTHR19897 (PANTHER); IPR006605 (PROSITE_PROFILES); IPR009017 (SUPERFAMILY)
2386	c45300_g1_i1_len_340_path_1_0_339_1	9	laminin subunit gamma- partial	113	2.21E-48	78.60%	0.105	IPR008211 (SMART); IPR008979 (G3DSA:2.60.120.GENE3D); IPR008211 (PFAM); PTHR10574:SF231 (PANTHER); PTHR10574 (PANTHER); IPR008211 (PROSITE_PROFILES)
2387	c4542_g1_i1_len_150_path_128_0_149_2	2	vitellogenin partial	50	8.67E-17	77.80%	0.099	IPR001846 (PFAM); IPR001846 (PROSITE_PROFILES)
2388	c4542_g2_i1_len_405_path_637_0_404_4	14	vitellogenin partial	135	5.05E-39	65.40%	0.101	no IPS match
2389	c45450_g1_i1_len_318_path_296_0_317_3	10	neuroligin- y-linked isoform x1	106	1.92E-46	84.40%	0.145	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559:SF157 (PANTHER); PTHR11559 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY)
2390	c45473_g1_i1_len_1481_path_1_0_1480_4	92	#NAME?	494	0	77.20%	0.115	IPR001830 (PFAM); IPR023214 (G3DSA:3.40.50.GENE3D); IPR003337 (TIGRFAM); G3DSA:3.40.50.2000 (GENE3D); IPR006379 (TIGRFAM); IPR003337 (PFAM); PTHR10788 (PANTHER); PTHR10788:SF6 (PANTHER); SSF53756 (SUPERFAMILY); IPR023214 (SUPERFAMILY)
2391	c45484_g1_i1_len_292_path_270_0_291_0	6	basement membrane-specific heparan sulfate proteoglycan core protein	98	5.14E-32	66.10%	0.106	IPR013783 (G3DSA:2.60.40.GENE3D); SSF48726 (SUPERFAMILY)
2392	c45485_g1_i1_len_797_path_1_0_796_2	57	tyrosine-protein kinase dnt-like	265	6.87E-114	83.10%	0.116	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR001245 (PFAM); IPR016253 (PIRSF); PTHR24416 (PANTHER); PTHR24416:SF256 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
2393	c45488_g1_i1_len_695_path_1_0_694_1	27	c-type lectin domain family 4 member g-like isoform x2	232	1.97E-09	46.60%	0.109	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY)
2394	c4561_g1_i1_len_414_path_1025_0_169_317_170_413_3	14	trafficking protein particle complex subunit 1-like isoform x3	138	5.03E-08	71.00%	0.252	IPR007233 (PFAM)
2395	c4561_g1_i2_len_560_path_1_0_315_317_316_559_3	26	trafficking protein particle complex subunit 1	187	9.68E-74	87.70%	0.252	G3DSA:3.30.450.70 (GENE3D); IPR007233 (PFAM); PTHR23249:SF16 (PANTHER); IPR007233 (PANTHER); IPR011012 (SUPERFAMILY)
2396	c45627_g1_i1_len_405_path_1_0_404_0	14	neural- partial	135	3.31E-32	59.80%	0.109	G3DSA:2.10.25.10 (GENE3D); IPR000742 (PROSITE_PROFILES)
2397	c45684_g1_i1_len_646_path_624_0_645_4	15	CG4553	215	3.28E-29	62.70%	0.151	Coil (COILS); Coil (COILS); IPR010487 (PFAM); PTHR21133 (PANTHER); PTHR21133:SF0 (PANTHER)
2398	c45751_g1_i1_len_627_path_1_0_626_4	10	45 kda calcium-binding protein	209	1.77E-83	72.20%	0.107	IPR002048 (SMART); IPR011992 (G3DSA:1.10.238.GENE3D); IPR028974 (G3DSA:4.10.1080.GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PF13833 (PFAM); PTHR10827 (PANTHER); IPR027240 (PTHR10827:PANTHER); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)
2399	c45805_g1_i1_len_592_path_570_0_591_3	14	aldehyde dehydrogenase 16 member a1	198	9.72E-82	75.40%	0.15	IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF98 (PANTHER); IPR016161 (SUPERFAMILY); IPR016161 (SUPERFAMILY)

2400	c4581_g1_i1_len_1977_path_1955_0_1976_1	116	frizzled 4	659	0	72.90%	0.143	IPR000539 (PRINTS); IPR020067 (SMART); IPR020067 (PFAM); IPR000539 (PFAM); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR026551 (PTHR11309:PANTHER); IPR015526 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017981 (PROSITE_PROFILES); IPR020067 (PROSITE_PROFILES); IPR020067 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2401	c45933_g1_i1_len_352_path_1_0_351_4	8	voltage-gated sodium channel	117	1.07E-53	82.30%	0.102	IPR028814 (PTHR10037:PANTHER); PTHR10037 (PANTHER)
2402	c45943_g1_i1_len_348_path_1_0_347_1	7	aael005869- partial	116	1.34E-24	60.40%	0.117	IPR014784 (G3DSA:2.60.120.GENE3D); PF03712 (PFAM); IPR000945 (PANTHER); IPR014783 (PROSITE_PATTERNS); IPR008977 (SUPERFAMILY)
2403	c46054_g1_i1_len_377_path_355_0_376_0	7	reelin- partial	126	4.08E-29	67.70%	0.096	PTHR11841 (PANTHER)
2404	c46146_g1_i1_len_989_path_1_0_988_3	44	tyrosine-protein kinase hopscotch	330	1.29E-90	66.00%	0.152	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24418 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2405	c46180_g1_i1_len_270_path_1_0_269_4	8	sec14 domain and spectrin repeat-containing protein 1	90	2.11E-28	84.10%	0.103	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF148 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
2406	c46188_g1_i1_len_1315_path_1_0_1314_5	62	ankyrin repeat protein partial	438	4.62E-24	50.30%	0.103	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2407	c46192_g1_i1_len_347_path_325_0_346_1	8	xanthine partial	116	7.21E-16	68.50%	0.156	IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF65 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)
2408	c46283_g1_i1_len_215_path_232_0_214_4	2	von willebrand factor d and egf domain-containing partial	72	2.90E-24	80.10%	0.153	IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
2409	c46354_g1_i1_len_469_path_1_0_468_1	9	c-type mannose receptor 2-like	156	8.65E-15	48.60%	0.107	IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
2410	c46367_g1_i1_len_629_path_607_0_628_0	10	zinc finger protein 658b-like	210	2.24E-31	58.00%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2411	c46376_g1_i1_len_320_path_1_0_319_3	6	membrane-associated guanylate ww and pdz domain-containing protein 2	107	2.27E-56	85.00%	0.134	G3DSA:3.30.63.10 (GENE3D); IPR008145 (PFAM); PTHR10316 (PANTHER); PTHR10316:SF40 (PANTHER); IPR020590 (PROSITE_PATTERNS); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
2412	c46386_g1_i1_len_231_path_1_0_230_0	7	chaperone	77	2.37E-30	85.10%	0.111	G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); PTHR19375:SF155 (PANTHER); PTHR19375 (PANTHER); SSF53067 (SUPERFAMILY)
2413	c46530_g1_i1_len_801_path_779_0_800_5	36	lactase-phlorizin hydrolase-like	267	2.50E-98	69.80%	0.173	IPR001360 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001360 (PANTHER); IPR017853 (SUPERFAMILY)
2414	c46549_g1_i1_len_431_path_409_0_430_4	14	---NA---	144			0.135	Coil (COILS); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016187 (SUPERFAMILY)

2415	c46551_g1_i1_len_1028_path_1006_0_1027_2	32	plexin-a4	342	0	83.50%	0.099	IPR016201 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); G3DSA:3.30.1680.10 (GENE3D); IPR002165 (PFAM); IPR001627 (PFAM); PTHR22625 (PANTHER); PTHR22625:SF16 (PANTHER); IPR001627 (PROSITE_PROFILES); IPR016201 (SUPERFAMILY); IPR001627 (SUPERFAMILY)
2416	c46572_g1_i1_len_282_path_260_0_281_4	4	laminin beta 1	94	6.58E-27	73.70%	0.117	Coil (COILS); IPR001800 (SUPERFAMILY)
2417	c4659_g1_i1_len_2081_path_1_0_845_847_8_46_2080_4	231	uncharacterized threonine-rich gpi-anchored glyco isoform x7	694	0	90.60%	0.271	Coil (COILS); IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR024678 (PFAM); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR13902 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2418	c46668_g1_i1_len_551_path_529_0_550_1	24	wd repeat-containing protein 5	184	8.14E-114	98.00%	0.114	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847 (PANTHER); PTHR22847:SF308 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2419	c46897_g1_i1_len_276_path_1_0_32_34_33_113_34_114_194_34_195_275_5	15	hypothetical protein CAPTEDRAFT_145620	92	1.45E-14	51.90%	0.093	no IPS match
2420	c46934_g1_i1_len_296_path_1_0_295_2	7	hemiceitin-2 isoform x2	98	2.16E-14	58.80%	0.115	IPR003598 (SMART); IPR003599 (SMART); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF158 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
2421	c47099_g1_i1_len_757_path_1_0_756_1	32	carbohydrate sulfotransferase 11-like	252	6.91E-16	48.00%	0.405 Y	IPR005331 (PFAM); IPR018011 (PANTHER); PTHR12137:SF29 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
2422	c47191_g1_i1_len_350_path_29_0_349_3	5	voltage-gated sodium partial	117	1.82E-54	92.50%	0.121	IPR027359 (G3DSA:1.20.120.GENE3D); IPR005821 (PFAM); PTHR10037 (PANTHER); IPR028814 (PTHR10037:PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF81324 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2423	c47316_g1_i1_len_347_path_325_0_346_4	4	sodium channel protein para isoform x5	116	5.35E-58	86.00%	0.116	IPR001696 (PRINTS); IPR028814 (PTHR10037:PANTHER); PTHR10037 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
2424	c47494_g1_i1_len_366_path_1_0_365_0	8	hyaluronidase ph-20	122	7.77E-28	66.80%	0.099	Coil (COILS); IPR018155 (PRINTS); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); PTHR11769:SF8 (PANTHER); IPR018155 (PANTHER); IPR017853 (SUPERFAMILY)
2425	c47554_g1_i1_len_1583_path_3_0_1582_1	138	f-box wd repeat-containing protein 7	528	0	87.90%	0.102	IPR020472 (PRINTS); IPR001810 (SMART); IPR001680 (SMART); G3DSA:1.20.1280.50 (GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001810 (PFAM); PTHR22844 (PANTHER); PTHR22844:SF116 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001810 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR001810 (SUPERFAMILY)
2426	c47779_g1_i1_len_713_path_691_0_712_0	26	nucleoporin seh1 isoform x2	238	4.75E-140	90.60%	0.105	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR11024 (PANTHER); PTHR11024:SF3 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2427	c47871_g1_i1_len_400_path_378_0_399_1	8	polypeptide n-acetylgalactosaminyltransferase partial	133	2.28E-69	83.00%	0.104	IPR000772 (PFAM); G3DSA:2.80.10.50 (GENE3D); PTHR11675:SF24 (PANTHER); PTHR11675 (PANTHER); IPR000772 (PROSITE_PROFILES); IPR000772 (SUPERFAMILY); IPR029044 (SUPERFAMILY)
2428	c47887_g1_i1_len_340_path_318_0_339_4	4	14-3-3 family protein	113	1.68E-40	75.60%	0.115	IPR000308 (PRINTS); IPR023410 (SMART); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); IPR023410 (SUPERFAMILY)
2429	c47985_g1_i1_len_407_path_411_0_406_1	9	er degradation-enhancing alpha-mannosidase-like 3	136	6.06E-35	90.70%	0.149	IPR001382 (PRINTS); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); PTHR11742:SF38 (PANTHER); IPR001382 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001382 (SUPERFAMILY)

2430	c48007_g1_i1_len_464_path_1_0_463_5	6	xanthine dehydrogenase oxidase	154	9.40E-51	69.30%	0.126	IPR005107 (SMART); G3DSA:3.30.390.50 (GENE3D); IPR005107 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR005107 (SUPERFAMILY)
2431	c48076_g1_i1_len_473_path_451_0_472_2	12	death-associated protein kinase partial	157	2.57E-47	83.60%	0.132	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); IPR020675 (PANTHER); IPR020676 (PTHR22964:PANTHER); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2432	c48128_g1_i1_len_2193_path_2171_0_2192_5	263	glycoside catalytic core	731	5.97E-94	53.40%	0.642Y	Coil (COILS); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001547 (PFAM); PTHR31308 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017853 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2433	c48169_g1_i1_len_978_path_1_0_977_2	60	dnak protein	326	4.34E-141	79.00%	0.101	Coil (COILS); Coil (COILS); IPR013126 (PRINTS); IPR013126 (PFAM); IPR029047 (G3DSA:2.60.34.GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF142 (PANTHER); IPR029047 (SUPERFAMILY); IPR029048 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
2434	c48577_g1_i1_len_900_path_878_0_899_0	21	serine-aspartate repeat protein f	300	5.14E-18	51.30%	0.186	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2435	c48577_g1_i1_len_900_path_878_0_899_4	21	aael005189- partial	300	1.38E-96	66.00%	0.099	IPR003598 (SMART); IPR003599 (SMART); IPR008160 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF50 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2436	c48631_g1_i1_len_602_path_1_0_601_5	20	mitochondrial cardiolipin hydrolase-like	200	1.27E-45	72.40%	0.182	IPR025202 (PFAM); G3DSA:3.30.870.10 (GENE3D); PTHR21248 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001736 (PROSITE_PROFILES); SSF56024 (SUPERFAMILY); TMhelix (TMHMM)
2437	c48685_g1_i1_len_312_path_290_0_311_5	4	interference hedgehog-like	104	5.67E-19	60.00%	0.126	IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
2438	c48691_g1_i1_len_360_path_1_0_359_1	6	carboxypeptidase b	120	4.82E-39	67.80%	0.116	IPR000834 (PRINTS); IPR000834 (SMART); G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY)
2439	c48714_g1_i1_len_324_path_302_0_323_4	9	serine threonine-protein kinase sbk1	108	3.11E-47	80.50%	0.11	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24359:SF18 (PANTHER); PTHR24359 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2440	c48842_g1_i1_len_397_path_455_0_396_0	7	tyrosine-protein kinase src64b	133	1.24E-64	86.60%	0.125	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2441	c49004_g1_i1_len_397_path_1_0_396_1	8	xanthine dehydrogenase oxidase	132	5.72E-58	79.20%	0.149	IPR002888 (G3DSA:1.10.150.GENE3D); IPR002888 (PFAM); IPR012675 (G3DSA:3.10.20.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF65 (PANTHER); IPR002888 (SUPERFAMILY); IPR001041 (SUPERFAMILY)
2442	c49201_g1_i1_len_323_path_301_0_322_1	4	mitogen-activated protein kinase kinase kinase 15 isoform x1	108	6.29E-64	97.00%	0.103	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR11584:SF371 (PANTHER); PTHR11584 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2443	c49292_g1_i1_len_545_path_523_0_544_2	16	laminin subunit alpha-like	181	2.02E-73	74.30%	0.099	no IPS match
2444	c49306_g1_i1_len_244_path_1_0_243_5	4	chaperone protein	81	5.73E-21	74.30%	0.103	IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24077 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
2445	c49422_g1_i1_len_1533_path_1_0_1532_0	87	adenylate cyclase type partial	511	1.23E-27	77.00%	0.256	IPR001054 (G3DSA:3.30.70.GENE3D); IPR001054 (PFAM); PTHR11920:SF16 (PANTHER); PTHR11920 (PANTHER); IPR018297 (PROSITE_PATTERNS); IPR001054 (PROSITE_PROFILES); IPR029787 (SUPERFAMILY)
2446	c49731_g1_i1_len_513_path_1_0_512_0	9	aldehyde oxidase	171	8.75E-49	70.40%	0.116	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908:SF65 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)

2447	c49764_g1_i1_len_444_path_422_0_443_3	6	aminopeptidase n	148	3.77E-55	76.20%	0.098	G3DSA:1.10.390.10 (GENE3D); IPR001930 (PANTHER); PTHR11533:SF148 (PANTHER); SSF55486 (SUPERFAMILY)
2448	c49781_g1_i1_len_596_path_574_0_595_4	19	neuroendocrine convertase 2	199	3.75E-125	91.00%	0.102	IPR015500 (PRINTS); IPR000209 (PFAM); IPR000209 (G3DSA:3.40.50.GENE3D); IPR015500 (PANTHER); PTHR10795:SF11 (PANTHER); IPR022398 (PROSITE_PATTERNS); IPR023827 (PROSITE_PATTERNS); IPR000209 (SUPERFAMILY)
2449	c49830_g1_i1_len_312_path_290_0_311_3	8	transducin beta-like protein 3	104	6.40E-33	73.90%	0.17	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19854 (PANTHER); PTHR19854:SF15 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2450	c49944_g1_i1_len_409_path_387_0_408_2	6	polypeptide n-acetylgalactosaminyltransferase 5 isoform x2	136	8.49E-62	83.00%	0.102	IPR000772 (SMART); IPR000772 (PFAM); G3DSA:2.80.10.50 (GENE3D); PTHR11675:SF39 (PANTHER); PTHR11675 (PANTHER); IPR000772 (PROSITE_PROFILES); IPR000772 (SUPERFAMILY)
2451	c49986_g1_i1_len_233_path_211_0_232_1	3	chemosensory protein	78	1.04E-07	55.50%	0.188	IPR005055 (PFAM); IPR005055 (G3DSA:1.10.2080.GENE3D); IPR005055 (PANTHER); IPR005055 (SUPERFAMILY)
2452	c50058_g1_i1_len_279_path_257_0_278_4	8	ankyrin repeat domain-containing protein 54	93	5.32E-32	76.90%	0.109	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24197:SF33 (PANTHER); PTHR24197 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2453	c50194_g1_i1_len_573_path_573_0_572_5	20	glyceraldehyde-3-phosphate type i family protein	191	1.30E-81	76.10%	0.102	IPR020831 (PRINTS); IPR020828 (SMART); IPR020829 (PFAM); IPR020828 (PFAM); G3DSA:3.30.360.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR10836:SF31 (PANTHER); IPR020831 (PANTHER); IPR020830 (PROSITE_PATTERNS); SSF55347 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
2454	c50227_g1_i1_len_1135_path_1_0_192_194_193_663_194_664_1134_2	35	c protein immunoglobulin-a-binding beta antigen	378	2.43E-14	35.60%	0.125	no IPS match
2455	c50227_g1_i1_len_1135_path_1_0_192_194_193_663_194_664_1134_3	35	preprotachykinin a	379	3.50E-48	54.60%	0.103	no IPS match
2457	c5047_g1_i1_len_151_path_337_0_150_1	3	serine protease nudel	50	3.14E-21	82.10%	0.119	IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (SUPERFAMILY)
2456	c50477_g1_i1_len_1174_path_1184_0_1173_2	36	stromal cell-derived factor 2	391	3.42E-52	77.40%	0.111	IPR016093 (SMART); G3DSA:2.80.10.50 (GENE3D); IPR027005 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016093 (PROSITE_PROFILES); IPR016093 (PROSITE_PROFILES); IPR016093 (SUPERFAMILY)
2461	c506_g1_i1_len_1624_path_53_0_1623_1	152	periodic tryptophan protein 1 homolog	541	1.43E-151	64.20%	0.121	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR14091 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2458	c50616_g1_i1_len_954_path_932_0_953_0	13	fukutin-related protein	318	6.97E-107	64.20%	0.275	IPR007074 (PFAM); PTHR13627:SF25 (PANTHER); PTHR13627 (PANTHER)
2460	c5062_g1_i1_len_481_path_1_0_480_4	11	low-density lipoprotein receptor-related protein 4-like	160	6.37E-06	63.00%	0.11	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
2459	c50625_g1_i1_len_324_path_1_0_323_3	6	zinc finger	108	5.40E-44	67.40%	0.147	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2462	c50784_g1_i1_len_413_path_1_0_412_0	3	d chain coupling of remote alternating-access transport mechanisms for protons and substrates in the multidrug efflux pump acrb	138	3.30E-14	54.10%	0.241	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2463	c50796_g1_i1_len_331_path_1_0_330_2	10	zinc finger protein 282	110	1.31E-19	57.10%	0.125	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

2464	c508_g1_i2_len_758_path_1_0_497_499_498_757_2	14	lipophorin receptor	252	1.31E-84	76.70%	0.187	IPR000033 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); IPR000033 (PFAM); PF14670 (PFAM); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF63825 (SUPERFAMILY); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF247 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
2465	c50920_g1_i1_len_337_path_1_0_336_3	5	hydroxybutyrate dehydrogenase	113	4.64E-40	73.20%	0.107	Coil (COILS); IPR003137 (PFAM); G3DSA:3.50.30.30 (GENE3D); SSF52025 (SUPERFAMILY)
2466	c50954_g1_i1_len_817_path_795_0_816_1	10	er degradation-enhancing alpha-mannosidase-like 3	272	7.95E-42	68.80%	0.102	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF159 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
2467	c51108_g1_i1_len_876_path_1_0_875_5	22	dnaj homolog subfamily c member 11	292	1.54E-137	80.90%	0.103	G3DSA:2.10.70.10 (GENE3D); SSF57603 (SUPERFAMILY); SSF57603 (SUPERFAMILY)
2468	c51137_g1_i1_len_642_path_1_0_320_1_321_641_2	19	kielin chordin-like protein	214	6.50E-17	41.20%	0.133	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2469	c51355_g1_i1_len_279_path_1_0_278_0	8	serine protease	93	1.50E-16	58.60%	0.101	IPR005390 (PRINTS); IPR000276 (PRINTS); IPR000276 (PFAM); G3DSA:1.20.1070.10 (GENE3D); PTHR24243:SF28 (PANTHER); PTHR24243 (PANTHER); IPR000276 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017452 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2470	c5141_g2_i1_len_371_path_349_0_370_5	6	neuromedin-u receptor 1	123	6.55E-64	90.70%	0.21	IPR002791 (PFAM); PTHR12260:SF1 (PANTHER); PTHR12260 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
2471	c51469_g1_i1_len_310_path_1_0_309_1	6	upf0364 protein c6orf211 homolog	103	1.06E-22	76.10%	0.123	IPR003595 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); PTHR19134:SF277 (PANTHER); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); IPR029021 (SUPERFAMILY)
2472	c5154_g1_i1_len_357_path_179_0_51_178_5_2_77_114_78_141_178_142_167_114_168_2_31_178_232_257_255_258_2	4	rho gtpase-activating protein 39 isoform x2	119	1.09E-07	54.00%	0.232	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2473	c51642_g1_i1_len_404_path_1_0_403_3	27	tyrosine-protein phosphatase 69d	135	7.78E-54	81.40%	0.143	IPR004254 (PANTHER); PTHR20855:SF15 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2474	c51692_g1_i1_len_628_path_1_0_627_4	10	fasciclin- partial	209	3.81E-20	48.60%	0.22	IPR004254 (PFAM); IPR004254 (PANTHER); PTHR20855:SF15 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2475	c5172_g1_i1_len_481_path_1_0_407_1137_4_08_480_5	13	adiponectin receptor protein	160	9.53E-14	81.60%	0.236	IPR004254 (PFAM); IPR004254 (PANTHER); PTHR20855:SF15 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2476	c5172_g1_i2_len_543_path_1_0_407_409_40_8_542_4	19	adiponectin receptor protein	181	1.42E-41	90.30%	0.304	G3DSA:2.20.100.10 (GENE3D); PTHR13723 (PANTHER)
2477	c51845_g1_i1_len_291_path_1_0_290_5	4	a disintegrin and metalloproteinase with thrombospondin motifs 7-like	97	7.62E-42	76.70%	0.113	IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.30.30 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF137 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
2478	c51948_g1_i1_len_275_path_253_0_274_3	6	dnak protein	92	1.29E-38	88.50%	0.13	IPR000209 (PFAM); IPR000209 (G3DSA:3.40.50.GENE3D); IPR015500 (PANTHER); PTHR10795:SF9 (PANTHER); IPR022398 (PROSITE_PATTERNS); IPR000209 (SUPERFAMILY)
2479	c51999_g1_i1_len_406_path_384_0_405_0	7	proprotein convertase subtilisin kexin type 7 isoform x2	136	2.34E-63	82.50%	0.134	

2480	c5201_g1_i1_len_477_path_53_0_20_26_21_227_282_228_248_26_249_455_282_456_476_5	23	polyubiquitin-b-like isoform 1	159	1.40E-106	99.00%	0.102	IPR019956 (PRINTS); IPR000626 (SMART); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); G3DSA:3.10.20.90 (GENE3D); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY)
2481	c52214_g1_i1_len_347_path_325_0_346_5	6	zinc finger protein 708-like	115	7.10E-17	57.10%	0.099	IPR015880 (SMART); PF12874 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2482	c52403_g1_i1_len_532_path_1_0_531_3	14	slit-like partial	178	4.84E-56	60.20%	0.112	PR00019 (PRINTS); IPR003591 (SMART); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
2483	c52698_g1_i1_len_368_path_346_0_367_0	6	zinc finger protein	123	4.23E-25	58.50%	0.123	IPR015880 (SMART); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2484	c52781_g1_i1_len_261_path_1_0_260_1	5	adp-ribosylation factor-like protein 4a	87	2.20E-41	92.30%	0.163	IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF121 (PANTHER); PTHR11711 (PANTHER); IPR027417 (SUPERFAMILY)
2485	c52805_g1_i1_len_258_path_236_0_257_4	4	aael010835- partial	86	1.42E-48	95.50%	0.104	IPR001245 (PRINTS); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR23257 (PANTHER); IPR027258 (PTHR23257:PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2486	c53028_g1_i1_len_340_path_1_0_339_1	11	zonadhesion-like partial	113	1.71E-11	51.20%	0.113	IPR000998 (PFAM); PTHR23282:SF75 (PANTHER); PTHR23282 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
2487	c53142_g1_i1_len_429_path_407_0_428_4	10	low-density lipoprotein receptor-related protein 4-like	143	4.90E-11	50.20%	0.13	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
2488	c53247_g1_i1_len_572_path_1_0_571_4	32	carboxypeptidase n subunit 2	191	7.38E-33	57.40%	0.2	IPR003591 (SMART); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); SSF52058 (SUPERFAMILY)
2489	c53370_g1_i1_len_343_path_1_0_342_5	16	plexin domain-containing protein 2	114	1.56E-45	82.50%	0.118	PTHR13055:SF12 (PANTHER); PTHR13055 (PANTHER)
2490	c53492_g1_i1_len_823_path_801_0_822_1	739	ecdysteroid-regulated 16 kda protein	274	1.17E-17	54.20%	0.450Y	IPR003172 (SMART); IPR003172 (G3DSA:2.60.40.GENE3D); IPR003172 (PFAM); PTHR11306 (PANTHER); SignalP-noTM (SIGNALP_EUK); IPR014756 (SUPERFAMILY)
2491	c53513_g1_i1_len_231_path_1_0_230_0	2	uncharacterized mitochondrial protein g00810-like	77	4.96E-12	70.90%	0.131	PTHR11439 (PANTHER)
2492	c53564_g1_i1_len_504_path_482_0_503_2	11	reticulocalbin-2	168	2.56E-27	87.40%	0.101	IPR011992 (G3DSA:1.10.238.GENE3D); PTHR10827:SF48 (PANTHER); PTHR10827 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)
2493	c53650_g1_i1_len_271_path_1_0_270_1	4	de-cadherin isoform x1	90	2.65E-32	81.40%	0.099	IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24026:SF39 (PANTHER); PTHR24026 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY)
2494	c5366_g1_i1_len_1794_path_1817_0_1645_3463_1646_1669_3665_1670_1793_0	72	PREDICTED: uncharacterized protein LOC105185459 isoform X3	598	4.08E-07	49.00%	0.1	IPR002172 (PRINTS); IPR002172 (SMART); IPR003609 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); G3DSA:3.50.4.10 (GENE3D); IPR003014 (PFAM); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR003609 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

2495	c53721_g1_i1_len_442_path_420_0_441_0	16	low quality protein: sco-spondin	148	1.13E-19	52.70%	0.104	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); PTHR10529:SF208 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
2496	c53853_g1_i1_len_290_path_1_0_289_3	6	tgf-beta receptor type-1	97	4.22E-54	94.40%	0.263	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); IPR000333 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2497	c5402_g2_i1_len_322_path_1_0_321_4	8	angiogenic factor with g patch and fha domains 1-like	107	2.29E-16	63.00%	0.127	no IPS match
2498	c5406_g2_i1_len_146_path_211_0_145_2	1	polypeptide n-acetylgalactosaminyltransferase 9	48	3.34E-22	91.80%	0.173	PTHR11675 (PANTHER)
2499	c54144_g1_i1_len_356_path_334_0_355_3	19	low-density lipoprotein receptor-related protein 2	119	1.04E-57	85.90%	0.115	IPR000033 (SMART); IPR011042 (G3DSA:2.120.10.GENE3D); IPR000033 (PFAM); PTHR10529:SF210 (PANTHER); PTHR10529 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY)
2500	c54183_g1_i1_len_687_path_665_0_686_0	18	serine protease	229	7.95E-57	81.10%	0.109	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); PTHR24256:SF103 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2501	c54206_g1_i1_len_256_path_234_0_255_3	4	vacuolar-sorting protein snf8-like	86	2.20E-22	93.00%	0.176	Coil (COILS); IPR007286 (PFAM); PTHR12806:SF0 (PANTHER); IPR007286 (PANTHER)
2502	c54301_g1_i1_len_466_path_444_0_465_4	15	retinol dehydrogenase 11-like	155	8.71E-58	71.60%	0.390Y	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF305 (PANTHER); PTHR24316 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
2503	c54416_g1_i1_len_256_path_1_0_255_0	8	mam and ldl-receptor class a domain-containing protein 1	86	2.62E-13	57.90%	0.102	IPR000998 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
2504	c54527_g1_i1_len_301_path_1_0_300_4	8	ankyrin repeat-containing protein	100	4.91E-56	87.80%	0.175	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2505	c54538_g1_i1_len_312_path_1_0_311_0	10	zinc finger protein 492-like	104	1.89E-29	74.00%	0.13	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2506	c54741_g1_i1_len_150_path_128_0_149_4	2	chemosensory protein	50	6.70E-18	84.60%	0.152	IPR005055 (G3DSA:1.10.2080.GENE3D); IPR005055 (PFAM); IPR005055 (PANTHER); PTHR11257:SF4 (PANTHER); IPR005055 (SUPERFAMILY)
2507	c5496_g2_i1_len_359_path_553_0_358_2	3	peptidylglycine alpha-hydroxylating monooxygenase	119	7.40E-63	83.50%	0.11	IPR000323 (PFAM); PF03712 (PFAM); IPR014784 (G3DSA:2.60.120.GENE3D); IPR000323 (G3DSA:2.60.120.GENE3D); PTHR10680 (PANTHER); IPR014783 (PROSITE_PATTERNS); IPR008977 (SUPERFAMILY); IPR008977 (SUPERFAMILY)
2508	c55149_g1_i1_len_740_path_1_0_739_4	10	low quality protein: de-cadherin	247	2.62E-58	63.20%	0.1	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027:SF276 (PANTHER); PTHR24027 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
2509	c55870_g1_i1_len_251_path_1_0_250_3	2	von willebrand factor type egf and pentraxin domain-containing protein 1	84	4.26E-15	60.90%	0.129	IPR011641 (PFAM); IPR009030 (SUPERFAMILY)
2510	c5589_g2_i1_len_1062_path_743_0_1061_5	50	atrial natriuretic peptide-converting enzyme-like	354	2.90E-46	61.60%	0.1	Coil (COILS); IPR002172 (SMART); IPR020067 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR020067 (PFAM); IPR002172 (PFAM); PTHR10529:SF209 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR020067 (PROSITE_PROFILES); IPR020067 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
2511	c56015_g1_i1_len_363_path_1_0_362_3	8	snare domain containing protein	121	8.01E-18	74.80%	0.164	Coil (COILS); IPR000727 (SMART); IPR000727 (PFAM); G3DSA:1.20.5.110 (GENE3D); PTHR19957 (PANTHER); IPR028669 (PTHR19957:PANTHER); IPR006012 (PROSITE_PATTERNS); IPR000727 (PROSITE_PROFILES); IPR010989 (SUPERFAMILY)

2512	c56015_g1_i1_len_363_path_1_0_362_5	8	protein isoform partial	121	1.22E-08	67.80%	0.106	G3DSA:1.20.58.70 (GENE3D); IPR010989 (SUPERFAMILY)
2513	c56108_g1_i1_len_361_path_1_0_360_1	4	glycosyltransferase 1 domain-containing protein 1	120	1.98E-30	74.70%	0.136	G3DSA:3.40.50.2000 (GENE3D); IPR001296 (PFAM); PTHR12526:SF331 (PANTHER); PTHR12526 (PANTHER); SSF53756 (SUPERFAMILY) PR00019 (PRINTS); IPR003591 (SMART); SM00364 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR025875 (PFAM); PTHR23155 (PANTHER); IPR027036 (PTHR23155:PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
2514	c56161_g1_i1_len_408_path_386_0_407_4	6	leucine-rich repeat protein soc-2 homolog	136	1.04E-72	93.10%	0.213	IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF136 (PANTHER); IPR002172 (PROSITE_PROFILES); IPR011330 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
2515	c56357_g1_i1_len_379_path_1_0_378_2	5	chitin deacetylase 1	126	1.59E-78	97.90%	0.103	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); PTHR23223:SF146 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2516	c56540_g1_i1_len_401_path_379_0_400_1	27	krueppel-like factor 15	134	2.71E-23	90.90%	0.103	IPR000668 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); IPR013128 (PANTHER); PTHR12411:SF287 (PANTHER); SSF54001 (SUPERFAMILY)
2517	c56629_g1_i1_len_479_path_1_0_478_4	6	cysteine protease and a protease	160	3.49E-41	68.30%	0.134	IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418 (PANTHER); PTHR24418:SF190 (PANTHER); IPR011009 (SUPERFAMILY)
2518	c56730_g1_i1_len_158_path_136_0_157_2	1	tyrosine-protein kinase src42a	52	3.49E-29	94.60%	0.104	IPR000242 (PRINTS); IPR003595 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
2519	c56863_g1_i1_len_250_path_228_0_249_1	4	tyrosine-protein phosphatase 10d-like	83	5.18E-21	82.50%	0.131	IPR028820 (PTHR10037:PANTHER); PTHR10037 (PANTHER)
2520	c57049_g1_i1_len_359_path_337_0_358_5	4	sodium channel protein 60e-like isoform x7	119	5.50E-45	83.80%	0.149	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY)
2521	c57066_g1_i1_len_265_path_243_0_264_4	4	---NA---	88			0.105	PF14828 (PFAM); PTHR11339:SF223 (PANTHER); PTHR11339 (PANTHER)
2522	c57205_g1_i1_len_256_path_1_0_255_3	4	dorsal-ventral patterning protein sog	86	2.44E-27	76.60%	0.105	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PF13895 (PFAM); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2523	c57447_g1_i1_len_349_path_327_0_348_4	5	frazzled protein	116	2.60E-08	50.30%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2524	c57448_g1_i1_len_267_path_245_0_266_0	4	zinc finger protein 39-like isoform x1	89	2.56E-13	61.40%	0.103	IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR11475:SF58 (PANTHER); PTHR11475 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2525	c57458_g1_i1_len_451_path_1_0_450_4	9	pdgf vegf receptor	150	4.18E-15	50.80%	0.099	IPR000961 (SMART); IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR017892 (PFAM); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24351:SF68 (PANTHER); PTHR24351 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2526	c57476_g1_i1_len_981_path_959_0_980_3	14	ribosomal protein s6 kinase alpha- partial	327	0	92.10%	0.141	Coil (COILS); IPR010326 (PFAM); IPR010326 (PANTHER); PTHR21292:SF1 (PANTHER)
2527	c5769_g1_i1_len_2387_path_1_0_1291_1293_1292_2386_1	219	exocyst complex component 3	796	0	74.20%	0.103	IPR019734 (SMART); IPR011990 (G3DSA:1.25.40.GENE3D); IPR013105 (PFAM); PF13414 (PFAM); PTHR24078 (PANTHER); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF48452 (SUPERFAMILY)
2528	c58028_g1_i1_len_470_path_448_0_469_2	8	dnaj homolog subfamily c member 3-like	156	1.70E-51	73.10%	0.452 Y	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2529	c58475_g1_i1_len_352_path_1_0_351_0	4	partner of bursicon	118	1.14E-14	71.50%	0.23	

2530	c58587_g1_i1_len_406_path_384_0_405_0	7	gastrula zinc finger	136	3.13E-30	59.60%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY);
2531	c5874_g1_i1_len_532_path_510_0_531_1	15	serine protease easter-like isoform x1	177	3.00E-25	53.40%	0.311	IPR006604 (SMART); IPR022700 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24260 (PANTHER); PTHR24260:SF3 (PANTHER); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
2532	c58845_g1_i1_len_288_path_1_0_287_4	5	ecto-nox disulfide-thiol exchanger partial	96	9.95E-47	85.80%	0.102	Coil (COILS); IPR012677 (G3DSA:3.30.70.GENE3D); PF13893 (PFAM); PTHR16001 (PANTHER); IPR000504 (PROSITE_PROFILES); SSF54928 (SUPERFAMILY)
2533	c5892_g1_i1_len_625_path_974_0_244_372_245_624_2	29	heat shock protein 70	208	7.10E-138	98.90%	0.224	Coil (COILS); IPR013126 (PRINTS); IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); IPR029048 (G3DSA:1.20.1270.GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR029047 (SUPERFAMILY); IPR029048 (SUPERFAMILY)
2534	c59522_g1_i1_len_427_path_405_0_426_3	8	polypeptide n-acetylgalactosaminyltransferase 35a	143	4.35E-26	66.90%	0.113	PTHR11675:SF14 (PANTHER); PTHR11675 (PANTHER)
2535	c59536_g1_i1_len_145_path_1_0_144_4	1	hypothetical protein L798_13682, partial	48	7.42E-13	73.30%	0.122	G3DSA:2.10.25.10 (GENE3D); PF14670 (PFAM); SSF57196 (SUPERFAMILY)
2536	c59604_g1_i1_len_259_path_237_0_258_0	4	plexin domain-containing protein 2	87	9.21E-32	78.00%	0.105	PTHR13055:SF12 (PANTHER); PTHR13055 (PANTHER)
2537	c5974_g1_i1_len_316_path_294_0_315_3	4	fibrillin-2-like	106	2.55E-45	80.60%	0.126	IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR011398 (PANTHER); PTHR24039:SF20 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
2538	c5974_g2_i1_len_144_path_708_0_143_0	1	fibrillin-1- partial	48	4.86E-09	72.20%	0.124	IPR017878 (G3DSA:3.90.290.GENE3D); IPR017878 (PFAM); IPR017878 (SUPERFAMILY)
2539	c5983_g1_i1_len_589_path_567_0_588_4	12	a disintegrin and metalloproteinase with thrombospondin motifs 18	196	1.04E-29	57.10%	0.104	IPR006586 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001590 (PFAM); PTHR13723 (PANTHER); IPR001590 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY)
2540	c6059_g1_i1_len_1735_path_1905_0_1676_4_6_1677_1734_4	98	mitochondrial import inner membrane translocase subunit tim8 a-like	578	1.39E-19	80.90%	0.137	IPR004217 (PFAM); IPR004217 (G3DSA:1.10.287.GENE3D); PTHR21535 (PANTHER); IPR004217 (SUPERFAMILY)
2541	c6059_g1_i2_len_1883_path_1905_0_1676_3_581_1677_1824_46_1825_1882_5	102	mitochondrial import inner membrane translocase subunit tim8 a	627	3.00E-30	82.20%	0.411Y	IPR004217 (PFAM); IPR004217 (G3DSA:1.10.287.GENE3D); PTHR21535 (PANTHER); IPR004217 (SUPERFAMILY)
2542	c60825_g1_i1_len_378_path_1_0_377_4	8	de-cadherin- partial	126	3.72E-20	58.30%	0.11	IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); PTHR24027:SF285 (PANTHER); IPR015919 (SUPERFAMILY)
2543	c6091_g1_i1_len_1396_path_10_0_1395_4	195	ras-related protein rab-8a isoform x2	465	3.32E-135	95.90%	0.128	IPR001806 (PRINTS); IPR024156 (SMART); IPR002041 (SMART); IPR020849 (SMART); IPR003579 (SMART); IPR003578 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR001806 (PFAM); PTHR24073:SF22 (PANTHER); PTHR24073 (PANTHER); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
2544	c60959_g1_i1_len_260_path_1_0_259_1	2	leucine-rich repeat-containing protein 17	87	9.45E-10	62.80%	0.103	G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365:SF233 (PANTHER); PTHR24365 (PANTHER); SSF52058 (SUPERFAMILY)
2545	c6100_g2_i1_len_1379_path_271_0_1378_1	33	calcium-activated chloride channel regulator 1-like	460	1.45E-101	53.70%	0.136	IPR002035 (SMART); IPR015394 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); PF13519 (PFAM); PTHR10579 (PANTHER); PTHR10579:SF8 (PANTHER); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
2546	c61025_g1_i1_len_177_path_1_0_176_1	2	dnak protein	59	4.25E-25	91.70%	0.128	IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.90.640.10 (GENE3D); PTHR19375 (PANTHER); SSF53067 (SUPERFAMILY)
2547	c6109_g1_i1_len_1295_path_1_0_527_529_5_28_605_607_606_1294_2	129	annexin b9-like isoform x2	431	6.21E-128	72.80%	0.231	IPR001464 (PRINTS); IPR002391 (PRINTS); IPR018502 (SMART); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); SSF47874 (SUPERFAMILY)

2548	c6117_g1_i1_len_1175_path_1153_0_512_166_513_513_1667_514_1174_0	52	dentin sialophosphoprotein isoform x1	392	9.81E-116	64.20%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2549	c6127_g1_i1_len_854_path_53_0_853_5	873	Adrenodoxin, mitochondrial	284	3.88E-52	76.90%	0.123	IPR001055 (PRINTS); IPR012675 (G3DSA:3.10.20.GENE3D); IPR001041 (PFAM); PTHR23426:SF21 (PANTHER); PTHR23426 (PANTHER); IPR018298 (PROSITE_PATTERNS); IPR001041 (PROSITE_PROFILES); IPR001041 (SUPERFAMILY)
2550	c6130_g1_i1_len_143_path_1_0_142_3	2	reelin isoform x2	48	1.63E-11	66.60%	0.107	G3DSA:2.10.25.10 (GENE3D); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
2551	c6130_g2_i1_len_871_path_1089_0_870_5	30	low quality protein: reelin-like	290	2.16E-60	57.70%	0.206	IPR011040 (G3DSA:2.120.10.GENE3D); PTHR11841 (PANTHER); IPR011040 (SUPERFAMILY)
2552	c6131_g1_i1_len_1255_path_53_0_1254_4	489	estradiol 17-beta-dehydrogenase 8	418	1.17E-88	72.40%	0.273	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR013968 (SMART); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF254 (PANTHER); PTHR24316 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
2553	c6141_g1_i1_len_1215_path_2593_0_13_141_5_14_1214_5	38	cytochrome p450 2j2-like	405	2.33E-112	61.40%	0.129	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
2555	c6166_g1_i1_len_1485_path_1_0_1484_4	54	disintegrin and metalloproteinase domain-containing protein 10-like	495	0	78.30%	0.105	IPR001762 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); PF13688 (PFAM); IPR001762 (G3DSA:4.10.70.GENE3D); IPR001762 (PFAM); PTHR11905:SF4 (PANTHER); PTHR11905 (PANTHER); IPR001762 (PROSITE_PROFILES); IPR001590 (PROSITE_PROFILES); IPR001762 (SUPERFAMILY); SSF55486 (SUPERFAMILY)
2556	c6166_g2_i1_len_444_path_2925_0_443_3	22	disintegrin and metalloproteinase domain-containing protein 10 isoform x3	148	4.65E-46	67.90%	0.157	PTHR11905:SF4 (PANTHER); PTHR11905 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
2554	c61666_g1_i1_len_250_path_1_0_249_2	4	leucine-rich transmembrane	83	4.54E-14	66.00%	0.116	PR00019 (PRINTS); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
2557	c62039_g1_i1_len_259_path_237_0_258_1	8	tyrosine-protein phosphatase	86	5.41E-37	83.80%	0.132	IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
2558	c6209_g1_i1_len_1308_path_1286_0_1307_2	102	twitchin isoform x4	436	0	83.70%	0.116	PR00014 (PRINTS); IPR003599 (SMART); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF155 (PANTHER); PTHR19897 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
2559	c6215_g1_i1_len_309_path_1_0_308_1	10	von willebrand factor type egf and pentraxin domain-containing protein 1 isoform x2	103	2.69E-14	54.50%	0.1	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)

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2576	c6636_g1_i1_len_540_path_568_0_539_2	24	zinc finger protein 26-like	180	5.94E-22	56.30%	0.113	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2577	c6637_g1_i1_len_610_path_53_0_609_2	17	glutamyl aminopeptidase-like	203	3.86E-17	54.20%	0.138	IPR014782 (PFAM); IPR001930 (PANTHER); PTHR11533:SF165 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF63737 (SUPERFAMILY); TMhelix (TMHMM)
2578	c6663_g1_i1_len_373_path_221_0_249_121_250_372_1	11	insulin-like growth factor-binding protein complex acid labile subunit-like	124	1.34E-20	57.40%	0.108	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PFAM); PTHR24365 (PANTHER); SSF52058 (SUPERFAMILY)
2579	c6703_g2_i1_len_156_path_354_0_155_0	2	ankyrin repeat domain-containing protein 27-like	52	2.01E-14	73.70%	0.223	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2580	c672_g1_i1_len_1810_path_53_0_1809_5	1208	ras-related protein rab-1a	603	4.37E-130	93.90%	0.154	IPR001806 (PRINTS); IPR020849 (SMART); IPR003578 (SMART); IPR024156 (SMART); IPR002041 (SMART); IPR003579 (SMART); IPR001806 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR24073 (PANTHER); PTHR24073:SF455 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2581	c6795_g1_i1_len_2263_path_2291_0_2262_5	176	cytochrome p450 cyp44	754	0	65.70%	0.305	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24292:SF0 (PANTHER); PTHR24292 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
2582	c68270_g1_i1_len_851_path_1_0_850_2	31	gastrula zinc finger	283	9.27E-68	56.70%	0.097	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2583	c68271_g1_i1_len_1148_path_1_0_1147_4	114	tho complex subunit 3	383	0	87.00%	0.104	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR015943 (G3DSA:2.130.10.GENE3D); IPR011659 (PFAM); IPR001680 (PFAM); PTHR22839 (PANTHER); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
2584	c68459_g1_i1_len_2322_path_1_0_2321_3	101	fez family zinc finger protein 2	774	0	76.50%	0.15	Coil (COILS); IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

2585	c68472_g1_i1_len_1541_path_1_0_1540_4	82	neuroendocrine partial	514	1.76E-86	61.20%	0.106	IPR000209 (G3DSA:3.40.50.GENE3D); IPR000209 (PFAM); IPR002884 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); IPR015500 (PANTHER); PTHR10795:SF340 (PANTHER); IPR023828 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008979 (SUPERFAMILY); IPR000209 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2586	c68487_g1_i1_len_358_path_1_0_357_3	8	kn motif and ankyrin repeat domain-containing protein 1	120	6.05E-46	77.60%	0.165	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24168:SF19 (PANTHER); PTHR24168 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2587	c68577_g1_i1_len_733_path_711_0_732_1	18	agap008807-pa-like protein	244	2.46E-48	57.50%	0.618 Y	IPR015816 (G3DSA:2.30.230.GENE3D); IPR001747 (PFAM); PTHR23345:SF11 (PANTHER); PTHR23345 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001747 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR015819 (SUPERFAMILY)
2588	c68638_g1_i1_len_1676_path_1_0_1675_5	58	zinc finger and btb domain-containing protein 24	558	9.00E-67	55.70%	0.139	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2589	c68643_g1_i1_len_1071_path_1049_0_1070_3	84	complement c1q tumor necrosis factor-related protein 6 precursor	357	1.08E-19	52.20%	0.122	Coil (COILS); IPR001073 (PRINTS); IPR001073 (SMART); IPR008983 (G3DSA:2.60.120.GENE3D); IPR001073 (PFAM); PTHR22923:SF51 (PANTHER); PTHR22923 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY); TMhelix (TMHMM)
2590	c68671_g1_i1_len_809_path_1_0_808_2	32	dehydrogenase reductase sdr family member on chromosome x-like isoform x1	269	3.02E-72	62.30%	0.114	IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); SSF51735 (SUPERFAMILY)
2591	c68672_g1_i1_len_271_path_249_0_270_3	5	transient receptor potential channel pyrexia-like	91	1.78E-19	68.30%	0.115	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PF13857 (PFAM); PTHR24188 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2592	c6874_g1_i1_len_324_path_494_0_164_1010_165_323_1	18	zinc finger protein	108	8.60E-11	63.10%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2593	c68764_g1_i1_len_724_path_702_0_723_4	12	envelope partial	241	2.54E-19	43.00%	0.136	IPR013755 (G3DSA:3.30.387.GENE3D); IPR013754 (G3DSA:2.60.98.GENE3D); IPR011998 (PFAM); IPR011998 (SUPERFAMILY)
2594	c68789_g1_i1_len_529_path_1_0_528_1	12	zinc finger protein 846 isoform x2	176	1.97E-39	58.50%	0.103	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2595	c6880_g1_i1_len_1452_path_1430_0_1451_2	84	low quality protein: cubilin	484	4.20E-81	54.50%	0.22	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR10127:SF569 (PANTHER); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)

2596	c68834_g1_i1_len_705_path_1_0_704_3	27	cub and sushi domain-containing protein 3-like	235	1.11E-08	47.20%	0.201	IPR000859 (SMART); IPR000859 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); PTHR22991:SF23 (PANTHER); PTHR22991 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); TMhelix (TMHMM)
2597	c68861_g1_i1_len_2686_path_1_0_2685_4	3379	heat shock 70 kda protein cognate 3	895	0	93.90%	0.15	Coil (COILS); Coil (COILS); IPR013126 (PRINTS); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.30.30 (GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); G3DSA:3.90.640.10 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF157 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029048 (SUPERFAMILY); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2598	c68881_g1_i1_len_449_path_1_0_448_1	4	probable serine carboxypeptidase cpvl isoform x2	150	1.60E-22	71.30%	0.109	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); PTHR11802:SF30 (PANTHER); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
2599	c68985_g1_i1_len_1327_path_1305_0_1326_0	60	#NAME?	443	0	81.70%	0.125	G3DSA:3.40.50.2000 (GENE3D); IPR001830 (PFAM); G3DSA:3.40.50.2000 (GENE3D); PTHR10788:SF6 (PANTHER); PTHR10788 (PANTHER); SSF53756 (SUPERFAMILY)
2600	c69004_g1_i1_len_1639_path_1617_0_1638_2	98	carbohydrate sulfotransferase 11-like	546	1.38E-66	55.30%	0.374Y	IPR005331 (PFAM); IPR018011 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
2601	c69037_g1_i1_len_1276_path_1254_0_1275_3	2260	histone 1o	426	2.51E-29	71.80%	0.126	IPR005819 (PRINTS); IPR005818 (SMART); IPR005818 (PFAM); IPR011991 (G3DSA:1.10.10.GENE3D); PTHR11467 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005818 (PROSITE_PROFILES); SSF46785 (SUPERFAMILY)
2602	c69072_g1_i1_len_2236_path_1_0_2235_0	143	transcription initiation factor tfiid subunit 5	746	0	83.40%	0.108	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR007582 (PFAM); IPR001680 (PFAM); PTHR19879 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR006594 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); SSF160897 (SUPERFAMILY); IPR017986 (SUPERFAMILY)
2603	c69092_g1_i1_len_426_path_404_0_425_0	7	r-spondin- partial	142	1.07E-13	59.50%	0.109	G3DSA:2.20.100.10 (GENE3D); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY)
2604	c69098_g1_i1_len_955_path_3_0_954_3	23	von willebrand factor type egf and pentraxin domain-containing protein 1	319	5.03E-13	42.60%	0.12	IPR000436 (SMART); IPR000562 (SMART); IPR000562 (PFAM); IPR000436 (PFAM); IPR000562 (G3DSA:2.10.10.GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325:SF330 (PANTHER); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR013806 (SUPERFAMILY)
2605	c69106_g1_i1_len_331_path_1_0_330_5	11	habp2-prov protein	110	1.40E-19	58.50%	0.2	IPR001314 (PRINTS); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2609	c692_g1_i1_len_1697_path_1619_0_434_46_435_1450_3068_1451_1573_3068_1574_169_6_5	63	low-density lipoprotein receptor-related protein 2	565	4.88E-23	64.20%	0.103	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
2606	c6924_g1_i1_len_828_path_1_0_430_432_43_1_827_0	40	serine protease easter	276	3.22E-45	61.30%	0.107	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

2607	c69251_g1_i1_len_680_path_1_0_679_5	23	tyrosine-protein kinase hopscotch	226	1.98E-60	67.80%	0.117	IPR001245 (PRINTS); IPR020635 (SMART); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418:SF206 (PANTHER); PTHR24418 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY) IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
2608	c69276_g1_i1_len_1014_path_1_0_1013_4	33	receptor-type tyrosine-protein phosphatase eta-partial	338	5.93E-56	65.80%	0.159	Coil (COILS); IPR015880 (SMART); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2610	c69379_g1_i1_len_1556_path_1534_0_1555_2	46	isoform cra_a	518	1.63E-50	56.10%	0.097	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR010909 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR010909 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2611	c6941_g1_i1_len_1521_path_47_0_38_85_39_518_46_519_1397_1443_1398_1520_1	96	papilin isoform x2	507	2.87E-107	63.20%	0.14	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR010909 (PFAM); IPR013098 (PFAM); PTHR10489 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR010909 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2612	c6941_g1_i2_len_1041_path_47_0_38_46__3_9_917_1443_918_1040_1	55	papilin-like isoform x8	347	1.60E-55	67.20%	0.129	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR010909 (PFAM); IPR013098 (PFAM); PTHR10489 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR010909 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2613	c69424_g1_i1_len_564_path_1_0_563_4	12	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfpheX133) (epstein-barr virus-induced zinc finger protein) (znf-eB) (ct-zfp48) (zinc finger protein	188	2.06E-25	58.00%	0.105	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2614	c69430_g1_i1_len_3614_path_1_0_3613_2	195	collagen alpha-1 chain	1204	0	66.20%	0.099	IPR001442 (SMART); IPR001442 (G3DSA:2.170.240.GENE3D); IPR001442 (PFAM); IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF397 (PANTHER); IPR001442 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
2615	c69430_g1_i1_len_3614_path_1_0_3613_4	195	mucin 17-like protein	1205	3.19E-116	43.20%	0.219	no IPS match
2616	c69431_g1_i1_len_604_path_1_0_603_1	16	peptidyl-alpha-hydroxyglycine alpha-amidating lyase 2-like	201	5.55E-25	63.20%	0.239	PTHR10680 (PANTHER)
2617	c69434_g1_i1_len_349_path_327_0_348_1	4	tubulointerstitial nephritis antigen-like	116	4.50E-34	64.40%	0.254	IPR001212 (PFAM); PTHR12411:SF15 (PANTHER); IPR013128 (PANTHER); IPR001212 (PROSITE_PATTERNS)
2618	c69451_g1_i1_len_358_path_336_0_357_1	6	protein fam132a-like isoform x1	119	1.64E-25	64.50%	0.121	IPR006052 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); PTHR24019:SF9 (PANTHER); PTHR24019 (PANTHER); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY)
2619	c69458_g1_i1_len_540_path_518_0_539_5	13	transcriptional repressor ctcf	180	5.88E-108	89.50%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24375 (PANTHER); PTHR24375:SF1 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

2620	c69476_g1_i1_len_361_path_1_0_360_0	5	gamma-glutamyltranspeptidase 1-like	121	5.02E-39	79.60%	0.139	IPR000101 (PRINTS); IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF8 (PANTHER); IPR029055 (SUPERFAMILY)
2621	c6953_g1_i1_len_894_path_922_0_893_3	62	abnormal spindle-like microcephaly-associated protein homolog	298	4.35E-88	65.10%	0.129	PR00014 (PRINTS); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013098 (PFAM); PTHR19900 (PANTHER); PTHR19900:SF44 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2622	c69644_g1_i1_len_293_path_271_0_292_2	3	agrin-like isoform x6	97	3.46E-23	61.80%	0.103	IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); PTHR10913 (PANTHER); PTHR10913:SF45 (PANTHER); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY)
2623	c69660_g1_i1_len_399_path_377_0_398_4	6	cbpb_astas ame: full=carboxypeptidase b	133	4.28E-44	67.20%	0.108	IPR000834 (SMART); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
2624	c69661_g1_i1_len_422_path_1_0_421_0	7	5 -nucleotidase	141	7.19E-55	76.40%	0.096	IPR006179 (PRINTS); IPR008334 (G3DSA:3.90.550.GENE3D); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11575:SF21 (PANTHER); IPR006179 (PANTHER); IPR029052 (SUPERFAMILY); IPR008334 (SUPERFAMILY)
2625	c69691_g1_i1_len_422_path_1_0_421_4	8	exostosin- partial	141	1.58E-68	84.20%	0.147	IPR015338 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); PTHR11062 (PANTHER); IPR027673 (PTHR11062:PANTHER); IPR029044 (SUPERFAMILY)
2626	c69696_g1_i1_len_373_path_351_0_372_1	7	aldehyde dehydrogenase family 16 member a1-like	124	1.68E-59	89.60%	0.1	IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF98 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
2627	c6983_g1_i1_len_1657_path_1635_0_1656_5	3013	clotting factor b-like	552	2.00E-66	60.30%	0.299	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2628	c69915_g1_i1_len_880_path_1_0_879_1	27	maguk p55 subfamily member 7 isoform x2	293	8.47E-152	79.30%	0.111	IPR004172 (SMART); IPR001452 (SMART); IPR001478 (SMART); IPR001478 (PFAM); IPR011511 (PFAM); IPR014775 (PFAM); G3DSA:2.30.30.40 (GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR23122:SF14 (PANTHER); PTHR23122 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR004172 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001452 (SUPERFAMILY); SSF101288 (SUPERFAMILY)
2629	c69969_g1_i1_len_1124_path_1102_0_1123_0	35	insulin-like receptor	375	3.58E-116	64.50%	0.11	IPR006212 (SMART); IPR000494 (G3DSA:3.80.20.GENE3D); IPR000494 (G3DSA:3.80.20.GENE3D); G3DSA:2.10.220.10 (GENE3D); IPR006211 (PFAM); G3DSA:2.10.220.10 (GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000494 (PFAM); PTHR24416 (PANTHER); IPR028792 (PTHR24416:PANTHER); IPR009030 (SUPERFAMILY); SSF52058 (SUPERFAMILY)
2630	c69970_g1_i1_len_1261_path_1239_0_1260_5	64	perlucin-like protein	420	6.32E-19	53.30%	0.108	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2631	c70054_g1_i1_len_756_path_734_0_755_1	23	protein toll	252	9.15E-33	50.50%	0.411 Y	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365:SF249 (PANTHER); PTHR24365 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
2632	c70152_g1_i1_len_777_path_755_0_776_0	20	gamma-glutamyltranspeptidase 1-like	259	1.33E-48	54.50%	0.285	IPR000101 (PRINTS); IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF18 (PANTHER); IPR029055 (SUPERFAMILY)
2633	c70173_g1_i1_len_852_path_1_0_851_2	403	hemagglutinin amebocyte aggregation factor-like	284	9.27E-30	57.60%	0.446 Y	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
2634	c7030_g1_i1_len_774_path_353_0_340_728_341_773_4	22	xylosylprotein beta4-	258	1.77E-108	71.50%	0.123	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR027995 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)

[illegible]

2660	c71796_g1_i1_len_714_path_1_0_713_0	12	low quality protein: zinc finger protein gfi-1	238	8.53E-15	61.60%	0.133	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2661	c71801_g1_i1_len_501_path_479_0_500_3	16	inversin- partial	167	7.65E-51	71.60%	0.360 Y	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); PTHR24178 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2662	c71870_g1_i1_len_816_path_794_0_815_2	19	deleted in autism protein 1	272	5.88E-58	55.30%	0.121	IPR022049 (PFAM); PTHR32073:SF7 (PANTHER); PTHR32073 (PANTHER); IPR020519 (PRODOM); IPR011009 (SUPERFAMILY)
2663	c72084_g1_i1_len_972_path_950_0_971_3	24	85 88 kda calcium-independent phospholipase a2	324	6.25E-75	64.10%	0.234	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24139 (PANTHER); PTHR24139:SF33 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2664	c72110_g1_i1_len_848_path_826_0_847_5	24	neuroligin- y-linked	282	2.87E-115	76.50%	0.167	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559:SF157 (PANTHER); PTHR11559 (PANTHER); IPR029058 (SUPERFAMILY)
2665	c72198_g1_i1_len_393_path_1_0_392_0	17	lipophorin receptor	131	2.88E-07	48.25%	0.104	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
2666	c72301_g1_i1_len_598_path_576_0_597_0	298	histone h2a-like	200	1.13E-79	97.30%	0.246	IPR002119 (PRINTS); IPR002119 (SMART); IPR007125 (PFAM); IPR009072 (G3DSA:1.10.20.GENE3D); PTHR23430:SF45 (PANTHER); PTHR23430 (PANTHER); IPR002119 (PROSITE_PATTERNS); IPR009072 (SUPERFAMILY)
2667	c72365_g1_i1_len_315_path_1_0_314_1	6	pancreatic triacylglycerol lipase-like	105	1.67E-43	79.60%	0.212	IPR000734 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR013818 (PFAM); IPR000734 (PANTHER); PTHR11610:SF8 (PANTHER); IPR029058 (SUPERFAMILY)
2668	c72415_g1_i1_len_1102_path_1080_0_1101_1	33	zinc finger protein 492-like	367	2.55E-22	71.80%	0.116	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2669	c72512_g1_i1_len_350_path_328_0_349_1	10	gastrula zinc finger	117	3.97E-34	70.60%	0.099	IPR015880 (SMART); PF13912 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2670	c72540_g1_i1_len_333_path_313_0_332_4	3	zinc finger and btb domain-containing protein	111	6.41E-17	59.60%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

2671	c72545_g1_i1_len_651_path_565_0_476_104_2_477_563_1042_564_650_4	28	gastrula zinc finger protein - partial	217	2.68E-33	53.00%	0.1	IPR015880 (SMART); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2672	c7262_g1_i1_len_1914_path_1892_0_1913_1	595	dorsal-ventral patterning protein tolloid	638	0	79.50%	0.192	Coil (COILS); IPR001506 (PRINTS); IPR006026 (SMART); IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000859 (PFAM); PTHR10127:SF304 (PANTHER); PTHR10127 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
2673	c72656_g1_i1_len_596_path_1_0_595_5	24	gastrula zinc finger	198	3.75E-23	63.50%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2674	c72720_g1_i1_len_264_path_1_0_263_0	4	cd4-specific ankyrin repeat protein	88	4.45E-13	60.80%	0.113	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24182 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2675	c72727_g1_i1_len_351_path_1_0_350_5	9	carboxypeptidase e	117	4.40E-28	66.00%	0.108	PF13620 (PFAM); IPR014766 (G3DSA:2.60.40.GENE3D); PTHR11532 (PANTHER); IPR008969 (SUPERFAMILY)
2676	c72856_g1_i1_len_428_path_406_0_427_0	5	transient receptor potential channel pyrexia	143	1.12E-56	78.70%	0.137	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24161 (PANTHER); IPR030288 (PTHR24161:PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2677	c72912_g1_i1_len_625_path_603_0_624_0	30	low quality protein: titin-like	209	3.86E-55	62.40%	0.124	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2678	c7293_g1_i1_len_665_path_643_0_664_2	71	trypsinogen 2	221	1.02E-73	66.60%	0.888Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
2679	c7293_g2_i1_len_219_path_1285_0_218_0	13	transmembrane protease serine 13	73	1.70E-14	75.90%	0.106	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2680	c73016_g1_i1_len_798_path_776_0_797_1	20	zinc finger protein 316-like	266	3.75E-12	67.30%	0.191	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2681	c73107_g1_i1_len_810_path_1_0_809_1	11	GK10945	270	9.63E-20	76.60%	0.1	IPR001916 (PRINTS); IPR001916 (SMART); G3DSA:1.10.530.10 (GENE3D); IPR001916 (PFAM); PTHR11407 (PANTHER); IPR001916 (PROSITE_PROFILES); IPR023346 (SUPERFAMILY)
2682	c73234_g1_i1_len_627_path_605_0_626_0	14	ephrin-b2 isoform x1	209	6.94E-89	80.90%	0.105	IPR001799 (PRINTS); IPR001799 (PFAM); IPR008972 (G3DSA:2.60.40.GENE3D); IPR001799 (PANTHER); PTHR11304:SF29 (PANTHER); IPR001799 (PRODOM); IPR001799 (PROSITE_PROFILES); IPR008972 (SUPERFAMILY)
2683	c73248_g1_i1_len_780_path_758_0_779_3	44	beta- -galactosyltransferase 7	260	1.88E-122	81.50%	0.102	IPR003859 (PRINTS); IPR027995 (PFAM); IPR027791 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR003859 (PANTHER); PTHR19300:SF1 (PANTHER); IPR029044 (SUPERFAMILY)

2684	c73295_g1_i1_len_1235_path_1_0_1234_5	39	liver carboxylesterase 2-like	411	4.97E-24	50.60%	0.109	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559 (PANTHER); PTHR11559:SF157 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
2685	c73313_g1_i1_len_774_path_752_0_773_0	1436	kazal-type serine proteinase inhibitor 3	258	3.94E-24	56.90%	0.504Y	IPR002350 (SMART); IPR002350 (PFAM); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); G3DSA:3.30.60.30 (GENE3D); PTHR10913:SF46 (PANTHER); PTHR10913 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SignalIP-TM (SIGNALP_EUK); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2686	c73410_g1_i1_len_514_path_492_0_513_2	15	carboxypeptidase b-like	171	1.30E-26	56.20%	0.678Y	G3DSA:3.40.630.10 (GENE3D); IPR003146 (G3DSA:3.30.70.GENE3D); IPR003146 (PFAM); PTHR11705 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR009020 (SUPERFAMILY)
2687	c73414_g1_i1_len_407_path_1_0_406_4	56	protein	136	3.34E-30	82.60%	0.444 Y	no IPS match
2688	c73455_g1_i1_len_1052_path_1_0_1051_1	239	---NA---	351			0.108	Coil (COILS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
2689	c73458_g1_i1_len_783_path_761_0_782_0	27	protein phosphatase 1 regulatory subunit 16a isoform x4	261	2.69E-105	77.60%	0.103	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24186 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2690	c73536_g1_i1_len_201_path_1_0_200_4	2	isoform a	67	1.13E-25	89.90%	0.139	IPR024079 (G3DSA:3.40.390.GENE3D); PTHR11905 (PANTHER); PTHR11905:SF121 (PANTHER); SSF55486 (SUPERFAMILY)
2691	c73607_g1_i1_len_608_path_1_0_607_5	17	leucine-rich repeat-containing protein 15-like	202	8.45E-32	53.50%	0.205	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24373 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
2692	c73736_g1_i1_len_273_path_251_0_272_5	6	leucine-rich repeat-containing protein 19-like isoform x1	91	9.53E-10	58.80%	0.123	PR00019 (PRINTS); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365:SF265 (PANTHER); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
2693	c73773_g1_i1_len_140_path_2_0_139_5	0	very low-density lipoprotein receptor	46	1.40E-07	71.40%	0.111	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
2694	c73784_g1_i1_len_352_path_1_0_351_4	11	zinc finger and scan domain-containing protein 2-like isoform x1	117	1.15E-64	87.60%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2695	c73835_g1_i1_len_686_path_1_0_685_2	11	pr domain zinc finger protein 4	228	2.73E-31	69.50%	0.105	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR027775 (PANTHER); PTHR10032:SF157 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2696	c73853_g1_i1_len_530_path_508_0_529_2	8	papain family cysteine protease containing protein	176	5.66E-30	53.60%	0.155	IPR000668 (SMART); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR013128 (PANTHER); PTHR12411:SF316 (PANTHER); IPR025660 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
2697	c73920_g1_i1_len_1204_path_1_0_1203_0	65	ste20-related kinase adapter protein alpha	402	1.39E-145	65.70%	0.098	G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24361:SF273 (PANTHER); PTHR24361 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2698	c7398_g1_i2_len_294_path_272_0_175_448_176_293_3	8	abl interactor 2 isoform x1	98	7.51E-39	86.60%	0.099	IPR001452 (PRINTS); IPR001452 (SMART); IPR001452 (PFAM); G3DSA:2.30.30.40 (GENE3D); IPR028457 (PANTHER); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY)

[illegible]

2713	c75151_g1_i1_len_690_path_668_0_689_4	7	zinc finger protein zfat-like	230	3.57E-28	62.90%	0.719Y	IPR015880 (SMART); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
2714	c75203_g1_i1_len_1022_path_1000_0_1021_3	31	shootin-1	341	1.70E-26	52.70%	0.108	Coil (COILS); Coil (COILS); Coil (COILS)
2715	c75245_g1_i1_len_818_path_1_0_817_5	24	asparagine-rich zinc finger protein azf1-like isoform x2	272	5.90E-65	69.00%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2716	c7546_g1_i1_len_801_path_1_0_800_5	36	down syndrome cell adhesion molecule-like protein dscam2	267	6.39E-136	84.30%	0.102	IPR003961 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF567 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
2717	c75553_g1_i1_len_296_path_1_0_295_4	13	retinol dehydrogenase 14-like	99	6.23E-10	63.20%	0.119	PTHR24320 (PANTHER)
2718	c75590_g1_i1_len_413_path_391_0_412_2	7	mitogen-activated protein kinase-binding protein 1-like isoform x1	137	1.68E-63	86.80%	0.137	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847 (PANTHER); PTHR22847:SF332 (PANTHER); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2719	c75608_g1_i1_len_814_path_792_0_813_0	24	cytochrome p450 18a1	272	1.12E-101	77.80%	0.12	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300:SF116 (PANTHER); PTHR24300 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
2720	c75665_g1_i1_len_494_path_472_0_493_1	8	17-beta-hydroxysteroid dehydrogenase 13-like	165	1.49E-40	70.00%	0.129	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF214 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
2721	c75806_g1_i1_len_426_path_404_0_425_3	6	gamma-glutamyl hydrolase-like	142	3.68E-20	69.50%	0.111	IPR029062 (G3DSA:3.40.50.GENE3D); IPR011697 (PFAM); IPR015527 (PANTHER); PTHR11315:SF2 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY); TMhelix (TMHMM)
2722	c75881_g1_i1_len_711_path_689_0_710_1	26	dipeptidyl peptidase 9 isoform x1	237	1.17E-103	75.60%	0.18	IPR002469 (G3DSA:2.140.10.GENE3D); IPR002469 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11731 (PANTHER); PTHR11731:SF110 (PANTHER); IPR029058 (SUPERFAMILY); SSF82171 (SUPERFAMILY)
2723	c7610_g1_i1_len_1554_path_41_0_1457_40_1458_1553_0	1804	p-selectin- partial	518	4.21E-14	40.00%	0.374Y	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325:SF321 (PANTHER); PTHR19325 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); TMhelix (TMHMM)
2724	c76148_g1_i1_len_581_path_1_0_580_2	19	transforming growth factor-beta-induced protein ig-h3-like	193	6.84E-83	65.40%	0.102	IPR000782 (SMART); IPR000782 (PFAM); IPR000782 (G3DSA:2.30.180.GENE3D); PTHR10900:SF73 (PANTHER); PTHR10900 (PANTHER); IPR011489 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY)
2725	c7622_g1_i1_len_317_path_295_0_76_372_7_7_316_4	10	carboxypeptidase partial	106	7.65E-29	75.10%	0.11	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
2726	c7631_g1_i1_len_1191_path_1169_0_1190_2	168	peroxisomal trans-2-enoyl- reductase-like	397	1.05E-126	74.10%	0.135	IPR002347 (PRINTS); PF13561 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24317 (PANTHER); SSF51735 (SUPERFAMILY)

2727	c76348_g1_i1_len_721_path_1_0_720_3	18	plexin- partial	241	3.91E-118	83.80%	0.103	Coil (COILS); IPR013548 (PFAM); PTHR22625 (PANTHER); PTHR22625:SF16 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
2728	c76440_g1_i1_len_249_path_17_0_248_0	4	esterase fe4	83	1.15E-25	73.40%	0.126	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR019826 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
2729	c7661_g1_i1_len_1019_path_997_0_982_13_983_1018_4	618	27 kda hemolymph	340	1.34E-30	49.50%	0.203	IPR009832 (PFAM); PTHR20997 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
2730	c76639_g1_i1_len_360_path_338_0_359_0	9	adp-dependent glucokinase-like	120	1.63E-38	73.20%	0.176	IPR029056 (G3DSA:3.40.1190.GENE3D); IPR007666 (PFAM); PTHR21208:SF1 (PANTHER); IPR007666 (PANTHER); IPR007666 (PROSITE_PROFILES); IPR029056 (SUPERFAMILY)
2731	c76653_g1_i1_len_534_path_512_0_533_1	10	low-density lipoprotein receptor-related protein partial	178	1.62E-29	57.50%	0.11	IPR000859 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR002172 (PFAM); IPR000859 (PFAM); PTHR10529 (PANTHER); PTHR10529:SF216 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR000859 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
2732	c76734_g1_i1_len_830_path_1_0_829_2	13	sodium channel protein para	276	1.44E-137	89.50%	0.118	IPR010526 (PFAM); IPR005821 (PFAM); IPR027359 (G3DSA:1.20.120.GENE3D); PTHR10037 (PANTHER); IPR028814 (PTHR10037:PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF81324 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2733	c76810_g1_i1_len_328_path_1_0_327_1	9	glycoside hydrolase family 1	109	8.42E-33	80.70%	0.109	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001360 (PFAM); IPR001360 (PANTHER); IPR018120 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
2734	c77155_g1_i1_len_488_path_1_0_487_4	8	vascular endothelial growth factor receptor 1-like	163	2.73E-18	57.40%	0.104	G3DSA:1.10.510.10 (GENE3D); IPR001956 (G3DSA:2.60.40.GENE3D); IPR001245 (PFAM); PTHR24416:SF298 (PANTHER); PTHR24416 (PANTHER); IPR011009 (SUPERFAMILY)
2735	c77273_g1_i1_len_412_path_1_0_411_1	103	glycosyl-phosphatidylinositol-linked carbonic anhydrase	137	1.28E-11	54.70%	0.32	IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); IPR023561 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
2736	c77400_g1_i1_len_249_path_227_0_248_1	4	microtubule-associated serine threonine-protein kinase 3 isoform x3	83	1.25E-47	98.00%	0.121	IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24356 (PANTHER); PTHR24356:SF36 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2737	c77544_g1_i1_len_356_path_334_0_355_2	7	gastrula zinc finger protein	118	9.73E-23	59.30%	0.098	IPR015880 (SMART); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2738	c77569_g1_i1_len_673_path_651_0_672_4	18	otopettrin-2 isoform x1	224	2.42E-61	58.60%	0.201	IPR004878 (PFAM); IPR004878 (PANTHER); PTHR21522:SF37 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2739	c77687_g1_i1_len_375_path_353_0_374_0	8	ankyrin repeat-containing protein	125	1.10E-10	55.50%	0.121	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24182 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2740	c77816_g1_i1_len_452_path_430_0_451_2	8	transport and golgi organization protein 1	150	3.45E-16	63.70%	0.32	IPR011511 (PFAM); G3DSA:2.30.30.40 (GENE3D); IPR001452 (SUPERFAMILY)

2741	c77822_g1_i1_len_585_path_1_0_584_5	12	zinc finger and btb domain-containing protein partial	195	1.04E-22	59.60%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY);
2742	c77895_g1_i1_len_441_path_419_0_440_4	10	zinc finger protein 235-like	147	2.54E-32	61.40%	0.11	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY);
2743	c77920_g1_i1_len_429_path_407_0_428_0	6	maltase- intestinal isoform x2	143	5.02E-33	61.20%	0.099	PTHR22762 (PANTHER); PTHR22762:SF7 (PANTHER); IPR011013 (SUPERFAMILY)
2744	c77989_g1_i1_len_500_path_1_0_499_4	14	plexin-a4	167	3.77E-66	77.40%	0.101	IPR002909 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR002909 (PFAM); PTHR22625 (PANTHER); PTHR22625:SF16 (PANTHER); IPR014756 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
2745	c7852_g1_i1_len_1593_path_131_0_1592_4	61	zinc c2h2	531	8.38E-55	76.90%	0.153	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR23223 (PANTHER); PTHR23223:SF130 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2746	c78590_g1_i1_len_304_path_282_0_303_2	6	zinc finger and btb domain-containing protein 49	101	4.72E-13	62.20%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2747	c78598_g1_i1_len_496_path_1_0_495_5	8	zinc finger	165	1.52E-74	84.20%	0.11	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); PTHR23228 (PANTHER); PTHR23228:SF78 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2748	c78628_g1_i1_len_402_path_1_0_401_5	11	bone morphogenetic protein receptor type-2	134	3.31E-57	80.20%	0.135	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR23255:SF52 (PANTHER); IPR000333 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2749	c7879_g1_i1_len_1098_path_1_0_1097_2	184	superoxide dismutase	366	5.85E-59	66.10%	0.158	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); IPR001424 (SUPERFAMILY)
2750	c78826_g1_i1_len_412_path_390_0_411_3	10	zinc finger protein	138	1.20E-25	60.50%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2751	c78885_g1_i1_len_170_path_1_0_169_5	1	ectonucleotide pyrophosphatase phosphodiesterase family member 3	56	5.74E-11	71.40%	0.147	IPR002591 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); IPR024873 (PANTHER); IPR017850 (SUPERFAMILY)
2752	c78996_g1_i1_len_412_path_1_0_411_5	8	leucine-rich repeat and transmembrane domain-containing protein 1	137	9.02E-11	58.30%	0.103	PR00019 (PRINTS); IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)

2753	c79020_g1_i1_len_484_path_1_0_483_4	16	carbohydrate sulfotransferase 11 isoform x1	161	1.56E-28	57.30%	0.123	IPR005331 (PFAM); PTHR12137:SF29 (PANTHER); IPR018011 (PANTHER)
2754	c79204_g1_i1_len_324_path_1_0_323_1	6	low quality protein: glypican-1	108	6.30E-16	77.60%	0.103	IPR001863 (PFAM); PTHR10822:SF25 (PANTHER); IPR001863 (PANTHER)
2755	c79268_g1_i1_len_1274_path_1252_0_1273_4	27	lethal isoform a	425	5.56E-54	91.30%	0.235	IPR024084 (G3DSA:3.40.718.GENE3D); IPR024084 (PFAM); IPR001804 (PANTHER); PTHR11835:SF34 (PANTHER); IPR019818 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53659 (SUPERFAMILY); TMhelix (TMHMM)
2756	c79392_g1_i1_len_256_path_1_0_255_4	2	cre-lrp-1 protein	85	3.86E-13	76.10%	0.12	IPR000033 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); IPR000033 (PROSITE_PROFILES)
2757	c7943_g1_i1_len_3519_path_3497_0_1658_5_156_1659_1661_5159_1662_3518_5	218	low-density lipoprotein receptor-related protein 2	1173	3.20E-13	53.00%	0.101	IPR002172 (PRINTS); IPR002172 (SMART); IPR000998 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PFAM); IPR000859 (G3DSA:2.60.120.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
2758	c79458_g1_i1_len_310_path_1_0_309_0	5	tyrosine-protein kinase dnt	104	2.85E-41	78.70%	0.1	G3DSA:3.30.200.20 (GENE3D); IPR001245 (PFAM); PTHR24416 (PANTHER); PTHR24416:SF302 (PANTHER); IPR011009 (SUPERFAMILY)
2759	c79460_g1_i1_len_362_path_360_0_361_0	2	repetin	121	1.33E-08	47.78%	0.101	no IPS match
2760	c79461_g1_i1_len_159_path_1_0_158_2	1	xanthine dehydrogenase oxidase-like	53	1.09E-18	85.00%	0.127	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR008274 (SUPERFAMILY)
2761	c79571_g1_i1_len_537_path_515_0_536_2	9	zinc finger protein 239- partial	179	4.44E-45	71.60%	0.151	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2763	c7961_g1_i1_len_1506_path_1484_0_1505_0	68	endoplasmic reticulum resident protein 44 isoform x2	502	0	79.10%	0.178	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PF13848 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF49 (PANTHER); PTHR18929 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
2762	c79617_g1_i1_len_141_path_1_0_140_1	0	5 -nucleotidase-like	47	5.73E-12	82.70%	0.142	IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11575:SF20 (PANTHER); IPR006179 (PANTHER); IPR029052 (SUPERFAMILY)
2764	c79739_g1_i1_len_684_path_662_0_683_1	25	zinc finger protein 235	228	2.80E-12	48.70%	0.1	IPR015880 (SMART); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2765	c7979_g1_i1_len_949_path_927_0_948_5	388	poly -specific endoribonuclease homolog	316	4.92E-79	63.40%	0.306	IPR018998 (PFAM); PTHR12439 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SSF142877 (SUPERFAMILY)
2766	c79826_g1_i1_len_752_path_730_0_751_5	16	g-protein coupled receptor mth2	250	2.17E-50	62.20%	0.249	IPR000832 (PFAM); PTHR12011:SF244 (PANTHER); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017981 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

2780	c80978_g1_i1_len_268_path_1_0_6_8_7_93_8_94_180_8_181_267_4	1	zinc c2h2 type	89	8.70E-15	56.70%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2781	c81076_g1_i1_len_454_path_432_0_453_4	13	transcriptional repressor ctcf-like isoform x1	151	1.02E-88	91.90%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24375:SF1 (PANTHER); PTHR24375 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2782	c81114_g1_i1_len_293_path_271_0_292_1	8	de-cadherin isoform x1	98	8.96E-25	67.60%	0.098	IPR002126 (PRINTS); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); PTHR24027:SF276 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY)
2783	c8117_g1_i1_len_748_path_39_0_31_70_32_32_19_33_747_2	24	---NA---	249			0.344Y	no IPS match
2784	c8135_g1_i1_len_312_path_479_0_18_481_1_9_311_2	7	tyrosine-protein phosphatase partial	104	1.08E-48	91.30%	0.144	PR00014 (PRINTS); IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19134 (PANTHER); PTHR19134:SF204 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
2785	c8135_g1_i2_len_443_path_41_0_149_481_1_50_442_1	21	tyrosine-protein phosphatase lar isoform x4	148	2.05E-74	87.40%	0.118	PR00014 (PRINTS); IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19134 (PANTHER); PTHR19134:SF204 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
2786	c81464_g1_i1_len_441_path_419_0_440_1	9	transforming growth factor-beta-induced protein ig-h3-like isoform x6	147	8.63E-49	67.00%	0.174	IPR000782 (SMART); IPR000782 (PFAM); IPR000782 (G3DSA:2.30.180.GENE3D); PTHR10900 (PANTHER); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY)
2787	c81560_g1_i1_len_216_path_1_0_215_1	2	er degradation-enhancing alpha-mannosidase-like 3	72	2.80E-39	92.20%	0.111	IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); PTHR11742:SF38 (PANTHER); IPR001382 (PANTHER); IPR001382 (SUPERFAMILY)
2788	c8169_g1_i1_len_1150_path_1178_0_827_52_828_1149_0	402	otogelin- partial	384	7.96E-17	38.60%	0.202	no IPS match
2789	c81816_g1_i1_len_473_path_1_0_472_2	18	insulin degrading	157	5.58E-48	72.90%	0.139	IPR007863 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); PTHR11851:SF108 (PANTHER); PTHR11851 (PANTHER); IPR011249 (SUPERFAMILY)
2790	c81885_g1_i1_len_559_path_537_0_558_4	8	neurexin-4 isoform x2	186	2.70E-81	78.20%	0.185	IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF556 (PANTHER); IPR001791 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
2791	c8224_g1_i1_len_1142_path_1120_0_1141_2	85	balbiani ring protein 3	380	6.84E-18	49.80%	0.104	IPR000072 (SMART); IPR000072 (PFAM); IPR004153 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); PTHR11633:SF1 (PANTHER); PTHR11633 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000072 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY); TMhelix (TMHMM)

2792	c82332_g1_i1_len_866_path_844_0_865_0	19	neurogenic locus protein partial	289	3.67E-125	74.80%	0.102	PR00010 (PRINTS); IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); PTHR24044:SF216 (PANTHER); PTHR24044 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR009030 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY);
2793	c82333_g1_i1_len_437_path_1_0_436_4	6	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	146	5.70E-26	53.20%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY);
2794	c8251_g1_i1_len_1609_path_1639_0_1227_2_866_1228_1229_54_1230_1608_2	71	probable g-protein coupled receptor 133 isoform x2	536	1.79E-54	53.00%	0.202	IPR000832 (PFAM); PTHR12011:SF222 (PANTHER); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
2795	c82584_g1_i1_len_374_path_1_0_373_1	6	ectonucleotide pyrophosphatase phosphodiesterase family member 5	125	4.64E-22	60.20%	0.102	IPR002591 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); IPR024873 (PANTHER); PTHR10151:SF70 (PANTHER); IPR017850 (SUPERFAMILY)
2796	c82758_g1_i1_len_517_path_1_0_516_4	6	fras1-related extracellular matrix protein 1-like	172	6.52E-19	50.30%	0.115	PTHR15036 (PANTHER)
2797	c8297_g1_i1_len_336_path_1_0_335_4	9	achain crystal structure of engineered northeast structural genomics consortium target	112	1.13E-19	55.50%	0.13	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2798	c8308_g1_i1_len_378_path_356_0_377_4	8	ring finger and spry domain-containing protein 1-like	126	2.24E-15	82.00%	0.108	IPR001841 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); PF13920 (PFAM); IPR001841 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY)
2799	c8308_g2_i1_len_320_path_1008_0_319_5	6	ring finger and spry domain-containing protein 1-like	106	2.71E-40	75.20%	0.202	IPR003877 (PFAM); PTHR13363 (PANTHER); IPR001870 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
2800	c8310_g1_i1_len_279_path_1_0_278_3	4	zinc finger protein 195- partial	93	3.81E-24	66.10%	0.112	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2801	c832_g1_i1_len_485_path_61_0_91_60_92_4_84_1	16	glutamyl aminopeptidase-like	162	1.70E-19	53.20%	0.263	G3DSA:1.10.390.10 (GENE3D); IPR001930 (PANTHER); PTHR11533:SF165 (PANTHER); SSF55486 (SUPERFAMILY)

2802	c8331_g2_i1_len_673_path_217_0_672_1	17	fibronectin type-iii domain-containing protein 3a-like isoform x5	224	1.80E-78	74.10%	0.111	IPR00014 (PRINTS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19900 (PANTHER); PTHR19900:SF50 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
2803	c83334_g1_i1_len_369_path_1_0_368_3	10	chemosensory protein	123	2.24E-52	85.50%	0.352Y	IPR005055 (G3DSA:1.10.2080.GENE3D); IPR005055 (PFAM); PTHR11257:SF4 (PANTHER); IPR005055 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR005055 (SUPERFAMILY); TMhelix (TMHMM)
2804	c83348_g1_i1_len_349_path_1_0_348_1	4	protein kinase domain-containing cytoplasmic isoform x2	116	2.04E-21	54.00%	0.099	no IPS match
2805	c83371_g1_i1_len_397_path_375_0_396_0	14	PREDICTED: uncharacterized protein LOC103569758	133	2.06E-15	63.60%	0.106	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
2806	c83452_g1_i1_len_308_path_1_0_307_0	4	zinc finger protein 37-like	103	2.98E-17	64.90%	0.11	IPR015880 (SMART); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2807	c83760_g1_i1_len_543_path_521_0_542_3	8	zinc finger protein 683 isoform x2	181	3.75E-15	52.10%	0.098	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2808	c83852_g1_i1_len_503_path_1_0_502_2	8	zinc finger protein 484-like	167	6.37E-47	63.20%	0.119	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2809	c83913_g1_i1_len_276_path_1_0_275_1	5	prenylcysteine oxidase	92	1.32E-13	62.10%	0.097	IPR010795 (PFAM); IPR017046 (PANTHER)
2810	c8405_g1_i1_len_461_path_439_0_88_528_8_9_104_544_105_460_3	2782	ribosomal protein s26	154	2.07E-59	89.80%	0.103	IPR000892 (PFAM); IPR000892 (PANTHER); IPR000892 (PROSITE_PATTERNS)
2811	c84085_g1_i1_len_538_path_1_0_537_0	15	dnaj homolog subfamily c member 3	180	6.14E-73	74.00%	0.103	Coil (COILS); IPR019734 (SMART); IPR013105 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PF13414 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF132 (PANTHER); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY); SSF48452 (SUPERFAMILY)
2812	c84136_g1_i1_len_263_path_241_0_262_5	6	cadherin-related tumor suppressor	87	2.95E-27	71.10%	0.099	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027:SF268 (PANTHER); PTHR24027 (PANTHER); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY)
2813	c8414_g1_i1_len_294_path_1_0_293_0	8	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	98	5.17E-18	65.40%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2814	c8416_g2_i1_len_583_path_469_0_582_5	16	limbic system-associated membrane protein	194	4.31E-58	69.60%	0.125	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR19831:SF47 (PANTHER); PTHR19831 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)

2825	c84918_g1_i1_len_403_path_381_0_402_0	7	cadherin- partial	135	6.38E-49	78.80%	0.13	IPR002126 (PRINTS); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027:SF45 (PANTHER); PTHR24027 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
2826	c8513_g1_i1_len_1905_path_1883_0_1904_1	137	von willebrand factor a domain-containing protein 8	635	0	74.60%	0.175	IPR011704 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR21610 (PANTHER); PTHR21610:SF9 (PANTHER); IPR027417 (SUPERFAMILY); IPR027417 (SUPERFAMILY)
2827	c8513_g2_i1_len_172_path_3914_0_171_4	2	von willebrand factor a domain-containing protein 8- partial	57	1.24E-24	93.20%	0.102	IPR011704 (PFAM); PTHR21610:SF9 (PANTHER); PTHR21610 (PANTHER)
2828	c85247_g1_i1_len_338_path_1_0_337_0	4	villin-1-like isoform x2	113	1.40E-41	73.10%	0.101	IPR007122 (PRINTS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY)
2829	c85284_g1_i1_len_253_path_231_0_252_5	6	carboxypeptidase d	84	2.78E-18	68.40%	0.107	PF13620 (PFAM); IPR014766 (G3DSA:2.60.40.GENE3D); PTHR11532 (PANTHER); IPR027062 (PTHR11532:PANTHER); IPR008969 (SUPERFAMILY) IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF251 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
2830	c8530_g1_i1_len_1549_path_1_0_1548_3	248	hydroxyacyl dehydrogenase	517	1.00E-128	83.60%	0.202	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23228 (PANTHER); PTHR23228:SF106 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2831	c85818_g1_i1_len_201_path_1_0_200_4	2	zinc finger protein gfi- partial	67	1.86E-38	98.20%	0.14	IPR006589 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR006047 (PFAM); IPR015902 (PANTHER); PTHR10357:SF77 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2832	c8592_g1_i1_len_2087_path_2065_0_1583_3 649_1584_2086_5	169	maltase partial	695	7.71E-61	65.00%	0.147	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24188 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2833	c86240_g1_i1_len_376_path_1_0_375_4	4	achain crystal structure of artificial ankyrin repeat protein_ank 1d4	125	4.51E-14	59.10%	0.232	IPR025705 (PRINTS); IPR029018 (G3DSA:3.30.379.GENE3D); IPR029019 (PFAM); IPR015883 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR22600 (PANTHER); PTHR22600:SF4 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029018 (SUPERFAMILY); IPR017853 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2834	c8626_g1_i1_len_1178_path_1206_0_1177_1	96	beta-n-acetylglucosaminidase-like partial	393	1.39E-83	59.30%	0.126	IPR000668 (PRINTS); IPR000668 (SMART); IPR000010 (SMART); IPR013201 (SMART); IPR013201 (PFAM); G3DSA:3.10.450.10 (GENE3D); G3DSA:3.90.70.10 (GENE3D); IPR000010 (PFAM); IPR000668 (PFAM); IPR013128 (PANTHER); PTHR12411:SF316 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR018073 (PROSITE_PATTERNS); IPR018073 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020381 (PRODOM); SSF54401 (SUPERFAMILY); SSF54403 (SUPERFAMILY); SSF54403 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2835	c8661_g1_i1_len_2206_path_1_0_2205_2	105	cysteine proteinase cg12163	735	0	66.60%	0.102	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR001245 (PFAM); PTHR24418 (PANTHER); PTHR24418:SF185 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2836	c86626_g1_i1_len_329_path_307_0_328_0	4	tyrosine-protein kinase shark	110	2.68E-46	82.80%	0.108	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
2837	c8665_g1_i1_len_933_path_1_0_932_5	88	urokinase-type plasminogen activator	311	7.24E-66	54.10%	0.1	IPR003410 (PFAM); PTHR24273 (PANTHER); PTHR24273:SF29 (PANTHER); IPR003410 (PROSITE_PROFILES)
2838	c8679_g1_i1_len_831_path_1734_0_44_1778 45_67_70_68_830_3	36	fibrillin-2 isoform x3	277	3.62E-25	59.40%	0.114	IPR011641 (PFAM)
2839	c8679_g1_i1_len_831_path_1734_0_44_1778 45_67_70_68_830_5	36	von willebrand factor type egf and pentraxin domain-containing protein 1-like	277	7.81E-08	44.60%	0.145	

2840	c87204_g2_i1_len_179_path_360_0_30_117_31_58_25_59_150_117_151_178_3	0	protein orf34	60	2.89E-06	63.50%	0.167	no IPS match
2841	c87461_g1_i1_len_194_path_1_0_193_1	1	receptor protein tyrosine	65	1.39E-26	80.70%	0.123	IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
2842	c87663_g1_i1_len_445_path_423_0_444_1	6	gastrula zinc finger protein - partial	148	8.62E-28	60.00%	0.11	IPR015880 (SMART); PF13913 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2843	c8769_g1_i1_len_1212_path_2794_0_1211_1	45	protein gdp2 homolog	404	3.25E-157	75.80%	0.187	IPR002589 (SMART); G3DSA:3.40.220.10 (GENE3D); IPR002589 (PFAM); PTHR11106:SF59 (PANTHER); PTHR11106 (PANTHER); IPR002589 (PROSITE_PROFILES); SSF52949 (SUPERFAMILY)
2844	c8774_g1_i1_len_403_path_1_0_402_0	8	phosphatidylinositol phosphatase partial	135	7.39E-38	65.90%	0.256	IPR000242 (PRINTS); IPR000242 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134:SF251 (PANTHER); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
2845	c8774_g2_i1_len_287_path_761_0_286_2	4	receptor-type tyrosine-protein phosphatase mu	95	2.16E-17	66.40%	0.106	IPR000242 (PRINTS); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134 (PANTHER); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
2846	c87892_g1_i1_len_670_path_648_0_669_5	12	leucine-rich repeat-containing protein 15	223	1.01E-25	54.70%	0.131	PR00019 (PRINTS); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
2847	c87899_g1_i1_len_506_path_1_0_505_5	17	translocation protein sec63 homolog	168	1.23E-73	80.60%	0.788Y	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24075:SF0 (PANTHER); IPR027137 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001623 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR001623 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2848	c88033_g1_i1_len_150_path_128_0_149_0	2	suppressor of tumorigenicity 14 protein	50	2.29E-08	76.20%	0.098	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR009003 (SUPERFAMILY)
2849	c88063_g1_i1_len_306_path_284_0_305_1	6	aldehyde oxidase	102	9.83E-28	72.50%	0.125	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF65 (PANTHER); IPR008274 (SUPERFAMILY)
2850	c8825_g1_i1_len_303_path_1_0_302_3	7	threonine synthase-like 2	89	2.75E-14	71.10%	0.14	PTHR10314 (PANTHER); IPR027457 (PTHR10314:PANTHER)
2851	c88784_g1_i1_len_250_path_1_0_249_0	4	arylsulfatase b-like	84	1.64E-26	74.80%	0.114	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342:SF206 (PANTHER); PTHR10342 (PANTHER); IPR017850 (SUPERFAMILY)
2852	c88792_g1_i1_len_275_path_253_0_274_1	4	peptidylglycine alpha-hydroxylating monooxygenase	92	2.42E-24	75.80%	0.281	IPR000323 (PFAM); IPR000323 (G3DSA:2.60.120.GENE3D); PTHR10680 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR008977 (SUPERFAMILY); TMhelix (TMHMM)
2853	c8889_g2_i1_len_821_path_1067_0_126_533_127_820_3	43	parkinson disease 7 domain-containing	274	9.37E-102	73.30%	0.236	IPR002818 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); PTHR11019 (PANTHER); PTHR11019:SF71 (PANTHER); IPR029062 (SUPERFAMILY)
2854	c8889_g2_i2_len_1054_path_173_0_359_533_360_1053_3	60	parkinson disease 7 domain-containing	352	9.33E-101	73.00%	0.236	IPR002818 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); PTHR11019 (PANTHER); PTHR11019:SF71 (PANTHER); IPR029062 (SUPERFAMILY)
2855	c8891_g1_i1_len_1988_path_1_0_1987_5	93	glucose dehydrogenase	662	0	66.90%	0.156	IPR007867 (PFAM); IPR000172 (PFAM); G3DSA:3.50.50.60 (GENE3D); IPR012132 (PIRSF); PTHR11552:SF77 (PANTHER); PTHR11552 (PANTHER); IPR000172 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54373 (SUPERFAMILY); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
2856	c8903_g1_i1_len_1315_path_1_0_1314_1	655	mitochondrial matrix protein p33	438	1.24E-85	67.40%	0.136	IPR003428 (G3DSA:3.10.280.GENE3D); IPR003428 (PFAM); PTHR10826 (PANTHER); PTHR10826:SF1 (PANTHER); IPR003428 (SUPERFAMILY)

2857	c8906_g1_i1_len_1163_path_2113_0_1162_0	49	aael008062- partial	388	2.67E-164	76.00%	0.103	IPR028974 (G3DSA:4.10.1080.GENE3D); IPR023413 (G3DSA:2.40.155.GENE3D); IPR003367 (PFAM); IPR008859 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10199:SF76 (PANTHER); PTHR10199 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR008859 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR017897 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR028974 (SUPERFAMILY); IPR028974 (SUPERFAMILY); IPR028974 (SUPERFAMILY)
2858	c8906_g2_i1_len_1079_path_1057_0_1078_5	63	aael008062- partial	359	7.50E-118	90.90%	0.1	IPR013320 (G3DSA:2.60.120.GENE3D); IPR008859 (PFAM); PTHR10199 (PANTHER); IPR008859 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
2859	c8907_g1_i1_len_729_path_713_0_728_5	28	epidermal growth factor receptor	243	7.33E-144	91.30%	0.713Y	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:4.10.1140.10 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24416:SF95 (PANTHER); PTHR24416 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR000719 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR011009 (SUPERFAMILY)
2860	c8907_g2_i1_len_379_path_357_0_378_0	11	epidermal growth factor receptor-like	127	1.40E-37	66.20%	0.104	IPR006212 (SMART); G3DSA:2.10.220.10 (GENE3D); IPR009030 (SUPERFAMILY)
2861	c89109_g1_i1_len_286_path_264_0_285_4	3	endothelin-converting enzyme 1-like	95	3.32E-15	64.20%	0.866Y	IPR008753 (PFAM); IPR000718 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF55486 (SUPERFAMILY)
2862	c89151_g1_i1_len_267_path_1_0_266_1	4	n-acetylgalactosaminyltransferase 7	89	2.99E-49	94.20%	0.11	IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); PTHR11675 (PANTHER); PTHR11675:SF15 (PANTHER); IPR029044 (SUPERFAMILY)
2863	c89557_g1_i1_len_439_path_417_0_438_4	12	protein ndnf-like	146	2.56E-19	50.10%	0.147	IPR019326 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); SignalP-TM (SIGNALP_GRAM_POSITIVE)
2864	c8967_g1_i1_len_1672_path_1650_0_1671_1	183	polycomb protein eed	557	0	85.10%	0.127	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR10253 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2865	c89844_g1_i1_len_390_path_1_0_389_2	7	phospholipase b-like 2 isoform x1	130	6.03E-34	70.90%	0.173	IPR007000 (PFAM); PTHR12370:SF3 (PANTHER); IPR007000 (PANTHER)
2866	c9009_g1_i1_len_447_path_475_0_446_0	10	guanylate cyclase 32e-like isoform x1	149	3.22E-35	65.10%	0.116	G3DSA:3.40.50.2300 (GENE3D); IPR001828 (PFAM); PTHR11920:SF281 (PANTHER); PTHR11920 (PANTHER); IPR028082 (SUPERFAMILY)
2867	c9032_g1_i1_len_664_path_692_0_663_3	20	aquaporin partial	222	1.48E-30	68.10%	0.409Y	IPR000425 (PRINTS); IPR023271 (G3DSA:1.20.1080.GENE3D); IPR000425 (PFAM); IPR000425 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023271 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2868	c90468_g1_i1_len_241_path_1_0_240_4	4	zinc finger protein partial	80	1.25E-17	61.40%	0.099	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2869	c9162_g2_i1_len_482_path_994_0_481_2	16	growth differentiation factor 8-like	160	8.33E-22	65.30%	0.115	IPR001839 (SMART); IPR001839 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); PTHR11848:SF126 (PANTHER); IPR015615 (PANTHER); IPR017948 (PROSITE_PATTERNS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)

2870	c9177_g1_i1_len_2328_path_53_0_2327_0	4432	heat shock 70 kda protein cognate 4	776	0	94.10%	0.156	Coil (COILS); IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.90.640.10 (GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.30.30 (GENE3D); G3DSA:3.30.420.40 (GENE3D); PTHR19375 (PANTHER); PTHR19375:SF142 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029047 (SUPERFAMILY); IPR029048 (SUPERFAMILY); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); TMhelix (TMHMM)
2871	c9195_g1_i1_len_1044_path_53_0_1043_4	192	d-dopachrome decarboxylase-a-like	348	1.09E-24	62.70%	0.139	IPR001398 (PFAM); G3DSA:3.30.429.10 (GENE3D); IPR001398 (PANTHER); PTHR11954:SF22 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001398 (PRODOM); IPR014347 (SUPERFAMILY); TMhelix (TMHMM)
2872	c9201_g1_i1_len_139_path_343_0_138_3	0	angiotensin-converting enzyme-like	47	1.50E-08	77.20%	0.11	IPR001548 (PFAM); SSF55486 (SUPERFAMILY)
2873	c9220_g1_i1_len_789_path_49_0_95_144_96_155_48_156_788_0	27	c3orf33 protein	263	9.22E-32	45.40%	0.102	IPR016071 (G3DSA:2.40.50.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016071 (SUPERFAMILY); TMhelix (TMHMM)
2874	c9220_g1_i2_len_729_path_49_0_95_48_96_728_0	27	c3orf33 protein	243	3.49E-21	44.70%	0.099	IPR016071 (G3DSA:2.40.50.GENE3D); IPR016071 (SUPERFAMILY)
2875	c9250_g1_i1_len_801_path_829_0_800_2	108	39s ribosomal protein mitochondrial	267	8.63E-107	73.00%	0.102	IPR008914 (G3DSA:3.90.280.GENE3D); IPR008914 (PFAM); PTHR11362 (PANTHER); PTHR11362:SF16 (PANTHER); IPR008914 (SUPERFAMILY)
2876	c92604_g1_i1_len_429_path_407_0_428_0	10	low quality protein: kinase d-interacting substrate of 220 kda-like	143	1.03E-65	86.00%	0.104	IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24139:SF10 (PANTHER); PTHR24139 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2877	c9303_g1_i1_len_3930_path_3941_0_3574_3_4_3575_3929_1	258	disks large 1 tumor suppressor isoform x7	1310	0	85.40%	0.108	Coil (COILS); IPR001478 (SMART); IPR001452 (SMART); IPR008145 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); G3DSA:2.30.30.40 (GENE3D); G3DSA:3.30.63.10 (GENE3D); IPR001478 (PFAM); IPR011511 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR008145 (PFAM); IPR016313 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001452 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
2878	c9326_g1_i1_len_2552_path_53_0_2551_1	206	ribosome biogenesis protein bop1 homolog	851	0	73.60%	0.105	IPR012953 (SMART); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR012953 (PFAM); PTHR17605 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR028598 (HAMAP); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2879	c93742_g1_i1_len_204_path_1_0_203_1	4	ankyrin repeat and sterile alpha motif domain-containing protein 1b	68	8.53E-27	93.20%	0.111	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24174 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2880	c94018_g1_i1_len_157_path_135_0_156_0	0	low-density lipoprotein receptor-related protein 4-like	53	1.93E-09	68.30%	0.103	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
2881	c94804_g1_i1_len_846_path_1_0_845_3	52	succinate-semialdehyde mitochondrial	282	2.96E-125	80.40%	0.19	IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF49 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
2882	c94840_g1_i1_len_1521_path_1499_0_1520_1	120	sepiapterin reductase-like	507	2.92E-81	63.70%	0.112	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); IPR006393 (TIGRFAM); PTHR24318:SF1 (PANTHER); PTHR24318 (PANTHER); SSF51735 (SUPERFAMILY)

								IPR002172 (PRINTS); IPR000033 (SMART); IPR002172 (SMART); IPR000742 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); IPR002172 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR000033 (PFAM); PTHR12106:SF7 (PANTHER); PTHR12106 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY);
2883	c94870_g1_i1_len_2225_path_1_0_2224_2	127	sortilin-related receptor-like	741	0	68.50%	0.136	
2884	c94924_g1_i1_len_399_path_377_0_398_0	29	dipeptidyl peptidase 9	133	1.22E-72	91.70%	0.189	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001375 (PFAM); PTHR11731 (PANTHER); PTHR11731:SF110 (PANTHER); IPR029058 (SUPERFAMILY) IPR000980 (PRINTS); IPR001245 (PRINTS); IPR020635 (SMART); IPR000980 (SMART); IPR000980 (PFAM); G3DSA:3.30.200.20 (GENE3D); IPR000980 (G3DSA:3.30.505.GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24418 (PANTHER); PTHR24418:SF192 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR000980 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); IPR000980 (SUPERFAMILY); TMhelix (TMHMM)
2885	c94963_g1_i1_len_1710_path_1_0_1709_1	143	tyrosine-protein kinase csk-like isoform x1	570	0	86.00%	0.322	IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR000242 (PFAM); IPR021613 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134:SF2 (PANTHER); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)
2886	c94972_g1_i1_len_2850_path_1_0_2849_0	210	receptor-type tyrosine-protein phosphatase n2	950	0	76.30%	0.103	IPR010562 (SMART); IPR010562 (PFAM); PTHR11008:SF9 (PANTHER); PTHR11008 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE)
2887	c94977_g1_i1_len_1042_path_1_0_835_837_836_938_837_939_1041_1	48	protein takeout	347	1.77E-69	56.70%	0.827Y	Coil (COILS); IPR005123 (PFAM); PTHR14049:SF9 (PANTHER); PTHR14049 (PANTHER)
2888	c95033_g1_i1_len_467_path_1_0_466_1	15	prolyl 3-hydroxylase 1-like	156	3.39E-27	77.10%	0.104	IPR015816 (G3DSA:2.30.230.GENE3D); IPR011030 (G3DSA:1.25.10.GENE3D); IPR001747 (PFAM); PTHR23345 (PANTHER); IPR001747 (PROSITE_PROFILES); IPR011030 (SUPERFAMILY)
2889	c95036_g1_i1_len_838_path_1_0_837_5	22	Apolipoprotein, partial	279	7.81E-50	53.70%	0.113	IPR006589 (SMART); IPR004193 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR013780 (G3DSA:2.60.40.GENE3D); IPR006048 (PFAM); IPR006047 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR006407 (PIRSF); IPR015902 (PANTHER); PTHR10357:SF110 (PANTHER); IPR017853 (SUPERFAMILY); IPR014756 (SUPERFAMILY); SSF51011 (SUPERFAMILY)
2890	c95043_g1_i1_len_2377_path_2355_0_2376_1	138	#NAME?	792	0	79.00%	0.181	

[illegible]

2899	c95408_g1_i1_len_381_path_359_0_380_1	6	agap012439-pa-like protein	127	2.19E-24	63.70%	0.102	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24131 (PANTHER); PTHR24131:SF6 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2901	c9541_g1_i1_len_721_path_749_0_720_0	24	peptidyl-prolyl cis-trans isomerase nima-interacting 1	241	2.41E-94	89.40%	0.104	Coil (COILS); IPR001202 (SMART); IPR001202 (PFAM); IPR000297 (PFAM); G3DSA:2.20.70.10 (GENE3D); G3DSA:3.10.50.40 (GENE3D); PTHR10657 (PANTHER); IPR023058 (PROSITE_PATTERNS); IPR001202 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001202 (PROSITE_PROFILES); IPR000297 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY); IPR001202 (SUPERFAMILY); TMhelix (TMHMM)
2900	c95417_g1_i1_len_882_path_860_0_881_0	22	macrophage mannose receptor 1-like	294	9.96E-39	47.90%	0.101	IPR001304 (SMART); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); PTHR22803:SF16 (PANTHER); PTHR22803 (PANTHER); IPR001304 (PROSITE_PROFILES); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR016187 (SUPERFAMILY)
2902	c95473_g1_i1_len_480_path_1_0_479_1	11	endoplasmic reticulum aminopeptidase 1- partial	160	2.01E-40	64.10%	0.111	IPR014782 (PRINTS); IPR014782 (PFAM); IPR001930 (PANTHER); PTHR11533:SF165 (PANTHER); SSF63737 (SUPERFAMILY); SSF55486 (SUPERFAMILY)
2903	c95474_g1_i1_len_2108_path_2086_0_2107_1	237	counting factor associated protein d-like	703	0	77.10%	0.172	IPR000668 (PRINTS); IPR000668 (SMART); IPR013201 (SMART); IPR013201 (PFAM); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR013128 (PANTHER); PTHR12411:SF284 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
2904	c95504_g1_i1_len_1703_path_1_0_1702_1	58	plexin- partial	568	0	92.80%	0.392Y	G3DSA:3.10.20.90 (GENE3D); IPR013548 (PFAM); PTHR22625 (PANTHER); IPR008936 (SUPERFAMILY)
2905	c95654_g1_i1_len_1554_path_1_0_1553_2	100	hypothetical protein CRE_06355	518	7.34E-07	44.00%	0.211	no IPS match
2906	c95654_g1_i1_len_1554_path_1_0_1553_5	100	collagen and calcium-binding egf domain-containing protein 1	518	5.94E-100	52.80%	0.277	Coil (COILS); IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); PF14670 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR008160 (PFAM); PTHR24023 (PANTHER); IPR013032 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
2907	c95709_g1_i1_len_1467_path_1_0_1334_1336_1335_1400_1336_1401_1466_1	123	nucleolar protein 58-like	489	0	82.90%	0.152	IPR012976 (SMART); IPR002687 (PFAM); IPR012976 (PFAM); IPR012974 (PFAM); PTHR10894 (PANTHER); IPR002687 (PROSITE_PROFILES); SSF89124 (SUPERFAMILY)

2915	c95901_g1_i1_len_3230_path_1_0_3229_3	831	coatomer subunit beta	1077	0	84.30%	0.123	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR016453 (PIRSF); IPR015943 (G3DSA:2.130.10.GENE3D); IPR006692 (PFAM); PTHR19876 (PANTHER); PTHR19876:SF2 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR011044 (SUPERFAMILY)
2916	c95969_g1_i1_len_730_path_1_0_729_3	143	myotrophin-like isoform 2	244	5.47E-55	84.20%	0.134	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24152 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM)
2917	c95985_g1_i1_len_489_path_1_0_488_2	7	partitioning defective 3 homolog	163	5.42E-50	66.70%	0.11	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR16484 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
2918	c95988_g1_i1_len_561_path_539_0_560_4	94	md-2-related lipid-recognition	187	3.60E-24	53.60%	0.785 Y	IPR003172 (SMART); IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306 (PANTHER); PTHR11306:SF4 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR014756 (SUPERFAMILY)
2919	c96020_g1_i1_len_622_path_1_0_621_4	22	hemocyte protein-glutamine gamma-glutamyltransferase-like	207	5.18E-87	76.70%	0.102	IPR013783 (G3DSA:2.60.40.GENE3D); IPR002931 (PFAM); IPR002931 (G3DSA:3.90.260.GENE3D); PTHR11590:SF40 (PANTHER); IPR023608 (PANTHER); SSF54001 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
2920	c96045_g1_i1_len_2226_path_1_0_2225_2	91	endoplasmic reticulum mannosyl-oligosaccharide - alpha-mannosidase	742	0	79.70%	0.101	IPR001382 (PRINTS); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); IPR001382 (PANTHER); PTHR11742:SF7 (PANTHER); IPR001382 (SUPERFAMILY)
2921	c96312_g1_i1_len_837_path_1_0_836_5	20	afadin isoform x1	279	1.35E-78	66.60%	0.111	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR10398 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
2922	c96315_g1_i1_len_283_path_261_0_282_5	10	Idlr2-a protein	94	1.20E-12	57.10%	0.12	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY)
2923	c96328_g1_i1_len_346_path_324_0_345_3	6	hemicentin-1	116	2.08E-38	71.20%	0.108	PR01705 (PRINTS); IPR000884 (SMART); IPR000884 (PFAM); G3DSA:2.20.100.10 (GENE3D); PTHR19897 (PANTHER); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
2924	c96343_g1_i1_len_725_path_1_0_724_3	9	laminin subunit alpha-1	242	1.72E-54	59.10%	0.107	IPR001791 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); PTHR10574:SF148 (PANTHER); PTHR10574 (PANTHER); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
2925	c96448_g1_i1_len_491_path_1_0_490_5	10	inversin protein	163	2.07E-67	77.00%	0.464 Y	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PF13637 (PFAM); PTHR24178 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR020683 (SUPERFAMILY)
2926	c96470_g1_i1_len_1804_path_1_0_1803_5	2962	carboxypeptidase b-like	601	9.10E-123	62.60%	0.184	IPR000834 (PRINTS); IPR000834 (SMART); IPR003146 (PFAM); IPR000834 (PFAM); IPR003146 (G3DSA:3.30.70.GENE3D); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009020 (SUPERFAMILY); SSF53187 (SUPERFAMILY)

2927	c96482_g1_i1_len_1810_path_1_0_1809_4	80	zinc finger protein 239-like isoform x2	603	2.94E-78	68.30%	0.116	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24377 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2928	c96492_g1_i1_len_349_path_327_0_348_4	12	fukutin-related protein	116	3.65E-09	60.40%	0.198	no IPS match
2929	c96606_g1_i1_len_1822_path_1800_0_1821_3	121	tyrosine-protein kinase src64b	608	0	79.70%	0.1	IPR000980 (PRINTS); IPR001245 (PRINTS); IPR001452 (PRINTS); IPR000980 (SMART); IPR001452 (SMART); IPR020635 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR000980 (G3DSA:3.30.505.GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR001452 (PFAM); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); IPR000980 (PFAM); PTHR24418 (PANTHER); PTHR24418:SF35 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR000980 (PROSITE_PROFILES); IPR000980 (SUPERFAMILY); IPR001452 (SUPERFAMILY); IPR011009 (SUPERFAMILY)
2930	c96634_g1_i1_len_481_path_459_0_480_1	13	gastrula zinc finger protein	160	1.20E-11	60.10%	0.113	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2931	c96701_g1_i1_len_1994_path_1972_0_1993_5	147	membrane metallo-endopeptidase-like 1-like	664	0	78.30%	0.106	IPR018497 (PRINTS); IPR018497 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR008753 (PFAM); PTHR11733:SF113 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
2932	c96810_g1_i1_len_504_path_482_0_503_0	15	ribonuclease oy	168	2.65E-39	58.90%	0.153	IPR001568 (PFAM); IPR001568 (G3DSA:3.90.730.GENE3D); IPR001568 (PANTHER); IPR001568 (SUPERFAMILY)
2933	c96829_g1_i1_len_1254_path_1232_0_1253_0	41	cyclin-h	418	2.95E-157	81.70%	0.128	IPR013763 (SMART); IPR006671 (PFAM); IPR013763 (G3DSA:1.10.472.GENE3D); IPR013763 (G3DSA:1.10.472.GENE3D); IPR027081 (TIGRFAM); IPR027081 (PTHR10026:PANTHER); IPR015429 (PANTHER); IPR013763 (SUPERFAMILY); IPR013763 (SUPERFAMILY)
2934	c96850_g1_i1_len_698_path_676_0_697_1	40	zinc finger protein 271-like	233	1.91E-18	66.60%	0.111	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
2935	c96892_g1_i1_len_427_path_1_0_426_0	12	epidermal growth factor receptor	143	1.55E-52	73.90%	0.101	IPR006212 (SMART); G3DSA:2.10.220.10 (GENE3D); IPR000494 (PFAM); IPR000494 (G3DSA:3.80.20.GENE3D); PF14843 (PFAM); PTHR24416:SF88 (PANTHER); PTHR24416 (PANTHER); IPR009030 (SUPERFAMILY); SSF52058 (SUPERFAMILY)
2936	c96922_g1_i1_len_486_path_1_0_485_0	9	low-density lipoprotein receptor-related protein 2	162	1.50E-81	87.10%	0.12	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

2937	c96935_g1_i1_len_868_path_846_0_867_0	37	iduronate 2- partial	290	2.04E-119	78.70%	0.532Y	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342 (PANTHER); PTHR10342:SF185 (PANTHER); IPR024607 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017850 (SUPERFAMILY)
2938	c96956_g1_i1_len_672_path_650_0_671_0	22	gastrula zinc finger	224	1.20E-68	63.40%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2939	c96990_g1_i1_len_619_path_597_0_618_1	16	caseinolytic peptidase b protein homolog	206	3.36E-53	76.20%	0.102	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); IPR020683 (PFAM); PTHR24193 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2940	c96993_g1_i1_len_788_path_766_0_787_2	22	oxysterol-binding protein 1- partial	262	1.48E-79	74.60%	0.1	IPR002110 (PRINTS); IPR002110 (SMART); PF13637 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24142 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2941	c97055_g1_i1_len_600_path_1_0_599_1	47	xanthine dehydrogenase	200	6.89E-84	83.80%	0.184	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR008274 (SUPERFAMILY)
2942	c97098_g1_i1_len_303_path_281_0_302_0	4	beta-galactosidase-1-like protein 2	101	2.79E-28	71.90%	0.123	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001944 (PFAM); PTHR23421:SF66 (PANTHER); IPR001944 (PANTHER); IPR017853 (SUPERFAMILY)
2943	c97102_g1_i1_len_2653_path_2558_0_2524_5083_2525_2556_5083_2557_2588_5083_2589_2620_5083_2621_2652_0	273	mucosa-associated lymphoid tissue lymphoma translocation protein 1-like	885	2.67E-64	46.70%	0.17	IPR015917 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR011029 (G3DSA:1.10.533.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000488 (PFAM); IPR013098 (PFAM); PF13895 (PFAM); IPR011600 (PFAM); IPR029030 (G3DSA:3.40.50.GENE3D); PTHR22576:SF20 (PANTHER); PTHR22576 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR001309 (PROSITE_PROFILES); SSF52129 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR011029 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
2944	c97146_g1_i1_len_700_path_678_0_699_1	39	PREDICTED: uncharacterized protein LOC105389730 isoform X2	233	7.69E-43	57.00%	0.123	IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY)
2945	c97181_g1_i1_len_497_path_475_0_496_5	12	lipoprotein receptor	165	7.06E-31	62.70%	0.277	IPR000832 (PFAM); PTHR12011:SF260 (PANTHER); PTHR12011 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
2946	c97248_g1_i1_len_598_path_1_0_597_0	29	kielin chordin-like protein isoform x2	200	1.35E-35	57.70%	0.108	IPR002223 (G3DSA:4.10.410.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PROSITE_PATTERNS); IPR000436 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
2947	c97322_g1_i1_len_286_path_1_0_285_1	4	---NA---	95			0.107	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
2948	c97358_g1_i1_len_239_path_217_0_238_2	2	beta-adrenergic receptor kinase 2-like	79	4.32E-48	98.60%	0.098	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24355:SF17 (PANTHER); PTHR24355 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
2949	c97375_g1_i1_len_544_path_522_0_543_1	22	deoxyribonuclease-1-like 2-like	181	8.45E-46	66.20%	0.101	IPR016202 (PRINTS); IPR016202 (SMART); IPR005135 (G3DSA:3.60.10.GENE3D); IPR005135 (PFAM); IPR016202 (PANTHER); IPR005135 (SUPERFAMILY)

2950	c97409_g1_i1_len_691_path_1_0_690_3	18	u4 u6 small nuclear ribonucleoprotein prp4	231	2.84E-114	87.10%	0.191	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR027106 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2951	c9743_g1_i1_len_494_path_1_0_493_4	6	coronin-2b-like isoform x2	165	5.16E-96	90.80%	0.101	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015505 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2952	c97464_g1_i1_len_316_path_1_0_315_2	8	zinc finger protein 420-like	105	9.51E-18	62.40%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2953	c97540_g1_i1_len_1697_path_1_0_1696_5	79	zinc finger protein 28 homolog	565	1.46E-50	53.00%	0.099	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF12874 (PFAM); PF13465 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
2954	c97595_g1_i1_len_263_path_241_0_262_3	4	partial	88	1.85E-49	95.20%	0.109	IPR011614 (G3DSA:2.40.180.GENE3D); IPR011614 (PFAM); IPR018028 (PANTHER); IPR018028 (PROSITE_PROFILES); IPR020835 (SUPERFAMILY)
2955	c97642_g1_i1_len_438_path_416_0_437_2	20	mam and ldl-receptor class a domain-containing protein 1-like	146	8.22E-41	60.10%	0.113	IPR000998 (SMART); IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
2956	c97650_g1_i1_len_716_path_694_0_715_2	32	retinol dehydrogenase 13-like	238	6.04E-99	76.20%	0.114	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320:SF55 (PANTHER); PTHR24320 (PANTHER); SSF51735 (SUPERFAMILY)
2957	c97706_g1_i1_len_1197_path_1175_0_1196_4	50	peptidyl-prolyl cis-trans isomerase d	399	7.08E-150	73.70%	0.095	Coil (COILS); IPR002130 (PRINTS); IPR019734 (SMART); IPR002130 (PFAM); IPR023114 (G3DSA:1.10.150.GENE3D); PF13414 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); IPR024936 (PANTHER); PTHR11071:SF78 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR002130 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); SSF48452 (SUPERFAMILY)
2958	c97747_g1_i1_len_384_path_362_0_383_3	6	low-density lipoprotein	128	4.02E-59	77.20%	0.117	IPR000033 (SMART); IPR011042 (G3DSA:2.120.10.GENE3D); IPR000033 (PFAM); PTHR10529 (PANTHER); PTHR10529:SF222 (PANTHER); SSF63825 (SUPERFAMILY)
2959	c97768_g1_i1_len_823_path_809_0_822_4	35	pdz domain-containing protein 11	274	1.74E-51	76.90%	0.119	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR14063 (PANTHER); TRANSMEMBRANE (PHOBIOUS); NON_CYTOPLASMIC_DOMAIN (PHOBIOUS); CYTOPLASMIC_DOMAIN (PHOBIOUS); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
2960	c97797_g1_i1_len_692_path_1_0_691_2	27	hemagglutinin	230	1.29E-43	59.50%	0.109	IPR023612 (PRINTS); G3DSA:1.10.390.10 (GENE3D); IPR013856 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); SSF55486 (SUPERFAMILY)
2961	c97978_g1_i1_len_266_path_1_0_265_5	3	guanine nucleotide-binding protein subunit beta-5	88	5.28E-43	92.30%	0.124	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19850:SF12 (PANTHER); IPR016346 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
2962	c98066_g1_i1_len_450_path_1_0_449_1	6	contactin	150	2.60E-24	54.60%	0.124	IPR003598 (SMART); PF13927 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)

2963	c98082_g1_i1_len_364_path_1_0_363_0	5	xanthine dehydrogenase oxidase isoform x2	122	1.36E-37	73.60%	0.123	G3DSA:3.30.390.50 (GENE3D); IPR002346 (PFAM); IPR016169 (G3DSA:3.30.465.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR016166 (PROSITE_PROFILES); IPR016166 (SUPERFAMILY)
2964	c98153_g1_i1_len_624_path_602_0_623_0	21	aminopeptidase n	208	1.15E-71	73.10%	0.116	IPR024571 (PFAM); IPR001930 (PANTHER); PTHR11533:SF148 (PANTHER) IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); PTHR23223:SF148 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2965	c98159_g1_i1_len_761_path_739_0_760_0	21	krueppel-like factor 3 isoform x1	254	4.16E-58	70.00%	0.105	IPR000782 (PFAM); IPR000782 (G3DSA:2.30.180.GENE3D); PTHR10900 (PANTHER); PTHR10900:SF73 (PANTHER); IPR000782 (PROSITE_PATTERNS); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY)
2966	c98208_g1_i1_len_469_path_447_0_468_0	16	transforming growth factor-beta-induced protein ig-h3-like	157	1.21E-56	66.60%	0.121	IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23074 (PANTHER); PTHR23074:SF74 (PANTHER); IPR027417 (SUPERFAMILY)
2967	c98259_g1_i1_len_258_path_1_0_257_2	7	vacuolar protein sorting-associated protein 4-like	86	2.48E-41	85.50%	0.12	IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11640 (PANTHER); PTHR11640:SF52 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
2968	c98280_g1_i1_len_375_path_353_0_374_2	6	irregular chiasm c-roughest protein isoform x1	125	7.02E-39	66.90%	0.15	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PANTHER); PTHR10316 (PANTHER); PTHR10316:SF40 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
2969	c98299_g1_i1_len_1998_path_1_0_1997_3	119	membrane-associated guanylate ww and pdz domain-containing protein 2	666	5.93E-166	77.70%	0.1	IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PFAM); IPR000436 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325:SF43 (PANTHER); PTHR19325 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000436 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR000436 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
2970	c98338_g1_i1_len_525_path_503_0_524_4	19	von willebrand factor type egf and pentraxin domain-containing protein 1-like	168	1.08E-38	58.40%	0.106	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24300 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
2971	c98459_g1_i1_len_641_path_1_0_640_0	10	cytochrome p450 2u1	214	6.98E-46	63.20%	0.117	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10529:SF222 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
2972	c98506_g1_i1_len_389_path_1_0_388_4	7	low-density lipoprotein	130	1.38E-33	59.00%	0.107	IPR002172 (SUPERFAMILY)
2973	c98525_g1_i1_len_274_path_252_0_273_0	4	neurexin-4 isoform x3	92	5.74E-31	76.40%	0.107	IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (SUPERFAMILY)
2974	c98527_g1_i1_len_324_path_1_0_323_1	6	isoform b	108	2.08E-45	85.00%	0.114	PR00010 (PRINTS); IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); PTHR24049:SF6 (PANTHER); PTHR24049 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
2975	c98533_g1_i1_len_925_path_1_0_924_4	110	---NA---	308			0.128	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
2976	c98555_g1_i1_len_424_path_402_0_423_5	9	thioredoxin 2	141	6.68E-33	71.20%	0.114	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR10438:SF235 (PANTHER); IPR005746 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
2977	c98592_g1_i1_len_236_path_1_0_235_2	3	moxd1-like protein 1	78	2.21E-12	65.10%	0.108	IPR000323 (G3DSA:2.60.120.GENE3D); IPR000323 (PFAM); PTHR10157:SF23 (PANTHER); IPR000945 (PANTHER); IPR008977 (SUPERFAMILY)

2978	c98630_g1_i1_len_762_path_1_0_761_2	20	apolipoprotein d-like	254	8.97E-24	51.40%	0.144	IPR003057 (PRINTS); IPR012674 (G3DSA:2.40.128.GENE3D); IPR000566 (PFAM); PTHR10612 (PANTHER); IPR022272 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)
2979	c98644_g1_i1_len_1598_path_1576_0_1597_5	56	low-density lipoprotein receptor class a domain-containing protein 3	532	5.59E-80	51.70%	0.853Y	IPR003599 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR002172 (PFAM); IPR013151 (PFAM); IPR023415 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SSF48726 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
2980	c98660_g1_i1_len_904_path_1_0_903_3	86	ankyrin repeat domain-containing protein 49-like	302	5.34E-62	65.80%	0.122	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24144 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2981	c98682_g1_i1_len_257_path_235_0_256_1	9	hypothetical protein	86	2.55E-06	51.00%	0.104	no IPS match
2982	c98682_g1_i1_len_257_path_235_0_256_5	9	collagen alpha-1 chain isoform x1	85	2.28E-07	65.40%	0.751 Y	IPR008160 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF372 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK)
2983	c98691_g1_i1_len_374_path_352_0_373_4	6	zinc finger protein 345 isoform x3	125	2.16E-13	56.00%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2984	c98731_g1_i1_len_704_path_1_0_703_3	20	aldehyde dehydrogenase family 2 member mitochondrial-like	235	1.47E-94	70.90%	0.107	IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); IPR015657 (PTHR11699:PANTHER); PTHR11699 (PANTHER); IPR016161 (SUPERFAMILY)
2985	c98857_g1_i1_len_394_path_1_0_393_1	4	zinc finger protein 84-like	131	1.64E-11	53.80%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2986	c99099_g1_i1_len_297_path_1_0_296_0	6	xanthine dehydrogenase	99	3.25E-39	83.70%	0.11	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)
2987	c99120_g1_i1_len_665_path_49_0_664_5	17	upf0764 protein c16orf89 homolog	221	1.44E-27	50.20%	0.135	no IPS match
2988	c99159_g1_i1_len_649_path_1_0_648_3	14	tyrosine-protein phosphatase non-receptor type 23	217	1.88E-95	69.40%	0.136	IPR000242 (PRINTS); IPR000242 (SMART); IPR003595 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); IPR028770 (PTHR19134:PANTHER); IPR016130 (PROSITE_PATTERNS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
2989	c99186_g1_i1_len_1275_path_1253_0_1274_1	35	ankyrin repeat family a protein 2-like	425	3.78E-73	68.30%	0.199	IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24124:SF6 (PANTHER); PTHR24124 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
2990	c99239_g1_i1_len_577_path_555_0_576_0	12	protocadherin fat 2	193	1.14E-78	78.90%	0.103	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); PTHR24026:SF40 (PANTHER); PTHR24026 (PANTHER); IPR020894 (PROSITE_PATTERNS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY)
2991	c99244_g1_i1_len_866_path_1_0_865_4	33	lysosomal alpha-glucosidase-like	289	1.41E-62	66.10%	0.162	IPR000322 (PFAM); PTHR22762:SF7 (PANTHER); PTHR22762 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51011 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

[illegible]

Supplementary Table 8: Venom gland tissue transcriptome (Trinity contigs that match against secreted proteins [UniProtSL0243])

Nr.	Contig name	Read Numbers	Blast result (evalue=10 ⁻⁵ , BlastP, Nr database)	Seq. length	min. evalue	mean similarity	SignalP	InterProScan
1	c100119_g1_i1_len_324_path_302_0_323_3	2	zinc finger protein 449 isoform x2	108	7.51E-15	69.10%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
2	c10019_g1_i1_len_1900_path_1_0_1899_4	63	spermine oxidase-like	629	1.03E-131	62.60%	0.171	IPR001613 (PRINTS); IPR002937 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR10742:SF255 (PANTHER); PTHR10742 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54373 (SUPERFAMILY); SSF51905 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
3	c100216_g1_i1_len_1066_path_1044_0_1065_0	8	lrr receptor-like serine threonine-protein kinase fls2	349	1.09E-140	69.30%	0.392 Y	IPR013210 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24420 (PANTHER); SSF52058 (SUPERFAMILY)
4	c10027_g1_i1_len_1364_path_1_0_284_2835_285_390_392_391_1363_1	12	cathepsin partial	455	1.01E-117	81.30%	0.129	IPR000668 (PRINTS); IPR000668 (SMART); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR013128 (PANTHER); PTHR12411:SF265 (PANTHER); IPR025661 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
5	c100538_g1_i1_len_407_path_1_0_406_0	2	adp-ribosylation factor-like protein 4a	136	1.11E-69	88.50%	0.111	IPR006689 (PRINTS); IPR024156 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF121 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
6	c101178_g1_i1_len_678_path_656_0_677_4	9	amine oxidase	226	4.93E-61	66.90%	0.13	G3DSA:1.10.405.10 (GENE3D); PF13450 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR10742 (PANTHER); PTHR10742:SF217 (PANTHER); SSF51905 (SUPERFAMILY)
7	c10145_g1_i1_len_1333_path_1_0_1332_4	65	follistatin-a isoform x2	439	7.69E-104	66.80%	0.17	IPR003645 (SMART); IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); IPR002350 (PFAM); PTHR10913:SF39 (PANTHER); PTHR10913 (PANTHER); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
8	c1016_g1_i1_len_1732_path_1_0_1731_1	798	nucleolar protein 56	577	0	87.50%	0.192	Coil (COILS); IPR012976 (SMART); IPR002687 (PFAM); IPR012974 (PFAM); IPR012976 (PFAM); PTHR10894 (PANTHER); PTHR10894:SF0 (PANTHER); IPR002687 (PROSITE_PROFILES); SSF89124 (SUPERFAMILY)
9	c101999_g1_i1_len_241_path_1_0_240_3	0	ncase_drops ame: full=neutral ceramidase short=n-cdase short=ncdase ame: full=acylsphingosine deacylase ame: full=n-acylsphingosine amidohydrolase flags: precursor	81	6.35E-23	71.30%	0.109	IPR006823 (PFAM); IPR006823 (PANTHER); PTHR12670:SF1 (PANTHER)
10	c102093_g1_i1_len_383_path_1_0_382_1	4	collagen alpha-1 chain-like	128	5.00E-58	86.90%	0.146	IPR000885 (SMART); IPR000885 (PFAM); PTHR24023:SF444 (PANTHER); PTHR24023 (PANTHER); IPR000885 (PRODOM); IPR000885 (PROSITE_PROFILES)
11	c103722_g1_i1_len_387_path_1_0_386_0	2	hypothetical protein DAPPUDRAFT_101895	129	1.18E-07	68.00%	0.1	IPR001881 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); IPR018097 (PROSITE_PATTERNS); SSF57196 (SUPERFAMILY)
12	c103735_g1_i1_len_354_path_1_0_353_0	2	leukotriene a-4 hydrolase	118	1.99E-59	84.90%	0.142	IPR014782 (PRINTS); IPR014782 (PFAM); G3DSA:1.10.390.10 (GENE3D); IPR001930 (PANTHER); PTHR11533:SF4 (PANTHER); SSF55486 (SUPERFAMILY)
13	c104895_g1_i1_len_224_path_202_0_223_4	2	alanine dehydrogenase	75	4.04E-41	98.60%	0.13	IPR007698 (SMART); IPR007698 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR10160 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY)
14	c10512_g1_i1_len_2062_path_53_0_2061_0	91	pyrroline-5-carboxylate dehydrogenase	682	0	80.50%	0.317	IPR016162 (G3DSA:3.40.605.GENE3D); IPR005931 (TIGRFAM); IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF18 (PANTHER); IPR016160 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM)

15	c10659_g1_i1_len_2017_path_43_0_948_42_949_2016_2	128	puromycin-sensitive aminopeptidase	666	6.60E-106	79.70%	0.109	Coil (COILS); IPR024571 (PFAM); IPR001930 (PANTHER); PTHR11533:SF163 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
16	c10692_g1_i1_len_2878_path_2856_0_288_3145_289_2877_4	123	fat-like cadherin-related tumor suppressor homolog isoform x1	959	2.00E-141	60.00%	0.105	IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); PTHR24026 (PANTHER); PTHR24026:SF39 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)
17	c1079_g1_i1_len_212_path_103_0_36_140_37_6_0_400_61_79_183_80_211_0	0	probable chitinase 3	71	7.67E-12	64.90%	0.106	IPR013781 (G3DSA:3.20.20.GENE3D)
18	c1080_g1_i1_len_1123_path_53_0_1122_2	51	n-acetylglucosamine-1-phosphotransferase subunit gamma-like	374	1.13E-71	60.30%	0.136	Coil (COILS); IPR009011 (G3DSA:2.70.130.GENE3D); PF13015 (PFAM); PTHR12630:SF6 (PANTHER); PTHR12630 (PANTHER); IPR009011 (SUPERFAMILY)
19	c10833_g1_i1_len_1502_path_55_0_1501_4	140	tl5a_tactr ame: full=techylectin-5a flags: precursor	501	4.40E-54	60.50%	0.118	Coil (COILS); IPR002181 (SMART); IPR002181 (PFAM); IPR014715 (G3DSA:4.10.530.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
20	c108622_g1_i1_len_161_path_1_0_160_2	0	sparc-related modular calcium-binding protein 2-like	53	1.52E-07	72.50%	0.108	IPR000716 (SMART); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY)
21	c109580_g1_i1_len_587_path_573_0_586_1	6281	anopheles stephensi ubiquitin	189	2.60E-85	97.30%	0.106	IPR019956 (PRINTS); IPR000626 (SMART); IPR001975 (PFAM); IPR000626 (PFAM); G3DSA:3.10.20.90 (GENE3D); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR000626 (PROSITE_PROFILES); IPR011332 (SUPERFAMILY); IPR029071 (SUPERFAMILY)
22	c109648_g1_i1_len_1383_path_5_0_1382_2	3370	adp-ribosylation factor-like protein 8b-a	455	6.48E-124	97.70%	0.108	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR003579 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR11711 (PANTHER); PTHR11711:SF122 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
23	c109726_g1_i1_len_438_path_416_0_437_3	3	tryptophan permease	146	3.06E-38	100.00%	0.106	IPR015422 (G3DSA:3.90.1150.GENE3D); IPR018227 (PFAM); PTHR32195 (PANTHER); PTHR32195:SF11 (PANTHER); IPR013061 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR015424 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
24	c109756_g1_i1_len_753_path_1_0_752_5	13	wnt10 protein	251	2.32E-41	80.10%	0.135	IPR005817 (PFAM); IPR005817 (PANTHER); PTHR12027:SF74 (PANTHER)
25	c110003_g1_i1_len_1658_path_1636_0_1657_3	42	allatostatin precursor protein	553	1.87E-29	54.70%	0.108	IPR010276 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
26	c110042_g1_i1_len_1639_path_1617_0_1638_1	45	cation channel sperm-associated protein 2	546	1.53E-75	55.00%	0.132	Coil (COILS); IPR027359 (G3DSA:1.20.120.GENE3D); IPR005821 (PFAM); PTHR10037 (PANTHER); IPR028747 (PTHR10037:PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF81324 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
27	c110109_g1_i1_len_1218_path_1196_0_1217_3	29	hypothetical protein DAPPUDRAFT_300634	406	9.32E-47	63.10%	0.191	IPR001916 (PRINTS); IPR001916 (SMART); IPR001916 (PFAM); G3DSA:1.10.530.10 (GENE3D); PTHR11407 (PANTHER); IPR019799 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001916 (PROSITE_PROFILES); IPR023346 (SUPERFAMILY)

28	c110167_g1_i1_len_1131_path_1_0_1130_4	28	tyrosine-protein phosphatase lar isoform x1	377	1.03E-27	74.10%	0.112	IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19134:SF199 (PANTHER); PTHR19134 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
29	c110212_g1_i1_len_2727_path_20_0_2726_2	117	fimbrial family protein	909	3.82E-120	99.50%	0.451 Y	IPR000259 (G3DSA:2.60.40.GENE3D); IPR000259 (PFAM); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR008966 (SUPERFAMILY)
30	c110231_g1_i1_len_293_path_1_0_292_3	1	exocyst complex component 6	98	1.21E-44	85.40%	0.155	IPR007225 (PANTHER)
31	c110269_g1_i1_len_2468_path_1_0_2467_4	170	mitogen-activated protein kinase 15-like	817	0	73.00%	0.177	IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24055:SF79 (PANTHER); PTHR24055 (PANTHER); IPR003527 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
32	c110337_g1_i1_len_1283_path_1261_0_1282_0	28	dentin sialophosphoprotein isoform x1	428	1.09E-119	68.70%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
33	c110350_g1_i1_len_496_path_1_0_495_1	4	venom serine protease 34-like	160	1.47E-13	53.80%	0.154	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
34	c110372_g1_i1_len_544_path_1_0_543_2	4	n-acetylmuramoyl-l-alanine amidase partial	181	1.69E-99	99.90%	0.102	IPR002508 (SMART); IPR003594 (G3DSA:3.30.565.GENE3D); IPR002508 (G3DSA:3.40.630.GENE3D); IPR002508 (PFAM); PTHR30404 (PANTHER); PTHR30404:SF0 (PANTHER); SSF53187 (SUPERFAMILY)
35	c110397_g1_i1_len_1015_path_1_0_1014_3	23	c-binding	339	4.06E-08	57.20%	0.103	IPR001846 (PFAM); PTHR11339 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001846 (PROSITE_PROFILES)

36	c110402_g1_i1_len_2389_path_2367_0_2388_0	76	guanine nucleotide-binding protein g g subunit beta-1	791	0	97.70%	0.13	Coil (COILS); IPR020472 (PRINTS); IPR001632 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR016346 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
37	c110502_g1_i1_len_1555_path_1_0_1554_2	156	lpxtg-motif cell wall anchor domain protein	512	9.50E-06	53.00%	0.099	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
38	c110615_g1_i1_len_894_path_1_0_893_0	6	chorion peroxidase-like	298	7.99E-100	69.60%	0.117	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
39	c110618_g1_i1_len_1064_path_1_0_1063_1	47	peptidyl-prolyl cis-trans isomerase h	355	1.96E-124	95.40%	0.101	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF58 (PANTHER); IPR020892 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
40	c110641_g1_i1_len_1404_path_1_0_1403_3	27	bone morphogenetic protein partial	468	4.92E-34	67.30%	0.103	IPR001839 (SMART); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001839 (PFAM); PTHR11848:SF131 (PANTHER); IPR015615 (PANTHER); IPR017948 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY); TMhelix (TMHMM)
41	c110643_g1_i1_len_2255_path_1_0_2254_0	120	glycoside catalytic core	752	8.81E-94	54.00%	0.16	Coil (COILS); IPR001547 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR31308 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY)
42	c110660_g1_i1_len_959_path_46_0_958_1	52	fibroblast growth factor receptor partial	314	7.01E-16	67.10%	0.101	IPR013783 (G3DSA:2.60.40.GENE3D); PTHR24416 (PANTHER); IPR028174 (PTHR24416:PANTHER); SSF48726 (SUPERFAMILY)
43	c110704_g1_i1_len_1330_path_1_0_1329_1	47	prophenol oxidase activating enzyme precursor	438	3.30E-48	52.10%	0.156	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR022700 (PFAM); IPR001254 (PFAM); PTHR24268:SF54 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
44	c11097_g2_i1_len_586_path_681_0_585_1	4	nedd4 family-interacting protein 1-like	195	4.51E-71	73.30%	0.109	IPR019325 (PFAM); PTHR13396 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

45	c111109_g1_i1_len_622_path_600_0_621_0	8	leucine-rich repeats and immunoglobulin-like domains protein 1	208	2.15E-45	86.10%	0.293	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR24367 (PANTHER); PTHR24367:SF245 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR007110 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
46	c111129_g1_i1_len_1087_path_1_0_876_878_877_981_878_982_1086_4	22	type iv secretion protein rhs	362	3.21E-14	59.00%	0.129	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
47	c111174_g1_i1_len_1187_path_1165_0_1186_4	9	formate dehydrogenase- large subunit	396	0	99.00%	0.212	IPR006963 (SMART); G3DSA:2.20.25.90 (GENE3D); G3DSA:3.40.228.10 (GENE3D); IPR006656 (PFAM); G3DSA:3.40.50.740 (GENE3D); IPR006963 (PFAM); PTHR11615 (PANTHER); PTHR11615:SF38 (PANTHER); IPR027467 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006963 (PROSITE_PROFILES); SSF53706 (SUPERFAMILY); TMhelix (TMHMM)
48	c111229_g1_i1_len_459_path_1_0_458_3	3	krueppel-like factor 15	153	1.01E-56	78.00%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223:SF146 (PANTHER); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
49	c111250_g1_i1_len_886_path_864_0_885_0	7	attractin-like protein partial	296	3.70E-98	65.70%	0.1	IPR016201 (SMART); IPR002049 (SMART); IPR002049 (PFAM); IPR002165 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10574 (PANTHER); PTHR10574:SF3 (PANTHER); SSF57196 (SUPERFAMILY)
50	c111460_g1_i1_len_1592_path_1570_0_1591_1	10	outer membrane autotransporter barrel domain protein	531	0	99.90%	0.291	IPR006315 (TIGRFAM); IPR012332 (G3DSA:2.160.20.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011050 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
51	c111472_g1_i1_len_268_path_1_0_267_5	0	chondroitin sulfate synthase 1	89	9.24E-08	74.30%	0.1	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
52	c111500_g1_i1_len_2313_path_2291_0_2312_2	20	protein fem-1 homolog c isoform x1	771	0	75.90%	0.103	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24182 (PANTHER); PTHR24182:SF9 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); IPR020683 (SUPERFAMILY)
53	c111535_g1_i1_len_471_path_1_0_470_4	21	potassium:sodium hyperpolarization activated	157	7.97E-08	61.60%	0.133	IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
54	c111547_g1_i1_len_1069_path_1_0_1068_5	14	hsp70 family protein	356	0	99.00%	0.112	IPR013126 (PRINTS); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF151 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY)
55	c111638_g1_i1_len_1336_path_1314_0_1335_3	27	ecto-nox disulfide-thiol exchanger 2	446	4.97E-112	77.10%	0.114	Coil (COILS); Coil (COILS); PTHR16001 (PANTHER)
56	c111841_g1_i1_len_827_path_805_0_826_4	19	neutral ceramidase	270	7.99E-61	65.00%	0.108	IPR006823 (PFAM); IPR006823 (PANTHER); PTHR12670:SF1 (PANTHER)
57	c112063_g1_i1_len_1236_path_1214_0_1235_2	44	endothelin-converting enzyme 1-like	412	2.59E-36	55.70%	0.246	G3DSA:1.10.1380.10 (GENE3D); IPR008753 (PFAM); IPR000718 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
58	c112098_g1_i1_len_915_path_1_0_914_1	6	lysosomal alpha-mannosidase	305	2.49E-89	65.70%	0.134	G3DSA:2.70.98.30 (GENE3D); IPR013780 (G3DSA:2.60.40.GENE3D); IPR011682 (PFAM); PTHR11607 (PANTHER); PTHR11607:SF3 (PANTHER); IPR011013 (SUPERFAMILY)

59	c112161_g1_i1_len_745_path_723_0_744_0	9	tissue factor pathway inhibitor 2	249	9.52E-34	51.60%	0.131	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
60	c112272_g1_i1_len_1408_path_1386_0_1407_0	23	endothelin-converting enzyme 1 isoform x2	470	1.89E-150	66.30%	0.27	IPR018497 (PRINTS); IPR018497 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR008753 (PFAM); IPR000718 (PANTHER); IPR029733 (PTHR11733:PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
61	c112359_g1_i1_len_573_path_551_0_572_0	4	hypoxanthine partial	191	7.20E-136	99.70%	0.138	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF64 (PANTHER); IPR008274 (SUPERFAMILY)
62	c112607_g1_i1_len_1962_path_1_0_1961_2	50	dual specificity mitogen-activated protein kinase kinase 4-like	654	0	89.90%	0.169	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24360:SF46 (PANTHER); PTHR24360 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
63	c112661_g1_i1_len_776_path_754_0_775_3	10	histone h2a	259	7.46E-79	99.90%	0.334	IPR002119 (PRINTS); IPR002119 (SMART); IPR009072 (G3DSA:1.10.20.GENE3D); IPR007125 (PFAM); PTHR23430:SF45 (PANTHER); PTHR23430 (PANTHER); IPR002119 (PROSITE_PATTERNS); IPR009072 (SUPERFAMILY)
64	c112698_g1_i1_len_1031_path_1_0_1030_4	21	beta-lactamase	344	0	99.80%	0.115	IPR000871 (PRINTS); PF13354 (PFAM); IPR012338 (G3DSA:3.40.710.GENE3D); IPR023650 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012338 (SUPERFAMILY)
65	c112765_g1_i1_len_830_path_1_0_829_1	14	hemocytin isoform x1	271	3.28E-14	47.00%	0.102	IPR006207 (PROSITE_PROFILES)
66	c113336_g1_i1_len_568_path_1_0_567_3	8	zinc finger and btb domain-containing protein 17	190	1.37E-70	55.50%	0.101	IPR015880 (SMART); PF13465 (PFAM); PF13909 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
67	c113356_g1_i1_len_1660_path_1_0_1659_2	29	low quality protein: otogelin	553	2.87E-17	43.70%	0.12	no IPS match
68	c113420_g1_i1_len_980_path_972_0_979_4	23	rac protein kinase drac-	321	1.62E-155	85.80%	0.157	IPR000961 (SMART); IPR002290 (SMART); IPR017892 (PFAM); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24351:SF64 (PANTHER); PTHR24351 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
69	c113461_g1_i1_len_711_path_1_0_710_0	11	epidermal growth factor-like protein 7	237	1.20E-29	49.90%	0.117	Coil (COILS); Coil (COILS); IPR001881 (SMART); IPR000742 (SMART); IPR000742 (PFAM); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR14949 (PANTHER); PTHR14949:SF14 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
70	c113632_g1_i1_len_1331_path_1309_0_1330_0	82	phospholipase lecithinase hemolysin	438	1.94E-14	44.90%	0.24	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)

71	c113786_g1_i1_len_516_path_1_0_515_3	3	netrin-g1 ligand	172	1.29E-70	78.20%	0.133	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR026906 (PFAM); PTHR24367 (PANTHER); PTHR24367:SF227 (PANTHER); SSF52058 (SUPERFAMILY)
72	c113825_g1_i1_len_1318_path_1304_0_1317_0	71	probable trna n6-adenosine threonylcarbamoyltransferase	440	0	89.00%	0.549 Y	IPR017861 (PRINTS); G3DSA:3.30.420.40 (GENE3D); IPR017861 (TIGRFAM); IPR000905 (PFAM); PTHR11735:SF6 (PANTHER); PTHR11735 (PANTHER); IPR017860 (PROSITE_PATTERNS); SignalP-noTM (SIGNALP_EUK); SSF53067 (SUPERFAMILY)
73	c114008_g1_i1_len_660_path_1_0_659_0	7	iron zinc purple acid phosphatase-like partial	220	6.44E-74	73.40%	0.195	IPR029052 (G3DSA:3.60.21.GENE3D); IPR018946 (PFAM); IPR015914 (G3DSA:2.60.40.GENE3D); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY); IPR008963 (SUPERFAMILY); TMhelix (TMHMM)
74	c114019_g1_i1_len_1382_path_1_0_1381_0	27	multiple pdz domain	461	2.79E-109	77.10%	0.113	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964:SF34 (PANTHER); PTHR19964 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
75	c114019_g1_i1_len_1382_path_1_0_1381_2	27	multiple pdz domain	460	5.42E-31	91.80%	0.182	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964:SF10 (PANTHER); PTHR19964 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
76	c114035_g1_i1_len_1169_path_3_0_1168_5	25	zinc finger protein 282	378	4.26E-15	58.80%	0.103	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
77	c114045_g1_i1_len_305_path_1_0_304_1	0	phenoloxidase subunit a3	102	5.60E-13	57.00%	0.138	IPR005204 (PFAM); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005204 (SUPERFAMILY)
78	c114240_g1_i1_len_1703_path_1_0_1702_2	76	26s protease regulatory subunit 6b	567	0	95.10%	0.099	Coil (COILS); IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR005937 (TIGRFAM); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23073 (PANTHER); PTHR23073:SF8 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
79	c1144_g1_i1_len_1014_path_3001_0_1012_4018_1013_1013_0	23	group 3 secretory phospholipase a2	338	1.19E-71	54.90%	0.104	Coil (COILS); IPR001211 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR12253 (PANTHER); IPR016090 (SUPERFAMILY)
80	c114450_g1_i1_len_796_path_1_0_795_0	9	vitellogenin- partial	260	1.46E-14	44.80%	0.12	PTHR23345 (PANTHER); PTHR23345:SF1 (PANTHER); IPR001846 (PROSITE_PROFILES)
81	c114620_g1_i1_len_1094_path_1_0_1093_2	27	krueppel-like factor 13	364	2.62E-50	82.60%	0.157	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
82	c11516_g1_i1_len_274_path_252_0_273_5	0	alpha-amylase	91	8.75E-58	99.40%	0.158	IPR013781 (G3DSA:3.20.20.GENE3D); IPR006047 (PFAM); IPR015902 (PANTHER); PTHR10357:SF11 (PANTHER); IPR017853 (SUPERFAMILY)
83	c11516_g2_i1_len_765_path_503_0_764_4	7	alpha-amylase	255	0	99.00%	0.099	IPR006589 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR006047 (PFAM); IPR015902 (PANTHER); PTHR10357:SF11 (PANTHER); IPR017853 (SUPERFAMILY)
84	c115247_g1_i1_len_317_path_295_0_316_1	2	aldehyde partial	106	3.67E-66	98.90%	0.11	IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); IPR015657 (PTHR11699:PANTHER); PTHR11699 (PANTHER); IPR016160 (PROSITE_PATTERNS); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)

85	c115416_g1_i1_len_1100_path_1_0_1099_3	14	u4 u6 small nuclear ribonucleoprotein prp4	367	0	83.90%	0.122	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR027106 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
86	c115766_g1_i1_len_869_path_1_0_868_1	15	sortilin-related receptor-like	284	3.35E-79	66.40%	0.104	IPR002172 (PRINTS); IPR002172 (SMART); G3DSA:4.10.1220.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR12106:SF7 (PANTHER); PTHR12106 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
87	c115833_g1_i1_len_1255_path_1_0_1254_1	65	kunitz-like protease inhibitor	418	1.03E-40	55.50%	0.142	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); IPR008037 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
88	c115838_g1_i1_len_636_path_1_0_635_5	7	27 kda hemolymph	212	1.20E-17	64.00%	0.112	IPR009832 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
89	c115841_g1_i1_len_992_path_1_0_991_0	6	lipoprotein	331	1.53E-107	99.40%	0.117	IPR000064 (PFAM); IPR000064 (G3DSA:3.90.1720.GENE3D); PTHR21666:SF194 (PANTHER); PTHR21666 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY)
90	c115877_g1_i1_len_597_path_575_0_596_4	9	catalase peroxidase partial	199	2.39E-138	99.90%	0.104	IPR002016 (PRINTS); G3DSA:1.10.420.10 (GENE3D); IPR002016 (PFAM); G3DSA:1.10.520.10 (GENE3D); PTHR30555 (PANTHER); PTHR30555:SF0 (PANTHER); IPR019793 (PROSITE_PATTERNS); IPR010255 (SUPERFAMILY)
91	c115912_g1_i1_len_479_path_459_0_478_2	3	oocyte zinc finger protein 6	159	3.55E-18	61.10%	0.184	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
92	c115984_g1_i1_len_1306_path_1284_0_1305_4	42	protein spaetzle	435	1.87E-28	54.30%	0.114	PTHR23199 (PANTHER); IPR029034 (SUPERFAMILY)
93	c11626_g1_i1_len_416_path_4_0_40_45_41_415_4	2	dnaj homolog subfamily a member 2	139	8.10E-41	76.30%	0.123	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24076 (PANTHER); PTHR24076:SF1 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
94	c116301_g1_i1_len_531_path_509_0_530_3	6	3-hydroxy acid dehydrogenase	177	2.36E-46	98.70%	0.369 Y	IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF78 (PANTHER); PTHR24322 (PANTHER); SignalP-TM (SIGNALP_GRAM_NEGATIVE); SSF51735 (SUPERFAMILY)
95	c116313_g1_i1_len_916_path_1_0_915_5	8	gamma-glutamyltransferase	305	0	99.90%	0.107	IPR000101 (PRINTS); IPR000101 (TIGRFAM); IPR000101 (PFAM); IPR000101 (PANTHER); PTHR11686:SF9 (PANTHER); IPR029055 (SUPERFAMILY)
96	c1164_g1_i1_len_1496_path_1524_0_1495_5	96	protein 60a	492	3.06E-121	66.20%	0.117	IPR002405 (PRINTS); IPR001839 (SMART); IPR001111 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); IPR001839 (PFAM); PTHR11848:SF54 (PANTHER); IPR015615 (PANTHER); IPR017948 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001839 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY); TMhelix (TMHMM)
97	c116535_g1_i1_len_1204_path_1182_0_1203_4	17	hypothetical protein BRAFLDRAFT_125057	401	1.52E-12	47.10%	0.112	no IPS match

98	c1167_g1_i1_len_1190_path_1_0_683_2393_684_695_697_696_1189_4	37	guanine nucleotide-binding protein subunit beta-5	391	5.14E-93	93.50%	0.12	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR016346 (PANTHER); PTHR19850:SF12 (PANTHER); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
99	c116829_g1_i1_len_551_path_1_0_550_0	26	40s ribosomal protein s26	178	2.70E-68	90.00%	0.108	IPR000892 (PFAM); IPR000892 (PANTHER); IPR000892 (PROSITE_PATTERNS)
100	c117037_g1_i1_len_2578_path_2556_0_2577_5	188	atp-dependent zinc metalloprotease yme1 homolog	859	0	75.30%	0.194	IPR003593 (SMART); IPR005936 (TIGRFAM); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR000642 (PFAM); G3DSA:1.10.8.60 (GENE3D); PTHR23076:SF37 (PANTHER); PTHR23076 (PANTHER); IPR003960 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005936 (HAMAP); SSF140990 (SUPERFAMILY); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
101	c117076_g1_i1_len_432_path_410_0_431_3	2	carbohydrate sulfotransferase partial	144	1.52E-52	70.50%	0.099	IPR005331 (PFAM); IPR018011 (PANTHER)
102	c117203_g1_i1_len_1545_path_1_0_1544_4	29	transmembrane protease serine partial	515	7.00E-13	76.70%	0.11	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
103	c117412_g1_i1_len_587_path_1_0_586_2	3	calumenin-like partial	195	2.69E-95	79.40%	0.108	IPR002048 (SMART); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); IPR002048 (PFAM); PTHR10827 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY)
104	c117490_g1_i1_len_291_path_1_0_290_3	2	twitchin- partial	97	4.46E-50	92.20%	0.191	PR00014 (PRINTS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR19897:SF142 (PANTHER); PTHR19897 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
105	c117563_g1_i1_len_1982_path_1960_0_1981_4	93	pleiotropic regulator 1	640	0	81.40%	0.251	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19923 (PANTHER); PTHR19923:SF0 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
106	c117605_g1_i1_len_2541_path_1_0_2540_3	76	translocation protein sec63 homolog	847	0	73.90%	0.148	IPR001623 (PRINTS); IPR004179 (SMART); IPR004179 (SMART); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR000008 (G3DSA:2.60.40.GENE3D); IPR004179 (PFAM); IPR001623 (PFAM); G3DSA:1.10.150.20 (GENE3D); G3DSA:1.10.3380.10 (GENE3D); PTHR24075:SF0 (PANTHER); IPR027137 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001623 (PROSITE_PROFILES); SSF158702 (SUPERFAMILY); IPR001623 (SUPERFAMILY); IPR014756 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
107	c117718_g1_i1_len_1773_path_1751_0_1772_2	59	multiple inositol polyphosphate phosphatase 1	587	1.28E-71	59.50%	0.192	IPR000560 (PFAM); IPR029033 (G3DSA:3.40.50.GENE3D); PTHR20963 (PANTHER); PTHR20963:SF8 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029033 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

108	c117757_g1_i1_len_943_path_1_0_942_0	21	immunoglobulin-like and fibronectin type iii domain containing 7	310	7.71E-18	55.90%	0.121	IPR026966 (PFAM); PTHR10489 (PANTHER); PTHR10489:SF553 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
109	c117786_g1_i1_len_475_path_1_0_474_5	4	metabotropic gaba-b receptor subtype isoform b	158	1.48E-21	96.10%	0.175	G3DSA:3.40.50.2300 (GENE3D); PTHR10519:SF3 (PANTHER); IPR002455 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR028082 (SUPERFAMILY); TMhelix (TMHMM)
110	c117844_g1_i1_len_899_path_877_0_898_1	12	limbic system-associated membrane protein	300	8.80E-40	56.00%	0.477 Y	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PF13895 (PFAM); PTHR19831 (PANTHER); PTHR19831:SF40 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
111	c11819_g1_i1_len_2411_path_4342_0_499_1909_500_2410_3	109	krueppel-like factor 10	804	1.75E-65	63.20%	0.669 Y	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR23223:SF21 (PANTHER); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
112	c118315_g1_i1_len_729_path_6_0_728_5	14	proactivator polypeptide	243	2.32E-10	72.40%	0.127	IPR008139 (SMART); IPR008138 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR11480:SF3 (PANTHER); PTHR11480 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008139 (PROSITE_PROFILES); IPR011001 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
113	c118357_g1_i1_len_1092_path_1070_0_1091_1	24	chondroitin sulfate synthase 1	364	2.98E-111	64.50%	0.101	IPR008428 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); PTHR12369:SF11 (PANTHER); PTHR12369 (PANTHER); IPR029044 (SUPERFAMILY)
114	c118503_g1_i1_len_538_path_696_0_537_5	4	exostosin-1-like isoform 1	179	1.87E-39	88.70%	0.115	IPR015338 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); PTHR11062:SF7 (PANTHER); PTHR11062 (PANTHER); IPR029044 (SUPERFAMILY)
115	c11858_g1_i1_len_740_path_718_0_739_0	6	venom serine protease bi-vsp-like	247	5.98E-45	67.00%	0.149	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF97 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
116	c11858_g2_i1_len_243_path_1435_0_242_2	0	venom protease-like	81	1.99E-13	62.20%	0.143	IPR006604 (SMART); IPR022700 (PFAM)
117	c118762_g1_i1_len_508_path_1_0_507_4	2	phosphoglycerate kinase	169	4.83E-93	99.90%	0.101	IPR015901 (G3DSA:3.40.50.GENE3D); IPR001576 (PFAM); IPR001576 (PANTHER); PTHR11406:SF0 (PANTHER); IPR001576 (SUPERFAMILY)
118	c11884_g1_i1_len_440_path_828_0_78_411_79_439_2	85	probable chitinase 3	146	7.78E-28	69.90%	0.114	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
119	c11884_g1_i2_len_397_path_375_0_35_411_36_396_1	75	chitinase-related protein 1	132	3.30E-28	71.50%	0.207	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
120	c119077_g1_i1_len_585_path_1_0_584_5	15	ribonuclease oy-like	195	6.62E-22	67.40%	0.109	IPR001568 (G3DSA:3.90.730.GENE3D); IPR001568 (PFAM); PTHR11240:SF1 (PANTHER); IPR001568 (PANTHER); IPR001568 (SUPERFAMILY)

121	c119134_g1_i1_len_375_path_353_0_374_3	5	dnaj homolog subfamily c member 10	125	1.82E-17	69.90%	0.147	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR24078:SF3 (PANTHER); PTHR24078 (PANTHER); IPR017937 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
122	c119266_g1_i1_len_640_path_618_0_639_4	4	zinc finger protein 678-like	213	1.70E-29	55.20%	0.098	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
123	c119398_g1_i1_len_701_path_1_0_700_2	5	protein lap4 isoform x5	233	1.13E-47	66.60%	0.1	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); IPR016313 (PANTHER); PTHR23119:SF28 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
124	c119462_g1_i1_len_515_path_1_0_514_0	6	echotoxin b2	172	8.79E-07	51.60%	0.117	IPR015926 (G3DSA:2.60.270.GENE3D); IPR015926 (SUPERFAMILY)
125	c119472_g1_i1_len_309_path_63_0_308_1	0	partial	96	1.55E-10	69.90%	0.118	IPR005203 (PFAM); IPR005203 (G3DSA:2.60.40.GENE3D); PTHR11511:SF24 (PANTHER); IPR013788 (PANTHER); IPR014756 (SUPERFAMILY)
126	c120115_g1_i1_len_1218_path_1_0_1217_0	10	oxidoreductase	406	0	99.80%	0.106	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PF13561 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF192 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
127	c12042_g1_i1_len_2291_path_1015_0_1272_228_7_1273_1757_1014_1758_2290_4	41	copa-type pol polypeptide	758	4.11E-50	49.80%	0.165	IPR001584 (PFAM); IPR013103 (PFAM); IPR012337 (G3DSA:3.30.420.GENE3D); PTHR11439 (PANTHER); PTHR11439:SF127 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001584 (PROSITE_PROFILES); IPR012337 (SUPERFAMILY)
128	c120581_g1_i1_len_784_path_1_0_783_1	9	low quality protein: zinc finger protein 233	261	2.79E-67	67.00%	0.116	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
129	c120650_g1_i1_len_368_path_346_0_367_4	4	actin-depolymerizing factor	123	2.34E-22	68.10%	0.103	IPR007122 (SMART); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR030004 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY)
130	c120823_g1_i1_len_221_path_1_0_220_1	0	---NA---	74			0.139	IPR001229 (PFAM); IPR001229 (G3DSA:2.100.10.GENE3D); IPR001229 (SUPERFAMILY)
131	c120889_g1_i1_len_671_path_4_0_670_2	4	aurora kinase a	223	1.61E-39	92.70%	0.258	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); IPR030616 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
132	c121260_g1_i1_len_293_path_271_0_292_5	2	proprotein convertase subtilisin kexin type 7 isoform x1	97	3.34E-44	85.40%	0.109	IPR000209 (PFAM); IPR000209 (G3DSA:3.40.50.GENE3D); IPR015500 (PANTHER); PTHR10795:SF9 (PANTHER); IPR023828 (PROSITE_PATTERNS); IPR000209 (SUPERFAMILY)
133	c121290_g1_i1_len_1093_path_1209_0_1092_4	6	glycogen branching partial	364	0	99.90%	0.109	IPR006589 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR006407 (TIGRFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR006047 (PFAM); IPR015902 (PANTHER); PTHR10357:SF110 (PANTHER); IPR017853 (SUPERFAMILY)
134	c121447_g1_i1_len_713_path_691_0_712_5	6	conserved hypothetical protein	237	3.33E-07	67.00%	0.286	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)

135	c121675_g1_i1_len_708_path_1_0_707_4	8	poly -specific endoribonuclease homolog	236	1.51E-56	61.60%	0.718 Y	IPR018998 (PFAM); PTHR12439 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF142877 (SUPERFAMILY)
136	c121686_g1_i1_len_290_path_268_0_289_4	2	protein sda1 homolog	97	3.94E-42	89.60%	0.206	IPR007949 (PFAM); IPR027312 (PTHR12730:PANTHER); PTHR12730 (PANTHER)
137	c12172_g2_i1_len_687_path_665_0_686_1	6	calcium calmodulin-dependent protein kinase kinase 1-like isoform x2	229	2.39E-55	88.90%	0.128	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); IPR020636 (PANTHER); PTHR24347:SF141 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
138	c1218_g1_i1_len_1397_path_1_0_908_910_909_1007_1009_1008_1396_0	136	d-aspartate oxidase	466	4.37E-99	63.60%	0.119	IPR006076 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR11530:SF0 (PANTHER); IPR023209 (PANTHER); IPR006181 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54373 (SUPERFAMILY); SSF51971 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
139	c1218_g1_i2_len_1298_path_1_0_908_1009_909_1297_0	72	d-aspartate oxidase	433	9.46E-79	56.90%	0.119	G3DSA:3.30.9.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR006076 (PFAM); PTHR11530:SF0 (PANTHER); IPR023209 (PANTHER); IPR006181 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51971 (SUPERFAMILY); SSF54373 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
140	c12203_g1_i1_len_1314_path_1_0_1313_2	11	partial	438	0	99.00%	0.261	IPR001661 (PFAM); IPR001661 (PANTHER); PTHR23403:SF1 (PANTHER); IPR018232 (PROSITE_PATTERNS); IPR008928 (SUPERFAMILY)
141	c12213_g1_i1_len_2408_path_2386_0_1296_368_3_1297_2407_2	119	endoplasmic reticulum resident protein 44 isoform x3	802	0	79.10%	0.154	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); PF13848 (PFAM); PTHR18929:SF49 (PANTHER); PTHR18929 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
142	c122163_g1_i1_len_546_path_1_0_545_5	8	fk506-binding protein 4	182	4.51E-46	75.80%	0.133	G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); IPR023566 (PANTHER); PTHR10516:SF274 (PANTHER); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY)
143	c122246_g1_i1_len_327_path_1_0_326_3	3	tyrosine-protein kinase dnt	109	6.71E-31	69.10%	0.12	IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24416 (PANTHER); PTHR24416:SF256 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
144	c122499_g1_i1_len_350_path_328_0_349_0	3	low quality protein: von willebrand factor type egf and pentraxin domain-containing protein 1-like	117	6.43E-42	75.50%	0.102	IPR011641 (PFAM); G3DSA:2.10.50.10 (GENE3D); PTHR24049 (PANTHER); PTHR24049:SF6 (PANTHER); IPR009030 (SUPERFAMILY)
145	c12265_g1_i1_len_1818_path_1_0_1817_0	99	periodic tryptophan protein 2 homolog	606	0	79.00%	0.108	IPR001680 (SMART); IPR001680 (PFAM); IPR007148 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR015943 (G3DSA:2.130.10.GENE3D); IPR027145 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR011047 (SUPERFAMILY)
146	c12266_g1_i1_len_1412_path_1_0_1411_1	1001	peptidyl-prolyl cis-trans isomerase e	465	2.39E-168	84.30%	0.107	IPR002130 (PRINTS); IPR000504 (SMART); IPR029000 (G3DSA:2.40.100.GENE3D); IPR000504 (PFAM); IPR012677 (G3DSA:3.30.70.GENE3D); IPR002130 (PFAM); PTHR11071:SF242 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR000504 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); SSF54928 (SUPERFAMILY)

147	c12316_g1_i1_len_3218_path_3196_0_1562_475_9_1563_3217_2	384	basement membrane-specific heparan sulfate proteoglycan core protein	1072	3.14E-105	59.60%	0.104	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013151 (PFAM); PTHR10489 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
148	c123169_g1_i1_len_1103_path_1081_0_1102_4	14	secreted salivary gland	368	2.22E-30	50.30%	0.107	IPR004991 (PFAM); IPR023307 (G3DSA:2.170.15.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF56973 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
149	c12324_g1_i1_len_1660_path_1_0_1246_2516_1_247_1659_3	26	l-xylulose 3-keto-l-gulonate kinase	554	0	97.70%	0.134	IPR018484 (PFAM); IPR018389 (PFAM); IPR004682 (TIGRFAM); G3DSA:3.30.420.40 (GENE3D); PTHR10196:SF10 (PANTHER); PTHR10196 (PANTHER); SSF53067 (SUPERFAMILY); SSF53850 (SUPERFAMILY)
150	c123450_g1_i1_len_660_path_1_0_659_1	6	lysine--trna partial	220	2.19E-158	99.00%	0.15	IPR018149 (PRINTS); IPR004364 (PFAM); IPR004365 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); G3DSA:3.30.930.10 (GENE3D); IPR018150 (PANTHER); PTHR22594:SF25 (PANTHER); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY); IPR012340 (SUPERFAMILY)
151	c123713_g1_i1_len_570_path_699_0_569_0	25	mucin core	190	1.08E-11	73.50%	0.1	IPR007947 (PFAM); IPR007947 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
152	c12373_g1_i1_len_152_path_25_0_151_4	4	carboxypeptidase	51	3.09E-12	80.30%	0.13	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
153	c12472_g1_i1_len_1168_path_44_0_1096_1141_1097_1167_5	14	---NA---	389			0.118	Coil (COILS); Coil (COILS)
154	c1253_g1_i1_len_1246_path_1_0_1245_0	78	apolipoprotein d	416	1.15E-07	45.50%	0.129	IPR012674 (G3DSA:2.40.128.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011038 (SUPERFAMILY)
155	c12538_g1_i1_len_2147_path_1_0_1302_1304_1_303_2146_3	31	peroxisomal multifunctional enzyme type 2	716	0	71.90%	0.139	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR013968 (SMART); IPR002198 (PFAM); IPR003033 (G3DSA:3.30.1050.GENE3D); IPR029069 (G3DSA:3.10.129.GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002539 (PFAM); PF13452 (PFAM); IPR029069 (G3DSA:3.10.129.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF2 (PANTHER); IPR020904 (PROSITE_PATTERNS); IPR029069 (SUPERFAMILY); SSF51735 (SUPERFAMILY); IPR029069 (SUPERFAMILY)
156	c12538_g1_i2_len_2171_path_1_0_1302_4311_1_303_1326_1304_1327_2170_3	31	peroxisomal multifunctional enzyme type 2	724	0	72.70%	0.139	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR013968 (SMART); PF13452 (PFAM); IPR003033 (G3DSA:3.30.1050.GENE3D); IPR029069 (G3DSA:3.10.129.GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002539 (PFAM); IPR029069 (G3DSA:3.10.129.GENE3D); IPR002198 (PFAM); PTHR24316 (PANTHER); PTHR24316:SF2 (PANTHER); IPR020904 (PROSITE_PATTERNS); IPR029069 (SUPERFAMILY); IPR029069 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
157	c126362_g1_i1_len_538_path_1_0_537_1	4	lysine--trna partial	179	1.78E-128	99.90%	0.155	IPR018149 (PRINTS); IPR004365 (PFAM); IPR004364 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); G3DSA:3.30.930.10 (GENE3D); PTHR22594:SF25 (PANTHER); IPR018150 (PANTHER); IPR006195 (PROSITE_PROFILES); IPR012340 (SUPERFAMILY); SSF55681 (SUPERFAMILY)

158	c12674_g1_i1_len_1465_path_1_0_1392_1394_1_393_1416_1394_1417_1440_1394_1441_1464_4	31	phospholipid scramblase 2 isoform x1	488	2.50E-132	81.80%	0.101	IPR005552 (PFAM); PTHR23248:SF26 (PANTHER); IPR005552 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR025659 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
159	c12686_g1_i1_len_1200_path_1_0_1199_2	103249	serine proteinase stubble	393	5.53E-40	52.20%	0.23	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
160	c127139_g1_i1_len_675_path_502_0_326_829_3_27_500_829_501_674_5	14	gastrula zinc finger	219	4.00E-36	53.40%	0.098	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
161	c12730_g1_i1_len_1118_path_1_0_1117_3	143	estradiol 17-beta-dehydrogenase 8	373	3.86E-86	72.20%	0.12	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316 (PANTHER); PTHR24316:SF254 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
162	c127669_g1_i1_len_389_path_1_0_388_1	2	lysine--trna ligase	130	8.40E-88	100.00%	0.101	G3DSA:3.30.930.10 (GENE3D); IPR004364 (PFAM); PTHR22594:SF25 (PANTHER); IPR018150 (PANTHER); SSF55681 (SUPERFAMILY)
163	c127922_g1_i1_len_484_path_1_0_483_4	4	thioredoxin	161	2.54E-100	99.60%	0.343 Y	PR00421 (PRINTS); IPR005746 (TIGRFAM); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10438:SF253 (PANTHER); IPR005746 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
164	c12796_g1_i1_len_1101_path_1079_0_1100_0	35	preproneuropeptide f i	362	1.39E-17	63.88%	0.168	IPR020392 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001955 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
165	c12847_g1_i1_len_1341_path_1319_0_1106_242_6_1107_1107_2427_1108_1340_2	72	chitinase partial	441	1.18E-91	70.20%	0.1	IPR011583 (SMART); IPR002557 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); IPR002557 (PFAM); IPR002557 (G3DSA:2.170.140.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR029070 (SUPERFAMILY)
166	c12858_g1_i1_len_241_path_169_0_240_1	13	trypsin partial	80	2.19E-12	64.10%	0.106	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24250 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
167	c12876_g1_i1_len_1384_path_2_0_1244_2844_1_245_1245_1247_1246_1383_0	34	contactin associated protein 1	462	1.65E-50	50.70%	0.101	Coil (COILS); IPR000885 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); PTHR10127 (PANTHER); PTHR10127:SF575 (PANTHER); IPR002181 (SUPERFAMILY)
168	c128889_g1_i1_len_279_path_1_0_278_5	2	low quality protein: glutathione peroxidase 3-like	93	5.26E-14	67.80%	0.107	IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PANTHER); PTHR11592:SF21 (PANTHER); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
169	c129036_g1_i1_len_694_path_672_0_693_2	4	---NA---	231			0.113	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
170	c129414_g1_i1_len_489_path_467_0_488_1	4	#NAME?	163	1.43E-52	81.50%	0.137	IPR001830 (PFAM); G3DSA:3.40.50.2000 (GENE3D); PTHR10788:SF6 (PANTHER); PTHR10788 (PANTHER); SSF53756 (SUPERFAMILY)

171	c129442_g1_i1_len_302_path_1_0_301_0	0	zinc c2h2 type domain-containing protein	101	3.54E-20	58.50%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
172	c12958_g1_i1_len_2203_path_2181_0_843_3025_844_2202_2	72	von willebrand factor a domain-containing protein partial	728	0	70.80%	0.126	Coil (COILS); IPR002035 (SMART); PF13519 (PFAM); PTHR21610 (PANTHER); PTHR21610:SF9 (PANTHER); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
173	c12975_g1_i1_len_993_path_971_0_439_1411_440_441_1413_442_992_1	76	tyrosine-protein kinase wsck	325	9.66E-40	65.50%	0.124	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24418 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
174	c13023_g1_i1_len_1229_path_1207_0_1228_0	181	transcriptional repressor protein yy1-like	398	2.38E-108	95.20%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR14003:SF10 (PANTHER); PTHR14003 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
175	c130346_g1_i1_len_464_path_442_0_463_2	6	semaphorin-1a isoform x2	154	7.41E-13	78.30%	0.265	IPR001627 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR11036:SF66 (PANTHER); IPR027231 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001627 (SUPERFAMILY); TMhelix (TMHMM)
176	c130812_g1_i1_len_437_path_1_0_436_4	4	zinc finger	146	4.80E-67	86.10%	0.177	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24391:SF9 (PANTHER); PTHR24391 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
177	c1310_g1_i1_len_1155_path_1133_0_470_1604_471_1154_2	33	low-density lipoprotein receptor-related protein 1-like	379	1.02E-08	72.80%	0.106	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
178	c1310_g1_i2_len_1641_path_2265_0_956_1604_957_1640_2	61	ves g 5 allergen	541	9.84E-46	52.40%	0.574 Y	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR002172 (SMART); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR014044 (SUPERFAMILY); TMhelix (TMHMM)
179	c13109_g1_i1_len_977_path_125_0_743_112_744_755_124_756_976_0	29	zinc metalloprotease	321	5.10E-10	60.20%	0.205	G3DSA:1.10.390.10 (GENE3D); TMhelix (TMHMM); TMhelix (TMHMM)
180	c13157_g1_i1_len_736_path_762_0_123_885_124_126_25_127_735_2	43	protein pygopus	237	1.99E-58	87.40%	0.098	IPR001965 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); IPR019787 (PFAM); PTHR23194 (PANTHER); PTHR23194:SF15 (PANTHER); IPR019786 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR019787 (PROSITE_PROFILES); IPR011011 (SUPERFAMILY)

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188	c13292_g1_i1_len_1084_path_49_0_448_497_449_1083_2	31	syntaxin-16 isoform x4	361	1.02E-104	70.80%	0.155	IPR000727 (SMART); IPR006011 (PFAM); IPR000727 (PFAM); G3DSA:1.20.58.70 (GENE3D); PTHR19957:SF83 (PANTHER); PTHR19957 (PANTHER); IPR006012 (PROSITE PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000727 (PROSITE_PROFILES); IPR010989 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
189	c13315_g1_i1_len_1882_path_1_0_1881_0	135	4-trimethylaminobutyraldehyde partial	628	0	74.30%	0.176	IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699:SF114 (PANTHER); PTHR11699 (PANTHER); IPR016160 (PROSITE PATTERNS); IPR029510 (PROSITE PATTERNS); IPR016161 (SUPERFAMILY)
190	c133397_g1_i1_len_328_path_1_0_327_0	1	parkinson disease 7 domain-containing protein 1-like isoform x1	105	1.69E-41	72.60%	0.176	IPR002818 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); IPR029062 (SUPERFAMILY)
191	c13376_g1_i1_len_270_path_254_0_221_557_222_269_2	0	probable chitinase 3	90	1.69E-06	55.00%	0.105	Coil (COILS); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
192	c134251_g1_i1_len_313_path_67_0_312_0	0	tryptase partial	105	5.71E-06	56.00%	0.145	G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
193	c1344_g1_i1_len_1803_path_1781_0_1802_0	21	cyclin-dependent kinase 17-like isoform x1	601	0	85.90%	0.102	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24056:SF128 (PANTHER); PTHR24056 (PANTHER); IPR008271 (PROSITE PATTERNS); IPR017441 (PROSITE PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
194	c13494_g1_i1_len_2261_path_1_0_1400_1402_1401_1402_1404_1403_2260_1	80	zinc finger protein 239-like isoform x2	748	1.25E-76	68.00%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24377 (PANTHER); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
195	c13501_g1_i1_len_1025_path_1_0_1024_1	16	ly6 plaur domain-containing protein 1-like	335	1.02E-37	74.00%	0.102	G3DSA:2.10.60.10 (GENE3D); PTHR31171 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF57302 (SUPERFAMILY)
196	c135253_g1_i1_len_173_path_197_0_172_4	0	---NA---	58			0.168	no IPS match
197	c13591_g1_i1_len_1321_path_1_0_1320_1	3443	ion transport peptide isoform x2	440	4.90E-30	77.90%	0.124	IPR001166 (PRINTS); IPR000346 (PRINTS); IPR001166 (G3DSA:1.10.2010.GENE3D); IPR001166 (PFAM); IPR018251 (PROSITE PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001166 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
198	c13598_g1_i1_len_1205_path_1_0_1204_4	775049	serine protease 27-like	394	5.73E-42	55.00%	0.438 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE PATTERNS); IPR018114 (PROSITE PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

199	c13605_g1_i1_len_1660_path_1648_0_1659_2	18211	suppressor of tumorigenicity 14 protein	544	1.38E-67	53.40%	0.17	IPR002172 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); IPR002172 (PFAM); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
200	c13611_g1_i1_len_2033_path_1_0_2032_3	22159	enolase isoform x2	672	0	89.70%	0.122	IPR000941 (PRINTS); IPR020810 (PFAM); IPR000941 (TIGRFAM); IPR020811 (PFAM); IPR029065 (G3DSA:3.20.20.GENE3D); IPR029017 (G3DSA:3.30.390.GENE3D); IPR000941 (PANTHER); IPR020809 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000941 (HAMAP); IPR029065 (SUPERFAMILY); IPR029017 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
201	c13639_g1_i1_len_534_path_642_0_423_1066_4_24_430_1073_431_533_0	16	type i restriction enzyme	178	7.35E-08	69.50%	0.112	Coil (COILS); TMhelix (TMHMM)
202	c136476_g1_i1_len_1172_path_1_0_1171_3	32	70 kda heat shock partial	391	0	88.30%	0.1	Coil (COILS); IPR013126 (PRINTS); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); G3DSA:3.90.640.10 (GENE3D); IPR029048 (G3DSA:1.20.1270.GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029048 (SUPERFAMILY)
203	c136533_g1_i1_len_1658_path_1_0_1657_0	58	von willebrand factor like 2	553	1.33E-14	41.70%	0.098	IPR001007 (PROSITE_PATTERNS)
204	c136609_g1_i1_len_984_path_1_0_983_5	16	serine threonine-protein kinase 11	328	2.06E-103	74.80%	0.112	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24347:SF1 (PANTHER); IPR020636 (PANTHER); IPR008271 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
205	c136637_g1_i1_len_311_path_289_0_310_0	9301	chitinase 2	104	6.50E-16	73.90%	0.12	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
206	c136668_g1_i1_len_2176_path_2154_0_2175_1	45	neural cell adhesion molecule 1-b	719	2.50E-71	57.20%	0.107	IPR003599 (SMART); IPR003598 (SMART); IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831:SF48 (PANTHER); PTHR19831 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
207	c13674_g1_i1_len_1130_path_31_0_110_30_111_174_30_175_238_204_239_1129_5	9	protein twisted gastrulation	376	4.39E-68	74.80%	0.1	IPR006761 (PFAM); IPR006761 (PANTHER); PTHR12312:SF15 (PANTHER)
208	c136777_g1_i1_len_579_path_557_0_578_4	6	hth-type transcriptional regulator malt	193	2.59E-72	100.00%	0.112	no IPS match
209	c136814_g1_i1_len_1623_path_1601_0_1622_1	117	acetylcholine receptor subunit alpha-type acr-16	535	6.06E-112	59.90%	0.171	IPR006201 (PRINTS); IPR006029 (PFAM); IPR006202 (G3DSA:2.70.170.GENE3D); IPR027361 (G3DSA:1.20.120.GENE3D); IPR006202 (PFAM); PTHR18945:SF490 (PANTHER); IPR006201 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006029 (SUPERFAMILY); IPR006202 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

[illegible]

229	c137924_g1_i1_len_853_path_831_0_852_1	16	krueppel-like factor 5	284	3.06E-46	96.20%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
230	c13799_g1_i1_len_2238_path_1_0_1469_1471_1_470_1604_1606_1605_2237_5	46	nephrin isoform x1	746	1.25E-158	65.40%	0.101	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013162 (PFAM); PTHR11640:SF31 (PANTHER); PTHR11640 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
231	c13799_g1_i2_len_2103_path_1_0_1469_1606_1_470_2102_5	43	nephrin isoform x1	701	1.27E-135	64.80%	0.101	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013098 (PFAM); PTHR11640:SF31 (PANTHER); PTHR11640 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
232	c138092_g1_i1_len_302_path_280_0_301_3	2	plexin- partial	101	2.28E-46	86.50%	0.107	IPR001627 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22625:SF16 (PANTHER); PTHR22625 (PANTHER); IPR001627 (PROSITE_PROFILES); IPR001627 (SUPERFAMILY)
233	c13811_g1_i1_len_601_path_1_0_559_1242_560_574_607_575_600_1	46	vp302_lycmc ame: full=venom protein 302 flags: precursor	200	2.45E-14	55.80%	0.718 Y	PTHR14186:SF8 (PANTHER); IPR011390 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR000867 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009030 (SUPERFAMILY)
234	c13811_g1_i2_len_632_path_1_0_559_561_560_605_607_606_631_1	55	vp302_lycmc ame: full=venom protein 302 flags: precursor	211	2.43E-14	56.00%	0.718 Y	PTHR14186:SF8 (PANTHER); IPR011390 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000867 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR009030 (SUPERFAMILY)
235	c138187_g1_i1_len_742_path_1_0_741_5	8	leukotriene a-4 hydrolase	247	1.98E-106	76.80%	0.096	IPR014782 (PRINTS); IPR014782 (PFAM); IPR001930 (PANTHER); PTHR11533:SF4 (PANTHER); SSF63737 (SUPERFAMILY); SSF55486 (SUPERFAMILY)
236	c13837_g1_i1_len_529_path_1_0_528_2	9	tyrosine-protein kinase dnt	176	6.67E-44	88.00%	0.399 Y	IPR001245 (PRINTS); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416 (PANTHER); PTHR24416:SF302 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
237	c138408_g1_i1_len_1460_path_1438_0_1459_2	39	zinc finger protein 271-like	480	1.97E-63	66.30%	0.097	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
238	c138539_g2_i1_len_194_path_420_0_193_1	0	hypothetical protein Y032_0001g415	65	1.09E-08	64.50%	0.1	no IPS match

239	c138695_g1_i1_len_1209_path_1_0_1208_3	17	zinc finger	403	6.36E-16	47.70%	0.104	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24375:SF106 (PANTHER); PTHR24375 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
240	c138874_g1_i1_len_1266_path_1244_0_1265_3	28	melanopsin-like isoform x1	422	2.05E-78	60.90%	0.121	IPR000276 (PRINTS); IPR000276 (PFAM); G3DSA:1.20.1070.10 (GENE3D); PTHR24242 (PANTHER); PTHR24242:SF154 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017452 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
241	c138901_g1_i1_len_1314_path_1_0_1313_2	59	internalin a	438	3.81E-126	68.50%	0.109	SM00364 (SMART); IPR003591 (SMART); IPR001611 (PFAM); IPR025875 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155:SF408 (PANTHER); PTHR23155 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
242	c138982_g1_i1_len_2375_path_2353_0_2374_1	208	wd repeat-containing protein 82	786	0	94.80%	0.15	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19861 (PANTHER); PTHR19861:SF2 (PANTHER); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
243	c139006_g1_i1_len_1369_path_1_0_1368_2	64	beta-galactosidase and hygromycin phosphotransferase fusion protein	456	0	100.00%	0.113	IPR006101 (PRINTS); IPR006104 (PFAM); IPR013812 (G3DSA:2.60.40.GENE3D); IPR006102 (PFAM); IPR006103 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR10066:SF57 (PANTHER); PTHR10066 (PANTHER); IPR023230 (PROSITE_PATTERNS); IPR023232 (PROSITE_PATTERNS); IPR006102 (SUPERFAMILY); IPR008979 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
244	c139125_g1_i1_len_1454_path_1432_0_1453_0	23	endoplasmic reticulum mannosyl-oligosaccharide - alpha-mannosidase	485	3.88E-135	81.30%	0.105	IPR001382 (PRINTS); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); PTHR11742:SF7 (PANTHER); IPR001382 (PANTHER); IPR001382 (SUPERFAMILY)
245	c139137_g1_i1_len_1934_path_1912_0_1933_3	32	cgmp-dependent protein isozyme 2 forms cd4 t1 t3a t3b	645	0	91.30%	0.115	Coil (COILS); IPR002374 (PRINTS); IPR000961 (SMART); IPR002290 (SMART); IPR000595 (SMART); IPR014710 (G3DSA:2.60.120.GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR002374 (PIRSF); IPR000595 (PFAM); IPR000719 (PFAM); IPR014710 (G3DSA:2.60.120.GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24353:SF65 (PANTHER); PTHR24353 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); IPR018488 (PROSITE_PATTERNS); IPR000595 (PROSITE_PROFILES); IPR000595 (PROSITE_PROFILES); IPR000961 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); IPR018490 (SUPERFAMILY); IPR018490 (SUPERFAMILY)

246	c13944_g2_i1_len_301_path_1_0_300_5	2	protein p21-like	100	6.59E-35	96.30%	0.099	IPR001938 (SMART); IPR001938 (G3DSA:2.60.110.GENE3D); IPR001938 (PFAM); IPR001938 (PANTHER); IPR001938 (PROSITE_PROFILES); IPR001938 (SUPERFAMILY)
247	c139731_g1_i1_len_562_path_6_0_453_460_454_507_460_508_561_2	16	hypothetical protein	182	8.29E-09	57.00%	0.148	no IPS match
248	c139783_g1_i1_len_1150_path_1_0_1149_4	32	nardilysin-like isoform x2	383	3.16E-98	66.00%	0.266	IPR011237 (G3DSA:3.30.830.GENE3D); IPR007863 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); PTHR11851:SF108 (PANTHER); PTHR11851 (PANTHER); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY)
249	c139846_g1_i1_len_1208_path_1_0_1207_0	19	plasma alpha-l-fucosidase	398	8.65E-63	81.40%	0.746 Y	IPR016286 (PRINTS); IPR000933 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR000933 (PFAM); IPR000933 (PANTHER); PTHR10030:SF26 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017853 (SUPERFAMILY)
250	c139882_g1_i1_len_671_path_649_0_670_2	10	angiopoietin-2-like isoform x4	223	2.05E-09	60.90%	0.117	IPR002181 (SMART); IPR014716 (G3DSA:3.90.215.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); IPR002181 (SUPERFAMILY)
251	c140090_g1_i1_len_461_path_439_0_460_1	5	exocyst complex component 6	154	2.39E-80	80.60%	0.205	IPR007225 (PANTHER)
252	c14066_g1_i1_len_250_path_1_0_249_3	0	draper splice variant 1	84	2.43E-19	66.70%	0.103	G3DSA:2.170.300.10 (GENE3D); PTHR24035 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES)
253	c14066_g2_i1_len_338_path_455_0_337_5	3	multiple epidermal growth factor-like domains protein 10 isoform x1	112	1.56E-34	68.30%	0.11	PR00011 (PRINTS); IPR002049 (SMART); IPR002049 (PFAM); IPR013032 (PFAM); G3DSA:2.170.300.10 (GENE3D); PTHR24035 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
254	c140765_g1_i1_len_1477_path_1465_0_1476_4	56	vanin-like protein 1	485	4.58E-38	52.20%	0.156	IPR003010 (G3DSA:3.60.110.GENE3D); IPR003010 (PFAM); IPR012101 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003010 (PROSITE_PROFILES); IPR003010 (SUPERFAMILY)
255	c140847_g1_i1_len_1232_path_1210_0_1231_1	26	nas-15 protein	411	1.20E-44	60.10%	0.119	IPR001506 (PRINTS); IPR006026 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY)
256	c140903_g1_i1_len_995_path_3_0_994_1	5	---NA---	332			0.11	Coil (COILS)
257	c140903_g1_i1_len_995_path_3_0_994_2	5	---NA---	331			0.115	Coil (COILS)
258	c140964_g1_i1_len_1196_path_1_0_1195_0	53	endonuclease mitochondrial	393	1.24E-127	83.80%	0.15	IPR020821 (SMART); IPR001604 (SMART); IPR020821 (G3DSA:3.40.570.GENE3D); IPR001604 (PFAM); PTHR13966 (PANTHER); IPR018524 (PROSITE_PATTERNS); SSF54060 (SUPERFAMILY)
259	c140993_g1_i1_len_723_path_701_0_722_2	7	alpha-amylase	241	1.31E-174	99.00%	0.108	IPR013781 (G3DSA:3.20.20.GENE3D); IPR006047 (PFAM); IPR017853 (SUPERFAMILY)
260	c14110_g2_i1_len_312_path_795_0_287_1083_2_88_311_0	2	type iii restriction endonuclease subunit m	104	7.86E-08	62.80%	0.115	no IPS match
261	c141152_g1_i1_len_863_path_841_0_862_1	12	---NA---	288			0.488 Y	IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR003961 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR003961 (SUPERFAMILY)
262	c141442_g1_i1_len_822_path_1_0_821_5	14	prostaglandin f synthase-like isoform x4	274	1.12E-85	72.80%	0.115	IPR020471 (PRINTS); IPR023210 (PFAM); IPR020471 (PIRSF); IPR023210 (G3DSA:3.20.20.GENE3D); PTHR11732:SF133 (PANTHER); IPR001395 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
263	c141597_g1_i1_len_497_path_1_0_496_0	5	acid sphingomyelinase-like phosphodiesterase partial	166	4.54E-14	54.25%	0.098	PTHR10340 (PANTHER)
264	c141669_g1_i1_len_767_path_745_0_766_2	13	trypsin 3	255	2.52E-33	63.80%	0.179	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24260 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
265	c141689_g1_i1_len_491_path_469_0_490_2	6	gels_homam ame: full= cytoplasmic ame: full=actin-depolymerizing factor short=adf	163	8.18E-49	78.50%	0.2	IPR007122 (PRINTS); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007123 (PFAM); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY)

266	c141855_g1_i1_len_872_path_1_0_871_4	4	nad binding domain of 6-phosphogluconate dehydrogenase family protein	291	3.28E-165	99.00%	0.117	IPR016040 (G3DSA:3.40.50.GENE3D); IPR029154 (PFAM); IPR015815 (PIRSF); IPR006115 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); PTHR22981 (PANTHER); SSF51735 (SUPERFAMILY); IPR008927 (SUPERFAMILY)
267	c142079_g1_i1_len_518_path_496_0_517_0	5	furin-like protease isoform 1-crr isoform x2	173	2.95E-16	45.70%	0.099	G3DSA:2.10.220.10 (GENE3D); IPR009030 (SUPERFAMILY)
268	c142207_g1_i1_len_639_path_1_0_638_3	19	secreted salivary gland	213	3.20E-10	70.80%	0.168	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF85 (PANTHER); PTHR24268 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
269	c142266_g1_i1_len_851_path_860_0_850_0	24	---NA---	284			0.161	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
270	c142266_g1_i1_len_851_path_860_0_850_1	24	---NA---	284			0.312	no IPS match
271	c142266_g1_i1_len_851_path_860_0_850_2	24	---NA---	283			0.356 Y	no IPS match
272	c142337_g1_i1_len_1033_path_1_0_1032_2	28	sortilin-related receptor	344	3.35E-137	73.70%	0.124	IPR000033 (SMART); IPR002172 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR000033 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR12106:SF7 (PANTHER); PTHR12106 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY)
273	c142390_g1_i1_len_1132_path_1110_0_1131_3	14	chi11_metan ame: full=endochitinase 11 ame: full=chitinase 11 flags: precursor	378	1.74E-06	77.00%	0.354 Y	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
274	c142390_g1_i1_len_1132_path_1110_0_1131_5	14	periplasmic endochitinase	377	0	99.00%	0.11	IPR003610 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR003610 (G3DSA:2.10.10.GENE3D); IPR003610 (PFAM); PTHR11177:SF120 (PANTHER); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY); IPR003610 (SUPERFAMILY)
275	c14244_g1_i1_len_1031_path_1061_0_829_1890_830_830_54_831_1030_1	50	transcription initiation factor tfiid subunit 5	344	3.97E-98	84.20%	0.139	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19879 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
276	c142919_g1_i1_len_2242_path_2234_0_2241_4	190	poc1 centriolar protein homolog a	747	0	73.60%	0.104	Coil (COILS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847:SF319 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
277	c143025_g1_i1_len_435_path_413_0_434_0	3	glycosyl-phosphatidylinositol-linked carbonic anhydrase	145	2.13E-13	54.20%	0.268	IPR001148 (PFAM); IPR001148 (G3DSA:3.10.200.GENE3D); IPR023561 (PANTHER); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
278	c143234_g1_i1_len_722_path_1_0_721_5	16	serine threonine-protein phosphatase pp1-beta catalytic subunit-like	240	1.36E-170	98.20%	0.115	IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668:SF204 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
279	c143258_g1_i1_len_1015_path_1029_0_1014_2	12	zinc finger protein 235-like isoform x2	338	8.42E-32	62.30%	0.306	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

								PR00019 (PRINTS); IPR003591 (SMART); SM00364 (SMART); SM00365 (SMART); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24365 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
280	c143443_g1_i1_len_1182_path_1160_0_1181_3	16	leucine rich repeat protein	394	2.26E-27	55.40%	0.252	Coil (COILS); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23122:SF32 (PANTHER); PTHR23122 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
281	c143464_g1_i1_len_660_path_1_0_659_2	25	maguk p55 subfamily member partial	220	2.91E-23	87.60%	0.251	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
282	c143570_g1_i1_len_717_path_695_0_716_4	10	zinc finger protein 484-like	239	6.66E-48	61.40%	0.108	IPR004911 (PFAM); IPR004911 (PANTHER)
283	c14364_g1_i1_len_957_path_985_0_956_5	38	gamma-interferon-inducible lysosomal thiol reductase	307	6.45E-24	53.30%	0.163	IPR006212 (SMART); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
284	c143692_g1_i1_len_1010_path_1_0_1009_4	23	cysteine-rich with egf-like domain protein 2	337	1.53E-30	69.20%	0.099	IPR008373 (PRINTS); IPR003119 (SMART); IPR008139 (SMART); IPR011001 (G3DSA:1.10.225.GENE3D); IPR011001 (G3DSA:1.10.225.GENE3D); IPR007856 (PFAM); IPR003119 (PFAM); IPR008138 (PFAM); PTHR11480 (PANTHER); PTHR11480:SF3 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR008139 (PROSITE_PROFILES); IPR003119 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR008139 (PROSITE_PROFILES); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); IPR011001 (SUPERFAMILY); TMhelix (TMHMM)
285	c14427_g1_i1_len_1166_path_1_0_1165_5	13	proactivator polypeptide-like	388	1.46E-107	61.80%	0.424 Y	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
286	c144270_g1_i1_len_952_path_1_0_951_1	21	polycystic kidney disease protein 2	317	3.58E-07	71.17%	0.124	IPR002165 (PFAM); IPR015915 (G3DSA:2.120.10.GENE3D); PF13854 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF223 (PANTHER); SSF117281 (SUPERFAMILY)
287	c144606_g1_i1_len_347_path_1_0_346_0	5	attractin-like protein 1	116	9.53E-36	70.80%	0.127	

288	c144677_g1_i1_len_2052_path_2030_0_2051_1	26	acetylornithine deacetylase	684	0	99.00%	0.118	IPR002933 (PFAM); IPR010169 (TIGRFAM); IPR011650 (PFAM); G3DSA:3.40.630.10 (GENE3D); IPR011650 (G3DSA:3.30.70.GENE3D); PTHR11014:SF75 (PANTHER); PTHR11014 (PANTHER); IPR001261 (PROSITE_PATTERNS); IPR001261 (PROSITE_PATTERNS); IPR010169 (HAMAP); SSF53187 (SUPERFAMILY); IPR011650 (SUPERFAMILY)
289	c144709_g1_i1_len_563_path_541_0_562_0	4	transcriptional regulator partial	188	1.84E-126	98.80%	0.138	no IPS match
290	c144797_g1_i1_len_248_path_226_0_247_4	0	nitrate reductase catalytic partial	83	3.55E-51	100.00%	0.111	IPR006656 (PFAM); G3DSA:3.40.228.10 (GENE3D); PTHR11615:SF123 (PANTHER); PTHR11615 (PANTHER); SSF53706 (SUPERFAMILY)
291	c144968_g1_i1_len_1140_path_1_0_1139_1	20	peptidyl-prolyl cis-trans isomerase-like 2	380	8.38E-152	80.30%	0.168	Coil (COILS); IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF147 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
292	c144970_g1_i1_len_671_path_58_0_670_3	10	peptidyl-alpha-hydroxyglycine alpha-amidating lyase 1	224	3.75E-82	67.90%	0.108	IPR000720 (PRINTS); IPR011042 (G3DSA:2.120.10.GENE3D); IPR001258 (PFAM); PTHR10680 (PANTHER); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY)
293	c145030_g1_i1_len_652_path_630_0_651_3	8	isocitrate dehydrogenase	218	4.13E-66	83.50%	0.187	IPR024084 (G3DSA:3.40.718.GENE3D); IPR024084 (PFAM); PTHR11835:SF42 (PANTHER); IPR001804 (PANTHER); SSF53659 (SUPERFAMILY); TMhelix (TMHMM)
294	c145126_g1_i1_len_1316_path_1_0_1315_3	13	sco- partial	439	1.32E-15	53.90%	0.356 Y	IPR025155 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
295	c145226_g1_i1_len_750_path_652_0_551_1204_552_650_1204_651_749_4	15	---NA---	250			0.105	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
296	c145749_g1_i1_len_334_path_1_0_333_1	2	---NA---	111			0.501 Y	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY)
297	c1464_g2_i1_len_849_path_827_0_848_4	9	proclotting enzyme	283	2.93E-08	74.00%	0.116	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24264 (PANTHER); PTHR24264:SF9 (PANTHER); IPR009003 (SUPERFAMILY)
298	c146601_g1_i1_len_368_path_1_0_367_4	4	ankyrin repeat-containing protein	123	3.35E-13	59.10%	0.118	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
299	c146914_g1_i1_len_737_path_715_0_736_3	14	down syndrome cell adhesion molecule-like protein dscam2	246	7.34E-20	63.90%	0.156	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR10489:SF580 (PANTHER); PTHR10489 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
300	c147018_g1_i1_len_658_path_636_0_657_4	7	---NA---	219			0.103	IPR017905 (G3DSA:1.20.120.GENE3D); PTHR12645 (PANTHER); IPR017905 (PROSITE_PROFILES); IPR017905 (SUPERFAMILY)
301	c147062_g1_i1_len_513_path_491_0_512_4	3	attractin-like protein 1 isoform x1	171	1.75E-37	80.70%	0.121	PTHR10574:SF3 (PANTHER); PTHR10574 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
302	c147306_g1_i1_len_536_path_514_0_535_0	4	leucine-rich repeat and calponin homology domain-containing protein 2-like	179	4.65E-51	71.70%	0.122	IPR001715 (SMART); IPR001715 (PFAM); IPR001715 (G3DSA:1.10.418.GENE3D); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001715 (PROSITE_PROFILES); IPR001715 (SUPERFAMILY); TMhelix (TMHMM)
303	c147397_g1_i1_len_453_path_431_0_452_2	5	ejaculatory bulb-specific protein 3	151	9.01E-37	70.00%	0.554 Y	IPR005055 (PFAM); IPR005055 (G3DSA:1.10.2080.GENE3D); IPR005055 (PANTHER); PTHR11257:SF2 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_EUK); IPR005055 (SUPERFAMILY); TMhelix (TMHMM)

304	c14754_g1_i1_len_382_path_637_0_91_732_92_381_0	0	zinc finger protein	128	1.62E-21	56.70%	0.1	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
305	c1476_g1_i1_len_1590_path_1568_0_1589_0	50	nitrilase homolog 1-like	530	0	69.50%	0.136	Coil (COILS); IPR001310 (PFAM); IPR003010 (PFAM); IPR003010 (G3DSA:3.60.110.GENE3D); IPR011146 (G3DSA:3.30.428.GENE3D); PTHR23088 (PANTHER); PTHR23088:SF5 (PANTHER); IPR019808 (PROSITE_PATTERNS); IPR001110 (PROSITE_PATTERNS); IPR011146 (PROSITE_PROFILES); IPR003010 (PROSITE_PROFILES); IPR003010 (SUPERFAMILY); IPR011146 (SUPERFAMILY)
306	c147604_g1_i1_len_824_path_1_0_823_1	23	beta- -n-acetylgalactosaminyltransferase bre-4-like	275	1.01E-41	69.20%	0.123	IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); PTHR19300:SF30 (PANTHER); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
307	c147690_g1_i1_len_745_path_723_0_744_4	6	protease do	248	1.86E-142	100.00%	0.105	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR22939 (PANTHER); PTHR22939:SF79 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
308	c147752_g1_i1_len_472_path_450_0_471_2	17	nidogen-2 isoform x5	157	3.21E-23	54.60%	0.429 Y	IPR000716 (SMART); IPR000716 (PFAM); IPR000716 (G3DSA:4.10.800.GENE3D); IPR022339 (PANTHER); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY); IPR000716 (SUPERFAMILY); TMhelix (TMHMM)
309	c147893_g1_i1_len_915_path_893_0_914_0	37	stromal cell-derived factor 2	300	7.11E-95	75.50%	0.402 Y	IPR016093 (SMART); G3DSA:2.80.10.50 (GENE3D); IPR016093 (PFAM); IPR027005 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016093 (PROSITE_PROFILES); IPR016093 (PROSITE_PROFILES); IPR016093 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR016093 (SUPERFAMILY)
310	c148014_g1_i1_len_775_path_753_0_774_0	11	mam and ldl-receptor class a domain-containing protein 2-like	259	8.96E-41	60.50%	0.149	IPR000998 (SMART); IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PATTERNS); IPR000998 (PROSITE_PATTERNS); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
311	c148014_g1_i1_len_775_path_753_0_774_2	11	mlrp2_acrmi ame: full=mam and ldl-receptor class a domain-containing protein 2 ame: full=skeletal organic matrix mam and ldl-receptor 2 short=som mam and ldl-receptor partial	258	1.40E-07	55.86%	0.107	IPR000998 (PFAM); PTHR23282 (PANTHER); PTHR23282:SF75 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
312	c148055_g1_i1_len_457_path_1_0_456_4	3	tyrosine-protein kinase receptor tie-1-like isoform x1	152	3.57E-09	62.30%	0.106	G3DSA:2.10.25.10 (GENE3D); IPR013032 (PFAM); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES)
313	c14850_g1_i1_len_754_path_1_0_306_308_307_753_4	29	peptidyl-prolyl cis-trans isomerase cyp11 isoform x1	243	1.50E-105	88.10%	0.133	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF229 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
314	c14850_g1_i2_len_870_path_1_0_306_1685_307_422_308_423_869_3	8	peptidyl-prolyl cis-trans isomerase g isoform x2	282	9.30E-28	75.80%	0.181	IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); PTHR11071:SF229 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
315	c14850_g1_i2_len_870_path_1_0_306_1685_307_422_308_423_869_4	8	peptidyl-prolyl cis-trans isomerase cyp11-like isoform x2	282	2.70E-70	88.70%	0.133	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF229 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
316	c148556_g1_i1_len_686_path_1_0_685_2	5	serine proteinase stubble	228	4.83E-62	71.00%	0.183	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

317	c148572_g1_i1_len_594_path_572_0_593_2	6	ligand of numb protein x 2	198	1.25E-44	68.40%	0.154	IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR19964 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
318	c148734_g1_i1_len_389_path_367_0_388_3	4	tryptophan partial	130	4.81E-84	100.00%	0.105	IPR018227 (PFAM); PTHR32195:SF11 (PANTHER); PTHR32195 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
319	c149051_g1_i1_len_256_path_1_0_255_0	0	transmembrane protease serine 2	86	1.31E-14	64.20%	0.414 Y	IPR001314 (PRINTS); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24250 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
320	c149257_g1_i1_len_1229_path_1207_0_1228_0	53	---NA---	410			0.111	Coil (COILS)
321	c149257_g1_i1_len_1229_path_1207_0_1228_1	53	---NA---	410			0.106	Coil (COILS)
322	c149492_g1_i1_len_282_path_260_0_281_5	2	glutamate synthase	94	9.85E-52	93.90%	0.149	PR00419 (PRINTS); G3DSA:1.10.1060.10 (GENE3D); G3DSA:3.50.50.60 (GENE3D); PF13450 (PFAM); IPR028261 (PFAM); PTHR11938 (PANTHER); PTHR11938:SF61 (PANTHER); SSF51905 (SUPERFAMILY)
323	c149638_g1_i1_len_225_path_203_0_224_2	0	gastrula zinc finger protein	75	6.36E-12	65.80%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
324	c149791_g1_i1_len_987_path_1_0_986_3	6	broad-complex isoform a-nze	329	2.19E-46	63.70%	0.178	Coil (COILS); IPR000210 (SMART); G3DSA:3.30.710.10 (GENE3D); IPR013069 (PFAM); PTHR23110 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000210 (PROSITE_PROFILES); IPR011333 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
325	c149794_g1_i1_len_572_path_1_0_571_1	5	basement membrane-specific heparan sulfate proteoglycan core protein	191	5.84E-52	77.20%	0.098	IPR001791 (SMART); IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10574:SF247 (PANTHER); PTHR10574 (PANTHER); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
326	c149869_g1_i1_len_1070_path_1048_0_1069_5	6	enolase	356	0	100.00%	0.123	IPR000941 (PRINTS); IPR029065 (G3DSA:3.20.20.GENE3D); IPR020811 (PFAM); IPR029017 (G3DSA:3.30.390.GENE3D); IPR020810 (PFAM); IPR000941 (TIGRFAM); IPR000941 (PANTHER); IPR020809 (PROSITE_PATTERNS); IPR000941 (HAMAP); IPR029065 (SUPERFAMILY); IPR029017 (SUPERFAMILY)
327	c149933_g1_i1_len_1137_path_1115_0_1136_0	21	von willebrand factor type egf and pentraxin domain-containing protein 1	379	4.89E-168	77.60%	0.125	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325:SF340 (PANTHER); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
328	c150363_g1_i1_len_751_path_729_0_750_5	8	cerebellin-3	250	4.96E-07	50.20%	0.108	IPR001073 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001073 (PROSITE_PROFILES); IPR008983 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
329	c150404_g1_i1_len_422_path_1_0_421_0	3	low quality protein: zinc finger protein 233	141	2.16E-39	66.60%	0.116	IPR015880 (SMART); IPR007087 (PFAM); PF13913 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

330	c150547_g1_i1_len_757_path_2_0_756_1	9	ecdysis triggering hormone receptor isoform a	252	5.89E-43	85.80%	0.102	IPR000276 (PRINTS); G3DSA:1.20.1070.10 (GENE3D); IPR000276 (PFAM); PTHR24239 (PANTHER); PTHR24239:SF5 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017452 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
331	c15071_g2_i1_len_186_path_1013_0_185_3	0	molecular chaperone partial	62	1.00E-35	99.80%	0.123	IPR013126 (PRINTS); IPR013126 (PFAM); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF173 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY)
332	c150776_g1_i1_len_989_path_1_0_988_2	8	aminoacylase-1a-like isoform x1	329	2.33E-88	76.50%	0.126	IPR011650 (G3DSA:3.30.70.GENE3D); IPR002933 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11014:SF8 (PANTHER); PTHR11014 (PANTHER); IPR001261 (PROSITE_PATTERNS); IPR001261 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53187 (SUPERFAMILY)
333	c151066_g1_i1_len_633_path_1_0_632_2	4	antigen partial	211	4.96E-138	100.00%	0.15	IPR012332 (G3DSA:2.160.20.GENE3D); IPR011050 (SUPERFAMILY)
334	c15109_g1_i1_len_397_path_508_0_394_58_395_396_4	2	collagen alpha-1 chain-like	132	6.93E-29	81.80%	0.573 Y	IPR000885 (SMART); IPR000885 (PFAM); PTHR24023:SF441 (PANTHER); PTHR24023 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR000885 (PRODOM); IPR000885 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK)
335	c151500_g1_i1_len_768_path_1_0_767_0	10	retinol dehydrogenase 12- partial	256	3.23E-83	70.00%	0.099	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); SSF51735 (SUPERFAMILY)
336	c151635_g1_i1_len_490_path_468_0_489_1	2	n-acetylmuramoyl-l-alanine amidase	163	6.99E-113	99.00%	0.103	IPR002508 (SMART); IPR002508 (PFAM); IPR002508 (G3DSA:3.40.630.GENE3D); PTHR30404:SF0 (PANTHER); PTHR30404 (PANTHER); SSF53187 (SUPERFAMILY)
337	c151643_g1_i1_len_465_path_1_0_464_1	5	oxidoreductase with nad -binding rossmann-fold	155	5.25E-109	100.00%	0.107	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF68 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
338	c152187_g1_i1_len_427_path_1_0_426_3	5	YEDN_ECOLIRecName: Full=Putative uncharacterized protein YedN	143	4.13E-94	99.70%	0.16	G3DSA:3.80.10.10 (GENE3D); SSF52058 (SUPERFAMILY)
339	c152326_g1_i1_len_669_path_647_0_668_1	4	dentin matrix protein 4-like	223	1.06E-20	76.00%	0.114	IPR009581 (PFAM); IPR024869 (PANTHER); PTHR12450:SF8 (PANTHER)
340	c15236_g1_i1_len_549_path_1_0_34_36_35_548_2	6	pre-b cell enhancing factor	178	3.38E-37	81.40%	0.127	IPR016471 (PTHR11098:PANTHER); IPR007229 (PANTHER)
341	c15236_g1_i2_len_574_path_1113_0_59_36_60_573_0	3	nicotinamide phosphoribosyltransferase	187	1.45E-36	79.90%	0.221	IPR007229 (PANTHER); IPR016471 (PTHR11098:PANTHER)
342	c152400_g1_i1_len_627_path_1_0_626_1	6	neurexin-4 isoform x1	203	2.41E-22	62.10%	0.335	IPR000421 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); PTHR24543 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000421 (PROSITE_PROFILES); IPR008979 (SUPERFAMILY)
343	c153243_g1_i1_len_427_path_1_0_426_2	5	hypothetical protein, partial	142	4.52E-16	44.40%	0.147	PTHR24023:SF405 (PANTHER); PTHR24023 (PANTHER)
344	c153243_g1_i1_len_427_path_1_0_426_3	5	collagen alpha-2 chain	143	2.11E-22	60.40%	0.119	IPR008160 (PFAM); PTHR24023:SF379 (PANTHER); PTHR24023 (PANTHER)
345	c154025_g1_i1_len_383_path_1_0_382_1	1	apolipoprotein d-like	122	4.98E-13	56.30%	0.104	IPR000566 (PFAM); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612 (PANTHER); IPR011038 (SUPERFAMILY)
346	c15450_g1_i1_len_835_path_1649_0_834_5	6	cell filamentation protein fic	278	9.58E-114	100.00%	0.184	IPR003812 (G3DSA:1.10.3290.GENE3D); IPR003812 (PFAM); IPR003812 (PROSITE_PROFILES); IPR003812 (SUPERFAMILY)
347	c15450_g2_i1_len_847_path_825_0_846_0	6	peptidyl-prolyl cis-trans isomerase a	283	3.54E-93	92.00%	0.101	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF192 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
348	c155295_g1_i1_len_238_path_216_0_237_5	2	antigen partial	79	1.30E-41	98.00%	0.111	IPR006315 (TIGRFAM); IPR005546 (G3DSA:2.40.128.GENE3D); IPR005546 (PFAM); IPR005546 (SUPERFAMILY)
349	c155411_g1_i1_len_765_path_743_0_764_0	10	transferrin 2	255	8.05E-100	62.10%	0.113	IPR001156 (PRINTS); IPR001156 (SMART); G3DSA:3.40.190.10 (GENE3D); G3DSA:3.40.190.10 (GENE3D); G3DSA:3.40.190.10 (GENE3D); IPR001156 (PFAM); PTHR11485 (PANTHER); PTHR11485:SF18 (PANTHER); IPR001156 (PROSITE_PROFILES); IPR001156 (PROSITE_PROFILES); SSF53850 (SUPERFAMILY); SSF53850 (SUPERFAMILY)

350	c155466_g1_i1_len_347_path_325_0_346_1	3	zinc finger partial	116	4.87E-19	60.30%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
351	c155618_g1_i1_len_324_path_1_0_323_5	2	tyrosine-protein kinase hopscotch	108	1.38E-42	80.00%	0.155	IPR001245 (PRINTS); IPR020635 (SMART); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24418 (PANTHER); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
352	c15576_g1_i1_len_1966_path_3794_0_234_72_2_35_1965_1	61	hypothetical protein DAPPUDRAFT_316225	649	6.64E-58	50.40%	0.425 Y	IPR001190 (PRINTS); IPR002557 (SMART); IPR017448 (SMART); IPR002557 (PFAM); IPR017448 (G3DSA:3.10.250.GENE3D); IPR001190 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); PTHR23301 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001190 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR017448 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
353	c15576_g1_i2_len_1802_path_1_0_70_72_71_18_01_2	66	hypothetical protein DAPPUDRAFT_316225	594	1.41E-58	50.10%	0.187	IPR001190 (PRINTS); IPR002557 (SMART); IPR017448 (SMART); IPR017448 (G3DSA:3.10.250.GENE3D); IPR016186 (G3DSA:3.10.100.GENE3D); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002557 (PFAM); IPR001190 (PFAM); PTHR23301 (PANTHER); IPR001190 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR002557 (PROSITE_PROFILES); IPR017448 (SUPERFAMILY); IPR016187 (SUPERFAMILY); IPR002557 (SUPERFAMILY); IPR002557 (SUPERFAMILY)
354	c156046_g1_i1_len_235_path_1_0_234_0	0	isoform b	74	3.22E-17	78.80%	0.116	IPR024079 (G3DSA:3.40.390.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
355	c15610_g1_i1_len_1640_path_53_0_1639_2	67	cleavage stimulation factor subunit 1-like	537	0	85.70%	0.302	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22840:SF8 (PANTHER); PTHR22840 (PANTHER); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
356	c1562_g1_i1_len_686_path_51_0_83_25_84_685_2	6	upf0669 protein c6orf120 homolog	228	2.27E-37	63.30%	0.187	PTHR31703 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
357	c1562_g1_i2_len_848_path_51_0_83_134_84_24_5_25_246_847_2	7	upf0669 protein c6orf120 homolog	282	1.51E-36	63.20%	0.123	PTHR31703 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
358	c156361_g1_i1_len_410_path_1_0_409_1	3	protein lap4 isoform x4	137	4.40E-68	91.00%	0.138	IPR003591 (SMART); IPR025875 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155:SF31 (PANTHER); PTHR23155 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
359	c156435_g1_i1_len_331_path_1_0_330_0	1	Usherin	111	1.98E-06	59.00%	0.203	IPR002049 (SMART); IPR002049 (PFAM); G3DSA:2.10.25.10 (GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)

371	c163171_g1_i1_len_754_path_1_0_753_1	21	hemagglutinin amebocyte aggregation factor-like	251	3.05E-40	62.30%	0.611 Y	PF14704 (PFAM); IPR026645 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
372	c163189_g1_i1_len_2428_path_2408_0_2427_0	6946	hemocyanin subunit type 1 precursor	802	0	75.70%	0.421 Y	IPR013788 (PRINTS); IPR000896 (PFAM); IPR005203 (PFAM); IPR005204 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005203 (G3DSA:2.60.40.GENE3D); IPR005204 (G3DSA:1.20.1370.GENE3D); PTHR11511:SF5 (PANTHER); IPR013788 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR002227 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR014756 (SUPERFAMILY); IPR005204 (SUPERFAMILY); IPR008922 (SUPERFAMILY)
373	c163202_g1_i1_len_1270_path_1248_0_1269_0	47	phosphatidylinositol -trisphosphate 3-phosphatase and dual-specificity protein phosphatase pten isoform x4	417	6.88E-123	70.90%	0.118	IPR003595 (SMART); G3DSA:2.60.40.1110 (GENE3D); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000340 (PFAM); IPR014020 (PFAM); PTHR12305 (PANTHER); IPR016130 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029023 (PROSITE_PROFILES); IPR014020 (PROSITE_PROFILES); IPR000008 (SUPERFAMILY); IPR029021 (SUPERFAMILY)
374	c163284_g1_i1_len_1774_path_1752_0_1773_2	1156	serine protease easter-like	585	1.66E-71	54.70%	0.307	IPR001314 (PRINTS); IPR006604 (SMART); IPR001254 (SMART); IPR022700 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); PTHR24260:SF3 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
375	c163461_g1_i1_len_1898_path_1_0_1897_1	90	counting factor associated protein d-like	626	0	77.90%	0.105	IPR000668 (PRINTS); IPR000668 (SMART); IPR013201 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); IPR013201 (PFAM); IPR013128 (PANTHER); PTHR12411:SF284 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
376	c163473_g1_i1_len_494_path_472_0_493_1	10	tyrosine-protein kinase transmembrane receptor ror2	165	4.88E-67	92.20%	0.112	IPR001245 (PRINTS); IPR020635 (SMART); IPR001245 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24416 (PANTHER); PTHR24416:SF63 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
377	c163547_g1_i1_len_1377_path_1_0_1376_4	16	protein	459	0	98.90%	0.128	IPR001117 (PFAM); IPR011707 (PFAM); IPR008972 (G3DSA:2.60.40.GENE3D); IPR008972 (G3DSA:2.60.40.GENE3D); IPR011706 (PFAM); PTHR11709:SF2 (PANTHER); PTHR11709 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008972 (SUPERFAMILY); IPR008972 (SUPERFAMILY); IPR008972 (SUPERFAMILY)
378	c163573_g1_i1_len_1979_path_1_0_1978_0	42	cd109 antigen	660	0	64.00%	0.105	IPR008930 (G3DSA:1.50.10.GENE3D); IPR011626 (PFAM); PTHR11412:SF85 (PANTHER); PTHR11412 (PANTHER); IPR008930 (SUPERFAMILY)
379	c163578_g1_i1_len_351_path_329_0_350_2	1	outer membrane autotransporter barrel domain partial	117	2.16E-70	97.70%	0.096	IPR012332 (G3DSA:2.160.20.GENE3D)

									IPR015880 (SMART); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
380	c163602_g1_i1_len_1086_path_1064_0_1085_5	36	zinc finger protein 658b-like	362	5.54E-31	57.40%	0.111		Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR006594 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR006594 (PFAM); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR006594 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017252 (HAMAP); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); SSF109925 (SUPERFAMILY)
381	c16368_g1_i1_len_2111_path_2089_0_2110_1	1147	lissencephaly-1 homolog	696	0	90.90%	0.171		Coil (COILS); IPR000467 (SMART); IPR000467 (PFAM); PTHR13948 (PANTHER); IPR000467 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES)
382	c163785_g1_i1_len_1861_path_1839_0_1860_3	135	rna-binding protein 5-like	621	4.72E-151	64.90%	0.103		IPR000895 (PRINTS); IPR023416 (SMART); IPR014306 (TIGRFAM); IPR023416 (G3DSA:2.60.40.GENE3D); IPR023416 (PFAM); PTHR10395 (PANTHER); PTHR10395:SF8 (PANTHER); IPR023418 (PROSITE_PATTERNS); IPR023416 (SUPERFAMILY)
383	c163857_g1_i1_len_1077_path_1_0_1076_2	39	5-hydroxyisourate hydrolase	354	1.84E-33	68.20%	0.1		Coil (COILS); IPR003593 (SMART); IPR000194 (PFAM); IPR000793 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005864 (TIGRFAM); IPR004100 (PFAM); IPR028987 (G3DSA:1.20.5.GENE3D); IPR005722 (TIGRFAM); IPR024034 (G3DSA:1.10.1140.GENE3D); G3DSA:2.40.10.170 (GENE3D); IPR002146 (PFAM); IPR005722 (PTHR15184:PANTHER); PTHR15184 (PANTHER); IPR020003 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005722 (HAMAP); IPR002146 (HAMAP); IPR027417 (SUPERFAMILY); IPR000793 (SUPERFAMILY); IPR028987 (SUPERFAMILY); IPR004100 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
384	c163965_g1_i1_len_6440_path_6418_0_6439_1	450	atp synthase beta subunit	2147	0	98.90%	0.206		IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR011047 (SUPERFAMILY); IPR017986 (SUPERFAMILY); IPR017986 (SUPERFAMILY)
385	c164043_g1_i1_len_2589_path_1_0_2588_2	74	telomerase protein component 1-like	863	2.39E-36	42.10%	0.101		IPR029052 (G3DSA:3.60.21.GENE3D); PTHR12905 (PANTHER); IPR029052 (SUPERFAMILY)
386	c164112_g1_i1_len_454_path_1_0_453_1	2	metallophosphoesterase domain-containing protein 1	151	1.02E-65	76.00%	0.107		

387	c164204_g1_i1_len_2138_path_2116_0_2137_1	57	zinc finger protein ozf-like	705	4.78E-28	53.00%	0.174	IPR015880 (SMART); IPR000210 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013069 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); G3DSA:3.30.710.10 (GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR000210 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); IPR011333 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
388	c164337_g1_i1_len_1647_path_1625_0_1646_0	24	isoform cra_b	549	1.07E-75	78.50%	0.136	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24348 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
389	c164337_g1_i1_len_1647_path_1625_0_1646_2	24	serine threonine-protein kinase ulk3	549	1.74E-93	66.50%	0.417 Y	Coil (COILS); IPR002290 (SMART); IPR007330 (SMART); IPR007330 (G3DSA:1.20.58.GENE3D); IPR007330 (PFAM); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); IPR007330 (G3DSA:1.20.58.GENE3D); PTHR24348 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR007330 (SUPERFAMILY); IPR011009 (SUPERFAMILY); IPR007330 (SUPERFAMILY)
390	c164501_g1_i1_len_138_path_1_0_137_1	0	chromosome 8 open reading frame isoform cra_a	46	6.25E-16	87.40%	0.213	PTHR22878 (PANTHER)
391	c164501_g1_i1_len_138_path_1_0_137_3	0	polymerase (dna directed) isoform cra_c	46	3.65E-19	91.00%	0.548 Y	PR02045 (PRINTS); PTHR12138 (PANTHER); SignalP-noTM (SIGNALP_EUK)
392	c164501_g1_i1_len_138_path_1_0_137_5	0	5 -nucleotidase domain containing isoform cra_d	46	1.41E-15	80.80%	0.176	PTHR16213 (PANTHER)
393	c164567_g1_i1_len_1464_path_1442_0_1463_0	16	cellulose partial	488	0	98.00%	0.144	IPR002037 (PRINTS); IPR012341 (G3DSA:1.50.10.GENE3D); IPR018513 (PFAM); IPR002037 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008928 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
394	c164636_g1_i1_len_2828_path_1_0_2827_1	96	peptidoglycan-associated lipoprotein	943	1.25E-121	99.70%	0.118	IPR006664 (PRINTS); IPR014169 (TIGRFAM); IPR006665 (PFAM); IPR006665 (G3DSA:3.30.1330.GENE3D); PTHR30128 (PANTHER); IPR006690 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006665 (PROSITE_PROFILES); IPR006665 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
395	c164650_g1_i1_len_962_path_940_0_961_1	10	zinc finger protein 160-like	321	7.20E-43	58.60%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
396	c16469_g1_i1_len_1917_path_3691_0_67_1865_68_1916_3	174	a disintegrin and metalloproteinase with thrombospondin motifs 18	639	2.31E-60	55.10%	0.11	IPR006586 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001590 (PFAM); PTHR13723 (PANTHER); IPR001590 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY)
397	c16469_g1_i2_len_1868_path_1846_0_18_1865_19_1867_3	173	a disintegrin and metalloproteinase with thrombospondin motifs 18	617	1.39E-60	55.10%	0.11	IPR006586 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001590 (PFAM); PTHR13723 (PANTHER); IPR001590 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY)

[illegible]

413	c166157_g1_i1_len_619_path_597_0_618_0	4	lipophorin receptor	207	3.30E-82	73.50%	0.127	IPR002172 (PRINTS); IPR002172 (SMART); IPR000742 (SMART); IPR001881 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PF14670 (PFAM); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
414	c166162_g1_i1_len_1047_path_1025_0_1046_2	11	oocyte zinc finger protein xlc0f22	349	3.18E-19	53.10%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
415	c166233_g1_i1_len_1107_path_1085_0_1106_1	14	short-chain dehydrogenase reductase family 16c member 6-like	369	1.79E-34	73.90%	0.142	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF214 (PANTHER); PTHR24316 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
416	c166247_g1_i1_len_1231_path_1_0_1230_2	32	fukutin-related partial	410	1.20E-26	72.00%	0.286	IPR007074 (PFAM); PTHR13627:SF25 (PANTHER); PTHR13627 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
417	c166254_g1_i1_len_1700_path_1_0_1699_0	102	aael005189- partial	561	3.87E-128	69.30%	0.129	IPR003112 (SMART); IPR003112 (PFAM); PTHR23192 (PANTHER); PTHR23192:SF33 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003112 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM)
418	c166307_g1_i1_len_1202_path_1180_0_1201_1	17	partial	401	4.62E-152	99.50%	0.123	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF22 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)
419	c166657_g1_i1_len_705_path_1_0_704_1	6	adhesive serine protease	235	2.89E-26	67.30%	0.12	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
420	c166657_g1_i1_len_705_path_1_0_704_2	6	trypsin- partial	235	5.87E-12	73.40%	0.15	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24258 (PANTHER); PTHR24258:SF4 (PANTHER); IPR009003 (SUPERFAMILY)
421	c166681_g1_i1_len_816_path_1_0_815_5	12	xanthine dehydrogenase oxidase	272	1.60E-20	85.70%	0.099	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)
422	c166891_g1_i1_len_956_path_1_0_955_4	19	collagen alpha 1 chain	319	9.73E-57	55.70%	0.12	IPR016186 (G3DSA:3.10.100.GENE3D); IPR010515 (PFAM); PTHR24023 (PANTHER); IPR026917 (PTHR24023:PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
423	c166969_g1_i1_len_1251_path_1229_0_1250_1	23	prolyl 3-hydroxylase 2-like isoform x1	417	3.03E-105	68.90%	0.107	Coil (COILS); IPR006620 (SMART); IPR005123 (PFAM); PTHR14049 (PANTHER); PTHR14049:SF9 (PANTHER); IPR005123 (PROSITE_PROFILES)

424	c167092_g1_i1_len_1486_path_1_0_1485_2	68	3-ketodihydrosphingosine reductase	495	3.10E-119	71.70%	0.117	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); PTHR24320:SF1 (PANTHER); IPR020904 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
425	c167139_g1_i1_len_1415_path_1_0_1414_5	31	tight junction protein zo-3	466	3.09E-42	73.50%	0.1	Coil (COILS); IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR19964:SF22 (PANTHER); PTHR19964 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
426	c167153_g1_i1_len_248_path_226_0_247_5	0	zinc finger protein	82	1.23E-13	58.70%	0.097	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
427	c167480_g1_i1_len_631_path_1_0_630_2	17	protein bv8	210	2.60E-20	59.30%	0.191	G3DSA:2.10.80.10 (GENE3D)
428	c167578_g1_i1_len_1656_path_1634_0_1655_0	92	serine protease mitochondrial	547	3.10E-130	73.50%	0.296	IPR001940 (PRINTS); IPR001478 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PF13365 (PFAM); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR22939:SF69 (PANTHER); PTHR22939 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001478 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); IPR001478 (SUPERFAMILY)
429	c167628_g1_i1_len_1263_path_1_0_1262_0	26	dipeptidyl peptidase 1 isoform x1	421	4.27E-164	70.00%	0.208	IPR000668 (PRINTS); IPR000668 (SMART); G3DSA:3.90.70.10 (GENE3D); IPR014882 (G3DSA:2.40.128.GENE3D); IPR014882 (PFAM); IPR000668 (PFAM); IPR013128 (PANTHER); PTHR12411:SF314 (PANTHER); IPR000169 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54001 (SUPERFAMILY); IPR014882 (SUPERFAMILY); TMhelix (TMHMM)
430	c167713_g1_i1_len_629_path_1_0_628_4	11	inner membrane lipoprotein yiad	210	1.56E-136	99.90%	0.278	IPR006664 (PRINTS); IPR006665 (PFAM); PF13488 (PFAM); IPR006665 (G3DSA:3.30.1330.GENE3D); PTHR30128 (PANTHER); PTHR30128:SF0 (PANTHER); IPR006690 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006665 (PROSITE_PROFILES); SignalIP-TM (SIGNALP_GRAM_POSITIVE); IPR006665 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
431	c167809_g1_i1_len_1718_path_1696_0_1717_4	41	chondroitin sulfate synthase 1-like	573	2.80E-86	53.00%	0.279	IPR008428 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); PTHR12369:SF11 (PANTHER); PTHR12369 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM)
432	c168114_g1_i1_len_709_path_687_0_708_0	8	vitellogenin receptor	237	7.14E-44	56.70%	0.104	IPR002172 (PRINTS); IPR000742 (SMART); IPR001881 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); IPR001881 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10529:SF204 (PANTHER); PTHR10529 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

433	c168235_g1_i1_len_581_path_559_0_580_5	4	xanthine dehydrogenase	193	1.02E-80	76.60%	0.115	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)
434	c168636_g1_i1_len_656_path_634_0_655_4	4	zinc finger protein 883-like isoform x1	219	2.13E-20	53.30%	0.147	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24375 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
435	c16878_g1_i1_len_636_path_2835_0_17_2222_1_8_635_4	12	26s protease regulatory subunit 8	212	6.95E-90	95.90%	0.265	Coil (COILS); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23073:SF12 (PANTHER); PTHR23073 (PANTHER); IPR027417 (SUPERFAMILY)
436	c16878_g1_i2_len_1431_path_1409_0_812_2222_813_1430_4	49	26s protease regulatory subunit 8	477	0	98.00%	0.265	Coil (COILS); IPR003593 (SMART); IPR005937 (TIGRFAM); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23073 (PANTHER); PTHR23073:SF12 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
437	c16885_g1_i1_len_1184_path_1979_0_278_2240_279_280_1163_281_1009_1892_1010_1096_18_92_1097_1183_3	25	zinc c2h2 type domain-containing protein	390	8.68E-21	55.70%	0.101	IPR015880 (SMART); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
438	c168938_g1_i1_len_1339_path_20_0_1338_2	8	protease 3	446	0	99.10%	0.101	IPR011237 (G3DSA:3.30.830.GENE3D); IPR011237 (G3DSA:3.30.830.GENE3D); IPR007863 (PFAM); PTHR11851 (PANTHER); PTHR11851:SF85 (PANTHER); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY); IPR011249 (SUPERFAMILY)
439	c16904_g1_i1_len_225_path_71_0_85_155_86_2_24_0	0	chitinase partial	75	2.64E-16	62.70%	0.114	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
440	c169362_g1_i1_len_810_path_788_0_809_2	7	pdz domain-containing protein 2	270	3.38E-29	85.50%	0.17	IPR001478 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001478 (PFAM); PTHR19964 (PANTHER); PTHR19964:SF22 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
441	c16944_g1_i1_len_1709_path_107_0_711_818_7_12_713_106_714_1708_1	71	sepiapterin reductase-like	570	2.21E-80	63.70%	0.112	IPR002347 (PRINTS); IPR006393 (TIGRFAM); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24318:SF1 (PANTHER); PTHR24318 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY)
442	c169480_g1_i1_len_568_path_546_0_567_1	27	sterile alpha motif domain-containing protein 13	184	3.64E-12	85.30%	0.119	IPR013761 (G3DSA:1.10.150.GENE3D); IPR021129 (PFAM); PTHR12247 (PANTHER); PTHR12247:SF66 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR013761 (SUPERFAMILY); TMhelix (TMHMM)
443	c169507_g1_i1_len_842_path_1_0_841_5	13	thioredoxin domain-containing protein 11	280	1.09E-38	54.80%	0.146	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929:SF61 (PANTHER); PTHR18929 (PANTHER); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
444	c169557_g1_i1_len_358_path_1_0_357_2	2	heat shock protein 70 b2	119	1.50E-27	76.40%	0.105	IPR029048 (G3DSA:1.20.1270.GENE3D); PTHR19375 (PANTHER); PTHR19375:SF142 (PANTHER); IPR029048 (SUPERFAMILY)
445	c169560_g1_i1_len_800_path_1_0_799_0	73	trafficking protein particle complex subunit 1 isoform x1	262	7.57E-07	71.00%	0.231	IPR007233 (PFAM)
446	c169637_g1_i1_len_278_path_256_0_277_2	0	cysteine-rich secretory protein 2-like isoform x1	92	3.03E-45	79.40%	0.139	IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); PTHR10334:SF188 (PANTHER); IPR014044 (SUPERFAMILY)

447	c169643_g1_i1_len_954_path_1_0_953_4	9	carbonic anhydrase-related protein 10	318	3.62E-51	84.10%	0.124	IPR001148 (SMART); IPR001148 (G3DSA:3.10.200.GENE3D); IPR001148 (PFAM); IPR023561 (PANTHER); PTHR18952:SF85 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
448	c169698_g1_i1_len_691_path_1_0_690_2	11	serine-aspartate repeat protein f	230	3.98E-12	64.10%	0.109	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
449	c169698_g1_i1_len_691_path_1_0_690_3	11	collagen alpha-1 chain	231	1.46E-13	69.90%	0.357 Y	IPR008160 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
450	c169979_g1_i1_len_2422_path_1_0_2421_0	137	polypeptide n-acetylgalactosaminyltransferase 5 isoform x2	802	0	88.70%	0.124	IPR000772 (SMART); IPR029044 (G3DSA:3.90.550.GENE3D); G3DSA:2.80.10.50 (GENE3D); IPR001173 (PFAM); IPR000772 (PFAM); PTHR11675:SF39 (PANTHER); PTHR11675 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000772 (PROSITE_PROFILES); IPR029044 (SUPERFAMILY); IPR000772 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
451	c169998_g1_i1_len_953_path_931_0_952_3	7	beta-d- partial	318	0	99.80%	0.115	IPR006101 (PRINTS); IPR008979 (G3DSA:2.60.120.GENE3D); IPR006103 (PFAM); IPR013812 (G3DSA:2.60.40.GENE3D); IPR006104 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR006102 (PFAM); PTHR10066 (PANTHER); PTHR10066:SF58 (PANTHER); IPR023232 (PROSITE_PATTERNS); IPR023230 (PROSITE_PATTERNS); IPR008979 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR006102 (SUPERFAMILY)
452	c170015_g1_i1_len_1704_path_1_0_1703_1	30	zinc finger protein 436-like isoform x2	568	5.66E-42	59.80%	0.103	IPR000210 (SMART); IPR015880 (SMART); G3DSA:3.30.710.10 (GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013069 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR000210 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); IPR011333 (SUPERFAMILY); TMhelix (TMHMM)
453	c170298_g1_i1_len_1319_path_1297_0_1318_5	22	fat-like cadherin-related tumor suppressor homolog isoform x1	439	9.65E-144	76.20%	0.165	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24026:SF39 (PANTHER); PTHR24026 (PANTHER); IPR020894 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); TMhelix (TMHMM)
454	c170333_g1_i1_len_469_path_1_0_468_2	5	diuretic hormone class 2 isoform x1	156	3.80E-18	92.60%	0.153	no IPS match
455	c1706_g2_i1_len_295_path_1303_0_294_2	0	protein disulfide-isomerase tmx3 isoform x1	98	7.72E-38	78.00%	0.737 Y	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929:SF82 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY)
456	c170924_g1_i1_len_1041_path_1_0_1040_2	10	beta-secretase 1	347	5.16E-107	59.90%	0.121	IPR009119 (PRINTS); IPR021109 (G3DSA:2.40.70.GENE3D); IPR021109 (G3DSA:2.40.70.GENE3D); IPR001461 (PFAM); IPR001461 (PANTHER); PTHR13683:SF245 (PANTHER); IPR021109 (SUPERFAMILY)

[illegible]

470	c17270_g1_i1_len_1969_path_2037_0_1772_42_1773_1968_0	215	coatomer subunit beta -like	650	0	77.10%	0.138	IPR006692 (PFAM); PTHR19876 (PANTHER); PTHR19876:SF2 (PANTHER)
471	c17281_g1_i1_len_1774_path_1752_0_1256_300_9_1257_1773_0	41	wee1-like protein kinase	592	0	74.20%	0.257	IPR002290 (SMART); IPR017164 (PIRSF); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR11042:SF69 (PANTHER); PTHR11042 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
472	c172826_g1_i1_len_784_path_1_0_783_2	14	carbohydrate sulfotransferase 11-like	261	2.48E-48	64.60%	0.101	IPR005331 (PFAM); IPR018011 (PANTHER); PTHR12137:SF29 (PANTHER); TMhelix (TMHMM); TMhelix (TMHMM)
473	c17285_g2_i1_len_1039_path_1017_0_1038_1	41	mannosyl-oligosaccharide -alpha-mannosidase ia isoform x1	346	2.25E-49	87.00%	0.112	IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); PTHR11742:SF6 (PANTHER); IPR001382 (PANTHER); IPR001382 (SUPERFAMILY)
474	c17302_g1_i1_len_1330_path_62_0_750_813_75_1_756_819_757_1329_2	56	tyrosine-protein phosphatase	443	4.94E-33	84.60%	0.111	IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134 (PANTHER); PTHR19134:SF274 (PANTHER); IPR016130 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
475	c17323_g1_i1_len_1016_path_1_0_249_251_250_250_252_251_1015_2	268	micos complex subunit mic27	332	1.31E-26	54.80%	0.185	IPR019166 (PFAM); PTHR14564 (PANTHER); PTHR14564:SF1 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
476	c173255_g1_i1_len_919_path_897_0_918_0	21	complement component q subcomponent-like protein	307	8.57E-37	60.90%	0.523 Y	IPR001073 (PRINTS); IPR001073 (SMART); IPR001073 (PFAM); IPR008983 (G3DSA:2.60.120.GENE3D); PTHR22923 (PANTHER); PTHR22923:SF51 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001073 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR008983 (SUPERFAMILY); TMhelix (TMHMM)
477	c173325_g1_i1_len_906_path_884_0_905_1	8	protein fam172a-like isoform x2	295	5.18E-59	71.50%	0.106	IPR019154 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR21357 (PANTHER); IPR029058 (SUPERFAMILY)
478	c1735_g1_i1_len_796_path_3841_0_19_3843_20_795_0	21	otogelin- partial	266	8.76E-10	43.20%	0.103	no IPS match
479	c1735_g1_i2_len_1908_path_1937_0_1131_3843_1132_1907_2	56	otogelin- partial	636	6.95E-15	42.20%	0.1	no IPS match
480	c173597_g1_i1_len_1458_path_1_0_1457_0	21	vitellogenin fused with superoxide dismutase	486	5.27E-45	47.40%	0.109	IPR001846 (SMART); IPR001846 (PFAM); PTHR23345 (PANTHER); PTHR23345:SF1 (PANTHER); IPR001846 (PROSITE_PROFILES)
481	c173967_g1_i1_len_688_path_1_0_687_0	12	prostaglandin-endoperoxide synthase 2	230	2.57E-102	74.30%	0.121	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11903:SF10 (PANTHER); PTHR11903 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
482	c173990_g1_i1_len_470_path_448_0_469_0	6	latrophilin cir1-like isoform x1	157	5.64E-36	80.00%	0.293	IPR000832 (PFAM); PTHR12011 (PANTHER); PTHR12011:SF258 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
483	c173990_g1_i1_len_470_path_448_0_469_2	6	latrophilin cir1-like	156	8.13E-32	93.30%	0.274	IPR000832 (PFAM); PTHR12011:SF258 (PANTHER); PTHR12011 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017981 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM)

484	c17402_g1_i1_len_2191_path_2268_0_301_25_3_02_2190_3	2822	limulus clotting factor c	724	1.08E-88	43.00%	0.221	IPR002172 (PRINTS); IPR000742 (SMART); IPR000436 (SMART); IPR002172 (SMART); IPR001254 (SMART); IPR001881 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000436 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001254 (PFAM); G3DSA:2.10.70.10 (GENE3D); PF14670 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR24265 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR000436 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR009003 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
485	c174292_g1_i1_len_774_path_752_0_773_4	6	ankyrin repeat domain protein	253	1.97E-16	54.30%	0.106	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
486	c17450_g1_i2_len_2780_path_2758_0_2389_514_8_2390_2568_5327_2569_2569_5328_2570_277_9_0	156	angiotensin-converting enzyme-like	927	3.00E-162	61.70%	0.271	Coil (COILS); IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM)
487	c174633_g1_i1_len_590_path_568_0_589_2	3	glucose-6-phosphate isomerase	196	5.67E-73	99.80%	0.315	IPR001672 (PFAM); G3DSA:3.40.50.10490 (GENE3D); IPR001672 (PANTHER); PTHR11469:SF7 (PANTHER); IPR001672 (PROSITE_PROFILES); SSF53697 (SUPERFAMILY)
488	c174771_g1_i1_len_666_path_1_0_665_5	18	---NA---	216			0.111	G3DSA:2.40.10.10 (GENE3D); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
489	c174797_g1_i1_len_296_path_274_0_295_0	1	---NA---	99			0.274	IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
490	c17500_g1_i1_len_2037_path_3841_0_837_25_8_38_2036_2	123	carboxypeptidase n subunit 2	679	6.91E-96	58.90%	0.173	SM00365 (SMART); IPR003591 (SMART); PF13516 (PFAM); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); IPR025875 (PFAM); PTHR24365 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
491	c17500_g1_i2_len_1356_path_3841_0_837_4678_838_1355_2	131	carboxypeptidase n subunit 2	452	7.41E-29	55.10%	0.173	IPR003591 (SMART); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24373:SF98 (PANTHER); PTHR24373 (PANTHER); SSF52058 (SUPERFAMILY)

492	c175075_g1_i1_len_566_path_584_0_565_1	6	serrate partial	189	8.54E-29	77.10%	0.259	IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); PTHR24044 (PANTHER); PTHR24044:SF222 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
493	c175082_g1_i1_len_183_path_1_0_182_2	2	microtubule-associated serine threonine-protein kinase 3 isoform x3	61	1.49E-32	98.00%	0.116	G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24356 (PANTHER); PTHR24356:SF36 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
494	c175506_g1_i1_len_651_path_629_0_650_1	12	peptidyl-prolyl cis-trans isomerase-like 4	211	1.08E-76	84.10%	0.141	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF156 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
495	c17559_g1_i1_len_1939_path_1979_0_1938_1	12556	trypsin- partial	639	5.18E-59	55.90%	0.228	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
496	c1756_g1_i1_len_3011_path_7743_0_99_934_10_0_3010_3	115454	levansucrase	1004	0	99.30%	0.245	IPR023296 (G3DSA:2.115.10.GENE3D); IPR003469 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023296 (SUPERFAMILY)
497	c1756_g1_i2_len_3844_path_1_0_932_934_933_3843_0	171791	hypothetical protein ECP02989421_5334	1282	2.20E-81	90.60%	0.149	TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
498	c1756_g1_i2_len_3844_path_1_0_932_934_933_3843_3	171791	levansucrase	1282	0	99.30%	0.245	IPR023296 (G3DSA:2.115.10.GENE3D); IPR003469 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023296 (SUPERFAMILY)
499	c1758_g1_i1_len_1492_path_1534_0_1491_0	10626	peptidyl-prolyl cis-trans isomerase	491	5.25E-99	93.00%	0.201	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF116 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
500	c17612_g1_i1_len_1225_path_1_0_464_466_465_605_607_606_827_829_828_994_996_995_122_4_0	67	dehydrogenase reductase sdr family member 7	404	7.23E-109	67.50%	0.141	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF31 (PANTHER); PTHR24322 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
501	c17612_g1_i2_len_1084_path_1_0_464_607_465_686_829_687_853_996_854_1083_0	30	dehydrogenase reductase sdr family member 7	357	2.69E-77	55.70%	0.141	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF244 (PANTHER); PTHR24322 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

502	c17612_g1_i3_len_1058_path_1_0_464_466_465_605_607_606_827_996_828_1057_0	32	dehydrogenase reductase sdr family member 7	348	1.55E-82	69.00%	0.141	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF244 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
503	c17621_g1_i1_len_1123_path_129_0_1122_3	23	venom dipeptidyl peptidase 4 isoform x3	375	8.70E-26	70.80%	0.102	IPR001375 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11731 (PANTHER); PTHR11731:SF93 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY)
504	c176318_g1_i1_len_899_path_813_0_724_1538_725_811_1538_812_898_4	16	zinc finger protein	300	3.19E-42	53.70%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
505	c17634_g1_i1_len_1032_path_1_0_1031_5	25221	venom allergen 3-like	337	3.19E-45	50.10%	0.750 Y	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR014044 (SUPERFAMILY)
506	c17648_g1_i1_len_2631_path_2609_0_1853_446_3_1854_1854_4464_1855_2630_2	651	titin isoform x14	864	2.53E-166	74.50%	0.102	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF149 (PANTHER); PTHR19897 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
507	c17660_g1_i1_len_1709_path_1787_0_1211_299_6_1212_1214_26_1215_1708_2	782	retinal dehydrogenase 1-like	564	0	80.00%	0.252	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF145 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
508	c176715_g1_i1_len_867_path_845_0_866_0	11	carcinolectin 5b partial	289	1.19E-43	66.60%	0.101	IPR002181 (SMART); IPR002181 (PFAM); IPR014715 (G3DSA:4.10.530.GENE3D); IPR014716 (G3DSA:3.90.215.GENE3D); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); TMhelix (TMHMM)
509	c176993_g1_i1_len_512_path_1_0_511_2	4	zinc finger protein with krab and scan domains 4	170	1.57E-18	62.00%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

510	c17700_g1_i1_len_2316_path_2119_0_840_5735_841_2315_1	313	tolloid-like protein 2 isoform x1	766	1.11E-144	70.20%	0.1	IPR002172 (SMART); IPR000859 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (PFAM); PTHR10127:SF557 (PANTHER); PTHR10127 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
511	c17700_g1_i2_len_2141_path_2119_0_840_2960_841_2140_1	194	tolloid-like protein 2 isoform x1	708	8.27E-127	71.90%	0.1	IPR002172 (SMART); IPR000859 (SMART); IPR000859 (G3DSA:2.60.120.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000859 (PFAM); PTHR10127 (PANTHER); PTHR10127:SF557 (PANTHER); IPR000859 (PROSITE_PROFILES); IPR000859 (PROSITE_PROFILES); IPR000859 (SUPERFAMILY); IPR000859 (SUPERFAMILY)
512	c177129_g1_i1_len_507_path_485_0_506_2	4	insulin-degrading enzyme	169	6.33E-66	78.60%	0.114	IPR011237 (G3DSA:3.30.830.GENE3D); PTHR11851 (PANTHER); PTHR11851:SF85 (PANTHER); IPR011249 (SUPERFAMILY)
513	c177612_g1_i1_len_326_path_1_0_325_5	0	proclotting enzyme	108	1.28E-08	47.00%	0.457 Y	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
514	c17764_g1_i1_len_1612_path_1445_0_976_19_9_77_1103_2545_1104_1357_2545_1358_1611_0	38	acidic phospholipase a2 pa4 isoform x2	538	1.61E-42	57.30%	0.875 Y	IPR001211 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR12253 (PANTHER); IPR013090 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR016090 (SUPERFAMILY); TMhelix (TMHMM)
515	c178015_g1_i1_len_351_path_329_0_350_1	2	hypothetical protein DAPPUDRAFT_332703	117	8.19E-40	60.50%	0.103	IPR001846 (PFAM); IPR014853 (PFAM); PTHR23361:SF13 (PANTHER); PTHR23361 (PANTHER); IPR001846 (PROSITE_PROFILES)
516	c17806_g1_i1_len_868_path_227_0_826_81_827_867_2	14	bone morphogenetic protein 4-like	289	4.81E-55	67.30%	0.151	IPR001111 (PFAM); PTHR11848:SF131 (PANTHER); IPR015615 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
517	c17807_g1_i1_len_1434_path_1412_0_574_1987_575_1433_4	1693	mitochondrial matrix protein p33	470	4.29E-85	67.40%	0.1	IPR003428 (PFAM); IPR003428 (G3DSA:3.10.280.GENE3D); PTHR10826:SF1 (PANTHER); PTHR10826 (PANTHER); IPR003428 (SUPERFAMILY)
518	c17807_g1_i2_len_1452_path_1412_0_574_2894_575_592_1987_593_1451_4	995	mitochondrial matrix protein p33	476	1.68E-82	66.70%	0.1	IPR003428 (PFAM); IPR003428 (G3DSA:3.10.280.GENE3D); PTHR10826:SF1 (PANTHER); PTHR10826 (PANTHER); IPR003428 (SUPERFAMILY)
519	c178085_g1_i1_len_524_path_502_0_523_4	5	tyrosine-protein kinase transmembrane receptor ror isoform x2	175	1.98E-18	100.00%	0.126	G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416 (PANTHER); PTHR24416:SF309 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
520	c17836_g1_i1_len_1703_path_53_0_1702_2	71	interleukin-1 receptor-associated kinase 4	560	2.82E-119	59.90%	0.159	IPR002290 (SMART); IPR000719 (PFAM); IPR011029 (G3DSA:1.10.533.GENE3D); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR029397 (PFAM); PTHR24419:SF0 (PANTHER); PTHR24419 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011029 (SUPERFAMILY); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
521	c17839_g1_i1_len_1821_path_1_0_1153_1155_1_154_1820_0	38	serpin 3	601	1.36E-82	58.90%	0.167	IPR023796 (SMART); IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); G3DSA:3.30.497.10 (GENE3D); PTHR11461:SF52 (PANTHER); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
522	c17839_g1_i2_len_1367_path_1_0_1153_3620_1_154_1366_0	31	serpin 3	456	1.96E-84	59.90%	0.167	IPR023796 (SMART); IPR023796 (PFAM); G3DSA:2.30.39.10 (GENE3D); G3DSA:3.30.497.10 (GENE3D); IPR000215 (PANTHER); PTHR11461:SF52 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)

523	c178411_g1_i1_len_503_path_481_0_502_5	7	succinate-semialdehyde mitochondrial	167	7.65E-51	83.80%	0.121	IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF49 (PANTHER); IPR016161 (SUPERFAMILY)
524	c17890_g1_i1_len_2370_path_55_0_2369_0	968	tribbles homolog 2	784	1.36E-119	71.80%	0.107	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR22961:SF4 (PANTHER); IPR024104 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
525	c17905_g1_i1_len_1133_path_969_0_403_1373_404_470_1960_471_502_1373_503_569_1960_570_601_1373_602_6_3	1117	thioredoxin 1	372	1.76E-48	83.30%	0.478 Y	PR00421 (PRINTS); IPR013766 (PFAM); IPR005746 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005746 (PANTHER); IPR017937 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
526	c17909_g1_i1_len_1408_path_1386_0_1407_5	89	moxd1 homolog 2- partial	469	1.51E-27	59.40%	0.881 Y	IPR005018 (SMART); IPR005018 (PFAM); PTHR10157:SF23 (PANTHER); IPR000945 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR005018 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SSF49344 (SUPERFAMILY)
527	c179482_g1_i1_len_262_path_303_0_261_4	0	chitinase 10 precursor	87	6.78E-23	70.60%	0.101	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR017853 (SUPERFAMILY)
528	c17962_g1_i2_len_370_path_1_0_182_184_183_369_5	19	allergen 5	117	2.92E-07	69.80%	0.263	IPR002413 (PRINTS); IPR014044 (G3DSA:3.40.33.GENE3D); TMhelix (TMHMM)
529	c17962_g1_i3_len_984_path_1329_0_109_1439_110_796_184_797_983_5	565	val5_vesmc ame: full=venom allergen 5 ame: full=antigen 5 ame: full=cysteine-rich venom protein short=crvp flags: precursor	322	5.28E-06	70.00%	0.264	IPR002413 (PRINTS); IPR014044 (G3DSA:3.40.33.GENE3D)
530	c179635_g1_i1_len_388_path_366_0_387_1	3	zinc finger protein 735	129	1.13E-42	73.70%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
531	c179951_g1_i1_len_346_path_1_0_345_3	2	low-density lipoprotein receptor-related protein 1b-like	116	5.79E-14	63.00%	0.432 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
532	c179963_g1_i1_len_451_path_429_0_450_4	10	transcription factor e4f1-like	150	6.50E-35	65.30%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
533	c18025_g1_i1_len_1161_path_1191_0_108_1300_109_110_1302_111_1160_1	3072	eukaryotic translation initiation factor 3 subunit i-like	380	3.10E-180	84.20%	0.157	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19877 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR027525 (HAMAP); IPR017986 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)

534	c18091_g1_i1_len_2158_path_53_0_329_383_33_0_350_404_351_2157_0	80	zinc finger protein 135-like isoform x2	720	1.21E-71	56.50%	0.172	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
535	c18100_g1_i1_len_2101_path_2186_0_2100_1	1183	arylsulfatase b	700	8.04E-173	64.80%	0.216	G3DSA:3.30.1120.10 (GENE3D); IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342-SF206 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM)
536	c182504_g1_i1_len_493_path_471_0_492_0	2	leucine-rich repeat-containing protein partial	165	1.82E-52	78.70%	0.279	IPR003591 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR23155-SF466 (PANTHER); PTHR23155 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
537	c18269_g1_i1_len_1960_path_2096_0_1959_0	1099	clotting factor b-like	646	1.25E-65	60.30%	0.217	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
538	c18271_g1_i1_len_1777_path_1855_0_1776_2	116	wd40 repeat-containing protein smu1	586	0	93.80%	0.108	IPR020472 (PRINTS); IPR006594 (SMART); IPR006595 (SMART); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22848 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR006595 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR006594 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
539	c18283_g1_i1_len_1179_path_1338_0_58_1397_59_120_1458_121_162_159_163_1178_1	286704	prostasin- partial	379	2.02E-46	55.30%	0.173	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
540	c182841_g1_i1_len_156_path_1_0_155_2	0	early growth response partial	47	9.31E-15	77.00%	0.11	IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
541	c183142_g1_i1_len_321_path_299_0_320_1	1	phenoloxidase subunit a3	107	8.90E-25	60.70%	0.116	IPR008922 (G3DSA:1.10.1280.GENE3D); IPR000896 (PFAM); PTHR11511-SF4 (PANTHER); IPR013788 (PANTHER); IPR008922 (SUPERFAMILY)

542	c18323_g1_i1_len_1878_path_1_0_239_4232_24_0_1877_2	55	ankyrin isoform p	626	0	93.20%	0.129	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24123 (PANTHER); PTHR24123:SF0 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); IPR020683 (SUPERFAMILY)
543	c18336_g1_i2_len_2346_path_2324_0_2061_438_6_2062_2345_0	108	glutamate-rich wd repeat-containing protein 1	782	0	72.30%	0.106	IPR020472 (PRINTS); IPR001680 (SMART); IPR022052 (PFAM); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22850:SF6 (PANTHER); PTHR22850 (PANTHER); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
544	c18361_g1_i1_len_1058_path_1134_0_924_2056_925_927_25_928_1057_4	30	bola-like protein 3	353	3.20E-31	78.90%	0.216	IPR002634 (PFAM); G3DSA:3.30.70.1500 (GENE3D); PTHR12735 (PANTHER); PTHR12735:SF4 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002634 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
545	c184011_g1_i1_len_397_path_375_0_396_4	2	2-hydroxy-3-oxopropionate reductase	132	4.26E-81	100.00%	0.131	IPR006115 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR029154 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); PTHR22981 (PANTHER); PTHR22981:SF42 (PANTHER); SSF51735 (SUPERFAMILY); IPR008927 (SUPERFAMILY)
546	c18408_g1_i1_len_817_path_2823_0_41_2029_4_2_243_2231_244_816_0	43	dehydrogenase reductase sdr family member on chromosome partial	273	3.88E-26	61.80%	0.113	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320 (PANTHER); PTHR24320:SF55 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
547	c18408_g1_i2_len_1413_path_1391_0_637_2029_638_839_2231_840_1412_2	81	retinol dehydrogenase 12	471	3.49E-95	61.60%	0.237	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); PTHR24320:SF55 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
548	c18408_g1_i3_len_1211_path_1391_0_637_2231_638_1210_2	42	retinol dehydrogenase 12	403	8.12E-53	65.00%	0.237	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); PTHR24320:SF55 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
549	c184101_g1_i1_len_192_path_1_0_71_73_72_10_1_73_102_131_73_132_161_73_162_191_3	0	allatostatin precursor protein	64	6.39E-24	71.30%	0.108	IPR010276 (PFAM)
550	c184189_g1_i1_len_537_path_515_0_536_0	5	zinc finger protein 112-like	179	3.17E-33	64.50%	0.216	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
551	c18420_g1_i1_len_1984_path_53_0_134_188_13_5_135_189_136_979_1031_980_1844_1940_184_5_1845_1941_1846_0	218	27 kda hemolymph	662	3.53E-29	49.50%	0.384 Y	IPR009832 (PFAM); PTHR20997 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)

552	c18420_g1_i2_len_888_path_1055_0_22_1031_23_887_0	76	27 kda hemolymph	296	1.07E-26	48.60%	0.203	IPR009832 (PFAM); PTHR20997 (PANTHER)
553	c184991_g1_i1_len_163_path_1_0_162_5	2	membrane alanyl aminopeptidase	54	2.73E-29	100.00%	0.168	IPR014782 (PRINTS); G3DSA:1.10.390.10 (GENE3D); IPR014782 (PFAM); PTHR11533:SF163 (PANTHER); IPR001930 (PANTHER); SSF55486 (SUPERFAMILY)
554	c185590_g1_i1_len_232_path_1_0_231_2	2	acyl- -binding domain-containing protein 4 isoform x1	77	1.04E-16	62.80%	0.688 Y	PF13900 (PFAM); PTHR16213 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
555	c18593_g1_i1_len_880_path_858_0_879_3	406	secreted metalloprotease mcp02	287	1.39E-09	48.20%	0.165	IPR025711 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
556	c186765_g1_i1_len_239_path_227_0_238_1	2	dynein heavy chain axonemal isoform 2	80	7.29E-28	76.60%	0.208	PTHR22878 (PANTHER)
557	c186765_g1_i1_len_239_path_227_0_238_4	2	tak1-binding protein isoform cra_b	80	1.61E-21	70.90%	0.121	PF13900 (PFAM); PTHR16213 (PANTHER)
558	c186765_g1_i1_len_239_path_227_0_238_5	2	unnamed portein product	79	1.61E-29	76.40%	0.185	PR02045 (PRINTS); PTHR12138 (PANTHER)
559	c18719_g2_i1_len_949_path_2475_0_460_2935_461_948_1	64	wd repeat domain 5	316	7.47E-53	86.40%	0.103	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22847:SF308 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
560	c18719_g2_i2_len_1207_path_2475_0_460_25_461_1009_574_1010_1206_1	30	protein will die slowly-like	402	0	93.80%	0.103	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847:SF308 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
561	c18719_g2_i3_len_1353_path_2475_0_460_25_461_1009_2155_1010_1352_1	27	protein will die slowly-like	451	0	93.20%	0.103	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22847:SF308 (PANTHER); PTHR22847 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
562	c187364_g1_i1_len_314_path_1_0_313_5	1	suppressor of tumorigenicity 14 protein	104	4.14E-08	63.50%	0.149	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24275:SF50 (PANTHER); PTHR24275 (PANTHER); IPR009003 (SUPERFAMILY)
563	c18816_g1_i1_len_2422_path_1_0_227_229_228_228_230_229_2421_5	62	von willebrand factor like 1	800	3.35E-24	40.20%	0.099	IPR014853 (SMART); IPR001007 (PROSITE_PATTERNS); PD968187 (PRODOM); IPR001007 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY)
564	c1883_g1_i1_len_1069_path_1049_0_474_1526_475_1068_5	39	ferritin 2	356	6.56E-68	80.70%	0.13	IPR008331 (PFAM); IPR012347 (G3DSA:1.20.1260.GENE3D); IPR001519 (PANTHER); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY)
565	c1886_g1_i1_len_333_path_1_0_332_5	3	agap004066-pa-like protein	111	8.95E-16	84.30%	0.212	IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)
566	c18900_g1_i1_len_565_path_1_0_564_1	28	zinc-responsiveness transcriptional activator	183	1.40E-13	64.10%	0.139	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
567	c18900_g2_i1_len_1261_path_1133_0_1260_2	111	zinc finger protein 658b-like	420	1.16E-42	63.00%	0.211	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

568	c18954_g1_i1_len_1677_path_1755_0_497_2253_498_521_3454_522_522_3455_523_529_2284_530_555_102_556_1_1	74	exocyst complex component 6b-like isoform 1	544	5.06E-159	80.50%	0.306	Coil (COILS); Coil (COILS); IPR007225 (PFAM); IPR007225 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
569	c1898_g1_i1_len_1608_path_1_0_1201_1203_12_02_1409_1411_1410_1442_1411_1443_1475_14_11_1476_1508_1411_3	61	gastrula zinc finger	536	2.12E-72	55.30%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
570	c1898_g1_i1_len_1608_path_1_0_1201_1203_12_02_1409_1411_1410_1442_1411_1443_1475_14_11_1476_1508_1411_4	61	choline-binding surface protein a	536	8.86E-07	62.50%	0.105	Coil (COILS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
571	c1902_g1_i1_len_1648_path_53_0_1647_3	3374	universal minicircle sequence binding protein	542	3.76E-29	53.60%	0.189	Coil (COILS); Coil (COILS); IPR001878 (SMART); IPR001878 (G3DSA:4.10.60.GENE3D); IPR001878 (PFAM); IPR001878 (G3DSA:4.10.60.GENE3D); PTHR23002 (PANTHER); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (PROSITE_PROFILES); IPR001878 (SUPERFAMILY); IPR001878 (SUPERFAMILY); IPR001878 (SUPERFAMILY)
572	c19020_g3_i1_len_365_path_1219_0_364_4	1	n-acetylated-alpha-linked acidic dipeptidase-like protein	122	4.05E-39	75.40%	0.116	G3DSA:3.40.630.10 (GENE3D); IPR007484 (PFAM); PTHR10404 (PANTHER); SSF53187 (SUPERFAMILY)
573	c19172_g1_i1_len_2425_path_1_0_2424_0	91	phospholipase a2	809	1.44E-26	48.90%	0.161	IPR016090 (SMART); IPR016090 (PFAM); IPR016090 (G3DSA:1.20.90.GENE3D); PTHR11716:SF45 (PANTHER); IPR001211 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPRO016090 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
574	c19208_g1_i1_len_1620_path_1_0_1433_1435_1_434_1434_1436_1435_1458_3416_1459_1587_1_460_1588_1748_5	1155	endoplasmic reticulum resident protein 29	535	2.98E-93	71.10%	0.466 Y	Coil (COILS); IPR011679 (PFAM); IPR011679 (G3DSA:1.20.1150.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012883 (PFAM); PTHR12211 (PANTHER); PTHR12211:SF0 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011679 (SUPERFAMILY); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
575	c19208_g1_i2_len_1749_path_1_0_1433_1435_1_434_1434_1436_1435_1458_3416_1459_1587_1_460_1588_1748_5	1035	endoplasmic reticulum resident protein 29	578	1.59E-84	63.80%	0.493 Y	Coil (COILS); IPR011679 (PFAM); IPR011679 (G3DSA:1.20.1150.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012883 (PFAM); PTHR12211:SF0 (PANTHER); PTHR12211 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (SUPERFAMILY); IPR011679 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

585	c19850_g1_i1_len_460_path_1_0_18_20_19_373_375_374_389_391_390_459_0	708	ribosomal protein s26	154	3.38E-59	89.80%	0.103	IPR000892 (PFAM); IPR000892 (PANTHER); IPR000892 (PROSITE PATTERNS)
586	c19850_g1_i2_len_459_path_947_0_17_20_18_3_72_375_373_388_391_389_458_2	553	ribosomal protein s26	153	1.77E-59	89.20%	0.114	IPR000892 (PFAM); IPR000892 (PANTHER); IPR000892 (PROSITE PATTERNS)
587	c19937_g2_i1_len_336_path_454_0_268_15_269_335_2	1	serine protease 33	112	7.82E-06	50.00%	0.501 Y	G3DSA:2.40.10.10 (GENE3D); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
588	c19967_g1_i1_len_1172_path_1223_0_54_1277_55_55_25_56_568_2450_569_1171_1	112	mitochondrial	391	1.35E-40	76.60%	0.112	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR10438:SF254 (PANTHER); IPR005746 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
589	c19967_g1_i2_len_618_path_2448_0_14_2450_1_5_617_2	5	mitochondrial	206	4.29E-43	76.60%	0.465 Y	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10438:SF254 (PANTHER); IPR005746 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY)
590	c20019_g1_i1_len_1520_path_1_0_1519_5	46	zinc finger protein 658-like isoform x1	506	1.42E-34	56.90%	0.1	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
591	c20132_g1_i2_len_2392_path_227_0_2234_226_2235_2391_2	105	cadherin-related tumor suppressor	797	7.94E-14	44.90%	0.262	IPR002126 (PRINTS); IPR002126 (SMART); IPR002126 (G3DSA:2.60.40.GENE3D); IPR002126 (PFAM); IPR002126 (G3DSA:2.60.40.GENE3D); PTHR24027 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002126 (PROSITE_PROFILES); IPR015919 (SUPERFAMILY); IPR015919 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
592	c20204_g1_i1_len_958_path_105_0_957_3	52	adiponectin receptor protein	314	3.97E-21	77.70%	0.101	IPR004254 (PFAM); PTHR20855:SF15 (PANTHER); IPR004254 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
593	c2037_g1_i1_len_1527_path_1505_0_1526_1	111	perq amino acid-rich with gyf domain-containing protein 2-like	509	2.60E-36	63.40%	0.11	IPR000884 (SMART); IPR002223 (PFAM); IPR000884 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); G3DSA:2.20.100.10 (GENE3D); PTHR11311 (PANTHER); IPR020901 (PROSITE PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR000884 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR000884 (SUPERFAMILY); TMhelix (TMHMM)

594	c20382_g1_i1_len_1560_path_1671_0_37_3412_38_41_1846_42_1559_0	173	gastrula zinc finger	514	4.87E-42	55.60%	0.121	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY);
595	c20382_g1_i2_len_1693_path_1671_0_37_1709_38_174_1846_175_1692_1	187	gastrula zinc finger	558	3.79E-41	56.70%	0.208	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
596	c20445_g1_i1_len_1631_path_3808_0_72_311_73_687_1872_688_1630_0	48	twitchin isoform x2	544	0	76.40%	0.109	Coil (COILS); IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897:SF148 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY);
597	c20484_g1_i1_len_656_path_734_0_655_2	2519	transmembrane protease serine 9-like	213	8.17E-23	56.70%	0.104	IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
598	c20538_g1_i1_len_1430_path_103_0_495_598_4_96_496_102_497_1429_4	76	ras-related protein rab-39b	477	6.42E-124	88.00%	0.131	IPR001806 (PRINTS); IPR024156 (SMART); IPR003579 (SMART); IPR003578 (SMART); IPR020849 (SMART); IPR002041 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR001806 (PFAM); PTHR24073 (PANTHER); PTHR24073:SF376 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
599	c20542_g2_i1_len_1700_path_3681_0_1101_178_4_1102_1125_1808_1126_1699_0	37	membrane metallo-endopeptidase-like 1-like	567	2.22E-179	82.00%	0.125	IPR018497 (PRINTS); IPR008753 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); IPR000718 (PANTHER); PTHR11733:SF113 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
600	c20561_g3_i1_len_2335_path_3014_0_2263_527_8_2264_2287_5706_2288_2334_2	44	hydroxysteroid dehydrogenase-like protein 2	778	3.93E-164	76.40%	0.14	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF273 (PANTHER); PTHR24322 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
601	c2058_g1_i1_len_346_path_324_0_345_4	3	xylosyltransferase oxt	115	6.55E-33	59.40%	0.177	no IPS match

602	c2064_g1_i1_len_1288_path_2268_0_1287_5	25	calcium calmodulin-dependent protein kinase	429	3.62E-101	91.70%	0.106	IPR008145 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:3.30.63.10 (GENE3D); IPR008145 (PFAM); PTHR23122 (PANTHER); PTHR23122:SF7 (PANTHER); IPR020590 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
603	c2064_g2_i1_len_518_path_1_0_517_1	4	peripheral plasma membrane protein cask isoform x2	173	2.98E-104	91.00%	0.1	IPR001452 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR011511 (PFAM); PTHR23122:SF7 (PANTHER); PTHR23122 (PANTHER); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY)
604	c2065_g1_i1_len_1939_path_1_0_182_184_183_1938_0	98	secreted frizzled-related protein 3	647	2.56E-78	59.70%	0.133	Coil (COILS); IPR018933 (SMART); IPR020067 (SMART); IPR018933 (PFAM); G3DSA:2.40.50.120 (GENE3D); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR020067 (PFAM); PTHR11309:SF83 (PANTHER); IPR015526 (PANTHER); IPR020067 (PROSITE_PROFILES); IPR001134 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY); IPR020067 (SUPERFAMILY)
605	c2065_g1_i2_len_2189_path_1_0_182_4127_183_432_184_433_2188_1	99	secreted frizzled-related protein 3	730	5.53E-78	59.90%	0.213	Coil (COILS); IPR018933 (SMART); IPR020067 (SMART); IPR020067 (G3DSA:1.10.2000.GENE3D); IPR018933 (PFAM); IPR020067 (PFAM); G3DSA:2.40.50.120 (GENE3D); PTHR11309:SF83 (PANTHER); IPR015526 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001134 (PROSITE_PROFILES); IPR020067 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY); IPR020067 (SUPERFAMILY)
606	c20692_g1_i1_len_2589_path_2643_0_2412_53_2413_2588_0	118	low-density lipoprotein receptor	857	1.39E-15	40.90%	0.234	IPR002172 (PRINTS); IPR000859 (SMART); IPR000998 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000859 (G3DSA:2.60.120.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR000859 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR000998 (PFAM); PTHR23282 (PANTHER); PTHR23282:SF75 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000859 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR000859 (SUPERFAMILY); TMhelix (TMHMM)
607	c20697_g3_i1_len_638_path_616_0_637_4	4	atp-dependent partial	213	5.04E-146	99.00%	0.121	IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23076:SF10 (PANTHER); PTHR23076 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
608	c20723_g1_i2_len_885_path_515_0_542_514_543_884_3	19	calumenin partial	290	1.01E-13	83.00%	0.161	IPR011992 (G3DSA:1.10.238.GENE3D); IPR018247 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)

609	c20732_g1_i1_len_1919_path_1989_0_172_2161_173_699_96_700_1918_0	221	zinc finger protein 850-like isoform x1	634	1.26E-48	55.40%	0.113	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
610	c20732_g1_i2_len_1392_path_1989_0_172_96_173_1391_1	131	zinc finger protein 850-like isoform x1	458	1.18E-49	55.60%	0.145	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
611	c20747_g1_i1_len_671_path_919_0_177_111_178_670_0	34	adrenodoxin-like mitochondrial	217	9.22E-77	84.70%	0.156	IPR001055 (PRINTS); IPR012675 (G3DSA:3.10.20.GENE3D); IPR001041 (PFAM); PTHR23426 (PANTHER); PTHR23426:SF1 (PANTHER); IPR018298 (PROSITE_PATTERNS); IPR001041 (PROSITE_PROFILES); IPR001041 (SUPERFAMILY)
612	c20747_g1_i2_len_758_path_919_0_177_24_178_264_111_265_757_0	34	adrenodoxin-like mitochondrial	246	9.16E-73	86.90%	0.155	IPR001055 (PRINTS); IPR012675 (G3DSA:3.10.20.GENE3D); IPR001041 (PFAM); PTHR23426:SF1 (PANTHER); PTHR23426 (PANTHER); IPR018298 (PROSITE_PATTERNS); IPR001041 (PROSITE_PROFILES); IPR001041 (SUPERFAMILY)
613	c20948_g1_i1_len_1045_path_1125_0_363_79_364_1044_5	60	plasma alpha-l-fucosidase	348	1.02E-08	62.83%	0.101	PTHR10030:SF26 (PANTHER); IPR000933 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
614	c20958_g1_i1_len_1057_path_1_0_1056_4	10	myoneurin-like isoform x1	352	1.78E-84	70.20%	0.101	IPR015880 (SMART); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13909 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF19 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
615	c20984_g1_i1_len_2650_path_56_0_2649_4	195	exocyst complex component 3	877	0	74.20%	0.135	Coil (COILS); IPR010326 (PFAM); IPR010326 (PANTHER); PTHR21292:SF1 (PANTHER)
616	c21003_g1_i1_len_1457_path_1435_0_1456_2	74	omega-amidase nit2-like	485	3.56E-144	82.80%	0.500 Y	IPR003010 (PFAM); IPR003010 (G3DSA:3.60.110.GENE3D); PTHR23088 (PANTHER); PTHR23088:SF20 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003010 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR003010 (SUPERFAMILY); TMhelix (TMHMM)

[illegible]

Supplementary Table 8

630	c2155_g1_i1_len_1610_path_1638_0_1609_0	86	peptidyl-alpha-hydroxyglycine alpha-amidating lyase 2-like	531	1.02E-109	60.20%	0.716 Y	IPR000720 (PRINTS); IPR001258 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR10680 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF101898 (SUPERFAMILY)
631	c2156_g2_i1_len_740_path_1430_0_739_3	17	proprotein convertase subtilisin kexin type 7-like isoform x1	247	4.43E-68	58.30%	0.645 Y	IPR008979 (G3DSA:2.60.120.GENE3D); IPR002884 (PFAM); IPR015500 (PANTHER); PTHR10795:SF9 (PANTHER); SignalP-noTM (SIGNALP_EUK); IPR008979 (SUPERFAMILY)
632	c21574_g1_i1_len_2100_path_2188_0_359_74_3_60_377_92_378_2099_0	109	annexin a4	700	4.27E-90	66.90%	0.102	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF47874 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
633	c21574_g1_i2_len_2082_path_2188_0_359_92_3_60_2081_0	134	annexin a4	694	1.24E-91	67.90%	0.102	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF47874 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
634	c21583_g1_i1_len_1343_path_1436_0_443_1879_444_1342_1	18	inactive tyrosine-protein kinase 7-like	448	3.84E-143	62.00%	0.211	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR26391:SF14 (PANTHER); PTHR26391 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
635	c21589_g1_i1_len_3409_path_1_0_2040_2042_2_041_2064_2042_2065_2088_4187_2089_3408_0	625	zinc finger protein on ecdysone puffs	1131	1.50E-55	63.50%	0.131	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); G3DSA:1.10.601.10 (GENE3D); PF12874 (PFAM); IPR026811 (PTHR15491:PANTHER); PTHR15491 (PANTHER); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)

636	c21590_g1_i2_len_3280_path_991_0_2823_63_2_824_3279_1	207	zinc finger protein 184-like	1075	0	59.00%	0.163	Coil (COILS); IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
637	c2176_g1_i1_len_1158_path_53_0_1157_1	39	dentin matrix protein 4-like	374	0	85.00%	0.099	IPR009581 (PFAM); PTHR12450:SF8 (PANTHER); IPR024869 (PANTHER) IPR002130 (PRINTS); IPR001680 (SMART); IPR002130 (PFAM); IPR001680 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR015943 (G3DSA:2.130.10.GENE3D); IPR024936 (PANTHER); PTHR11071:SF228 (PANTHER); IPR017986 (PROSITE_PROFILES); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); IPR017986 (SUPERFAMILY)
638	c21787_g1_i1_len_2282_path_53_0_2281_2	193	peptidylprolyl isomerase domain and wd repeat-containing protein 1	755	0	84.50%	0.108	IPR023796 (SMART); G3DSA:2.30.39.10 (GENE3D); G3DSA:3.30.497.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023796 (SUPERFAMILY); TMhelix (TMHMM)
639	c21812_g1_i1_len_1612_path_1_0_538_540_539_1611_4	72	serine proteinase inhibitor b3	532	5.13E-73	53.90%	0.173	Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR007148 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19853:SF0 (PANTHER); PTHR19853 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR017986 (SUPERFAMILY)
640	c2183_g1_i1_len_3115_path_55_0_1068_1123_1_069_1069_27_1070_3114_2	176	wd repeat-containing protein 3	1032	0	73.90%	0.325	IPR001806 (PRINTS); IPR024156 (SMART); IPR002041 (SMART); IPR003578 (SMART); IPR003579 (SMART); IPR020849 (SMART); IPR001806 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR24073 (PANTHER); PTHR24073:SF456 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
641	c21835_g1_i2_len_1636_path_371_0_187_160_1_88_1635_0	292	ras-related protein rab-10	546	3.17E-116	92.90%	0.209	G3DSA:3.30.1120.10 (GENE3D); IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342:SF206 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)
642	c21845_g1_i1_len_1560_path_1600_0_1385_298_4_1386_1388_2987_1389_1559_4	59	arylsulfatase b-like	514	7.72E-143	66.20%	0.171	IPR001846 (SMART); IPR015255 (PFAM); IPR001846 (PFAM); PTHR23345:SF1 (PANTHER); PTHR23345 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001846 (PROSITE_PROFILES); IPR015819 (SUPERFAMILY)
643	c21858_g1_i1_len_2656_path_2634_0_236_2871_237_238_2873_239_376_3011_377_2655_5	265	vitellogenin 2	879	2.10E-66	43.80%	0.129	IPR001846 (SMART); IPR001846 (PFAM); IPR015255 (PFAM); PTHR23345:SF1 (PANTHER); PTHR23345 (PANTHER); IPR001846 (PROSITE_PROFILES); IPR015819 (SUPERFAMILY)
644	c21858_g1_i2_len_2718_path_5267_0_438_3011_439_2717_5	139	vitellogenin 2	906	2.38E-62	43.70%	0.129	IPR001846 (SMART); IPR001846 (PFAM); IPR015255 (PFAM); PTHR23345:SF1 (PANTHER); PTHR23345 (PANTHER); IPR001846 (PROSITE_PROFILES); IPR015819 (SUPERFAMILY)

645	c21876_g1_i1_len_1674_path_1652_0_1673_2	48	hemacentin-2 isoform x3	552	1.05E-90	67.40%	0.204	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR23279 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
646	c21890_g2_i2_len_365_path_1_0_212_562_213_364_4	63	trypsin-like proteinase	109	6.31E-08	72.30%	0.275	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24275 (PANTHER); IPR009003 (SUPERFAMILY)
647	c21925_g2_i1_len_459_path_1107_0_304_1411_305_310_62_311_458_0	2417	isoform b	153	4.75E-26	55.00%	0.101	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
648	c22032_g1_i2_len_1576_path_141_0_104_245_1_05_239_140_240_1575_0	37	---NA---	526			0.104	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
649	c22052_g1_i2_len_1192_path_61_0_362_424_36_3_1036_60_1037_1191_3	26	sortilin-related receptor-like	398	7.32E-55	58.20%	0.117	IPR013783 (G3DSA:2.60.40.GENE3D); PTHR12106 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (SUPERFAMILY); TMhelix (TMHMM)
650	c22052_g1_i3_len_1216_path_61_0_362_2465_3_63_386_424_387_1060_60_1061_1215_3	22	sortilin-related receptor-like	406	9.96E-55	56.80%	0.117	IPR013783 (G3DSA:2.60.40.GENE3D); PTHR12106 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (SUPERFAMILY); TMhelix (TMHMM)
651	c22159_g1_i1_len_1292_path_49_0_882_2629_8_83_888_48_889_1291_3	1165	isoform b	425	6.91E-48	62.20%	0.149	IPR003585 (SMART); IPR027789 (PFAM); IPR001050 (PANTHER); PTHR10915:SF1 (PANTHER); IPR030479 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
652	c22271_g1_i1_len_2501_path_105_0_2500_2	222	inversin-like isoform x3	827	1.96E-58	74.30%	0.219	IPR000048 (SMART); IPR002110 (SMART); IPR000048 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24178 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000048 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
653	c22296_g1_i1_len_404_path_1645_0_172_1818_173_223_1869_224_403_3	0	hypothetical protein DAPPUDRAFT_54608, partial	135	1.53E-07	43.00%	0.323	G3DSA:2.40.10.10 (GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
654	c22300_g1_i1_len_696_path_73_0_135_24_136_156_229_157_188_260_189_695_1	9	brasiliensin precursor	232	1.15E-27	49.80%	0.117	IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); PTHR10913 (PANTHER); PTHR10913:SF46 (PANTHER); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY); SSF100895 (SUPERFAMILY)
655	c2234_g1_i1_len_1236_path_53_0_1235_5	49	ras-related protein rab-4b	404	6.47E-135	94.30%	0.225	IPR001806 (PRINTS); IPR003579 (SMART); IPR003578 (SMART); IPR020849 (SMART); IPR024156 (SMART); IPR002041 (SMART); IPR001806 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR24073:SF387 (PANTHER); PTHR24073 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)

656	c22444_g1_i1_len_2328_path_2406_0_2327_0	103	maltase 2-like	776	0	65.50%	0.103	IPR006589 (SMART); G3DSA:3.90.400.10 (GENE3D); IPR006047 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR015902 (PANTHER); PTHR10357:SF76 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY)
657	c22466_g1_i1_len_1838_path_729_0_1490_2329_1491_1491_25_1492_1837_2	54	microfibrillar-associated protein 1-like	607	9.90E-176	78.00%	0.1	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR009730 (PFAM); IPR009730 (PANTHER); PTHR15327:SF0 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
658	c22466_g1_i2_len_1574_path_729_0_1490_2329_1491_1491_2330_1492_1573_2	54	microfibrillar-associated protein 1-like	524	4.09E-177	77.80%	0.1	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR009730 (PFAM); IPR009730 (PANTHER); PTHR15327:SF0 (PANTHER)
659	c225_g1_i1_len_2167_path_53_0_2166_0	310	dehydrogenase reductase sdr family member 11-like	716	5.76E-111	77.10%	0.165	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR013968 (SMART); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF78 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
660	c22705_g2_i1_len_450_path_2473_0_87_551_88_204_2829_205_449_0	4	ves g 5 allergen	150	1.14E-21	55.90%	0.359 Y	IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014044 (SUPERFAMILY)
661	c22717_g1_i2_len_1429_path_1904_0_867_224_868_1428_0	35	cyclin-dependent kinase 6-like	477	2.07E-137	78.80%	0.099	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24056 (PANTHER); PTHR24056:SF180 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
662	c22782_g1_i1_len_2191_path_2169_0_2190_0	203	lethal giant larvae protein homolog 1-like isoform x5	725	0	75.60%	0.167	IPR000664 (PRINTS); IPR001680 (SMART); IPR013577 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR10241:SF28 (PANTHER); PTHR10241 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR011047 (SUPERFAMILY); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
663	c2280_g1_i1_len_1405_path_1_0_460_462_461_1404_0	35	plasma kallikrein	469	1.72E-29	48.70%	0.159	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
664	c2280_g1_i2_len_579_path_1_0_460_2906_461_578_0	8	mite allergen der f 3-like	193	1.42E-07	47.60%	0.159	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24276 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR009003 (SUPERFAMILY)
665	c2281_g2_i1_len_146_path_594_0_145_1	0	---NA---	49			0.106	no IPS match
666	c22877_g1_i1_len_1771_path_2032_0_191_142_192_1770_1	180	polycomb protein eed	585	0	85.20%	0.139	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR10253 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)

667	c22877_g1_i2_len_1720_path_1_0_140_142_141_1719_1	176	polycomb protein eed	568	0	84.80%	0.101	IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR10253 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
668	c22914_g1_i1_len_1638_path_53_0_1637_2	49	aldehyde dimeric nadp-preferring isoform x4	540	0	74.30%	0.108	IPR012394 (PIRSF); IPR016163 (G3DSA:3.40.309.GENE3D); IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF15 (PANTHER); IPR029510 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM)
669	c22979_g1_i1_len_711_path_6519_0_91_6610_9_2_92_318_93_425_621_426_642_6988_643_643_160_644_710_2	32	carboxyl cholinesterase 5bs	237	2.15E-08	64.10%	0.104	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); PTHR11559:SF142 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
670	c22979_g1_i2_len_2517_path_319_0_301_621_3_02_518_6988_519_519_837_520_2516_1	171	venom carboxylesterase-6 isoform x2	839	2.87E-136	58.30%	0.132	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559 (PANTHER); IPR019819 (PROSITE_PATTERNS); IPR019826 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY)
671	c22979_g1_i3_len_285_path_621_0_216_25_217_284_2	0	carboxyl cholinesterase 5bs	95	5.62E-09	67.00%	0.909 Y	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR029058 (SUPERFAMILY)
672	c22998_g1_i1_len_997_path_1075_0_965_2082_966_996_0	107	e3 ubiquitin-protein ligase rnf185-like isoform x2	333	8.34E-88	81.00%	0.113	IPR001841 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); PF13923 (PFAM); PTHR12313:SF3 (PANTHER); PTHR12313 (PANTHER); IPR017907 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001841 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
673	c23129_g1_i1_len_3022_path_103_0_2310_2411_2311_2311_102_2312_3021_2	514	titin- partial	1000	2.55E-153	70.40%	0.1	PR00014 (PRINTS); IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF142 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
674	c23132_g1_i1_len_1012_path_2578_0_123_934_124_287_1113_288_488_1314_489_1011_1	38	zinc metalloproteinase nas-13	337	3.99E-30	60.90%	0.151	IPR001506 (PRINTS); IPR006026 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)
675	c23132_g1_i2_len_544_path_2536_0_20_1314_2_1_543_1	11	cre-nas-7 protein	181	1.02E-09	58.30%	0.127	IPR001506 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)
676	c23134_g1_i1_len_2816_path_5573_0_19_2780_20_35_2796_36_89_2850_90_2815_2	80	transcriptional regulator	938	0	99.60%	0.104	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR000843 (SMART); IPR000843 (PFAM); G3DSA:3.40.50.2300 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR001761 (PFAM); PF13561 (PFAM); G3DSA:3.40.50.2300 (GENE3D); IPR010982 (G3DSA:1.10.260.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF166 (PANTHER); IPR000843 (PROSITE_PATTERNS); IPR020904 (PROSITE_PATTERNS); IPR000843 (PROSITE_PROFILES); SSF51735 (SUPERFAMILY); IPR028082 (SUPERFAMILY); IPR010982 (SUPERFAMILY)

677	c23134_g1_i2_len_2801_path_5691_0_20_2796_21_74_2850_75_2800_2	80	transcriptional regulator	933	0	99.50%	0.107	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR000843 (SMART); G3DSA:3.40.50.2300 (GENE3D); G3DSA:3.40.50.2300 (GENE3D); IPR010982 (G3DSA:1.10.260.GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR000843 (PFAM); PF13561 (PFAM); IPR001761 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF166 (PANTHER); IPR000843 (PROSITE_PATTERNS); IPR020904 (PROSITE_PATTERNS); IPR000843 (PROSITE_PROFILES); IPR028082 (SUPERFAMILY); IPR010982 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
678	c23151_g1_i1_len_1059_path_1_0_184_186_185_1058_2	84	3-hydroxyisobutyrate dehydrogenase	347	2.17E-42	55.30%	0.297	IPR013328 (G3DSA:1.10.1040.GENE3D); IPR006115 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR029154 (PFAM); PTHR22981:SF7 (PANTHER); PTHR22981 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008927 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
679	c23151_g1_i2_len_1178_path_1_0_184_2090_18_5_303_186_304_1177_1	67	3-hydroxyisobutyrate dehydrogenase	387	1.31E-64	55.10%	0.156	IPR006115 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); IPR029154 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22981:SF7 (PANTHER); PTHR22981 (PANTHER); IPR029752 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY); IPR008927 (SUPERFAMILY)
680	c23163_g1_i1_len_1504_path_1139_0_321_2248_322_714_1459_715_1503_2	64	#NAME?	495	5.42E-140	79.20%	0.114	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PF13561 (PFAM); PTHR24315:SF2 (PANTHER); PTHR24315 (PANTHER); SSF51735 (SUPERFAMILY)
681	c23191_g1_i1_len_1692_path_1670_0_1453_312_4_1454_1464_3135_1465_1691_1	313	scp-like extracellular domain containing protein 1	558	6.86E-43	53.30%	0.794 Y	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR002172 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
682	c23201_g1_i1_len_2340_path_2318_0_1042_481_9_1043_1052_4829_1053_2339_5	63	cyclin-c	780	1.16E-161	91.00%	0.102	IPR013763 (SMART); IPR006671 (PFAM); IPR013763 (G3DSA:1.10.472.GENE3D); IPR015429 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013763 (SUPERFAMILY); IPR013763 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
683	c23224_g1_i1_len_333_path_2957_0_332_4	2	---NA---	111			0.142	no IPS match
684	c23225_g1_i2_len_728_path_458_0_403_862_40_4_727_0	4	dnaj homolog subfamily b member 12-like	243	1.83E-65	76.50%	0.101	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24077 (PANTHER); PTHR24077:SF239 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
685	c23242_g1_i1_len_1543_path_1_0_573_575_574_675_677_676_884_3294_885_1542_2	210	3-hydroxybutyrate dehydrogenase type 2	504	2.78E-43	76.30%	0.116	IPR003560 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24321 (PANTHER); PTHR24321:SF3 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY)
686	c23242_g1_i2_len_1484_path_1_0_573_677_574_782_886_783_825_3294_826_1483_2	238	3-hydroxybutyrate dehydrogenase type 2	484	1.48E-94	75.80%	0.116	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24321:SF3 (PANTHER); PTHR24321 (PANTHER); IPR020904 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
687	c23242_g1_i3_len_1586_path_1_0_573_575_574_675_677_676_884_886_885_927_3294_928_15_85_2	367	3-hydroxybutyrate dehydrogenase type 2	518	3.02E-118	81.00%	0.116	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24321:SF3 (PANTHER); PTHR24321 (PANTHER); IPR020904 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)

700	c23656_g2_i2_len_1236_path_1920_0_460_2380_461_554_1458_555_809_1168_810_1235_3	14	gastrula zinc finger	412	2.78E-60	54.90%	0.11	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
701	c23690_g1_i1_len_2193_path_2116_0_1431_465_5_1432_1570_3630_1571_2192_2	21998	disulfide isomerase	723	0	80.20%	0.545 Y	PR00421 (PRINTS); IPR005792 (TIGRFAM); IPR005788 (TIGRFAM); PF13848 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF48 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
702	c23690_g1_i2_len_2136_path_2116_0_1431_354_8_1432_1513_3630_1514_2135_2	29327	protein disulfide-isomerase	704	0	80.70%	0.545 Y	PR00421 (PRINTS); PF13848 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR005788 (TIGRFAM); IPR005792 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF48 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
703	c23749_g1_i1_len_1583_path_1712_0_963_3177_964_1382_258_1383_1408_3199_1409_1469_2_58_1470_1495_3199_1	80	zinc finger protein 84-like	528	4.66E-41	48.70%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
704	c23780_g1_i1_len_1184_path_1164_0_102_1267__103_625_1790_626_787_1952_788_966_2133_967_1183_2	53	peroxisomal trans-2-enoyl- reductase-like	388	1.13E-127	74.60%	0.131	IPR002347 (PRINTS); PF13561 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24317 (PANTHER); SSF51735 (SUPERFAMILY)
705	c23780_g1_i2_len_953_path_2367_0_31_1267__32_554_1952_555_733_2131_734_735_2133_73_6_952_0	26	peroxisomal trans-2-enoyl- reductase-like	312	3.11E-91	61.20%	0.177	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24317 (PANTHER); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
706	c23780_g1_i3_len_1115_path_2367_0_31_1267__32_554_1790_555_716_1952_717_895_2131_8_96_897_2133_898_0	54	peroxisomal trans-2-enoyl- reductase-like	366	1.36E-126	74.10%	0.177	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PF13561 (PFAM); PTHR24317 (PANTHER); SSF51735 (SUPERFAMILY)

707	c23838_g1_i2_len_1501_path_1479_0_385_1865_386_1500_4	74	matrix metalloproteinase-9	500	5.40E-10	41.30%	0.126	IPR000562 (SMART); IPR000562 (G3DSA:2.10.10.GENE3D); IPR000562 (PFAM); IPR000562 (G3DSA:2.10.10.GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000562 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY); TMhelix (TMHMM)
708	c23851_g1_i2_len_1323_path_1_0_560_3074_561_562_564_563_805_809_806_1322_3	35	fibroblast growth factor receptor-like 1	441	1.16E-27	63.60%	0.106	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19890 (PANTHER); PTHR19890:SF5 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
709	c23852_g1_i1_len_1428_path_1568_0_1054_262_2_1055_1078_49_1079_1079_116_1080_1094_1_32_1095_1427_1	2204	uncharacterized oxidoreductase	470	1.07E-84	69.80%	0.133	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF237 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
710	c23854_g1_i1_len_868_path_959_0_82_116_83_867_0	424	histone h2a-like	284	3.43E-79	96.80%	0.214	IPR002119 (PRINTS); IPR002119 (SMART); IPR007125 (PFAM); IPR009072 (G3DSA:1.10.20.GENE3D); PTHR23430:SF45 (PANTHER); PTHR23430 (PANTHER); IPR002119 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009072 (SUPERFAMILY); TMhelix (TMHMM)
711	c23863_g1_i2_len_1016_path_994_0_122_1117_123_285_1280_286_289_1284_290_375_1370_3_76_1015_2	137	l-xylulose reductase	332	3.60E-114	78.00%	0.119	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR013968 (SMART); IPR016040 (G3DSA:3.40.50.GENE3D); PF13561 (PFAM); PTHR24311:SF6 (PANTHER); PTHR24311 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
712	c23896_g1_i1_len_1656_path_1734_0_1655_2	788	er membrane protein complex subunit 10	540	6.85E-72	63.70%	0.276	PTHR21397 (PANTHER); IPR029615 (PTHR21397:PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
713	c23915_g1_i1_len_2340_path_53_0_2339_5	941	multiple inositol polyphosphate phosphatase 1	780	4.59E-142	61.20%	0.304	IPR029033 (G3DSA:3.40.50.GENE3D); IPR000560 (PFAM); PTHR20963:SF8 (PANTHER); PTHR20963 (PANTHER); IPR000560 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029033 (SUPERFAMILY); TMhelix (TMHMM)
714	c2392_g2_i1_len_486_path_647_0_485_2	4	PREDICTED: hypothetical protein LOC100647042	162	1.14E-17	52.70%	0.245	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24258 (PANTHER); PTHR24258:SF96 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

744	c24483_g1_i1_len_1391_path_1_0_1390_2	1973	hemagglutinin amebocyte aggregation factor-like	457	2.12E-40	61.10%	0.224	PF14704 (PFAM); IPR026645 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
745	c24508_g1_i1_len_1396_path_1374_0_549_1924_550_1142_2517_1143_1395_0	65	gastrula zinc finger	466	2.16E-49	57.90%	0.104	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
746	c24508_g1_i2_len_701_path_2747_0_107_1924_108_700_2	17	gastrula zinc finger protein - partial	233	3.55E-32	65.00%	0.197	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
747	c24519_g2_i1_len_1225_path_3545_0_563_4107_564_564_4108_565_1224_2	115	ankyrin repeat domain-containing protein 16-like	408	2.23E-112	63.60%	0.104	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24181 (PANTHER); PTHR24181:SF20 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
748	c24553_g2_i1_len_2142_path_1_0_14_16_15_21_41_1	186	n-sulphoglucosamine partial	714	0	78.30%	0.752 Y	Coil (COILS); G3DSA:3.30.1120.10 (GENE3D); IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342:SF76 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017850 (SUPERFAMILY)
749	c24553_g2_i2_len_2484_path_5120_0_356_16_3_57_2483_1	188	n-sulphoglucosamine partial	828	0	78.30%	0.134	Coil (COILS); IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); PTHR10342 (PANTHER); PTHR10342:SF76 (PANTHER); IPR024607 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY)
750	c24558_g1_i1_len_1322_path_480_0_753_1234_754_775_1256_776_1076_422_1077_1321_2	12025	granulins- partial	434	3.89E-38	51.30%	0.292	IPR000118 (SMART); IPR000118 (PFAM); PTHR12274:SF1 (PANTHER); PTHR12274 (PANTHER); IPR000118 (PROSITE_PATTERNS); IPR000118 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF57277 (SUPERFAMILY)

751	c24558_g1_i2_len_1503_path_480_0_753_1234_754_775_1256_776_1076_241_1077_1257_422_1258_1502_2	8528	granulins- partial	494	1.07E-37	51.20%	0.292	IPR000118 (SMART); IPR000118 (PFAM); PTHR12274:SF1 (PANTHER); PTHR12274 (PANTHER); IPR000118 (PROSITE_PATTERNS); IPR000118 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF57277 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
752	c24586_g1_i1_len_1956_path_2034_0_1955_3	1601	cytosolic non-specific dipeptidase	646	0	81.50%	0.453 Y	G3DSA:3.40.630.10 (GENE3D); IPR002933 (PFAM); IPR011650 (PFAM); IPR011650 (G3DSA:3.30.70.GENE3D); PTHR11014:SF51 (PANTHER); PTHR11014 (PANTHER); IPR001261 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); TMhelix (TMHMM)
753	c24588_g1_i2_len_921_path_79_0_663_67_664_702_67_703_741_1460_742_764_1483_765_803_1483_804_842_148_0	11	---NA---	307			0.131	CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
754	c24591_g1_i1_len_1125_path_2367_0_35_211_3_6_1124_1	37	zinc finger protein partial	370	6.11E-15	64.00%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
755	c24591_g2_i1_len_262_path_2367_0_35_2402_3_6_261_1	0	zinc finger protein 358	87	4.11E-15	64.80%	0.124	IPR015880 (SMART); PF13913 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
756	c24591_g3_i1_len_723_path_2662_0_249_2911_250_255_186_256_300_2960_301_337_124_338_722_2	12	zinc finger protein 358	241	4.84E-24	59.00%	0.12	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
757	c24597_g1_i1_len_1560_path_1622_0_1161_278_3_1162_1162_70_1163_1559_0	75	sh3 domain-containing ring finger protein 3 isoform x1	520	2.70E-68	52.70%	0.116	IPR001452 (SMART); G3DSA:2.30.30.40 (GENE3D); IPR001452 (PFAM); PTHR10661 (PANTHER); PTHR10661:SF7 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); TMhelix (TMHMM)
758	c24622_g1_i1_len_1600_path_1704_0_715_14_7_16_1599_2	90	uv radiation resistance-associated gene protein	533	1.52E-39	66.30%	0.097	Coil (COILS); PTHR15157 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
759	c24687_g1_i1_len_1589_path_53_0_1588_0	87	---NA---	530			0.112	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
760	c24687_g1_i1_len_1589_path_53_0_1588_1	87	cation channel sperm-associated protein subunit gamma	530	2.54E-07	56.00%	0.107	Coil (COILS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)

761	c24687_g1_i1_len_1589_path_53_0_1588_2	87	cation channel sperm-associated protein subunit gamma	529	6.71E-06	54.00%	0.111	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
762	c24707_g1_i1_len_1795_path_105_0_1794_5	101	peroxisomal biogenesis factor 7	598	3.80E-143	73.00%	0.161	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22850 (PANTHER); PTHR22850:SF98 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR01680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
763	c24738_g1_i1_len_1594_path_738_0_475_5831_476_477_763_478_1098_1384_1099_1103_1389_1104_1496_1782_1_0	54	protein d2-like isoform x2	524	2.83E-89	79.20%	0.33	IPR008914 (PFAM); IPR008914 (G3DSA:3.90.280.GENE3D); PTHR11362 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008914 (SUPERFAMILY); TMhelix (TMHMM)
764	c24738_g1_i2_len_1066_path_738_0_475_5831_476_477_5064_478_1065_0	67	protein d2-like isoform x1	356	1.75E-63	75.50%	0.33	IPR008914 (PFAM); IPR008914 (G3DSA:3.90.280.GENE3D); PTHR11362 (PANTHER); IPR008914 (SUPERFAMILY)
765	c24738_g1_i3_len_916_path_4492_0_94_738_95_570_25_571_915_2	51	phosphatidylethanolamine-binding protein	299	6.22E-64	78.50%	0.118	IPR008914 (G3DSA:3.90.280.GENE3D); IPR008914 (PFAM); PTHR11362 (PANTHER); IPR008914 (SUPERFAMILY)
766	c24782_g2_i1_len_2510_path_433_0_952_1386_953_954_1388_955_1930_2364_1931_2509_2	370	proclotting enzyme	821	1.15E-129	64.00%	0.214	IPR001314 (PRINTS); IPR006604 (SMART); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268:SF81 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
767	c24808_g1_i1_len_863_path_55_0_668_886_669_862_5	278	peptidyl-prolyl cis-trans isomerase-like 3-like	287	3.45E-48	59.70%	0.144	IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
768	c24808_g1_i2_len_1025_path_55_0_668_724_669_830_886_831_1024_5	673	peptidyl-prolyl cis-trans isomerase-like 3	341	1.27E-96	91.00%	0.145	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
769	c24834_g1_i1_len_1967_path_1_0_1919_1921_1_920_1938_4097_1939_1966_1	244	coatomer subunit alpha	648	0	81.70%	0.115	IPR010714 (PFAM); IPR006692 (PFAM); PTHR19876 (PANTHER)
770	c24933_g1_i2_len_1751_path_849_0_25_976_26_1054_2005_1055_1750_1	56	coagulation factor xi	584	1.69E-61	61.80%	0.121	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
771	c24949_g1_i1_len_1027_path_105_0_1026_3	798	protein them6	337	4.26E-32	55.60%	0.114	PF13279 (PFAM); IPR029069 (G3DSA:3.10.129.GENE3D); PTHR12475 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029069 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

772	c24982_g2_i1_len_495_path_724_0_86_810_87_329_1053_330_353_3184_354_383_3214_384_407_5964_408_470_3_3	8	zinc finger protein	165	5.88E-30	56.90%	0.119	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
773	c24982_g3_i2_len_759_path_2771_0_389_1053_390_413_1077_414_435_1099_436_758_3	11	zinc finger protein	253	1.10E-21	52.20%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24375:SF106 (PANTHER); PTHR24375 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
774	c24989_g1_i1_len_791_path_53_0_342_52_343_431_1706_432_432_483_433_489_1616_490_501_557_502_790_0	23	peptidase s8	264	2.72E-24	69.00%	0.361 Y	IPR007280 (PFAM); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
775	c25072_g2_i1_len_896_path_3050_0_447_3495_448_461_130_462_895_4	20	upf0454 protein c12orf49 homolog	299	7.49E-109	76.00%	0.1	IPR019352 (PFAM); IPR019352 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
776	c25095_g2_i1_len_611_path_3077_0_246_3322_247_276_3322_277_306_2857_307_414_1658_415_444_1658_445_4_4	7	repetitive proline-rich cell wall protein 2- partial	204	3.83E-18	42.50%	0.108	no IPS match
777	c25112_g1_i1_len_2141_path_53_0_347_399_348_350_402_351_2140_3	232	ww domain-containing oxidoreductase	708	3.87E-164	74.70%	0.669 Y	Coil (COILS); IPR002347 (PRINTS); IPR001202 (SMART); G3DSA:2.20.70.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316 (PANTHER); PTHR24316:SF115 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001202 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR001202 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
778	c25117_g1_i1_len_403_path_639_0_402_2	301	transmembrane protease serine 9- partial	134	3.22E-20	54.90%	0.104	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
779	c2520_g1_i1_len_1334_path_1_0_1333_4	181	neurofilament triplet h protein	445	4.15E-09	52.20%	0.107	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
780	c25203_g1_i1_len_1264_path_802_0_799_1602_800_1010_1679_1011_1263_3	21	alcohol dehydrogenase	422	2.91E-108	67.20%	0.147	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); PTHR11732:SF183 (PANTHER); IPR001395 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
781	c25203_g2_i1_len_1267_path_3465_0_578_1602_579_789_4251_790_1266_5	17	alcohol dehydrogenase	422	1.17E-16	68.90%	0.283	IPR023210 (G3DSA:3.20.20.GENE3D); IPR001395 (PANTHER); PTHR11732:SF183 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023210 (SUPERFAMILY); TMhelix (TMHMM)
782	c25222_g1_i1_len_1428_path_843_0_1039_50_1040_1427_1	1652	ribosome biogenesis protein wdr12 homolog	470	0	74.50%	0.136	IPR020472 (PRINTS); IPR001680 (SMART); IPR012972 (PFAM); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19855 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR028599 (HAMAP); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)

783	c25243_g1_i1_len_2102_path_78_0_23_102_24_249_324_250_1127_1200_1128_2101_1	2744	adp-ribosylation factor 2	695	1.27E-116	95.70%	0.109	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR003579 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR11711:SF153 (PANTHER); PTHR11711 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
784	c25243_g1_i2_len_2101_path_4447_0_22_102_23_248_324_249_1126_1200_1127_2100_0	2762	adp-ribosylation factor 2	695	1.08E-116	95.70%	0.11	IPR006689 (PRINTS); IPR024156 (SMART); IPR006687 (SMART); IPR003579 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711:SF153 (PANTHER); PTHR11711 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
785	c25243_g1_i3_len_2073_path_103_0_220_324_221_1098_1200_1099_2072_2	2770	adp-ribosylation factor 4	685	2.73E-112	93.20%	0.157	IPR006689 (PRINTS); IPR024156 (SMART); IPR006687 (SMART); IPR003579 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF153 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
786	c25266_g1_i1_len_1618_path_3274_0_1053_25_1054_1617_2	21543	glyceraldehyde-3-phosphate dehydrogenase	533	0	89.90%	0.126	IPR020831 (PRINTS); IPR020828 (SMART); IPR006424 (TIGRFAM); IPR020829 (PFAM); G3DSA:3.30.360.10 (GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020828 (PFAM); IPR020831 (PANTHER); IPR020830 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); SSF55347 (SUPERFAMILY)
787	c25266_g1_i2_len_2119_path_3274_0_1053_432_7_1054_2118_2	27390	glyceraldehyde-3-phosphate dehydrogenase	700	0	90.30%	0.126	IPR020831 (PRINTS); IPR020828 (SMART); G3DSA:3.30.360.10 (GENE3D); IPR020828 (PFAM); IPR006424 (TIGRFAM); IPR016040 (G3DSA:3.40.50.GENE3D); IPR020829 (PFAM); IPR020831 (PANTHER); IPR020830 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); SSF55347 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
788	c25267_g1_i1_len_1787_path_1765_0_1786_0	152	aael003561- partial	596	7.46E-24	52.80%	0.144	IPR001211 (PRINTS); IPR016090 (SMART); IPR016090 (G3DSA:1.20.90.GENE3D); IPR016090 (PFAM); PTHR11716:SF45 (PANTHER); IPR001211 (PANTHER); IPR013090 (PROSITE_PATTERNS); IPR013090 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016090 (SUPERFAMILY); TMhelix (TMHMM)

789	c25270_g1_i3_len_2912_path_2890_0_744_3635_745_1477_4368_1478_2160_5051_2161_2308_5199_2309_2911_0	128	wd repeat-containing protein 36	965	0	69.70%	0.157	IPR001680 (SMART); IPR001680 (PFAM); IPR007319 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR13889 (PANTHER); PTHR13889:SF2 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR017986 (SUPERFAMILY)
790	c25309_g1_i1_len_2232_path_2210_0_1342_355_3_1343_1343_3554_1344_2231_0	190	dnaj homolog subfamily c member 3-like	744	0	74.20%	0.142	Coil (COILS); IPR001623 (PRINTS); IPR019734 (SMART); IPR001623 (SMART); IPR011990 (G3DSA:1.25.40.GENE3D); IPR001623 (G3DSA:1.10.287.GENE3D); IPR013105 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); PF13414 (PFAM); IPR001623 (PFAM); PTHR24078 (PANTHER); IPR026901 (PTHR24078:PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR019734 (PROSITE_PROFILES); IPR001623 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY); IPR001623 (SUPERFAMILY); SSF48452 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
791	c25332_g1_i1_len_1386_path_448_0_353_372_3_54_1385_0	908	prolyl 3-hydroxylase partial	462	1.38E-121	66.30%	0.221	IPR011990 (G3DSA:1.25.40.GENE3D); PTHR13986:SF8 (PANTHER); PTHR13986 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
792	c25356_g1_i1_len_899_path_1113_0_12_1126_13_707_2744_708_898_2	30	low quality protein: titin-like	294	9.78E-134	88.60%	0.1	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR010939 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF149 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
793	c25356_g1_i2_len_1134_path_2225_0_247_1126_248_942_2744_943_1133_0	34	low quality protein: titin-like	373	1.70E-176	88.20%	0.099	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR010939 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897:SF149 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
794	c25356_g1_i3_len_1135_path_1113_0_12_1126_13_707_1821_708_1134_2	29	isoform z	378	2.16E-159	79.20%	0.1	IPR003598 (SMART); IPR003599 (SMART); IPR010939 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897:SF149 (PANTHER); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
795	c25410_g1_i1_len_1899_path_3767_0_109_18_110_1483_1392_1484_1485_1394_1486_1898_5	164	zinc finger protein 37 homolog isoform x1	633	7.19E-70	64.00%	0.14	IPR000210 (SMART); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); G3DSA:3.30.710.10 (GENE3D); IPR013069 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR000210 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); IPR011333 (SUPERFAMILY); TMhelix (TMHMM)

796	c25410_g1_i2_len_1805_path_2_0_15_18_16_1_389_1392_1390_1391_1394_1392_1804_5	160	zinc finger protein 37 homolog	595	2.24E-57	64.00%	0.14	IPR000210 (SMART); IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); G3DSA:3.30.710.10 (GENE3D); IPR013069 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR000210 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); IPR011333 (SUPERFAMILY); TMhelix (TMHMM)
797	c25427_g1_i1_len_1784_path_1812_0_1783_2	712	atpase family aaa domain-containing protein 1-b	588	1.68E-164	77.60%	0.122	IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23074:SF20 (PANTHER); PTHR23074 (PANTHER); IPR003960 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY)
798	c25433_g1_i1_len_2356_path_2384_0_893_3278_894_897_3282_898_962_3347_963_964_3349_965_2355_2	221	neural cell adhesion molecule ncam-140 and ncam-180	777	2.16E-16	57.60%	0.283	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
799	c25446_g1_i1_len_402_path_103_0_45_1523_46_231_50_232_401_1	39	chymotrypsin-like elastase family member 2a	134	3.50E-11	60.00%	0.126	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); PTHR24268:SF72 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
800	c25446_g1_i2_len_465_path_103_0_45_1523_46_231_1561_232_232_1260_233_464_1	37	chymotrypsin-like elastase family member 2a	155	9.83E-12	58.20%	0.126	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); PTHR24268:SF72 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
801	c25446_g1_i4_len_288_path_103_0_45_1523_46_231_1561_232_232_335_233_287_1	14	chymotrypsin-like elastase family member 2a	96	5.15E-18	59.70%	0.126	IPR001314 (PRINTS); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
802	c25506_g2_i1_len_1196_path_1389_0_959_332_960_1061_2447_1062_1195_4	328	26s proteasome non-atpase regulatory subunit 10	399	1.11E-77	71.40%	0.128	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24199 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
803	c25550_g1_i1_len_1928_path_3593_0_675_1688_676_879_1892_880_1927_3	55	otog_mouse ame: full=otogelin flags: precursor	643	3.23E-11	41.60%	0.1	no IPS match
804	c25550_g1_i1_len_1928_path_3593_0_675_1688_676_879_1892_880_1927_4	55	otogelin-like protein	643	4.14E-15	47.60%	0.116	no IPS match
805	c25560_g1_i1_len_1305_path_1333_0_96_1430_97_312_1646_313_1304_2	107	serine threonine-protein kinase sbk1	435	7.03E-148	71.40%	0.325	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24359 (PANTHER); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR000719 (PROSITE_PROFILES); SignalP-TM (SIGNALP GRAM POSITIVE); IPR011009 (SUPERFAMILY)

806	c25560_g1_i2_len_1223_path_2613_0_14_1430_15_230_1646_231_1222_1	104	serine threonine-protein kinase sbk1	408	1.14E-147	70.80%	0.138	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24359 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
807	c25640_g1_i1_len_1234_path_481_0_20_782_21_44_806_45_1233_3	43	dnaj homolog subfamily c member 30-like	412	1.26E-26	51.20%	0.114	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF171 (PANTHER); IPR018253 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
808	c25648_g1_i1_len_1521_path_101_0_1520_5	1319	ferritin 1-like protein a	507	2.51E-45	64.70%	0.312	IPR012347 (G3DSA:1.20.1260.GENE3D); IPR008331 (PFAM); IPR001519 (PANTHER); PTHR11431:SF29 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY)
809	c25692_g1_i1_len_243_path_329_0_7_337_8_18_743_19_242_3	0	zinc finger and scan domain-containing protein 2	81	2.16E-12	61.90%	0.109	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
810	c25811_g1_i1_len_760_path_927_0_323_514_32_4_759_2	17	sortilin-related receptor	253	7.03E-07	58.67%	0.872 Y	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
811	c25811_g1_i2_len_491_path_927_0_323_1248_3_24_439_1364_440_490_2	24	suppressor of tumorigenicity 14 protein	163	1.65E-12	50.30%	0.872 Y	IPR002172 (SMART); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24256:SF20 (PANTHER); PTHR24256 (PANTHER); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
812	c25812_g1_i1_len_1601_path_53_0_1600_2	131	insulin-like growth factor-binding protein 7 precursor	533	6.49E-73	59.10%	0.480 Y	IPR003598 (SMART); IPR002350 (SMART); IPR003599 (SMART); IPR000867 (SMART); IPR000867 (PFAM); IPR002350 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); G3DSA:3.30.60.30 (GENE3D); IPR011390 (PANTHER); PTHR14186:SF9 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR000867 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR009030 (SUPERFAMILY); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
813	c25846_g3_i2_len_294_path_2033_0_122_2156_123_293_4	0	hypothetical protein Y032_0089g2326	98	2.26E-07	62.50%	0.104	IPR011991 (G3DSA:1.10.10.GENE3D)
814	c25868_g1_i1_len_1223_path_2648_0_18_14_19_73_2402_74_202_69_203_900_2579_901_902_771_903_1222_0	130	adp-ribosylation factor-like protein 16	408	2.89E-40	67.90%	0.127	IPR006689 (PRINTS); IPR024156 (SMART); IPR006687 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711:SF42 (PANTHER); PTHR11711 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

815	c25868_g1_i2_len_1090_path_1_0_12_14_13_67_69_68_765_767_766_769_771_770_1089_0	153	adp-ribosylation factor-like protein 16	364	8.18E-41	67.70%	0.114	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF42 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
816	c25879_g1_i1_len_1421_path_6765_0_97_1962_98_1420_5	26	agap000560-pa-like protein	473	0	74.20%	0.102	IPR003593 (SMART); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23076 (PANTHER); PTHR23076:SF47 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
817	c25879_g1_i2_len_3284_path_1_0_1960_1962_1_961_3283_5	398	agap000560-pa-like protein	1094	0	77.80%	0.102	IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR000642 (PFAM); IPR005936 (TIGRFAM); PTHR23076 (PANTHER); PTHR23076:SF47 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR005936 (HAMAP); SSF140990 (SUPERFAMILY); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
818	c25894_g1_i1_len_493_path_4516_0_84_1707_8_5_205_1828_206_231_4100_232_466_1828_467_492_1	12	zinc finger protein	164	6.09E-29	56.30%	0.103	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
819	c25894_g3_i1_len_788_path_2075_0_98_2174_9_9_100_2176_101_138_2214_139_173_2248_174_634_2709_635_706_0	50	zinc finger protein xfin-like isoform x1	263	3.57E-16	60.50%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
820	c25894_g3_i2_len_884_path_2075_0_98_2174_9_9_100_2176_101_138_2214_139_173_2248_174_634_2709_635_706_0	59	zinc finger protein xfin-like isoform x1	289	7.22E-16	60.20%	0.109	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
821	c25919_g1_i1_len_1216_path_1270_0_173_2992_174_175_1446_176_295_3007_296_303_1574_304_304_1575_305_2	338	mitochondrial acyl carrier protein 1 isoform b	393	1.37E-44	66.60%	0.225	IPR009081 (PFAM); IPR009081 (G3DSA:1.10.1200.GENE3D); PTHR20863:SF5 (PANTHER); PTHR20863 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003231 (PRODOM); IPR003231 (HAMAP); IPR009081 (PROSITE_PROFILES); IPR009081 (SUPERFAMILY)
822	c25919_g1_i2_len_1292_path_1270_0_173_2992_174_175_1446_176_295_3007_296_303_1574_304_304_1575_305_2	605	mitochondrial acyl carrier protein 1 isoform b	419	6.66E-48	67.90%	0.225	IPR009081 (G3DSA:1.10.1200.GENE3D); IPR009081 (PFAM); PTHR20863 (PANTHER); PTHR20863:SF5 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003231 (PRODOM); IPR003231 (HAMAP); IPR009081 (PROSITE_PROFILES); IPR009081 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

823	c25919_g1_i3_len_1283_path_1270_0_173_2992_174_175_2608_176_286_3007_287_294_1574_295_295_1575_296_2	508	nadh dehydrogenase isoform 1	416	1.16E-49	76.60%	0.223	IPR009081 (PFAM); IPR009081 (G3DSA:1.10.1200.GENE3D); PTHR20863:SF5 (PANTHER); PTHR20863 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003231 (PRODOM); IPR003231 (HAMAP); IPR009081 (PROSITE_PROFILES); IPR009081 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
824	c25936_g1_i1_len_1508_path_1507_0_507_2014_508_509_13_510_1380_3006_1381_1383_288_6_1384_1507_0	104	stereocilin	503	5.32E-18	46.60%	0.099	IPR026061 (PTHR23412:PANTHER); IPR026664 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
825	c25959_g1_i1_len_390_path_1563_0_389_1	161	transmembrane protease serine 11d-like isoform 2	124	2.90E-06	59.00%	0.16	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR009003 (SUPERFAMILY)
826	c25959_g2_i1_len_522_path_500_0_521_1	424	coagulation factor xi	174	7.48E-28	54.90%	0.466 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
827	c25966_g1_i1_len_831_path_1001_0_830_5	3766	isoform a	271	1.25E-33	55.30%	0.12	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
828	c25966_g2_i1_len_438_path_416_0_50_467_51_52_469_53_437_0	1015	transmembrane protease serine 9	146	2.64E-07	44.60%	0.22	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009003 (SUPERFAMILY)
829	c25996_g1_i1_len_1410_path_1388_0_264_1653_265_274_1663_275_1222_2611_1223_1265_26_54_1266_1409_1	488359	suppressor of tumorigenicity 14 protein homolog	462	6.09E-43	50.10%	0.731 Y	IPR001314 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); PTHR24256 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
830	c26026_g2_i2_len_1815_path_1743_0_554_2298_555_1417_6762_1418_1814_0	482	kunitz bovine pancreatic trypsin inhibitor domain protein	605	7.04E-47	61.60%	0.105	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY)
831	c26041_g1_i1_len_1342_path_189_0_934_2911_935_959_100_960_1316_2931_1317_1341_0	52	abhydrolase domain-containing protein 2 isoform x1	442	1.22E-174	76.90%	0.201	IPR029058 (G3DSA:3.40.50.GENE3D); IPR000073 (PFAM); IPR012020 (PIRSF); PTHR10794:SF35 (PANTHER); PTHR10794 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
832	c26069_g2_i1_len_2718_path_2696_0_2396_509_3_2397_2401_7366_2402_2717_0	150	neuropeptides capa receptor-like	900	3.40E-148	74.00%	0.137	Coil (COILS); IPR005390 (PRINTS); IPR000276 (PRINTS); IPR000276 (PFAM); G3DSA:1.20.1070.10 (GENE3D); PTHR24243:SF107 (PANTHER); PTHR24243 (PANTHER); IPR000276 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017452 (PROSITE_PROFILES); SSF81321 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

843	c26292_g1_i1_len_882_path_952_0_105_1057_1 06_287_96_288_840_1789_841_881_1	60	adp-ribosylation factor-like protein 2	294	1.20E-109	93.70%	0.2	IPR006689 (PRINTS); IPR003579 (SMART); IPR006687 (SMART); IPR024156 (SMART); IPR006689 (PFAM); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF26 (PANTHER); PTHR11711 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
844	c26292_g1_i2_len_700_path_952_0_105_96_106_658_1789_659_699_2	26	adp-ribosylation factor-like protein 2	233	2.26E-69	91.40%	0.1	IPR006689 (PRINTS); IPR024156 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF26 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
845	c26332_g1_i1_len_972_path_2326_0_154_221_155_949_2544_950_971_2	228	isoamyl acetate-hydrolyzing esterase 1 homolog	318	6.23E-65	65.00%	0.228	PF13472 (PFAM); IPR013830 (G3DSA:3.40.50.GENE3D); PTHR14209 (PANTHER); IPR013830 (SUPERFAMILY)
846	c26332_g1_i2_len_1037_path_1_0_219_221_22_0_1014_2544_1015_1036_1	300	isoamyl acetate-hydrolyzing esterase 1 homolog	340	1.97E-73	65.70%	0.119	IPR013830 (G3DSA:3.40.50.GENE3D); IPR001087 (PFAM); PTHR14209 (PANTHER); IPR013830 (SUPERFAMILY)
847	c26347_g1_i1_len_2383_path_2559_0_2045_480_3_2046_2382_3	134	Glucosylceramidase	795	1.53E-161	68.80%	0.126	IPR001139 (PRINTS); IPR013780 (G3DSA:2.60.40.GENE3D); IPR001139 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001139 (PANTHER); PTHR11069:SF7 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY)
848	c26347_g1_i2_len_2581_path_2559_0_2045_460_5_2046_2243_4803_2244_2580_3	176	glucosylceramidase-like	861	5.39E-180	66.20%	0.126	IPR001139 (PRINTS); IPR013780 (G3DSA:2.60.40.GENE3D); IPR001139 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001139 (PANTHER); PTHR11069:SF7 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); SSF51011 (SUPERFAMILY)
849	c26353_g1_i1_len_2323_path_2779_0_2322_4	1095	pdgf- and vegf-related factor 1-like precursor	769	5.26E-53	55.80%	0.309	IPR000072 (SMART); IPR029034 (G3DSA:2.10.90.GENE3D); IPR000072 (PFAM); PTHR11633:SF1 (PANTHER); PTHR11633 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000072 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
850	c26358_g2_i1_len_1506_path_53_0_1505_1	5106	serpin 3	502	1.15E-98	63.50%	0.127	IPR023796 (SMART); G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); G3DSA:3.30.497.10 (GENE3D); IPR000215 (PANTHER); IPR023795 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023796 (SUPERFAMILY)
851	c26368_g1_i1_len_1947_path_221_0_214_435_2_15_216_220_217_893_23_894_929_59_930_19_46_2	244	protein shifted isoform x1	649	0	81.10%	0.145	IPR013309 (PRINTS); IPR003306 (SMART); IPR000742 (SMART); IPR003306 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR013032 (PFAM); PTHR24838 (PANTHER); PTHR24838:SF276 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003306 (PRODOM); IPR000742 (PROSITE_PROFILES); IPR003306 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)

852	c26368_g1_i2_len_1911_path_221_0_214_435_2 15_216_220_217_893_59_894_1910_2	240	wnt inhibitory factor 1	637	0	82.70%	0.145	IPR013309 (PRINTS); IPR000742 (SMART); IPR003306 (SMART); IPR003306 (PFAM); IPR013032 (PFAM); G3DSA:2.170.300.10 (GENE3D); PTHR24838:SF276 (PANTHER); PTHR24838 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003306 (PRODOM); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR003306 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)
853	c26405_g1_i1_len_1887_path_2194_0_1208_340 1_1209_1325_3515_1326_1886_5	271	low quality protein: hemocytin-like	621	4.77E-75	53.50%	0.114	IPR006207 (SMART); IPR006208 (PFAM); PTHR11339:SF229 (PANTHER); PTHR11339 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); SSF57603 (SUPERFAMILY); SSF57603 (SUPERFAMILY)
854	c26409_g1_i1_len_1346_path_409_0_283_692_2 84_462_204_463_1345_5	4475	annexin b10-like	443	2.72E-117	70.90%	0.119	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF47874 (SUPERFAMILY)
855	c26409_g1_i2_len_1346_path_409_0_283_25_28 4_462_204_463_1345_5	2818	annexin b10-like	443	3.82E-116	71.10%	0.119	Coil (COILS); IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF47874 (SUPERFAMILY)
856	c26423_g1_i1_len_2151_path_2129_0_411_2541 _412_413_2543_414_1353_3483_1354_1678_44 76_1679_1681_4479_2	227	btb poz domain-containing protein 17	717	0	75.30%	0.138	IPR011705 (SMART); IPR000210 (SMART); IPR011705 (PFAM); IPR013069 (PFAM); G3DSA:3.30.710.10 (GENE3D); PTHR24410 (PANTHER); PTHR24410:SF9 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000210 (PROSITE_PROFILES); IPR011333 (SUPERFAMILY)
857	c26441_g1_i2_len_3192_path_691_0_1378_2068 _1379_1380_630_1381_2283_3914_2284_2287_ 3920_2288_3191_2	520	myotrophin-like isoform 2	1055	4.97E-52	84.20%	0.141	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24152 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

858	c26472_g1_i1_len_2411_path_275_0_629_904_6_30_648_231_649_2333_2603_2334_2353_143_2354_2410_1	1334	histone 1o	804	7.16E-28	70.00%	0.119	IPR005819 (PRINTS); IPR005818 (SMART); IPR011991 (G3DSA:1.10.10.GENE3D); IPR005818 (PFAM); PTHR11467 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005818 (PROSITE_PROFILES); SSF46785 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
859	c26479_g1_i1_len_1692_path_105_0_1691_0	52	retinol dehydrogenase 13-like	564	3.21E-138	75.10%	0.104	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320:SF55 (PANTHER); PTHR24320 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
860	c26487_g1_i1_len_2042_path_185_0_1245_164_1246_1918_144_1919_2041_2	189	adp-dependent glucokinase-like	680	0	71.30%	0.226	IPR007666 (PFAM); IPR029056 (G3DSA:3.40.1190.GENE3D); IPR007666 (PANTHER); PTHR21208:SF1 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007666 (PROSITE_PROFILES); IPR029056 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
861	c26493_g1_i2_len_890_path_2208_0_793_174_7_94_889_1	22	insulin-like growth factor-binding protein 2-b-like	297	5.52E-25	66.50%	0.11	IPR000867 (SMART); IPR000867 (PFAM); IPR011390 (PANTHER); PTHR14186:SF8 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000867 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
862	c26493_g1_i3_len_1692_path_2208_0_793_3001_794_899_3402_900_1691_1	123	cysteine-rich motor neuron 1	556	3.58E-66	62.00%	0.11	Coil (COILS); IPR000867 (SMART); IPR000867 (PFAM); PTHR14186:SF8 (PANTHER); IPR011390 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000867 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
863	c26516_g1_i1_len_2373_path_2547_0_1484_403_1_1485_1499_88_1500_1531_4076_1532_1533_180_1534_1674_421_0	157	vacuolar protein sorting-associated protein 4a-like	791	0	88.00%	0.183	IPR003593 (SMART); IPR007330 (SMART); IPR015415 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR007330 (PFAM); IPR007330 (G3DSA:1.20.58.GENE3D); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); PTHR23074 (PANTHER); PTHR23074:SF72 (PANTHER); IPR003960 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); IPR007330 (SUPERFAMILY)
864	c26537_g1_i1_len_1057_path_1802_0_741_329_742_870_2670_871_875_2675_876_923_2722_9_24_942_694_943_10_2	22	hyaluronidase precursor	352	1.07E-76	59.10%	0.258	Coil (COILS); IPR018155 (PRINTS); IPR001329 (PRINTS); IPR018155 (PFAM); IPR018155 (PIRSF); IPR013785 (G3DSA:3.20.20.GENE3D); PTHR11769:SF8 (PANTHER); IPR018155 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
865	c26537_g1_i2_len_477_path_53_0_275_329_276_404_2670_405_409_2675_410_457_2722_458_476_1	7	putative hyaluronoglucosaminidase	159	3.55E-07	55.00%	0.18	IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); IPR018155 (PANTHER); IPR017853 (SUPERFAMILY)
866	c26539_g1_i1_len_1433_path_4141_0_483_2733_484_1432_5	47	fas1_scham ame: full=fasciclin-1 ame: full=fasciclin i short=fas i short=fcn flags: precursor	477	1.08E-84	64.90%	0.099	IPR000782 (SMART); IPR000782 (PFAM); IPR000782 (G3DSA:2.30.180.GENE3D); PTHR10900 (PANTHER); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY)
867	c26539_g1_i2_len_1782_path_1903_0_521_74_5_22_832_2733_833_1781_5	99	fasciclin-1 isoform x2	587	5.29E-122	59.40%	0.099	IPR000782 (SMART); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
868	c26539_g1_i3_len_1281_path_53_0_20_74_21_3_31_2733_332_1280_5	39	fas1_scham ame: full=fasciclin-1 ame: full=fasciclin i short=fas i short=fcn flags: precursor	427	1.68E-107	62.90%	0.099	IPR000782 (SMART); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900 (PANTHER); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY)
869	c26550_g1_i1_len_932_path_111_0_838_71_839_845_78_846_909_2110_910_931_3	60	phospholipase a2 isozymes pa3a pa3b pa5	311	4.11E-50	46.80%	0.227	IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PFAM); PTHR12253 (PANTHER); PTHR12253:SF8 (PANTHER); IPR016090 (SUPERFAMILY)

870	c26585_g1_i1_len_2431_path_259_0_2430_1	1151	brain peptide idl-like protein	804	7.66E-110	88.40%	0.103	IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR20967 (PANTHER); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
871	c26589_g1_i1_len_3647_path_5444_0_153_5597_154_3646_0	205	transducin beta-like protein 2	1216	7.95E-143	69.20%	0.129	Coil (COILS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22847 (PANTHER); PTHR22847:SF380 (PANTHER); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
872	c26592_g2_i1_len_382_path_1558_0_160_1719_161_191_2028_192_255_1814_256_306_57_307_313_64_314_381_1	3	cre-ptr-16 protein	127	1.75E-17	57.80%	0.111	PTHR23022 (PANTHER); PTHR23022:SF64 (PANTHER)
873	c26598_g1_i1_len_1306_path_162_0_1305_1	605	glutaminy-peptide cyclotransferase-like	435	9.87E-116	68.90%	0.161	G3DSA:3.40.630.10 (GENE3D); IPR007484 (PFAM); PTHR12283 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY)
874	c26629_g1_i1_len_1996_path_207_0_1995_5	1456	cd166 antigen	659	3.64E-116	56.30%	0.154	IPR003598 (SMART); IPR003599 (SMART); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013162 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11640:SF52 (PANTHER); PTHR11640 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
875	c26639_g2_i1_len_1963_path_3193_0_18_73_19_1387_656_1388_1962_4	266	mitochondrial 10-formyltetrahydrofolate dehydrogenase	649	0	91.80%	0.125	IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699:SF118 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
876	c26639_g2_i2_len_590_path_641_0_14_656_15_589_4	8	cg8665-like partial	197	3.78E-111	90.80%	0.125	IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF118 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
877	c26642_g1_i1_len_236_path_891_0_20_46_21_6_0_202_61_89_998_90_111_252_112_235_2	0	---NA---	78			0.123	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24275 (PANTHER); IPR009003 (SUPERFAMILY)
878	c26693_g1_i1_len_1256_path_475_0_1075_234_1076_1255_0	4	---NA---	419			0.11	no IPS match

887	c26762_g1_i4_len_1892_path_41_0_290_331_29 1_349_3949_350_350_3248_351_647_3545_648 _649_390_650_833_2	237	protein vein	625	8.58E-36	61.10%	0.126	IPR000742 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR11100 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
888	c26798_g1_i1_len_1501_path_2649_0_1500_2	1589	chymotrypsinogen a	493	8.64E-95	58.30%	0.343 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); PTHR24260:SF47 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
889	c26800_g1_i1_len_1179_path_209_0_1178_5	2790	thioredoxin peroxidase	387	3.41E-118	88.20%	0.109	IPR000866 (PFAM); IPR019479 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
890	c26860_g1_i1_len_1256_path_35_0_916_951_91 7_917_34_918_1255_0	6181	thioredoxin peroxidase	413	6.68E-137	86.30%	0.247	IPR012336 (G3DSA:3.40.30.GENE3D); IPR019479 (PFAM); IPR000866 (PFAM); PTHR10681:SF101 (PANTHER); PTHR10681 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
891	c26909_g1_i1_len_2790_path_1_0_2789_3	19756	tissue factor pathway inhibitor 2	925	6.59E-33	62.30%	0.103	Coil (COILS); IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR020901 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR002223 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
892	c26929_g1_i1_len_1983_path_2011_0_1337_334 9_1338_1982_0	32771	calreticulin	654	0	84.20%	0.223	Coil (COILS); IPR001580 (PRINTS); IPR001580 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR11073:SF8 (PANTHER); IPR001580 (PANTHER); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009033 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
893	c27017_g1_i1_len_653_path_186_0_59_1397_60 _652_0	11	calcium calmodulin-dependent protein kinase type 1	212	3.96E-53	96.90%	0.099	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24347:SF116 (PANTHER); IPR020636 (PANTHER); IPR008271 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
894	c27020_g1_i1_len_1048_path_101_0_1047_3	67718	venom allergen 3-like	342	1.40E-49	51.90%	0.450 Y	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
895	c27030_g1_i1_len_388_path_739_0_268_364_26 9_309_1047_310_331_1953_332_387_2	18858	chitinase 2	129	5.21E-34	64.50%	0.112	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
896	c27030_g1_i2_len_300_path_183_0_116_300_11 7_133_317_134_180_364_181_221_1047_222_2 43_1953_244_299_1	4118	chitinase 2	100	3.63E-30	66.30%	0.107	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF45 (PANTHER); IPR001579 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)

897	c27034_g2_i1_len_2081_path_2251_0_638_2890_639_2080_0	100	collagen alpha-1 chain	689	1.31E-92	48.90%	0.103	IPR016186 (G3DSA:3.10.100.GENE3D); IPR008160 (PFAM); IPR010515 (PFAM); PTHR24023 (PANTHER); PTHR24023:SF471 (PANTHER); IPR016187 (SUPERFAMILY)
898	c27034_g2_i1_len_2081_path_2251_0_638_2890_639_2080_5	100	gram-positive signal peptide ysirk family	688	2.70E-28	39.00%	0.098	TMhelix (TMHMM)
899	c27034_g2_i2_len_697_path_2251_0_638_6468_639_696_0	9	collagen alpha-1 chain-like isoform x1	233	1.62E-20	55.00%	0.103	IPR008160 (PFAM); PTHR24023 (PANTHER)
900	c27034_g2_i2_len_697_path_2251_0_638_6468_639_696_5	9	threonine-rich gpi-anchored partial	232	9.10E-20	46.90%	0.155	no IPS match
901	c27035_g1_i1_len_571_path_1318_0_72_1391_7_3_89_1670_90_96_1677_97_114_933_115_242_888_243_254_4_255_2	20036	lpxtg-motif cell wall anchor domain protein	190	8.06E-08	43.33%	0.094	no IPS match
902	c27035_g1_i3_len_493_path_1318_0_72_1391_7_3_89_1670_90_96_1415_97_128_899_129_159_1650_160_163_887_2	6285	hypothetical protein NEMVEDRAFT_v1g149369	164	1.33E-08	51.00%	0.095	no IPS match
903	c27035_g1_i4_len_619_path_1318_0_72_1391_7_3_89_1670_90_96_1415_97_128_899_129_159_930_160_162_933_1_2	29154	spore wall protein 2-like	206	1.19E-07	43.00%	0.095	no IPS match
904	c27055_g1_i1_len_2022_path_53_0_1739_1791_1740_2021_5	93	insulin-like growth factor-binding protein complex acid labile subunit	668	9.73E-85	54.10%	0.13	IPR003591 (SMART); IPR000483 (SMART); SM00365 (SMART); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24373 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
905	c27065_g1_i1_len_1555_path_1830_0_41_25_42_89_73_90_186_1967_187_227_2008_228_262_2043_263_308_3804_1	165	zinc finger protein 235-like	513	1.86E-39	49.10%	0.142	IPR015880 (SMART); IPR003656 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY);
906	c27065_g1_i2_len_1507_path_1830_0_41_73_42_138_1967_139_179_2008_180_214_2043_215_260_3804_261_1506_1	156	zinc finger protein 235-like	497	1.01E-39	49.10%	0.131	IPR003656 (SMART); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY);

907	c27065_g2_i1_len_1703_path_3513_0_133_1967_134_174_6354_175_209_2043_210_255_2089_256_1702_2	104	zinc finger protein 235-like	567	2.32E-28	43.50%	0.099	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
908	c27078_g1_i1_len_2921_path_3161_0_733_260_734_895_422_896_2920_2	283	phospholipase a-2-activating protein	968	0	65.90%	0.122	IPR001680 (SMART); IPR013535 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR015155 (PFAM); IPR001680 (PFAM); PTHR19849 (PANTHER); PTHR19849:SF0 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR013535 (PROSITE_PROFILES); IPR015155 (PROSITE_PROFILES); IPR016024 (SUPERFAMILY); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
909	c27078_g1_i2_len_2759_path_3161_0_733_422_734_2758_2	302	phospholipase a-2-activating	914	0	60.00%	0.122	IPR001680 (SMART); IPR013535 (PFAM); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR015155 (PFAM); PTHR19849 (PANTHER); PTHR19849:SF0 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR013535 (PROSITE_PROFILES); IPR015155 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); IPR016024 (SUPERFAMILY); TMhelix (TMHMM)
910	c27083_g2_i1_len_2659_path_2926_0_558_6050_559_719_3646_720_1682_4609_1683_2658_0	1327	14-3-3 protein zeta isoform x2	887	8.10E-163	95.70%	0.133	Coil (COILS); IPR000308 (PRINTS); IPR023410 (SMART); IPR023410 (PFAM); G3DSA:1.20.190.20 (GENE3D); IPR000308 (PANTHER); IPR023409 (PROSITE_PATTERNS); IPR023409 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023410 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
911	c27088_g1_i1_len_1624_path_1735_0_328_2063_329_329_117_330_883_2616_884_884_71_885_1132_2863_1133_1_5	107	macro domain-containing protein 2	541	1.83E-83	69.40%	0.101	Coil (COILS); IPR002589 (SMART); IPR002589 (PFAM); G3DSA:3.40.220.10 (GENE3D); PTHR11106 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002589 (PROSITE_PROFILES); SSF52949 (SUPERFAMILY); TMhelix (TMHMM)
912	c27088_g1_i2_len_824_path_117_0_553_71_554_801_3442_802_823_3	16	o-acetyl-adp-ribose deacetylase macrod2-like	275	1.70E-65	78.80%	0.114	IPR002589 (SMART); G3DSA:3.40.220.10 (GENE3D); IPR002589 (PFAM); PTHR11106 (PANTHER); IPR002589 (PROSITE_PROFILES); SSF52949 (SUPERFAMILY)
913	c27096_g1_i1_len_2393_path_241_0_1105_1346_1106_1122_198_1123_1771_2679_1772_2392_0	173	inactive dipeptidyl peptidase 10	798	0	62.10%	0.112	IPR002469 (G3DSA:2.140.10.GENE3D); IPR001375 (PFAM); IPR002469 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11731 (PANTHER); PTHR11731:SF22 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF82171 (SUPERFAMILY); IPR029058 (SUPERFAMILY)
914	c27101_g1_i1_len_1141_path_1326_0_1140_1	140921	transmembrane protease serine 4	380	1.10E-39	52.30%	0.317	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
915	c27103_g2_i2_len_679_path_3525_0_19_2871_2_0_112_2964_113_457_21_458_678_1	33	zinc finger protein 717-like	226	2.67E-12	47.40%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)

916	c27103_g2_i3_len_1414_path_2118_0_505_3568_506_508_2625_509_754_2871_755_847_2964_848_1192_21_1193_1	57	zinc finger protein 717-like	471	1.40E-11	45.60%	0.282	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
917	c27129_g1_i1_len_1139_path_1185_0_294_1480_295_295_1481_296_1138_2	220	vacuolar-sorting protein snf8-like	379	1.23E-121	83.60%	0.121	Coil (COILS); IPR011991 (G3DSA:1.10.10.GENE3D); IPR011991 (G3DSA:1.10.10.GENE3D); IPR007286 (PFAM); IPR007286 (PANTHER); PTHR12806:SF0 (PANTHER); SSF46785 (SUPERFAMILY); SSF46785 (SUPERFAMILY)
918	c27138_g1_i1_len_2047_path_1_0_441_4358_44_2_447_449_448_461_463_462_836_838_837_20_46_2	169	serine threonine-protein phosphatase 6 regulatory ankyrin repeat subunit c-like	682	1.60E-95	55.00%	0.219	IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
919	c27156_g1_i1_len_1653_path_3573_0_175_318_176_635_778_636_1167_1308_1168_1299_1440_1300_1652_1	802	ectonucleotide pyrophosphatase phosphodiesterase family member 6	545	1.89E-119	55.50%	0.113	IPR017849 (G3DSA:3.40.720.GENE3D); IPR002591 (PFAM); IPR024873 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY)
920	c27156_g1_i2_len_553_path_3946_0_20_778_21_552_1	71	ectonucleotide pyrophosphatase phosphodiesterase family member 7-like	184	2.44E-30	56.30%	0.136	IPR017849 (G3DSA:3.40.720.GENE3D); IPR002591 (PFAM); IPR024873 (PANTHER); IPR017850 (SUPERFAMILY)
921	c27156_g1_i3_len_1726_path_69_0_248_318_24_9_708_778_709_1240_1308_1241_1372_1440_1_373_1725_2	771	ectonucleotide pyrophosphatase phosphodiesterase family member 6	569	1.95E-119	55.60%	0.228	IPR006612 (SMART); IPR017849 (G3DSA:3.40.720.GENE3D); IPR006612 (PFAM); IPR002591 (PFAM); IPR024873 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006612 (PROSITE_PROFILES); SSF57716 (SUPERFAMILY); IPR017850 (SUPERFAMILY)
922	c27162_g1_i1_len_313_path_176_0_312_5	21533	snake venom serine protease da-36	97	4.06E-06	76.00%	0.102	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24275 (PANTHER); IPR009003 (SUPERFAMILY)
923	c27200_g1_i1_len_1570_path_1648_0_1569_2	314	hydroxyacyl dehydrogenase	510	6.58E-129	83.60%	0.141	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF251 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
924	c27203_g1_i1_len_660_path_1558_0_534_305_5_35_659_0	11	peptidyl-prolyl cis-trans isomerase ppif	220	2.93E-37	53.50%	0.108	IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF202 (PANTHER); IPR024936 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); TMhelix (TMHMM)
925	c27203_g1_i2_len_1140_path_1558_0_534_2092_535_582_129_583_839_446_840_1139_0	107	peptidyl-prolyl cis-trans	375	1.80E-36	53.50%	0.108	IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF202 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
926	c27232_g1_i1_len_398_path_789_0_31_818_32_32_102_33_56_842_57_302_1084_303_354_113_6_355_397_5	686	carboxypeptidase b-like	132	4.76E-13	53.80%	0.683 Y	IPR003146 (G3DSA:3.30.70.GENE3D); IPR003146 (PFAM); PTHR11705 (PANTHER); SignalP-noTM (SIGNALP_EUK); IPR009020 (SUPERFAMILY)
927	c27255_g3_i2_len_1545_path_1_0_378_380_37_9_1175_13509_1176_1178_13512_1179_1544_5	601	nucleoporin seh1 isoform x2	509	0	84.70%	0.281	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR11024 (PANTHER); PTHR11024:SF3 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)

928	c27256_g5_i1_len_2117_path_2873_0_163_6065_164_1085_6987_1086_1526_7426_1527_1880_1904_1881_2116_2	185	von willebrand domain-containing protein	693	1.42E-133	55.90%	0.202	IPR002035 (SMART); IPR002035 (G3DSA:3.40.50.GENE3D); PF13768 (PFAM); PTHR10338 (PANTHER); PTHR10338:SF95 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
929	c27256_g5_i2_len_1440_path_2873_0_163_6065_164_1085_7426_1086_1439_2	48	von willebrand domain-containing protein	474	9.71E-105	59.70%	0.202	IPR002035 (SMART); PF13768 (PFAM); IPR002035 (G3DSA:3.40.50.GENE3D); PTHR10338:SF95 (PANTHER); PTHR10338 (PANTHER); IPR002035 (PROSITE_PROFILES); IPR002035 (SUPERFAMILY)
930	c27266_g1_i1_len_1617_path_1645_0_941_2585_942_954_2598_955_1192_2836_1193_1198_2842_1199_1616_1	211	beta- -galactosyltransferase 7	532	1.92E-126	72.30%	0.229	IPR003859 (PRINTS); IPR027995 (PFAM); IPR027791 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); PTHR19300:SF1 (PANTHER); IPR003859 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
931	c27267_g1_i1_len_1529_path_1552_0_172_1725_173_189_1742_190_306_39_307_736_2288_737_738_2290_739_13_1	168	upf0378 protein kiaa0100	504	2.87E-61	54.20%	0.091	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
932	c27281_g1_i1_len_2082_path_1469_0_1364_2831_1365_1367_1351_1368_1505_2970_1506_1508_1468_1509_2037_2	247	lysine--trna ligase isoform x2	687	0	86.50%	0.109	Coil (COILS); IPR018149 (PRINTS); IPR004365 (PFAM); IPR004364 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); G3DSA:3.30.930.10 (GENE3D); IPR002313 (TIGRFAM); IPR002313 (PIRSF); PTHR22594:SF4 (PANTHER); IPR018150 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002313 (HAMAP); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY); IPR012340 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
933	c27289_g4_i1_len_2179_path_1_0_374_376_375_398_400_399_1198_1200_1199_1230_1232_1231_1489_1491_1490_5	87	zinc finger protein 501 isoform x2	720	7.27E-11	60.20%	0.1	IPR000210 (SMART); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013069 (PFAM); G3DSA:3.30.710.10 (GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR000210 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); IPR011333 (SUPERFAMILY)
934	c27302_g1_i2_len_1968_path_4457_0_125_4583_126_1330_1159_1331_1967_5	185	cytochrome p450	656	0	69.50%	0.333	Coil (COILS); IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24290:SF0 (PANTHER); PTHR24290 (PANTHER); IPR017972 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
935	c27305_g4_i1_len_1536_path_2484_0_102_2263_103_131_2292_132_219_2380_220_1138_2937_1139_1535_0	138	ankyrin repeat family a protein 2	507	3.55E-72	67.70%	0.135	Coil (COILS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); PTHR24124:SF6 (PANTHER); PTHR24124 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
936	c27353_g1_i1_len_1350_path_4590_0_755_5367_756_756_5368_757_758_92_759_1349_2	6127	ferritin	443	1.55E-82	84.70%	0.338	Coil (COILS); IPR012347 (G3DSA:1.20.1260.GENE3D); IPR008331 (PFAM); IPR001519 (PANTHER); IPR014034 (PROSITE_PATTERNS); IPR014034 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
937	c27364_g1_i1_len_1296_path_291_0_320_200_321_1216_1668_1217_1295_0	215	venom allergen 5-like	427	2.95E-15	50.40%	0.11	IPR001283 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); PTHR10334:SF153 (PANTHER); IPR001283 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

Supplementary Table 8

944	c27439_g2_i1_len_1679_path_357_0_1154_1512_1155_1355_3672_1356_1678_4	54	alcohol dehydrogenase	560	1.12E-113	66.10%	0.107	IPR020471 (PRINTS); IPR023210 (G3DSA:3.20.20.GENE3D); IPR023210 (PFAM); IPR001395 (PANTHER); PTHR11732:SF183 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR023210 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
945	c27443_g1_i2_len_2155_path_1_0_1023_1025_1_024_1490_1492_1491_1612_3381_1613_1697_3_182_1698_1721_348_2	152	dnaj homolog subfamily c member 7	718	0	74.50%	0.103	IPR001623 (PRINTS); IPR001623 (SMART); IPR019734 (SMART); IPR013105 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); IPR001623 (PFAM); PF13414 (PFAM); IPR011990 (G3DSA:1.25.40.GENE3D); IPR019734 (PFAM); PTHR24078:SF140 (PANTHER); PTHR24078 (PANTHER); IPR018253 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR019734 (PROSITE_PROFILES); IPR013026 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR001623 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); IPR019734 (PROSITE_PROFILES); SSF48452 (SUPERFAMILY); IPR001623 (SUPERFAMILY); SSF48452 (SUPERFAMILY); TMhelix (TMHMM)
946	c27443_g1_i3_len_715_path_3004_0_18_1025_1_9_485_1492_486_607_3099_608_690_3182_691_714_2	45	dnaj homolog subfamily c member 7	238	9.51E-60	77.90%	0.102	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF139 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
947	c27452_g1_i2_len_846_path_4526_0_133_1880_134_643_228_644_845_3	82	map7 domain-containing protein 1-like isoform x1	276	6.77E-11	55.00%	0.126	Coil (COILS); Coil (COILS)
948	c27452_g1_i4_len_1396_path_1196_0_683_1880_684_1193_228_1194_1395_3	71	map7 domain-containing protein 1-like isoform x12	460	6.49E-11	50.50%	0.126	Coil (COILS); Coil (COILS)
949	c27458_g1_i1_len_1151_path_1073_0_304_2213_305_435_2583_436_1150_2	113	acyl- delta desaturase	383	1.13E-163	76.50%	0.137	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351 (PANTHER); PTHR11351:SF28 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
950	c27458_g1_i2_len_1020_path_1073_0_304_2583_305_1019_0	115	acyl- delta desaturase	340	8.77E-118	82.70%	0.331	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351:SF28 (PANTHER); PTHR11351 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
951	c27512_g1_i1_len_1535_path_315_0_175_490_1_76_215_47_216_260_573_261_1501_1807_1502_1534_1	1124	serine protease 56	506	7.92E-11	43.90%	0.103	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
952	c27512_g1_i2_len_1525_path_315_0_175_490_1_76_215_47_216_260_573_261_1501_3478_1502_1524_1	1088	serine protease 56	503	7.35E-11	43.90%	0.103	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
953	c27520_g1_i1_len_1507_path_105_0_1388_1490_1389_1506_0	145668	carboxypeptidase b-like	495	2.40E-126	62.40%	0.332	IPR000834 (PRINTS); IPR000834 (SMART); IPR003146 (PFAM); IPR003146 (G3DSA:3.30.70.GENE3D); G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); IPR000834 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); IPR009020 (SUPERFAMILY); TMhelix (TMHMM)

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962	c27635_g1_i1_len_1723_path_199_0_527_722_5 28_738_125_739_1273_1466_1274_1275_78_12 76_1722_1	195	3-hydroxyisobutyrate mitochondrial	574	9.07E-151	81.30%	0.233	IPR006115 (PFAM); IPR029154 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); IPR011548 (TIGRFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22981:SF51 (PANTHER); PTHR22981 (PANTHER); IPR002204 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008927 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
963	c27635_g1_i2_len_1063_path_199_0_527_125_5 28_1062_1	50	3-hydroxyisobutyrate mitochondrial	354	1.11E-50	75.90%	0.233	IPR006115 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR22981:SF44 (PANTHER); PTHR22981 (PANTHER); IPR002204 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY)
964	c27644_g1_i1_len_1864_path_1931_0_454_2386 _455_511_2442_512_513_66_514_591_2521_59 2_1191_18_1192_11_0	300	notchless protein homolog 1	615	5.39E-169	79.80%	0.119	IPR020472 (PRINTS); IPR001680 (SMART); IPR012972 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19848 (PANTHER); PTHR19848:SF0 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
965	c27644_g1_i1_len_1864_path_1931_0_454_2386 _455_511_2442_512_513_66_514_591_2521_59 2_1191_18_1192_11_1	300	notchless protein homolog 1 isoform x2	615	5.69E-69	89.80%	0.106	IPR001632 (PRINTS); IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19848 (PANTHER); PTHR19848:SF0 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
966	c27644_g1_i2_len_1055_path_1931_0_454_2521 _455_1054_1	45	notchless protein homolog 1 isoform x1	352	2.37E-96	80.80%	0.106	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19848 (PANTHER); PTHR19848:SF0 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
967	c27655_g1_i1_len_2712_path_2123_0_1633_516 8_1634_1650_3757_1651_1750_3857_1751_183 8_3945_1839_2137_0	340	agap005714-pa-like protein	897	6.51E-146	53.90%	0.099	IPR000742 (SMART); IPR000436 (SMART); IPR001881 (SMART); PF14670 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR003410 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR001881 (PFAM); IPR023413 (G3DSA:2.40.155.GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PTHR24034 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000742 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR003410 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR009030 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
968	c27655_g1_i2_len_2607_path_2123_0_1633_375 7_1634_1733_3945_1734_2032_4244_2033_221 0_5960_2211_2211_0	383	agap005714-pa-like protein	862	5.82E-152	53.60%	0.099	IPR000436 (SMART); IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR023413 (G3DSA:2.40.155.GENE3D); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); PF14670 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR003410 (PFAM); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR24034 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000436 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR003410 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR009030 (SUPERFAMILY); IPR000436 (SUPERFAMILY)

969	c27655_g1_i3_len_2624_path_2123_0_1633_516 8_1634_1650_3757_1651_1750_3945_1751_204 9_4244_2050_2227_0	316	agap005714-pa-like protein	868	3.25E-146	53.90%	0.099	IPR000436 (SMART); IPR000742 (SMART); IPR001881 (SMART); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR003410 (PFAM); IPR023413 (G3DSA:2.40.155.GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); PF14670 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR24034 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000436 (PROSITE_PROFILES); IPR003410 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR000436 (SUPERFAMILY); IPR009030 (SUPERFAMILY); IPR000436 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)
970	c27655_g1_i4_len_2695_path_2123_0_1633_375 7_1634_1733_3857_1734_1821_3945_1822_212 0_4244_2121_2298_0	381	agap005714-pa-like protein	892	8.45E-156	52.70%	0.099	IPR000742 (SMART); IPR001881 (SMART); IPR000436 (SMART); IPR023413 (G3DSA:2.40.155.GENE3D); IPR003410 (PFAM); PF14670 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR001881 (PFAM); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24034 (PANTHER); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR003410 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY); IPR000436 (SUPERFAMILY); SSF57196 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR000436 (SUPERFAMILY); SSF57196 (SUPERFAMILY)
971	c27666_g1_i1_len_2487_path_2967_0_2486_3	17601	membrane metallo-endopeptidase-like 1-like	821	0	67.90%	0.125	IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); IPR008753 (PFAM); IPR000718 (PANTHER); PTHR11733:SF113 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
972	c27716_g1_i1_len_606_path_950_0_423_1374_4 24_474_1425_475_605_1	603	atrial natriuretic peptide-converting enzyme	197	3.67E-13	52.50%	0.104	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); PTHR10529:SF208 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
973	c27718_g2_i1_len_1344_path_3041_0_934_77_9 35_1343_5	81	peptidyl-prolyl cis-trans isomerase nima-interacting 1-like	448	4.42E-70	85.10%	0.102	Coil (COILS); IPR001202 (SMART); IPR000297 (PFAM); G3DSA:3.10.50.40 (GENE3D); G3DSA:2.20.70.10 (GENE3D); IPR001202 (PFAM); PTHR10657 (PANTHER); IPR001202 (PROSITE_PATTERNS); IPR023058 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000297 (PROSITE_PROFILES); IPR001202 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY); IPR001202 (SUPERFAMILY); TMhelix (TMHMM)

974	c27732_g1_i1_len_1242_path_3129_0_40_1858_41_821_130_822_1241_0	162	ferritin 2 light chain homologue	414	4.28E-35	53.70%	0.621 Y	IPR012347 (G3DSA:1.20.1260.GENE3D); IPR008331 (PFAM); IPR001519 (PANTHER); PTHR11431:SF28 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR009040 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR009078 (SUPERFAMILY)
975	c27732_g1_i2_len_1474_path_1585_0_272_1858_273_1053_130_1054_1473_1	226	ferritin 2 light chain homologue	491	8.54E-35	53.50%	0.104	IPR008331 (PFAM); IPR012347 (G3DSA:1.20.1260.GENE3D); IPR001519 (PANTHER); PTHR11431:SF28 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009040 (PROSITE_PROFILES); IPR009078 (SUPERFAMILY)
976	c27733_g1_i1_len_1340_path_1538_0_436_68_4_37_454_86_455_786_2319_787_788_111_789_1_316_3005_1317_133_1	1007	projectin short variant	441	4.57E-40	49.60%	0.1	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
977	c27746_g1_i1_len_2350_path_1293_0_921_4036_922_1303_4418_1304_1381_4496_1382_1559_4674_1560_1561_46_1	253	annexin b9-like isoform x1	778	8.96E-133	60.00%	0.208	IPR001464 (PRINTS); IPR018502 (SMART); IPR018502 (PFAM); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); IPR018502 (G3DSA:1.10.220.GENE3D); PTHR10502 (PANTHER); IPR018252 (PROSITE_PATTERNS); IPR018252 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF47874 (SUPERFAMILY); TMhelix (TMHMM)
978	c27749_g1_i1_len_1065_path_961_0_19_789_20_68_838_69_467_439_468_628_2602_629_1064_0	1674	low quality protein: glutathione peroxidase 1-like	350	6.24E-87	79.30%	0.138	IPR000889 (PRINTS); IPR000889 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PANTHER); PTHR11592:SF23 (PANTHER); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
979	c27749_g1_i2_len_1067_path_767_0_21_789_22_70_838_71_469_439_470_630_2602_631_1066_2	1690	low quality protein: glutathione peroxidase 1-like	350	6.24E-87	79.30%	0.125	IPR000889 (PRINTS); IPR000889 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR11592:SF23 (PANTHER); IPR000889 (PANTHER); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
980	c27749_g1_i3_len_1018_path_2023_0_21_838_2_2_420_439_421_581_2602_582_1017_1	1796	low quality protein: glutathione peroxidase 1-like	334	8.55E-87	78.50%	0.139	IPR000889 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PFAM); PTHR11592:SF23 (PANTHER); IPR000889 (PANTHER); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
981	c27749_g1_i4_len_552_path_185_0_190_3545_1_91_205_390_206_208_75_209_255_439_256_41_6_3583_417_437_36_0	162	low quality protein: glutathione peroxidase 1-like	179	1.46E-22	73.70%	0.194	IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PANTHER); PTHR11592:SF24 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
982	c27762_g1_i1_len_1579_path_43_0_929_973_93_0_1048_1092_1049_1050_1094_1051_1138_118_1_1139_1139_21_11_5	396	dnaj homolog subfamily c member 9	520	1.67E-85	75.60%	0.115	Coil (COILS); Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF166 (PANTHER); IPR018253 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
983	c27797_g1_i1_len_1903_path_155_0_21_29_22_82_4094_83_1902_1	293	torsin-1b-like isoform x2	628	8.52E-35	53.60%	0.266	IPR027417 (G3DSA:3.40.50.GENE3D); IPR010448 (PFAM); IPR010448 (PANTHER); IPR030553 (PTHR10760:PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
984	c27797_g1_i2_len_1841_path_4022_0_20_4094_21_1840_2	293	torsin-1b-like isoform x2	607	8.54E-35	53.20%	0.271	IPR027417 (G3DSA:3.40.50.GENE3D); IPR010448 (PFAM); IPR030553 (PTHR10760:PANTHER); IPR010448 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

985	c27823_g1_i1_len_3207_path_1_0_254_256_255_2265_2267_2266_3206_2	243	serine threonine-protein phosphatase 2a catalytic subunit alpha isoform	1069	0	97.70%	0.171	Coil (COILS); IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668:SF216 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
986	c27844_g1_i1_len_483_path_1_0_146_148_147_175_944_176_246_1015_247_336_1105_337_48_2_3	1398	carboxypeptidase b	161	5.36E-26	70.40%	0.14	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
987	c27844_g1_i1_len_483_path_1_0_146_148_147_175_944_176_246_1015_247_336_1105_337_48_2_4	1398	carboxypeptidase b-like	161	5.09E-27	75.70%	0.195	G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PTHR11705 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53187 (SUPERFAMILY); TMhelix (TMHMM)
988	c27844_g2_i1_len_492_path_2133_0_155_148_1_56_184_177_185_491_4	1312	carboxypeptidase b	164	5.19E-65	69.40%	0.12	IPR000834 (SMART); IPR000834 (PFAM); G3DSA:3.40.630.10 (GENE3D); PTHR11705 (PANTHER); SSF53187 (SUPERFAMILY)
989	c27856_g1_i3_len_1113_path_1853_0_142_1996_143_395_334_396_535_2607_536_1112_2	194	ankyrin repeat domain-containing protein 12-like isoform x1	371	1.43E-35	65.10%	0.462 Y	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24149 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
990	c27856_g1_i4_len_1333_path_1853_0_142_1996_143_395_334_396_535_2388_536_538_468_53_9_755_2607_756_13_2	363	ankyrin repeat domain-containing protein partial	444	1.18E-48	71.40%	0.462 Y	IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24149 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
991	c27856_g1_i5_len_1261_path_3256_0_70_1996_71_323_334_324_463_2388_464_466_468_467_683_2607_684_1260_2	327	ankyrin repeat domain-containing protein partial	420	1.97E-49	66.20%	0.252	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR002110 (PFAM); PTHR24149 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
992	c27866_g1_i1_len_674_path_2403_0_4_2408_5_5_520_6_673_3	18	dbh-like monooxygenase protein 1-like protein	225	3.50E-15	66.70%	0.177	IPR005018 (PFAM); IPR000945 (PANTHER); PTHR10157:SF23 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR005018 (PROSITE_PROFILES)
993	c27869_g2_i1_len_1688_path_3725_0_170_1621_171_374_5600_375_375_1826_376_510_1961_511_1687_1	151	wd repeat domain-containing protein 83	551	5.62E-139	80.10%	0.114	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22842 (PANTHER); IPR019775 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
994	c27869_g2_i2_len_1444_path_1558_0_62_1621_63_266_1961_267_1443_2	149	wd repeat domain-containing protein 83	475	5.59E-99	78.30%	0.454 Y	IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22842 (PANTHER); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
995	c27884_g1_i1_len_424_path_1_0_423_2	17222	aael000389- partial	141	6.37E-29	73.00%	0.274	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)

996	c2789_g1_i1_len_548_path_526_0_438_965_439_547_0	23	kunitz and ntr domain-containing protein 2	183	4.55E-15	68.20%	0.467 Y	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); TMhelix (TMHMM)
997	c2789_g1_i2_len_493_path_526_0_438_1074_439_492_0	18	protease inhibitor-like	165	1.65E-15	67.40%	0.467 Y	IPR002223 (PRINTS); IPR002223 (SMART); IPR002223 (PFAM); IPR002223 (G3DSA:4.10.410.GENE3D); PTHR10083 (PANTHER); IPR020901 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002223 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); TMhelix (TMHMM)
998	c27942_g1_i1_len_1746_path_1878_0_99_1978_100_783_2657_784_785_102_786_1745_2	559	alpha-aminoadipic semialdehyde dehydrogenase	576	0	83.70%	0.17	IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); PTHR11699 (PANTHER); PTHR11699:SF144 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
999	c27960_g1_i1_len_1144_path_343_0_813_1151_814_822_340_823_900_1236_901_910_196_911_1143_0	316580	plasma kallikrein	382	4.99E-53	55.90%	0.444 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1000	c27977_g1_i1_len_965_path_1031_0_403_2055_404_538_2352_539_928_1822_929_964_1	90	peptidyl-prolyl cis-trans isomerase-like 1	322	6.28E-92	71.30%	0.153	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY); IPR029000 (SUPERFAMILY)
1001	c27977_g1_i2_len_831_path_1031_0_403_2352_404_793_1821_794_794_1822_795_830_1	251	peptidyl-prolyl cis-trans isomerase-like 1	265	1.48E-100	91.30%	0.153	IPR002130 (PRINTS); IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1002	c27978_g1_i1_len_1466_path_3566_0_93_1742_94_250_3978_251_256_1905_257_1465_2	355	leucine-rich repeat-containing protein 57	483	1.11E-96	75.60%	0.268	IPR003591 (SMART); IPR001611 (PFAM); IPR025875 (PFAM); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
1003	c27978_g1_i3_len_1694_path_1546_0_195_1742_196_352_3156_353_478_3978_479_484_1905_485_1693_2	340	leucine-rich repeat-containing protein 57	559	2.16E-93	76.10%	0.218	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR025875 (PFAM); PTHR23155 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
1004	c27978_g1_i4_len_1592_path_3566_0_93_1742_94_250_3156_251_376_3978_377_382_1905_383_1591_2	333	leucine-rich repeat-containing protein 57	525	5.64E-94	76.10%	0.268	IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR025875 (PFAM); PTHR23155 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)

1005	c27978_g1_i5_len_1568_path_1546_0_195_1742_196_352_3978_353_358_1905_359_1567_2	382	leucine-rich repeat-containing protein 57	517	4.86E-96	75.60%	0.218	IPR003591 (SMART); IPR025875 (PFAM); G3DSA:3.80.10.10 (GENE3D); G3DSA:3.80.10.10 (GENE3D); IPR001611 (PFAM); PTHR23155 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
1006	c27990_g1_i1_len_1575_path_321_0_311_100_3_12_1574_4	319	receptor-type tyrosine-protein phosphatase n2	515	0	86.40%	0.232	IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134 (PANTHER); PTHR19134:SF2 (PANTHER); IPR016130 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); TMhelix (TMHMM)
1007	c27990_g1_i2_len_2998_path_321_0_311_632_3_12_779_268_780_1734_100_1735_2997_4	2414	receptor-type tyrosine-protein phosphatase n2	989	0	87.30%	0.232	IPR000242 (PRINTS); IPR000242 (SMART); IPR003595 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134:SF2 (PANTHER); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1008	c28000_g2_i1_len_1299_path_1487_0_459_1947_460_596_2084_597_641_1375_642_714_1448_715_746_2231_747_0	347	huga_polan ame: full=hyaluronidase short=hya ame: full=hyaluronoglucosaminidase ame: allergen=pol a 2 flags: partial	433	6.05E-73	57.40%	0.254	IPR018155 (PRINTS); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); IPR018155 (PANTHER); PTHR11769:SF8 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY)
1009	c28000_g2_i2_len_1299_path_1487_0_459_4306_460_550_1486_551_596_2084_597_641_2128_642_714_1448_715_0	630	hyaluronidase-like	433	9.52E-74	56.90%	0.254	IPR018155 (PRINTS); IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); PTHR11769:SF8 (PANTHER); IPR018155 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY)
1010	c28011_g1_i1_len_2870_path_2848_0_1818_466_7_1819_1820_4669_1821_1870_4719_1871_187_1_4720_1872_2240_2	635	hemocytin isoform x1	951	3.85E-26	41.20%	0.118	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM)
1011	c28023_g1_i1_len_1812_path_53_0_580_634_58_1_581_635_582_740_794_741_742_796_743_91_5_969_916_919_973_2	482	reticulocalbin-2	598	3.85E-131	73.80%	0.308	IPR002048 (SMART); IPR011992 (G3DSA:1.10.238.GENE3D); IPR011992 (PFAM); PTHR10827:SF48 (PANTHER); PTHR10827 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); SSF47473 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1012	c28024_g3_i1_len_1205_path_7135_0_139_4139_140_1204_4	71	acyl- delta desaturase	402	5.69E-104	70.80%	0.178	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1013	c28024_g3_i2_len_1789_path_3415_0_186_3602_187_723_4139_724_1788_4	171	acyl- delta desaturase	596	1.77E-128	72.50%	0.178	IPR015876 (PRINTS); IPR005804 (PFAM); PTHR11351:SF28 (PANTHER); PTHR11351 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1014	c28026_g1_i1_len_1419_path_275_0_201_222_2_02_437_52_438_584_853_585_587_140_588_14_18_2	394	sortilin-related receptor-like	467	2.49E-17	59.10%	0.118	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1015	c28042_g1_i1_len_1155_path_1458_0_70_1529_71_188_1647_189_241_1698_242_300_135_301_337_1793_338_510_3	84621	chymotrypsinogen 2-like	385	5.59E-46	56.70%	0.414 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1016	c28049_g1_i1_len_1051_path_1685_0_580_2263_581_609_2292_610_731_2413_732_732_536_7_33_1050_1	235	trypsin i-p1-like	350	2.36E-31	56.20%	0.102	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1017	c28049_g1_i2_len_1280_path_1685_0_580_268_581_693_554_694_1279_1	165	transmembrane protease serine 9-like	421	2.24E-31	56.20%	0.102	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1018	c28057_g2_i1_len_2240_path_2720_0_1272_399_2_1273_1466_23_1467_1622_4341_1623_1630_4349_1631_1702_50_0	164	arylsulfatase a-like	747	0	68.40%	0.177	PF14707 (PFAM); IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); PTHR10342:SF22 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1019	c28057_g2_i2_len_2149_path_2720_0_1272_399_2_1273_1466_23_1467_1622_6104_1623_1627_4349_1628_1699_44_0	194	arylsulfatase a-like	717	0	68.00%	0.177	PF14707 (PFAM); G3DSA:3.30.1120.10 (GENE3D); IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342:SF22 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1020	c28057_g2_i3_len_1958_path_2720_0_1272_23_1273_1428_4341_1429_1436_4349_1437_1508_4421_1509_1923_48_0	129	arylsulfatase a-like	653	5.04E-153	71.20%	0.177	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF22 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR024607 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1021	c28064_g1_i1_len_2391_path_105_0_2390_0	228	esterase fe4	797	2.85E-144	58.20%	0.389 Y	IPR002018 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11559 (PANTHER); IPR019826 (PROSITE_PATTERNS); IPR019819 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1022	c28068_g1_i1_len_2660_path_127_0_381_509_3_82_1381_1509_1382_1382_1510_1383_2462_9_0_2463_2659_1	959	n-acetylated-alpha-linked acidic dipeptidase	881	0	59.30%	0.235	IPR003137 (PFAM); IPR007365 (PFAM); IPR007365 (G3DSA:1.20.930.GENE3D); G3DSA:3.40.630.10 (GENE3D); G3DSA:3.50.30.30 (GENE3D); IPR007484 (PFAM); PTHR10404 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53187 (SUPERFAMILY); SSF52025 (SUPERFAMILY); IPR007365 (SUPERFAMILY); TMhelix (TMHMM)
1023	c28078_g1_i1_len_2080_path_4427_0_137_2511_138_163_2537_164_894_6792_895_897_3268_898_1734_4105_2	119	apolipoprotein d-like	688	1.04E-57	62.70%	0.766 Y	IPR003057 (PRINTS); IPR012674 (G3DSA:2.40.128.GENE3D); IPR000566 (PFAM); PTHR10612:SF7 (PANTHER); PTHR10612 (PANTHER); IPR022272 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)
1024	c28078_g2_i1_len_1161_path_2291_0_219_2511_220_245_4726_246_1160_0	108	apolipoprotein d-like	387	1.11E-41	60.50%	0.205	IPR003057 (PRINTS); IPR012674 (G3DSA:2.40.128.GENE3D); IPR000566 (PFAM); PTHR10612:SF7 (PANTHER); PTHR10612 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011038 (SUPERFAMILY); TMhelix (TMHMM)
1025	c28096_g1_i1_len_2264_path_2343_0_542_2886_543_1489_3833_1490_1703_4045_1704_1823_78_1824_2263_0	76	cytochrome p450 6k1-like	755	3.68E-126	59.00%	0.131	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24292 (PANTHER); PTHR24292:SF24 (PANTHER); IPR017972 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1026	c28106_g1_i1_len_1066_path_1_0_1038_3131_1_039_1039_1041_1040_1065_2	10974	low quality protein: galectin-4	355	5.60E-52	50.40%	0.157	IPR001079 (SMART); IPR001079 (SMART); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001079 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR11346 (PANTHER); IPR001079 (PROSITE_PROFILES); IPR001079 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1027	c28113_g1_i1_len_2354_path_1_0_370_4988_37_1_2353_4	305	trichohyalin isoform x4	772	3.15E-150	66.50%	0.1	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR027881 (PFAM); PTHR15742 (PANTHER); PTHR15742:SF0 (PANTHER)
1028	c28129_g3_i1_len_1944_path_9887_0_1098_795_0_1099_1136_11022_1137_1139_1953_1140_19_43_2	236	cation channel sperm-associated protein subunit gamma	642	2.68E-08	52.50%	0.111	Coil (COILS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)

1029	c28134_g1_i1_len_2823_path_263_0_329_590_3 30_340_36_341_819_1077_820_1128_115_1129 _1357_1613_1358_1_5	3405	projectin short variant	915	0	79.80%	0.259	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1030	c28134_g1_i2_len_2805_path_263_0_329_590_3 30_340_36_341_819_1077_820_1128_115_1129 _1357_1613_1358_1_5	4099	projectin short variant	909	0	80.80%	0.259	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1031	c28134_g1_i3_len_2163_path_263_0_329_590_3 30_340_36_341_819_1077_820_1128_115_1129 _1357_184_1358_16_5	3658	myosin light chain smooth muscle-like	695	0	75.50%	0.259	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1032	c28134_g1_i4_len_2496_path_263_0_329_590_3 30_340_36_341_819_115_820_1048_1613_1049 _1689_2254_1690_1_5	2739	projectin short variant	806	0	74.50%	0.259	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1033	c28134_g1_i5_len_1854_path_263_0_329_25_33 0_340_36_341_819_115_820_1048_184_1049_1 354_2560_1355_137_5	1880	isoform c	592	8.19E-174	68.30%	0.259	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1034	c28134_g1_i6_len_2823_path_263_0_329_590_3 30_340_36_341_819_1077_820_1128_115_1129 _1357_1613_1358_1_5	3971	projectin short variant	915	0	80.00%	0.259	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)

1035	c28140_g1_i3_len_702_path_1075_0_25_1101_2 6_65_1141_66_220_2272_221_239_1028_240_4 20_982_421_681_27_5	17	translocase of inner mitochondrial membrane 8 homolog b	234	5.90E-33	78.30%	0.113	IPR004217 (G3DSA:1.10.287.GENE3D); IPR004217 (PFAM); PTHR21535:SF25 (PANTHER); PTHR21535 (PANTHER); IPR004217 (SUPERFAMILY)
1036	c28158_g3_i1_len_1608_path_1_0_249_251_250 _877_1344_878_1033_1500_1034_1428_4436_1 429_1447_1914_144_3	80	calnexin-like isoform x2	536	8.57E-134	76.30%	0.111	IPR001580 (PRINTS); IPR013320 (G3DSA:2.60.120.GENE3D); IPR001580 (PFAM); PTHR11073:SF1 (PANTHER); IPR001580 (PANTHER); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR018124 (PROSITE_PATTERNS); IPR009033 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1037	c28158_g3_i3_len_1572_path_503_0_213_251_2 14_841_1344_842_997_1500_998_1392_4436_1 393_1411_1914_141_3	101	calnexin-like isoform x2	524	1.76E-88	77.80%	0.111	IPR001580 (PRINTS); IPR001580 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR11073:SF1 (PANTHER); IPR001580 (PANTHER); IPR018124 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013320 (SUPERFAMILY)
1038	c28177_g1_i1_len_1907_path_105_0_1906_2	1011	abhydrolase domain-containing protein 15-like	631	1.55E-79	57.60%	0.254	IPR000073 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR10794 (PANTHER); PTHR10794:SF28 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1039	c28200_g1_i1_len_1851_path_1341_0_1140_248 2_1141_1181_695_1182_1273_4942_1274_1274 _4943_1275_1275_7_2	607	superoxide dismutase	611	2.29E-45	67.20%	0.134	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY)
1040	c28206_g1_i1_len_4265_path_8526_0_159_8686 _160_194_6012_195_232_6050_233_2031_347 6_2032_3788_523_5	103	protein rhsa	1421	0	98.50%	0.153	IPR001826 (PRINTS); IPR006530 (PFAM); IPR001826 (PFAM); IPR022385 (TIGRFAM); IPR006530 (TIGRFAM); PTHR32305:SF6 (PANTHER); PTHR32305 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1041	c28239_g1_i1_len_1866_path_2030_0_1180_320 9_1181_1203_3232_1204_1204_3233_1205_160 0_3624_1601_1601_1	150	methylmalonate-semialdehyde dehydrogenase	616	0	88.40%	0.103	IPR016163 (G3DSA:3.40.309.GENE3D); IPR010061 (TIGRFAM); IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); IPR010061 (PTHR11699:PANTHER); PTHR11699 (PANTHER); IPR016160 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM)
1042	c28252_g1_i2_len_1588_path_53_0_884_938_88 5_1360_1414_1361_1372_2910_1373_1437_297 5_1438_1468_3844_3	348	polyubiquitin-c-like isoform 2	530	8.63E-141	99.00%	0.111	IPR019956 (PRINTS); IPR000626 (SMART); G3DSA:3.10.20.90 (GENE3D); IPR000626 (PFAM); PTHR10666 (PANTHER); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); IPR019954 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR000626 (PROSITE_PROFILES); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); IPR029071 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1043	c28261_g1_i1_len_1136_path_2644_0_435_3078 _436_690_3333_691_952_3595_953_1028_5166 _1029_1032_25_103_1	105	iduronate 2- partial	379	1.96E-147	77.20%	0.462 Y	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342 (PANTHER); PTHR10342:SF185 (PANTHER); IPR024607 (PROSITE_PATTERNS); SignalP-noTM (SIGNALP_EUK); IPR017850 (SUPERFAMILY)
1044	c28261_g1_i2_len_2028_path_2644_0_435_3333 _436_697_5166_698_701_3674_702_2027_1	288	iduronate 2-sulfatase	669	1.07E-73	62.80%	0.462 Y	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342:SF185 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); SignalP-noTM (SIGNALP_EUK); IPR017850 (SUPERFAMILY)

1045	c28261_g1_i3_len_2359_path_2644_0_435_3078_436_690_3333_691_952_3595_953_1028_5166_1029_1032_3674_1_1	467	iduronate 2-sulfatase	779	0	67.60%	0.462 Y	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); G3DSA:3.30.1120.10 (GENE3D); PTHR10342:SF185 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR017850 (SUPERFAMILY)
1046	c28268_g1_i1_len_2001_path_1_0_845_847_846_2000_3	8093	gamma-glutamyltranspeptidase 1-like isoform x3	661	0	66.10%	0.33	IPR000101 (PRINTS); IPR000101 (PFAM); IPR000101 (TIGRFAM); IPR000101 (PANTHER); PTHR11686:SF15 (PANTHER); IPR029055 (SUPERFAMILY)
1047	c28270_g1_i2_len_2739_path_53_0_543_597_54_4_545_599_546_805_859_806_807_861_808_17_80_1834_1781_2738_5	718	tyrosine-protein phosphatase non-receptor type 9 isoform x1	906	0	67.60%	0.135	IPR000242 (PRINTS); IPR000242 (SMART); IPR003595 (SMART); IPR000242 (PFAM); IPR001251 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR001251 (G3DSA:3.40.525.GENE3D); PTHR19134:SF232 (PANTHER); PTHR19134 (PANTHER); IPR016130 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001251 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); IPR001251 (SUPERFAMILY)
1048	c28274_g1_i1_len_2065_path_2251_0_228_87_2_29_2064_3	8301	peptidyl-prolyl cis-trans isomerase 5	682	1.24E-111	86.30%	0.406 Y	IPR002130 (PRINTS); IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF63 (PANTHER); IPR024936 (PANTHER); IPR020892 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1049	c28279_g2_i1_len_933_path_3533_0_149_1022_150_932_4	33	15-hydroxyprostaglandin dehydrogenase	311	1.60E-54	64.60%	0.119	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24310 (PANTHER); SSF51735 (SUPERFAMILY)
1050	c28279_g2_i2_len_1392_path_3949_0_100_4048_101_125_4073_126_179_4126_180_195_3493_196_379_793_380_3_4	132	15-hydroxyprostaglandin dehydrogenase	458	7.43E-64	62.90%	0.119	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24310 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY)
1051	c28287_g2_i1_len_3550_path_1211_0_63_1210_64_817_1074_818_1415_2622_1416_1434_2641_1435_3549_3	2595	long form-like	1184	0	86.30%	0.123	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); IPR002928 (PFAM); PTHR13140 (PANTHER); PTHR13140:SF164 (PANTHER); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY); SSF90257 (SUPERFAMILY)
1052	c28299_g1_i1_len_866_path_45_0_306_352_307_746_3185_747_747_2874_748_865_1	196	hypothetical protein BRAFLDRAFT_71031	289	2.32E-15	50.25%	0.106	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1053	c28299_g1_i3_len_1368_path_45_0_306_352_30_7_746_3185_747_747_792_748_1148_1193_114_9_1149_1194_1150_1	429	c3orf33 protein	448	1.95E-30	45.30%	0.106	IPR016071 (G3DSA:2.40.50.GENE3D); IPR016071 (SUPERFAMILY); TMhelix (TMHMM)
1054	c28306_g1_i1_len_1241_path_1368_0_501_2724_502_1240_2	258	prohormone-1-like	407	1.22E-29	77.80%	0.107	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1055	c28311_g1_i1_len_720_path_2547_0_15_2563_1_6_168_2716_169_565_3113_566_697_5448_698_719_2	153	ras-related protein rab-1a	240	1.15E-126	95.20%	0.155	IPR001806 (PRINTS); IPR002041 (SMART); IPR003579 (SMART); IPR024156 (SMART); IPR003578 (SMART); IPR020849 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); IPR001806 (PFAM); PTHR24073:SF455 (PANTHER); PTHR24073 (PANTHER); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1056	c28311_g1_i2_len_1796_path_2547_0_15_2563_16_168_2716_169_565_3113_566_697_3245_69_8_781_3329_782_10_2	515	ras-related protein rab-1a	598	2.83E-130	93.90%	0.155	IPR001806 (PRINTS); IPR003579 (SMART); IPR003578 (SMART); IPR002041 (SMART); IPR020849 (SMART); IPR024156 (SMART); IPR001806 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR24073 (PANTHER); PTHR24073:SF455 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1057	c28311_g1_i3_len_1411_path_2716_0_396_3329_397_645_5_646_1410_1	193	ras-related protein rab- partial	470	5.03E-85	98.00%	0.181	IPR001806 (PRINTS); IPR003578 (SMART); IPR024156 (SMART); IPR002041 (SMART); IPR003579 (SMART); IPR020849 (SMART); IPR001806 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR24073:SF455 (PANTHER); PTHR24073 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1058	c28332_g1_i1_len_2295_path_307_0_2294_2	3750	angiotensin-converting enzyme-like	759	0	71.20%	0.159	IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); SSF55486 (SUPERFAMILY)
1059	c28334_g6_i1_len_1981_path_6955_0_1980_0	2832	methyltransferase-like protein 23	661	4.11E-94	76.60%	0.104	IPR000582 (PRINTS); IPR002110 (SMART); IPR000504 (SMART); IPR029063 (G3DSA:3.40.50.GENE3D); IPR019410 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR000582 (PFAM); IPR020683 (PFAM); IPR000504 (PFAM); IPR014352 (G3DSA:1.20.80.GENE3D); IPR012677 (G3DSA:3.30.70.GENE3D); PTHR24119:SF0 (PANTHER); PTHR24119 (PANTHER); IPR000582 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR000504 (PROSITE_PROFILES); IPR000582 (SUPERFAMILY); SSF54928 (SUPERFAMILY); IPR020683 (SUPERFAMILY); IPR029063 (SUPERFAMILY)
1060	c28361_g1_i1_len_2064_path_121_0_2063_2	424	carbonic anhydrase 1	682	2.04E-103	69.30%	0.107	IPR001148 (SMART); IPR001148 (G3DSA:3.10.200.GENE3D); IPR001148 (PFAM); IPR023561 (PANTHER); IPR018338 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001148 (PROSITE_PROFILES); IPR001148 (SUPERFAMILY)
1061	c28363_g1_i1_len_2317_path_2295_0_1935_485_2_1936_1952_4248_1953_2316_2	160	nicotinic acetylcholine receptor subunit alpha10	766	3.68E-105	59.10%	0.301	IPR006201 (PRINTS); IPR027361 (G3DSA:1.20.120.GENE3D); IPR006029 (PFAM); IPR006202 (G3DSA:2.70.170.GENE3D); IPR006202 (PFAM); PTHR18945:SF490 (PANTHER); IPR006201 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006202 (SUPERFAMILY); IPR006029 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1062	c28374_g5_i1_len_2075_path_7193_0_55_845_5_6_2074_4	51	PREDICTED: uncharacterized protein C15orf61-like	692	4.20E-57	77.40%	0.235	IPR029245 (PFAM)
1063	c28396_g1_i1_len_1132_path_1496_0_64_280_6_5_106_98_107_145_300_146_749_2239_750_7_63_137_764_861_0	141	i-type lysozyme	378	1.50E-35	65.20%	0.12	IPR008597 (PFAM); IPR008597 (PANTHER); IPR018247 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1064	c28396_g1_i2_len_1159_path_1496_0_64_279_6_5_65_280_66_107_72_108_133_98_134_172_30_0_173_776_2239_0	138	i-type lysozyme	387	1.80E-35	64.50%	0.13	IPR008597 (PFAM); IPR008597 (PANTHER); IPR018247 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1065	c28450_g1_i1_len_1704_path_33_0_796_830_79_7_798_832_799_1071_1105_1072_1080_1114_1_081_1676_3773_167_1	354	46 kda fk506-binding nuclear protein	562	9.30E-47	73.30%	0.248	Coil (COILS); G3DSA:3.10.50.40 (GENE3D); IPR001179 (PFAM); IPR023566 (PANTHER); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY); IPR024057 (SUPERFAMILY)
1066	c28483_g2_i1_len_2544_path_5816_0_387_1384_388_770_1057_771_1132_1273_1133_1477_72_85_1478_1751_1972_1	122	plexin domain-containing protein partial	848	3.62E-136	59.00%	0.335	IPR016201 (SMART); G3DSA:3.30.1680.10 (GENE3D); PTHR13055 (PANTHER); PTHR13055:SF12 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1067	c28483_g2_i2_len_435_path_1183_0_89_1273_9_0_434_2	0	plexin domain-containing protein partial	145	1.04E-31	62.30%	0.107	IPR016201 (SMART); G3DSA:3.30.1680.10 (GENE3D); PTHR13055:SF12 (PANTHER); PTHR13055 (PANTHER)

[illegible]

1071	c28484_g2_i4_len_2135_path_4543_0_90_4634_91_1170_6257_1171_1277_1951_1278_2134_2	58	zinc finger protein 2 homolog	711	0	70.80%	0.108	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1072	c28488_g2_i1_len_2440_path_1639_0_529_341_530_530_342_531_568_2204_569_688_290_689_2425_7814_2426_2_2	638	angiotensin-converting enzyme-like	813	0	78.50%	0.113	IPR001548 (PRINTS); IPR001548 (PFAM); IPR001548 (PANTHER); PTHR10514:SF17 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1073	c28540_g2_i1_len_2301_path_8248_0_1258_950_6_1259_1260_4479_1261_1600_4893_1601_163_2_4924_1633_1650_1	201	wd repeat-containing protein 61	767	5.56E-153	87.10%	0.101	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR22841 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)
1074	c28542_g2_i1_len_2933_path_3010_0_2932_1	524	sel1l protein	972	0	77.70%	0.259	Coil (COILS); IPR006597 (SMART); IPR011990 (G3DSA:1.25.40.GENE3D); IPR011990 (G3DSA:1.25.40.GENE3D); IPR006597 (PFAM); PTHR11102:SF55 (PANTHER); PTHR11102 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF81901 (SUPERFAMILY); SSF81901 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1075	c28558_g1_i3_len_770_path_3267_0_205_1756_206_532_2083_533_769_3	22	---NA---	257			0.13	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1076	c28572_g1_i1_len_1648_path_1822_0_43_3535_44_48_1872_49_1647_3	242	serine proteinase stubble-like	550	4.84E-69	56.10%	0.102	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)

1077	c28587_g1_i1_len_2413_path_2920_0_520_3441_521_940_3864_941_1313_4763_1314_1457_49_07_1458_2412_3	184	low-density lipoprotein receptor-related protein partial	799	2.26E-57	48.20%	0.118	IPR002172 (PRINTS); IPR002172 (SMART); IPR001881 (SMART); IPR000742 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR011042 (G3DSA:2.120.10.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001881 (PFAM); PTHR10529 (PANTHER); PTHR10529:SF204 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1078	c28587_g1_i2_len_3135_path_2920_0_520_3441_521_940_3861_941_943_3864_944_1316_4237_1317_1842_4763_1_3	298	vitellogenin receptor	1039	1.86E-48	49.30%	0.118	IPR002172 (PRINTS); IPR002172 (SMART); IPR000742 (SMART); IPR001881 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001881 (PFAM); PTHR10529:SF204 (PANTHER); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1079	c28587_g1_i2_len_3135_path_2920_0_520_3441_521_940_3861_941_943_3864_944_1316_4237_1317_1842_4763_1_4	298	low-density lipoprotein receptor-related protein 1-like	1039	4.38E-28	51.20%	0.191	IPR000033 (SMART); IPR011042 (G3DSA:2.120.10.GENE3D); G3DSA:2.10.25.10 (GENE3D); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1080	c28587_g1_i3_len_2942_path_2920_0_520_3441_521_940_3861_941_943_3864_944_1316_4237_1317_1842_4763_1_3	307	vitellogenin receptor	975	2.43E-85	45.80%	0.118	IPR002172 (PRINTS); IPR001881 (SMART); IPR000033 (SMART); IPR002172 (SMART); IPR000742 (SMART); IPR002172 (PFAM); IPR001881 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); PTHR10529:SF204 (PANTHER); IPR018097 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); SSF57196 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); SSF63825 (SUPERFAMILY); TMhelix (TMHMM)
1081	c28592_g1_i1_len_1276_path_1304_0_167_1472_168_433_2914_434_446_1749_447_447_3095_448_459_1762_460_2	298	meprin a subunit beta	420	1.53E-50	58.10%	0.196	IPR001506 (PRINTS); IPR006026 (SMART); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1082	c28592_g1_i2_len_1231_path_2768_0_122_1472_123_388_3081_389_400_1748_401_401_1749_402_402_3095_403_2	311	meprin a subunit beta	405	6.17E-51	58.30%	0.26	IPR001506 (PRINTS); IPR006026 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); PTHR10127 (PANTHER); SSF55486 (SUPERFAMILY)

1083	c28595_g1_i1_len_2012_path_1_0_534_536_535_707_709_708_2011_1	8335	fk506-binding protein 2 isoform x2	663	8.01E-94	78.10%	0.603	Y	IPR011992 (PFAM); IPR001179 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); G3DSA:3.10.50.40 (GENE3D); IPR023566 (PANTHER); PTHR10516:SF252 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001179 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF47473 (SUPERFAMILY); SSF54534 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1084	c28595_g1_i2_len_1839_path_1_0_534_709_535_1838_1	7585	fk506-binding protein 2 isoform x2	605	6.55E-98	79.60%	0.603	Y	IPR011992 (G3DSA:1.10.238.GENE3D); IPR001179 (PFAM); IPR011992 (PFAM); G3DSA:3.10.50.40 (GENE3D); IPR023566 (PANTHER); PTHR10516:SF252 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR002048 (PROSITE_PROFILES); IPR002048 (PROSITE_PROFILES); IPR001179 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF54534 (SUPERFAMILY); SSF47473 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1085	c28611_g1_i1_len_476_path_4896_0_58_1815_5_9_475_2	17	dehydrogenase reductase sdr family member 4-like isoform x1	158	1.92E-38	75.10%	0.188		IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF239 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1086	c28611_g1_i2_len_2198_path_3185_0_801_1812_802_804_1815_805_1221_2232_1222_1368_23_79_1369_1429_2440_1	216	dehydrogenase reductase sdr family member 4-like isoform x1	733	8.37E-103	74.70%	0.453	Y	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PF13561 (PFAM); PTHR24322:SF239 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1087	c28611_g1_i3_len_1615_path_1593_0_218_1812_219_221_1815_222_638_2232_639_785_2379_786_846_2440_847_0	232	dehydrogenase reductase sdr family member 4-like isoform x1	539	7.76E-105	74.60%	0.301		IPR002347 (PRINTS); IPR002198 (PRINTS); PF13561 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF239 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1088	c28624_g1_i1_len_1964_path_1992_0_1963_4	301	chymotrypsinogen b isoform x2	643	5.46E-133	64.30%	0.189		IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.20.100.10 (GENE3D); PTHR24265 (PANTHER); PTHR24265:SF76 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000884 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1089	c28625_g1_i1_len_1859_path_105_0_456_562_4_57_458_564_459_709_815_710_925_1029_926_1614_1716_1615_2	119	adp-ribosylation factor-like protein 3	619	1.25E-86	65.60%	0.245	IPR006689 (PRINTS); IPR024156 (SMART); IPR006687 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711:SF15 (PANTHER); PTHR11711 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1090	c28625_g1_i2_len_1643_path_105_0_456_562_4_57_458_564_459_709_1029_710_1398_1716_1_399_1403_1721_1_2	73	adp-ribosylation factor-like protein 3	547	3.34E-87	65.50%	0.245	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF15 (PANTHER); PTHR11711 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1091	c28635_g1_i1_len_1203_path_1236_0_29_2458_30_30_1266_31_98_1334_99_100_1336_101_30_3_1539_304_306_15_5	3080	hornerin isoform x2	393	2.38E-29	48.00%	0.761 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1092	c28636_g1_i1_len_1626_path_313_0_1625_4	511	prophenoloxidase activating factor	537	3.83E-132	65.60%	0.119	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1093	c28638_g1_i4_len_1750_path_713_0_329_1043_330_535_1249_536_678_1392_679_1749_2	821	di-n-acetylchitobiase	575	1.17E-113	63.00%	0.410 Y	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF146 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1094	c28644_g2_i1_len_539_path_1002_0_75_1122_7_6_538_1	68	serine protease inhibitor dipetalogastin-like	180	3.46E-08	60.70%	0.338	IPR002350 (SMART); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY)
1095	c28644_g2_i2_len_930_path_1002_0_75_1078_7_6_119_1122_120_582_1582_583_583_23_584_6_87_1686_688_712_1_0	190	serine protease inhibitor kazal-type 6-like isoform x1	310	4.78E-09	62.20%	0.293	IPR002350 (SMART); G3DSA:3.30.60.30 (GENE3D); IPR002350 (PFAM); IPR002350 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); TMhelix (TMHMM)
1096	c28657_g1_i1_len_295_path_4578_0_16_1228_1_7_294_4	10	flowering locus t a1	93	1.54E-10	56.30%	0.11	IPR008914 (PFAM); IPR008914 (G3DSA:3.90.280.GENE3D); PTHR11362 (PANTHER); IPR008914 (SUPERFAMILY)

1097	c28657_g1_i2_len_1938_path_3101_0_913_4015_914_916_4018_917_952_967_953_976_991_977_1132_4300_1133_5	713	flowering locus protein t	646	3.46E-24	60.40%	0.159	IPR008914 (PFAM); IPR008914 (G3DSA:3.90.280.GENE3D); PTHR11362 (PANTHER); IPR001858 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008914 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1098	c28674_g1_i1_len_2368_path_53_0_1512_1564_1513_1529_1581_1530_2298_2350_2299_2299_2351_2300_2367_0	316	heat shock 70 kda protein cognate 4	778	5.12E-49	87.30%	0.168	IPR013126 (PFAM); IPR029048 (G3DSA:1.20.1270.GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029048 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1099	c28686_g2_i1_len_1401_path_3867_0_1253_512_1_1254_1294_5162_1295_1295_2570_1296_1296_6167_1297_1320_0	47	carboxypeptidase d	462	7.48E-148	72.70%	0.102	IPR000834 (PRINTS); IPR000834 (SMART); IPR014766 (G3DSA:2.60.40.GENE3D); G3DSA:3.40.630.10 (GENE3D); IPR000834 (PFAM); PF13620 (PFAM); PTHR11532 (PANTHER); IPR000834 (PROSITE_PATTERNS); IPR000834 (PROSITE_PATTERNS); SSF53187 (SUPERFAMILY); IPR008969 (SUPERFAMILY)
1100	c28688_g1_i1_len_1699_path_1971_0_463_2428_464_464_129_465_1144_306_1145_1698_0	229	kielin chordin-like protein	561	1.34E-34	48.20%	0.162	IPR01791 (SMART); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
1101	c28694_g1_i1_len_233_path_446_0_192_4050_1_93_232_4	12	chitinase partial	78	1.26E-18	63.70%	0.101	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR017853 (SUPERFAMILY)
1102	c28694_g2_i1_len_238_path_812_0_76_889_77_150_986_151_180_6103_181_187_3804_188_23_7_4	467	chitinase partial	79	3.88E-21	65.70%	0.112	IPR001223 (PFAM); IPR029070 (G3DSA:3.10.50.GENE3D); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR029070 (SUPERFAMILY)
1103	c28694_g3_i1_len_396_path_3929_0_7_3606_8_31_3630_32_98_3697_99_170_986_171_200_44_84_201_242_4818_2_4	23414	chitinase partial	132	6.01E-34	60.30%	0.107	IPR029070 (G3DSA:3.10.50.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR029070 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1104	c28694_g4_i1_len_563_path_5320_0_125_5440_126_167_5174_168_191_5504_192_215_5222_2_16_252_6016_253_2_3	2471	chitinase 2	188	1.75E-51	68.50%	0.327	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); IPR001579 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1105	c28699_g2_i1_len_1988_path_53_0_1204_1256_1205_1218_1270_1219_1219_2762_1220_1799_3212_1800_1987_1	203	low quality protein: agrin	657	8.42E-39	52.00%	0.343 Y	IPR002350 (SMART); G3DSA:2.40.50.120 (GENE3D); IPR004850 (PFAM); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); PTHR10913:SF45 (PANTHER); PTHR10913 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR004850 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1106	c28699_g2_i2_len_1973_path_53_0_1204_2762_1205_1784_3212_1785_1972_1	200	low quality protein: agrin	652	1.26E-38	52.00%	0.343 Y	IPR002350 (SMART); IPR004850 (PFAM); IPR002350 (PFAM); G3DSA:2.40.50.120 (GENE3D); G3DSA:3.30.60.30 (GENE3D); PTHR10913 (PANTHER); PTHR10913:SF45 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002350 (PROSITE_PROFILES); IPR004850 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1107	c28754_g1_i1_len_1056_path_1_0_611_1026_612_1055_1	31	dnaj homolog subfamily b member 11	352	3.76E-96	81.40%	0.510 Y	IPR001623 (PRINTS); IPR001623 (SMART); G3DSA:2.60.260.20 (GENE3D); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24077:SF210 (PANTHER); PTHR24077 (PANTHER); IPR018253 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001623 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); IPR001623 (SUPERFAMILY); TMhelix (TMHMM)
1108	c28754_g1_i2_len_1562_path_1_0_611_613_612_1024_1026_1025_1468_1470_1469_1480_1482_1481_1549_1470_1_1	83	dnaj homolog subfamily b member 11	521	0	84.20%	0.510 Y	IPR001623 (PRINTS); IPR001623 (SMART); G3DSA:2.60.260.20 (GENE3D); IPR001623 (G3DSA:1.10.287.GENE3D); G3DSA:2.60.260.20 (GENE3D); IPR002939 (PFAM); IPR001623 (PFAM); PTHR24077:SF210 (PANTHER); PTHR24077 (PANTHER); IPR018253 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); IPR008971 (SUPERFAMILY); IPR001623 (SUPERFAMILY); IPR008971 (SUPERFAMILY); TMhelix (TMHMM)
1109	c28757_g3_i1_len_1359_path_1843_0_620_2460_621_648_3959_649_1358_5	103	xanthine dehydrogenase oxidase	447	1.62E-11	55.10%	0.194	IPR002888 (G3DSA:1.10.150.GENE3D); IPR002888 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002888 (SUPERFAMILY)
1110	c28777_g1_i1_len_1945_path_209_0_804_1010_805_1830_2034_1831_1857_2034_1858_1884_2061_1885_1905_208_1	251	carbohydrate sulfotransferase 11	648	7.09E-30	49.50%	0.14	IPR005331 (PFAM); IPR018011 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1111	c28786_g1_i1_len_2008_path_2464_0_1243_370_5_1244_1244_52_1245_1268_223_1269_1298_9_8_1299_1329_4012_0	699	tyrosine--trna cytoplasmic	662	0	72.00%	0.129	IPR002307 (PRINTS); G3DSA:1.10.240.10 (GENE3D); IPR002547 (PFAM); IPR002307 (TIGRFAM); IPR012340 (G3DSA:2.40.50.GENE3D); IPR014729 (G3DSA:3.40.50.GENE3D); IPR002305 (PFAM); PTHR11946 (PANTHER); IPR002547 (PROSITE_PROFILES); IPR010987 (SUPERFAMILY); SSF52374 (SUPERFAMILY); IPR012340 (SUPERFAMILY)
1112	c28786_g1_i2_len_2233_path_2464_0_1243_370_5_1244_1244_52_1245_1268_223_1269_1298_3_757_1299_1523_98_0	1249	tyrosine--trna cytoplasmic	737	0	79.80%	0.129	IPR002307 (PRINTS); IPR014729 (G3DSA:3.40.50.GENE3D); IPR002305 (PFAM); IPR012340 (G3DSA:2.40.50.GENE3D); IPR002307 (TIGRFAM); IPR002547 (PFAM); G3DSA:1.10.240.10 (GENE3D); PTHR11946 (PANTHER); IPR002547 (PROSITE_PROFILES); IPR012340 (SUPERFAMILY); SSF52374 (SUPERFAMILY); IPR010987 (SUPERFAMILY)
1113	c28791_g1_i1_len_2023_path_2282_0_1523_379_8_1524_1525_221_1526_2022_1	306	uncharacterized family 31 glucosidase k1a1161 isoform x4	668	8.33E-90	69.30%	0.146	IPR000322 (PFAM); PTHR22762:SF73 (PANTHER); PTHR22762 (PANTHER); SSF51011 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1114	c28803_g1_i1_len_2551_path_449_0_1237_94_1_238_1641_169_1642_1719_247_1720_1936_18_1937_2132_2495_21_2	178	pitslre serine threonine-protein kinase cdc21	850	0	81.70%	0.109	Coil (COILS); IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24056 (PANTHER); PTHR24056:SF107 (PANTHER); IPR008271 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1115	c28803_g1_i2_len_2474_path_449_0_1237_94_1_238_1641_247_1642_1858_2300_1859_1859_18_1860_2055_2495_2_2	208	pitslre serine threonine-protein kinase cdc21	824	0	86.10%	0.109	Coil (COILS); IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24056:SF107 (PANTHER); PTHR24056 (PANTHER); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1116	c28814_g1_i1_len_1861_path_253_0_789_3956_790_799_1052_800_1434_252_1435_1623_1867_1624_1645_1889_1_1	2234	superoxide dismutase	604	2.84E-79	85.20%	0.156	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); PTHR10003:SF33 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001424 (SUPERFAMILY)
1117	c28814_g1_i2_len_1838_path_253_0_789_1043_790_798_1052_799_1433_252_1434_1622_1889_1623_1837_1	2817	superoxide dismutase	597	2.41E-79	84.90%	0.156	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003:SF33 (PANTHER); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY)
1118	c28820_g2_i1_len_2144_path_1771_0_1151_780_1152_1363_3132_1364_2143_3	190	tyrosine-protein phosphatase lar-like isoform x1	715	5.78E-118	83.20%	0.136	IPR013106 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); IPR013106 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR23279:SF9 (PANTHER); PTHR23279 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1119	c28820_g2_i2_len_1386_path_1771_0_1151_780_1152_1363_6655_1364_1385_4	141	tyrosine-protein phosphatase lar-like isoform x1	462	4.90E-100	87.20%	0.149	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR23279 (PANTHER); PTHR23279:SF9 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1120	c28825_g2_i1_len_1734_path_3327_0_707_1067_7_708_917_6906_918_1733_3	107	gilt-like protein	578	7.82E-56	64.50%	0.133	IPR004911 (PFAM); IPR004911 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1121	c28825_g2_i3_len_1630_path_6092_0_813_6906_814_1629_3	150	gamma-interferon-inducible lysosomal thiol reductase-like	544	1.05E-59	63.20%	0.133	IPR004911 (PFAM); IPR004911 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1122	c28848_g1_i2_len_1797_path_2593_0_619_3211_620_620_3212_621_797_4737_798_818_3407_819_842_3431_843_1	333	sparc	599	6.60E-110	80.90%	0.1	Coil (COILS); IPR003645 (SMART); IPR011992 (G3DSA:1.10.238.GENE3D); G3DSA:3.30.60.30 (GENE3D); IPR019577 (PFAM); PTHR13866:SF14 (PANTHER); PTHR13866 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR001999 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF100895 (SUPERFAMILY); SSF47473 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1123	c28851_g1_i1_len_1097_path_1213_0_454_1665_455_595_92_596_743_1951_744_1096_0	631	neuferricin -like protein	360	1.15E-81	66.50%	0.109	IPR001199 (PFAM); IPR001199 (G3DSA:3.10.120.GENE3D); PTHR10281:SF4 (PANTHER); PTHR10281 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001199 (SUPERFAMILY); TMhelix (TMHMM)

1124	c28851_g1_i2_len_956_path_1213_0_454_92_455_602_1951_603_955_0	171	neuferricin-like isoform 2	313	1.17E-51	55.60%	0.109	IPR001199 (PFAM); IPR001199 (G3DSA:3.10.120.GENE3D); PTHR10281:SF4 (PANTHER); PTHR10281 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001199 (SUPERFAMILY); TMhelix (TMHMM)
1125	c28854_g1_i1_len_1936_path_157_0_1538_1692_1539_1541_1695_1542_1935_0	152	adp-ribosylation factor-like protein 4a	640	9.29E-109	86.80%	0.13	IPR006689 (PRINTS); IPR006687 (SMART); IPR003579 (SMART); IPR024156 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR11711:SF121 (PANTHER); PTHR11711 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1126	c28859_g1_i1_len_1582_path_3354_0_165_1726_166_1123_2684_1124_1125_2686_1126_1581_1	272	estradiol 17-beta-dehydrogenase 12	521	4.10E-70	65.60%	0.142	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF68 (PANTHER); PTHR24316 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1127	c28859_g1_i2_len_1582_path_1560_0_165_1726_166_1123_2684_1124_1125_2686_1126_1581_1	280	hydroxysteroid (17-beta)	521	9.73E-79	62.00%	0.275	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF68 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
1128	c28859_g1_i3_len_1929_path_3354_0_165_3519_166_512_1726_513_1470_2684_1471_1472_2_686_1473_1928_0	286	estradiol 17-beta-dehydrogenase 12	637	1.92E-69	65.40%	0.2	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316 (PANTHER); PTHR24316:SF68 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1129	c28860_g1_i1_len_1745_path_1_0_560_562_561_564_566_565_1551_1553_1552_1646_3658_16_47_1713_1715_1714_5	229	factor d-like protein	581	1.12E-78	51.10%	0.112	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1130	c28867_g1_i1_len_2360_path_2718_0_1291_535_8_1292_2359_1	239	casein kinase ii subunit alpha	787	0	95.60%	0.16	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24054:SF28 (PANTHER); PTHR24054 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1131	c28867_g1_i2_len_2642_path_2718_0_1291_401_0_1292_2217_7778_2218_2219_7978_2220_223_0_24_2231_2641_1	491	casein kinase ii subunit alpha	875	0	95.10%	0.16	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24054 (PANTHER); PTHR24054:SF28 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1132	c28873_g1_i1_len_1405_path_1_0_536_538_537_537_539_538_660_662_661_822_824_823_102_2_1173_1023_1286_1	117	epidermal retinol dehydrogenase 2	468	4.31E-110	71.00%	0.115	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF289 (PANTHER); PTHR24316 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)

1133	c28873_g1_i3_len_1392_path_1_0_536_538_537_537_539_538_660_824_661_860_1024_861_1009_1173_1010_1273_1	99	epidermal retinol dehydrogenase 2-like	464	1.36E-68	56.80%	0.115	Coil (COILS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF289 (PANTHER); PTHR24316 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1134	c28873_g1_i4_len_1554_path_1_0_536_538_537_537_539_538_660_824_661_822_824_823_1022_1024_1023_1171_1	187	epidermal retinol dehydrogenase 2-like isoform x2	518	1.48E-111	71.70%	0.115	Coil (COILS); IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316 (PANTHER); PTHR24316:SF289 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1135	c28874_g1_i1_len_1715_path_422_0_4_228_5_26_447_27_1033_1454_1034_1714_3	245	transitional endoplasmic reticulum atpase ter94	561	0	93.10%	0.098	IPR003593 (SMART); G3DSA:1.10.8.60 (GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); IPR015415 (PFAM); PTHR23077:SF69 (PANTHER); PTHR23077 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
1136	c28885_g1_i1_len_1843_path_1495_0_663_2159_664_859_2354_860_1298_26_1299_1392_2886_1393_1398_2908_1_4	145	otogelin-like protein	609	1.50E-12	45.30%	0.098	no IPS match
1137	c28885_g1_i2_len_1405_path_1495_0_663_2159_664_859_25_860_860_26_861_954_2886_955_960_2908_961_1061_4	61	otogelin-like protein	463	7.97E-09	45.30%	0.098	no IPS match
1138	c28885_g1_i3_len_1200_path_3009_0_20_2159_21_216_2354_217_655_26_656_749_2886_750_755_2908_756_856_4	69	otogelin-like protein	400	5.29E-10	47.10%	0.098	no IPS match
1139	c28885_g2_i1_len_1776_path_3051_0_935_77_936_1775_4	99	otogelin-like protein	586	7.85E-11	43.50%	0.103	no IPS match
1140	c28885_g2_i1_len_1776_path_3051_0_935_77_936_1775_5	99	otogelin-like protein	586	3.07E-10	41.80%	0.117	PD968187 (PRODOM)
1141	c28909_g1_i1_len_1948_path_2445_0_1726_732_4_1727_1728_7326_1729_1747_4189_1748_1802_4244_1803_1877_4	1321	inactive hydroxysteroid dehydrogenase-like protein 1	649	6.60E-107	68.20%	0.298	Coil (COILS); IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316:SF317 (PANTHER); PTHR24316 (PANTHER); IPR020904 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY)
1142	c28910_g1_i1_len_1750_path_399_0_239_636_240_1292_1682_1293_1316_398_1317_1405_22_1406_1749_0	2299	bola-like protein 2-like	574	1.24E-33	83.10%	0.164	IPR002634 (G3DSA:3.30.300.GENE3D); IPR002634 (PFAM); PTHR12735 (PANTHER); PTHR12735:SF2 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002634 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1143	c28930_g3_i2_len_451_path_5821_0_95_7970_96_96_7971_97_116_5362_117_450_4	1	isocitrate lyase family partial	150	1.98E-67	99.90%	0.175	IPR006254 (PFAM); IPR015813 (G3DSA:3.20.20.GENE3D); PTHR21631 (PANTHER); PTHR21631:SF10 (PANTHER); IPR015813 (SUPERFAMILY)
1144	c28938_g3_i1_len_1918_path_6801_0_15_6748_16_112_1180_113_620_3162_621_727_64_728_796_2494_797_1917_1	4059	gamma-glutamyl hydrolase	633	2.10E-92	66.30%	0.105	IPR029062 (G3DSA:3.40.50.GENE3D); IPR011697 (PFAM); IPR015527 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1145	c28938_g3_i2_len_1811_path_6801_0_15_6748_1810_1	2599	gamma-glutamyl hydrolase-like	597	2.86E-45	70.00%	0.105	IPR011697 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); PTHR11315:SF2 (PANTHER); IPR015527 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
1146	c28938_g3_i2_len_1811_path_6801_0_15_6748_1810_2	2599	gamma-glutamyl hydrolase-like	597	1.29E-29	67.70%	0.154	IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY); TMhelix (TMHMM)
1147	c28938_g3_i3_len_2071_path_6579_0_168_6748_169_265_1180_266_773_3162_774_880_64_88_1_949_2494_950_20_1	4069	gamma-glutamyl hydrolase	684	6.28E-92	66.30%	0.132	IPR029062 (G3DSA:3.40.50.GENE3D); IPR011697 (PFAM); IPR015527 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1148	c28938_g4_i1_len_446_path_7474_0_46_2096_4_7_445_1	28	gamma-glutamyl hydrolase	149	1.63E-38	65.90%	0.29	IPR011697 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1149	c28939_g2_i1_len_1533_path_4126_0_124_859_125_1532_0	158	gtp-binding protein sar1b	511	2.05E-68	93.10%	0.788 Y	IPR006689 (PRINTS); IPR006687 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF107 (PANTHER); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006687 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1150	c28939_g2_i2_len_1917_path_1_0_248_250_249_508_859_509_1916_0	202	gtp-binding protein sar1	639	3.92E-123	93.90%	0.249	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR005225 (TIGRFAM); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711:SF133 (PANTHER); PTHR11711 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006687 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1151	c28939_g2_i3_len_1715_path_553_0_46_250_47_306_859_307_1714_2	204	gtp-binding protein sar1	571	1.60E-123	93.20%	0.113	IPR006689 (PRINTS); IPR006687 (SMART); IPR024156 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR11711:SF133 (PANTHER); PTHR11711 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006687 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1152	c28940_g1_i1_len_3541_path_8022_0_1796_70_1797_1797_2492_1798_1821_15224_1822_1832_15245_1833_1839_4	159	arginine abc periplasmic arginine-binding protein	1180	0	99.40%	0.123	IPR001320 (SMART); IPR001638 (SMART); IPR005768 (TIGRFAM); IPR021909 (PFAM); G3DSA:3.40.190.10 (GENE3D); G3DSA:3.40.190.10 (GENE3D); PF00497 (PFAM); PTHR18966 (PANTHER); PTHR18966:SF152 (PANTHER); IPR018313 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53850 (SUPERFAMILY)
1153	c28947_g1_i1_len_2374_path_2619_0_1943_455_8_1944_2373_1	836	zinc metalloproteinase nas-13-like isoform 1	791	6.68E-133	54.80%	0.291	IPR001506 (PRINTS); IPR003582 (SMART); IPR006026 (SMART); IPR024079 (G3DSA:3.40.390.GENE3D); IPR001506 (PFAM); IPR003582 (PFAM); PTHR10127 (PANTHER); PTHR10127:SF550 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003582 (PROSITE_PROFILES); IPR003582 (PROSITE_PROFILES); IPR003582 (PROSITE_PROFILES); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1154	c28955_g1_i1_len_2783_path_351_0_2782_0	13171	intestinal mucin-like	921	1.48E-21	41.00%	0.1	IPR006207 (SMART); IPR001007 (SMART); IPR001007 (PFAM); IPR001007 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES)
1155	c28981_g1_i1_len_1961_path_2088_0_1235_78_1236_1960_3	403	thioredoxin-like protein 1 isoform x1	654	1.01E-149	81.20%	0.143	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR010400 (G3DSA:2.60.120.GENE3D); IPR010400 (PFAM); IPR013766 (PFAM); IPR005746 (PANTHER); IPR017937 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR010400 (PROSITE_PROFILES); IPR008979 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1156	c28985_g1_i1_len_656_path_776_0_366_1143_3_67_407_1184_408_438_1215_439_655_5	21	zinc finger protein 658-like	218	2.11E-14	62.90%	0.113	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1157	c28985_g2_i1_len_1287_path_2865_0_629_3495_630_645_3511_646_1085_4875_1086_1207_40_69_1208_1238_4100_0	71	zinc finger protein 570-like	429	2.03E-28	57.80%	0.16	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1158	c2899_g1_i1_len_1178_path_2215_0_193_26_19_4_1177_0	20	thioredoxin-related transmembrane protein 2 homolog	393	1.03E-111	78.90%	0.106	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR15853 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)

1159	c29002_g1_i1_len_563_path_180_0_19_200_20_562_2	39	low quality protein: otogelin	187	3.12E-07	44.50%	0.102	no IPS match
1160	c29002_g1_i2_len_1531_path_3853_0_987_200_988_1530_1	132	otogelin-like protein	510	1.08E-12	45.20%	0.102	no IPS match
1161	c29002_g2_i2_len_1636_path_2977_0_749_1346_750_1635_4	255	low quality protein: otogelin	545	1.24E-13	47.00%	0.102	PD968187 (PRODOM)
1162	c29005_g1_i1_len_1291_path_53_0_297_351_29_8_537_5294_538_1290_1	47	partial	426	3.52E-38	90.70%	0.256	IPR024156 (SMART); IPR006689 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF146 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1163	c29005_g2_i1_len_2241_path_3014_0_559_351_560_799_3813_800_1641_4652_1642_1642_804_1643_2240_1	191	adp-ribosylation factor-like protein 5b	747	1.54E-106	94.30%	0.344 Y	IPR006689 (PRINTS); IPR024156 (SMART); IPR006687 (SMART); IPR006689 (PFAM); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR11711 (PANTHER); PTHR11711:SF146 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1164	c29011_g1_i1_len_556_path_808_0_52_861_53_411_1691_412_412_1692_413_437_1331_438_4_60_1692_461_485_1_5	41348	chondroitin proteoglycan partial	176	2.94E-14	57.40%	0.101	IPR002557 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002557 (PFAM); PTHR23301 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY)
1165	c29043_g1_i1_len_1867_path_1393_0_26_1258_27_1100_2492_1101_1640_10912_1641_1866_2	511	cyclin-g-associated kinase-like	622	2.27E-152	78.10%	0.153	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR23172 (PANTHER); PTHR23172:SF19 (PANTHER); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1166	c29043_g1_i2_len_1661_path_1393_0_26_1258_27_1100_10236_1101_1660_2	250	cyclin-g-associated kinase-like	553	2.67E-152	78.40%	0.153	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR23172 (PANTHER); PTHR23172:SF19 (PANTHER); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1167	c29043_g2_i1_len_2810_path_2690_0_2809_3	113	aldehyde mitochondrial	937	0	85.50%	0.163	IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699:SF151 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1168	c29074_g1_i1_len_2322_path_1_0_262_5014_26_3_263_5015_264_274_276_275_275_277_276_7_07_709_708_708_71_5	298	laccase isoform d	761	0	61.90%	0.121	IPR001117 (PFAM); IPR008972 (G3DSA:2.60.40.GENE3D); IPR008972 (G3DSA:2.60.40.GENE3D); IPR008972 (G3DSA:2.60.40.GENE3D); IPR011706 (PFAM); IPR011707 (PFAM); PTHR11709 (PANTHER); PTHR11709:SF33 (PANTHER); IPR002355 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008972 (SUPERFAMILY); IPR008972 (SUPERFAMILY); IPR008972 (SUPERFAMILY)

1169	c29090_g1_i1_len_2238_path_77_0_1551_62_15_52_1563_74_1564_1667_1743_1668_1671_1747_1672_2237_2	140303	transmembrane protease serine 4	739	6.90E-40	53.10%	0.396 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1170	c29091_g1_i1_len_1102_path_1_0_243_2276_24_4_497_499_498_566_3516_567_761_763_762_7_98_800_799_1101_1	75244	transmembrane serine protease	367	4.88E-45	54.20%	0.677 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1171	c29091_g1_i2_len_1100_path_1_0_243_245_244_497_499_498_566_567_593_595_594_677_679_678_761_763_1	216342	isoform a	367	3.29E-44	53.50%	0.677 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1172	c29107_g2_i1_len_2214_path_1_0_1010_8481_1_011_1011_8482_1012_1018_1020_1019_1030_8_501_1031_1034_850_0	32715	plasma kallikrein	732	3.11E-41	55.20%	0.152	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1173	c29109_g1_i1_len_2327_path_6_0_741_748_742_743_750_744_1451_1458_1452_2326_3	261	prophenoloxidase activating factor	770	2.27E-125	67.70%	0.117	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); PTHR24268:SF95 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1174	c29126_g1_i1_len_1184_path_1687_0_272_261_273_694_2374_695_717_120_718_1183_0	72458	proclotting enzyme-like	388	4.27E-50	55.20%	0.546 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-TM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)

1175	c29128_g1_i1_len_1331_path_74_0_23_98_24_9 3_809_94_244_959_245_246_120_247_330_104 4_331_1057_1771_1_5	150	beta- -n-acetylglactosaminyl transferase (bre-4)	443	4.35E-25	67.80%	0.147	IPR027995 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR003859 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1176	c29128_g1_i2_len_1906_path_143_0_414_98_41 5_484_625_485_668_809_669_819_959_820_82 1_120_822_905_104_5	389	beta- -n-acetylglactosaminyltransferase bre-4	628	8.81E-92	70.50%	0.147	IPR003859 (PRINTS); IPR027995 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR003859 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1177	c29128_g1_i3_len_1010_path_143_0_414_98_41 5_484_625_485_668_809_669_819_959_820_82 1_120_822_905_194_3	221	beta- -n-acetylglactosaminyltransferase bre-4	330	2.75E-87	73.50%	0.163	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR027995 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
1178	c29128_g1_i4_len_826_path_143_0_414_98_415 _484_809_485_635_959_636_637_120_638_721 1940_722_722_194_3	58	beta- -n-acetylglactosaminyl transferase (bre-4)	269	2.36E-19	70.80%	0.163	IPR029044 (G3DSA:3.90.550.GENE3D); IPR027995 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
1179	c29128_g1_i4_len_826_path_143_0_414_98_415 _484_809_485_635_959_636_637_120_638_721 1940_722_722_194_5	58	beta- -n-acetylglactosaminyltransferase bre-4	268	4.14E-20	71.70%	0.163	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR003859 (PANTHER); IPR029044 (SUPERFAMILY)
1180	c29159_g1_i1_len_2722_path_5828_0_666_57_6 67_2721_0	467	monocarboxylate transporter 10 isoform x1	901	1.46E-168	72.50%	0.091	G3DSA:1.20.1250.20 (GENE3D); IPR011701 (PFAM); PTHR11360:SF90 (PANTHER); PTHR11360 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020846 (PROSITE_PROFILES); IPR020846 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

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1187	c29241_g2_i1_len_2602_path_2978_0_306_308_307_764_3741_765_1372_4349_1373_1376_4353_1377_1582_4559_1	843	alpha beta hydrolase domain-containing protein 13	859	1.73E-137	75.10%	0.241	IPR029059 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR12277 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1188	c29248_g1_i1_len_2471_path_3073_0_16_789_17_417_84_418_496_747_497_779_3845_780_803_182_804_1395_3	363	chorion peroxidase-like	818	8.80E-97	68.50%	0.139	IPR019791 (PRINTS); IPR019791 (G3DSA:1.10.640.GENE3D); IPR019791 (PFAM); PTHR11475 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
1189	c29248_g1_i1_len_2471_path_3073_0_16_789_17_417_84_418_496_747_497_779_3845_780_803_182_804_1395_5	363	hypothetical protein DAPPUDRAFT_196945	818	1.09E-76	63.20%	0.115	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
1190	c29274_g1_i1_len_1721_path_1938_0_461_228_462_462_229_463_644_2578_645_662_2596_663_1720_5	661	aldose reductase	565	6.95E-152	77.50%	0.538 Y	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); IPR001395 (PANTHER); PTHR11732:SF202 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); IPR018170 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR023210 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1191	c29291_g1_i1_len_1797_path_1703_0_100_1804_101_102_102_103_750_5482_751_1415_907_1416_1796_0	384	superoxide dismutase	592	8.81E-62	68.70%	0.203	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY); IPR001424 (SUPERFAMILY); TMhelix (TMHMM)
1192	c29291_g1_i2_len_1127_path_103_0_80_5482_81_745_907_746_1126_2	237	superoxide dismutase	368	5.98E-63	67.80%	0.115	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); IPR001424 (SUPERFAMILY); IPR001424 (SUPERFAMILY)
1193	c29291_g1_i3_len_1718_path_78_0_23_102_24_671_5482_672_1336_907_1337_1717_2	381	superoxide dismutase	565	7.48E-62	68.70%	0.11	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY); IPR001424 (SUPERFAMILY); TMhelix (TMHMM)
1194	c29291_g1_i4_len_1021_path_267_0_639_907_640_1020_1	49	superoxide dismutase	333	2.15E-24	71.00%	0.125	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (PFAM); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY)

1195	c29291_g1_i5_len_1775_path_3699_0_78_1804_79_80_102_81_728_5482_729_1393_907_1394_1774_2	390	superoxide dismutase	584	8.72E-62	68.60%	0.201	IPR001424 (PRINTS); IPR001424 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); IPR001424 (G3DSA:2.60.40.GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); IPR018152 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001424 (SUPERFAMILY); IPR001424 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1196	c29302_g1_i1_len_1580_path_3261_0_875_1798_876_901_2502_902_1579_0	57	scp-like extracellular domain containing protein 1	520	9.15E-37	49.00%	0.356 Y	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR014044 (SMART); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001283 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1197	c29302_g2_i1_len_1937_path_952_0_847_1798_848_873_4161_874_1831_7386_1832_1850_513_2_1851_1893_5175_2	104	ves g 5 allergen	645	2.13E-41	51.40%	0.271	IPR002413 (PRINTS); IPR001283 (PRINTS); IPR002172 (SMART); IPR014044 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR018244 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR014044 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1198	c29328_g1_i1_len_2864_path_215_0_1226_1439_1227_1230_110_1231_2863_5	279	serine proteinase stubble	949	2.17E-104	61.80%	0.172	Coil (COILS); IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF95 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1199	c29331_g1_i2_len_1846_path_105_0_612_715_6_13_615_52_616_1096_1198_1097_1252_1354_1_253_1845_0	515	upf0764 protein c16orf89 homolog	610	2.88E-46	47.50%	0.239	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1200	c29341_g1_i1_len_1310_path_3_0_55_59_56_5_37_541_538_671_675_672_859_3499_860_860_917_861_1309_2	108	carbonyl reductase	431	3.41E-98	74.80%	0.119	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF58 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1201	c29341_g1_i2_len_1363_path_3_0_55_59_56_5_37_541_538_671_675_672_859_3499_860_860_864_861_893_897_2	206	carbonyl reductase	448	1.72E-126	74.90%	0.119	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF58 (PANTHER); SSF51735 (SUPERFAMILY)
1202	c29360_g3_i1_len_1609_path_611_0_608_7820_609_768_1380_769_778_1390_779_1344_6082_1345_1347_5422_13_1	234789	pdgf- and vegf-related factor 1-like precursor	530	1.08E-38	53.10%	0.201	IPR000072 (SMART); IPR000072 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); PTHR11633 (PANTHER); PTHR11633:SF1 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR000072 (PROSITE_PROFILES); IPR029034 (SUPERFAMILY)
1203	c29368_g1_i1_len_1913_path_293_0_1292_4277_1293_1293_214_1294_1912_0	556	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 3-like	633	1.55E-137	74.40%	0.105	IPR006620 (SMART); IPR005123 (PFAM); PTHR14650 (PANTHER); PTHR14650:SF1 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005123 (PROSITE_PROFILES)

1204	c29370_g1_i1_len_2262_path_2239_0_570_2810_571_589_2829_590_1942_5032_1943_1943_4_182_1944_1959_4_0	285	n-acetylglucosamine-6-sulfatase-like isoform x1	748	1.88E-171	61.10%	0.265	IPR017849 (G3DSA:3.40.720.GENE3D); IPR000917 (PFAM); PTHR10342:SF208 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017850 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1205	c29380_g1_i2_len_2326_path_3281_0_1357_608_1358_2115_3010_2116_2145_927_2146_2325_4	141	zinc finger protein 470-like	775	8.57E-56	63.30%	0.159	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1206	c29383_g3_i1_len_2162_path_6862_0_38_2757_39_83_2802_84_473_3192_474_551_3270_552_576_13518_577_601_1	86	transposable element tcb1 partial	715	9.79E-25	61.50%	0.224	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1207	c2939_g1_i1_len_1555_path_1531_0_1004_3105_1005_1006_2536_1007_1554_2	39	cd109 antigen	511	6.78E-118	76.00%	0.205	IPR009048 (PFAM); IPR009048 (G3DSA:2.60.40.GENE3D); IPR008930 (G3DSA:1.50.10.GENE3D); IPR011626 (PFAM); PTHR11412:SF85 (PANTHER); PTHR11412 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008930 (SUPERFAMILY); IPR009048 (SUPERFAMILY)
1208	c29395_g1_i2_len_1647_path_1789_0_96_1886_97_156_2110_157_326_2280_327_458_2412_45_9_490_4076_491_56_2	43	nicotinic acetylcholine receptor subunit alpha10	543	7.79E-87	55.90%	0.15	Coil (COILS); IPR006201 (PRINTS); IPR027361 (G3DSA:1.20.120.GENE3D); IPR006202 (G3DSA:2.70.170.GENE3D); IPR006202 (PFAM); IPR006029 (PFAM); IPR006201 (PANTHER); PTHR18945:SF481 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006202 (SUPERFAMILY); IPR006029 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1209	c29395_g1_i3_len_1811_path_1789_0_96_1886_97_156_1946_157_311_2101_312_320_2110_32_1_490_4764_491_62_1	119	nicotinic acetylcholine receptor subunit alpha10	598	2.78E-98	55.40%	0.266	Coil (COILS); IPR002394 (PRINTS); IPR006201 (PRINTS); IPR006202 (PFAM); IPR006029 (PFAM); IPR027361 (G3DSA:1.20.120.GENE3D); IPR006202 (G3DSA:2.70.170.GENE3D); IPR006201 (PANTHER); PTHR18945:SF481 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR006202 (SUPERFAMILY); IPR006029 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1210	c29403_g1_i1_len_1327_path_1899_0_676_3408_677_678_3410_679_681_2579_682_690_283_6_91_704_506_705_95_0	1514	macrophage migration inhibitory factor	435	3.02E-37	69.80%	0.11	G3DSA:3.30.429.10 (GENE3D); IPR001398 (PFAM); IPR001398 (PANTHER); PTHR11954:SF6 (PANTHER); IPR001398 (PRODOM); IPR014347 (SUPERFAMILY)
1211	c29404_g1_i1_len_2223_path_2201_0_845_3047_846_1505_3707_1506_1507_3709_1508_1890_4092_1891_1893_2	302	alpha-mannosidase 2	735	1.36E-160	58.80%	0.1	G3DSA:2.70.98.30 (GENE3D); IPR011682 (PFAM); G3DSA:1.10.287.530 (GENE3D); IPR015341 (PFAM); IPR013780 (G3DSA:2.60.40.GENE3D); PTHR11607 (PANTHER); PTHR11607:SF4 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR028995 (SUPERFAMILY); IPR011013 (SUPERFAMILY); TMhelix (TMHMM)

1212	c29417_g1_i2_len_1178_path_251_0_699_951_7_00_998_147_999_1177_4	19	low quality protein: beta-mannosidase	393	3.92E-31	66.30%	0.358 Y	IPR008979 (G3DSA:2.60.120.GENE3D); IPR006104 (PFAM); IPR028369 (PTHR10066:PANTHER); PTHR10066 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008979 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1213	c29417_g2_i1_len_2274_path_4512_0_6_4519_7_169_1677_170_327_4838_328_329_1794_330_649_22_650_1025_1_4	393	beta-mannosidase	758	0	62.50%	0.128	IPR013812 (G3DSA:2.60.40.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR006102 (PFAM); IPR006103 (PFAM); PTHR10066 (PANTHER); IPR028369 (PTHR10066:PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006102 (SUPERFAMILY); IPR017853 (SUPERFAMILY); IPR006102 (SUPERFAMILY); IPR006102 (SUPERFAMILY)
1214	c29417_g2_i2_len_396_path_2_0_19_22_20_395_4	6	beta-mannosidase	132	4.31E-41	75.20%	0.114	IPR013781 (G3DSA:3.20.20.GENE3D); PTHR10066 (PANTHER); IPR028369 (PTHR10066:PANTHER); IPR017853 (SUPERFAMILY)
1215	c29428_g1_i1_len_2184_path_287_0_249_537_2_50_251_256_252_1084_1366_1085_1085_271_1086_1231_1512_2	892	serine-threonine kinase receptor-associated protein	721	0	85.50%	0.113	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19877 (PANTHER); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1216	c29459_g7_i1_len_1655_path_10619_0_938_124_939_1654_1	93	polypeptide n-acetylgalactosaminyltransferase partial	552	1.54E-29	77.70%	0.102	PTHR11675 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY)
1217	c29459_g7_i1_len_1655_path_10619_0_938_124_939_1654_2	93	polypeptide n-acetylgalactosaminyltransferase 2	551	1.03E-11	51.00%	0.111	IPR000772 (SMART); IPR000772 (PFAM); G3DSA:2.80.10.50 (GENE3D); PTHR11675:SF24 (PANTHER); PTHR11675 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000772 (PROSITE_PROFILES); IPR000772 (SUPERFAMILY); TMhelix (TMHMM)
1218	c29459_g7_i2_len_1677_path_10619_0_938_102_939_960_124_961_1676_1	77	polypeptide n-acetylgalactosaminyltransferase partial	559	1.81E-29	77.70%	0.102	PTHR11675 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY)
1219	c29459_g7_i2_len_1677_path_10619_0_938_102_939_960_124_961_1676_2	77	polypeptide n-acetylgalactosaminyltransferase 2	559	8.59E-12	51.00%	0.111	IPR000772 (SMART); IPR000772 (PFAM); G3DSA:2.80.10.50 (GENE3D); PTHR11675 (PANTHER); PTHR11675:SF24 (PANTHER); IPR000772 (PROSITE_PROFILES); IPR000772 (SUPERFAMILY)
1220	c29464_g1_i1_len_1634_path_1768_0_98_110_99_1162_2927_1163_1164_2929_1165_1200_29_65_1201_1209_29_0	488	epoxide hydrolase 4	539	6.69E-102	62.10%	0.097	IPR000639 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR000073 (PFAM); PTHR10992:SF721 (PANTHER); PTHR10992 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1221	c29473_g3_i1_len_960_path_7628_0_399_2069_400_426_2096_427_595_2265_596_746_4806_7_47_959_1	38	probable serine carboxypeptidase cpvl	315	4.39E-17	79.20%	0.465 Y	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); IPR001563 (PANTHER); IPR018202 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1235	c29554_g2_i1_len_2918_path_3020_0_137_3158_138_2917_1	796	cathepsin d	973	0	80.70%	0.149	IPR001461 (PRINTS); IPR021109 (G3DSA:2.40.70.GENE3D); IPR001461 (PFAM); IPR021109 (G3DSA:2.40.70.GENE3D); IPR012848 (PFAM); IPR001461 (PANTHER); PTHR13683:SF230 (PANTHER); IPR001969 (PROSITE_PATTERNS); IPR001969 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR021109 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1236	c29591_g10_i1_len_1165_path_19478_0_156_83_18_157_160_35744_161_180_35764_181_194_3_6113_195_1164_3	48	gamma-interferon-inducible lysosomal thiol reductase	389	1.74E-48	57.20%	0.251	IPR004911 (PFAM); IPR004911 (PANTHER); PTHR13234:SF8 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1237	c29591_g10_i2_len_990_path_35777_0_19_3611_3_20_989_3	30	gamma-interferon-inducible lysosomal thiol reductase	330	2.64E-49	57.20%	0.251	IPR004911 (PFAM); PTHR13234:SF8 (PANTHER); IPR004911 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1238	c29603_g1_i1_len_3001_path_554_0_114_668_1_15_115_121_116_116_669_117_250_803_251_2_51_804_252_122_3	195	neutral alpha-glucosidase ab-like	997	0	75.30%	0.105	IPR025887 (PFAM); IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF54 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011013 (SUPERFAMILY); SSF51011 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1239	c29603_g1_i2_len_665_path_7091_0_73_2954_7_4_664_3	9	neutral alpha-glucosidase ab-like	208	1.51E-82	76.70%	0.105	IPR025887 (PFAM); IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF54 (PANTHER); IPR011013 (SUPERFAMILY)
1240	c29605_g1_i1_len_1307_path_1726_0_106_361_107_166_328_167_579_2303_580_581_2305_58_2_1306_0	320	pacifastin light chain	431	4.39E-16	50.70%	0.103	IPR008037 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020862 (PROSITE_PROFILES); IPR020862 (PROSITE_PROFILES); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); IPR008037 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1241	c29607_g1_i1_len_1464_path_3013_0_19_1446_20_199_1626_200_225_1652_226_1234_2661_1_235_1463_1	209	zinc finger protein 569-like	481	1.05E-25	48.00%	0.181	IPR015880 (SMART); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1242	c29607_g1_i3_len_1456_path_1434_0_11_1446_12_191_1626_192_217_1652_218_1226_2661_1_227_1455_2	209	zinc finger protein 569-like	478	9.78E-26	47.90%	0.242	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1243	c29608_g1_i1_len_2043_path_2414_0_661_3076_662_663_3078_664_1302_56_1303_1382_378_7_1383_1383_408_2	380	serine threonine-protein phosphatase 2b catalytic subunit 2-like isoform x2	681	0	94.90%	0.106	IPR006186 (PRINTS); IPR006186 (SMART); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); PTHR11668:SF186 (PANTHER); PTHR11668 (PANTHER); IPR006186 (PROSITE_PATTERNS); IPR029052 (SUPERFAMILY)
1244	c29621_g1_i1_len_2487_path_3451_0_309_3760_310_312_1338_313_1475_4921_1476_1496_4_942_1497_1524_0	497	mucin-5b- partial	824	5.77E-17	44.00%	0.208	IPR025155 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1245	c29622_g1_i1_len_2269_path_2475_0_235_4921_236_236_2711_237_1187_114_1188_1618_40_86_1619_2268_1	433	u3 small nucleolar rna-interacting protein 2 isoform x2	752	1.45E-178	75.00%	0.153	Coil (COILS); IPR020472 (PRINTS); IPR001680 (SMART); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19865 (PANTHER); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1246	c29625_g2_i2_len_209_path_4476_0_112_8115_113_117_8120_118_137_8140_138_208_1	0	zinc finger protein partial	70	2.94E-12	67.10%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1247	c29625_g5_i1_len_308_path_267_0_51_6393_52_81_319_82_96_8107_97_104_8115_105_109_8_120_110_129_8147_2	3	zinc finger protein 347-like	102	1.72E-20	63.00%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1248	c29625_g5_i2_len_278_path_267_0_51_319_52_66_8107_67_74_8115_75_79_8120_80_99_8147_100_108_677_109_2	0	zinc finger protein 135-like	92	1.40E-15	56.80%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1249	c29640_g6_i1_len_1597_path_10897_0_408_241_8_409_492_2502_493_1518_3528_1519_1548_1_0480_1549_1596_1	68	ras suppressor protein 1	532	6.67E-156	87.60%	0.099	SM00364 (SMART); IPR003591 (SMART); IPR025875 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1250	c29642_g1_i1_len_2058_path_1_0_109_111_110_343_345_344_363_365_364_559_4401_560_68_5_561_686_2057_5	822	protein tumorous imaginal mitochondrial-like isoform x2	679	0	75.00%	0.188	IPR001623 (PRINTS); IPR001623 (SMART); IPR001305 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); G3DSA:2.60.260.20 (GENE3D); IPR001305 (G3DSA:2.10.230.GENE3D); IPR002939 (PFAM); IPR001623 (PFAM); PTHR24076 (PANTHER); PTHR24076:SF79 (PANTHER); IPR018253 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012724 (HAMAP); IPR001623 (PROSITE_PROFILES); IPR001305 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); IPR008971 (SUPERFAMILY); IPR008971 (SUPERFAMILY); IPR001305 (SUPERFAMILY); TMhelix (TMHMM)
1251	c29642_g1_i2_len_2122_path_1_0_109_111_110_343_345_344_363_365_364_559_4337_560_62_3_4401_624_749_56_5	754	protein tumorous imaginal mitochondrial-like isoform x2	701	0	75.00%	0.188	IPR001623 (PRINTS); IPR001623 (SMART); G3DSA:2.60.260.20 (GENE3D); IPR002939 (PFAM); IPR001305 (PFAM); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001305 (G3DSA:2.10.230.GENE3D); PTHR24076 (PANTHER); PTHR24076:SF79 (PANTHER); IPR018253 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012724 (HAMAP); IPR001305 (PROSITE_PROFILES); IPR001305 (PROSITE_PROFILES); IPR008971 (SUPERFAMILY); IPR001623 (SUPERFAMILY); IPR001305 (SUPERFAMILY); IPR008971 (SUPERFAMILY); TMhelix (TMHMM)

1252	c29642_g1_i3_len_1932_path_1_0_109_111_110_343_345_344_363_365_364_559_561_560_193_1_5	893	protein tumorous imaginal mitochondrial-like isoform x2	637	0	75.00%	0.188	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001305 (G3DSA:2.10.230.GENE3D); IPR001305 (PFAM); G3DSA:2.60.260.20 (GENE3D); IPR002939 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24076 (PANTHER); PTHR24076:SF79 (PANTHER); IPR018253 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001305 (PROSITE_PROFILES); IPR012724 (HAMAP); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); IPR008971 (SUPERFAMILY); IPR001305 (SUPERFAMILY); IPR008971 (SUPERFAMILY); TMhelix (TMHMM)
1253	c29649_g1_i1_len_2027_path_3271_0_123_3394_124_716_130_717_2026_0	266	ankyrin-1-like isoform x2	676	0	80.30%	0.154	IPR002110 (PRINTS); IPR001496 (SMART); IPR001496 (SMART); IPR002110 (SMART); IPR001496 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR002110 (PFAM); PTHR24133 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR001496 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); SSF158235 (SUPERFAMILY); IPR020683 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1254	c29664_g2_i4_len_1312_path_1759_0_878_1356_1_879_879_2636_880_1311_2	39	syntaxin-12	437	1.69E-96	72.40%	0.103	IPR006011 (SMART); IPR000727 (SMART); G3DSA:1.20.58.70 (GENE3D); PF14523 (PFAM); IPR000727 (PFAM); PTHR19957:SF87 (PANTHER); PTHR19957 (PANTHER); IPR006012 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000727 (PROSITE_PROFILES); IPR010989 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1255	c29664_g2_i5_len_1026_path_1759_0_878_1356_1_879_879_1414_880_930_9820_931_961_459_0_962_967_9856_2	15	syntaxin-12	342	1.38E-97	72.50%	0.103	IPR006011 (SMART); IPR000727 (SMART); PF14523 (PFAM); IPR000727 (PFAM); G3DSA:1.20.58.70 (GENE3D); PTHR19957:SF87 (PANTHER); PTHR19957 (PANTHER); IPR006012 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000727 (PROSITE_PROFILES); IPR010989 (SUPERFAMILY); TMhelix (TMHMM)
1256	c29667_g1_i1_len_1036_path_51_0_55_107_56_72_2891_73_76_2895_77_182_234_183_446_49_8_447_693_744_694_4	150	peroxiredoxin partial	345	5.68E-116	83.50%	0.141	G3DSA:3.30.1020.10 (GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR019479 (PFAM); IPR000866 (PFAM); PTHR10681:SF77 (PANTHER); PTHR10681 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
1257	c29676_g1_i1_len_2725_path_483_0_52_377_53_55_380_56_1224_1700_1225_1226_430_1227_1765_154_1766_2	920	heat shock 70 kda protein cognate 5	908	0	89.00%	0.127	Coil (COILS); IPR013126 (PRINTS); IPR029048 (G3DSA:1.20.1270.GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR012725 (TIGRFAM); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.90.640.10 (GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.30.30 (GENE3D); IPR013126 (PFAM); PTHR19375 (PANTHER); PTHR19375:SF173 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR012725 (HAMAP); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
1258	c29682_g2_i1_len_822_path_1895_0_477_2373_478_482_2378_483_667_172_668_701_2596_70_2_727_172_728_761_1	874	---NA---	274			0.172	no IPS match
1259	c29703_g1_i3_len_2089_path_645_0_1243_644_1244_1396_328_1397_1476_408_1477_1478_20_35_1479_1842_4920_4	456	hypothetical protein L798_04491	690	6.64E-34	62.20%	0.128	IPR013783 (G3DSA:2.60.40.GENE3D); PTHR21104 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1260	c29703_g1_i4_len_2137_path_645_0_1243_596_1244_1291_644_1292_1444_328_1445_1524_408_1525_1526_2035_4	424	hypothetical protein L798_04491	706	7.69E-34	62.20%	0.128	IPR013783 (G3DSA:2.60.40.GENE3D); PTHR21104 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
1261	c29703_g1_i5_len_2009_path_645_0_1243_644_1244_1396_408_1397_1398_2035_1399_1762_4920_1763_1765_239_5	525	hypothetical protein L798_04491	663	6.44E-34	63.40%	0.112	IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR21104 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
1262	c29713_g2_i1_len_957_path_1_0_197_199_198_956_0	77	ankyrin sam and basic leucine zipper domain-containing protein 1-like	319	3.01E-63	68.40%	0.099	IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24157 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1263	c29718_g2_i1_len_598_path_940_0_169_1110_170_334_1603_335_409_7335_410_450_7376_451_527_2627_528_55_2	174	si:dkey- protein	199	4.47E-21	61.60%	0.16	PF14704 (PFAM); IPR026645 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1264	c29718_g2_i2_len_449_path_3681_0_45_2760_46_99_2395_100_124_7784_125_185_1603_186_260_7917_261_301_0	300	dermatopontin 3	150	2.19E-21	62.10%	0.203	PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1265	c29718_g2_i3_len_446_path_1421_0_17_1110_18_182_1603_183_257_7335_258_298_7376_299_375_2627_376_404_0	184	si:dkey- protein	149	9.40E-22	60.80%	0.18	PF14704 (PFAM); IPR026645 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1266	c29718_g3_i1_len_870_path_2295_0_99_2395_100_124_3803_125_288_3967_289_363_3661_364_399_4075_400_42_0	524	hemagglutinin amebocyte aggregation factor-like	285	4.11E-39	61.70%	0.282	PF14704 (PFAM); IPR026645 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1267	c29718_g4_i2_len_1564_path_3803_0_163_7152_164_274_4075_275_302_4102_303_853_2548_854_1563_1	243	dermatopontin 2	515	1.12E-35	59.20%	0.112	PF14704 (PFAM); IPR026645 (PANTHER)
1268	c29718_g5_i1_len_175_path_1291_0_129_363_130_174_4	0	hemagglutinin amebocyte aggregation factor-like	58	2.47E-12	66.50%	0.151	PF14704 (PFAM); IPR026645 (PANTHER)
1269	c29718_g6_i1_len_407_path_1_0_361_363_362_406_4	191	hemagglutinin amebocyte aggregation factor-like	128	1.18E-14	66.40%	0.132	PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1270	c29733_g1_i1_len_2204_path_2899_0_1320_422_0_1321_1336_4236_1337_1947_4847_1948_1974_7583_1975_1980_1	427	contactin associated protein 1	735	5.72E-69	51.50%	0.138	Coil (COILS); IPR001073 (SMART); IPR008983 (G3DSA:2.60.120.GENE3D); IPR000885 (PFAM); IPR001073 (PFAM); IPR014716 (G3DSA:3.90.215.GENE3D); PTHR10127:SF575 (PANTHER); PTHR10127 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001073 (PROSITE_PROFILES); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY); IPR008983 (SUPERFAMILY); IPR002181 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1278	c29759_g2_i1_len_1563_path_2227_0_793_626_794_1036_554_1037_1180_3440_1181_1181_528_1182_1552_4457_2	200	zinc finger and scan domain-containing protein 2-like	521	9.70E-23	55.40%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1279	c29759_g2_i2_len_1611_path_2227_0_793_3014_794_841_626_842_1084_554_1085_1228_3440_1229_1229_528_12_2	234	zinc finger protein 235-like	537	8.40E-23	52.50%	0.102	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1280	c29780_g6_i1_len_1532_path_24313_0_37_2435_0_38_53_24366_54_1060_14426_1061_1329_25_758_1330_1531_1	444	zinc finger protein zpr1	503	0	74.20%	0.123	IPR004457 (SMART); IPR004457 (TIGRFAM); IPR004457 (PFAM); PTHR10876 (PANTHER); PTHR10876:SF0 (PANTHER)
1281	c29780_g6_i2_len_716_path_19643_0_12_28759_13_23_28770_24_36_14263_37_199_14426_20_0_468_22085_469_7_1	10	zinc finger protein partial	239	7.09E-26	73.20%	0.113	IPR004457 (SMART); IPR004457 (PFAM); PTHR10876 (PANTHER); PTHR10876:SF0 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
1282	c29795_g1_i3_len_269_path_130_0_21_152_22_245_5983_246_268_2	4	serine protease inhibitor serpin-like protein	89	3.03E-08	72.20%	0.22	G3DSA:2.30.39.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); PTHR11461:SF52 (PANTHER); IPR023795 (PROSITE_PATTERNS); IPR023796 (SUPERFAMILY)
1283	c29808_g1_i1_len_1381_path_2895_0_122_3018_123_208_1358_209_209_1359_210_216_1366_217_271_1421_272_2	268	copper chaperone for superoxide dismutase	455	2.81E-111	77.00%	0.434 Y	IPR001424 (PRINTS); IPR001424 (PFAM); IPR006121 (PFAM); IPR001424 (G3DSA:2.60.40.GENE3D); G3DSA:3.30.70.100 (GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006121 (PROSITE_PROFILES); IPR001424 (SUPERFAMILY); IPR006121 (SUPERFAMILY)
1284	c29808_g1_i2_len_1280_path_1250_0_107_1358_108_108_1359_109_115_1366_116_170_1421_171_202_1421_203_0	322	copper chaperone for superoxide dismutase	422	8.25E-112	77.00%	0.17	IPR001424 (PRINTS); IPR001424 (G3DSA:2.60.40.GENE3D); IPR006121 (PFAM); IPR001424 (PFAM); G3DSA:3.30.70.100 (GENE3D); PTHR10003 (PANTHER); IPR018152 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006121 (PROSITE_PROFILES); IPR001424 (SUPERFAMILY); IPR006121 (SUPERFAMILY)
1285	c29820_g1_i2_len_2316_path_669_0_449_1118_450_452_272_453_643_176_644_730_341_731_933_1590_934_948_1	214	serine protease nudel	772	2.97E-40	51.40%	0.126	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); PTHR10529:SF222 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001190 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR017448 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1286	c29824_g1_i1_len_2478_path_2781_0_1658_443_7_1659_1865_100_1866_1966_4742_1967_1971_254_1972_2006_47_0	1131	extracellular matrix protein partial	820	5.62E-22	40.10%	0.106	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); TMhelix (TMHMM)

1287	c29825_g1_i2_len_785_path_4447_0_73_5560_7_4_91_5578_92_109_54_110_133_3098_134_234_1718_235_784_1	40	platelet-activating factor acetylhydrolase	262	4.81E-41	59.90%	0.156	IPR005065 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR005065 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1288	c29825_g1_i3_len_1480_path_1618_0_99_1718_100_649_5704_650_1287_2906_1288_1479_1	497	platelet-activating factor acetylhydrolase	487	2.00E-102	57.20%	0.192	Coil (COILS); IPR005065 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR005065 (PANTHER); IPR029058 (SUPERFAMILY)
1289	c29835_g2_i1_len_868_path_10807_0_867_3	780	glutathione peroxidase 7	290	1.53E-75	70.60%	0.251	IPR000889 (PRINTS); IPR000889 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR11592:SF10 (PANTHER); IPR000889 (PANTHER); IPR029760 (PROSITE_PATTERNS); IPR029759 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
1290	c29839_g1_i1_len_1703_path_852_0_820_1665_821_1269_2109_1270_1270_633_1271_1279_21_18_1280_1702_2	7378101	probable chitinase 3	567	3.86E-128	56.90%	0.21	IPR002557 (SMART); IPR011583 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR013781 (G3DSA:3.20.20.GENE3D); IPR029070 (G3DSA:3.10.50.GENE3D); IPR002557 (PFAM); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR001579 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR017853 (SUPERFAMILY); IPR029070 (SUPERFAMILY); IPR002557 (SUPERFAMILY)
1291	c29848_g1_i1_len_256_path_1_0_255_0	0	villin-1-like isoform x1	86	5.89E-26	69.80%	0.1	IPR029006 (G3DSA:3.40.20.GENE3D); IPR007122 (PANTHER); IPR030016 (PTHR11977:PANTHER); SSF82754 (SUPERFAMILY)
1292	c29848_g2_i1_len_1628_path_2640_0_790_4272_791_797_498_798_1120_706_1121_1161_3793_1162_1172_1004_1_0	245	villin-1-like isoform x1	543	4.78E-146	66.00%	0.102	IPR007122 (PRINTS); IPR007122 (SMART); IPR003128 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR003128 (G3DSA:1.10.950.GENE3D); IPR003128 (PFAM); IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR029006 (G3DSA:3.40.20.GENE3D); IPR007122 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003128 (PROSITE_PROFILES); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY); IPR003128 (SUPERFAMILY); TMhelix (TMHMM)
1293	c29849_g1_i1_len_3440_path_3560_0_2646_760_6_2647_2648_6207_2649_2651_6210_2652_280_2_7650_2803_2804_1	512	retinoid-inducible serine carboxypeptidase	1141	7.13E-141	67.40%	0.12	IPR001563 (PRINTS); IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11802:SF3 (PANTHER); IPR001563 (PANTHER); IPR018202 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1294	c29862_g1_i1_len_2594_path_4016_0_154_6926_155_211_4228_212_235_7006_236_320_4331_321_373_752_374_4_5	108	zinc finger protein 699-like	858	1.92E-32	55.00%	0.11	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1295	c29863_g14_i1_len_987_path_4110_0_986_1	22	high affinity nerve growth factor	322	9.00E-32	74.30%	0.18	IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24418:SF198 (PANTHER); PTHR24418 (PANTHER); IPR008266 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011009 (SUPERFAMILY)
1296	c29865_g6_i1_len_3235_path_3969_0_43_4013_44_1598_5568_1599_3234_0	360	lamin dm0-like isoform x1	1079	3.59E-164	74.40%	0.152	Coil (COILS); Coil (COILS); Coil (COILS); Coil (COILS); G3DSA:1.20.5.170 (GENE3D); IPR001664 (PFAM); IPR001322 (G3DSA:2.60.40.GENE3D); IPR001322 (PFAM); IPR001664 (PANTHER); IPR027696 (PTHR23239:PANTHER); IPR018039 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF64593 (SUPERFAMILY); IPR001322 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1297	c29879_g1_i1_len_2432_path_4646_0_164_4810_165_168_2176_169_211_4855_212_1100_955_1101_1222_5864_12_0	686	low quality protein: hemocytin	806	2.55E-79	47.10%	0.175	IPR001846 (SMART); IPR014853 (PFAM); G3DSA:2.10.25.10 (GENE3D); IPR001846 (PFAM); PTHR11339 (PANTHER); PTHR11339:SF25 (PANTHER); IPR001846 (PROSITE_PROFILES); IPR001846 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY)
1298	c29879_g2_i1_len_1637_path_4646_0_164_2172_165_168_2176_169_211_77_212_1091_955_10_92_1213_2025_1214_0	119	hemocytin-like isoform x3	546	2.20E-37	46.10%	0.17	G3DSA:2.10.25.10 (GENE3D); IPR001846 (PFAM); IPR014853 (PFAM); IPR001846 (PROSITE_PROFILES); IPR002919 (SUPERFAMILY)
1299	c29891_g1_i1_len_2528_path_1_0_166_168_167_1045_11184_1046_1924_2995_1925_2206_11_352_2207_2220_1_0	380	chorion partial	843	9.56E-39	47.10%	0.169	IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); IPR029590 (PTHR11475:PANTHER); PTHR11475 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1300	c29891_g1_i1_len_2528_path_1_0_166_168_167_1045_11184_1046_1924_2995_1925_2206_11_352_2207_2220_1_2	380	hypothetical protein DAPPUDRAFT_308673	842	3.64E-06	69.25%	0.15	IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR029585 (PTHR11475:PANTHER); IPR010255 (SUPERFAMILY)
1301	c29891_g1_i2_len_3280_path_10338_0_728_111_84_729_1607_1926_1608_2461_2780_2462_24_63_2782_2464_26_1	653	chorion peroxidase-like	1093	7.02E-169	57.40%	0.203	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY)
1302	c29891_g1_i3_len_3597_path_1_0_166_168_167_1045_11184_1046_1924_1926_1925_2778_27_80_2779_2780_27_0	895	chorion peroxidase-like	1199	2.40E-169	55.40%	0.169	IPR019791 (PRINTS); IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR019791 (PROSITE_PROFILES); IPR010255 (SUPERFAMILY); TMhelix (TMHMM)
1303	c29899_g1_i1_len_3205_path_1_0_574_576_575_575_577_576_576_578_577_3204_5	973	transforming growth factor-beta-induced protein ig-h3	1068	0	55.80%	0.483 Y	Coil (COILS); IPR000782 (SMART); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900:SF73 (PANTHER); PTHR10900 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY)
1304	c29902_g1_i1_len_2094_path_1117_0_64_231_6_5_67_234_68_346_1457_347_358_7722_359_4_59_7786_460_465_1	280	probable cytochrome p450 49a1	698	5.78E-143	62.70%	0.138	IPR001128 (PRINTS); IPR002401 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24305:SF49 (PANTHER); PTHR24305 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
1305	c29922_g1_i1_len_1828_path_4784_0_1310_266_3_1311_1350_25_1351_1362_37_1363_1827_5	39	protein creg1	602	1.42E-68	76.20%	0.126	PF13883 (PFAM); IPR012349 (G3DSA:2.30.110.GENE3D); PTHR13343 (PANTHER); PTHR13343:SF17 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012349 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1306	c29922_g1_i2_len_1462_path_1724_0_106_1831_107_161_1886_162_209_1934_210_212_1937_213_352_2075_353_5	44	protein creg1	487	5.04E-55	77.30%	0.126	PF13883 (PFAM); IPR012349 (G3DSA:2.30.110.GENE3D); PTHR13343 (PANTHER); PTHR13343:SF12 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012349 (SUPERFAMILY)
1307	c29925_g18_i1_len_2202_path_20871_0_567_21_438_568_572_3252_573_1129_7738_1130_1427_28743_1428_1836_0	476	serine threonine-protein kinase grp-like	728	0	74.20%	0.123	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24344 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1308	c29928_g1_i1_len_2982_path_3377_0_24_3402_25_978_4345_979_988_35_989_1449_4812_14_50_1526_4889_15_3	1402	hemocyanin subunit type 1 precursor	987	0	69.60%	0.195	IPR013788 (PRINTS); IPR005203 (PFAM); IPR005203 (G3DSA:2.60.40.GENE3D); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR000896 (PFAM); IPR005204 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR013788 (PANTHER); IPR013788 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); IPR002227 (PROSITE_PATTERNS); IPR014756 (SUPERFAMILY); IPR005204 (SUPERFAMILY); IPR008922 (SUPERFAMILY)
1309	c29957_g2_i1_len_2333_path_6375_0_17_6393_18_40_6416_41_212_6588_213_1294_13633_1_295_1295_7667_1_0	1168	chitinase domain-containing protein 1 isoform x1	778	3.60E-146	70.30%	0.128	IPR011583 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); PTHR11177:SF135 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1310	c29957_g2_i2_len_1336_path_6375_0_17_6393_18_40_6416_41_212_6588_213_1294_749_129_5_1299_754_1300_0	839	chitinase domain-containing protein 1 isoform x1	446	1.86E-118	67.40%	0.128	IPR011583 (SMART); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
1311	c29957_g2_i3_len_2162_path_11298_0_18_6393_19_41_6588_42_1123_13633_1124_1124_766_7_1125_2161_0	970	chitinase domain-containing protein 1 isoform x1	721	9.38E-147	70.30%	0.198	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF135 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1312	c29969_g2_i1_len_907_path_9165_0_18_9184_1_9_21_9187_22_38_274_39_39_275_40_40_276_41_42_9208_43_61_1	40	xanthine dehydrogenase	302	2.55E-66	83.60%	0.101	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008274 (SUPERFAMILY)
1313	c29969_g2_i3_len_862_path_7243_0_233_5522_234_861_1	33	xanthine dehydrogenase	287	6.35E-109	80.60%	0.11	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR008274 (SUPERFAMILY)
1314	c29969_g2_i5_len_680_path_7243_0_233_3398_234_679_1	4	xanthine dehydrogenase oxidase-like	227	1.33E-34	86.50%	0.11	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); PTHR11908:SF32 (PANTHER); PTHR11908 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008274 (SUPERFAMILY)
1315	c29973_g36_i1_len_2302_path_21957_0_1224_2_3181_1225_1225_23182_1226_2301_4	1825	cathepsin I	767	2.39E-176	81.00%	0.139	IPR000668 (PRINTS); IPR000668 (SMART); IPR013201 (SMART); IPR013201 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR000668 (PFAM); PTHR12411:SF57 (PANTHER); IPR013128 (PANTHER); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1316	c29974_g1_i1_len_2667_path_430_0_223_654__ 224_1934_3363_1935_1937_706_1938_2221_36 41_2222_2222_93_0	181	hemocyte protein-glutamine gamma- partial	889	0	70.20%	0.166	IPR002931 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR002931 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR001102 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR008958 (PFAM); IPR002931 (G3DSA:3.90.260.GENE3D); IPR023608 (PANTHER); PTHR11590:SF40 (PANTHER); IPR008958 (SUPERFAMILY); SSF54001 (SUPERFAMILY); IPR014756 (SUPERFAMILY); IPR008958 (SUPERFAMILY)
1317	c29974_g1_i2_len_2988_path_7339_0_107_1218 _108_133_1243_134_544_654_545_2255_3363 _2256_2258_706_0	178	hemocyte protein-glutamine gamma- partial	996	0	70.40%	0.378 Y	IPR002931 (SMART); IPR008958 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR002931 (G3DSA:3.90.260.GENE3D); IPR002931 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR001102 (PFAM); IPR023608 (PANTHER); PTHR11590:SF40 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008958 (SUPERFAMILY); IPR008958 (SUPERFAMILY); SSF54001 (SUPERFAMILY); IPR014756 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1318	c29981_g1_i1_len_3040_path_3315_0_536_3851 _537_538_156_539_686_4000_687_708_7038_7 09_710_4047_711_9_5	846	sulfhydryl oxidase 1-like	1008	2.20E-139	54.10%	0.321	IPR017905 (G3DSA:1.20.120.GENE3D); IPR013766 (PFAM); IPR017905 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR22897:SF8 (PANTHER); PTHR22897 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017905 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR017905 (SUPERFAMILY); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1319	c29982_g1_i1_len_534_path_9336_0_24_5106_2 5_170_2708_171_175_2180_176_340_384_341_ 392_1871_393_533_5	196885	transmembrane protease serine 6	178	3.75E-26	50.80%	0.098	IPR001314 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); IPR001254 (PFAM); G3DSA:4.10.1220.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
1320	c29982_g2_i1_len_1128_path_111_0_81_677_82 _101_213_102_272_384_273_324_2925_325_38 8_1358_389_845_98_4	191528	low-density lipoprotein receptor-related protein 2-like	376	1.34E-49	55.70%	0.800 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
1321	c29982_g2_i2_len_892_path_9625_0_75_1281_7 6_152_1358_153_609_9821_610_728_5984_729 _891_4	88749	low-density lipoprotein receptor-related protein 2-like	297	2.24E-41	57.80%	0.800 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)

1322	c29982_g3_i1_len_1222_path_6252_0_306_9955_307_308_9625_309_384_9674_385_921_9821_922_1040_3561_104_4	381583	suppressor of tumorigenicity 14 protein	407	6.43E-56	51.30%	0.791 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001254 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNAIP_EUK); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1323	c29982_g4_i1_len_563_path_8117_0_226_8343_227_236_5022_237_311_1154_312_351_8465_352_562_0	118055	secreted salivary gland	180	4.57E-20	57.60%	0.282	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1324	c29982_g5_i1_len_447_path_962_0_191_1154_192_231_1599_232_446_0	29390	peptidase s1 and s6 chymotrypsin hap	143	3.57E-14	66.70%	0.109	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1325	c29986_g1_i1_len_2346_path_2694_0_837_3531_838_841_160_842_1393_5968_1394_1408_409_8_1409_1432_352_1_4	181822	venom serine carboxypeptidase-like	775	4.80E-129	63.90%	0.209	IPR001563 (PRINTS); IPR001563 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PANTHER); IPR018202 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM)
1326	c30020_g3_i1_len_2007_path_13697_0_20_1391_4_21_1192_1517_1193_1218_9302_1219_1743_9827_1744_1767_13_2	40	flavin-containing monooxygenase fmo gs-ox-like 4	669	5.10E-112	62.40%	0.105	IPR000960 (PRINTS); G3DSA:3.50.50.60 (GENE3D); IPR020946 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR23023 (PANTHER); PTHR23023:SF4 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51905 (SUPERFAMILY); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
1327	c30020_g3_i2_len_2306_path_25_0_319_13914_320_1491_1517_1492_1517_9302_1518_2042_9827_2043_2066_134_1	48	flavin-containing monooxygenase fmo gs-ox-like 4	769	1.57E-144	64.00%	0.114	IPR000960 (PRINTS); IPR020946 (PFAM); G3DSA:3.50.50.60 (GENE3D); G3DSA:3.50.50.60 (GENE3D); PTHR23023:SF4 (PANTHER); PTHR23023 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51905 (SUPERFAMILY); SSF51905 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1328	c30025_g1_i1_len_318_path_1051_0_21_298_22_200_8920_201_317_1	376	chondroitin proteoglycan partial	106	1.55E-09	59.60%	0.176	IPR002557 (SMART); IPR002557 (G3DSA:2.170.140.GENE3D); IPR002557 (PFAM); PTHR23301 (PANTHER); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY)
1329	c30025_g1_i2_len_3319_path_1973_0_248_8920_249_365_2330_366_467_784_468_535_1662_536_598_2557_599_6_1	98406	c-type lectin	1101	4.81E-15	50.50%	0.116	IPR002557 (SMART); IPR002557 (PFAM); IPR002557 (G3DSA:2.170.140.GENE3D); PTHR11177:SF153 (PANTHER); PTHR11177 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR002557 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1330	c30044_g10_i1_len_1427_path_28325_0_60_157 38_61_67_33841_68_85_33859_86_91_134_92_498_541_499_557_1_1	82	zinc finger protein 501-like	476	1.46E-22	47.40%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1331	c30044_g3_i1_len_2721_path_16335_0_300_185 59_301_318_16654_319_330_15397_331_345_33594_346_354_1542_0	433	zinc finger protein	907	4.43E-30	51.80%	0.104	Coil (COILS); IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1332	c30044_g5_i1_len_784_path_2484_0_27_33668_28_37_9606_38_59_9628_60_77_34503_78_78_34504_79_84_3329_2	18	zinc finger protein	261	1.86E-12	58.60%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1333	c30044_g5_i3_len_1254_path_2484_0_27_33668_28_37_9606_38_59_9628_60_77_34503_78_78_34504_79_84_3329_2	52	zinc finger protein	418	1.39E-17	57.30%	0.101	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1334	c30044_g6_i2_len_807_path_27201_0_184_3393_9_185_190_33945_191_205_33960_206_208_23_852_209_292_23936_1	9	zinc finger protein	269	2.38E-17	56.40%	0.109	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1335	c30044_g8_i1_len_1438_path_21677_0_1282_49_47_1283_1362_5027_1363_1398_33526_1399_1_406_10750_1407_14_2	61	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	479	5.58E-31	56.90%	0.106	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1336	c30063_g1_i1_len_3031_path_2312_0_233_9268_234_248_2561_249_293_13719_294_308_1373_4_309_323_9160_32_1	866	hemagglutinin	1005	4.84E-121	58.80%	0.127	IPR023612 (PRINTS); IPR001570 (PFAM); IPR025711 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); IPR011096 (PFAM); IPR013856 (PFAM); IPR007280 (PFAM); G3DSA:1.10.390.10 (GENE3D); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1337	c30063_g1_i2_len_2334_path_2312_0_233_2546_234_248_2561_249_293_13719_294_308_2621_309_330_2643_331_1	2619	hemagglutinin	772	1.88E-126	55.80%	0.127	IPR023612 (PRINTS); G3DSA:1.10.390.10 (GENE3D); IPR001570 (PFAM); IPR011096 (PFAM); IPR007280 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); IPR025711 (PFAM); IPR013856 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF55486 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1338	c30063_g2_i1_len_2070_path_13346_0_20_1284_1_21_285_13719_286_300_13734_301_315_563_9_316_2046_14113_2	553	hemagglutinin	684	8.54E-127	56.00%	0.218	IPR023612 (PRINTS); IPR013856 (PFAM); IPR011096 (PFAM); IPR007280 (PFAM); IPR001570 (PFAM); G3DSA:1.10.390.10 (GENE3D); IPR013856 (G3DSA:3.10.170.GENE3D); SSF55486 (SUPERFAMILY)
1339	c30064_g2_i1_len_1089_path_384_0_51_436_52_65_450_66_90_6711_91_104_3897_105_285_6_819_286_286_6820_2	752	bursicon alpha	356	1.33E-60	85.50%	0.16	IPR004133 (PFAM); PTHR11339 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1340	c30064_g2_i10_len_1838_path_2861_0_625_348_7_626_944_3806_945_1034_6819_1035_1035_6_820_1036_1143_418_1	684	bursicon alpha	600	2.01E-32	85.10%	0.258	TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1341	c30064_g2_i2_len_714_path_5085_0_19_4186_2_0_340_4507_341_407_4574_408_713_2	469	bursicon alpha	231	1.10E-10	82.40%	0.103	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1342	c30064_g2_i3_len_907_path_384_0_51_436_52_65_450_66_90_6711_91_104_6820_105_212_41_86_213_533_4507_5_0	654	bursicon alpha	296	5.58E-32	86.40%	0.263	TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1343	c30064_g2_i4_len_1546_path_5573_0_151_3487_152_470_3806_471_560_3896_561_561_3897_562_742_6819_743_1	757	bursicon alpha	504	1.90E-59	86.20%	0.129	IPR004133 (PFAM); PTHR11339 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1344	c30064_g2_i5_len_1072_path_5485_0_87_3897_88_268_6819_269_269_6820_270_377_4186_37_8_698_4507_699_76_0	744	bursicon alpha	351	5.69E-60	82.90%	0.123	IPR004133 (PFAM); PTHR11339 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR006207 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1345	c30064_g2_i6_len_1113_path_384_0_51_436_52_65_450_66_90_6711_91_104_3806_105_194_3_896_195_195_3897_0	230	bursicon alpha	365	2.83E-60	85.80%	0.284	IPR004133 (PFAM); PTHR11339 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1346	c30064_g2_i7_len_998_path_384_0_51_436_52_65_450_66_90_6711_91_104_3806_105_194_68_19_195_195_6820_1_1	665	bursicon alpha	326	2.81E-32	83.30%	0.232	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1347	c30064_g2_i8_len_1364_path_5573_0_151_3487_152_470_3806_471_560_6819_561_561_6820_562_669_4186_670_2	672	bursicon alpha	443	4.43E-32	84.20%	0.108	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1348	c30064_g2_i9_len_1180_path_384_0_51_436_52_65_450_66_90_6711_91_104_3806_105_194_3_896_195_195_3897_0	752	cg13419	387	2.52E-60	85.40%	0.284	IPR004133 (PFAM); PTHR11339 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006207 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM)
1349	c30069_g1_i1_len_1258_path_196_0_68_136_69_138_349_139_175_386_176_255_3453_256_8_79_1086_880_903_3	211	histone h1	412	2.83E-38	72.40%	0.216	IPR005819 (PRINTS); IPR005818 (SMART); IPR005818 (PFAM); IPR011991 (G3DSA:1.10.10.GENE3D); PTHR11467 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR005818 (PROSITE_PROFILES); SSF46785 (SUPERFAMILY)

1350	c30069_g1_i2_len_1274_path_196_0_68_264_69_84_136_85_154_349_155_191_386_192_271_3_453_272_895_10_3	236	histone h1	418	2.68E-38	71.40%	0.216	IPR005819 (PRINTS); IPR005818 (SMART); IPR011991 (G3DSA:1.10.10.GENE3D); IPR005818 (PFAM); PTHR11467 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR005818 (PROSITE_PROFILES); SSF46785 (SUPERFAMILY)
1351	c30077_g3_i1_len_1270_path_1653_0_75_1729_76_78_1732_79_107_14637_108_122_5484_123_163_1815_164_193_0	339	cytolysin src-1-like	424	2.19E-21	52.50%	0.18	IPR015926 (G3DSA:2.60.270.GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR015926 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1352	c30077_g3_i2_len_1286_path_1653_0_75_9178_76_78_1732_79_107_1761_108_161_1815_162_191_1844_192_336_1	451	cytolysin src-1-like isoform x2	422	8.95E-25	51.20%	0.108	IPR015926 (G3DSA:2.60.270.GENE3D); IPR009104 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR015926 (SUPERFAMILY); TMhelix (TMHMM)
1353	c30077_g4_i1_len_327_path_1103_0_162_14716_163_184_14738_185_185_14739_186_205_571_1_206_326_0	2	---NA---	109			0.109	no IPS match
1354	c30116_g1_i1_len_1367_path_1527_0_16_4146_17_82_1610_83_346_1872_347_359_1885_360_445_4236_446_792_3	354	ras-related protein rab-37 isoform x2	451	6.28E-112	86.10%	0.236	IPR001806 (PRINTS); IPR020849 (SMART); IPR003579 (SMART); IPR003578 (SMART); IPR024156 (SMART); IPR002041 (SMART); IPR001806 (PFAM); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR24073:SF342 (PANTHER); PTHR24073 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1355	c30116_g1_i2_len_1476_path_3255_0_17_1610_18_281_1872_282_294_1885_295_380_4236_38_1_727_2316_728_72_3	353	ras-related protein rab-37 isoform x2	487	4.68E-112	87.40%	0.161	IPR001806 (PRINTS); IPR003579 (SMART); IPR002041 (SMART); IPR020849 (SMART); IPR024156 (SMART); IPR003578 (SMART); IPR001806 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); PTHR24073 (PANTHER); PTHR24073:SF342 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1356	c30116_g1_i3_len_1333_path_1527_0_16_4146_17_82_1610_83_346_1872_347_359_1885_360_445_4236_446_792_5	237	ras-related protein rab-37 isoform x2	439	5.44E-112	86.60%	0.118	IPR001806 (PRINTS); IPR003578 (SMART); IPR003579 (SMART); IPR020849 (SMART); IPR002041 (SMART); IPR024156 (SMART); IPR005225 (TIGRFAM); IPR001806 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR24073 (PANTHER); PTHR24073:SF342 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1357	c30116_g1_i4_len_1541_path_1527_0_16_4146_17_82_1610_83_346_1872_347_359_1885_360_445_4236_446_792_3	365	ras-related protein rab-37 isoform x2	509	1.31E-111	87.50%	0.161	IPR001806 (PRINTS); IPR024156 (SMART); IPR020849 (SMART); IPR003578 (SMART); IPR002041 (SMART); IPR003579 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR001806 (PFAM); PTHR24073 (PANTHER); PTHR24073:SF342 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1358	c30116_g1_i5_len_1640_path_2975_0_115_4146_116_181_1610_182_445_1872_446_458_1885_459_544_4236_545_3	376	ras-related protein rab-37 isoform x2	547	4.35E-111	87.10%	0.161	IPR001806 (PRINTS); IPR020849 (SMART); IPR003579 (SMART); IPR024156 (SMART); IPR002041 (SMART); IPR003578 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR001806 (PFAM); IPR005225 (TIGRFAM); PTHR24073:SF342 (PANTHER); PTHR24073 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1359	c30117_g1_i1_len_1521_path_6045_0_129_4676_130_131_4870_132_179_2284_180_215_5468_216_248_2353_249_0	199	zinc finger protein 85-like isoform x1	507	1.02E-26	53.40%	0.11	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1360	c30117_g1_i2_len_1583_path_2080_0_122_4797_123_184_5678_185_185_4862_186_193_4870_194_241_2284_242_2	187	zinc finger protein 37-like	527	1.47E-26	55.30%	0.105	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1361	c30117_g1_i3_len_1968_path_2080_0_122_2203_123_203_2284_204_239_2320_240_272_2353_273_362_2443_363_0	479	zinc finger protein 239-like	650	4.50E-26	53.40%	0.126	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1362	c30119_g1_i1_len_2699_path_1267_0_83_934_8_4_447_1713_448_881_2146_882_2596_7513_25_97_2611_7582_2612_1	162	gastrula zinc finger	900	1.25E-51	51.80%	0.163	IPR001713 (PRINTS); IPR015880 (SMART); IPR000010 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); IPR000010 (PFAM); G3DSA:3.10.450.10 (GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR018073 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF54403 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1363	c30124_g1_i2_len_2560_path_2722_0_720_3442_721_721_5785_722_745_3466_746_1320_4041_1321_1321_5537_1_2	572	di-n-acetylchitobiase	853	6.85E-91	59.10%	0.256	IPR011583 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF146 (PANTHER); IPR001579 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPRO17853 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1364	c30135_g4_i1_len_1782_path_4557_0_0_4558_1_24_13134_25_255_5611_256_257_5613_258_3_49_13455_350_369_4	147	apolipoprotein d	594	1.74E-09	45.20%	0.153	IPR000566 (PFAM); IPR012674 (G3DSA:2.40.128.GENE3D); PTHR10612:SF7 (PANTHER); PTHR10612 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPRO11038 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1365	c30148_g1_i1_len_1140_path_636_0_93_10492_94_97_10496_98_99_10498_100_100_10499_101_108_10507_109_1_2	364870	isoform a	372	6.34E-51	56.90%	0.604 Y	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1366	c30148_g1_i2_len_1147_path_636_0_93_730_94_100_10499_101_108_10507_109_141_10540_142_184_821_185_26_2	139510	isoform a	375	2.76E-49	56.80%	0.602 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR009003 (SUPERFAMILY)
1367	c30148_g1_i3_len_883_path_6849_0_143_10589_144_176_899_177_322_10791_323_327_9571_328_362_1085_363_0	87362	26kda protease	295	1.14E-48	56.80%	0.328	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1368	c30148_g1_i4_len_385_path_6849_0_143_10589_144_176_10620_177_384_0	5382	---NA---	129			0.323	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR009003 (SUPERFAMILY)
1369	c30158_g1_i2_len_244_path_1777_0_49_9668_5_0_123_1901_124_126_1904_127_160_4156_161_177_3403_178_236_1	0	zinc finger protein 558	81	9.01E-15	61.50%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1370	c30158_g1_i3_len_701_path_2131_0_289_10854_290_700_1	46	zinc finger protein 213	228	1.56E-21	61.80%	0.11	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1371	c30158_g1_i4_len_1671_path_10390_0_0_10391_1_5_1162_6_108_10419_109_123_1280_124_187_10466_188_229_1	287	zinc finger protein 850-like isoform x1	549	2.12E-44	57.70%	0.102	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1383	c30248_g3_i1_len_4379_path_14285_0_38_1432_4_39_62_16808_63_837_18356_838_838_7628_839_1666_8446_166_1	913	map kinase-interacting serine threonine-protein kinase 1	1460	0	77.10%	0.687 Y	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24349 (PANTHER); IPR008271 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
1384	c30248_g3_i2_len_4614_path_7457_0_170_1835_6_171_171_7628_172_999_8446_1000_1150_85_96_1151_1153_270_0	905	map kinase-interacting serine threonine-protein kinase 1	1538	0	82.40%	0.1	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24349 (PANTHER); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
1385	c30248_g3_i3_len_3712_path_7457_0_170_1835_6_171_171_7628_172_999_8446_1000_1150_85_96_1151_1153_270_0	905	map kinase-interacting serine threonine-protein kinase 1	1238	0	80.60%	0.1	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24349 (PANTHER); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);
1386	c30248_g3_i7_len_1237_path_7457_0_170_1835_6_171_171_7628_172_999_1679_1000_1236_0	122	map kinase-interacting serine threonine-protein kinase 1-like	413	8.05E-147	88.90%	0.1	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24349 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY);
1387	c30266_g2_i4_len_4331_path_3562_0_2687_516_06_2688_2695_51614_2696_2700_50895_2701_2845_26955_2846_2_5	198	bacterial transcriptional regulator family protein	1443	4.62E-63	100.00%	0.107	IPR029016 (G3DSA:3.30.450.GENE3D); IPR014757 (PFAM); PTHR30136:SF6 (PANTHER); PTHR30136 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR014757 (PROSITE_PROFILES); IPR029016 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM);
1388	c30268_g13_i1_len_1789_path_13728_0_441_14_169_442_442_8506_443_549_14276_550_574_1_6022_575_1788_5	146	beta- -n-acetylgalactosaminyltransferase bre-4	590	1.40E-123	66.70%	0.143	IPR003859 (PRINTS); IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR027995 (PFAM); IPR003859 (PANTHER); PTHR19300:SF30 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM);
1389	c30271_g18_i1_len_1992_path_11337_0_1991_3	85	trehalase-like isoform x1	664	6.60E-100	69.40%	0.105	IPR001661 (PRINTS); IPR001661 (PFAM); PTHR23403:SF1 (PANTHER); IPR001661 (PANTHER); IPR018232 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008928 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM);

1390	c30271_g19_i9_len_947_path_8421_0_185_3558_0_186_188_8610_189_946_3	68	cysteine string protein	316	3.20E-106	76.20%	0.162	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF5 (PANTHER); IPR018253 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1391	c30275_g19_i2_len_1731_path_10179_0_543_32_832_544_1730_1	46	alk tyrosine kinase receptor isoform x1	577	2.62E-108	57.70%	0.138	IPR000998 (SMART); IPR002172 (SMART); IPR000998 (PFAM); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR23282 (PANTHER); IPR023415 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
1392	c30284_g7_i1_len_884_path_2188_0_45_247_46_85_2273_86_102_2290_103_149_2337_150_15_9_2347_160_538_27_1	48	sortilin-related receptor	295	1.68E-10	54.20%	0.231	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1393	c30284_g7_i2_len_1260_path_223_0_23_247_24_63_7603_64_80_2290_81_127_11838_128_128_2347_129_507_272_0	60	low-density lipoprotein receptor-related protein 2-like	420	1.71E-12	45.20%	0.385 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1394	c30313_g1_i3_len_1134_path_1_0_130_5071_13_1_135_137_136_157_159_158_225_5097_226_2_28_5100_229_316_2_3	569	histone h2b	372	1.16E-64	99.00%	0.108	IPR000558 (PRINTS); IPR000558 (SMART); IPR007125 (PFAM); IPR009072 (G3DSA:1.10.20.GENE3D); IPR000558 (PANTHER); IPR000558 (PROSITE_PATTERNS); IPR009072 (SUPERFAMILY)
1395	c30315_g8_i1_len_1581_path_2785_0_656_2855_2_657_659_3444_660_1455_4240_1456_1580_4	1600	torsin- partial	520	6.83E-110	66.80%	0.13	Coil (COILS); IPR010448 (PFAM); IPR009724 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR010448 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1396	c30315_g8_i2_len_1680_path_2785_0_656_2760_657_657_2761_658_702_28498_703_707_2850_4_708_717_28514_7_4	1100	torsin- partial	553	8.43E-103	60.90%	0.13	Coil (COILS); IPR027417 (G3DSA:3.40.50.GENE3D); IPR009724 (PFAM); IPR010448 (PFAM); IPR010448 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1397	c30341_g1_i1_len_1218_path_3299_0_181_3476_182_196_1225_197_250_4565_251_294_3587_295_344_4826_345_0	17300	ves g 5 allergen	400	1.77E-46	52.80%	0.383 Y	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (PFAM); IPR014044 (G3DSA:3.40.33.GENE3D); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR014044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1398	c30343_g1_i1_len_2320_path_2548_0_361_2910_362_376_2925_377_524_3071_525_526_3073_527_1013_3558_101_2	855	phenoloxidase subunit a3	757	0	60.70%	0.612 Y	IPR013788 (PRINTS); IPR005203 (PFAM); IPR008922 (G3DSA:1.10.1280.GENE3D); IPR005203 (G3DSA:2.60.40.GENE3D); IPR000896 (PFAM); IPR005204 (G3DSA:1.20.1370.GENE3D); IPR005204 (PFAM); PTHR11511:SF24 (PANTHER); IPR013788 (PANTHER); IPR002227 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); IPR013788 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR008922 (SUPERFAMILY); IPR005204 (SUPERFAMILY); IPR014756 (SUPERFAMILY)
1399	c30343_g1_i2_len_793_path_5805_0_361_4431_362_792_2	34	phenoloxidase subunit a3-like	248	2.14E-53	60.10%	0.099	IPR005203 (PFAM); IPR005203 (G3DSA:2.60.40.GENE3D); PTHR11511:SF24 (PANTHER); IPR013788 (PANTHER); IPR014756 (SUPERFAMILY)
1400	c30346_g1_i3_len_1794_path_927_0_414_1342_415_500_1428_501_513_6066_514_577_6113_578_586_6122_587_5_2	355	probable cytochrome p450 49a1	592	2.10E-137	60.50%	0.265	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (PFAM); IPR001128 (G3DSA:1.10.630.GENE3D); PTHR24305:SF49 (PANTHER); PTHR24305 (PANTHER); IPR017972 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001128 (SUPERFAMILY); TMhelix (TMHMM)
1401	c30368_g1_i1_len_740_path_2300_0_69_9482_7_0_73_9486_74_93_198_94_201_306_202_324_9_240_325_355_3748_2	94156	low-density lipoprotein receptor-related protein 2 isoform x2	246	1.34E-38	56.50%	0.783 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1402	c30368_g1_i2_len_1910_path_3392_0_72_9482_73_76_9486_77_96_2393_97_113_2410_114_142_3533_143_204_30_2	995917	suppressor of tumorigenicity 14 partial	628	6.12E-79	52.20%	0.391 Y	IPR002172 (PRINTS); IPR001254 (SMART); IPR002172 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24256 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)
1403	c30368_g1_i3_len_1480_path_3392_0_72_9482_73_76_3468_77_113_2410_114_142_7166_143_697_4674_698_744_2	615193	suppressor of tumorigenicity 14 protein	486	3.84E-53	52.30%	0.518 Y	IPR001314 (PRINTS); IPR001254 (SMART); IPR002172 (SMART); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001254 (PFAM); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-TM (SIGNALP_EUK); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM)

1404	c30382_g13_i1_len_1594_path_48049_0_571_15326_572_642_15398_643_1078_15834_1079_1434_42551_1435_145_4	175	maguk p55 subfamily member 6 isoform x2	526	7.67E-19	79.60%	0.146	IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23122 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1405	c30382_g13_i2_len_2383_path_15325_0_0_15326_1_71_15397_72_72_15398_73_508_16390_509_1975_33883_1976_4	256	maguk p55 subfamily member 6 isoform x1	789	0	76.90%	0.269	IPR001452 (SMART); IPR008145 (SMART); IPR001478 (SMART); IPR004172 (SMART); IPR001478 (G3DSA:2.30.42.GENE3D); IPR011511 (PFAM); IPR001478 (PFAM); G3DSA:3.30.63.10 (GENE3D); IPR008145 (PFAM); G3DSA:2.30.30.40 (GENE3D); IPR014775 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23122 (PANTHER); IPR020590 (PROSITE_PATTERNS); IPR004172 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR008144 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); IPR027417 (SUPERFAMILY); IPR001478 (SUPERFAMILY); SSF101288 (SUPERFAMILY)
1406	c30382_g13_i3_len_2854_path_48049_0_571_15326_572_642_15397_643_643_15398_644_1079_16390_1080_2546_3	294	calcium calmodulin-dependent serine protein kinase	946	0	75.30%	0.109	IPR001478 (SMART); IPR001452 (SMART); IPR004172 (SMART); IPR008145 (SMART); G3DSA:3.30.63.10 (GENE3D); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); G3DSA:2.30.30.40 (GENE3D); IPR014775 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR008145 (PFAM); IPR011511 (PFAM); PTHR23122 (PANTHER); IPR020590 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR004172 (PROSITE_PROFILES); IPR008144 (PROSITE_PROFILES); IPR001478 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); IPR001478 (SUPERFAMILY); IPR027417 (SUPERFAMILY); SSF101288 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1407	c30386_g1_i1_len_1409_path_1867_0_46_1914_47_168_2036_169_180_2048_181_1014_2869_1015_1021_116_1_0	476	marginal zone b- and b1-cell-specific	461	4.73E-42	56.40%	0.19	PTHR15881:SF1 (PANTHER); PTHR15881 (PANTHER)
1408	c30416_g2_i1_len_1898_path_5764_0_109_5874_110_113_5878_114_155_5920_156_169_5934_170_299_6064_300_1	82423	matrix metalloproteinase-9 precursor	633	2.99E-14	50.30%	0.787 Y	IPR001314 (PRINTS); IPR000562 (SMART); IPR001254 (SMART); IPR000562 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR000562 (G3DSA:2.10.10.GENE3D); IPR001254 (PFAM); IPR000562 (G3DSA:2.10.10.GENE3D); PTHR24260 (PANTHER); PTHR24260:SF51 (PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR009003 (SUPERFAMILY); IPR013806 (SUPERFAMILY); IPR013806 (SUPERFAMILY); TMhelix (TMHMM)
1409	c30416_g2_i2_len_3809_path_5764_0_109_5874_110_113_5878_114_155_5920_156_169_5934_170_299_6064_300_1	121765	matrix metalloproteinase 9	1270	4.89E-17	49.30%	0.787 Y	IPR000562 (SMART); IPR001254 (SMART); IPR000562 (G3DSA:2.10.10.GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR000562 (G3DSA:2.10.10.GENE3D); IPR000562 (PFAM); PTHR24260 (PANTHER); PTHR24260:SF51 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR000562 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR000562 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); IPR013806 (SUPERFAMILY); IPR009003 (SUPERFAMILY); IPR013806 (SUPERFAMILY); TMhelix (TMHMM)

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1416	c30425_g2_i2_len_1853_path_7069_0_213_2893_214_228_6748_229_274_7341_275_315_6248_316_344_7409_345_5	525	low quality protein: gastrula zinc finger	617	1.21E-46	56.20%	0.1		IPR015880 (SMART); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1417	c30425_g2_i3_len_1936_path_2443_0_290_6943_291_301_2744_302_338_2781_339_450_2893_451_465_6748_466_4	223	zinc finger protein 699-like	640	6.73E-59	54.90%	0.104		IPR015880 (SMART); PF13912 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1418	c30425_g2_i4_len_1700_path_7069_0_213_2893_214_228_6748_229_274_7341_275_315_6248_316_344_7409_345_5	322	gastrula zinc finger protein - partial	566	9.79E-47	55.60%	0.389 Y		IPR015880 (SMART); IPR007087 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1419	c30425_g2_i5_len_1599_path_2443_0_290_6943_291_301_2744_302_338_2781_339_450_2893_451_465_6748_466_3	82	gastrula zinc finger	528	4.16E-61	56.40%	0.113		IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

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1424	c30439_g13_i2_len_2511_path_1825_0_1822_36_48_1823_1923_21617_1924_1945_39494_1946_1953_39502_1954_1_3	93	zinc finger protein 782-like	837	2.66E-55	51.10%	0.108	IPR015880 (SMART); PF13912 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1425	c30447_g1_i1_len_1206_path_871_0_181_1053_182_379_1251_380_385_1257_386_409_1281_410_487_5616_48_4	3	hypothetical protein DAPPUDRAFT_194525	402	1.43E-49	41.00%	0.24	IPR013781 (G3DSA:3.20.20.GENE3D); IPR017853 (SUPERFAMILY)
1426	c30465_g8_i4_len_1460_path_34871_0_87_2851_9_88_111_28543_112_351_36118_352_369_361_36_370_371_36138_4	114	---NA---	487			0.115	Coil (COILS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM)
1427	c30465_g8_i4_len_1460_path_34871_0_87_2851_9_88_111_28543_112_351_36118_352_369_361_36_370_371_36138_5	114	---NA---	486			0.111	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1428	c30474_g1_i1_len_1140_path_8396_0_44_13258_45_51_8448_52_155_10747_156_423_6770_42_4_462_4312_463_50_4	139	PREDICTED: putative uncharacterized protein ART2-like, partial	373	1.38E-09	70.10%	0.106	no IPS match
1429	c30474_g1_i4_len_1039_path_8396_0_44_13258_45_51_8448_52_155_10747_156_423_6770_42_4_462_4312_463_50_3	389	unnamed protein product	341	2.75E-09	72.10%	0.123	no IPS match
1430	c30486_g1_i1_len_1111_path_793_0_118_912_1_19_348_1142_349_1110_2	24	tyrosine-protein kinase receptor tie-1	370	9.97E-19	57.70%	0.11	G3DSA:2.170.300.10 (GENE3D); PTHR24416:SF125 (PANTHER); PTHR24416 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1431	c30486_g1_i2_len_889_path_21260_0_126_1142_127_888_2	32	tyrosine-protein kinase receptor tie-1	296	1.69E-18	57.90%	0.185	G3DSA:2.170.300.10 (GENE3D); PTHR24416 (PANTHER); PTHR24416:SF125 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1432	c30498_g16_i4_len_809_path_15533_0_750_162_84_751_752_8796_753_753_2320_754_808_4	17	agrin-like isoform x6	270	1.98E-26	79.70%	0.266	IPR013320 (G3DSA:2.60.120.GENE3D); IPR001791 (PFAM); PTHR10574 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR013320 (SUPERFAMILY)
1433	c30499_g2_i1_len_947_path_3833_0_399_2966_400_526_11958_527_531_4531_532_696_389_6_97_720_12009_721_0	15	dehydrogenase reductase sdr family member 11	316	2.77E-13	85.70%	0.109	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF310 (PANTHER); SSF51735 (SUPERFAMILY)
1434	c30499_g2_i1_len_947_path_3833_0_399_2966_400_526_11958_527_531_4531_532_696_389_6_97_720_12009_721_2	15	dehydrogenase reductase sdr family member 11 isoform x2	315	2.46E-11	78.10%	0.205	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1435	c30499_g2_i2_len_1061_path_3807_0_11_11881_12_25_3833_26_425_11916_426_428_4235_42_9_594_2966_595_72_2	100	dehydrogenase reductase sdr family member 11-like	353	5.10E-57	74.80%	0.117	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1436	c30499_g2_i3_len_1618_path_3833_0_399_2966_400_526_11958_527_531_469_532_666_604_667_1494_1432_1_0	125	dehydrogenase reductase sdr family member 11-like	534	8.58E-13	86.00%	0.109	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF310 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY)

1437	c30499_g2_i3_len_1618_path_3833_0_399_2966_400_526_11958_527_531_469_532_666_604_667_1494_1432_1_2	125	dehydrogenase reductase sdr family member 11-like	533	5.08E-54	75.00%	0.205	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF310 (PANTHER); SSF51735 (SUPERFAMILY)
1438	c30499_g2_i4_len_1813_path_3807_0_11_11881_12_25_3833_26_425_11916_426_428_4235_42_9_594_2966_595_72_2	154	dehydrogenase reductase sdr family member 11-like	598	2.84E-99	74.00%	0.117	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF310 (PANTHER); SSF51735 (SUPERFAMILY)
1439	c30499_g2_i5_len_1478_path_3833_0_399_2966_400_526_604_527_1354_1432_1355_1372_14_50_1373_1477_0	113	dehydrogenase reductase sdr family member 11-like	487	1.99E-17	67.90%	0.109	IPR016040 (G3DSA:3.40.50.GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322 (PANTHER); PTHR24322:SF310 (PANTHER); SSF51735 (SUPERFAMILY)
1440	c30499_g2_i5_len_1478_path_3833_0_399_2966_400_526_604_527_1354_1432_1355_1372_14_50_1373_1477_2	113	dehydrogenase reductase sdr family member 11-like	487	2.26E-10	81.10%	0.205	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY)
1441	c30499_g2_i6_len_1673_path_3807_0_11_11881_12_25_3833_26_425_11916_426_428_4235_42_9_594_2966_595_72_0	135	dehydrogenase reductase sdr family member 11-like	552	1.12E-14	72.20%	0.109	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER)
1442	c30499_g2_i6_len_1673_path_3807_0_11_11881_12_25_3833_26_425_11916_426_428_4235_42_9_594_2966_595_72_2	135	dehydrogenase reductase sdr family member 11	552	8.52E-55	77.00%	0.117	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY)
1443	c30499_g2_i7_len_630_path_7853_0_12_11881_13_26_3833_27_426_11916_427_429_7604_430_629_0	6	dehydrogenase reductase sdr family member 11-like	210	6.33E-14	85.20%	0.121	IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER); SSF51735 (SUPERFAMILY)
1444	c30501_g12_i1_len_2106_path_23657_0_1265_9_722_1266_2105_5	72	u4 u6 small nuclear ribonucleoprotein prp31	702	0	84.50%	0.133	IPR012976 (SMART); IPR012976 (PFAM); IPR019175 (PFAM); IPR002687 (PFAM); IPR027105 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002687 (PROSITE_PROFILES); SSF89124 (SUPERFAMILY); TMhelix (TMHMM)
1445	c30522_g10_i1_len_2579_path_24415_0_1645_2_6057_1646_1667_26079_1668_1807_26219_180_8_1823_26235_1824_2	112	abhydrolase domain-containing protein 16a	854	0	68.90%	0.146	IPR029058 (G3DSA:3.40.50.GENE3D); IPR029059 (PFAM); PTHR12277:SF44 (PANTHER); PTHR12277 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1446	c30522_g10_i2_len_2556_path_24415_0_1645_2_6079_1646_1785_31848_1786_1800_26235_180_1_1814_12570_1815_2	92	abhydrolase domain-containing protein 16a	846	0	69.00%	0.146	IPR029058 (G3DSA:3.40.50.GENE3D); IPR029059 (PFAM); PTHR12277:SF44 (PANTHER); PTHR12277 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029058 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1447	c30526_g1_i6_len_2022_path_5247_0_94_5342_95_807_6053_808_813_11626_814_1129_11234_1130_1140_6385_1_2	881	hemagglutinin amebocyte aggregation factor-like	674	2.96E-36	58.10%	0.219	PF14704 (PFAM); IPR026645 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1448	c30552_g4_i1_len_1303_path_20735_0_255_868_9_256_1302_3	29	cation channel sperm-associated protein subunit gamma	435	1.10E-07	48.00%	0.111	CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1449	c30552_g4_i1_len_1303_path_20735_0_255_868_9_256_1302_4	29	hypothetical protein TGVAND_316635A, partial	434	2.47E-08	59.00%	0.108	TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1455	c30580_g5_i1_len_902_path_5283_0_752_20742_753_755_20745_756_766_20756_767_769_20759_770_775_20765_0	11	slit homolog 3 partial	301	2.58E-15	68.40%	0.109	IPR000372 (SMART); IPR000372 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24369 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF52058 (SUPERFAMILY); TMhelix (TMHMM)
1456	c30587_g2_i1_len_696_path_3932_0_32_3965_3_3_347_3932_348_380_3965_381_695_3	9	zinc finger protein	232	6.46E-37	57.00%	0.1	IPR015880 (SMART); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); IPR000560 (PFAM); IPR029033 (G3DSA:3.40.50.GENE3D); PTHR11567 (PANTHER); PTHR11567:SF26 (PANTHER); IPR000560 (PROSITE_PATTERNS); IPR000560 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR029033 (SUPERFAMILY); TMhelix (TMHMM)
1457	c30603_g43_i1_len_1388_path_6125_0_505_663_1_506_979_59586_980_1387_2	76	prostatic acid phosphatase-like	457	1.99E-122	63.60%	0.456 Y	IPR000560 (PFAM); IPR029033 (G3DSA:3.40.50.GENE3D); PTHR11567 (PANTHER); PTHR11567:SF26 (PANTHER); IPR000560 (PROSITE_PATTERNS); IPR000560 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR029033 (SUPERFAMILY); TMhelix (TMHMM)
1458	c30603_g43_i2_len_1080_path_6125_0_505_663_1_506_979_7105_980_1037_7163_1038_1066_6_1575_1067_1079_2	77	lysosomal acid phosphatase	360	6.72E-102	66.80%	0.456 Y	IPR000560 (PFAM); IPR029033 (G3DSA:3.40.50.GENE3D); PTHR11567 (PANTHER); PTHR11567:SF26 (PANTHER); IPR000560 (PROSITE_PATTERNS); IPR000560 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR029033 (SUPERFAMILY)
1459	c30605_g3_i1_len_2413_path_7175_0_22_27573_23_31_27582_32_32_8149_33_78_8195_79_93_0_6868_931_2412_4	2941	beta-galactosidase-1-like protein 2	799	0	64.10%	0.103	IPR001944 (PRINTS); IPR013781 (G3DSA:3.20.20.GENE3D); IPR001944 (PFAM); IPR008979 (G3DSA:2.60.120.GENE3D); PTHR23421:SF66 (PANTHER); IPR001944 (PANTHER); IPR019801 (PROSITE_PATTERNS); IPR008979 (SUPERFAMILY); IPR017853 (SUPERFAMILY)
1460	c30615_g12_i1_len_1218_path_7349_0_794_426_4_795_818_4288_819_1217_1	122	adrenodoxin	401	4.46E-51	77.70%	0.112	IPR001055 (PRINTS); IPR012675 (G3DSA:3.10.20.GENE3D); IPR001041 (PFAM); PTHR23426 (PANTHER); PTHR23426:SF21 (PANTHER); IPR018298 (PROSITE_PATTERNS); IPR001041 (PROSITE_PROFILES); IPR001041 (SUPERFAMILY)
1461	c30619_g12_i2_len_1381_path_5381_0_350_573_2_351_1016_2147_1017_1380_3	129	coiled-coil domain-containing protein 134-like	456	1.96E-52	65.00%	0.266	IPR026321 (PFAM); IPR026321 (PANTHER)
1462	c30637_g6_i1_len_2291_path_499_0_70_16912_34_110_134_33631_135_141_33638_142_144_3_74_576_10589_577_3	568	utp--glucose-1-phosphate uridylyltransferase-like	764	0	84.40%	0.108	IPR002618 (PFAM); IPR029044 (G3DSA:3.90.550.GENE3D); IPR016267 (PTHR11952:PANTHER); IPR002618 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1463	c30640_g14_i1_len_1548_path_24478_0_109_25_34_110_134_33631_135_141_33638_142_144_3_3641_145_148_3364_1	121	zinc finger protein 431-like isoform x2	510	4.26E-37	53.70%	0.558 Y	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13912 (PFAM); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1464	c30648_g7_i6_len_1898_path_28787_0_651_236_59_652_653_23661_654_1743_2500_1744_1893_33100_1894_1897_1	86	dbh-like monooxygenase protein 1	633	2.42E-29	50.50%	0.108	IPR014784 (G3DSA:2.60.120.GENE3D); PF03712 (PFAM); IPR000945 (PANTHER); IPR014783 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008977 (SUPERFAMILY)

1465	c30665_g17_i1_len_1278_path_4809_0_93_1527_4_94_551_975_552_573_20600_574_1277_5	38	zinc finger protein	426	4.69E-25	49.10%	0.098	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PTHR24375:SF106 (PANTHER); PTHR24375 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
1466	c30675_g2_i1_len_1456_path_8724_0_41_11362_42_61_8785_62_104_8827_105_107_5207_108_132_12171_133_14_4	434416	low quality protein: suppressor of tumorigenicity 14 protein	485	1.30E-81	53.10%	0.102	IPR002172 (PRINTS); IPR001254 (SMART); IPR002172 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1467	c30675_g2_i2_len_1752_path_8724_0_41_8766_42_61_8785_62_104_5204_105_107_5207_108_132_8854_133_142_3	1228052	suppressor of tumorigenicity 14 protein homolog	584	1.60E-82	52.20%	0.754 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1468	c30675_g2_i3_len_1795_path_10781_0_128_109_10_129_164_10946_165_197_2027_198_234_14_475_235_245_2075_4	1612752	suppressor of tumorigenicity 14 partial	591	5.32E-80	52.40%	0.440 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY)

1469	c30675_g2_i4_len_1508_path_10781_0_128_109 10_129_164_10946_165_197_2027_198_234_14 475_235_245_2075_5	933783	suppressor of tumorigenicity 14 protein	495	8.84E-80	53.10%	0.109	IPR002172 (PRINTS); IPR002172 (SMART); IPR001254 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001254 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR001254 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1470	c30690_g6_i4_len_1954_path_2511_0_1682_208 00_1683_1686_21459_1687_1693_12270_1694_1953_1	104	cd109 antigen-like isoform x1	644	0	75.20%	0.168	IPR011626 (PFAM); IPR009048 (G3DSA:2.60.40.GENE3D); IPR008930 (G3DSA:1.50.10.GENE3D); IPR009048 (PFAM); PTHR11412:SF84 (PANTHER); PTHR11412 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008930 (SUPERFAMILY); IPR009048 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1471	c30690_g6_i5_len_2961_path_2511_0_1682_208 00_1683_1686_4197_1687_1704_4215_1705_1861_4371_1862_1872_1	176	cd109 antigen-like isoform x1	987	0	76.70%	0.168	IPR009048 (G3DSA:2.60.40.GENE3D); IPR009048 (PFAM); IPR011626 (PFAM); IPR008930 (G3DSA:1.50.10.GENE3D); PTHR11412 (PANTHER); PTHR11412:SF84 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008930 (SUPERFAMILY); IPR009048 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1472	c30693_g3_i1_len_342_path_23746_0_2_23751_3_20_23361_21_21_14650_22_69_14698_70_88_23425_89_98_2343_4	0	hypothetical protein Y032_0655g1201	114	2.94E-06	66.67%	0.115	no IPS match
1473	c30709_g7_i1_len_1162_path_7009_0_820_7830_821_844_11719_845_1161_3	53	basement membrane-specific heparan sulfate proteoglycan core isoform x4	382	1.27E-86	77.00%	0.135	IPR013106 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013106 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR23279 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1474	c30733_g7_i2_len_1607_path_18226_0_580_188_06_581_608_6218_609_1517_19742_1518_1606_0	97	muscle-specific protein 20	536	6.15E-88	86.20%	0.531 Y	IPR003096 (PRINTS); IPR001997 (PRINTS); IPR001715 (SMART); IPR000557 (PFAM); IPR001715 (PFAM); IPR001715 (G3DSA:1.10.418.GENE3D); PTHR18959:SF51 (PANTHER); PTHR18959 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001715 (PROSITE_PROFILES); IPR000557 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR001715 (SUPERFAMILY)
1475	c3074_g1_i1_len_2164_path_53_0_2163_2	63	n-acetylgalactosamine-6-sulfatase isoform x1	715	0	70.50%	0.097	PF14707 (PFAM); IPR000917 (PFAM); G3DSA:3.30.1120.10 (GENE3D); IPR017849 (G3DSA:3.40.720.GENE3D); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342:SF27 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR017850 (SUPERFAMILY)

1484	c30779_g6_i3_len_1519_path_10524_0_1301_11_820_1302_1302_2862_1303_1326_19535_1327_1337_18710_1338_1_4	86	39s ribosomal protein mitochondrial	500	1.13E-141	68.70%	0.258	IPR008914 (G3DSA:3.90.280.GENE3D); IPR008914 (PFAM); PTHR11362:SF16 (PANTHER); PTHR11362 (PANTHER); IPR008914 (SUPERFAMILY)
1485	c30779_g6_i6_len_1526_path_10524_0_1301_11_820_1302_1302_2862_1303_1326_19535_1327_1337_18710_1338_1_5	94	39s ribosomal protein mitochondrial	502	7.37E-142	68.70%	0.139	IPR008914 (PFAM); IPR008914 (G3DSA:3.90.280.GENE3D); PTHR11362 (PANTHER); PTHR11362:SF16 (PANTHER); IPR008914 (SUPERFAMILY)
1486	c30785_g27_i1_len_700_path_39635_0_2_39638_3_4_39640_5_11_14214_12_699_1	41	epididymal secretory protein e1	218	6.28E-24	58.90%	0.283	IPR003172 (SMART); IPR003172 (PFAM); IPR003172 (G3DSA:2.60.40.GENE3D); PTHR11306:SF3 (PANTHER); PTHR11306 (PANTHER); IPR014756 (SUPERFAMILY)
1487	c30796_g1_i1_len_1068_path_139_0_56_12713_57_71_12728_72_87_976_88_174_12814_175_1_75_12815_176_187_0	40	5 -nucleotidase	356	2.67E-76	81.30%	0.125	IPR029052 (G3DSA:3.60.21.GENE3D); IPR006179 (PANTHER); PTHR11575:SF7 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029052 (SUPERFAMILY)
1488	c30809_g14_i2_len_466_path_16491_0_222_108_65_223_465_4	5	agap002578-pa-like protein	149	1.57E-57	85.90%	0.109	IPR027359 (G3DSA:1.20.120.GENE3D); IPR005821 (PFAM); IPR005447 (PTHR10037:PANTHER); PTHR10037 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF81324 (SUPERFAMILY)
1489	c30818_g8_i1_len_2855_path_34544_0_0_26742_1_1426_25878_1427_1527_28268_1528_2854_4	238	sparc-related modular calcium-binding protein 1-like isoform x2	952	2.09E-123	56.80%	0.105	IPR000716 (SMART); IPR002350 (SMART); IPR002350 (PFAM); IPR000716 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR011992 (G3DSA:1.10.238.GENE3D); IPR000716 (G3DSA:4.10.800.GENE3D); IPR019577 (PFAM); PTHR12352 (PANTHER); PTHR12352:SF3 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000716 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR000716 (SUPERFAMILY); SSF47473 (SUPERFAMILY); IPR000716 (SUPERFAMILY); SSF100895 (SUPERFAMILY); SSF47473 (SUPERFAMILY)
1490	c30818_g8_i2_len_1667_path_25639_0_238_258_78_239_339_28268_340_1666_4	79	sparc-related modular calcium-binding protein 1-like isoform x2	556	2.33E-124	57.10%	0.105	IPR000716 (SMART); IPR002350 (SMART); IPR000716 (G3DSA:4.10.800.GENE3D); IPR019577 (PFAM); G3DSA:3.30.60.30 (GENE3D); IPR000716 (PFAM); IPR002350 (PFAM); IPR011992 (G3DSA:1.10.238.GENE3D); PTHR12352 (PANTHER); PTHR12352:SF3 (PANTHER); IPR018247 (PROSITE_PATTERNS); IPR000716 (PROSITE_PATTERNS); IPR018247 (PROSITE_PATTERNS); IPR000716 (PROSITE_PROFILES); IPR000716 (PROSITE_PROFILES); IPR002350 (PROSITE_PROFILES); SSF47473 (SUPERFAMILY); IPR000716 (SUPERFAMILY); SSF100895 (SUPERFAMILY); IPR000716 (SUPERFAMILY); SSF47473 (SUPERFAMILY)
1491	c30823_g14_i1_len_662_path_15372_0_371_208_37_372_382_20949_383_385_20954_386_661_0	6	unknown	221	3.23E-07	56.00%	0.121	IPR000477 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000742 (PROSITE_PROFILES); TMhelix (TMHMM); TMhelix (TMHMM)
1492	c30906_g1_i1_len_1956_path_1_0_1955_0	1140	adp-ribosylation factor 1	652	1.08E-126	98.50%	0.11	IPR006689 (PRINTS); IPR003579 (SMART); IPR006687 (SMART); IPR024156 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); IPR005225 (TIGRFAM); PTHR11711:SF118 (PANTHER); PTHR11711 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1493	c30930_g1_i1_len_1434_path_1412_0_1433_2	6308	virulence metalloprotease	471	2.84E-16	54.20%	0.13	IPR025711 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1494	c30934_g1_i1_len_2590_path_1_0_2589_2	82	aminopeptidase n	863	0	100.00%	0.375 Y	IPR014782 (PRINTS); IPR012779 (TIGRFAM); IPR024601 (PFAM); IPR024601 (G3DSA:1.25.50.GENE3D); IPR014782 (PFAM); G3DSA:1.10.390.10 (GENE3D); IPR001930 (PANTHER); PTHR11533:SF152 (PANTHER); SSF63737 (SUPERFAMILY); SSF55486 (SUPERFAMILY)
1495	c30963_g1_i1_len_2256_path_1_0_2255_2	67	lachesin-like isoform x1	752	4.06E-86	73.00%	0.285	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR23279:SF12 (PANTHER); PTHR23279 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1496	c31076_g1_i1_len_1748_path_1726_0_1747_2	91	integrin-linked protein kinase	582	0	87.10%	0.229	IPR002110 (SMART); IPR002110 (PFAM); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR23257 (PANTHER); PTHR23257:SF30 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020683 (PROSITE_PROFILES); IPR000719 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); IPR020683 (SUPERFAMILY); TMhelix (TMHMM)
1497	c31104_g1_i1_len_684_path_1_0_683_1	8	udp-n-acetyl-d-mannosaminuronic acid transferase	228	3.42E-142	99.30%	0.114	IPR004629 (PFAM); IPR004629 (TIGRFAM)
1498	c31234_g1_i1_len_786_path_1_0_785_2	9	hypothetical protein L798_00519	262	1.75E-30	50.20%	0.101	IPR002157 (PFAM); IPR008930 (G3DSA:1.50.10.GENE3D); PTHR10559:SF12 (PANTHER); IPR002157 (PANTHER); IPR008930 (SUPERFAMILY)
1499	c31319_g1_i1_len_889_path_1_0_888_0	63	hemagglutinin amebocyte aggregation factor-like	297	1.29E-29	57.60%	0.269	PF14704 (PFAM); IPR026645 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1500	c31501_g1_i1_len_887_path_1_0_886_3	15	serine protease easter-like	296	1.23E-40	59.30%	0.171	IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF54 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1501	c31501_g1_i1_len_887_path_1_0_886_4	15	serine protease easter	296	7.05E-16	71.20%	0.139	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24260 (PANTHER); PTHR24260:SF3 (PANTHER); IPR018114 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1502	c31508_g1_i1_len_1184_path_1_0_1183_2	28	threonine synthase-like 2	394	7.16E-106	73.10%	0.634 Y	IPR029144 (PFAM); G3DSA:3.40.50.1100 (GENE3D); IPR029144 (G3DSA:3.90.1380.GENE3D); PTHR10314 (PANTHER); IPR027457 (PTHR10314:PANTHER); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR001926 (SUPERFAMILY)
1503	c31650_g1_i1_len_549_path_527_0_548_0	8	wnt8-like protein 1	178	3.31E-34	65.60%	0.1	IPR005817 (SMART); IPR005817 (PFAM); IPR005817 (PANTHER); IPR026540 (PTHR12027:PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS)
1504	c31656_g1_i1_len_1551_path_1529_0_1550_1	59	folate receptor alpha-like	512	3.59E-80	68.10%	0.299	IPR018143 (PFAM); PTHR10517:SF3 (PANTHER); IPR004269 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1505	c3168_g1_i1_len_1934_path_363_0_784_23_785_942_181_943_1933_0	95	prenylcysteine oxidase-like	645	2.58E-58	56.70%	0.237	IPR010795 (PFAM); IPR017046 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1506	c3168_g1_i1_len_1934_path_363_0_784_23_785_942_181_943_1933_1	95	prenylcysteine oxidase-like	645	3.83E-57	64.10%	0.173	PF13450 (PFAM); IPR010795 (PFAM); G3DSA:3.50.50.60 (GENE3D); IPR017046 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51905 (SUPERFAMILY)
1507	c3168_g1_i2_len_1776_path_363_0_784_181_785_1775_1	86	prenylcysteine oxidase-like	592	1.12E-137	59.30%	0.173	PF13450 (PFAM); G3DSA:3.50.50.60 (GENE3D); IPR010795 (PFAM); IPR017046 (PANTHER); SSF51905 (SUPERFAMILY)
1508	c31681_g1_i1_len_2123_path_2101_0_2122_4	64	zinc finger protein 226 isoform x1	702	2.22E-47	56.70%	0.108	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1509	c31703_g1_i1_len_471_path_1_0_470_3	2	carbohydrate sulfotransferase 11-like isoform x1	154	2.11E-31	67.90%	0.108	IPR005331 (PFAM); PTHR12137:SF30 (PANTHER); IPR018011 (PANTHER)
1510	c31764_g1_i1_len_878_path_1_0_877_3	5	zinc finger protein 239-like	293	6.25E-26	59.20%	0.157	IPR015880 (SMART); G3DSA:3.30.710.10 (GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR013069 (PFAM); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR000210 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR011333 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1511	c31845_g1_i1_len_727_path_1_0_726_3	6	zinc finger protein 271-like	243	1.73E-49	55.80%	0.098	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1512	c31914_g1_i1_len_896_path_1_0_895_0	53	spermatogenesis-associated protein 5	293	4.49E-141	82.30%	0.104	Coil (COILS); IPR003593 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR003959 (PFAM); G3DSA:1.10.8.60 (GENE3D); PTHR23077 (PANTHER); PTHR23077:SF27 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)

1513	c32007_g2_i1_len_1594_path_2302_0_940_3243_941_942_3245_943_1029_3332_1030_1053_3528_1054_1593_1	52	zinc finger protein	531	6.91E-41	54.60%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1514	c32070_g1_i1_len_1979_path_1_0_1978_1	98	katanin p60 atpase-containing subunit a-like 1	660	0	82.00%	0.317	IPR003593 (SMART); IPR015415 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:1.10.8.60 (GENE3D); IPR003959 (PFAM); PTHR23074 (PANTHER); PTHR23074:SF65 (PANTHER); IPR003960 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); IPR028596 (HAMAP); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1515	c32133_g1_i1_len_1678_path_1_0_1677_4	63	ikaros family zinc finger protein	559	4.69E-93	51.80%	0.101	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1516	c32186_g1_i1_len_1627_path_1_0_1626_0	115	flavin-containing monooxygenase fmo gs-ox4-like isoform x1	537	6.38E-134	62.90%	0.308	IPR000960 (PRINTS); G3DSA:3.50.50.60 (GENE3D); IPR020946 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR23023:SF4 (PANTHER); PTHR23023 (PANTHER); SSF51905 (SUPERFAMILY); SSF51905 (SUPERFAMILY); TMhelix (TMHMM)
1517	c32210_g1_i1_len_513_path_491_0_512_3	8	lipase 3-like	171	1.97E-47	70.90%	0.157	IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11005:SF6 (PANTHER); PTHR11005 (PANTHER); IPR029058 (SUPERFAMILY)
1518	c32221_g1_i1_len_1311_path_1289_0_1310_0	23	retinol dehydrogenase 13	437	1.50E-111	71.10%	0.134	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320:SF38 (PANTHER); PTHR24320 (PANTHER); IPR020904 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY)
1519	c32435_g1_i1_len_385_path_363_0_384_2	1	retinol dehydrogenase 13-like	128	3.53E-35	74.30%	0.243	IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24320 (PANTHER); PTHR24320:SF38 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1520	c32656_g1_i1_len_1935_path_1_0_1934_1	61	antigen partial	645	0	99.00%	0.235	IPR024973 (PFAM); IPR012332 (G3DSA:2.160.20.GENE3D); PTHR12338 (PANTHER)
1521	c32756_g1_i1_len_518_path_496_0_517_2	4	retinol dehydrogenase 11-like	172	5.41E-59	72.00%	0.315	IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF305 (PANTHER); PTHR24316 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM)
1522	c33010_g1_i1_len_313_path_1_0_312_5	2	hemagglutinin	104	6.33E-16	57.60%	0.128	IPR001570 (PFAM); G3DSA:1.10.390.10 (GENE3D); SSF55486 (SUPERFAMILY)

1523	c33123_g1_i1_len_1645_path_1_0_1644_1	42	serine threonine-protein kinase nek7	542	4.29E-178	91.10%	0.145	IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); IPR000719 (PFAM); PTHR24362:SF228 (PANTHER); PTHR24362 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1524	c33144_g1_i1_len_1074_path_1_0_1073_1	9	pentapeptide repeats family protein	358	0	100.00%	0.117	IPR025726 (PFAM)
1525	c33176_g1_i1_len_678_path_726_0_677_2	6	gelsolin	226	3.18E-35	75.30%	0.244	IPR029006 (G3DSA:3.40.20.GENE3D); IPR007122 (PANTHER); IPR030004 (PTHR11977:PANTHER); SSF55753 (SUPERFAMILY)
1526	c33193_g1_i1_len_1369_path_1_0_1368_2	45	insulin-degrading enzyme isoform x2	456	3.77E-97	70.60%	0.107	IPR007863 (PFAM); IPR011237 (G3DSA:3.30.830.GENE3D); PTHR11851 (PANTHER); PTHR11851:SF109 (PANTHER); IPR011249 (SUPERFAMILY)
1527	c33273_g1_i1_len_380_path_358_0_379_1	1	hsp70 family protein	127	1.47E-83	100.00%	0.11	IPR029047 (G3DSA:2.60.34.GENE3D); IPR013126 (PFAM); IPR029048 (G3DSA:1.20.1270.GENE3D); PTHR19375 (PANTHER); PTHR19375:SF173 (PANTHER); IPR029047 (SUPERFAMILY)
1528	c33490_g1_i1_len_536_path_514_0_535_4	8	dna-specific endonuclease i	179	1.17E-66	100.00%	0.107	IPR007346 (PFAM); SSF54060 (SUPERFAMILY)
1529	c33527_g1_i1_len_1192_path_1_0_1191_0	8	carbohydrate binding domain-containing protein	398	3.07E-70	99.30%	0.125	IPR007419 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1530	c33609_g1_i1_len_1423_path_1_0_1422_0	27	aspartate--trna mitochondrial	475	0	72.10%	0.107	IPR002312 (PRINTS); IPR004364 (PFAM); IPR004524 (TIGRFAM); IPR004115 (G3DSA:3.30.1360.GENE3D); G3DSA:3.30.930.10 (GENE3D); IPR029351 (PFAM); IPR004524 (PTHR22594:PANTHER); IPR018150 (PANTHER); IPR006195 (PROSITE_PROFILES); IPR004115 (SUPERFAMILY); SSF55681 (SUPERFAMILY)
1531	c33635_g1_i1_len_981_path_959_0_980_5	12	glucose dehydrogenase	327	1.26E-71	63.00%	0.102	G3DSA:3.30.560.10 (GENE3D); IPR000172 (PFAM); G3DSA:3.50.50.60 (GENE3D); IPR007867 (PFAM); PTHR11552 (PANTHER); PTHR11552:SF77 (PANTHER); IPR000172 (PROSITE_PATTERNS); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY)
1532	c33786_g1_i1_len_612_path_1076_0_611_1	3	50MGP	204	1.06E-14	50.20%	0.235	PTHR11008 (PANTHER); PTHR11008:SF13 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR020234 (PRODOM)
1533	c33913_g1_i1_len_926_path_1_0_925_0	12	collagen alpha-1 chain	309	3.22E-20	58.60%	0.101	IPR008160 (PFAM); PTHR24023:SF372 (PANTHER); PTHR24023 (PANTHER)
1534	c33913_g1_i1_len_926_path_1_0_925_2	12	cre-let-2 protein	308	1.32E-17	62.10%	0.114	IPR008160 (PFAM)
1535	c33913_g1_i1_len_926_path_1_0_925_3	12	serine-aspartate repeat protein f	309	2.17E-18	42.60%	0.246	no IPS match
1536	c33949_g1_i1_len_619_path_1_0_618_4	4	phosphoglycerol transferase partial	206	7.49E-150	99.40%	0.127	IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342 (PANTHER); PTHR10342:SF182 (PANTHER); IPR017850 (SUPERFAMILY)
1537	c34084_g1_i1_len_534_path_1_0_533_2	4	thioredoxin domain-containing protein 5	178	3.99E-45	71.10%	0.281	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR005788 (TIGRFAM); PTHR18929 (PANTHER); PTHR18929:SF52 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1538	c34109_g1_i1_len_241_path_1_0_240_3	0	neutral ceramidase-like	81	5.19E-28	77.70%	0.11	IPR006823 (PFAM); PTHR12670:SF1 (PANTHER); IPR006823 (PANTHER)
1539	c34160_g1_i1_len_163_path_1_0_162_5	0	acyl- -binding domain-containing protein 4 isoform x1	54	2.70E-06	72.50%	0.116	no IPS match
1540	c34174_g1_i1_len_514_path_1_0_513_5	6	glucosidase 2 subunit beta	171	2.67E-63	70.70%	0.107	Coil (COILS); PF13015 (PFAM); IPR009011 (G3DSA:2.70.130.GENE3D); IPR026874 (PTHR12630:PANTHER); PTHR12630 (PANTHER); IPR009011 (SUPERFAMILY)
1541	c34275_g1_i1_len_1017_path_995_0_1016_1	14	sulfatase family protein	339	0	99.00%	0.102	G3DSA:3.30.1120.10 (GENE3D); IPR000917 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); PTHR10342:SF160 (PANTHER); PTHR10342 (PANTHER); IPR024607 (PROSITE_PATTERNS); IPR017850 (SUPERFAMILY)
1542	c34326_g1_i1_len_2145_path_2123_0_2144_1	81	cyclin-dependent kinase 14 isoform x1	715	0	89.50%	0.109	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24056:SF155 (PANTHER); PTHR24056 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1543	c34357_g1_i1_len_250_path_1_0_249_1	2	von willebrand factor a domain-containing protein 8	83	6.14E-13	99.20%	0.167	PTHR21610 (PANTHER); PTHR21610:SF9 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)

1552	c35225_g1_i1_len_1025_path_1_0_1024_2	15	cytochrome p450 cyp44	336	1.23E-95	67.50%	0.1	IPR002401 (PRINTS); IPR001128 (PRINTS); IPR001128 (G3DSA:1.10.630.GENE3D); IPR001128 (PFAM); PTHR24291 (PANTHER); PTHR24291:SF1 (PANTHER); IPR017972 (PROSITE_PATTERNS); IPR001128 (SUPERFAMILY)
1553	c35275_g1_i1_len_606_path_1_0_605_1	6	glycerophosphoryl diester phosphodiesterase	202	1.01E-134	99.70%	0.221	IPR030395 (PFAM); IPR017946 (G3DSA:3.20.20.GENE3D); PTHR23344:SF7 (PANTHER); IPR004129 (PANTHER); IPR030395 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR017946 (SUPERFAMILY)
1554	c35304_g1_i1_len_1060_path_1_0_1059_1	15	protein gdp2 homolog	353	3.62E-115	74.30%	0.209	IPR002589 (SMART); IPR002589 (PFAM); G3DSA:3.40.220.10 (GENE3D); PTHR11106:SF59 (PANTHER); PTHR11106 (PANTHER); IPR002589 (PROSITE_PROFILES); SSF52949 (SUPERFAMILY)
1555	c35381_g1_i1_len_624_path_602_0_623_1	7	6-phospho-beta- partial	208	2.30E-120	98.00%	0.117	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001360 (PFAM); IPR001360 (PANTHER); PTHR10353:SF35 (PANTHER); IPR018120 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
1556	c35533_g1_i1_len_1016_path_1002_0_1015_3	595	mitochondrial manganese superoxide dismutase	333	3.23E-121	86.10%	0.11	Coil (COILS); IPR001189 (PRINTS); G3DSA:1.10.287.990 (GENE3D); IPR019832 (PFAM); IPR019831 (PFAM); IPR001189 (PANTHER); PTHR11404:SF6 (PANTHER); IPR019833 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR019831 (SUPERFAMILY); IPR019832 (SUPERFAMILY); TMhelix (TMHMM)
1557	c35602_g1_i1_len_274_path_252_0_273_4	0	serine threonine-protein kinase mark2-like isoform x10	91	2.42E-56	99.80%	0.101	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:1.10.510.10 (GENE3D); PTHR24346 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1558	c36079_g1_i1_len_609_path_1_0_608_1	5	aldehyde partial	203	5.48E-143	99.10%	0.119	IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF97 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
1559	c36098_g1_i1_len_840_path_1_0_839_1	27	ankyrin repeat domain-containing protein 49-like	280	3.20E-61	68.40%	0.145	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24144 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1560	c36177_g1_i1_len_1295_path_1_0_1294_4	25	dehydrogenase reductase sdr family member 11-like	432	1.58E-103	74.50%	0.13	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF310 (PANTHER); PTHR24322 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1561	c36555_g1_i1_len_554_path_532_0_553_4	5	6-phospho-beta-glucosidase	185	2.18E-125	99.50%	0.123	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001360 (PFAM); PTHR10353:SF31 (PANTHER); IPR001360 (PANTHER); IPR018120 (PROSITE_PATTERNS); IPR017853 (SUPERFAMILY)
1562	c36683_g1_i1_len_1269_path_1_0_1268_5	35	leukocyte elastase inhibitor a-like	423	2.47E-49	56.60%	0.149	IPR023796 (SMART); G3DSA:3.30.497.10 (GENE3D); IPR023796 (PFAM); IPR000215 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023796 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1563	c37095_g1_i1_len_1052_path_14_0_1051_0	44	apolipoprotein a-i-binding protein	345	9.82E-109	77.50%	0.103	IPR004443 (PFAM); IPR004443 (TIGRFAM); IPR004443 (G3DSA:3.40.50.GENE3D); PTHR13232 (PANTHER); IPR004443 (HAMAP); IPR004443 (PROSITE_PROFILES); IPR004443 (SUPERFAMILY)
1564	c372_g1_i1_len_1243_path_33_0_1162_1195_1163_32_1164_1242_2	2513	steroid dehydrogenase	407	1.35E-115	68.80%	0.199	Coil (COILS); IPR002198 (PRINTS); IPR002347 (PRINTS); IPR002198 (PFAM); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24316:SF68 (PANTHER); PTHR24316 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1565	c3723_g1_i1_len_1098_path_53_0_1097_5	70	protein spaetzle	356	8.86E-28	51.90%	0.141	PTHR23199 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029034 (SUPERFAMILY); TMhelix (TMHMM)

1566	c37329_g1_i1_len_541_path_519_0_540_0	7	14-3-3 zeta	181	1.72E-51	92.10%	0.128	Coil (COILS); IPR000308 (PRINTS); IPR023410 (SMART); G3DSA:1.20.190.20 (GENE3D); IPR023410 (PFAM); IPR000308 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023410 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1567	c37416_g1_i1_len_505_path_1_0_504_1	4	polypeptide n-acetylgalactosaminyltransferase 1	168	1.21E-45	72.90%	0.103	IPR029044 (G3DSA:3.90.550.GENE3D); IPR001173 (PFAM); PTHR11675 (PANTHER); PTHR11675:SF27 (PANTHER); IPR029044 (SUPERFAMILY)
1568	c37579_g1_i1_len_838_path_816_0_837_0	12	thrombospondin type-1 domain-containing protein 4-like	280	4.55E-23	57.10%	0.638 Y	IPR000884 (SMART); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); PTHR13723 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000884 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR000884 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1569	c37589_g1_i1_len_1210_path_1188_0_1209_1	25	e3 ubiquitin-protein ligase partial	403	2.34E-143	66.30%	0.11	Coil (COILS); IPR001841 (SMART); IPR002110 (SMART); IPR013083 (G3DSA:3.30.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR013083 (G3DSA:3.30.40.GENE3D); PF13920 (PFAM); IPR020683 (PFAM); IPR002110 (PFAM); PTHR24202 (PANTHER); PTHR24202:SF4 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR020683 (PROSITE_PROFILES); IPR001841 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR001841 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); SSF57850 (SUPERFAMILY)
1570	c37684_g1_i1_len_259_path_237_0_258_4	0	group 3 secretory phospholipase a2-like	86	1.19E-23	69.40%	0.155	IPR016090 (G3DSA:1.20.90.GENE3D); IPR001211 (PFAM); PTHR12253 (PANTHER); IPR016090 (SUPERFAMILY)
1571	c37781_g1_i1_len_1166_path_1144_0_1165_4	19	down syndrome cell adhesion molecule isoform bc	389	1.49E-85	65.60%	0.207	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PF13895 (PFAM); PTHR10489 (PANTHER); PTHR10489:SF567 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1572	c37875_g1_i1_len_1149_path_1127_0_1148_5	17	neural ectodermal development factor imp-l2	383	9.88E-44	51.70%	0.218	IPR003599 (SMART); IPR003598 (SMART); PF13895 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1573	c37931_g1_i1_len_425_path_1_0_424_1	4	serine endoprotease partial	142	8.91E-92	99.00%	0.116	IPR001940 (PRINTS); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PF13365 (PFAM); PTHR22939 (PANTHER); IPR009003 (SUPERFAMILY)
1574	c37943_g1_i1_len_1061_path_1_0_1060_3	47	a disintegrin and metalloproteinase with thrombospondin motifs 2	349	3.69E-15	49.50%	0.151	IPR002870 (PFAM); PTHR13723 (PANTHER)
1575	c37950_g1_i1_len_992_path_1_0_991_5	38	prolow-density lipoprotein receptor-related protein 1-like	330	3.47E-31	54.80%	0.115	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1576	c3812_g1_i1_len_306_path_438_0_29_103_30_1_25_19_126_209_103_210_305_0	0	aggrecan core protein	102	4.92E-08	51.50%	0.235	no IPS match
1577	c38320_g1_i1_len_722_path_700_0_721_0	9	protein disulfide-isomerase-like	241	4.27E-20	73.60%	0.144	IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF56 (PANTHER); PTHR18929 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)

1578	c3837_g1_i1_len_2345_path_635_0_987_634_98_8_2344_4	58	neuroglian-like isoform x2	782	0	75.50%	0.108	IPR003599 (SMART); IPR003598 (SMART); IPR003961 (SMART); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF553 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1579	c3837_g1_i2_len_1673_path_318_0_315_634_31_6_1672_4	27	neuroglian-like isoform 2	558	0	79.20%	0.108	IPR003961 (SMART); IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR10489 (PANTHER); PTHR10489:SF553 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1580	c384_g1_i1_len_1016_path_53_0_1015_3	106	thioredoxin 2	339	2.57E-34	70.70%	0.152	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR005746 (PANTHER); PTHR10438:SF235 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
1581	c3845_g1_i1_len_813_path_1_0_192_194_193_8_12_4	18	protein disulfide	271	1.51E-104	79.70%	0.099	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF85 (PANTHER); PTHR18929 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); TMhelix (TMHMM)
1582	c3845_g1_i2_len_655_path_1616_0_34_194_35_654_4	15	protein disulfide	210	2.32E-105	79.90%	0.099	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929 (PANTHER); PTHR18929:SF85 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1583	c38524_g1_i1_len_808_path_1_0_807_2	66	spondin-2 isoform x1	263	8.17E-13	75.30%	0.154	IPR009465 (PFAM); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009465 (PROSITE_PROFILES); TMhelix (TMHMM)
1584	c38776_g1_i1_len_272_path_250_0_271_4	0	von willebrand factor c and egf domain-containing protein	85	1.97E-07	54.30%	0.107	IPR001007 (SMART); IPR001007 (PFAM); G3DSA:2.10.70.10 (GENE3D); IPR001007 (PROSITE_PATTERNS); IPR001007 (PROSITE_PROFILES); SSF57603 (SUPERFAMILY)
1585	c38881_g1_i1_len_444_path_1_0_443_1	6	protein sidekick-1	148	1.04E-10	55.50%	0.145	IPR003598 (SMART); IPR003599 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
1586	c39099_g1_i1_len_534_path_1_0_533_2	5	carbohydrate binding domain protein	178	1.47E-116	99.40%	0.104	IPR003610 (SMART)
1587	c39156_g1_i1_len_525_path_503_0_524_3	5	glutathione peroxidase	175	1.63E-08	64.50%	0.297	IPR000889 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR000889 (PANTHER); IPR029760 (PROSITE_PATTERNS); IPR000889 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1588	c39208_g1_i1_len_1063_path_1_0_1062_0	44	---NA---	355			0.172	Coil (COILS)
1589	c39223_g1_i1_len_1321_path_1_0_1320_0	24	angio-associated migratory cell	434	2.85E-81	65.20%	0.597 Y	IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR19857 (PANTHER); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR011047 (SUPERFAMILY)
1590	c393_g1_i1_len_1178_path_1195_0_341_2370_3_42_1177_4	32	krueppel-like factor 6 isoform x1	393	1.49E-109	63.30%	0.105	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); PTHR23223:SF132 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1591	c39395_g1_i1_len_583_path_561_0_582_0	4	endoplasmic reticulum mannosyl-oligosaccharide - alpha-mannosidase	195	2.66E-77	81.20%	0.104	IPR001382 (PRINTS); IPR001382 (G3DSA:1.50.10.GENE3D); IPR001382 (PFAM); IPR001382 (PANTHER); PTHR11742:SF7 (PANTHER); IPR001382 (SUPERFAMILY)
1592	c3965_g1_i1_len_1534_path_2483_0_1446_3930_1447_1473_3956_1474_1506_3930_1507_1533_1	99	calcium activated chlorine	511	5.36E-18	54.60%	0.108	IPR003961 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10579 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR003961 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1593	c3976_g1_i1_len_2029_path_1_0_1265_1267_1266_2028_3	94	p38 mitogen-activated protein kinase	671	0	89.70%	0.11	Coil (COILS); IPR008352 (PRINTS); IPR002290 (SMART); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24055:SF110 (PANTHER); PTHR24055 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR003527 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1594	c39841_g1_i1_len_1106_path_1084_0_1105_2	8	receptor-type tyrosine-protein phosphatase mu- partial	368	1.21E-46	54.20%	0.106	Coil (COILS); IPR000242 (PRINTS); IPR003595 (SMART); IPR000242 (SMART); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR19134:SF81 (PANTHER); PTHR19134 (PANTHER); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY)
1595	c39866_g1_i1_len_503_path_481_0_502_0	4	apical endosomal glycoprotein	168	1.83E-19	68.60%	0.105	IPR000998 (PFAM); PTHR23282 (PANTHER); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY)
1596	c40070_g1_i1_len_613_path_1_0_612_0	6	fimbrial family protein	205	1.48E-105	100.00%	0.104	IPR000259 (PFAM); IPR000259 (G3DSA:2.60.40.GENE3D); IPR008966 (SUPERFAMILY)
1597	c40289_g1_i1_len_295_path_1_0_294_1	3	hemocyte protein-glutamine gamma- glutamyltransferase-like	98	1.33E-29	74.30%	0.122	IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR029021 (G3DSA:3.90.190.GENE3D); IPR000242 (PFAM); PTHR11590:SF40 (PANTHER); IPR023608 (PANTHER); IPR008958 (SUPERFAMILY); IPR008958 (SUPERFAMILY)
1598	c4065_g1_i1_len_340_path_1_0_88_90_89_112_1067_113_339_1	5	zinc finger protein 501-like	113	2.95E-21	61.20%	0.101	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1599	c4065_g2_i1_len_328_path_898_0_145_90_146_169_114_170_327_1	1	zinc c2h2 type	109	5.54E-14	61.10%	0.12	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1600	c40782_g1_i1_len_1328_path_1306_0_1327_1	32	nicotinamide phosphoribosyltransferase-like	443	1.99E-153	82.30%	0.107	IPR007229 (PFAM); G3DSA:3.20.140.10 (GENE3D); IPR007229 (PANTHER); IPR016471 (PTHR11098:PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002638 (SUPERFAMILY)
1601	c41039_g1_i1_len_562_path_540_0_561_2	3	cathepsin I	187	1.53E-96	81.80%	0.199	IPR000668 (PRINTS); IPR000668 (SMART); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); PTHR12411:SF57 (PANTHER); IPR013128 (PANTHER); IPR025661 (PROSITE_PATTERNS); IPR025660 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); SSF54001 (SUPERFAMILY)
1602	c41726_g1_i1_len_948_path_1_0_947_1	12	beta- -n-acetylgalactosaminyltransferase bre-4	316	4.14E-24	87.20%	0.105	IPR029044 (G3DSA:3.90.550.GENE3D); IPR027791 (PFAM); IPR003859 (PANTHER); PTHR19300:SF30 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029044 (SUPERFAMILY); TMhelix (TMHMM)

1603	c4249_g1_i1_len_1083_path_17_0_564_677_565_1082_0	18	peroxisome biogenesis factor 10-like	355	2.26E-71	57.30%	0.128	IPR001841 (SMART); IPR001841 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); IPR006845 (PFAM); IPR025654 (PANTHER); IPR017907 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001841 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY)
1604	c4249_g1_i2_len_1178_path_17_0_564_582_565_659_677_660_1177_2	22	peroxisome biogenesis factor 10	386	9.22E-26	60.20%	0.111	IPR001841 (SMART); PF13923 (PFAM); IPR013083 (G3DSA:3.30.40.GENE3D); IPR025654 (PANTHER); IPR017907 (PROSITE_PATTERNS); IPR001841 (PROSITE_PROFILES); SSF57850 (SUPERFAMILY)
1605	c42763_g1_i1_len_448_path_1_0_447_4	3	laminin beta 1	149	4.41E-62	74.40%	0.124	IPR002049 (SMART); G3DSA:2.10.25.10 (GENE3D); IPR002049 (PFAM); PTHR10574 (PANTHER); PTHR10574:SF238 (PANTHER); IPR002049 (PROSITE_PATTERNS); IPR013015 (PROSITE_PROFILES); IPR002049 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
1606	c4294_g1_i1_len_1431_path_53_0_1430_4	81	mitochondrial cardiolipin hydrolase-like	477	1.85E-60	66.40%	0.186	G3DSA:3.30.870.10 (GENE3D); IPR025202 (PFAM); PTHR21248 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001736 (PROSITE_PROFILES); SSF56024 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1607	c42985_g1_i1_len_364_path_342_0_363_1	2	protein kinase dc2	121	4.56E-76	95.90%	0.125	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); PTHR24353 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1608	c4304_g1_i1_len_492_path_1_0_491_1	3	trna binding domain protein	164	4.01E-73	99.90%	0.103	IPR012340 (G3DSA:2.40.50.GENE3D); IPR002547 (PFAM); PTHR11586 (PANTHER); IPR002547 (PROSITE_PROFILES); IPR012340 (SUPERFAMILY)
1609	c43104_g1_i1_len_1067_path_1_0_1066_5	7	epsilon-sarcoglycan isoform x2	355	1.12E-87	61.50%	0.119	IPR008908 (PFAM); IPR001304 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR008908 (PANTHER); PTHR10132:SF14 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM)
1610	c43125_g1_i1_len_431_path_1_0_430_4	0	low-density lipoprotein receptor-related protein partial	144	4.06E-07	41.67%	0.31	NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR002172 (SUPERFAMILY)
1611	c43246_g1_i1_len_900_path_1_0_899_4	9	protein kinase c-binding protein nell1-like isoform x2	300	2.26E-68	60.60%	0.104	IPR001007 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR001007 (PFAM); PTHR24042:SF4 (PANTHER); PTHR24042 (PANTHER); IPR001007 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR001007 (PROSITE_PROFILES); IPR001007 (PROSITE_PROFILES); SSF57603 (SUPERFAMILY); SSF57603 (SUPERFAMILY)
1612	c43419_g1_i1_len_251_path_229_0_250_4	2	3-hydroxyisobutyrate dehydrogenase	84	5.28E-37	90.60%	0.121	IPR016040 (G3DSA:3.40.50.GENE3D); IPR029154 (PFAM); IPR006115 (PFAM); IPR013328 (G3DSA:1.10.1040.GENE3D); PTHR22981:SF7 (PANTHER); PTHR22981 (PANTHER); IPR008927 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
1613	c44048_g1_i1_len_599_path_577_0_598_2	6	alpha c-terminal all-beta domain protein	199	1.75E-141	98.00%	0.116	IPR017853 (SUPERFAMILY)
1614	c4440_g1_i1_len_1388_path_1366_0_1387_4	43	guanylate kinase isoform x2	458	1.62E-89	83.40%	0.247	IPR008145 (SMART); IPR017665 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:3.30.63.10 (GENE3D); IPR008145 (PFAM); PTHR23117 (PANTHER); PTHR23117:SF13 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008144 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1615	c44660_g1_i1_len_423_path_1_0_422_1	2	carcinolectin 5a isoform	141	1.27E-24	65.40%	0.164	IPR002181 (SMART); IPR014716 (G3DSA:3.90.215.GENE3D); IPR014715 (G3DSA:4.10.530.GENE3D); IPR002181 (PFAM); PTHR19143 (PANTHER); IPR020837 (PROSITE_PATTERNS); IPR002181 (PROSITE_PROFILES); IPR002181 (SUPERFAMILY)
1616	c45002_g1_i1_len_247_path_1_0_246_0	0	flagellar hook-associated protein 1 domain protein	83	3.85E-49	100.00%	0.15	IPR002371 (PRINTS); PTHR30033:SF0 (PANTHER); PTHR30033 (PANTHER)

1617	c45221_g1_i1_len_206_path_1_0_205_5	2	zinc c2h2 type domain-containing protein	68	5.67E-10	57.60%	0.099	IPR015880 (SMART); IPR007087 (PFAM); PF13894 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1618	c455_g1_i1_len_1151_path_304_0_1001_25_100_2_1150_2	31	zinc finger protein	383	3.35E-57	65.90%	0.133	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PF13465 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1619	c46046_g1_i1_len_536_path_1_0_512_514_513_533_535_534_535_2	3	heat shock 70 kda protein cognate 4	178	4.22E-53	84.10%	0.101	IPR029048 (G3DSA:1.20.1270.GENE3D); IPR013126 (PFAM); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029048 (SUPERFAMILY)
1620	c46352_g1_i1_len_767_path_761_0_766_0	17	trafficking protein particle complex subunit 1	256	6.05E-60	86.10%	0.19	IPR007233 (PFAM); G3DSA:3.30.450.70 (GENE3D); PTHR23249:SF16 (PANTHER); IPR007233 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR011012 (SUPERFAMILY); TMhelix (TMHMM)
1621	c46487_g1_i1_len_438_path_568_0_437_2	1	brca1-associated ring domain protein 1	146	9.51E-38	68.90%	0.102	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (PFAM); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24171:SF9 (PANTHER); PTHR24171 (PANTHER); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1622	c46728_g1_i1_len_583_path_561_0_582_4	14	aplp_manse ame: full=apolipophorins contains: ame: full=apolipophorin-2 ame: full=apolipophorin ii ame: full=apolp-2 contains: ame: full=apolipophorin-1 ame: full=apolipophorin i ame: full=apolp-1 flags: precursor	194	6.93E-22	51.50%	0.1	no IPS match
1623	c46764_g1_i1_len_290_path_1_0_289_4	1	tollod-like protein	97	5.53E-08	56.30%	0.101	IPR001506 (PRINTS); IPR001506 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D)
1624	c46893_g1_i1_len_334_path_312_0_333_0	2	#NAME?	112	5.29E-73	99.10%	0.101	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); IPR001395 (PANTHER); PTHR11732:SF100 (PANTHER); IPR018170 (PROSITE_PATTERNS); IPR023210 (SUPERFAMILY)
1625	c47090_g1_i1_len_442_path_1_0_441_4	3	acyloxyacyl hydrolase	147	2.92E-38	64.40%	0.144	PTHR15010 (PANTHER)
1626	c47119_g1_i1_len_978_path_956_0_977_0	5	protein fam3c-like	326	1.74E-23	63.50%	0.128	PTHR14592:SF7 (PANTHER); IPR026101 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1627	c47119_g1_i1_len_978_path_956_0_977_1	5	protein partial	326	1.11E-25	59.00%	0.276	PTHR14592:SF7 (PANTHER); IPR026101 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1628	c47237_g1_i1_len_484_path_1_0_483_1	11	neogenin isoform x3	161	6.07E-12	74.20%	0.107	IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
1629	c4773_g1_i1_len_916_path_944_0_915_2	32	perlucin-like protein	299	4.96E-22	53.70%	0.943 Y	Coil (COILS); IPR001304 (SMART); IPR016186 (G3DSA:3.10.100.GENE3D); IPR001304 (PFAM); PTHR22802 (PANTHER); IPR018378 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR001304 (PROSITE_PROFILES); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR016187 (SUPERFAMILY)
1630	c48133_g1_i1_len_706_path_1_0_705_3	5	allene oxide synthase-lipoxygenase partial	236	6.73E-76	70.00%	0.101	Coil (COILS); IPR013819 (PFAM); G3DSA:1.20.245.10 (GENE3D); PTHR11771:SF43 (PANTHER); IPR000907 (PANTHER); IPR013819 (PROSITE_PROFILES); IPR013819 (SUPERFAMILY)

1631	c4835_g1_i1_len_820_path_185_0_565_184_566_819_4	5	neuroglian isoform x1	273	2.66E-66	85.80%	0.125	IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489 (PANTHER); PTHR10489:SF553 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1632	c49415_g1_i1_len_352_path_330_0_351_2	2	lipase 3	117	2.94E-56	77.80%	0.117	IPR006693 (PFAM); IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11005 (PANTHER); IPR029058 (SUPERFAMILY)
1633	c49923_g1_i1_len_459_path_1_0_458_1	4	pa domain-containing protein	153	5.61E-44	77.60%	0.102	IPR003137 (PFAM); G3DSA:3.50.30.30 (GENE3D); PTHR22702 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1634	c50010_g1_i1_len_860_path_838_0_859_2	7	muscle calcium channel subunit alpha-1 isoform x1	286	3.06E-17	79.00%	0.323	IPR005821 (PFAM); IPR027359 (G3DSA:1.20.120.GENE3D); PTHR10037:SF195 (PANTHER); PTHR10037 (PANTHER); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1635	c50256_g1_i1_len_217_path_195_0_216_2	0	zinc finger protein	72	3.61E-12	58.70%	0.098	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1636	c50412_g1_i1_len_458_path_1_0_457_1	1	short-chain dehydrogenase reductase family 16c member partial	153	5.97E-61	74.70%	0.12	IPR002347 (PRINTS); IPR002198 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24316 (PANTHER); PTHR24316:SF289 (PANTHER); SSF51735 (SUPERFAMILY)
1637	c5093_g1_i2_len_1452_path_1_0_565_567_566_1451_0	69	adiponectin receptor protein	484	0	80.70%	0.139	IPR004254 (PFAM); PTHR20855:SF15 (PANTHER); IPR004254 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1638	c5095_g1_i2_len_1038_path_2823_0_482_25_48_3_1037_4	34	transposase	346	7.70E-43	57.50%	0.123	no IPS match
1639	c5111_g1_i1_len_1307_path_1_0_1306_0	42	histone-lysine n-methyltransferase prdm9-like	430	1.88E-55	65.50%	0.109	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1640	c51614_g1_i1_len_318_path_1_0_317_3	2	locomotion-related protein hikaru genki-like	106	1.08E-40	77.00%	0.149	IPR000436 (SMART); IPR000436 (PFAM); G3DSA:2.10.70.10 (GENE3D); G3DSA:2.10.70.10 (GENE3D); PTHR19325:SF340 (PANTHER); PTHR19325 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY); IPR000436 (SUPERFAMILY)
1641	c51656_g1_i1_len_234_path_212_0_233_1	0	peptidyl-alpha-hydroxyglycine alpha-amidating lyase 1	78	1.09E-08	64.10%	0.103	PTHR10680 (PANTHER)
1642	c52085_g1_i1_len_618_path_596_0_617_0	4	sulfakinin precursor	206	3.06E-09	75.11%	0.101	IPR013152 (PROSITE_PATTERNS); IPR013152 (PROSITE_PATTERNS)

1643	c5300_g1_i1_len_911_path_889_0_910_0	18	cathepsin I-associated protein	304	3.94E-62	59.30%	0.435 Y	IPR000782 (SMART); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); PTHR10900 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY)
1644	c53660_g1_i1_len_333_path_1_0_332_2	0	peripheral plasma membrane protein cask isoform x2	111	4.11E-58	96.90%	0.412 Y	IPR001478 (G3DSA:2.30.42.GENE3D); PTHR23122:SF7 (PANTHER); PTHR23122 (PANTHER); IPR001478 (SUPERFAMILY)
1645	c5375_g2_i1_len_738_path_1866_0_676_855_677_700_879_701_737_3	26	serine protease nudel	240	1.05E-34	75.10%	0.136	IPR002172 (SMART); IPR002172 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR001254 (PFAM); PTHR24256 (PANTHER); PTHR24256:SF95 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
1646	c5410_g1_i1_len_1978_path_53_0_1977_2	9092	retinal dehydrogenase 1-like	653	0	82.10%	0.113	IPR016163 (G3DSA:3.40.309.GENE3D); IPR016162 (G3DSA:3.40.605.GENE3D); IPR015590 (PFAM); PTHR11699:SF145 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016160 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR016161 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1647	c5439_g1_i1_len_697_path_1_0_696_0	14	transmembrane protease serine 12	233	8.69E-23	62.00%	0.136	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1648	c5443_g1_i1_len_1530_path_1_0_1433_4442_1434_1529_2	50	limbic system-associated membrane protein	510	5.00E-150	69.70%	0.122	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR19831 (PANTHER); PTHR19831:SF47 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1649	c5443_g1_i2_len_2184_path_1_0_1433_1435_1434_2183_2	102	limbic system-associated membrane protein	722	1.99E-146	68.50%	0.122	IPR003599 (SMART); IPR003598 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF47 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1650	c5493_g1_i2_len_2028_path_2006_0_663_2670_664_2027_2	75	ccr4-not transcription complex subunit 6-like isoform x1	676	0	85.10%	0.114	IPR003591 (SMART); IPR005135 (PFAM); G3DSA:3.80.10.10 (GENE3D); IPR005135 (G3DSA:3.60.10.GENE3D); PTHR12121:SF34 (PANTHER); PTHR12121 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR005135 (SUPERFAMILY); SSF52058 (SUPERFAMILY)
1651	c5494_g1_i1_len_1432_path_1_0_741_743_742_916_918_917_1431_5	30	upf0364 protein c6orf211 homolog	477	1.74E-121	62.40%	0.21	IPR002791 (PFAM); PTHR12260 (PANTHER); PTHR12260:SF1 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002791 (SUPERFAMILY)
1652	c5494_g1_i2_len_1432_path_1_0_741_3040_742_916_918_917_1431_5	23	upf0364 protein c6orf211 homolog	477	9.38E-121	62.60%	0.21	IPR002791 (PFAM); PTHR12260 (PANTHER); PTHR12260:SF1 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002791 (SUPERFAMILY)
1653	c5575_g1_i1_len_468_path_1_0_467_1	4	ectonucleoside triphosphate diphosphohydrolase 4	156	1.71E-53	72.90%	0.115	IPR000407 (PFAM); IPR000407 (PANTHER); PTHR11782:SF37 (PANTHER); IPR000407 (PROSITE_PATTERNS)
1654	c56053_g1_i1_len_1800_path_1824_0_1799_0	45	t-lymphocyte activation antigen cd86-like	600	1.29E-115	84.90%	0.104	IPR013106 (SMART); IPR003598 (SMART); IPR003599 (SMART); PF13895 (PFAM); IPR013106 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR23279 (PANTHER); PTHR23279:SF1 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1655	c56076_g1_i1_len_1783_path_1761_0_1782_3	6690	cathepsin b	590	7.38E-164	78.80%	0.118	IPR000668 (PRINTS); IPR000668 (SMART); IPR012599 (PFAM); IPR000668 (PFAM); G3DSA:3.90.70.10 (GENE3D); IPR013128 (PANTHER); IPR015643 (PTHR12411:PANTHER); IPR025660 (PROSITE_PATTERNS); IPR025661 (PROSITE_PATTERNS); IPR000169 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54001 (SUPERFAMILY); TMhelix (TMHMM)
1656	c56120_g1_i1_len_2244_path_2222_0_2243_2	8392	protein disulfide-isomerase a3	740	0	78.60%	0.183	PR00421 (PRINTS); IPR012336 (G3DSA:3.40.30.GENE3D); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005792 (TIGRFAM); IPR013766 (PFAM); PF13848 (PFAM); IPR005788 (TIGRFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929:SF60 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY); IPR012336 (SUPERFAMILY)
1657	c56260_g1_i1_len_643_path_1_0_642_0	3	partial	215	2.23E-32	83.40%	0.101	IPR011614 (PFAM); IPR011614 (G3DSA:2.40.180.GENE3D); IPR018028 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR018028 (PROSITE_PROFILES); IPR020835 (SUPERFAMILY)
1658	c56449_g1_i1_len_861_path_1_0_860_1	8	urokinase-type plasminogen activator	287	1.78E-29	63.90%	0.133	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY); TMhelix (TMHMM)
1659	c5651_g1_i1_len_495_path_1_0_125_127_126_4_94_4	19	zinc finger protein 227	159	7.34E-41	73.00%	0.107	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
1660	c56573_g1_i1_len_745_path_1_0_744_1	17	transcription factor e4f1-like	248	6.15E-17	75.90%	0.103	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1661	c56682_g1_i1_len_280_path_258_0_279_2	2	lipase 3	93	5.58E-24	70.00%	0.168	IPR029058 (G3DSA:3.40.50.GENE3D); PTHR11005:SF6 (PANTHER); PTHR11005 (PANTHER); IPR029058 (SUPERFAMILY)
1662	c5675_g1_i1_len_1109_path_1216_0_1108_4	40	chitotriosidase-1 isoform x1	362	8.47E-30	52.30%	0.106	IPR002557 (SMART); IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); IPR002557 (PFAM); IPR002557 (G3DSA:2.170.140.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF112 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002557 (PROSITE_PROFILES); IPR017853 (SUPERFAMILY); IPR002557 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1663	c56859_g1_i1_len_901_path_879_0_900_5	465	ecdysteroid-regulated 16 kda protein	294	1.42E-17	54.20%	0.393 Y	IPR003172 (SMART); IPR003172 (G3DSA:2.60.40.GENE3D); IPR003172 (PFAM); PTHR11306 (PANTHER); IPR014756 (SUPERFAMILY)
1664	c56929_g1_i1_len_789_path_767_0_788_2	5	ankyrin repeat-containing protein	263	7.53E-13	60.90%	0.1	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)

1665	c57239_g1_i1_len_1070_path_1048_0_1069_1	15	dnaj homolog dnj-5	350	2.74E-135	70.70%	0.833 Y	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PF14901 (PFAM); PTHR24078 (PANTHER); PTHR24078:SF141 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR001623 (SUPERFAMILY)
1666	c57255_g1_i1_len_645_path_1_0_644_5	6	peptidyl-glycine alpha-amidating monooxygenase partial	215	3.53E-67	63.40%	0.12	IPR000720 (PRINTS); PF03712 (PFAM); IPR000323 (G3DSA:2.60.120.GENE3D); IPR014784 (G3DSA:2.60.120.GENE3D); PTHR10680:SF13 (PANTHER); PTHR10680 (PANTHER); IPR014783 (PROSITE_PATTERNS); IPR008977 (SUPERFAMILY); IPR008977 (SUPERFAMILY)
1667	c57265_g1_i1_len_791_path_1_0_790_5	6	outer membrane autotransporter barrel domain protein	263	0	98.00%	0.104	IPR012332 (G3DSA:2.160.20.GENE3D); IPR006315 (TIGRFAM); IPR005546 (G3DSA:2.40.128.GENE3D); IPR004899 (PFAM); IPR005546 (PFAM); PTHR12338 (PANTHER); IPR005546 (PROSITE_PROFILES); IPR011050 (SUPERFAMILY); IPR005546 (SUPERFAMILY)
1668	c5739_g1_i1_len_2003_path_2011_0_2002_5	236	glucose-6-phosphate isomerase	667	0	87.70%	0.103	IPR001672 (PRINTS); IPR023096 (G3DSA:1.10.1390.GENE3D); IPR001672 (PFAM); G3DSA:3.40.50.10490 (GENE3D); IPR001672 (PANTHER); PTHR11469:SF4 (PANTHER); IPR018189 (PROSITE_PATTERNS); IPR018189 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001672 (PROSITE_PROFILES); IPR001672 (HAMAP); SSF53697 (SUPERFAMILY)
1669	c57455_g1_i1_len_1465_path_1_0_1464_3	18	upf0364 protein partial	489	1.80E-113	61.00%	0.101	Coil (COILS); IPR002791 (PFAM); PTHR12260:SF1 (PANTHER); PTHR12260 (PANTHER); IPR002791 (SUPERFAMILY)
1670	c57509_g1_i1_len_754_path_1_0_753_0	8	beta-lactamase	252	0	99.70%	0.635 Y	IPR012338 (G3DSA:3.40.710.GENE3D); IPR001466 (PFAM); PTHR22935 (PANTHER); PTHR22935:SF58 (PANTHER); IPR001586 (PROSITE_PATTERNS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); IPR012338 (SUPERFAMILY)
1671	c57516_g1_i1_len_1883_path_1861_0_1882_2	60	wd repeat-containing protein 37	627	0	76.80%	0.12	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR19855:SF12 (PANTHER); PTHR19855 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY)
1672	c57680_g1_i1_len_715_path_1_0_714_1	14	adenosine monophosphate-protein transferase ficd homolog	238	9.11E-123	83.90%	0.105	IPR003812 (PFAM); IPR003812 (G3DSA:1.10.3290.GENE3D); PTHR13504:SF12 (PANTHER); PTHR13504 (PANTHER); IPR003812 (PROSITE_PROFILES); IPR003812 (SUPERFAMILY)
1673	c57713_g1_i1_len_1166_path_1_0_1165_5	33	adp-ribosylation factor-like protein 3	380	1.74E-109	93.90%	0.558 Y	IPR006689 (PRINTS); IPR024156 (SMART); IPR003579 (SMART); IPR006687 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR005225 (TIGRFAM); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF124 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR024156 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); IPR027417 (SUPERFAMILY); TMhelix (TMHMM)
1674	c57754_g1_i1_len_1807_path_1785_0_1806_1	50	tripartite motif-containing protein 2-like isoform x5	602	9.84E-155	85.60%	0.116	IPR001258 (PFAM); IPR011042 (G3DSA:2.120.10.GENE3D); PTHR24103 (PANTHER); PTHR24103:SF1 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); IPR013017 (PROSITE_PROFILES); SSF101898 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1675	c5785_g1_i1_len_1008_path_986_0_1007_1	11	hypoxanthine partial	336	2.74E-147	100.00%	0.146	IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908:SF64 (PANTHER); PTHR11908 (PANTHER); IPR008274 (SUPERFAMILY)
1676	c57872_g1_i1_len_1484_path_1_0_1483_1	63	dipeptidyl peptidase 9	488	0	81.40%	0.126	IPR029058 (G3DSA:3.40.50.GENE3D); IPR002469 (G3DSA:2.140.10.GENE3D); IPR001375 (PFAM); IPR002469 (PFAM); PTHR11731:SF110 (PANTHER); PTHR11731 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF82171 (SUPERFAMILY); IPR029058 (SUPERFAMILY)
1677	c57873_g1_i1_len_1128_path_1_0_1127_4	12	thioredoxin	376	6.21E-97	96.90%	0.183	PR00421 (PRINTS); IPR005746 (TIGRFAM); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); IPR005746 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1678	c57916_g1_i1_len_2466_path_1_0_2465_2	78	eukaryotic translation initiation factor 2-alpha kinase 3	822	2.02E-112	52.50%	0.173	IPR002290 (SMART); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR11042:SF86 (PANTHER); PTHR11042 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008271 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM)
1679	c5799_g1_i1_len_1329_path_1307_0_949_2257_950_1328_1	26	myosin-binding protein fast-type-like	443	3.18E-38	57.60%	0.099	IPR003599 (SMART); IPR003598 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR020675 (PANTHER); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY)
1680	c57991_g1_i1_len_1416_path_1_0_1415_0	67	lachesin	472	9.18E-88	66.30%	0.124	IPR003598 (SMART); IPR003599 (SMART); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19831 (PANTHER); PTHR19831:SF43 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1681	c58054_g1_i1_len_622_path_600_0_621_5	5	peptidyl-prolyl cis-trans rhodopsin-specific isozyme	207	4.93E-79	75.90%	0.101	IPR002130 (PRINTS); IPR002130 (PFAM); IPR024936 (PIRSF); IPR029000 (G3DSA:2.40.100.GENE3D); IPR024936 (PANTHER); PTHR11071:SF11 (PANTHER); IPR020892 (PROSITE_PATTERNS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1682	c5817_g1_i1_len_971_path_1204_0_730_246_731_970_1	31	reticulon nogo	319	3.43E-58	63.80%	0.720 Y	IPR003591 (SMART); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR24367 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); SSF52058 (SUPERFAMILY)
1683	c58207_g1_i1_len_348_path_326_0_347_3	1	upf0378 protein kiaa0100-like	116	3.82E-48	83.50%	0.107	IPR019443 (PFAM); PTHR15678 (PANTHER); PTHR15678:SF6 (PANTHER)
1684	c58241_g1_i1_len_216_path_194_0_215_5	0	protein	72	3.35E-31	80.30%	0.113	no IPS match
1685	c58254_g1_i1_len_2695_path_2713_0_2694_0	120	kr domain protein	899	6.34E-148	99.00%	0.113	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322 (PANTHER); PTHR24322:SF265 (PANTHER); IPR020904 (PROSITE_PATTERNS); SSF51735 (SUPERFAMILY)
1686	c58419_g1_i1_len_1419_path_1_0_1418_5	30	mam and ldl-receptor class a domain-containing protein 2-like	468	2.26E-12	57.20%	0.138	IPR002172 (SMART); G3DSA:4.10.1220.10 (GENE3D); IPR023415 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1687	c5848_g1_i1_len_1037_path_1_0_1036_5	19	mam and ldl-receptor class a domain-containing protein 1	345	6.45E-21	48.80%	0.183	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (G3DSA:4.10.400.GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR002172 (G3DSA:4.10.400.GENE3D); IPR013032 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY); SSF57196 (SUPERFAMILY); TMhelix (TMHMM)

1688	c5848_g2_i1_len_321_path_2029_0_320_4	2	mam and ldl-receptor class a domain-containing protein 1	107	2.83E-14	61.40%	0.104	IPR002172 (SMART); IPR000998 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); IPR002172 (PFAM); PTHR23282 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR002172 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR002172 (SUPERFAMILY)
1689	c5859_g1_i1_len_1917_path_1_0_1916_1	113	cyclin-dependent kinase 9-like	639	0	93.40%	0.109	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24056:SF158 (PANTHER); PTHR24056 (PANTHER); IPR008271 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1690	c5862_g1_i1_len_1345_path_1_0_1344_2	76	bone morphogenetic protein 4	448	7.47E-14	45.60%	0.118	Coil (COILS); IPR001111 (PFAM); IPR015615 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1691	c58782_g1_i1_len_1725_path_1_0_1724_4	41	basement membrane-specific heparan sulfate proteoglycan core isoform x2	575	1.38E-103	75.40%	0.119	IPR003598 (SMART); IPR013106 (SMART); IPR003599 (SMART); PF13895 (PFAM); IPR013106 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR23279 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1692	c58907_g1_i1_len_1495_path_1473_0_1494_3	51	heat-shock protein 105	499	0	77.80%	0.105	IPR013126 (PRINTS); G3DSA:3.90.640.10 (GENE3D); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); IPR029047 (G3DSA:2.60.34.GENE3D); PTHR19375:SF78 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY)
1693	c58993_g1_i1_len_1635_path_1_0_1634_2	87	carbohydrate sulfotransferase 11-like	539	1.54E-66	55.10%	0.642 Y	IPR005331 (PFAM); IPR018011 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK)
1694	c5914_g2_i1_len_884_path_3561_0_408_1350_4_09_883_0	16	serine threonine-protein kinase mark2-like isoform x10	289	5.94E-48	78.60%	0.145	G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24346 (PANTHER); PTHR24346:SF23 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1695	c5914_g2_i2_len_1196_path_629_0_720_1350_7_21_1195_0	18	serine threonine-protein kinase mark2-like isoform x10	393	2.85E-36	90.00%	0.239	G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); PTHR24346:SF23 (PANTHER); PTHR24346 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1696	c5931_g1_i1_len_2473_path_4_0_1805_1810_18_06_1807_1812_1808_2472_2	76	ectonucleoside triphosphate diphosphohydrolase 2-like isoform x4	824	6.96E-105	54.40%	0.447 Y	IPR000407 (PFAM); IPR000407 (PANTHER); IPR000407 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1697	c59326_g1_i1_len_1565_path_1_0_1564_0	35	nucleolar protein 58-like	522	0	82.80%	0.114	IPR012976 (SMART); IPR012974 (PFAM); IPR002687 (PFAM); IPR012976 (PFAM); PTHR10894 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002687 (PROSITE_PROFILES); SSF89124 (SUPERFAMILY); TMhelix (TMHMM)
1698	c59468_g1_i1_len_1776_path_1_0_1775_3	53	fmrf_musdo ame: full=fmrfamide neuropeptides contains: ame: full= amide-2 contains: ame: full= amide-3 contains: ame: full= amide-4 contains: ame: full= amide-5 contains: ame: full= amide-6 contains: ame: full= amide-7 contains: ame: full= amide-8 ame: full= amide-10 contains: ame: full= amide-9 ame: full= amide-11 ame: full= amide-12 ame: full= amide-13 contains: ame: full= amide-14 contains: ame: full= amide-15 contains: ame: full= amide-17 contains: ame: full= amide-16 contains: ame: full= amide-18 flags: precursor	592	1.31E-19	58.60%	0.609 Y	IPR002544 (PFAM); PTHR20986:SF1 (PANTHER); PTHR20986 (PANTHER); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-noTM (SIGNALP_EUK)

1699	c59567_g1_i1_len_1396_path_1_0_1395_2	17	early growth response	465	1.14E-113	55.80%	0.113	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR10042 (PANTHER); PTHR10042:SF24 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1700	c59678_g1_i1_len_1479_path_1_0_1478_5	18	carbohydrate sulfotransferase 11-like	493	3.20E-34	50.70%	0.108	IPR005331 (PFAM); IPR018011 (PANTHER); PTHR12137:SF33 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1701	c59868_g1_i1_len_904_path_1_0_903_1	8	melanotransferrin	301	8.23E-118	79.40%	0.204	IPR001156 (PRINTS); IPR001156 (SMART); IPR001156 (PFAM); G3DSA:3.40.190.10 (GENE3D); G3DSA:3.40.190.10 (GENE3D); PTHR11485 (PANTHER); PTHR11485:SF18 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001156 (PROSITE_PROFILES); SSF53850 (SUPERFAMILY)
1702	c59895_g1_i1_len_1570_path_1548_0_1569_3	17	lysyl-trna synthetase	524	0	99.90%	0.105	IPR018149 (PRINTS); G3DSA:3.30.930.10 (GENE3D); IPR004364 (PFAM); IPR004525 (PTHR22594:PANTHER); IPR018150 (PANTHER); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY)
1703	c60159_g1_i1_len_1580_path_1558_0_1579_1	148	tropinone reductase 2-like	527	6.54E-134	83.50%	0.168	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); IPR002198 (PFAM); PTHR24322:SF111 (PANTHER); PTHR24322 (PANTHER); IPR020904 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF51735 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1704	c60227_g1_i1_len_960_path_950_0_959_2	33	wnt1-inducible-signaling pathway protein 3	320	6.70E-16	52.20%	0.205	IPR000867 (SMART); IPR000867 (PFAM); PTHR11348 (PANTHER); IPR000867 (PROSITE_PROFILES); IPR009030 (SUPERFAMILY)
1705	c60409_g1_i1_len_1355_path_1333_0_1354_0	23	xanthine dehydrogenase partial	452	0	80.90%	0.113	IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (PFAM); IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); IPR008274 (G3DSA:3.30.365.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR008274 (SUPERFAMILY)
1706	c60432_g1_i1_len_717_path_1_0_716_4	7	neurogenic locus notch	234	1.62E-108	89.70%	0.119	PR00010 (PRINTS); IPR001881 (SMART); IPR000742 (SMART); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); G3DSA:2.10.25.10 (GENE3D); IPR000742 (PFAM); G3DSA:2.10.25.10 (GENE3D); PTHR24033 (PANTHER); PTHR24033:SF36 (PANTHER); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR018097 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); IPR013032 (PROSITE_PATTERNS); PD936484 (PRODOM); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); IPR009030 (SUPERFAMILY)
1707	c60441_g1_i1_len_1829_path_1_0_1828_4	22	penicillin-binding protein 1a	610	0	99.00%	0.384 Y	IPR001264 (PFAM); G3DSA:1.10.3810.10 (GENE3D); IPR011816 (TIGRFAM); IPR012340 (G3DSA:2.40.50.GENE3D); IPR012338 (G3DSA:3.40.710.GENE3D); IPR001460 (PFAM); PTHR32282 (PANTHER); PTHR32282:SF5 (PANTHER); IPR023346 (SUPERFAMILY); IPR012338 (SUPERFAMILY)

[illegible]

1723	c62315_g1_i1_len_690_path_668_0_689_3	4	tryptophan-specific transport protein	230	3.17E-121	98.80%	0.447 Y	IPR018227 (PFAM); PTHR32195 (PANTHER); PTHR32195:SF11 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1724	c62415_g1_i1_len_861_path_1_0_860_0	14	lipophorin receptor	287	2.49E-28	71.50%	0.715 Y	IPR002172 (PRINTS); IPR002172 (SMART); IPR002172 (PFAM); IPR002172 (G3DSA:4.10.400.GENE3D); PTHR10529 (PANTHER); IPR023415 (PROSITE_PATTERNS); IPR023415 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR002172 (PROSITE_PROFILES); IPR002172 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-TM (SIGNALP_GRAM_POSITIVE); IPR002172 (SUPERFAMILY); IPR002172 (SUPERFAMILY)
1725	c62478_g1_i1_len_1617_path_1595_0_1616_3	128	PREDICTED: uncharacterized protein LOC101859571	539	4.33E-06	39.00%	0.103	IPR000998 (SMART); IPR000998 (PFAM); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000998 (PROSITE_PROFILES); IPR000998 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); TMhelix (TMHMM)
1726	c62549_g1_i1_len_600_path_578_0_599_4	5	sonic hedgehog protein a	200	3.53E-40	56.60%	0.108	IPR001657 (PRINTS); IPR003586 (SMART); IPR028992 (G3DSA:2.170.16.GENE3D); IPR001767 (PFAM); PTHR11889 (PANTHER); IPR028992 (SUPERFAMILY)
1727	c62819_g1_i1_len_884_path_862_0_883_4	16	low quality protein: zinc finger protein 233	295	1.61E-32	60.80%	0.099	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1728	c62856_g1_i1_len_855_path_833_0_854_0	13	interstitial collagenase	285	3.24E-23	61.20%	0.153	IPR018487 (SMART); IPR000585 (G3DSA:2.110.10.GENE3D); IPR018487 (PFAM); PTHR10201 (PANTHER); IPR018486 (PROSITE_PATTERNS); IPR018487 (PROSITE_PROFILES); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY)
1729	c62871_g1_i1_len_300_path_278_0_299_3	3	prostaglandin g h synthase 2-like isoform x3	100	1.50E-35	70.30%	0.118	G3DSA:2.10.25.10 (GENE3D); PTHR11903 (PANTHER); PTHR11903:SF10 (PANTHER); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY)
1730	c63049_g1_i1_len_1484_path_1_0_1483_2	33	hemagglutinin proteinase	483	6.34E-102	55.00%	0.098	IPR023612 (PRINTS); IPR025711 (PFAM); IPR001570 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); G3DSA:1.10.390.10 (GENE3D); IPR011096 (PFAM); IPR013856 (PFAM); SSF55486 (SUPERFAMILY)
1731	c63088_g1_i1_len_315_path_1_0_314_3	3	adp-ribosylation factor 1	105	7.46E-60	99.80%	0.108	IPR024156 (SMART); IPR027417 (G3DSA:3.40.50.GENE3D); IPR006689 (PFAM); PTHR11711 (PANTHER); PTHR11711:SF104 (PANTHER); IPR024156 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1732	c63142_g1_i1_len_1992_path_1_0_1991_4	38	fidgetin-like protein 1	658	0	80.80%	0.102	IPR003593 (SMART); IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR015415 (PFAM); G3DSA:1.10.8.60 (GENE3D); PTHR23074 (PANTHER); PTHR23074:SF75 (PANTHER); IPR003960 (PROSITE_PATTERNS); IPR027417 (SUPERFAMILY)
1733	c63371_g1_i1_len_175_path_1_0_174_3	0	cg7386- partial	59	1.02E-08	65.90%	0.105	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR007087 (PFAM); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1734	c63665_g1_i1_len_792_path_797_0_791_1	23	peptidyl-prolyl cis-trans	264	6.03E-56	70.90%	0.098	IPR029000 (G3DSA:2.40.100.GENE3D); IPR002130 (PFAM); PTHR11071:SF193 (PANTHER); IPR024936 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)

1744	c6440_g1_i1_len_2317_path_2_0_2316_1	46156	heat shock 70 kda protein cognate 4	765	0	94.40%	0.168	Coil (COILS); IPR013126 (PRINTS); G3DSA:3.30.420.40 (GENE3D); G3DSA:3.90.640.10 (GENE3D); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); IPR029048 (G3DSA:1.20.1270.GENE3D); G3DSA:3.30.30.30 (GENE3D); PTHR19375:SF142 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029047 (SUPERFAMILY); IPR029048 (SUPERFAMILY); TMhelix (TMHMM)
1745	c64978_g1_i1_len_626_path_604_0_625_3	15	---NA---	204			0.153	IPR000742 (SMART); IPR023413 (G3DSA:2.40.155.GENE3D); IPR024731 (PFAM); IPR013032 (PROSITE_PATTERNS); IPR000152 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000742 (PROSITE_PROFILES); SSF57196 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1746	c65092_g1_i1_len_279_path_257_0_278_1	2	lysyl-trna synthetase	93	1.04E-46	90.50%	0.108	G3DSA:3.30.930.10 (GENE3D); IPR004364 (PFAM); IPR018150 (PANTHER); PTHR22594:SF25 (PANTHER); IPR006195 (PROSITE_PROFILES); SSF55681 (SUPERFAMILY)
1747	c65499_g1_i1_len_1025_path_1003_0_1024_1	15	serine partial	336	4.15E-36	63.10%	0.101	IPR029058 (G3DSA:3.40.50.GENE3D); IPR001563 (PFAM); PTHR11802:SF30 (PANTHER); IPR001563 (PANTHER); IPR029058 (SUPERFAMILY)
1748	c65619_g1_i1_len_595_path_573_0_594_0	7	5 -nucleotidase domain containing isoform cra_d	199	5.72E-25	68.80%	0.295	PF13900 (PFAM); PTHR16213 (PANTHER)
1749	c65619_g1_i1_len_595_path_573_0_594_4	7	mre11 meiotic recombination 11 homolog a (cerevisiae) isoform cra_b	198	1.04E-20	73.00%	0.146	PTHR22878 (PANTHER)
1750	c65772_g1_i1_len_860_path_838_0_859_2	129	collagen and calcium-binding egf domain-containing protein 1-like	281	4.60E-19	56.30%	0.105	IPR008160 (PFAM); PTHR24023 (PANTHER)
1751	c65772_g1_i1_len_860_path_838_0_859_4	129	large adhesin	282	3.04E-10	41.25%	0.153	no IPS match
1752	c65815_g1_i1_len_597_path_575_0_596_2	3	secreted frizzled-related protein 5	199	4.13E-56	57.40%	0.105	IPR018933 (PFAM); IPR020067 (G3DSA:1.10.2000.GENE3D); G3DSA:2.40.50.120 (GENE3D); IPR020067 (PFAM); PTHR11309:SF80 (PANTHER); IPR015526 (PANTHER); IPR001134 (PROSITE_PROFILES); IPR020067 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY); IPR020067 (SUPERFAMILY)
1753	c66072_g1_i1_len_609_path_1_0_608_2	9	penicillin-binding protein partial	203	2.85E-138	99.10%	0.159	IPR001264 (PFAM); IPR012338 (G3DSA:3.40.710.GENE3D); G3DSA:1.10.3810.10 (GENE3D); PTHR32282:SF1 (PANTHER); PTHR32282 (PANTHER); IPR023346 (SUPERFAMILY)
1754	c66172_g1_i1_len_889_path_867_0_888_1	30	gamma-interferon-inducible lysosomal thiol reductase	292	9.36E-44	51.40%	0.380 Y	IPR004911 (PFAM); IPR004911 (PANTHER); PTHR13234:SF8 (PANTHER)
1755	c66182_g2_i1_len_343_path_905_0_342_3	3	coatomer subunit alpha	115	2.39E-15	90.10%	0.111	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1756	c66287_g1_i1_len_1143_path_1121_0_1142_1	23	5 -nucleotidase	381	1.09E-125	70.80%	0.106	IPR008334 (PFAM); IPR008334 (G3DSA:3.90.780.GENE3D); IPR006179 (PANTHER); PTHR11575:SF7 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008334 (SUPERFAMILY); TMhelix (TMHMM)
1757	c66572_g1_i1_len_255_path_1_0_254_0	0	adamts-like protein 5	85	4.37E-11	70.10%	0.143	IPR010294 (PFAM); PTHR13723 (PANTHER)
1758	c66607_g1_i1_len_1033_path_1047_0_1032_4	5	superoxide dismutase	344	4.47E-65	96.80%	0.15	IPR001189 (PRINTS); IPR019831 (PFAM); G3DSA:1.10.287.990 (GENE3D); PTHR11404:SF9 (PANTHER); IPR001189 (PANTHER); IPR019831 (SUPERFAMILY)
1759	c66961_g1_i1_len_358_path_1_0_357_2	1	agrin-like isoform x5	119	1.85E-23	62.10%	0.103	G3DSA:2.40.50.120 (GENE3D); IPR004850 (PFAM); IPR004850 (PROSITE_PROFILES); IPR008993 (SUPERFAMILY)
1760	c6717_g1_i1_len_305_path_1_0_304_1	2	formate dehydrogenase h	102	2.67E-68	99.90%	0.109	G3DSA:2.20.25.90 (GENE3D); IPR006656 (PFAM); G3DSA:3.40.50.740 (GENE3D); PTHR11615:SF112 (PANTHER); PTHR11615 (PANTHER); IPR006963 (PROSITE_PROFILES); SSF53706 (SUPERFAMILY)
1761	c6717_g2_i1_len_293_path_565_0_292_3	0	formate dehydrogenase h	98	1.15E-60	98.00%	0.111	G3DSA:3.40.228.10 (GENE3D); IPR006656 (PFAM); PTHR11615 (PANTHER); PTHR11615:SF112 (PANTHER); SSF53706 (SUPERFAMILY)
1762	c67203_g1_i1_len_267_path_245_0_266_3	0	tat (twin-arginine translocation) pathway signal sequence domain protein	89	3.13E-59	99.80%	0.102	IPR006963 (PFAM); IPR006656 (PFAM); G3DSA:3.40.50.740 (GENE3D); G3DSA:2.20.25.90 (GENE3D); PTHR11615 (PANTHER); PTHR11615:SF37 (PANTHER); IPR006963 (PROSITE_PROFILES); SSF53706 (SUPERFAMILY)

1763	c67246_g1_i1_len_816_path_794_0_815_3	6	glycosyltransferase 1 domain-containing protein 1	272	1.83E-39	57.00%	0.233	PTHR12526:SF331 (PANTHER); PTHR12526 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF53756 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1764	c67964_g1_i1_len_388_path_366_0_387_1	1	serine endoprotease partial	129	3.78E-76	100.00%	0.108	IPR001940 (PRINTS); G3DSA:2.40.10.10 (GENE3D); IPR001478 (G3DSA:2.30.42.GENE3D); IPR001254 (PFAM); PTHR22939 (PANTHER); IPR001478 (SUPERFAMILY); IPR009003 (SUPERFAMILY)
1765	c68000_g1_i1_len_841_path_819_0_840_1	13	collagen triple helix repeat family protein	280	3.52E-07	50.00%	0.147	no IPS match
1766	c68000_g1_i1_len_841_path_819_0_840_4	13	#NAME?	280	3.18E-14	49.00%	0.112	no IPS match
1767	c68430_g1_i1_len_637_path_36_0_636_1	6	zinc finger and btb domain-containing protein 49-like isoform x2	212	3.60E-23	73.60%	0.099	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); TMhelix (TMHMM)
1768	c68704_g1_i1_len_492_path_1_0_491_0	7	dnaj homolog subfamily c member 25 homolog	164	9.74E-60	80.10%	0.415 Y	Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF125 (PANTHER); IPR018253 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); TMhelix (TMHMM)
1769	c68721_g1_i1_len_814_path_1_0_813_5	8	sugar partial	271	0	100.00%	0.1	IPR013781 (G3DSA:3.20.20.GENE3D); G3DSA:3.90.400.10 (GENE3D); IPR006047 (PFAM); PTHR10357:SF132 (PANTHER); IPR015902 (PANTHER); IPR017853 (SUPERFAMILY)
1770	c6964_g1_i1_len_2377_path_55_0_348_403_349_352_54_353_2376_2	1302	protein them6	786	2.44E-34	58.40%	0.114	Coil (COILS); IPR029069 (G3DSA:3.10.129.GENE3D); PF13279 (PFAM); PTHR12475 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR029069 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1771	c69984_g1_i1_len_154_path_1_0_153_3	2	ekc keops complex subunit tprkb isoform x2	52	2.71E-12	81.80%	0.176	no IPS match
1772	c69984_g1_i1_len_154_path_1_0_153_4	2	nfs1 nitrogen fixation 1 homolog (cerevisiae)	51	4.56E-19	83.20%	0.127	PF13900 (PFAM); PTHR16213 (PANTHER)
1773	c69984_g1_i1_len_154_path_1_0_153_5	2	coiled-coil domain-containing protein 122	51	4.13E-21	88.80%	0.13	PTHR12138 (PANTHER)
1774	c69992_g1_i1_len_734_path_1_0_733_0	15	probable nuclear transport factor 2 isoform x1	245	9.14E-63	81.90%	0.152	IPR002075 (PFAM); G3DSA:3.10.450.50 (GENE3D); PTHR12612 (PANTHER); IPR018222 (PROSITE_PROFILES); SSF54427 (SUPERFAMILY)
1775	c70102_g1_i1_len_669_path_649_0_668_2	2	eosinophil peroxidase	223	2.85E-08	61.90%	0.728 Y	IPR019791 (PFAM); IPR019791 (G3DSA:1.10.640.GENE3D); PTHR11475 (PANTHER); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SignalP-noTM (SIGNALP_EUK); IPR010255 (SUPERFAMILY)
1776	c70359_g1_i1_len_756_path_734_0_755_1	5	chaperone protein	252	2.97E-150	99.90%	0.106	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001305 (G3DSA:2.10.230.GENE3D); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001305 (PFAM); G3DSA:2.60.260.20 (GENE3D); PTHR24076:SF78 (PANTHER); PTHR24076 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001305 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY); IPR001305 (SUPERFAMILY)
1777	c71276_g1_i1_len_542_path_1_0_541_0	2	tout- isoform a	176	2.55E-80	78.30%	0.351 Y	IPR004263 (PFAM); PTHR11062 (PANTHER); PTHR11062:SF7 (PANTHER)
1778	c71289_g1_i1_len_351_path_1_0_350_1	2	choline partial	117	1.58E-76	98.20%	0.103	IPR007867 (PFAM); G3DSA:3.50.50.60 (GENE3D); G3DSA:3.30.560.10 (GENE3D); PTHR11552 (PANTHER); SSF51905 (SUPERFAMILY); SSF54373 (SUPERFAMILY)
1779	c71366_g1_i1_len_142_path_120_0_141_4	0	isoform j	47	1.61E-08	67.80%	0.105	IPR029070 (G3DSA:3.10.50.GENE3D); IPR029070 (SUPERFAMILY)

1780	c72_g1_i1_len_1469_path_1522_0_1468_2	82	c-type lectin 4	489	3.38E-94	77.90%	0.362 Y	IPR016186 (G3DSA:3.10.100.GENE3D); PTHR21407:SF5 (PANTHER); PTHR21407 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001304 (PROSITE_PROFILES); IPR016187 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1781	c72560_g1_i1_len_144_path_122_0_143_2	0	geisolin-like allergen der f 16	48	3.96E-12	68.60%	0.108	IPR007123 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); IPR030016 (PTHR11977:PANTHER); IPR007122 (PANTHER); SSF55753 (SUPERFAMILY) IPR001314 (PRINTS); IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1782	c7375_g2_i1_len_1534_path_2256_0_1533_2	32	venom protease-like	506	2.08E-70	56.00%	0.215	PR00014 (PRINTS); IPR003961 (SMART); IPR003598 (SMART); IPR003599 (SMART); IPR003961 (PFAM); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR19897 (PANTHER); PTHR19897:SF155 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY)
1783	c7376_g1_i1_len_601_path_1_0_600_5	5	low quality protein: twitchin-like	200	1.20E-83	78.90%	0.119	PR00014 (PRINTS); IPR003961 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF142 (PANTHER); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1784	c7376_g2_i1_len_716_path_1875_0_715_3	6	twitchin isoform x4	239	2.34E-118	86.00%	0.197	PR00014 (PRINTS); IPR003961 (SMART); IPR013098 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); IPR003961 (PFAM); PTHR19897 (PANTHER); PTHR19897:SF142 (PANTHER); IPR003961 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); IPR003961 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1785	c73893_g1_i1_len_231_path_209_0_230_3	0	n-acetyl galactosaminyl transferase	77	1.62E-17	85.40%	0.159	IPR029044 (G3DSA:3.90.550.GENE3D); IPR001173 (PFAM); PTHR11675 (PANTHER); IPR029044 (SUPERFAMILY)
1786	c74300_g1_i1_len_482_path_1_0_481_4	8	gram negative bacteria binding protein 1	161	6.63E-47	68.10%	0.102	IPR013320 (G3DSA:2.60.120.GENE3D); IPR000757 (PFAM); PTHR10963:SF4 (PANTHER); PTHR10963 (PANTHER); IPR013320 (SUPERFAMILY) IPR001672 (PRINTS); IPR001672 (PFAM); G3DSA:3.40.50.10490 (GENE3D); IPR023096 (G3DSA:1.10.1390.GENE3D); IPR001672 (PANTHER); PTHR11469:SF7 (PANTHER); IPR018189 (PROSITE_PATTERNS); IPR001672 (PROSITE_PROFILES); SSF53697 (SUPERFAMILY)
1787	c74308_g1_i1_len_525_path_1_0_524_5	1	glucose-6-phosphate partial	175	2.71E-114	100.00%	0.11	Coil (COILS); G3DSA:3.30.200.20 (GENE3D); IPR000719 (PFAM); IPR020636 (PANTHER); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY) IPR012341 (G3DSA:1.50.10.GENE3D); IPR002037 (PFAM); IPR008928 (SUPERFAMILY)
1788	c74795_g1_i1_len_173_path_159_0_172_4	0	calcium calmodulin-dependent protein kinase type 1 isoform x2	58	1.21E-26	96.80%	0.095	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1789	c75202_g1_i1_len_363_path_383_0_362_2	2	endo- -d- partial	121	6.26E-82	100.00%	0.12	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF14 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY)
1790	c75670_g1_i1_len_261_path_1_0_260_3	0	zinc c2h2 type	87	4.12E-15	59.30%	0.126	IPR013856 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); SSF55486 (SUPERFAMILY)
1791	c7616_g1_i1_len_627_path_1443_0_13_642_14_65_694_66_96_724_97_595_694_596_626_0	13	plasmid recombination protein	209	2.17E-08	45.00%	0.106	no IPS match
1792	c76668_g1_i1_len_189_path_167_0_188_0	0	elastase	63	4.01E-13	68.60%	0.106	IPR013856 (PFAM); IPR013856 (G3DSA:3.10.170.GENE3D); SSF55486 (SUPERFAMILY)
1793	c7719_g1_i1_len_646_path_670_0_263_933_264_267_24_268_645_1	28	antigen 5 scp domain-containing	215	4.53E-12	55.30%	0.387 Y	IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); IPR014044 (SUPERFAMILY)
1794	c77954_g1_i1_len_679_path_1_0_678_0	4	laminin subunit alpha	227	2.47E-23	69.30%	0.113	IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (SUPERFAMILY) IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24139 (PANTHER); PTHR24139:SF26 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM)
1795	c784_g1_i1_len_825_path_1286_0_450_242_451_824_1	16	developmental protein cactus	270	2.70E-25	70.70%	0.114	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24139 (PANTHER); PTHR24139:SF26 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY); TMhelix (TMHMM)

1796	c784_g1_i2_len_615_path_1_0_240_242_241_61_4_1	5	nf-kappa-b inhibitor cactus-like	200	3.85E-51	72.00%	0.14	IPR002110 (SMART); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24139 (PANTHER); PTHR24139:SF26 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1797	c7868_g1_i1_len_472_path_478_0_425_904_426_471_2	2	serine protease nudel	157	2.16E-18	81.10%	0.132	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009003 (SUPERFAMILY)
1798	c80517_g1_i1_len_328_path_306_0_327_5	1	zinc finger protein 271 (zinc finger protein 7) (zinc finger protein znfphe133) (epstein-barr virus-induced zinc finger protein) (znf-eb) (ct-zfp48) (zinc finger protein)	109	7.79E-18	62.20%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR007087 (PFAM); PF13912 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF14 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1799	c8052_g1_i1_len_534_path_1_0_510_1076_511_533_3	4	aurora kinase a-like	173	2.03E-25	96.60%	0.1	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); IPR030616 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1800	c80640_g1_i1_len_142_path_120_0_141_1	0	retinol dehydrogenase 13-like	47	1.44E-19	92.40%	0.099	IPR002347 (PRINTS); IPR016040 (G3DSA:3.40.50.GENE3D); PTHR24320 (PANTHER); PTHR24320:SF55 (PANTHER); SSF51735 (SUPERFAMILY)
1801	c8150_g1_i1_len_2436_path_53_0_2435_1	137	carboxypeptidase e	812	0	73.90%	0.134	IPR000834 (PRINTS); IPR000834 (SMART); IPR014766 (G3DSA:2.60.40.GENE3D); G3DSA:3.40.630.10 (GENE3D); PF13620 (PFAM); IPR000834 (PFAM); PTHR11532:SF41 (PANTHER); PTHR11532 (PANTHER); IPR000834 (PROSITE_PATTERNS); IPR000834 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR008969 (SUPERFAMILY); SSF53187 (SUPERFAMILY); TMhelix (TMHMM)
1802	c82439_g1_i1_len_1193_path_1_0_1192_0	34	endo-beta- -glucanase	391	7.77E-114	72.60%	0.195	IPR012341 (G3DSA:1.50.10.GENE3D); IPR001701 (PFAM); PTHR22298 (PANTHER); PTHR22298:SF17 (PANTHER); IPR018221 (PROSITE_PATTERNS); IPR008928 (SUPERFAMILY)
1803	c82456_g1_i1_len_535_path_513_0_534_0	26	retinal dehydrogenase 1	172	2.14E-68	89.50%	0.101	IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF145 (PANTHER); IPR016161 (SUPERFAMILY)
1804	c82625_g1_i1_len_1833_path_1_0_1832_0	120	laminin subunit alpha	605	1.68E-130	54.60%	0.132	IPR001791 (SMART); IPR001791 (PFAM); IPR013320 (G3DSA:2.60.120.GENE3D); IPR013320 (G3DSA:2.60.120.GENE3D); PTHR10574 (PANTHER); PTHR10574:SF39 (PANTHER); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR001791 (PROSITE_PROFILES); IPR013320 (SUPERFAMILY); IPR013320 (SUPERFAMILY)
1805	c82725_g1_i1_len_1842_path_7_0_1841_3	30	zinc finger protein zfat-like	614	2.42E-39	57.50%	0.106	Coil (COILS); IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13894 (PFAM); PF13465 (PFAM); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1806	c82743_g1_i1_len_169_path_147_0_168_1	144	midgut chitinase	56	3.41E-11	66.20%	0.104	IPR001223 (PFAM); IPR013781 (G3DSA:3.20.20.GENE3D); PTHR11177 (PANTHER); PTHR11177:SF45 (PANTHER); IPR017853 (SUPERFAMILY)
1807	c82774_g1_i1_len_2623_path_10_0_2622_5	6061	heat shock 70 kda protein cognate 3	868	0	93.90%	0.257	Coil (COILS); Coil (COILS); IPR013126 (PRINTS); IPR029048 (G3DSA:1.20.1270.GENE3D); G3DSA:3.90.640.10 (GENE3D); G3DSA:3.30.30.30 (GENE3D); G3DSA:3.30.420.40 (GENE3D); IPR013126 (PFAM); IPR029047 (G3DSA:2.60.34.GENE3D); G3DSA:3.30.420.40 (GENE3D); PTHR19375:SF157 (PANTHER); PTHR19375 (PANTHER); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); IPR018181 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR029047 (SUPERFAMILY); SSF53067 (SUPERFAMILY); SSF53067 (SUPERFAMILY); IPR029048 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)

1808	c82789_g1_i1_len_1219_path_1_0_1218_3	24	alpha- -mannosyl-glycoprotein 4-beta-n-acetylglucosaminyltransferase a-like	400	6.70E-41	56.00%	0.164	IPR006759 (PFAM); IPR006759 (PANTHER); PTHR12062:SF5 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM)
1809	c82872_g1_i1_len_1701_path_1679_0_1700_4	14	cold shock protein	567	5.80E-41	99.40%	0.113	IPR002059 (PRINTS); IPR011129 (SMART); IPR012340 (G3DSA:2.40.50.GENE3D); IPR002059 (PFAM); PTHR11544 (PANTHER); IPR019844 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012340 (SUPERFAMILY)
1810	c82944_g1_i1_len_748_path_1_0_747_0	6	l-asparaginase 2	250	3.37E-161	99.00%	0.154	IPR006034 (PRINTS); IPR006034 (SMART); IPR006034 (PIRSF); IPR006034 (PFAM); IPR027474 (G3DSA:3.40.50.GENE3D); PIRSF500176 (PIRSF); IPR004550 (TIGRFAM); PTHR11707 (PANTHER); PTHR11707:SF4 (PANTHER); IPR027475 (PROSITE_PATTERNS); IPR020827 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR006034 (SUPERFAMILY); TMhelix (TMHMM)
1811	c83002_g1_i1_len_538_path_1_0_537_4	4	n-acetylmuramoyl-l-alanine amidase family partial	179	4.53E-107	100.00%	0.131	IPR002508 (SMART); IPR002508 (PFAM); IPR002508 (G3DSA:3.40.630.GENE3D); PTHR30404 (PANTHER); PTHR30404:SF0 (PANTHER); SSF53187 (SUPERFAMILY)
1812	c83042_g1_i1_len_1166_path_1_0_1165_5	20	ras-related protein rab-35	388	2.62E-128	94.70%	0.104	IPR001806 (PRINTS); IPR003579 (SMART); IPR020849 (SMART); IPR024156 (SMART); IPR002041 (SMART); IPR003578 (SMART); IPR005225 (TIGRFAM); IPR027417 (G3DSA:3.40.50.GENE3D); IPR001806 (PFAM); PTHR24073 (PANTHER); PTHR24073:SF428 (PANTHER); PS51419 (PROSITE_PROFILES); IPR027417 (SUPERFAMILY)
1813	c83082_g1_i1_len_979_path_1_0_978_1	9	aael017480- partial	326	7.49E-68	56.50%	0.102	IPR002110 (PRINTS); IPR002110 (SMART); PF13637 (PFAM); IPR020683 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); PTHR24198 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1814	c83202_g1_i1_len_1059_path_1037_0_1058_3	17	lachesin isoform x1	353	1.03E-80	76.50%	0.101	IPR003598 (SMART); PF13895 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013098 (PFAM); PTHR19831:SF43 (PANTHER); PTHR19831 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY); TMhelix (TMHMM)
1815	c83295_g1_i1_len_2089_path_2067_0_2088_3	36	maguk p55 subfamily member 7 isoform x4	697	4.36E-179	87.30%	0.105	IPR001452 (SMART); IPR008145 (SMART); IPR011511 (PFAM); IPR008145 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); G3DSA:3.30.63.10 (GENE3D); G3DSA:2.30.30.40 (GENE3D); PTHR23122:SF14 (PANTHER); PTHR23122 (PANTHER); IPR020590 (PROSITE_PATTERNS); IPR008144 (PROSITE_PROFILES); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY); IPR027417 (SUPERFAMILY)
1816	c83425_g1_i1_len_1946_path_1_0_1945_2	73	calcium calmodulin-dependent protein kinase ii isoform a	648	0	93.60%	0.138	IPR002290 (SMART); IPR000719 (PFAM); IPR013543 (PFAM); G3DSA:3.10.450.50 (GENE3D); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); IPR020636 (PANTHER); PTHR24347:SF108 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR017441 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR000719 (PROSITE_PROFILES); SSF54427 (SUPERFAMILY); IPR011009 (SUPERFAMILY)
1817	c83512_g1_i1_len_927_path_913_0_926_2	24306	translationally controlled tumor protein	302	4.80E-71	79.20%	0.159	IPR018105 (PRINTS); IPR018105 (PFAM); IPR011323 (G3DSA:2.170.150.GENE3D); IPR018105 (PANTHER); IPR011057 (SUPERFAMILY)

1826	c84306_g1_i1_len_1166_path_1144_0_1165_2	25	spondin-2 isoform x1	388	9.87E-137	80.60%	0.109	IPR009465 (PFAM); PTHR11311 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR009465 (PROSITE_PROFILES)
1827	c84356_g1_i1_len_1037_path_1015_0_1036_1	13	serine threonine-protein kinase plk1-like	346	8.47E-142	72.20%	0.111	IPR002290 (SMART); IPR000719 (PFAM); G3DSA:1.10.510.10 (GENE3D); G3DSA:3.30.200.20 (GENE3D); PTHR24345 (PANTHER); PTHR24345:SF49 (PANTHER); IPR008271 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1828	c84477_g1_i1_len_245_path_223_0_244_4	0	trypsin-like protein	82	6.22E-22	66.50%	0.111	IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); PTHR24256 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1829	c84539_g1_i1_len_742_path_18_0_741_4	4	protein tas	247	0	100.00%	0.105	IPR020471 (PRINTS); IPR023210 (PFAM); IPR023210 (G3DSA:3.20.20.GENE3D); IPR001395 (PANTHER); PTHR11732:SF112 (PANTHER); IPR023210 (SUPERFAMILY)
1830	c8461_g2_i1_len_1381_path_1359_0_1380_0	40	Agrin	461	2.59E-06	67.00%	0.136	IPR002350 (SMART); IPR002350 (PFAM); G3DSA:3.30.60.30 (GENE3D); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002350 (PROSITE_PROFILES); SSF100895 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1831	c84753_g1_i1_len_587_path_609_0_582_25_583_586_1	7	Hyaluronidase	196	1.20E-31	60.90%	0.106	IPR018155 (PFAM); IPR013785 (G3DSA:3.20.20.GENE3D); PTHR11769:SF8 (PANTHER); IPR018155 (PANTHER); IPR017853 (SUPERFAMILY)
1832	c84812_g1_i1_len_778_path_1_0_777_3	8	d-alanyl-d-alanine carboxypeptidase	260	1.87E-119	100.00%	0.104	IPR012907 (SMART); IPR012338 (G3DSA:3.40.710.GENE3D); IPR012907 (PFAM); IPR001967 (PFAM); IPR012907 (G3DSA:2.60.410.GENE3D); PTHR21581:SF3 (PANTHER); PTHR21581 (PANTHER); IPR012338 (SUPERFAMILY); IPR015956 (SUPERFAMILY)
1833	c84885_g1_i1_len_1045_path_1023_0_1044_2	15	mesencephalic astrocyte-derived neurotrophic factor homolog	348	6.57E-77	84.70%	0.166	IPR019345 (PFAM); IPR011001 (G3DSA:1.10.225.GENE3D); PTHR12990 (PANTHER); PTHR12990:SF5 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF68906 (SUPERFAMILY); TMhelix (TMHMM)
1834	c84914_g1_i1_len_354_path_332_0_353_4	2	partial	112	1.82E-54	82.60%	0.119	IPR000997 (PRINTS); IPR029058 (G3DSA:3.40.50.GENE3D); IPR002018 (PFAM); PTHR11559:SF154 (PANTHER); PTHR11559 (PANTHER); IPR019819 (PROSITE_PATTERNS); IPR029058 (SUPERFAMILY)
1835	c84923_g1_i1_len_569_path_1_0_568_0	3	glycosyl hydrolases 31 family protein	190	2.51E-130	99.00%	0.1	IPR025887 (PFAM); IPR000322 (PFAM); PTHR22762 (PANTHER); PTHR22762:SF38 (PANTHER); IPR017853 (SUPERFAMILY); IPR011013 (SUPERFAMILY)
1836	c84977_g1_i1_len_238_path_216_0_237_3	0	polypeptide n-acetylgalactosaminyltransferase 2-like	80	1.29E-35	83.10%	0.185	IPR000772 (PFAM); G3DSA:2.80.10.50 (GENE3D); PTHR11675 (PANTHER); PTHR11675:SF24 (PANTHER); IPR000772 (PROSITE_PROFILES); IPR000772 (SUPERFAMILY)
1837	c85049_g1_i1_len_1527_path_1_0_1526_5	49	purple acid phosphatase	509	0	74.40%	0.11	IPR025733 (PFAM); IPR004843 (PFAM); IPR029052 (G3DSA:3.60.21.GENE3D); IPR015914 (G3DSA:2.60.40.GENE3D); PTHR22953:SF9 (PANTHER); PTHR22953 (PANTHER); IPR008963 (SUPERFAMILY); IPR029052 (SUPERFAMILY)
1838	c85090_g1_i1_len_2708_path_2728_0_2707_2	81	malonyl -acyl carrier protein transacylase	902	0	97.80%	0.107	IPR002198 (PRINTS); IPR002347 (PRINTS); IPR020801 (SMART); IPR013968 (SMART); IPR002198 (PFAM); IPR003231 (TIGRFAM); IPR009081 (G3DSA:1.10.1200.GENE3D); IPR004410 (TIGRFAM); IPR014043 (PFAM); IPR016038 (G3DSA:3.40.47.GENE3D); IPR001227 (G3DSA:3.40.366.GENE3D); IPR016040 (G3DSA:3.40.50.GENE3D); G3DSA:3.30.70.250 (GENE3D); IPR014030 (PFAM); IPR011284 (TIGRFAM); IPR009081 (PFAM); PTHR24312:SF0 (PANTHER); PTHR24312 (PANTHER); IPR006162 (PROSITE_PATTERNS); IPR020904 (PROSITE_PATTERNS); IPR009081 (PROSITE_PROFILES); IPR003231 (HAMAP); IPR016036 (SUPERFAMILY); IPR016039 (SUPERFAMILY); IPR009081 (SUPERFAMILY); IPR016035 (SUPERFAMILY); SSF51735 (SUPERFAMILY)
1839	c8533_g1_i1_len_956_path_1018_0_383_1401_3_84_401_43_402_955_0	40	mitochondrial import inner membrane translocase subunit tim8 a	312	4.51E-31	80.90%	0.209	IPR004217 (PFAM); IPR006966 (PFAM); IPR004217 (G3DSA:1.10.287.GENE3D); PTHR21535 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR004217 (SUPERFAMILY)

1840	c85377_g1_i1_len_2711_path_2689_0_2710_3	51	ankyrin repeat protein	904	1.34E-39	54.60%	0.141	IPR002110 (PRINTS); IPR002110 (SMART); IPR002110 (PFAM); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); PTHR24198 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1841	c85451_g1_i1_len_787_path_765_0_786_1	14	dnaj homolog subfamily c member 21-like	262	4.28E-122	83.80%	0.122	Coil (COILS); Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (G3DSA:1.10.287.GENE3D); IPR001623 (PFAM); PTHR24078:SF150 (PANTHER); PTHR24078 (PANTHER); IPR018253 (PROSITE_PATTERNS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1842	c85493_g2_i1_len_571_path_454_0_570_5	3	c4b-binding protein beta chain	190	9.90E-25	81.10%	0.126	IPR000436 (SMART); G3DSA:2.10.70.10 (GENE3D); IPR000436 (PFAM); PTHR19325 (PANTHER); PTHR19325:SF340 (PANTHER); IPR000436 (PROSITE_PROFILES); IPR000436 (SUPERFAMILY)
1843	c85572_g1_i1_len_1317_path_1_0_1316_5	41	glucose dehydrogenase	439	1.01E-39	81.10%	0.127	G3DSA:3.30.560.10 (GENE3D); IPR007867 (PFAM); G3DSA:3.50.50.60 (GENE3D); PTHR11552:SF68 (PANTHER); PTHR11552 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SSF54373 (SUPERFAMILY); SSF51905 (SUPERFAMILY)
1844	c85584_g1_i1_len_1327_path_14_0_1326_2	20	dnaj homolog subfamily b member 9	442	4.05E-61	56.30%	0.201	Coil (COILS); IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24077 (PANTHER); IPR018253 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1845	c85681_g1_i1_len_642_path_620_0_641_5	4	membrane partial	214	2.20E-137	99.00%	0.097	IPR012332 (G3DSA:2.160.20.GENE3D)
1846	c86034_g1_i1_len_1455_path_1_0_1454_4	32	thioredoxin domain-containing protein 5	485	3.35E-35	70.50%	0.113	PR00421 (PRINTS); IPR013766 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1847	c86044_g1_i1_len_1256_path_1234_0_1255_2	45	activated cdc42 kinase 1 isoform x2	418	0	80.50%	0.108	IPR001245 (PRINTS); IPR020635 (SMART); G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); G3DSA:2.30.30.40 (GENE3D); IPR030220 (PTHR24418:PANTHER); PTHR24418 (PANTHER); IPR017441 (PROSITE_PATTERNS); IPR008266 (PROSITE_PATTERNS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY)
1848	c8612_g1_i1_len_430_path_81_0_61_80_62_429_0	895	60s acidic ribosomal protein p1	144	5.09E-31	93.40%	0.19	PF00428 (PFAM); PTHR21141 (PANTHER); IPR027534 (HAMAP)
1849	c8612_g1_i2_len_405_path_43_0_36_80_37_404_2	1365	60s acidic ribosomal protein p1	135	4.92E-31	92.80%	0.213	PF00428 (PFAM); PTHR21141 (PANTHER); IPR027534 (HAMAP)
1850	c86163_g1_i1_len_398_path_1_0_397_5	7	vesicle-fusing atpase 1	132	2.29E-72	90.40%	0.103	IPR003959 (PFAM); IPR027417 (G3DSA:3.40.50.GENE3D); PTHR23078 (PANTHER); IPR027417 (SUPERFAMILY)
1851	c86292_g1_i1_len_893_path_871_0_892_1	10	dnaj homolog subfamily c member 11	298	4.30E-139	81.80%	0.102	IPR001623 (PRINTS); IPR001623 (SMART); IPR001623 (PFAM); IPR001623 (G3DSA:1.10.287.GENE3D); PTHR24078 (PANTHER); PTHR24078:SF159 (PANTHER); IPR001623 (PROSITE_PROFILES); IPR001623 (SUPERFAMILY)
1852	c86316_g1_i1_len_605_path_583_0_604_0	7	lipophorin receptor	202	8.95E-111	86.20%	0.105	IPR000033 (SMART); IPR011042 (G3DSA:2.120.10.GENE3D); IPR000033 (PFAM); PTHR10529:SF208 (PANTHER); PTHR10529 (PANTHER); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); IPR000033 (PROSITE_PROFILES); SSF63825 (SUPERFAMILY)
1853	c86389_g1_i1_len_826_path_1_0_825_4	8	protein fem-1 homolog cg6966 isoform x1	275	3.91E-85	89.80%	0.337	IPR002110 (PRINTS); IPR002110 (SMART); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (G3DSA:1.25.40.GENE3D); IPR020683 (PFAM); IPR002110 (PFAM); PTHR24173 (PANTHER); PTHR24173:SF15 (PANTHER); IPR002110 (PROSITE_PROFILES); IPR020683 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR002110 (PROSITE_PROFILES); IPR020683 (SUPERFAMILY)
1854	c86497_g1_i1_len_262_path_240_0_261_4	0	endothelin-converting enzyme 1-like	81	5.98E-20	83.60%	0.121	IPR018497 (PFAM); IPR024079 (G3DSA:3.40.390.GENE3D); IPR000718 (PANTHER); PTHR11733:SF110 (PANTHER); SSF55486 (SUPERFAMILY)

1855	c86636_g1_i1_len_1130_path_1_0_1129_0	32	transforming growth factor-beta-induced protein ig-h3-like	377	4.24E-41	52.80%	0.351 Y	IPR000782 (SMART); IPR000782 (G3DSA:2.30.180.GENE3D); IPR000782 (PFAM); IPR000782 (G3DSA:2.30.180.GENE3D); PTHR10900 (PANTHER); IPR000782 (PROSITE_PROFILES); IPR000782 (PROSITE_PROFILES); IPR000782 (SUPERFAMILY); IPR000782 (SUPERFAMILY)
1856	c86799_g1_i1_len_1265_path_1_0_1264_1	116	leucine-rich repeat and calponin homology domain-containing protein 1-like	417	7.11E-120	65.60%	0.1	IPR003591 (SMART); SM00364 (SMART); IPR001611 (PFAM); IPR001611 (PFAM); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); PTHR23155:SF423 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1857	c86807_g1_i1_len_2146_path_1_0_2145_2	25	sel1 repeat family protein	715	2.67E-140	98.70%	0.102	IPR006597 (SMART); IPR011990 (G3DSA:1.25.40.GENE3D); IPR006597 (PFAM); PTHR11102 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF81901 (SUPERFAMILY); TMhelix (TMHMM)
1858	c86935_g1_i1_len_505_path_483_0_504_3	5	50-kda dystrophin-associated glycoprotein	169	5.16E-15	67.30%	0.117	IPR008908 (PFAM); IPR016186 (G3DSA:3.10.100.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10132:SF14 (PANTHER); IPR008908 (PANTHER); IPR016187 (SUPERFAMILY)
1859	c86969_g1_i1_len_1946_path_1_0_1945_4	649	peptidylglycine alpha-hydroxylating monooxygenase	642	2.45E-167	78.10%	0.136	IPR000720 (PRINTS); PF03712 (PFAM); IPR000323 (PFAM); IPR014784 (G3DSA:2.60.120.GENE3D); IPR000323 (G3DSA:2.60.120.GENE3D); PTHR10680 (PANTHER); IPR014783 (PROSITE_PATTERNS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR008977 (SUPERFAMILY); IPR008977 (SUPERFAMILY); IPR008977 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1860	c87070_g1_i1_len_704_path_682_0_703_0	15	xanthine dehydrogenase	235	4.53E-66	69.10%	0.113	IPR002346 (PFAM); IPR016167 (G3DSA:3.30.43.GENE3D); IPR016169 (G3DSA:3.30.465.GENE3D); PTHR11908 (PANTHER); PTHR11908:SF32 (PANTHER); IPR016166 (PROSITE_PROFILES); IPR016166 (SUPERFAMILY)
1861	c87110_g1_i1_len_487_path_465_0_486_4	9	partial	162	6.86E-16	66.60%	0.105	G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24276 (PANTHER); IPR009003 (SUPERFAMILY)
1862	c87211_g1_i1_len_750_path_1_0_749_5	38	peptidyl-prolyl cis-trans isomerase-like 6	244	2.07E-17	62.60%	0.109	IPR002130 (PFAM); IPR029000 (G3DSA:2.40.100.GENE3D); PTHR11071:SF210 (PANTHER); IPR024936 (PANTHER); IPR002130 (PROSITE_PROFILES); IPR029000 (SUPERFAMILY)
1863	c87222_g1_i1_len_2483_path_2485_0_2482_0	138	12 kda fk506-binding protein	828	1.20E-59	90.10%	0.245	IPR001179 (PFAM); G3DSA:3.10.50.40 (GENE3D); IPR023566 (PANTHER); PTHR10516:SF272 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001179 (PROSITE_PROFILES); SSF54534 (SUPERFAMILY); TMhelix (TMHMM)
1864	c87385_g1_i1_len_1357_path_1335_0_1356_2	20	early growth response	452	2.17E-82	67.90%	0.099	IPR015880 (SMART); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR23223 (PANTHER); PTHR23223:SF80 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1865	c877_g1_i1_len_1015_path_1_0_724_726_725_734_736_735_1014_0	17641	anti-lipopolysaccharide factor	327	3.36E-33	68.90%	0.316	IPR024509 (PFAM); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR024716 (PRODOM); TMhelix (TMHMM)
1866	c87854_g1_i1_len_807_path_785_0_806_5	7	hydroxymethylpyrimidine phosphomethylpyrimidine kinase	269	3.21E-162	99.90%	0.105	IPR004399 (TIGRFAM); IPR029056 (G3DSA:3.40.1190.GENE3D); IPR013749 (PFAM); PTHR20858 (PANTHER); PTHR20858:SF17 (PANTHER); IPR029056 (SUPERFAMILY)
1867	c88048_g1_i1_len_684_path_1_0_683_0	5	leucine-rich repeat-containing protein 70 isoform x1	228	2.50E-07	53.14%	0.106	G3DSA:3.80.10.10 (GENE3D); PTHR24369 (PANTHER); SSF52058 (SUPERFAMILY)
1868	c88158_g1_i1_len_265_path_1_0_264_1	0	---NA---	88			0.15	PTHR22878 (PANTHER)

[illegible]

[illegible]

1889	c90144_g1_i1_len_972_path_950_0_971_3	13	balbiani ring protein 3	324	2.71E-18	49.70%	0.666	Y	IPR000072 (SMART); IPR000072 (PFAM); IPR004153 (PFAM); IPR029034 (G3DSA:2.10.90.GENE3D); PTHR11633:SF1 (PANTHER); PTHR11633 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000072 (PROSITE_PROFILES); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); IPR029034 (SUPERFAMILY); TMhelix (TMHMM)
1890	c9018_g2_i4_len_2303_path_3441_0_1746_655_1747_1770_5211_1771_1901_502_1902_1925_5_365_1926_2302_0	96	cation channel sperm-associated protein subunit gamma	768	2.14E-09	49.67%	0.112		NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1891	c9018_g2_i4_len_2303_path_3441_0_1746_655_1747_1770_5211_1771_1901_502_1902_1925_5_365_1926_2302_1	96	cation channel sperm-associated protein subunit gamma	768	7.64E-10	52.50%	0.189		Coil (COILS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1892	c9018_g2_i4_len_2303_path_3441_0_1746_655_1747_1770_5211_1771_1901_502_1902_1925_5_365_1926_2302_2	96	ribosome-binding protein 1 isoform x1	767	6.18E-13	55.22%	0.12		TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1893	c90181_g1_i1_len_815_path_793_0_814_0	14	neprilysin 2 isoform x3	272	5.09E-104	72.00%	0.1		IPR018497 (PRINTS); IPR024079 (G3DSA:3.40.390.GENE3D); IPR018497 (PFAM); PTHR11733:SF113 (PANTHER); IPR000718 (PANTHER); SSF55486 (SUPERFAMILY)
1894	c9036_g1_i2_len_1820_path_1_0_1371_1373_1372_1399_2900_1400_1493_1429_1494_1503_30_03_1504_1819_2	40	repetitive proline-rich cell wall protein 2-like	606	5.53E-11	50.50%	0.136		no IPS match
1895	c90564_g1_i1_len_990_path_968_0_989_4	29	serine protease easter	330	1.59E-33	60.50%	0.1		IPR001314 (PRINTS); IPR001254 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268:SF81 (PANTHER); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1896	c9086_g1_i1_len_1025_path_1_0_493_495_494_1024_0	39	abl interactor 2-like	336	2.31E-34	94.80%	0.1		IPR001452 (PRINTS); IPR001452 (SMART); IPR001452 (PFAM); G3DSA:2.30.30.40 (GENE3D); IPR028457 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001452 (PROSITE_PROFILES); IPR001452 (SUPERFAMILY)
1897	c90934_g1_i1_len_516_path_494_0_515_1	9	sortilin-related receptor	172	2.03E-18	77.30%	0.106		G3DSA:2.130.10.140 (GENE3D); PTHR12106:SF7 (PANTHER); PTHR12106 (PANTHER); SSF110296 (SUPERFAMILY)
1898	c90969_g1_i1_len_525_path_1_0_524_3	10	peroxiredoxin 1	175	3.81E-60	91.70%	0.119		IPR000866 (PFAM); IPR019479 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10681 (PANTHER); PTHR10681:SF101 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1899	c9130_g1_i1_len_1626_path_1599_0_804_801_805_828_825_829_1625_4	134	pdz domain-containing protein 11	542	3.73E-50	76.80%	0.105		IPR001478 (SMART); IPR001478 (PFAM); IPR001478 (G3DSA:2.30.42.GENE3D); PTHR14063 (PANTHER); IPR001478 (PROSITE_PROFILES); IPR001478 (SUPERFAMILY)
1900	c9193_g1_i1_len_1915_path_1893_0_998_2892_999_1914_0	56	tyrosine-protein phosphatase 69d-like	639	3.07E-157	79.70%	0.133		IPR000242 (PRINTS); IPR000242 (SMART); IPR003595 (SMART); IPR000242 (PFAM); IPR029021 (G3DSA:3.90.190.GENE3D); IPR029021 (G3DSA:3.90.190.GENE3D); PTHR19134:SF277 (PANTHER); PTHR19134 (PANTHER); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000387 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR000242 (PROSITE_PROFILES); IPR000387 (PROSITE_PROFILES); IPR029021 (SUPERFAMILY); IPR029021 (SUPERFAMILY)

1901	c91971_g1_i1_len_483_path_461_0_482_3	2	kda midgut protein	155	6.12E-22	57.40%	0.261	SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TMhelix (TMHMM)
1902	c9203_g1_i1_len_1457_path_1_0_547_549_548_1456_3	151	leucine-rich repeat protein 1 isoform x2	486	2.42E-120	64.10%	0.263	PR00019 (PRINTS); IPR003591 (SMART); IPR001611 (PFAM); G3DSA:3.80.10.10 (GENE3D); PTHR23155 (PANTHER); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); IPR001611 (PROSITE_PROFILES); SSF52058 (SUPERFAMILY)
1903	c92079_g1_i1_len_714_path_1_0_713_2	15	zinc finger protein 420-like	238	2.15E-20	50.20%	0.119	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR007087 (PFAM); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1904	c92205_g1_i1_len_712_path_1_0_711_3	10	spondin-1-like	238	7.01E-87	69.20%	0.108	IPR002223 (PRINTS); IPR002223 (SMART); IPR000884 (SMART); IPR002223 (G3DSA:4.10.410.GENE3D); G3DSA:2.20.100.10 (GENE3D); IPR000884 (PFAM); IPR002223 (PFAM); PTHR11311 (PANTHER); PTHR11311:SF11 (PANTHER); IPR020901 (PROSITE_PATTERNS); IPR002223 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR000884 (PROSITE_PROFILES); IPR002223 (SUPERFAMILY); IPR000884 (SUPERFAMILY); IPR000884 (SUPERFAMILY)
1905	c9311_g1_i1_len_2782_path_2760_0_457_3218_458_2781_2	136	27 kda hemolymph	920	3.65E-44	57.00%	0.152	IPR009832 (PFAM); PTHR20997 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM)
1906	c93283_g1_i1_len_1025_path_1003_0_1024_2	6	succinate-semialdehyde partial	341	6.52E-111	99.30%	0.097	IPR015590 (PFAM); IPR016163 (G3DSA:3.40.309.GENE3D); PTHR11699 (PANTHER); PTHR11699:SF49 (PANTHER); IPR016161 (SUPERFAMILY)
1907	c9348_g1_i1_len_1308_path_1314_0_1307_0	86	thioredoxin-related transmembrane protein 1	436	4.83E-101	71.20%	0.462 Y	IPR012336 (G3DSA:3.40.30.GENE3D); IPR013766 (PFAM); PTHR18929:SF81 (PANTHER); PTHR18929 (PANTHER); IPR017937 (PROSITE_PATTERNS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1908	c9352_g1_i1_len_1303_path_1_0_1302_0	28	fasciclin-3 isoform x2	435	1.89E-28	46.20%	0.217	IPR003599 (SMART); IPR013098 (PFAM); IPR013162 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR11640 (PANTHER); PTHR11640:SF52 (PANTHER); IPR007110 (PROSITE_PROFILES); IPR007110 (PROSITE_PROFILES); SSF48726 (SUPERFAMILY); SSF48726 (SUPERFAMILY)
1909	c93564_g1_i1_len_185_path_163_0_184_3	0	probable chitinase 3	62	2.57E-14	72.90%	0.158	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF112 (PANTHER); PTHR11177 (PANTHER); IPR017853 (SUPERFAMILY)
1910	c93719_g1_i1_len_677_path_694_0_676_1	16	anti-lipopolysaccharide partial	226	1.61E-19	68.70%	0.764 Y	IPR024509 (PFAM); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); IPR024716 (PRODOM); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); TMhelix (TMHMM)
1911	c9392_g1_i1_len_1168_path_1896_0_1167_2	20	striatin- partial	389	0	90.00%	0.137	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); PTHR15653 (PANTHER); IPR019775 (PROSITE_PATTERNS); IPR019775 (PROSITE_PATTERNS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM)

1912	c9402_g1_i1_len_1309_path_1312_0_1308_1	222	trans-l-3-hydroxyproline dehydratase	436	3.79E-144	76.10%	0.174	IPR008794 (PFAM); G3DSA:3.10.310.10 (GENE3D); G3DSA:3.10.310.10 (GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SSF54506 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1913	c94066_g1_i1_len_734_path_30_0_733_1	14	---NA---	245			0.101	IPR029058 (G3DSA:3.40.50.GENE3D); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1914	c9413_g1_i1_len_1349_path_1327_0_109_1437_110_1348_1	68	matrix metalloproteinase-15-like	450	1.02E-93	74.80%	0.108	IPR018487 (SMART); IPR018487 (PFAM); IPR000585 (G3DSA:2.110.10.GENE3D); PTHR10201:SF135 (PANTHER); PTHR10201 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR018487 (PROSITE_PROFILES); IPR018487 (PROSITE_PROFILES); IPR018487 (PROSITE_PROFILES); IPR018487 (PROSITE_PROFILES); IPR000585 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1915	c94291_g1_i1_len_586_path_1_0_585_4	11	aldehyde oxidase	195	1.35E-17	81.10%	0.11	IPR002888 (G3DSA:1.10.150.GENE3D); IPR002888 (PFAM); PTHR11908:SF65 (PANTHER); PTHR11908 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR002888 (SUPERFAMILY)
1916	c94363_g1_i1_len_170_path_195_0_169_1	0	ppo2 protein	57	1.33E-13	77.60%	0.099	IPR008922 (G3DSA:1.10.1280.GENE3D); IPR000896 (PFAM); PTHR11511:SF24 (PANTHER); IPR013788 (PANTHER); IPR008922 (SUPERFAMILY)
1917	c9443_g1_i1_len_749_path_1570_0_592_510_593_622_501_623_631_510_632_661_501_662_670_510_671_700_501_5	30	---NA---	249			0.118	no IPS match
1918	c94882_g1_i1_len_326_path_1_0_325_3	4	probable chitinase 3	109	4.47E-18	75.50%	0.236	IPR013781 (G3DSA:3.20.20.GENE3D); IPR001223 (PFAM); PTHR11177:SF109 (PANTHER); PTHR11177 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR017853 (SUPERFAMILY); TMhelix (TMHMM)
1919	c95262_g1_i1_len_287_path_1_0_286_1	0	retinal dehydrogenase 1-like	96	3.49E-43	87.20%	0.113	IPR015590 (PFAM); IPR016162 (G3DSA:3.40.605.GENE3D); PTHR11699:SF145 (PANTHER); PTHR11699 (PANTHER); IPR029510 (PROSITE_PATTERNS); IPR016161 (SUPERFAMILY)
1920	c9548_g1_i1_len_1177_path_1_0_1044_1046_1045_1056_1058_1057_1176_2	57	alpha-mannosidase 2	392	5.88E-157	72.90%	0.112	IPR011682 (PFAM); G3DSA:2.70.98.30 (GENE3D); PTHR11607 (PANTHER); PTHR11607:SF22 (PANTHER); IPR011013 (SUPERFAMILY)
1921	c955_g1_i1_len_888_path_866_0_887_2	33	thioredoxin-dependent peroxide reductase	296	2.33E-127	84.70%	0.204	IPR000866 (PFAM); IPR019479 (PFAM); IPR012336 (G3DSA:3.40.30.GENE3D); PTHR10681:SF101 (PANTHER); PTHR10681 (PANTHER); IPR012336 (PROSITE_PROFILES); IPR012336 (SUPERFAMILY)
1922	c9605_g1_i1_len_1442_path_1_0_1441_2	126	tho complex subunit 3	475	0	86.90%	0.106	IPR020472 (PRINTS); IPR001680 (SMART); IPR015943 (G3DSA:2.130.10.GENE3D); IPR001680 (PFAM); IPR011659 (PFAM); IPR015943 (G3DSA:2.130.10.GENE3D); PTHR22839 (PANTHER); IPR019775 (PROSITE_PATTERNS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR001680 (PROSITE_PROFILES); IPR017986 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR001680 (PROSITE_PROFILES); IPR017986 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1923	c96160_g1_i1_len_232_path_1_0_231_3	0	tyrosine-protein kinase src64b	78	1.28E-09	81.60%	0.317	G3DSA:1.10.510.10 (GENE3D); IPR001245 (PFAM); PTHR24416:SF210 (PANTHER); PTHR24416 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)

1924	c96465_g1_i1_len_562_path_1_0_561_2	3	transmembrane protease serine 9-like	187	1.63E-24	54.90%	0.111	G3DSA:2.40.10.10 (GENE3D); IPR015420 (PFAM); PTHR24256:SF89 (PANTHER); PTHR24256 (PANTHER); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1925	c96512_g1_i1_len_606_path_1_0_605_5	4	otoancorin isoform x1	202	3.20E-23	51.20%	0.104	IPR026664 (PANTHER); PTHR23412:SF17 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1926	c96559_g1_i1_len_573_path_551_0_572_3	3	tyrosine-protein kinase src42a	191	7.74E-27	97.80%	0.211	IPR001245 (PFAM); G3DSA:3.30.200.20 (GENE3D); PTHR24418:SF190 (PANTHER); PTHR24418 (PANTHER); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR000719 (PROSITE_PROFILES); IPR011009 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM); TMhelix (TMHMM)
1927	c96607_g1_i1_len_465_path_1_0_464_0	7	gamma-glutamyl hydrolase	155	1.38E-48	65.80%	0.099	IPR011697 (PFAM); IPR029062 (G3DSA:3.40.50.GENE3D); IPR015527 (PANTHER); IPR015527 (PROSITE_PROFILES); IPR029062 (SUPERFAMILY)
1928	c96848_g1_i1_len_1090_path_1_0_1089_1	2	---NA---	363			0.246	no IPS match
1929	c96848_g1_i1_len_1090_path_1_0_1089_2	2	---NA---	363			0.178	CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS)
1930	c97082_g1_i1_len_637_path_615_0_636_2	6	leucomyosuppressin precursor	207	4.46E-15	68.90%	0.768 Y	TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_C_REGION (PHOBIUS); SIGNAL_PEPTIDE_H_REGION (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); SIGNAL_PEPTIDE_N_REGION (PHOBIUS); SIGNAL_PEPTIDE (PHOBIUS); TRANSMEMBRANE (PHOBIUS); SignalP-TM (SIGNALP_GRAM_POSITIVE); SignalP-noTM (SIGNALP_EUK); SignalP-noTM (SIGNALP_GRAM_NEGATIVE); TMhelix (TMHMM); TMhelix (TMHMM)
1931	c97286_g1_i1_len_497_path_475_0_496_5	4	alkaline phosphatase	165	1.29E-52	100.00%	0.106	IPR001952 (PFAM); IPR017849 (G3DSA:3.40.720.GENE3D); IPR017850 (SUPERFAMILY)
1932	c97605_g1_i1_len_898_path_1_0_897_0	16	venom allergen partial	300	1.54E-20	56.60%	0.129	IPR001283 (PRINTS); IPR002413 (PRINTS); IPR014044 (SMART); IPR014044 (G3DSA:3.40.33.GENE3D); IPR014044 (PFAM); IPR001283 (PANTHER); IPR018244 (PROSITE_PATTERNS); IPR014044 (SUPERFAMILY)
1933	c97826_g1_i1_len_491_path_469_0_490_5	5	odorant-binding protein 4	155	1.25E-44	72.00%	0.101	IPR006170 (PRINTS); IPR006170 (SMART); IPR023316 (G3DSA:1.10.238.GENE3D); IPR006170 (PFAM); PTHR11857:SF4 (PANTHER); PTHR11857 (PANTHER); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS); CYTOPLASMIC_DOMAIN (PHOBIUS); IPR023316 (SUPERFAMILY); TMhelix (TMHMM); TMhelix (TMHMM)
1934	c9816_g1_i1_len_1297_path_1_0_1296_1	20	venom serine protease	432	2.04E-63	52.60%	0.103	IPR001314 (PRINTS); IPR001254 (SMART); IPR006604 (SMART); IPR001254 (PFAM); G3DSA:2.40.10.10 (GENE3D); IPR022700 (PFAM); G3DSA:2.40.10.10 (GENE3D); G3DSA:2.40.10.10 (GENE3D); PTHR24268 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)
1935	c9825_g2_i1_len_1600_path_2466_0_1599_3	24	svil partial	534	1.04E-160	70.80%	0.126	IPR007122 (PRINTS); IPR003128 (SMART); IPR007122 (SMART); IPR029006 (G3DSA:3.40.20.GENE3D); IPR003128 (G3DSA:1.10.950.GENE3D); IPR007123 (PFAM); IPR003128 (PFAM); IPR029006 (G3DSA:3.40.20.GENE3D); PTHR11977:SF23 (PANTHER); IPR007122 (PANTHER); IPR003128 (PROSITE_PROFILES); SSF55753 (SUPERFAMILY); IPR003128 (SUPERFAMILY); SSF55753 (SUPERFAMILY); SSF55753 (SUPERFAMILY)
1936	c98876_g1_i1_len_447_path_451_0_446_1	5	zinc finger protein 502	136	2.41E-29	62.40%	0.099	IPR015880 (SMART); IPR007087 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409 (PANTHER); PTHR24409:SF13 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)

1937	c9912_g1_i2_len_659_path_1_0_482_484_483_658_2	10	adam 17-like protease	219	2.09E-67	70.20%	0.434 Y	IPR002870 (PFAM); PTHR11905 (PANTHER); PTHR11905:SF121 (PANTHER); CYTOPLASMIC_DOMAIN (PHOBIUS); NON_CYTOPLASMIC_DOMAIN (PHOBIUS); TRANSMEMBRANE (PHOBIUS)
1938	c99311_g1_i1_len_491_path_1_0_490_5	8	huga_polan ame: full=hyaluronidase short=hya ame: full=hyaluronoglucosaminidase ame: allergen=pol a 2 flags: partial	163	1.36E-39	62.90%	0.099	IPR018155 (PRINTS); IPR013785 (G3DSA:3.20.20.GENE3D); IPR018155 (PFAM); IPR018155 (PANTHER); PTHR11769:SF8 (PANTHER); IPR017853 (SUPERFAMILY)
1939	c99333_g1_i1_len_467_path_1_0_304_306_305_358_306_359_412_306_413_466_0	7	mucin binding protein	156	3.00E-10	56.30%	0.107	no IPS match
1940	c99333_g1_i1_len_467_path_1_0_304_306_305_358_306_359_412_306_413_466_3	7	collagen-like protein partial	156	7.46E-09	57.17%	0.114	IPR008160 (PFAM)
1941	c99470_g1_i1_len_289_path_267_0_288_2	2	down syndrome cell adhesion molecule-like protein dscam2	96	6.91E-25	70.10%	0.135	IPR003961 (PFAM); IPR013783 (G3DSA:2.60.40.GENE3D); PTHR10489:SF567 (PANTHER); PTHR10489 (PANTHER); IPR003961 (PROSITE_PROFILES); IPR003961 (SUPERFAMILY)
1942	c99590_g1_i1_len_228_path_1_0_227_3	0	zinc finger protein 891	76	2.77E-16	68.50%	0.131	IPR015880 (SMART); IPR013087 (G3DSA:3.30.160.GENE3D); PF13465 (PFAM); IPR013087 (G3DSA:3.30.160.GENE3D); PTHR24409:SF13 (PANTHER); PTHR24409 (PANTHER); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PATTERNS); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); IPR007087 (PROSITE_PROFILES); SSF57667 (SUPERFAMILY); SSF57667 (SUPERFAMILY)
1943	c99624_g1_i1_len_378_path_396_0_377_1	5	serine protease like protein	126	1.67E-23	63.80%	0.104	IPR001254 (SMART); G3DSA:2.40.10.10 (GENE3D); IPR001254 (PFAM); PTHR24265 (PANTHER); IPR018114 (PROSITE_PATTERNS); IPR001254 (PROSITE_PROFILES); IPR009003 (SUPERFAMILY)