Table S3. Detailed information on the identification of proteins in turkey inner perivitelline layer by MALDI TOF/TOF analysis.

Spot	Protein name	Gene symbol	Sequence coverage (%)	Mascot score	Calculated pI/ Nominal mass (Mr)	Precursor mass observed	Precursor mass theoretical	Peptide score	Peptide sequence
1	PREDICTED: calreticulin [Meleagris gallopavo] XP_010726340.1	CALR	54	583	43173/4.29	1147.6730	1146.6550	60	K.KVHVIFNYK.G
						1019.5789	1018.5600	53	K.VHVIFNYK.G
						1833.8756	1832.8469	63	K.VESGSLEDDWDFLPPK.K
						1961.9638	1960.9418	69	K.VESGSLEDDWDFLPPKK.I
						1586.7377	1585.7049	124	K.FAEEFGNETWGATK.E
	calreticulin, partial [Gallus gallus] AAS49610.1	CALR	56	583	47079/4.41	1147.6730	1146.6550	60	K.KVHVIFNYK.G
						1019.5789	1018.5600	53	K.VHVIFNYK.G
						1833.8756	1832.8469	63	K.VESGSLEDDWDFLPPK.K
						1961.9638	1960.9418	69	K.VESGSLEDDWDFLPPKK.I
2	PREDICTED: calreticulin [Meleagris gallopavo] AAS49610.1	CALR	40	345	43173/4.29	1019.5847	1018.5600	53	K.VHVIFNYK.G
						1586.7376	1585.7049	123	K.FAEEFGNETWGATK.E
						1320.6176	1319.5775	61	K.MKEQQDEEQR.Q
	calreticulin, partial [Gallus gallus] XP_010726340.1	CALR	45	458	47079/4.41	1072.5228	1071.4873	43	K.FYGDAEKDK.G
						1019.5847	1018.5600	53	K.VHVIFNYK.G
						1586.7376	1585.7049	123	K.FAEEFGNETWGATK.E
						1320.6176	1319.5775	61	K.MKEQQDEEQR.Q
3	calumenin [Numida meleagris] XP_021239488.1	CALU	12	169	36952/4.47	954.4915	953.4607	34	R.EQFVEFR.D
						1561.7619	1560.7168	90	R.HLVYESDQDKDGR.L
4	reticulocalbin-3-like, partial [Phasianus colchicus] XP_031467421.1	RCN3	16	278	26759/4.61	2994.3479	2993.3217	199	R.DLPGVPHDDTHGFSYDHDAFLGPEEAR.A
						1332.6459	1331.6470	68	R.AFQQLQPEESR.R
5	PREDICTED: protein disulfide-isomerase, partial [Meleagris gallopavo] XP_010719740.1	P4HB	42	466	45917/4.54	1175.6090	1174.5870	44	R.EADDIVSWLK.K
						1819.9068	1818.8901	35	K.ILFIFIDSDHSDNQR.I
						966.5626	965.5586	51	R.ILEFFGLK.K
						1341.6053	1340.5884	57	K.NFEEVAFDENK.N
						942.5228	941.5334	43	K.IHSFPTLK.F
						838.4044	837.4133	56	K.FFPAGSGR.N

6	PREDICTED: protein disulfide-isomerase, partial [Meleagris gallopavo] XP_010719740.1	P4HB	33	326	45917/4.54	1341.5709 942.5283 838.4150 1079.4965	1340.5884 941.5334 837.4133 1078.5043	66 42 56 45	K.NFEEVAFDENK.N K.IHSFPTLK.F K.FFPAGSGR.N R.NVIDYNGER.T
7	PREDICTED: complement component 1 Q subcomponent-binding protein, mitochondrial, partial [Meleagris gallopavo] XP_010720207.1	C1QBP	12	224	25785/4.52	1626.8451 1509.7407	1625.7798 1508.6783	103 110	K.VSGGWELEVHGTEAR.L R.EVSFQPTGESDWK.D
8	protein SET, partial [Cathartes aura] KFP47368.1	SET	46	471	16705/4.80	2195.0988 1273.7225 1208.6626 1840.8678	2194.0138 1272.7152 1207.6554 1839.8606	130 38 80 81	K.EQQEAIEHIDEVQNEIDR.L R.LNEQASEEILK.V R.VEVTEFEDIK.S R.IDFYFDENPYFENK.V
9	PREDICTED: complement component 1 Q subcomponent-binding protein, mitochondrial-like [Meleagris gallopavo] gi|733916121|ref|XP_01072020	C1QBP	12	224	25785/4.52	1626.8451 1509.7407	1625.7798 1508.6783	102 109	K.VSGGWELEVHGTEAR.L R.EVSFQPTGESDWK.D
10	PREDICTED: vimentin [Meleagris gallopavo] XP_010711008.2	VIM	29	385	46056/4.78	1115.5651 1254.5603 1093.5216 1836.7613	1114.5618 1253.5598 1092.5200 1835.7922	39 66 55 114	K.VELQELNDR.F R.LGDLYEEEMR.E K.FADLSEAANR.N R.DGQVINETSQHHDDLE
11	PREDICTED: vimentin [Meleagris gallopavo] XP_010711008.2	VIM	42	434	46056/4.78	1254.5552 1093.5192 1121.5748 1836.7516	1253.5598 1092.5200 1120.5764 1835.7922	83 59 30 118	R.LGDLYEEEMR.E K.FADLSEAANR.N R.EYQDLLNVK.M R.DGQVINETSQHHDDLE
12	PREDICTED: vimentin [Meleagris gallopavo] XP_010711008.2	VIM	40	384	46056/4.78	1254.5916 1309.6295 1093.5502 1836.8162	1253.5598 1308.5986 1092.5200 1835.7922	144 44 30 102	R.LGDLYEEEMR.E K.NLQEAEEWYK.S K.FADLSEAANR.N R.DGQVINETSQHHDDLE
13	PREDICTED: vimentin [Meleagris gallopavo] XP_010711008.2	VIM	25	353	46056/4.78	1254.5567 1093.5269 1836.7529	1253.5598 1092.5200 1835.7922	70 64 111	R.LGDLYEEEMR.E K.FADLSEAANR.N R.DGQVINETSQHHDDLE

14	PREDICTED: endoplasmin [Meleagris gallopavo] XP_003202424.1	HSP90B1	21	316	91683/4.81	1200.6555		46	K.FAFQAEVNR.M
15	Endoplasmin, partial [Phaethon lepturus] KFQ80494.1	HSP90B1	40	613	90377/4.82	1081.5562	1080.5352	66	K.FAFQAEVNR.M
						1200.6790	1199.6662	74	K.SILFVPNSAPR.G
						1595.7066	1594.7160	50	R.VFITDDFHDMMPK.Y
						973.4434	972.4341	54	K.YNDTFWK.E
						2355.0329	2354.0783	139	R.LTQSPCALVASQYGWSGNMER.I
16	Endoplasmin, partial [Struthio camelus australis] KFV83935.1	HSP90B1	34	456	90381/4.82	1081.5503	1080.5352	73	K.FAFQAEVNR.M
						1200.6796	1199.6662	73	K.SILFVPNSAPR.G
						2355.0346	2354.0783	121	R.LTQSPCALVASQYGWSGNMER.I
						876.4616	875.4501	46	K.TFEINPR.H
17	PREDICTED: heat shock protein HSP 90-alpha [Meleagris gallopavo] XP_010710229.1	HSP90AA1	27	922	84466/5.01	2255.9136	2254.9516	171	K.HNDDEQYAWESSAGGSFTVR.L
						1311.5643	1310.5626	85	K.EDQTEYLEER.R
						1217.6381	1216.6353	46	K.HSQFIGYPIR.L
						1833.7533	1832.7741	137	R.NPDDITNEEYGEFYK.S
						1513.7741	1512.7784	44	R.GVVDSEDLPLNISR.E
						948.4419	947.4389	51	K.FYEQFSK.N
						1168.5603	1167.5632	73	K.LGIHEDSQNR.K
						[illegible]	[illegible]	[illegible]	[illegible]
18	vimentin [Numida meleagris] XP_021243478.1	VIM	51	578	53271/5.13	1587.7411	1586.7900	38	R.TNEKVELQELNDR.F
						1115.5342	1114.5618	31	K.VELQELNDR.F
						1254.5314	1253.5598	93	R.LGDLYEEEMR.E
						1093.4910	1092.5200	59	K.FADLSEAANR.N
19	vimentin [Numida meleagris] XP_021243478.1	VIM	58	628	53271/5.13	1364.6965	1363.7208	34	R.YSLGSALRPSSAR.Y
						1587.7556	1586.7900	92	R.TNEKVELQELNDR.F
						1115.5385	1114.5618	48	K.VELQELNDR.F
						1254.5383	1253.5598	76	R.LGDLYEEEMR.E
						1093.4986	1092.5200	58	K.FADLSEAANR.N
						1836.7283	1835.7922	101	R.DGQVINETSQHHDDLE
20	transitional endoplasmic reticulum ATPase [Gallus gallus] NP_001038129.1	VCP	35	501	89953/5.14	1172.6220	1171.6601	45	R.GILLYGPPGTGK.T
						1329.6434	1328.6837	64	R.WALSQSNPSALR.E
						1578.7187	1577.7871	67	K.AIANECQANFISIK.G
						1190.4935	1189.5298	41	R.RDHFEEAMR.F
						1034.3897	1033.4287	60	R.DHFEEAMR.F

						1629.7299	1628.7981	52	R.KYEMFAQTLQQSR.G
	PREDICTED: transitional endoplasmic reticulum ATPase [Python bivittatus] XP_007442861.1	VCP	37	515	85157/5.17	1172.6220	1171.6601	45	R.GILLYGPPGTGK.T
						1329.6434	1328.6837	64	R.WALSQSNPSALR.E
						1578.7187	1577.7871	67	K.AIANECQANFISIK.G
						1190.4935	1189.5298	41	R.RDHFEEAMR.F
						1034.3897	1033.4287	60	R.DHFEEAMR.F
						1629.7299	1628.7981	52	R.KYEMFAQTLQQSR.G
21	PREDICTED: LOW QUALITY PROTEIN: hypoxia up-regulated protein 1-like [Meleagris gallopavo] gi|326933411|ref|XP_00321279	HYOU1	32	527	107246/5.11	1531.7943	1530.7790	53	K.QIDNPQVALYQSR.F
						1859.9298	1858.9174	54	K.DSGTQPQLQIQGIGFDR.T
						1492.7890	1491.7722	66	R.DAAVFPIQVEFTR.E
						1628.8045	1627.7954	90	K.QQSPPPDQAEAVHPK.E
22	PREDICTED: hypoxia up-regulated protein 1 [Meleagris gallopavo] XP_010722064.1	HYOU1	16	356	109121/5.12	1531.7307	1530.7790	83	K.QIDNPQVALYQSR.F
						1370.6421	1369.6878	59	R.FPEHELVKDEK.R
						1085.4970	1084.5302	32	K.LFNDQHPSK.D
						1628.7242	1627.7954	108	K.QQSPPPDQAEAVHPK.E
23	PREDICTED: hypoxia up-regulated protein 1 [Meleagris gallopavo] XP_010722064.1	HYOU1	21	495	109121/5.12	1531.7410	1530.7790	107	K.QIDNPQVALYQSR.F
						1370.6635	1369.6878	69	R.FPEHELVKDEK.R
						1693.7950	1692.8471	34	K.DAVITVPAYFNQAER.R
						1085.5105	1084.5302	55	K.LFNDQHPSK.D
						1628.7458	1627.7954	106	K.QQSPPPDQAEAVHPK.E
24	PREDICTED: hypoxia up-regulated protein 1 [Meleagris gallopavo] XP_010722064.1	HYOU1	23	451	109121/5.12	1531.7516	1530.7790	101	K.QIDNPQVALYQSR.F
						1331.6533	1330.6768	60	R.GLAEEFAEQPIK.D
						1693.8053	1692.8471	44	K.DAVITVPAYFNQAER.R
						1085.5132	1084.5302	36	K.LFNDQHPSK.D
						1628.7497	1627.7954	108	K.QQSPPPDQAEAVHPK.E
25	PREDICTED: hypoxia up-regulated protein 1 [Meleagris gallopavo] XP_010722064.1	HYOU1	11	373	109121/5.12	1531.8112	1530.7790	99	K.QIDNPQVALYQSR.F
						1859.9470	1858.9174	122	K.DSGTQPQLQIQGIGFDR.T
						1492.8067	1491.7722	91	R.DAAVFPIQVEFTR.E
26	PREDICTED: LOW QUALITY PROTEIN: hypoxia up-regulated protein 1-like [Meleagris gallopavo] gi|326933411|ref|XP_00321279	HYOU1	30	582	107246/ 5.11	1238.6357	1237.6376	52	R.LFGDSALGMSIK.T
						1531.7653	1530.7790	93	K.QIDNPQVALYQSR.F
						1859.8932	1858.9174	120	K.DSGTQPQLQIQGIGFDR.T
						1492.7605	1491.7722	89	R.DAAVFPIQVEFTR.E
						1628.7630	1627.7954	45	K.QQSPPPDQAEAVHPK.E

27	desmin [Meleagris gallopavo] XP_010711942.1	DES	53	431	53537/5.29	1268.6471	1267.5754	60	R.VAEMYEEELR.E
						1455.7825	1454.6790	132	R.FAGEAGGYQDTIAR.L
28	MICOS complex subunit MIC60 [Gallus gallus] NP_001006462.1	IMMT	38	558	79543/5.72	1222.6286	1221.5877	30	K.VEFEQNLSEK.L
						1824.8825	1823.8649	150	K.GIEQAVESHAVAEEEAR.K
						1353.7201	1352.6949	66	R.RVAHDWLTEAR.M
						1197.6241	1196.5938	80	R.VAHDWLTEAR.M
29	MICOS complex subunit MIC60 [Gallus gallus] NP_001006462.1	IMMT	43	531	79543/5.72	1824.8677	1823.8649	125	K.GIEQAVESHAVAEEEAR.K
						1023.5151	1022.5032	38	R.GVYSEEALR.A
						1353.7055	1352.6949	32	R.RVAHDWLTEAR.M
						1197.6094	1196.5938	58	R.VAHDWLTEAR.M
30	PREDICTED: alpha-actinin-1 isoform X5 [Pseudopodoces humilis] XP_005522612.1	ACTN1	34	513	107832/5.36	1392.6186	1391.6405	49	K.TFTAWCNSHLR.K
						1174.5835	1173.5965	33	K.EGLLLWCQR.K
						2051.8834	2050.9517	52	K.VLAVNQENEQLMEDYEK.L
						1028.5289	1027.5451	42	R.TIPWLENR.A
						1753.7790	1752.8179	78	K.KHEAFESDLAAHQDR.V
						1338.5901	1337.6034	45	K.GISQEQMNEFR.A
						993.4305	992.4464	42	R.ASFNHFDR.K
31	calmodulin, partial [Mauremys japonica] BAB32439.1	CALM1	34	351	15349/4.05	1352.6412	1351.5925	95	K.MKDTDSEEEIR.E
						1596.7490	1595.7063	69	K.DTDSEEEIREAFR.V
						1755.8943	1754.8475	159	R.VFDKDGDGYISAAELR.H
32	PREDICTED: LOW QUALITY PROTEIN: thioredoxin [Meleagris gallopavo] XP_003213740.2	TXN	46	269	12800/5.12	1522.7425	1521.7472	74	K.MIKPFFHSLCDK.F
						1538.7347	1537.7421	80	K.MIKPFFHSLCDK.F + Oxidation (M)
						1221.5351	1220.5358	62	K.CMPTFQFYK.N
						1237.5367	1236.5308	38	K.CMPTFQFYK.N + Oxidation (M)
						1107.5580	1106.5720	41	K.KVQFFSCANK.F
33	PREDICTED: hypothetical protein LOC100549033, partial [Meleagris gallopavo] gi|326934995|ref|XP_003213567.1|		37	316	15326/6.14	1660.7876	1659.7709	90	K.QQSVLGPEMEQMQR.S
						1692.7819	1691.7607	37	K.QQSVLGPEMEQMQR.S
						970.6026	969.5495	50	R.SNPLLGLEK.R
						1785.9153	1784.8846	136	K.GGEGIAAPIGPSSYPWAR.N
34	Coactosin-like, partial [Chlamydotis macqueenii] KFP43723.1	COTL1	39	353	16079/5.33	864.4536	863.4501	50	R.EAYNLVR.D
						1424.6692	1423.6620	106	R.DDATEVNWVTFK.Y
						934.4994	933.4920	49	K.EVVQNFAK.E
						1979.9245	1978.9524	107	K.EFVISDHKELDEDYIK.N

35	PREDICTED: eukaryotic translation initiation factor 5A-1 [Coturnix japonica] XP_015706238.1	EIF5A	40	211	17122/5.09	2160.9605 2176.9536 2032.8610 2048.8572	2159.9980 2175.9929 2031.9030 2047.8979	95 77 74 55	K.KYEDICPSTHNMDVPNIK.R K.KYEDICPSTHNMDVPNIK.R + Oxidation (M) K.YEDICPSTHNMDVPNIK.R
36	PREDICTED: protein canopy homolog 2 [Coturnix japonica] XP_015742545.1	CNPY2	34	354	22071/5.51	1203.5096 939.4707 1730.8475	1202.4921 938.4644 1729.8635	74 58 129	R.SQDLHCGACR.A K.TIQMGSFR.I R.INPDGSQSVVEVPYAR.S
37	PREDICTED: glutaredoxin-related protein 5, mitochondrial [Meleagris gallopavo] XP_003206758.3	GLRX5	21	150	23138/8.87	988.4961 1278.6601	987.4774 1277.6364	56 45	R.LHGVEDYR.A R.AHDVLQDPDLR.Q
38	40S ribosomal protein SA, partial [Podiceps cristatus] KFZ67637.1	RPSA	31	189	22782/4.93	1203.6649 1698.8602	1202.6408 1697.8526	74 46	K.FAAATGATPIAGR.F R.FTPGTFTNQIQAAFR.E
39	PREDICTED: 40S ribosomal protein SA-like [Meleagris gallopavo] gi|326922143|ref|XP_003207311.1|	RPSA	21	339	33115/4.80	1740.9610 1203.6696 1698.8627 1306.6543	1739.9417 1202.6408 1697.8526 1305.6387	76 106 47 45	R.AIVAIENPADVSVISSR.N K.FAAATGATPIAGR.F R.FTPGTFTNQIQAAFR.E R.YVDIAIPCNNK.G
40	PREDICTED: nucleophosmin, partial [Meleagris gallopavo] XP_019475889.1	NPM1	25	388	33459/4.90	1583.6787 2126.9364 1199.6420	1582.7223 2126.0168 1198.6611	111 171 76	K.VDDEENEHQLSLR.T K.DELHVVEAEALDYEGNPVK.V K.VIQALWQWR.Q
41	PREDICTED: nucleophosmin, partial [Meleagris gallopavo] XP_019475889.1	NPM1	39	407	33459/4.90	1583.7290 2126.9931 1199.6818	1582.7223 2126.0168 1198.6611	111 171 77	K.VDDEENEHQLSLR.T K.DELHVVEAEALDYEGNPVK.V K.VIQALWQWR.Q
42	PREDICTED: tropomyosin alpha-3 chain-like isoform 3 [Meleagris gallopavo] gi|326915866|ref|XP_003204233.1|	TPM3	26	210	32856/4.68	1243.6280 1284.7284	1242.6456 1283.7449	85 34	R.IQLVEEELDR.A R.KLVIIEGDLER.T

	PREDICTED: tropomyosin beta chain isoform X2 [Melopsittacus undulatus] XP_005152074.1	TPM2	37	391	31938/4.63	1399.8071 1243.7059 1727.9488 940.5026 1284.8030	1398.7467 1242.6456 1726.8849 939.4410 1283.7449	60 85 39 40 54	R.RIQLVEEELDR.A R.IQLVEEELDR.A R.IQLVEEELDRAQER.L K.HIAEEADR.K R.KLVVLEGELER.S
43	PREDICTED: tropomyosin alpha-1 chain isoform X4 [Gallus gallus] XP_015134265.1	TPM1	42	349	32848/4.65	1243.6599 940.4431 894.4595 1284.7557	1242.6456 939.4410 893.4606 1283.7449	94 50 36 61	R.IQLVEEELDR.A K.HIAEEADR.K R.KYEEVAR.K R.KLVIIEGDLER.A
	PREDICTED: tropomyosin alpha-3 chain-like isoform 3 [Meleagris gallopavo] gi|326915866|ref|XP_003204233.1|	TPM3	29	307	32856/4.68	1243.6599 940.4431 894.4595 1284.7557	1242.6456 939.4410 893.4606 1283.7449	94 50 36 59	R.IQLVEEELDR.A K.HIAEEADR.K R.KYEEVAR.K R.KLVIIEGDLER.T
44	cytoskeletal tropomyosin [Coturnix coturnix] CAA38180.1		21	183	28762/4.66	1243.6628 940.4520	1242.6456 939.4410	51 32	R.IQLVEEELDR.A K.HIAEEADR.K
45	PREDICTED: LOW QUALITY PROTEIN: keratin, type I cytoskeletal 19-like [Meleagris gallopavo] XP_003213149.2	KRT19	37	273	45752/4.87	1222.6458 1090.4977 1379.7229	1221.6353 1089.4879 1378.7204	44 68 57	K.TKFETEQALR.M K.DAEAWFHSK.T K.TRLEQEIATYR.Q
46	PREDICTED: LOW QUALITY PROTEIN: keratin, type I cytoskeletal 19-like [Meleagris gallopavo] XP_003213149.2	KRT19	15	151	45752/4.87	1222.6118 1090.4645 1379.6908	1221.6353 1089.4879 1378.7204	42 49 37	K.TKFETEQALR.M K.DAEAWFHSK.T K.TRLEQEIATYR.Q

47	PREDICTED: tubulin beta chain [Hippocampus comes] XP_019751599.1	TUBB	61	654	50070/4.77	1822.9276	1821.9156	122	R.EIVHIQAGQCGNQIGAK.F
						1958.9722	1957.9745	61	K.GHYTEGAELVDSVLDVVR.K
						1271.7323	1270.7220	152	R.KLAVNMVPFPR.L
						1287.7254	1286.7169	117	R.KLAVNMVPFPR.L + Oxidation (M)
						1659.8803	1658.8879	77	R.ALTVPELTQQVFDAK.N
						1696.8412	1695.8257	89	K.NSSYFVEWIPNNVK.T
	PREDICTED: tubulin beta-7 chain-like [Meleagris gallopavo] gi|326930217|ref|XP_003211247.1|	N/A	41	469	43207/4.87	1958.9722	1957.9745	61	K.GHYTEGAELVDSVLDVVR.K
						1271.7323	1270.7220	52	R.KLAVNMVPFPR.L
						1659.8803	1658.8879	77	R.ALTVPELTQQVFDAK.N
						1696.8412	1695.8257	89	K.NSSYFVEWIPNNVK.T
						1229.6079	1228.5910	76	R.ISEQFTAMFR.R
48	PREDICTED: tubulin beta-4A chain [Alligator sinensis] XP_006023414.1	TUBB4A	64	732	50110/4.82	1958.9579	1957.9745	173	K.GHYTEGAELVDSVLDVVR.K
						1077.5323	1076.5250	133	K.IREEYPDR.I
						1130.5943	1129.5880	85	R.FPGQLNADLR.K
						1258.6842	1257.6830	113	R.FPGQLNADLRK.L
						1271.7265	1270.7220	114	R.KLAVNMVPFPR.L
						1143.6293	1142.6270	56	K.LAVNMVPFPR.L
						1696.8201	1695.8257	91	K.NSSYFVEWIPNNVK.T
	PREDICTED: tubulin beta-2 chain-like [Meleagris gallopavo] gi|326917066|ref|XP_003204825.1|	TUBB2A	15	385	53458/4.84	1958.9579	1957.9745	173	K.GHYTEGAELVDSVLDVVR.K
						1077.5323	1076.5250	33	K.IREEYPDR.I
						1130.5943	1129.5880	85	R.FPGQLNADLR.K
						1271.7265	1270.7220	44	R.KLAVNMVPFPR.L
						1143.6293	1142.6270	56	K.LAVNMVPFPR.L
						1696.8201	1695.8257	90	K.NSSYFVEWIPNNVK.T
49	PREDICTED: ATP synthase subunit beta, mitochondrial [Falco cherrug] XP_014132675.1	ATP5F1B	49	886	53445/5.16	1406.6968	1405.6739	131	K.AHGGYSVFAGVGER.T
						2060.9907	2059.9884	139	R.EGNDLYHEMIESGVINLK.D
						1601.8302	1600.8031	115	K.VALVYGQMNEPPGAR.A
						2266.0927	2265.0770	198	R.IPSAVGYQPTLATDMGTMQER.I
50	PREDICTED: protein disulfide-isomerase A6 [Meleagris gallopavo] XP_010706217.1	PDIA6	34	798	49043/5.02	1957.0020	1955.9814	162	K.VGAVDADKHQSLGGQYGVR.G
						1201.6287	1200.6000	89	K.HQSLGGQYGVR.G
						1416.7846	1415.7620	46	R.TSEAIVDAALSALR.S
						1528.7791	1527.7569	126	K.NLEPEWAAAATEVK.E
						1559.8358	1558.8137	73	K.LAAVDATVNQMLASR.Y
						1695.8054	1694.7900	80	K.IFQKGEDPVDYDGGR.T

51	PREDICTED: LOW QUALITY PROTEIN: keratin, type I cytoskeletal 18 [Meleagris gallopavo] XP_019467106.1	KRT18	26	641	48440/5.13	1832.9250	1831.8813	175	R.LTPHSSAASVYAGAGGSGSR.I
						1135.5379	1134.4975	53	K.ETMQDLNER.L
						964.5141	963.5025	43	R.YEAELAIR.T
						1632.8422	1631.7751	174	R.SQNAGLEGSLAETEAR.Y
						1002.5077	1001.4778	58	R.GEEELAQAR.A
52	PREDICTED: tubulin alpha-1B chain-like [Meleagris gallopavo] gi|326922906|ref|XP_003207683.1|	TUBA1B	20	560	50804/4.94	2007.9859	2006.8858	160	K.TIGGGDDSFNTFFSETGAGK.H
						1410.8576	1409.7667	103	R.QLFHPEQLITGK.E
						1757.0521	1755.9559	93	R.IHFPLATYAPVISAEK.A
						1249.6157	1248.5453	58	K.YMACCLLYR.G
						1865.0047	1863.8971	112	R.AVCMLSNTTAIAEAWAR.L
						2330.0965	2329.0110	172	R.AFVHWYVGEGMEEGEFSEAR.E
	PREDICTED: tubulin alpha-1D chain-like [Miniopterus natalensis] XP_016052367.1		57	840	53715/4.89	2007.9859	2006.8858	167	K.TIGGGDDSFNTFFSETGAGK.H
						1410.8576	1409.7667	103	R.QLFHPEQLITGK.E
						1757.0521	1755.9559	93	R.IHFPLATYAPVISAEK.A
						1249.6157	1248.5453	58	K.YMACCLLYR.G
						1865.0047	1863.8971	112	R.AVCMLSNTTAIAEAWAR.L
						2330.0965	2329.0110	172	R.AFVHWYVGEGMEEGEFSEAR.E
53	PREDICTED: 78 kDa glucose-regulated protein [Egretta garzetta] XP_009645866.1	N/A	42	1300	68092/5.20	1566.7884	1565.7726	117	R.ITPSYVAFTPEGER.L
						1430.6924	1429.6838	102	R.TWNDPSVQQDIK.Y
						2016.0622	2015.0589	65	K.KVTHAVVTVPAYFNDAQR.Q
						1887.9717	1886.9639	152	K.VTHAVVTVPAYFNDAQR.Q
						1815.9912	1814.9890	125	R.IINEPTAAAIAYGLDKR.E
						1512.7532	1511.7442	115	R.AKFEELNMDLFR.S
						1313.6220	1312.6122	55	K.FEELNMDLFR.S
						1588.8658	1587.8468	101	K.KSDIDEIVLVGGSTR.I
						1460.7634	1459.7518	98	K.SDIDEIVLVGGSTR.I
						1934.0134	1933.0058	134	K.DNHLLGTFDLTGIPPAPR.G
						1974.9084	1973.9007	122	K.IEWLESHQDADIEDFK.A
54	tubulin alpha [Gallus gallus] prf||0703290B		39	708	46259/5.00	2007.8760	2006.8858	136	-.TIGGGDDSFNTFFSETGAGK.H
						1410.7798	1409.7667	94	R.QLFHPEQLITGK.E
						1756.9556	1755.9559	96	R.IHFPLATYAPVISAEK.A
						1249.5555	1248.5453	40	K.YMACCLLYR.G
						1864.9045	1863.8971	124	R.AVCMLSNTTAIAEAWAR.L
						2330.0114	2329.0110	146	R.AFVHWYVGEGMEEGEFSEAR.E

55	PREDICTED: actin, cytoplasmic 1 [Coturnix japonica] XP_015732105.1	ACTB	46	347	42161/5.37	976.4454 1198.7059 1960.9000 1515.7607 3183.6010 1132.5335	975.4410 1197.6982 1959.9036 1514.7419 3182.6071 1131.5197	36 49 45 82 42 53	K.AGFAGDDAPR.A R.AVFPSIVGRPR.H K.YPIEHGIITNWDDMEK.I K.IWHHTFYNELR.V R.TTGIVMDSGDGVTHTVPIYEGYAL-PHAILR.L R.GYSFTTTAER.E
56	Actin, alpha cardiac muscle 1, partial [Calypte anna] KFP01962.1	ACTC1	51	405	41169/5.56	976.4410 1130.5521 2356.1376	975.4410 1129.5404 2355.1529	60 81 139	K.AGFAGDDAPR.A R.GYSFVTTAER.E R.KDLYANNVLSGGTTMYPGIADR.M
57	PREDICTED: actin, cytoplasmic 2 [Coturnix japonica] XP_015735544.1	ACTG1	64	574	42121/5.31	976.4427 1198.7074 1960.9028 1515.7631 1132.5348	975.4410 1197.6982 1959.9036 1514.7419 1131.5197	64 50 50 82 59	K.AGFAGDDAPR.A R.AVFPSIVGRPR.H K.YPIEHGIITNWDDMEK.I K.IWHHTFYNELR.V R.GYSFTTTAER.E
58	PREDICTED: actin, cytoplasmic type 5 [Aptenodytes forsteri] XP_009277128.1		57	343	42098/5.30	976.4772 1198.7380 1171.6128 3183.6753	975.4410 1197.6982 1170.5638 3182.6071	47 44 77 76	K.AGFAGDDAPR.A R.AVFPSIVGRPR.H R.HQGVMVGMGQK.D R.TTGIVMDSGDGVTHTVPIYEGYAL-PHAILR.L
59	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	17	543	98702/7.62	1803.6548 1419.7207 2523.2612 1073.5734 1358.7767 2349.2207	1802.6658 1418.7154 2522.3129 1072.5665 1357.7718 2348.2641	119 102 114 49 44 96	R.DACLQAGCCFDDTDR.A R.GLSAQPYNLDSVR.L R.LVYENQLISTIDVQPGPHGSVTR.D R.DSVYILHAR.C K.VLRDPIYVEVR.L R.TQLVPVGPATLQLPFPSHYQR.F
60	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1		15	210	48706/5.58	1590.7381 1666.8834	1589.6859 1665.8297	80 54	R.GDPSAWSYGAEAHSR.A R.TNPAVIPIECHYPR.R
61	PREDICTED: eukaryotic initiation factor 4A-II-like [Meleagris gallopavo] gi|326926084|ref|XP_003209235.1|	EIF4A2	30	415	45743/5.50	1827.9069 1198.6655 1544.8275 1515.7334	1826.9315 1197.6717 1543.8471 1514.7769	136 38 107 60	R.GIYAYGFEKPSAIQQR.A K.ETQALVLAPTR.E K.LQAEAPHIVVGTPGR.V R.GFKDQIYEIFQK.L

62	PREDICTED: 60 kDa heat shock protein, mitochondrial [Meleagris gallopavo] XP_003207490.1	HSPD1	35	865	61108/5/79	1344.7049	1343.7085	106	R.TVIIEQSWGSPK.V
						1373.7002	1372.7027	102	R.GYISPYFINTAK.G
						1601.7371	1600.7443	89	K.CEFQDAYVLISEK.K
						2049.1316	2048.1378	146	K.KISSVQSIVPALEIANSHR.K
						1921.0389	1920.0428	173	K.ISSVQSIVPALEIANSHR.K
63	PREDICTED: heat shock cognate 71 kDa protein isoform X1 [Charadrius vociferus] XP_009889079.1	HSPA8	38	840	71607/5.33	1623.8614	1622.8318	88	K.HWPFTVVNDAGRPK.V
						1982.0141	1980.9905	153	K.TVTNAVVTVPAYFNDSQR.Q
						1691.7412	1690.7183	110	K.STAGDTHLGGEDFDNR.M
						1253.6323	1252.6088	79	R.FEELNADLFR.G
						2774.3340	2773.3195	47	K.QTQTFTTYSDNQPGVLIQVYEGER.A
						1303.6139	1302.5914	76	K.NSLESYAFNMK.A
						1745.8179	1744.8016	103	K.NQTAEKEEFEHQQK.E
64	PREDICTED: heat shock cognate 71 kDa protein isoform X3 [Pterocles gutturalis] XP_010083114.1	HSPA8	29	860	70258/5.37	1623.8497	1622.8318	79	K.HWPFTVVNDAGRPK.V
						1982.0121	1980.9905	160	K.TVTNAVVTVPAYFNDSQR.Q
						1691.7434	1690.7183	132	K.STAGDTHLGGEDFDNR.M
						1253.6291	1252.6088	77	R.FEELNADLFR.G
						2774.3451	2773.3195	129	K.QTQTFTTYSDNQPGVLIQVYEGER.A
						1303.6068	1302.5914	64	K.NSLESYAFNMK.A
						1745.8161	1744.8016	95	K.NQTAEKEEFEHQQK.E
65	PREDICTED: serum albumin [Meleagris gallopavo] XP_010707950.1	ALB	34	635	71740/5.73	1612.7396	1611.7351	76	K.ADPERNECFLSFK.V
						1096.5498	1095.5383	55	K.QQYSCGILK.K
						2330.0052	2329.0393	164	K.TDNPAECYANAQDQLNQHIK.E
						2647.1059	2646.1299	92	R.RQETTPINDNVSHCCSDSYAHR.R
66	PREDICTED: stress-70 protein, mitochondrial-like [Meleagris gallopavo] gi|326928269|ref|XP_003210303.1|	HSPA9	16	215	79550/7.13	1450.7145	1449.7100	66	R.TTPSVVAFTADGER.L
						1694.8309	1693.8424	39	K.NAVITVPAYFNDSQR.Q
						1242.6855	1241.6728	45	K.DAGQISGLNVLR.V
67	PREDICTED: serum albumin [Meleagris gallopavo] XP_010707950.1	ALB	40	278	71740/5.73	1612.7591	1611.7351	65	K.ADPERNECFLSFK.V
						1816.8623	1815.8461	98	K.TNCDLLSAHGEPDFLK.S
68	PREDICTED: stress-70 protein, mitochondrial [Meleagris gallopavo] XP_010717168.1	HSPA9	31	643	66135/5.56	974.4921	974.4921	32	K.VLENSEGAR.T
						1591.7674	1590.7791	87	R.QAVTNPHNTFYATK.R
						1694.8512	1693.8424	119	K.NAVITVPAYFNDSQR.Q
						1242.6856	1241.6728	76	K.DAGQISGLNVLR.V
						1645.8601	1644.8723	95	R.VINEPTAAALAYGLDK.S
						1290.6856	1289.6728	99	K.VQQTVQDLFGR.A

69	PREDICTED: serum albumin [Meleagris gallopavo] XP_010707950.1	ALB	30	321	71740/5.73	1612.7798	1611.7351	68	K.ADPERNECFLSFK.V
						2647.1834	2646.1299	123	R.RQETTPINDNVSHCCSDSYAHR.R
						1032.5198	1031.4706	37	K.LCSAPAEER.E
70	PREDICTED: T-complex protein 1 subunit epsilon [Meleagris gallopavo] XP_010706812.1	CCT5	25	596	56922/5.44	1093.5435	1092.5200	95	R.IADGYEQAAR.I
						1697.8668	1696.8607	96	K.GVIVDKDFSHPQMPK.E
						1610.8984	1609.8902	72	K.IAILTCPFEPPKPK.T
71	PREDICTED: T-complex protein 1 subunit theta isoform X1 [Meleagris gallopavo] XP_010720799.1	CCT5	23	345	60696/5.52	1323.6958	1322.6255	108	K.HYSGLEEAVYR.N
						1150.6424	1149.5818	57	K.FAEAFEAIPR.A
72	PREDICTED: hydroxymethylglutaryl-CoA synthase, cytoplasmic [Meleagris gallopavo] XP_010723686.1	HMGCS2	21	363	50003/5.51	1571.7706	1570.7450	101	M.PGSLPVNTESCWPK.D
						1184.5570	1183.5292	89	R.NSLSYDCIGR.L
						910.4869	909.4821	42	K.IHAQWQK.E
						1529.7231	1528.7045	72	K.LEDTYFDRDVEK.A
73	PREDICTED: keratin, type II cytoskeletal 8 isoform X2 [Meleagris gallopavo] XP_010726169.1	KRT8	39	210	51572/5.31	1197.6367	1196.6190	35	R.GLFEGYVGSLR.R
						1331.6429	1330.6265	44	K.NKYEEEINHR.T
						1079.5286	1078.5043	32	K.AQYEDIANR.S
74	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	31	535	48706/5.58	1590.7208	1589.6859	126	R.GDPSAWSYGAEAHSR.A
						1666.8683	1665.8297	82	R.TNPAVIPIECHYPR.R
						1366.6807	1365.6525	76	K.VTPADQGPDPQNK.A
						1144.5991	1143.5673	81	R.NTWVPVEGSR.D
						2111.8467	2110.8177	114	R.DVCSCCETGNCEPPALSR.R
75	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	9	297	98702/7.62	1803.6895	1802.6658	135	R.DACLQAGCCFDDTDR.A
						1419.7414	1418.7154	112	R.GLSAQPYNLDSVR.L
						1358.7921	1357.7718	36	K.VLRDPIYVEVR.L
76	PREDICTED: farnesyl pyrophosphate synthase [Meleagris gallopavo] XP_010721796.1	FDPS	37	319	29312/6.36	1209.5656	1208.5673	101	K.VDLSQFSEER.Y
						1448.6983	1447.7064	77	K.CSWLVVQCLQR.V
						1324.6795	1323.6857	56	K.VKELYETVGMR.A

77	PREDICTED: LOW QUALITY PROTEIN: 14-3-3 protein epsilon-like [Meleagris gallopavo] gi|326931332|ref|XP_003211786.1|	YWHAE	32	460	26884/4.74	1447.7488 2180.9738 2196.9763 1819.9711 2180.9738	1446.7024 2179.9328 2195.9277 1818.9298 2179.9328	68 132 35 110 132	K.VAGMDVELTVEER.N R.DNLTLWTSDMQGDGEEQNK.E R.DNLTLWTSDMQGDGEEQNK.E K.AASDIAMTELPPTHPIR.L R.DNLTLWTSDMQGDGEEQNK.E
78	PREDICTED: 14-3-3 protein epsilon isoform X2 [Haliaeetus albicilla] gi|700339038|ref|XP_009914457.1|	YWHAE	29	274	32321/5.57	1256.5656 1384.6531 1819.8661	1255.5833 1383.6783 1818.9298	77 40 91	R.YLAEFATGNDR.K R.YLAEFATGNDRK.E K.AASDIAMTELPPTHPIR.L
79	PREDICTED: clathrin light chain B-like [Meleagris gallopavo] gi|326928468|ref|XP_003210400.1|	CLTB	28	213	23097/4.60	947.4233 1074.5015	946.4508 1073.5141	33 45	K.VTEQEWR.E K.DLEEWNLR.Q
80	PREDICTED: 14-3-3 protein theta-like [Meleagris gallopavo] gi|326916470|ref|XP_003204530.1|	YWHAQ	26	234	28050/4.68	1532.7214 1108.5619	1531.7114 1107.5495	110 39	K.AVTEQGAELSNEER.N K.EMQPTHPIR.L
81	PREDICTED: 14-3-3 protein theta-like [Meleagris gallopavo] gi|326916470|ref|XP_003204530.1|	YWHAQ	27	364	28050/4.68	1532.7394 1268.5875 1396.6754 1108.5854	1531.7114 1267.5503 1395.6452 1107.5495	149 38 66 50	K.AVTEQGAELSNEER.N R.YLAEVACGDDR.K R.YLAEVACGDDRK.Q K.EMQPTHPIR.L
82	PREDICTED: 14-3-3 protein theta-like [Meleagris gallopavo] gi|326916470|ref|XP_003204530.1|	YWHAQ	38	318	28050/4.68	816.4643 1532.7880 1268.6322 1108.6241	815.4137 1531.7114 1267.5503 1107.5495	43 125 43 43	K.LAEQAER.Y K.AVTEQGAELSNEER.N R.YLAEVACGDDR.K K.EMQPTHPIR.L
83	PREDICTED: 14-3-3 protein theta-like [Meleagris gallopavo] gi|326916470|ref|XP_003204530	YWHAQ	38	275	28050/4.78	816.4562 1532.7544 1108.5901	815.4137 1531.7114 1107.5495	30 89 49	K.LAEQAER.Y K.AVTEQGAELSNEER.N K.EMQPTHPIR.L
84	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	32	720	48706/5.58	1590.6807 2456.2481 1869.9903 1666.8262	1589.6859 2455.2754 1868.9996 1665.8297	119 196 151 112	R.GDPSAWSYGAEAHSR.A R.AVAGSHPVAVQCQEAQLVVTVHR.D R.TLINYDPSPASNPVIIR.T R.TNPAVIPIECHYPR.R

85	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo]	ZP3	30	483	48706/5.58	1590.7032	1589.6859	123	R.GDPSAWSYGAEAHSR.A
						2456.2798	2455.2754	164	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1870.0130	1868.9996	144	R.TLINYDPSPASNPVIIR.T
86	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	29	691	48706/5.58	1590.6763	1589.6859	122	R.GDPSAWSYGAEAHSR.A
						2456.2301	2455.2754	176	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1869.9761	1868.9996	124	R.TLINYDPSPASNPVIIR.T
						1666.8211	1665.8297	100	R.TNPAVIPIECHYPR.R
87	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	27	696	48706/5.58	1590.7051	1589.6859	119	R.GDPSAWSYGAEAHSR.A
						2456.2587	2455.2754	180	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1870.0090	1868.9996	157	R.TLINYDPSPASNPVIIR.T
						1666.8458	1665.8297	87	R.TNPAVIPIECHYPR.R
88	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	30	867	48706/5.58	1590.7199	1589.6859	126	R.GDPSAWSYGAEAHSR.A
						2456.3110	2455.2754	174	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1870.0443	1868.9996	162	R.TLINYDPSPASNPVIIR.T
						1666.8778	1665.8297	96	R.TNPAVIPIECHYPR.R
						1144.5944	1143.5673	88	R.NTWVPVEGSR.D
89	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	29	697	48706/5.58	1590.6458	1589.6859	125	R.GDPSAWSYGAEAHSR.A
						2456.1683	2455.2754	165	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1869.9340	1868.9996	140	R.TLINYDPSPASNPVIIR.T
						1666.7799	1665.8297	84	R.TNPAVIPIECHYPR.R
						1144.5331	1143.5673	68	R.NTWVPVEGSR.D
90	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	32	871	48706/5.58	1590.6929	1589.6859	116	R.GDPSAWSYGAEAHSR.A
						2456.2394	2455.2754	151	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1869.9852	1868.9996	139	R.TLINYDPSPASNPVIIR.T
						1666.8323	1665.8297	102	R.TNPAVIPIECHYPR.R
						1366.6584	1365.6525	60	K.VTPADQGPDPQNK.A
						1144.5724	1143.5673	88	R.NTWVPVEGSR.D
						2111.7869	2110.8177	147	R.DVCSCCETGNCEPPALSR.R
91	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	32	549	48706/5.58	1590.6458	1589.6859	128	R.GDPSAWSYGAEAHSR.A
						2456.1683	2455.2754	46	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1869.9340	1868.9996	118	R.TLINYDPSPASNPVIIR.T
						1666.7799	1665.8297	105	R.TNPAVIPIECHYPR.R
						1144.5331	1143.5673	86	R.NTWVPVEGSR.D
92	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	24	364	48706/5.58	1590.6780	1589.6859	122	R.GDPSAWSYGAEAHSR.A
						1869.9797	1868.9996	114	R.TLINYDPSPASNPVIIR.T
						1144.5672	1143.5673	73	R.NTWVPVEGSR.D

93	PREDICTED: f-actin-capping protein subunit alpha-1-like [Meleagris gallopavo] gi|326933790|ref|XP_003212982.1|	CAPZA1	37	343	33194/5.78	1197.6918	1196.6877	52	R.LLLNNDNLLR.E
						2124.9237	2123.9735	125	R.EGAAHAFAQYNMDQFTPVK.I
						2028.9669	2028.0065	93	K.IQVHYYEDGNVQLVSHK.D
	PREDICTED: F-actin-capping protein subunit alpha-1, partial [Pelecanus crispus] XP_009491497.1	CAPZA1	43	357	31586/5.93	1197.6918	1196.6877	52	R.LLLNNDNLLR.E
						2124.9237	2123.9735	125	R.EGAAHAFAQYNMDQFTPVK.I
						2028.9669	2028.0065	93	K.IQVHYYEDGNVQLVSHK.D
94	PREDICTED: putative methyl-transferase DDB_G0268948 [Meleagris gallopavo] XP_003207431.2		15	156	30549/5.69	2552.2238	2551.1795	74	K.APSCTQLAVDVGCGSGQGTAFLAER.F
						1002.5503	1001.5182	41	R.EAWDQLLK.Y
						1178.6545	1177.6132	30	R.DTLLEFWVR.Y
95	PREDICTED: annexin A5 [Meleagris gallopavo] XP_010708237.1	ANXA5	26	342	36079/5.57	1268.6019	1267.6197	67	R.GTVTAFSPFDAR.A
						942.4865	941.5083	68	R.IFDAHALR.H
						1759.7232	1758.7770	124	K.QVYMQEYEANLEDK.I
96	PREDICTED: F-actin-capping protein subunit beta isoform X2 [Manacus vitellinus] XP_017941793.1	CAPZB	52	474	33678/6.97	1108.6147	1107.6400	31	R.RLPPQQIEK.N
						1518.6384	1517.6820	85	K.YDPPLEDGAMPSAR.L
						1534.6314	1533.6769	32	K.YDPPLEDGAMPSAR.L + Oxidation (M)
						1696.7649	1695.8216	110	R.KLEVEANNAFDQYR.D
						1568.6816	1567.7267	84	K.LEVEANNAFDQYR.D
						1171.5579	1170.5921	59	R.STLNEIYFGK.T
	PREDICTED: f-actin-capping protein subunit beta isoforms 1 and 2-like [Meleagris gallopavo] gi|326932494|ref|XP_003212351.1|	CAPZB	40	449	33119/5.15	1108.6147	1107.6400	31	R.RLPPQQIEK.N
						1518.6384	1517.6820	85	K.YDPPLEDGAMPSAR.L
						1534.6314	1533.6769	32	K.YDPPLEDGAMPSAR.L Oxidation (M)
						1696.7649	1695.8216	110	R.KLEVEANNAFDQYR.D
						1568.6816	1567.7267	84	K.LEVEANNAFDQYR.D
						1171.5579	1170.5921	59	R.STLNEIYFGK.T
97	Prohibitin, partial [Acanthisitta chloris] KFP76871.1	PHB	52	478	26459/5.40	1185.6310	1184.6513	67	K.DLQNVNITLR.I
						1410.8251	1409.8507	34	R.ILFRPVTAQLPR.I
						1444.6263	1443.6518	97	R.IFTSIGEDYDER.V
						1149.5598	1148.5826	52	R.FDAGELITQR.E
						1998.0092	1997.0793	30	K.AAELIANSLATAGDGLIELR.K
						1606.8055	1605.8362	116	R.KLEAAEDIAYQLSR.S

	PREDICTED: prohibitin-like [Meleagris gallopavo] gi|326934047|ref|XP_003213108.1|	PHB	37	230	14952/9.65	1185.6310 1410.8251 1444.6263	1184.6513 1409.8507 1443.6518	67 34 96	K.DLQNVNITLR.I R.ILFRPVTAQLPR.I R.IFTSIGEDYDER.V
98	PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial [Falco peregrinus] XP_005241954.1	NDUFS3	32	272	23430/5.55	1343.7633 909.4406 1551.8001 924.4597 1502.8294	1342.7092 908.4140 1550.7518 923.4348 1501.7776	42 38 44 37 39	K.SLADLTAVDVPSR.Q K.AANWYER.E R.ILTDYGFEGHPFR.K R.YDDEVKR.V R.VVAEPVELSQEFR.K
99	PREDICTED: peroxiredoxin-4-like [Meleagris gallopavo] gi|326913542|ref|XP_003203096.1	PRDX4	26	446	35453/6.34	1355.7286 1665.7867 1076.6234 1243.6537 1212.6341	1354.7146 1664.7794 1075.6026 1242.6391 1211.6186	79 131 65 50 76	K.FTHLAWINTPR.K K.DYGVYLEDQGHTLR.G R.GLFIIDDKR.I R.QITMNDLPVGR.S R.LVQAFQYTDK.H
100	PREDICTED: platelet-activating factor acetylhydrolase IB subunit beta-like [Meleagris gallopavo] gi|326933420|ref|XP_003212802.1|	PAFAH1B2	16	280	25636/5.66	2377.9359 2393.9198 958.4212	2376.9989 2392.9938 957.4239	183 142 43	MSHGDSNPAAVPHAAEDTQGDDR.W MSHGDSNPAAVPHAAEDTQGDDR.W + Oxidation (M) R.WMSQHNR.F
101	PREDICTED: ubiquitin carboxyl-terminal hydrolase isozyme L1, partial [Meleagris gallopavo] XP_010708612.1	UCHL1	37	315	25069/6.35	1649.8193 1521.7279 929.4612	1648.7944 1520.6994 928.4477	70 109 67	K.KFLDETADLSPEER.A K.FLDETADLSPEER.A R.FSAVAFCK.S
102	PREDICTED: protein disulfide-isomerase A3 [Meleagris gallopavo] XP_010716010.1	PDIA3	44	660	51211/5.84	1557.7893 1752.8397 1488.6925 1359.6441 1664.7379 1268.6576	1556.7988 1751.8479 1487.6715 1358.6507 1663.7512 1267.6601	116 108 68 66 93 77	K.FIGDKDASVVGFFR.D K.YEEDGEGVVLFRPSR.L K.GDKYVMQEEFSR.D R.FLQDYFDGNLK.K K.MDATANDVPSPYEVR.G R.GFPTIYFAPAGK.K
103	PREDICTED: protein disulfide-isomerase A3 [Meleagris gallopavo] XP_010716010.1	PDIA3	31	638	51211/5.84	1698.7863 1282.5359 1557.8183 1752.8691 1488.7173 1664.7689	1697.7645 1281.5109 1556.7988 1751.8479 1487.6715 1663.7512	64 58 76 98 44 106	K.IFRDGEESGTYDGPR.T R.DGEESGTYDGPR.T K.FIGDKDASVVGFFR.D K.YEEDGEGVVLFRPSR.L K.GDKYVMQEEFSR.D K.MDATANDVPSPYEVR.G

104	PREDICTED: cytosolic non-specific dipeptidase-like [Meleagris gallopavo] XP_010706997.1	CNDP2	17	532	53388/5.63	1422.6607	1421.6827	63	K.YIDEHQDLYVK.R
						1189.6027	1188.6139	65	K.TNQEFPVNIK.F
						1221.6273	1220.6336	38	K.NKPCITYGLR.G
						1161.5759	1160.5826	37	K.QFAELQSPNK.F
						1233.6357	1232.6401	45	K.TVFGVEPDLTR.E
						2065.9189	2064.9898	140	K.NVMLLPVGAADDGAHSONEK.L
105	PREDICTED: heterogeneous nuclear ribonucleoprotein K, partial [Acanthisitta chloris] XP_009068800.1	HNRNPK	34	390	34642/8.26	1780.8027	1779.7911	120	R.TDYNASVSVPDSSGPER.I
						1533.7912	1532.7875	57	K.IIPTLEEYQHYK.G
						1098.4614	1097.4448	68	K.GSDFDCELR.L
						1194.7097	1193.6921	80	R.NLPLPPPPPPR.G
106	actin-related protein 3 [Gallus gallus] NP_989638.1	ACTR3	37	634	47847/5.62	1540.7045	1539.7062	113	R.LPACVVDCGTGYTK.L
						1499.6989	1498.6875	31	R.HGIVEDWDLMER.F
						1782.9085	1781.9159	83	R.EREVGIPPEQSLETAK.A
						1228.5877	1227.5772	61	K.EFTIDVGYER.F
						1281.6609	1280.6547	81	K.NIVLSGGSTMFR.D
						1466.6856	1465.6871	73	K.KDYEEIGPSICR.H
						1338.5978	1337.5921	62	K.DYEEIGPSICR.H
	PREDICTED: actin-related protein 3-like [Meleagris gallopavo] gi|326923061|ref|XP_003207760.1|	ACTR3	35	509	46303/5.62	1499.6989	1498.6875	31	R.HGIVEDWDLMER.F
						1782.9085	1781.9159	83	R.EREVGIPPEQSLETAK.A
						1228.5877	1227.5772	61	K.EFTIDVGYER.F
						1281.6609	1280.6547	81	K.NIVLSGGSTMFR.D
						1466.6856	1465.6871	73	K.KDYEEIGPSICR.H
						1338.5978	1337.5921	62	K.DYEEIGPSICR.H
107	PREDICTED: thioredoxin domain-containing protein 5 isoform X2 [Meleagris gallopavo] XP_010706678.1	TXNDC5	42	402	37118/5.61	1856.8105	1855.8081	96	K.VDCTTDTPLCSEFGVR.G
						1266.6648	1265.6517	65	K.THIAEGNHFIK.F
						2023.8494	2022.8524	130	K.VDCTQHYEVCSENQVR.G
108	PREDICTED: serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform-like [Meleagris gallopavo] gi|326918444|ref|XP_003205498.1|	PPP2CA	32	258	37012/5.24	829.4252	828.4242	31	R.GGWGISPR.G
						1915.8324	1914.8254	67	R.AHQLVMEGYNWCHDR.N
						1340.6748	1339.6561	60	K.YSFLQFDPAPR.R

	PREDICTED: serine/threonine-protein phosphatase 2A catalytic subunit beta isoform [Melopsittacus undulatus] XP_005143054.1	PPP2CA	38	311	36081/5.22	1732.7922 829.4252 1915.8324 1340.6748	1731.7886 828.4242 1914.8254 1339.6561	41 31 67 60	K.ELDQWIEQLNECR.Q R.GGWGISPR.G R.AHQLVMEGYNWCHDR.N K.YSFLQFDPAPR.R
109	PREDICTED: eukaryotic translation initiation factor 2 subunit 1 [Meleagris gallopavo] gi|326920582|ref|XP_003206548.1|	EIF2S1	26	281	36441/5.07	981.4739 1244.6172 1214.6193	980.4604 1243.5986 1213.6013	33 51 44	R.TAWVFDDK.Y K.RPGYGAYDAFK.H R.YVMTTTTLER.T
110	PREDICTED: pyruvate dehydrogenase E1 component subunit beta, mitochondrial-like [Meleagris gallopavo] gi|326928041|ref|XP_003210193.1|	PDHA1	31	404	47133/ 5.91	1915.8977 1781.9119 1317.6719 1753.8593 1248.6525	1914.8919 1780.9004 1316.6394 1752.8505 1247.6220	83 53 58 67 46	R.DALNQALDEELERDER.V K.TCYMSAGAIPVPIVFR.G K.EGVECEVINLR.T R.IMEGSAFNYLDAPAVR. R.VTGADVPMPYAK.I
111	PREDICTED: pyruvate dehydrogenase E1 component subunit beta, mitochondrial-like [Meleagris gallopavo] gi|326928041|ref|XP_003210193.1|	PDHB	10	148	47133/5.91	1317.7020 1248.6708	1316.6394 1247.6220	34 46	K.EGVECEVINLR.T R.VTGADVPMPYAK.I
112	PREDICTED: alpha-soluble NSF attachment protein [Struthio camelus australis] XP_009673006.1	NAPA	40	423	36108/5.49	1239.5837 1577.7360 2546.1021 1492.6555	1238.5601 1576.7270 2545.1357 1491.6340	42 115 76 69	R.IEEACDIYAR.A K.HDAATNFVDAGNAFK.K K.AIAHYEQAADYYKGEESNSSANK.C K.YEEMFPAFTDSR.E
113	PREDICTED: LOW QUALITY PROTEIN: heat shock-related 70 kDa protein 2 [Meleagris gallopavo] XP_003206814.3	HSPA2	37	742	70083/5.74	1487.6948 1663.7902 1921.9464 1691.7060 1435.7096 1253.6154 1456.8104 1535.6690	1486.6940 1662.8035 1920.9694 1690.7183 1434.7078 1252.6088 1455.8046 1534.6722	82 67 105 104 63 54 71 72	R.TTPSYVAFTDTER.L K.NQVAMNPTNTIFDAK.R K.VQNAVITVPAYFNDSQR.Q K.STAGDTHLGGEDFDNR.M R.MVNHFVEEFKR.K R.FEELNADLFR.G K.GQIQEIVLVGGSTR.I R.NQMAEKEEYEHK.Q

114	PREDICTED: annexin A6 isoform X1 [Meleagris gallopavo] XP_003210442.2	ANXA6	33	381	75619/5.63	1073.4706	1072.4825	37	R.STAEYFAER.L
						2001.8907	2000.9552	116	R.GTVQPVGNFNDDGDAQVLR.K
						910.4597	909.4960	45	R.VFQEFIK.M
						1322.5928	1321.6197	50	K.MTNHDVEHAIR.K
						890.4658	889.5022	43	R.DAFVAIVR.S
115	PREDICTED: annexin A6 isoform X1 [Meleagris gallopavo] XP_003210442.2	ANXA6	60	1060	75619/5.63	1707.9080	1706.8839	32	K.GFGSDKDAILDLITSR.S
						1501.7857	1500.7572	101	R.TNQEIHDLVAAYK.D
						1819.8328	1818.8007	90	R.EEDDVVSEDLVEQDAK.D
						2359.0553	2358.0223	181	K.LCGGDDDAAGEFFPEAAQVAYR.M
						2001.9875	2000.9552	143	R.GTVQPVGNFNDDGDAQVLR.K
						2105.0279	2103.9973	164	R.NNQEIAAINEAYQQAYHK.S
						1322.6578	1321.6197	89	K.MTNHDVEHAIR.K
116	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	29	640	48706/5.58	1590.7128	1589.6859	122	R.GDPSAWSYGAEAHSR.A
						2456.2908	2455.2754	170	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1870.0197	1868.9996	122	R.TLINYDPSPASNPVIIR.T
						1666.8562	1665.8297	85	R.TNPAVIPIECHYPR.R
						1144.5835	1143.5673	74	R.NTWVPVEGSR.D
117	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	29	719	48706/5.58	1590.6943	1589.6859	119	R.GDPSAWSYGAEAHSR.A
						2456.2383	2455.2754	151	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1869.9937	1868.9996	155	R.TLINYDPSPASNPVIIR.T
						1666.8326	1665.8297	96	R.TNPAVIPIECHYPR.R
						1366.6564	1365.6525	62	K.VTPADQGPDPQNK.A
						1144.5743	1143.5673	82	R.NTWVPVEGSR.D
118	PREDICTED: LOW QUALITY PROTEIN: T-complex protein 1 subunit beta [Merops nubicus] XP_008941120.1	CCT2	17	324	52604/5.88	1419.8279	1418.8146	46	K.KIHPQTIIAGWR.A
						1291.7354	1290.7197	43	K.IHPQTIIAGWR.A
						1458.7157	1457.6899	50	K.AAVDHGDDEVKFR.E
						1130.5626	1129.5451	59	K.HGINCFINR.Q
119	PREDICTED: keratin, type II cytoskeletal cochleal [Meleagris gallopavo] XP_003206045.1	KRT2	40	840	53651/5.97	1112.6140	1111.6350	77	R.SVAVPGVSQIR.V
						1629.7290	1628.7794	161	K.AGGFGSSSLYNLGSANK.R
						1785.8255	1784.8805	58	K.AGGFGSSSLYNLGSANKR.I
						1017.4995	1016.5291	48	K.WSLLQDQK.T
						1079.4788	1078.5043	75	K.AQYEDIANR.S
						1441.6326	1440.6633	60	R.SRAEAESWYQSK.F
						1198.5033	1197.5302	73	R.AEAESWYQSK.F
						1153.5269	1152.5485	71	R.EYQELMNVK.L

120	ATPase inhibitor, mitochondrial, partial [Numida meleagris] XP_021231384.	ATP5IF1	25	248	17283/10.34	1310.5590 1438.6444	1309.5799 1437.6749	48 88	R.HHEEEIDHHK.K R.HHEEEIDHHKK.E
121	PREDICTED: 10 kDa heat shock protein, mitochondrial isoform X1 [Meleagris gallopavo] XP_010711708.1	HSPE1	67	508	11476/9.02	1035.5941 1327.7669 1265.6734 1076.5968 1573.8150	1034.5913 1326.7620 1264.6776 1075.5914 1572.8188	62 128 65 59 117	R.KFLPLFDR.V K.VLQATVVAVGSGAR.G R.GKDGEIHPVSVK.V K.VLLPEYGGTK.I K.IVLEDKDYYLFR.D
122	PREDICTED: cytochrome c oxidase subunit 6B1 [Meleagris gallopavo] XP_021231384.1	COX6B1	44	210	10545/7.66	1004.4824 1552.6597 1487.6294	1003.4835 1551.6677 1486.6299	34 49 72	R.FPNQNQTR.N R.NCWQNYLDFHR.C K.GADATPCQWYYR.V
123	ubiquitin-40S ribosomal protein S27a [Meleagris gallopavo] gi|1776497000|ref|XP_031408525.1|	UBB	14	269	23902/9.81	1523.8079 1039.5416 1081.5771	1522.7740 1038.5094 1080.5451	117 68 40	K.IQDKEGIPPDQQR.L K.EGIPPDQQR.L R.TLSDYNIQK.E
124	40S ribosomal protein S12 [Gallus gallus] NP_001264840.1	RPS12	42	338	15967/8.82	2134.9738 1751.0071 1061.5640 1042.5229	2133.9646 1749.9447 1060.5376 1041.5019	64 59 53 57	R.QAHLCVLASNCDEPMYVK.L K.LVEALCAEHQINLIK.V K.LGEWVGLCK.I K.DVIEEYFK.C
	PREDICTED: 40S ribosomal protein S12-like [Meleagris gallopavo] gi|326915903|ref|XP_003204251.1|	RPS12	42	307	15967/8.82	2135.0292 1751.0071 1061.6047 1042.5688	2133.9646 1749.9447 1060.5376 1041.5019	64 59 53 57	R.QAHLCVLASNCDEPMYVK.L K.LVEALCAEHQINLIK.V K.LGEWVGLCK.I K.DVIEEYFK.C
125	PREDICTED: peptidyl-prolyl cis-trans isomerase B, partial [Meleagris gallopavo] XP_019474804.1	PPIB	47	540	20003/9.12	1378.7023 1626.8173 1286.5744 1587.7383 1490.6622	1377.7140 1625.8236 1285.5761 1586.7365 1489.6772	108 89 105 61 83	K.TVENFVALATGEK.G R.VIKDFMIQGGDFTR.G K.DFMIQGGDFTR.G K.SIYGDRFPDENFK.L K.HYGPGWVSMANAGK.D + Oxidation (M)

126	PREDICTED: peptidyl-prolyl cis-trans isomerase B, partial [Meleagris gallopavo] XP_019474804.1	PPIB	46	341	20003/9.12	1286.5933 1587.7573 1490.6900 816.4066 1017.5419	1285.5761 1586.7365 1489.6772 815.4178 1016.5325	76 60 62 30 41	K.DFMIQGGDFTR.G K.SIYGDRFPDENFK.L K.HYGPGWVSMANAGK.D + Oxidation (M) K.TPWLDGK.H K.VLEGMDVVR.K
127	transgelin [Gallus gallus] NP_990825.1	TAGLN	45	197	22357/8.85	1182.5395 1337.6504 1353.6403	1181.5200 1336.6306 1352.6255	60 51 30	K.KYDDELEDR.L K.GASQAGMSYGRPR.Q K.GASQAGMSYGRPR.Q + Oxidation (M)
128	PREDICTED: ATP synthase subunit d, mitochondrial isoform X2 [Pterocles gutturalis] gi|704524989|ref|XP_010084405.1|	ATP5F1D	23	195	15653/9.27	1149.5589 1249.6256	1148.5614 1248.6350	89 79	K.AIDWAAFAER.V R.IAEYEQQLQK.L
129	PREDICTED: LOW QUALITY PROTEIN: cold-inducible RNA-binding protein-like [Meleagris gallopavo] gi|326918654|ref|XP_003205603.1|	CIRBP	39	170	18564/ 9.51	2345.1712 1559.7395	2344.1587 1558.7304	48 72	K.LFVGGLSFDTNEQSLEQVFSK.Y R.GFGFVTFENIDDAK.D
130	PREDICTED: mesencephalic astrocyte-derived neurotrophic factor, partial [Meleagris gallopavo] XP_019475495.1	MANF	40	366	22425/8.82	1533.7774 1362.6761 1206.5718	1532.7181 1361.6398 1205.5387	111 35 95	R.LCYYIGATSDAATK.I R.RILDDWGEACK.G R.ILDDWGEACK.G
131	PREDICTED: LOW QUALITY PROTEIN: cytochrome b-c1 complex subunit 7 [Meleagris gallopavo] XP_010707455.2	UQCRB	29	272	13507/9.24	1233.5727 1148.5507 1686.8036	1232.5614 1147.5509 1685.8188	71 48 89	K.WYYNAAGFNK.Y R.LPEDLYNER.M K.YEEDKPYLEPYLK.E
132	PREDICTED: cytochrome c oxidase subunit 6A1, mitochondrial [Meleagris gallopavo] XP_010718787.1	COX6A1	62	306	9749/9.10	1547.8450 1083.5952 1246.6460 2169.9646	1546.8117 1082.5621 1245.6142 2168.9763	37 35 76 98	1546.8117 K.HERPEFIR.Y R.TKPFPWGDGNK.T K.TLFHNPHTNALPTGYEDEN.-
133	PREDICTED: nucleoside diphosphate kinase-like [Meleagris gallopavo]	NME4	51	370	17399/7.79	1344.7445 1191.6435 1785.8706	1343.7561 1190.6448 1784.9091	103 33 106	R.TFIAIKPDGVQR.G K.DRPFYPGLVK.Y R.VMLGETNPADSKPGTIR.G

	gi|326931005|ref|XP_003211627.1|					1051.4852	1050.4917	56	R.GDFCIQVGR.N
134	PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Meleagris gallopavo] gi|326936164|ref|XP_003214127.1|	PPIA	34	203	11077/8.53	1096.5744	1095.5600	33	K.FADENFILK.H
						1491.7308	1490.7221	68	R.VKEGMNVVEAMER.C
						1264.5789	1263.5587	62	K.EGMNVVEAMER.C
135	PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Meleagris gallopavo] NP_001159798.1	PPIA	31	245	18084/8.29	1598.7906	1597.7381	36	R.IIPGFMCQGGDFTR.H
						1614.7838	1613.7331	45	R.IIPGFMCQGGDFTR.H + Oxidation (M)
						1096.6206	1095.5600	35	K.FADENFILK.H
						1491.7765	1490.7221	52	R.VKEGMNVVEAMER.C
						1264.6192	1263.5587	54	K.EGMNVVEAMER.C
136	peptidyl-prolyl cis-trans isomerase A [Gallus gallus] NP_001159798.1	PPIA	31	245	18084/8.29	1598.7906	1597.7381	36	R.IIPGFMCQGGDFTR.H
						1614.7838	1613.7331	45	R.IIPGFMCQGGDFTR.H + Oxidation (M)
						1096.6206	1095.5600	35	K.FADENFILK.H
						1491.7765	1490.7221	52	R.VKEGMNVVEAMER.C
						1264.6192	1263.5587	54	K.EGMNVVEAMER.C
137	glyceraldehyde-3-phosphate dehydrogenase [Meleagris gallopavo] NP_001290108.1	GAPDHS	26	509	35908/8.86	1091.4751	1090.4832	63	K.YDSTHGHFK.G
						1819.9060	1818.8968	134	K.IVSNASCTTNCLAPLAK.V
						1556.8118	1555.8029	120	R.VPTPNVSVVDLTCR.L
						1749.8044	1748.7794	118	K.LVSWYDNEFGYSNR.V
138	glyceraldehyde-3-phosphate dehydrogenase [Meleagris gallopavo] NP_001290108.1	GAPDHS	26	490	35908/8.86	1091.5107	1090.4832	60	K.YDSTHGHFK.G
						1819.9492	1818.8968	130	K.IVSNASCTTNCLAPLAK.V
						1556.8372	1555.8029	117	R.VPTPNVSVVDLTCR.L
						1749.8301	1748.7794	122	K.LVSWYDNEFGYSNR.V
139	PREDICTED: malate dehydrogenase, mitochondrial [Meleagris gallopavo] XP_003211747.1	MDH2	47	891	37435/8.83	1487.7626	1486.7490	96	K.GFLGPEQLPECLK.G
						1338.7213	1337.7126	82	K.GCDVVVIPAGVPR.K
						956.4521	955.4624	66	K.HGVYNPNR.I
						1120.6382	1119.6401	81	R.VSVPVIGGHAGK.T
						1370.7808	1369.7639	77	K.TIIPLISQCTPK.V
						1218.5957	1217.5928	70	K.VDFPQDQLEK.L
						1454.7062	1453.6983	101	K.AGAGSATLSMAYAGAR.F
						1195.5778	1194.5703	93	K.EGVIECSFVR.S
						1897.9205	1896.9357	94	R.SEETESPYFSTPLLLGK.N

140	PREDICTED: voltage-dependent anion-selective channel protein 2 [Corvus brachyrhynchos] XP_008641066.1	VDAC2	49	430	30274/8.62	840.4536	839.4541	67	K.GYGFGLVK.L
						1344.6676	1343.6398	106	K.WAEYGLTFTEK.W
						1428.7195	1427.6933	100	K.LTFDTTFSPNTGK.K
						1556.8182	1555.7882	78	K.LTFDTTFSPNTGKK.S
141	PREDICTED: calcyclin-binding protein, partial [Phaethon lepturus] XP_010280426.1	CACYBP	42	238	24936/8.55	1516.7872	1515.7681	52	K.LPAENVQVNFTER.S
						1192.5773	1191.5594	76	K.WECLTQVEK.E
142	glutathione S-transferase alpha class A1.2 [Meleagris gallopavo] NP_001290083.1	GSTA1	31	213	25269/8.75	1578.8188	1577.8314	85	K.VLKDHGHDFLVGNK.L
						1238.5854	1237.5840	94	K.DHGHDFLVGNK.L
143	glutathione S-transferase alpha class A2 [Meleagris gallopavo] gi|356640670|gb|AET31409.1|	GSTA2	19	242	25540/8.45	945.4854	944.4644	45	R.YFPVYEK.A
						1557.8204	1556.7947	91	K.ALKDHGQDYLVGNK.L
						932.5098	931.4876	35	K.FLQPGSQR.K
144	PREDICTED: epididymal secretory protein E1, partial [Meleagris gallopavo] XP_010710061.1		41	413	16360/7.11	812.3488	811.3535	40	R.FVDCGSK.D
						1557.7386	1556.7253	123	K.DGSIQEVNVSPCPR.Q
						1030.5449	1029.5277	61	K.SGIQCPIQK.G
						1068.5172	1067.5036	81	K.GHSYSYLNK.L
145	PREDICTED: phosphatidylethanolamine-binding protein 1 [Meleagris gallopavo] XP_003211138.2	PEBP1	35	316	20406/9.44	1560.8262	1559.8195	71	K.LYTLVLTDPDAPSR.K
						1457.6999	1456.6922	47	R.EWHHFLVTNMK.G + Oxidation (M)
						1324.6959	1323.6863	68	R.YVWLVYEQPK.Q
						1414.7128	1413.7034	79	K.QLACNEPILSNR.S
146	PREDICTED: peroxiredoxin-6, partial [Meleagris gallopavo] XP_010714011.1	PRDX6	40	486	23895/9.32	1395.6542	1394.6500	95	R.DFTPVCTTELGR.A
						1462.6742	1461.6736	57	K.DINAYNGDQPVEK.L
						1149.6625	1148.6594	78	R.VVFIFGPDKK.L
						1191.6726	1190.6659	106	K.LSILYPATTGR.N
						1842.8988	1841.9193	78	K.RGDSVMVVPTLPDEEAK.K
147	phosphoglycerate mutase 1 [Numida meleagris] XP_021255837.1	PGAM1	38	598	29044/7.07	1312.6460	1311.5956	92	R.HGESAWNLENR.F
						2070.9656	2069.8901	153	R.FCGWYDADLSPAGQQEAR.R
						1073.6047	1072.5665	84	R.HYGALTGLNK.A
						1882.9053	1881.8666	107	R.YADLTEDQLPTCESLK.D
						1150.7049	1149.6618	89	R.VLIAAHGNSLR.G

148	triosephosphate isomerase [Numida meleagris] XP_021251610.1	TPI1	48	517	26846/6.71	1082.6038	1081.5709	77	R.KFFVGGNWK.M
						954.4951	953.4760	58	K.FFVGGNWK.M
						1523.8200	1522.7892	117	K.DIGAAWVILGHSER.R
						1614.8480	1613.8162	67	R.RHVFGESDELIGQK.V
						1257.6439	1256.6109	85	K.SHVSDAVAQSTR.I
149	endoplasmic reticulum resident protein 29 precursor [Gallus gallus] NP_001263253.1	ERP29	16	206	28288/7.63	1247.5823	1246.5506	71	K.FDTQYPYGEK.Q
						1703.8916	1702.8526	99	K.ILEQGEEFAANEVVR.I
150	glutathione S-transferase alpha class A1.3 [Meleagris gallopavo] gi|290874550|gb|ADD65347.1|	GSTA1.3	31	236	25399/8.75	1578.8188	1577.8314	85	K.VLKDHGHDFLVGNK.L
						1238.5854	1237.5840	93	K.DHGHDFLVGNK.L
151	PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Cuculus canorus] gi|696957384|ref|XP_009560101.1|	EIF4H	14	235	37988/10.00	1393.7183	1392.6885	71	K.EALTYDGALLGDR.S
						1669.7198	1668.7049	51	R.GSSMDFREPTEEER.A
	eukaryotic translation initiation factor 4H isoform X2 [Numida meleagris] XP_021271760.1	EIF4H	28	244	25479/8.60	901.4569	900.4090	57	R.AYSSFGGGR.G
						1393.7565	1392.6885	71	K.EALTYDGALLGDR.S
						1669.7677	1668.7049	52	R.GSSMDFREPTEEER.A
152	PREDICTED: endoplasmic reticulum resident protein 29-like [Meleagris gallopavo] gi|326929719|ref|XP_003211004.1|	ERP29	12	210	28179/8.25	1247.5513	1246.5506	53	K.FDTQYPYGEK.Q
						1703.8447	1702.8526	109	K.ILEQGEEFAANEVVR.I
153	PREDICTED: ferritin heavy chain [Meleagris gallopavo] XP_019471620.1	FTH1	43	209	19793/5.83	1152.6129	1151.6047	73	K.QLGDHVTNLR.K
						1236.5543	1235.5532	71	K.YGMAEYLFDK.H
						1252.5498	1251.5482	79	K.YGMAEYLFDK.H + Oxidation (M)

154	PREDICTED: thioredoxin-dependent peroxide reductase, mitochondrial-like [Meleagris gallopavo] gi|733898322|ref|XP_010713240.1|	PRDX3	46	355	25810/7.60	1472.8323 1285.7672 1220.6970 833.4425	1471.8035 1284.7442 1219.6673 832.4290	108 48 83 33	R.DYGVLLEGPGIALR.G R.GLFIIDPNGVIK.H K.HLSINDLPVGR.S R.SVEETLR.L
155	cytochrome c oxidase subunit 5B, mitochondrial [Numida meleagris] XP_021230630.1	COX5B	25	187	14197/8.67	1483.8247 955.5746	1482.7678 954.5287	80 46	K.EDPNLVPSITDKR.I K.LIPHELPH.-
156	PREDICTED: alpha-enolase isoform X1 [Meleagris gallopavo] XP_010721061.1	ENO1	41	531	47651/6.30	1804.9245 1143.6063 1960.9014 1425.7181	1803.9366 1142.6084 1959.9174 1424.7187	117 67 171 102	R.AAVPSGASTGIYEALELR.D R.IGAEVYHNLK.N K.DATNVGDEGGFAPNILENK.E R.YISPDQLADLYK.G
157	Alpha-centractin, partial [Leptosomus discolor] KFQ10545.1	ACTR1A	40	361	41540/6.85	1073.5051 965.3310 1086.5146 1840.8150	1072.5375 964.3709 1085.5546 1839.9003	47 43 45 125	R.YPMEHGIVK.D K.DWNDMER.I R.IWQYVYSK.D K.AQYYLPDGSTIEIGSAR.F
158	PREDICTED: fructose-bisphosphate aldolase C-like [Meleagris gallopavo] gi|326931372|ref|XP_003211805.1|	ALDOC	30	291	39735/6.20	1671.8536 1173.6367 2231.9554	1670.8336 1172.6302 2230.9403	37 38 170	R.LNQIGVENTEENRR.L R.ALQASALSAWR.G K.YEGSGDDSGAAGQSLYVANHAY.-
159	calponin-3 [Gallus gallus] NP_001341600.1	CNN3	26	538	36758/6.14	1107.5852 1403.6668 1373.6185 1216.6416 939.4725 955.4714 1560.6480	1106.5608 1402.7238 1372.5864 1215.6030 938.4644 954.4593 1559.6165	89 68 78 90 44 38 93	K.GPSYGLSAEVK.N K.AGQSVIGLQMGTNK.C K.CASQAGMTAYGTR.R K.GASQAGMLAPGTR.R K.GMSVYGLGR.Q K.GMSVYGLGR.Q + Oxidation (M) R.DYHGQYSDQGIDY.-
	PREDICTED: calponin-3-like [Meleagris gallopavo] gi|326925093|ref|XP_003208756.1|	CNN3	24	435	34871/5.76	1403.6668 1373.6185 1216.6416 939.4725 955.4714	1402.7238 1372.5864 1215.6030 938.4644 954.4593	68 78 90 44 38	K.AGQSVIGLQMGTNK.C K.CASQAGMTAYGTR.R K.GASQAGMLAPGTR.R K.GMSVYGLGR.Q K.GMSVYGLGR.Q Oxidation (M)

						1560.6480	1559.6165	93	R.DYHGQYSDQGIDY.-
160	PREDICTED: S-formylglutathione hydrolase [Meleagris gallopavo] XP_003203382.1	ESD	26	248	32001/6.14	915.4236 1386.7249 1323.6759	914.3956 1385.6939 1322.6507	34 62 94	K.CFEGFQK.V K.LINANFPTDPER.M K.WEAYDATQLVK.S
161	PREDICTED: heterogeneous nuclear ribonucleoprotein H3 isoform X1 [Meleagris gallopavo] XP_010712575.1	HNRNPH3	24	311	34664/6.26	1271.6754 3210.2192 1241.5539 1257.5496	1270.6194 3209.1820 1240.5143 1256.5092	63 82 77 64	R.STGEAFVQFASK.E R.GGGGYDGGYGGFDDYGGYNNYGYG-SDGYDDR.M R.DGMDQGYGSVGR.M R.DGMDQGYGSVGR.M + Oxidation (M)
162	PREDICTED: lysosomal protective protein, partial [Meleagris gallopavo] XP_003212164.2	CTSA	11	248	52312/6.08	1073.4659 883.4451 1314.5360	1072.4614 882.4487 1313.5380	64 45 86	K.YNDYAWNK.I R.LFPEYSK.N K.DLQAFCCSEGK.C
163	Coactosin-like, partial [Cuculus canorus] KFO76261.1	COTL1	41	329	15280/5.29	864.4530 1424.6940 934.5056 1980.0404	863.4501 1423.6620 933.4920 1978.9524	34 110 32 101	R.EAYNLVR.D R.DDATEVNWVTFK.Y K.EVVQNFAK.E K.EFVISDHKELDEDYIK.N
164	serine/arginine-rich splicing factor 1 [Gallus gallus] NP_001107213.1	SRSF1	38	333	27889/10.37	995.5247 1123.5207 1401.7123 1162.6393	994.4356 1122.4254 1400.6031 1161.5414	53 45 97 79	R.DAEDAVYGR.D R.DGYDYDGYR.L R.EAGDVCYADVFR.D R.SHEGETAYIR.V
	PREDICTED: LOW QUALITY PROTEIN: serine/arginine-rich splicing factor 1 [Pelodiscus sinensis] XP_006138677.2	SRSF1	32	337	35919/9.20	995.5247 1123.5207 1401.7123 1162.6393	994.4356 1122.4254 1400.6031 1161.5414	53 45 97 79	R.DAEDAVYGR.D R.DGYDYDGYR.L R.EAGDVCYADVFR.D R.SHEGETAYIR.V
165	PREDICTED: cathepsin B-like [Meleagris gallopavo] gi|326916753|ref|XP_003204669.1|	CTSB	15	300	38520/5.64	1249.6978 1881.0359 1824.9476	1248.6251 1879.9289 1823.8472	61 156 55	K.HYGITSYGVPR.S K.SGVYQHVSGEQVGGHAIR.I R.GEDHCGIESEIVAGVPR.T

166	PREDICTED: L-lactate dehydrogenase B chain isoform X2 [Meleagris gallopavo] XP_010714086.1	LDHB	29	327	36762/6.71	1494.7939	1493.7726	49	K.IVADKDYAVTANSK.I
						1262.6430	1261.6085	48	R.VIGSGCNLDTAR.F
						1292.7097	1291.6772	85	K.QVVESAYEVIR.L
						1148.6222	1147.5873	76	K.SADTLWSIQK.D
167	PREDICTED: annexin A2 [Meleagris gallopavo] XP_019474821.1	ANXA2	51	669	39317/8.04	2011.9157	2010.9646	99	K.AYSNFDADRDAAALEAAIK.T
						1825.8296	1824.8741	120	K.TELEKDIISDTSGDFR.K
						2041.8465	2040.8946	159	R.CEDTSVIDYELIDQDAR.E
						1560.7193	1559.7541	76	K.SYSPYDMLESIKK.E
						1576.7128	1575.7490	52	K.SYSPYDMLESIKK.E + Oxidation (M)
						1405.6661	1404.6925	86	K.SLYYFIQQDTK.G
168	malate dehydrogenase, cytoplasmic isoform MDH1 [Gallus gallus] NP_001006395.1	MDH1	24	192	36748/6.92	1026.4859	1025.4600	31	K.ENFSCLTR.L
						1176.6638	1175.6299	55	K.GDFILTVQQR.G
						1393.7413	1392.7038	73	K.FVEGLPINDFSR.E
	PREDICTED: malate dehydrogenase, cytoplasmic-like [Meleagris gallopavo] gi|326914879|ref|XP_003203750.1|	MDH1	25	182	41370/7.55	1026.4859	1025.4600	31	K.ENFSCLTR.L
						1176.6638	1175.6299	55	K.GDFILTVQQR.G
						1393.7413	1392.7038	73	K.FVEGLPINDFSR.E
169	PREDICTED: heterogeneous nuclear ribonucleoprotein H3 isoform X1 [Meleagris gallopavo] XP_010712575.1	HNRNPH3	43	598	36676/6.60	1271.6135	1270.6194	66	R.STGEAFVQFASK.E
						3210.1109	3209.1820	153	R.GGGGYDGGYGGFDDYGGYNNYGYG-SDGYDDR.M
						1052.5391	1051.5411	51	
						1241.5117	1240.5143	89	R.VHIDIGADGR.A
						1918.7451	1917.7813	164	R.DGMDQGYGSVGR.M
									R.GSGNSGGYYGQGNMGGGGWR.G
170	PREDICTED: T-complex protein 1 subunit zeta [Meleagris gallopavo] XP_003211780.2	CCT6A	23	579	57064/6.70	1498.7705	1497.7576	112	K.QADLYISEGLHPR.I
						1028.6016	1027.5913	71	K.ALEVLEQVK.V
						937.5314	936.5141	51	R.GLVLDHGAR.H
						1148.5613	1147.5550	82	K.TEVSAGFFYK.S
						918.5356	917.5334	49	K.GFIVINQK.G
171	PREDICTED: LOW QUALITY PROTEIN: elongation factor 1-gamma, partial [Serinus canaria] gi|683941070|ref|XP_009098822.1|	EEF1G	10	169	40955/8.98	821.4833	820.4443	37	R.TFLVGER.V
						1237.7044	1236.6503	70	K.SPFVLDEFKR.K

172	succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial [Gallus gallus] NP_001006578.2	OXCT1	21	583	45556/5.65	1617.6706 1633.6936 2583.2373 1492.6876	1616.7141 1632.7090 2582.3017 1491.7317	114 68 201 99	R.MVSSYVGENAEFER.Q R.MVSSYVGENAEFER.Q + Oxidation (M) R.AGGAGIPAFYTSTGYGTLVQEGGAPIK.Y K.YNSDGTIAIASQPR.E
173	PREDICTED: aldehyde dehydrogenase, mitochondrial-like [Meleagris gallopavo] gi|326929711|ref|XP_003211000.1|	ALDH2	5	266	95672/6.37	1572.7348 1132.5570 1604.6972 1804.7865	1571.7732 1131.5825 1603.7341 1803.8315	80 77 85 111	K.IFINNEWHDAVSK.K R.AAFQLGSPWR.R K.TIPLDGDFFCYTR.H R.TYVQEDIYNEFVER.S
174	PREDICTED: aldehyde dehydrogenase, mitochondrial-like [Meleagris gallopavo] gi|326929711|ref|XP_003211000	ALDH2	28	538	95672/6.37	1572.7734 1132.5931 1604.7408 1804.8334	1571.7732 1131.5825 1603.7341 1803.8315	92 85 88 124	K.IFINNEWHDAVSK.K R.AAFQLGSPWR.R K.TIPLDGDFFCYTR.H R.TYVQEDIYNEFVER.S
	PREDICTED: aldehyde dehydrogenase, mitochondrial [Par XP_015499536.1us major] XP_015499536.1	ALDH2	28	527	57382/7.51	1572.7734 1132.5931 1604.7408 1804.8334 1534.7033	1571.7732 1131.5825 1603.7341 1803.8315 1533.6947	92 85 88 124 79	K.IFINNEWHDAVSK.K K.AAFQLGSPWR.R K.TIPLDGDFFCYTR.H R.TYVQEDIYNEFVER.S K.TEQGPQVDEEQFK.K
175	PREDICTED: ATP synthase subunit alpha, mitochondrial isoform X1 [Melopsittacus undulatus] XP_005145448.1	ATP5F1A	40	525	60155/9.07	1391.7018 1624.8881 1026.5928 1287.6900 1553.7338 892.4862	1390.6940 1623.8832 1025.5869 1286.6870 1552.7310 891.4814	31 53 49 80 114 31	K.TGTAEVSSILEER.I R.TGAIVDVPVGEELLGR.V K.AVDSLVPIGR.G K.HALIIYDDLSK.Q R.EAYPGDVFYLHSR.L K.LELAQYR.E
176	PREDICTED: ATP synthase subunit alpha, mitochondrial [Meleagris gallopavo] XP_010723474.1	ATP5F1A	27	397	55650/8.54	1391.7209 1624.9008 1287.7139 1553.7599	1390.6940 1623.8832 1286.6870 1552.7310	32 64 82 73	K.TGTAEVSSILEER.I R.TGAIVDVPVGEELLGR.V K.HALIIYDDLSK.Q R.EAYPGDVFYLHSR.L
177	PREDICTED: cytochrome b-c1 complex subunit 2, mitochondrial-like [Meleagris gallopavo] XP_010718246.1	UQCRC2	14	203	48939/6.86	1553.7677 1217.6901	1552.7344 1216.6564	73 68	K.TALANPLYCPDYR.I K.QVAEQFLNIR.S

178	PREDICTED: citrate synthase, mitochondrial, partial [Meleagris gallopavo] XP_010725496.2	CS	21	258	54330/7.00	1322.7110	1321.6415	47	R.DFIWNTLNSGR.V
						1167.7326	1166.6560	78	R.VVPGYGHAVLR.K
						1204.6928	1203.6288	35	K.YYTVLFGVSR.A
						1127.7141	1126.6499	32	R.ALGFPLERPK.S
179	PREDICTED: moesin isoform X2 [Meleagris gallopavo] XP_010713423.1	MSN	32	967	67231/5.88	976.5171	975.5389	77	K.QLFDQVVK.T
						1217.5759	1216.5836	36	K.LNKDQWEER.I
						1104.5717	1103.5764	82	K.IGFPWSEIR.N
						1310.6766	1309.6819	77	K.KAPDFVFYAPR.L
						1182.5876	1181.5869	80	K.APDFVFYAPR.L
						1472.7635	1471.7817	44	R.RKPDTIEVQQMK.A
						1387.6750	1386.6851	34	K.AQQELEEQTRR.A
						1661.7761	1660.8090	136	K.TQEQLAAEMAELTAR.I
						943.5295	942.5498	69	R.ITQLELAR.Q
						1031.5320	1030.5407	33	K.ALSSELANAR.D
						1402.5980	1401.6129	101	K.TANDMIHAENMR.L
180	PREDICTED: radixin-like [Meleagris gallopavo] gi|326914349|ref|XP_003203488.1|	RDX	11	203	68556/5.95	1248.5628	1247.5795	59	R.IQNWHEEHR.G
						1182.5717	1181.5869	61	K.APDFVFYAPR.L
181	PREDICTED: vinculin [Meleagris gallopavo] ACT78466.1	VCL	16	527	117476/6.06	1617.7521	1616.7981	69	R.AAQMLQADPYSVPAR.D
						1305.5931	1304.6221	58	R.QQELTHQEHR.V
						1175.5842	1174.6016	32	K.MSAEINEIIR.V
						2019.9109	2018.9922	53	K.GWLRDPNAPPGDAGEQAIR.Q
						1230.5483	1229.5677	61	R.WIDNPTVDDR.G
						1151.5509	1150.5627	33	R.LANVMMGPYR.Q
						2415.0894	2414.2077	56	K.LLAVAATAPSDTPNREEVFEER.A
						944.4129	943.4399	33	K.SFLDSGYR.I
182	PREDICTED: glycogen phosphorylase, liver form [Meleagris gallopavo] XP_010710458.1	PYGL	31	560	98753/6.03	1355.6750	1354.6670	66	R.DYYFALAHTVR.D
						1150.5244	1149.5091	50	R.TQQYYYER.D
						946.4695	945.4668	44	R.APNDFNLR.D
						1442.6892	1441.6878	78	R.VLYPNDNFFEGK.E
						1580.7517	1579.7518	84	R.DFAELEPDKFQNK.T
						1204.5959	1203.5812	63	K.VFADYEAYVK.C
						919.4881	918.4923	59	K.IPPPNEPR.E

183	PREDICTED: programmed cell death 6-interacting protein-like [Meleagris gallopavo] gi|326922173|ref|XP_003207326.1|	PDCD6IP	28	263	92548/6.02	1533.7543 1322.6243	1532.7524 1321.6051	73 34	K.HYQFASGAFQHIK.D K.KDNDFIYHDR.V
184	PREDICTED: ezrin [Meleagris gallopavo] XP_010705613.1	EZR	37	732	74449/6.68	976.5275 1031.5515 1535.7543 1104.5792 1310.6796 1182.5910	975.5389 1030.5560 1534.7715 1103.5764 1309.6819 1181.5869	73 48 101 71 53 89	K.QLFDQVVK.T R.KENPLQFR.F R.IQVWHAEHSGMLK.E K.IGFPWSEIR.N K.KAPDFVFYAPR.L K.APDFVFYAPR.L
185	PREDICTED: moesin isoform X2 [Meleagris gallopavo] XP_010713423.1	MSN	25	353	67231/5.88	976.5316 1310.6912 1182.5958	975.5389 1309.6819 1181.5869	47 35 67	K.QLFDQVVK.T K.KAPDFVFYAPR.L K.APDFVFYAPR.L
186	PREDICTED: isopentenyl-diphosphate Delta-isomerase 1-like [Meleagris gallopavo] gi|326921556|ref|XP_003207023.1|	IDI2	25	247	36857/6.64	1270.5616 1416.7180 1081.6378	1269.5520 1415.7085 1080.6219	35 83 47	K.NCHLNDNIDR.G R.AFSVFLFNTENK.L K.LIAETFLFK.W
187	Chain R, Cytochrome Bc1 Complex From Chicken With Fenamidone Bound gi|285803752|pdb|3L75|R		15	166	21751/6.07	1619.8553 1264.7097	1618.7740 1263.6320	88 39	-.VHNDVTVPDFSAYR.R K.LRDPQHDLDR.V
	PREDICTED: cytochrome b-c1 complex subunit Rieske, mitochondrial-like [Meleagris gallopavo] XP_003209829.2	UQCRFS1	14	161	27012/6.38	1996.8699 1840.7828 1264.6300	1995.8981 1839.7970 1263.6320	37 31 39	R.REDVLDATTSSQSSSEER.K R.EDVLDATTSSQSSSEER.K K.LRDPQHDLDR.V
188	PREDICTED: phosphatidylethanolamine-binding protein 1 [Meleagris gallopavo] XP_003211138.2	PEBP1	31	167	20406/9.44	1560.8224 1324.6955 1414.7185	1559.8195 1323.6863 1413.7034	33 46 47	K.LYTLVLTDPDAPSR.K R.YVWLVYEQPK.Q K.QLACNEPILSNR.S

189	PREDICTED: LOW QUALITY PROTEIN: T-complex protein 1 subunit eta [Cuculus canorus] gi|696994246|ref|XP_009564030.1|	CCT7	27	521	47839/6.58	1533.7256	1532.7333	44	K.KTFSYAGFEMQPK.K
						1405.6366	1404.6384	64	K.TFSYAGFEMQPK.K
						1421.6300	1420.6333	84	K.TFSYAGFEMQPK.K Oxidation (M)
						1565.7864	1564.7886	93	K.LPIGDVATQYFADR.D
						985.5254	984.5240	34	R.VPEEDLKR.T
						1133.5053	1132.5012	61	R.YNFFTGCPK.A
190	PREDICTED: alpha-enolase-like [Meleagris gallopavo] gi|326932384|ref|XP_003212299.1|	ENO1	24	411	47815/6.00	1143.6071	1142.6084	69	R.IGAEVYHNLK.N
						1960.8565	1959.9174	134	K.DATNVGDEGGFAPNILENK.E
						1425.7064	1424.7187	58	R.YISPDQLADLYK.G
191	PREDICTED: glutamine synthetase-like [Meleagris gallopavo] gi|326930228|ref|XP_003211252.1|	ASNS	15	189	43078/6.03	1630.8037	1629.7470	34	K.RHDYHICVYDPR.G
						1517.7237	1516.6583	83	R.QVGQDGFGYFEDR.R
192	PREDICTED: 26S protease regulatory subunit 10B-like [Meleagris gallopavo] gi|326921318|ref|XP_003206908.1|		33	443	42228/6.43	1219.6132	1218.6067	55	K.GCLLYGPPGTGK.T
						930.4129	929.4065	36	R.EMFNYAR.D
						1433.7960	1432.7786	39	R.KIHIDLPNEQAR.L
						1273.6444	1272.6350	91	K.HGEIDYEAIVK.L
						1368.6467	1367.6326	38	R.NVCTEAGMFAIR.A
						1580.7031	1579.6977	94	R.ADHDFVVQEDFMK.A
193	PREDICTED: synaptic vesicle membrane protein VAT-1 homolog [Meleagris gallopavo] XP_003213191.2	VAT1	34	312	53230/9.67	1268.6507	1267.6633	43	R.RGGSPGPGELSVR.V
						1763.6904	1762.7178	126	K.AVCGYDLGNMDEEYK.L
						1062.5768	1061.5869	61	K.LINLYNQGK.I
194	PREDICTED: endoplasmic reticulum resident protein 29-like [Meleagris gallopavo] gi|326929719|ref|XP_003211004.1|	ERP29	14	171	25670/7.66	1247.6232	1246.5506	76	K.FDTQYPYGEK.Q
						1703.9203	1702.8526	66	K.ILEQGEEFAANEVVR.I
195	PREDICTED: serpin H1 [Meleagris gallopavo] XP_010704578.1	SERPINH1	37	553	45681/8.74	1656.7807	1655.8195	75	R.LYGPASINFADDFVK.N
						1205.5526	1204.5625	68	K.KHYNYEHSK.I
						1077.4644	1076.4675	50	K.HYNYEHSK.I
						2087.9991	2087.0535	105	K.SINEWAAQTTDGKLPEVTK.D
						1580.6409	1579.6678	72	K.TNSILFIGR.L

196	PREDICTED: serpin H1 [Meleagris gallopavo] XP_010704578.1	SERPINH1	30	602	45681/8.74	1205.5760	1204.5625	66	K.KHYNYEHSK.I
						1077.4854	1076.4675	58	K.HYNYEHSK.I
						1420.6766	1419.6630	86	K.SINEWAAQTTDGK.L
						2088.0477	2087.0535	112	K.SINEWAAQTTDGKLPEVTK.D
						1580.6851	1579.6678	103	R.TGLYNYYDDEAEK.L
						1020.5974	1019.5764	85	K.TNSILFIGR.L
197	PREDICTED: serpin H1 [Meleagris gallopavo] XP_010704578.1	SERPINH1	17	252	45681/8.74	1205.5548	1204.5625	68	K.KHYNYEHSK.I
						1580.6548	1579.6678	62	R.TGLYNYYDDEAEK.L
						1020.5685	1019.5764	71	K.TNSILFIGR.L
198	PREDICTED: serpin H1-like [Meleagris gallopavo] gi|326914666|ref|XP_003203645.1|	SERPINH1	40	209	45610/ 8.28	2013.0673	2012.0223	43	K.LSSMIFIMPNHVEPLER.V
						1020.6259	1019.5764	54	K.TNSILFIGR.L
199	PREDICTED: elongation factor 1-alpha 1-like [Meleagris gallopavo] gi|326916312|ref|XP_003204452.1|	EEF1A1	8	166	50467/9.10	1404.7183	1403.7197	71	K.YYVTIIDAPGHR.D
						975.5761	974.5437	51	0 R.LPLQDVYK.I
200	PREDICTED: gelsolin isoform X2 [Meleagris gallopavo] XP_010719339.1	GSN	13	324	82630/5.82	2017.9431	2016.9752	94	R.DKDQTEGLGEAYISGHVAK.I
						1314.6870	1313.6728	77	K.VPFDAATLHTSR.A
						1220.6473	1219.6349	89	K.TPSAAYLWVGR.G
201	PREDICTED: annexin A6-like [Meleagris gallopavo] gi|326928554|ref|XP_003210442.1|	ANXA6	60	1160	75619/5.63	1707.9080	1706.8839	35	K.GFGSDKDAILDLITSR.S
						1501.7857	1500.7572	100	R.TNQEIHDLVAAYK.D
						1819.8328	1818.8007	89	R.EEDDVVSEDLVEQDAK.D
						2359.0553	2358.0223	180	K.LCGGDDDAAGEFFPEAAQVAYR.M
						2001.9875	2000.9552	142	R.GTVQPVGNFNDDGDAQVLR.K
						2105.0279	2103.9973	163	R.NNQEIAAINEAYQQAYHK.S
						1322.6578	1321.6197	88	K.MTNHDVEHAIR.K
202	PREDICTED: 26S protease regulatory subunit 7 [Picoides pubescens]	PSMC2	39	430	49030/5.72	1497.7981	1496.7947	70	K.QTLQSEQPLQVAR.C
						1418.7597	1417.7565	49	R.EVVETPLLHPER.F
						1379.5839	1378.5750	111	R.FDDGAGGDNEVQR.T
203	PREDICTED: perilipin-2 isoform X4 [Meleagris gallopavo] XP_010723996.1	PLIN2	12	253	48357/5.75	1928.9475	1927.9680	87	K.VEGFEVEVQKPSYYVR.L
						1238.6725	1237.6131	69	K.LYQSWVEWK.K
						2140.8220	2139.8689	45	K.NTGQNDDDESHSAEHIESR.T

204	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	24	225	48706/5.58	1590.6740 1869.9660 1666.8132	1589.6859 1868.9996 1665.8297	79 32 69	R.GDPSAWSYGAEAHSR.A R.TLINYDPSPASNPVIIR.T R.TNPAVIPIECHYPR.R
205	PREDICTED: thioredoxin domain-containing protein 5 isoform X2 [Meleagris gallopavo] XP_010706678.1	TXNDC5	12	138	37118/5.61	1856.8365 2023.8780	1855.8081 2022.8524	39 82	K.VDCTTDTPLCSEFGVR.G K.VDCTQHYEVCSENQVR.G
206	PREDICTED: cytoskeleton-associated protein 4 [Meleagris gallopavo] XP_019466286.1	CKAP4	39	641	49055/4.81	1724.7799 1439.6541 1196.5514 1122.5197 1668.7540 1351.6424	1723.8013 1438.6576 1195.5543 1121.5141 1667.7638 1350.6416	111 50 60 52 102 126	R.ERDFTSLENTVEER.L R.DFTSLENTVEER.L K.DAFGELQASMK.T K.WEENELFR.K K.ALETFESNSEGLESR.L K.FNSVEGSVDELR.S
207	PREDICTED: neutral alpha-glucosidase AB-like, partial [Gallus gallus] XP_015130042.1	GANAB	13	248	41885/6.28	1830.7548 1846.7403 1723.6725 1043.4638	1829.8367 1845.8316 1722.7485 1042.4760	109 54 92 31	K.VMDYVHGGGEAPQTDVR.W K.VMDYVHGGGEAPQTDVR.W + Oxidation (M) R.WNYQDEEDVAAVER.G R.YFTWDPSK.F
208	PREDICTED: phosphoglycerate kinase 1 [Meleagris gallopavo] XP_010713665.1	PGK1	52	374	41935/7.14	1634.8304 1769.0337 2010.9908 805.4498	1633.7849 1767.9883 2009.9364 804.4494	119 58 52 46	K.LGDVYVNDAFGTAHR.A K.ALESPERPFLAILGGAK.V K.VLNNMQIGNSLFDEEGSK.I+ Oxidation (M) K.FVEVVGR.A
209	PREDICTED: cytochrome b-c1 complex subunit 2, mitochondrial [Meleagris gallopavo] XP_010718246.1	UBB	16	214	48939/6.86	1553.7513 2129.0269 1217.6727	1552.7344 2128.0450 1216.6564	59 56 49	K.TALANPLYCPDYR.I K.ITSEQLHHFVQNNFTSAR.M K.QVAEQFLNIR.S
210	PREDICTED: heterogeneous nuclear ribonucleoprotein A3 homolog 1-like [Meleagris gallopavo] gi|326922673|ref|XP_003207572.1|	HNRNPA3	20	270	39688/8.94	1337.5723 1910.7006	1336.6268 1909.7827	30 181	K.WGTLTDCVVMR.D R.SSGSPYGGGYGSGSGSGGYGGR.R

211	PREDICTED: heterogeneous nuclear ribonucleoprotein A3 isoform X5 [Meleagris gallopavo] XP_010711878.1	HNRNPA3	22	299	40717/9.24	1337.6319 1882.9258 1910.7686	1336.6268 1881.9472 1909.7827	38 54 187	K.WGTLTDCVVMR.D K.IFVGGIKEDTEEYNLR.E R.SSGSPYGGGYGSGSGSGGYGGR.R
212	PREDICTED: acyl-CoA dehydrogenase family member 9, mitochondrial isoform X3 [Meleagris gallopavo] XP_019475592.1	ACAD9	17	309	65192/5.84	1386.6462 1239.6031 1217.5805	1385.6576 1238.5965 1216.5659	91 63 35	R.DFGGVTHGKPEDK.L R.KVDYGIMEER.G R.AYVCSHPLDR.T
213	PREDICTED: mothers against decapentaplegic homolog 2 isoform X2 [Picoides pubescens] XP_009899996.1	SMAD2	33	541	49807/6.67	1114.5881 1707.7867 1579.7055 1415.8693 1218.5733 838.3685	1113.5753 1706.7835 1578.6885 1414.8548 1217.5652 837.3769	32 76 85 37 70 43	K.GLPHVIYCR.L K.KDEVCVNPYHYQR.V K.DEVCVNPYHYQR.V R.VETPVLPPVLVPR.H R.YGWHPATVCK.I K.GWGAEYR.R
	PREDICTED: mothers against decapentaplegic homolog 2 isoform X2 [Pi XP_009899996.1coides pubescens]	SMAD2	33	541	49807/6.67	1114.5881 1707.7867 1579.7055 1415.8693 1218.5733	1113.5753 1706.7835 1578.6885 1414.8548 1217.5652	32 76 85 37 70	K.GLPHVIYCR.L K.KDEVCVNPYHYQR.V K.DEVCVNPYHYQR.V R.VETPVLPPVLVPR.H R.YGWHPATVCK.I
	PREDICTED: mothers against decapentaplegic homolog 3-like, partial [Meleagris gallopavo] gi|326926879|ref|XP_003209624.1|	SMAD3	15	365	46174/6.09	1707.7867 1579.7055 1415.8693 1218.5733 838.3685	1706.7835 1578.6885 1414.8548 1217.5652 837.3769	76 85 37 70 43	K.KDEVCVNPYHYQR.V K.DEVCVNPYHYQR.V R.VETPVLPPVLVPR.H R.YGWHPATVCK.I K.GWGAEYR.R
214	PREDICTED: EH domain-containing protein 3 [Meleagris gallopavo] XP_010713817.1	EHD3	24	441	60915/6.08	1236.6778 1332.6815 828.4228 1509.7641	1235.6411 1331.6503 827.4501 1508.7372	59 66 30 95	K.LNAFGNAFLNR.F K.ADQIETQQLMR.V R.DIQSLPR.N R.EHQISPGDFPNLR.K
215	PREDICTED: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial-like [Meleagris gallopavo] gi|326922595|ref|XP_003207534.1|	NDUFS1	14	276	80454/6.66	1594.7679 1627.7448 1064.5625	1593.7635 1626.7525 1063.5451	49 80 33	R.FASEVAGVDDLGTTGR.G R.LHEDINEEWISDK.T R.FEAPLFNAR.I

216	PREDICTED: lysyl-tRNA synthetase-like [Meleagris gallopavo] XP_010716411.1		20	202	68807/6.90	959.4135 1142.5195	958.4032 1141.5226	31 47	K.SEEEYFR.I R.FFDDLCAVR.N
217	PREDICTED: 4-trimethylaminobutyraldehyde dehydrogenase [Meleagris gallopavo] XP_003208605.2	ALDH9A1	10	173	54953/6.31	2018.9116 966.4831	2017.9229 965.4719	107 36	R.VEPVDGGQTEDVYEPATGR.V K.AAFQTWSR.M
218	PREDICTED: selenium-binding protein 1-A isoform X2 [Meleagris gallopavo] XP_010722315.1	N/A	14	147	53081/5.89	1296.7014 1469.7846	1295.6193 1468.7133	30 36	K.SPHYCQVIHR.L R.HNVLMSTEWGAPK.V
219	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP5-like [Meleagris gallopavo] gi|326933538|ref|XP_003212859.1|	FKBP5	21	332	51097/5.82	2087.1049 1604.8097 1053.6021	2086.0178 1603.7300 1052.5291	137 34 70	M.TTDEATKPEGEVQAAALAER.G K.RPGNEDEFPMIGDK.V R.YGFGEAGKPK.Y
220	PREDICTED: cytochrome b-c1 complex subunit 1, mitochondrial [Meleagris gallopavo] XP_010716826.1	UQCRC1	19	265	53290/6.36	2278.0922 1290.6564 1134.5590	2277.0696 1289.6364 1133.5353	65 36 64	R.VASEESSQPTCTVGVWIGAGSR.Y R.RISLEEWDSR.I R.ISLEEWDSR.I
221	PREDICTED: mothers against decapentaplegic homolog 3-like [Meleagris gallopavo] gi|326926879|ref|XP_003209624.1|	SMAD3	7	177	46174/6.09	1707.7704 1579.6873 1218.5711	1706.7835 1578.6885 1217.5652	73 34 47	K.KDEVCVNPYHYQR.V K.DEVCVNPYHYQR.V R.YGWHPATVCK.I
222	PREDICTED: ovotransferrin [Meleagris gallopavo] NP_001290136.1	N/A	11	382	79496/6.82	1671.7730 1333.6768 2537.0185 1047.5357	1670.7511 1332.6496 2535.9907 1046.5185	124 36 86 41	R.NAPYSGYSGAFHCLK.D R.IQWCAVGKDEK.S R.TGSCNFDEYFSEGCAPGSPPDSR.L K.YFGYTGALR.C
223	PREDICTED: ATP-dependent RNA helicase DDX3X isoform X2 [Meleagris gallopavo] XP_010723017.1	DDX3X	17	344	72453/6.54	1270.5468 1216.5661 2347.0084 1089.6051	1269.5374 1215.5520 2346.0223 1088.5978	59 91 52 36	K.QGFDSGGWSSSR.D R.DKDAYSSFGAR.S R.WCDKSDEDDWSKPLPPSER.L R.YTRPTPVQK.H

224	PREDICTED: cytochrome b-c1 complex subunit 2, mitochondrial isoform X2 [Gallus gallus] XP_010725496.2	UQCRC2	23	253	54330/7.00	1167.7177 1204.6826	1166.6560 1203.6288	81 49	R.VVPGYGHAVLR.K K.YYTVLFGVSR.A
225	PREDICTED: cytochrome b-c1 complex subunit 2, mitochondrial isoform X2 [Gallus gallus] XP_004945528.1	UQCRC2	17	176	48649/8.94	1559.8920 1217.7385	1558.8103 1216.6564	63 53	R.YETTANLGTAHLLR.L K.QVAEQFLNIR.S
226	PREDICTED: apolipoprotein A-I [Meleagris gallopavo] XP_010722021.1	APOA1	30	416	30593/5.58	1741.7885 1285.6330 1351.7479 1253.5881 1057.6186 1120.5891	1740.7856 1284.6172 1350.7296 1252.5724 1056.5927 1119.5747	59 49 51 75 54 45	R.SFWQHDDPQTPLDR.I K.LREDMAPYYK.E K.IRPFLDQFSTK.W K.WTEELEQYR.Q K.VVEQLSNLR.E K.MTPLVQEFR.E
227	PREDICTED: fatty acid-binding protein, heart [Meleagris gallopavo] XP_010721582.1	FABP3	25	216	14799/6.12	1445.6332 1497.6058	1444.6544 1496.6267	62 104	K.LVDTANFDEYMK.A K.LGEEFDETTADDR.H
228	PREDICTED: ubiquitin-conjugating enzyme E2 N-like [Meleagris gallopavo] gi|326911690|ref|XP_003202189.1|	UBE2N	11	184	28408/8.69	985.5443 1203.6176	984.5029 1202.5891	37 53	K.IYHPNVDK.L K.TNEAQAIETAR.A
229	PREDICTED: profilin-2 isoform X1 [Meleagris gallopavo] XP_019474798.1	PFN2	17	96	18736/8.89	1434.8053	1433.6899	83	K.SQGGEPTYNVAVGR.A
230	nucleoside diphosphate kinase [Anas platyrhynchos] XP_005016091.1	NME4	60	416	17475/7.72	1344.7863 1158.6344 1191.6735 1785.9400 1051.5253	1343.7561 1157.6081 1190.6448 1784.9091 1050.4917	100 62 35 68 54	R.TFIAIKPDGVQR.G K.FVHASEDLLK.Q K.DRPFYPGLVK.Y R.VMLGETNPADSKPGTIR.G R.GDFCIQVGR.N
231	peptidyl-prolyl cis-trans isomerase A [Gallus gallus] NP_001159798.1	PPIA	33	308	18084/8.29	1598.7896 1096.5949 1491.7596 1264.6012	1597.7381 1095.5600 1490.7221 1263.5587	75 72 34 40	R.IIPGFMCQGGDFTR.H K.FADENFILK.H R.VKEGMNVVEAMER.C K.EGMNVVEAMER.C

232	PREDICTED: mesencephalic astrocyte-derived neurotrophic factor, partial [Meleagris gallopavo] XP_019475495.1	MANF	40	423	22425/8.82	2231.0080	2230.0794	66	R.FYQSLKDDNVEFTPASIEK.E
						1533.6971	1532.7181	108	R.LCYYIGATSDAATK.I
						1973.9682	1973.0404	49	K.IINEVSKPMSHHIPVEK.I + Oxidation (M)
						1206.5143	1205.5387	78	R.ILDDWGEACK.G
233	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial-like [Meleagris gallopavo] gi|326912578|ref|XP_003202626.1|	NDUFA9	16	144	45665/8.95	1145.6363	1144.6604	33	R.IGSQVIIPYR.C
						962.4859	961.4981	37	K.TYALAGPNR.Y
234	PREDICTED: cholesterol side-chain cleavage enzyme, mitochondrial [Meleagris gallopavo] XP_010715503.1	CYP11A1	18	482	58499/9.25	1540.7122	1539.7252	103	K.EGGFHNVHNIMASK.F
						1133.6704	1132.6717	65	R.LHPVAVTLQR.Y
						1035.5374	1034.5396	38	K.EVILQDYR.I
						1828.8663	1827.8791	106	R.DPEVFPKPEQFNPER.W
						937.4741	936.4818	68	K.GLSFGFGPR.Q
235	PREDICTED: cholesterol side-chain cleavage enzyme, mitochondrial [Meleagris gallopavo] XP_010715503.1	CYP11A1	26	606	58499/9.25	1540.7463	1539.7252	88	K.EGGFHNVHNIMASK.F
						1408.6945	1407.6572	92	R.WTADFSHELFR.F
						1133.7045	1132.6717	71	R.LHPVAVTLQR.Y
						1035.5684	1034.5396	46	K.EVILQDYR.I
						1828.9271	1827.8791	106	R.DPEVFPKPEQFNPER.W
						820.4522	819.4313	44	R.WLVMGSK.H
						937.5156	936.4818	68	K.GLSFGFGPR.Q
236	PREDICTED: trifunctional enzyme subunit beta, mitochondrial isoform X2 [Meleagris gallopavo] XP_003204612.1	HADHB	22	423	51107/9.31	919.5221	918.5287	35	R.LAAAFAISR.V
						1122.5421	1121.5353	64	R.VEQDEYALR.S
						1197.5757	1196.5714	86	R.DFVYVSQDPK.D
						1416.7688	1415.7660	99	K.DQLLLGPTYATPK.V
237	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	7	321	98702/7.62	1803.6641	1802.6658	124	R.DACLQAGCCFDDTDR.A
						1419.7187	1418.7154	82	R.GLSAQPYNLDSVR.L
						1073.5734	1072.5665	54	R.DSVYILHAR.C
						1358.7622	1357.7718	41	K.VLRDPIYVEVR.L
238	PREDICTED: dihydrolipoyl dehydrogenase, mitochondrial-like [Meleagris gallopavo]	DLD	17	402	50607/7.17	1687.9965	1686.8954	115	K.ALLNNSHLYHLAHGK.D
						1127.7330	1126.6499	44	K.ALTGGIAHLFK.Q
						929.5966	928.5131	36	K.VVHVSGFGK.I
						1567.7879	1566.7413	46	K.SEEQLKEEGVEYK.I

	gi|326911238|ref|XP_003201968.1|					1510.7732	1509.7147	77	R.VCHAHPTVSEAFR.E
239	PREDICTED: LOW QUALITY PROTEIN: ornithine aminotransferase, mitochondrial [Meleagris gallopavo] XP_003208269.1	OAT	16	331	48811/7.12	1609.7563	1608.7784	86	K.TIQGPPSSDYIFER.E
						1736.8460	1735.8794	70	K.YGAHNYHPLPVALER.G
						1179.5870	1178.5720	77	K.GVYVWDVEGR.K
						1251.6563	1250.6560	57	K.IIFAAGNFWGR.T
240	PREDICTED: aflatoxin B1 aldehyde reductase member 2-like [Meleagris gallopavo] XP_019477922.1	AKR7A2	19	372	35769/6.80	1649.7539	1648.7515	77	R.LLDTAHMYAGGESER.I
						1374.6323	1373.6153	70	R.FFGNDWAQAYR.D
						1593.7970	1592.7794	74	K.DAYGSNAPSLTSAALR.W
						970.4923	969.4821	43	R.WLYHHSK.L
						1393.6360	1392.6245	54	K.LTAHDCPNYFR.-
241	PREDICTED: guanine nucleotide-binding protein subunit beta-2-like 1-like [Meleagris gallopavo] gi|326930102|ref|XP_003211191.1|	GNB2	44	388	35511/7.60	1192.5692	1191.5520	86	R.DETNYGIPQR.A
						1264.6557	1263.6459	87	R.LWDLTTGTTTR.R
						1366.6727	1365.6751	75	R.YWLCAATGPSIK.I
						860.4493	859.4440	30	K.IWDLEGK.I
242	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1-like [Meleagris gallopavo] gi|326921905|ref|XP_003207194.1|	HNRNPA2B1	38	415	38451/9.33	1087.4684	1086.4770	38	R.NYYEQWGK.L
						1879.9271	1878.9588	42	K.LFVGGIKEDTEEHHLR.D
						1050.4321	1049.4342	58	R.DYFEEYGK.I
						1695.7315	1694.7577	92	R.GFGFVTFDDHDPVDK.I
						1377.6224	1376.6222	76	R.GGGGNFGPGPGSNFR.G
243	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1-like [Meleagris gallopavo] gi|326921905|ref|XP_003207194.1|	HNRNPA2B1	25	198	38451/9.33	1087.5138	1086.4770	32	R.NYYEQWGK.L
						997.4808	996.4414	50	R.GGNFGFGDAR.G
						1377.6696	1376.6222	53	R.GGGGNFGPGPGSNFR.G
	PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1-like [Meleagris gallopavo]	HNRNPA2B1	25	198	38451/9.33	1087.5138	1086.4770	32	R.NYYEQWGK.L
						997.4808	996.4414	50	R.GGNFGFGDAR.G
						1377.6696	1376.6222	53	R.GGGGNFGPGPGSNFR.G

	gi|326921905|ref|XP_003207194.1|								
244	PREDICTED: apolipoprotein B-100 [Meleagris gallopavo] XP_010706280.1	APOB	3	121	525494/8.32	2190.9780 1337.6792	2189.9515 1336.6411	40 45	K.WTSPNFSDEGTHNSHATFR.V K.DYSLWEQAGLR.D
245	PREDICTED: apolipoprotein B-100 [Meleagris gallopavo] XP_010706280.1	APOB	2	443	525494/8.32	985.5338 1268.6758 1378.6264 2190.8903 1337.6343 944.5108	984.5393 1267.6925 1377.6459 2189.9515 1336.6411 943.5167	67 99 45 71 96 43	K.IPDFQLPR.I R.IPHTVTAPTFGK.L K.IQMQSGTAYSHR.L K.WTSPNFSDEGTHNSHATFR.V K.DYSLWEQAGLR.D K.YIIFFNK.Y
246	PREDICTED: U1 small nuclear ribonucleoprotein 70 kDa-like [Thamnophis sirtalis] XP_013921068.1	SNRNP70	18	148	23010/7.92	1652.8363 1413.6557	1651.8219 1412.6360	45 45	K.HHNQPYSGIAPYIR.E R.GYAFIEYEHER.D
247	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	17	343	98702/7.62	1803.5793 1419.6667 2300.9192	1802.6658 1418.7154 2300.0485	115 100 93	R.DACLQAGCCFDDTDR.A R.GLSAQPYNLDSVR.L R.IATDESYSSYHPDTDYPLVK.V
248	zona pellucida sperm-binding protein 1 precursor [Meleagris gallopavo] NP_001290145.1	ZP1	15	332	102104/8.46	1803.6707 1419.7363 1073.5827 1358.7868	1802.6658 1418.7154 1072.5665 1357.7718	121 77 57 49	R.DACLQAGCCFDDTDR.A R.GLSAQPYNLDSVR.L R.DSVYILHAR.C K.VLRDPIYVEVR.L
249	zona pellucida sperm-binding protein 1 precursor [Meleagris gallopavo] NP_001290145.1	ZP1	15	328	102104/8.46	1803.6495 1803.6495 1419.7089 1358.7643	2189.9663 1802.6658 1418.7154 1357.7718	30 142 89 47	R.YHYDCGDFGMQLLAFPTR.G R.DACLQAGCCFDDTDR.A R.GLSAQPYNLDSVR.L K.VLRDPIYVEVR.L
250	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	20	830	98702/7.62	2190.9709 936.4786 1803.6890 1419.7403 2523.3285 1073.5939	2189.9663 935.4713 1802.6658 1418.7154 2522.3129 1072.5665	143 38 145 84 146 72	R.YHYDCGDFGMQLLAFPTR.G K.VLDEFGTR.F R.DACLQAGCCFDDTDR.A R.GLSAQPYNLDSVR.L R.LVYENQLISTIDVQPGPHGSVTR.D R.DSVYILHAR.C

						1358.7974	1357.7718	55	K.VLRDPIYVEVR.L
						2349.2745	2348.2641	79	R.TQLVPVGPATLQLPFPSHYQR.F
	zona pellucida sperm-binding protein 1 precursor [Meleagris gallopavo] NP_001290145.1	ZP1	15	666	102104/8.46	2190.9709	2189.9663	143	R.YHYDCGDFGMQLLAFPTR.G
						936.4786	935.4713	38	K.VLDEFGTR.F
						1803.6890	1802.6658	145	R.DACLQAGCCFDDTDR.A
						1419.7403	1418.7154	84	R.GLSAQPYNLDSVR.L
						1073.5939	1072.5665	72	R.DSVYILHAR.C
						1358.7974	1357.7718	55	K.VLRDPIYVEVR.L
251	zona pellucida sperm-binding protein 1 precursor [Meleagris gallopavo] NP_001290145.1	ZP1	15	360	102104/8.46	1488.5975	1487.5960	56	R.DENMHGHHQPDR.G + Oxidation (M)
						1803.6615	1802.6658	142	R.DACLQAGCCFDDTDR.A
						1419.7214	1418.7154	96	R.GLSAQPYNLDSVR.L
						1358.7688	1357.7718	50	K.VLRDPIYVEVR.L
252	zona pellucida sperm-binding protein 1 precursor [Meleagris gallopavo] NP_001290145.1	ZP1	15	353	102104/8.46	1488.5838	1487.5960	53	R.DENMHGHHQPDR.G + Oxidation (M)
						1803.6427	1802.6658	139	R.DACLQAGCCFDDTDR.A
						1419.7104	1418.7154	99	R.GLSAQPYNLDSVR.L
						1358.7571	1357.7718	47	K.VLRDPIYVEVR.L
253	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	10	280	98702/7.62	1803.6346	1802.6658	135	R.DACLQAGCCFDDTDR.A
						1419.7058	1418.7154	105	R.GLSAQPYNLDSVR.L
254	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	13	482	98702/7.62	1488.5858	1487.5960	45	R.DENMHGHHQPDR.G + Oxidation (M)
						1803.6367	1802.6658	127	R.DACLQAGCCFDDTDR.A
						1419.7034	1418.7154	102	R.GLSAQPYNLDSVR.L
						1073.5626	1072.5665	89	R.DSVYILHAR.C
						1358.7598	1357.7718	52	K.VLRDPIYVEVR.L
255	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo]	ZP1	10	331	98702/7.62	1488.6248	1487.5960	40	R.DENMHGHHQPDR.G + Oxidation (M)
						1803.6684	1802.6658	131	R.DACLQAGCCFDDTDR.A
						1419.7277	1418.7154	101	R.GLSAQPYNLDSVR.L
256	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	10	390	98702/7.62	936.4677	935.4713	33	K.VLDEFGTR.F
						1488.5854	1487.5960	50	R.DENMHGHHQPDR.G + Oxidation (M)
						1803.6444	1802.6658	124	R.DACLQAGCCFDDTDR.A
						1419.7084	1418.7154	85	R.GLSAQPYNLDSVR.L
						1073.5670	1072.5665	50	R.DSVYILHAR.C

257	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo]	ZP1	9	241	98702/7.62	1803.6475 1419.7092 1073.5612	1802.6658 1418.7154 1072.5665	75 57 47	R.DACLQAGCCFDDTDR.A R.GLSAQPYNLDSVR.L R.DSVYILHAR.C
258	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo]	ZP1	10	237	98702/7.62	1803.7904 1419.8338 2301.1708	1802.6658 1418.7154 2300.0485	54 52 65	R.DACLQAGCCFDDTDR.A R.GLSAQPYNLDSVR.L R.IATDESYSSYHPDTDYPLVK.V
259	PREDICTED: LOW QUALITY PROTEIN: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] gi|326919872|ref|XP_00320620	ZP1	16	456	96950/8.00	1803.6418 1419.7069 2523.3058 1073.5716 1358.7634	1802.6658 1418.7154 2522.3129 1072.5665 1357.7718	110 91 60 65 39	R.DACLQAGCCFDDTDR.A R.GLSAQPYNLDSVR.L R.LVYENQLISTIDVQPGPHGSVTR.D R.DSVYILHAR.C K.VLRDPIYVEVR.L
260	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	16	442	98702/7.62	1803.6802 1419.7311 2523.3105 1073.5837	1802.6658 1418.7154 2522.3129 1072.5665	118 87 68 36	R.DACLQAGCCFDDTDR.A R.GLSAQPYNLDSVR.L R.LVYENQLISTIDVQPGPHGSVTR.D R.DSVYILHAR.C
261	PREDICTED: elongation factor 1-alpha 1-like [Meleagris gallopavo] gi|326916312|ref|XP_00320445	EEF1A1	8	199	50467/9.10	1404.7133 975.5383 1025.6039	1403.7197 974.5437 1024.6030	85 71 30	K.YYVTIIDAPGHR.D R.LPLQDVYK.I K.IGGIGTVPVGR.V
262	PREDICTED: elongation factor 1-alpha 1 [Pseudopodoces humilis] XP_005518198.1	EEF1A1	17	223	50468/9.10	1404.7562 1025.6357 3009.4372 3025.4371 3041.4320	1403.7197 1024.6030 3008.4082 3024.4031 3040.3980	82 33 89 63 39	K.YYVTIIDAPGHR.D K.IGGIGTVPVGR.V K.SGDAAIVDMIPGKPMCVESFSDYPPLGR.F K.SGDAAIVDMIPGKPMCVESFSDYPPLGR.F + Oxidation (M) K.SGDAAIVDMIPGKPMCVESFSDYPPLGR.F + 2 Oxidation (M)
263	PREDICTED: elongation factor 1-alpha 1-like [Meleagris gallopavo] gi|326916312|ref|XP_00320445	EEF1A1	8	179	50467/9.10	1404.7753 975.5823 1025.6491	1403.7197 974.5437 1024.6030	80 41 47	K.YYVTIIDAPGHR.D R.LPLQDVYK.I K.IGGIGTVPVGR.V
264	PREDICTED: aspartate aminotransferase, mitochondrial [Meleagris gallopavo] XP_003209725.3	GOT2	22	362	48223/9.15	1437.7524 918.4944 1134.5812 939.4206 994.4978	1436.7624 917.5083 1133.5829 938.4280 993.5066	84 37 71 32 48	R.YVTVQGISGTGSLR.I R.IGANFLQR.F R.DAGLQLQAYR.Y K.NMGLYGER.A R.AGAFTVICR.D

265	PREDICTED: aspartate aminotransferase, mitochondrial [Meleagris gallopavo]	GOT2	14	235	48223/9.15	1437.7711 918.4942 1134.5806	1436.7624 917.5083 1133.5829	43 38 60	R.YVTVQGISGTGSLR.I R.IGANFLQR.F R.DAGLQLQAYR.Y
266	PREDICTED: polyadenylate-binding protein 1-like [Meleagris gallopavo]	PABPN1	24	228	72992/ 9.58	1662.7354 1542.9250	1661.7396 1541.9293	55 71	K.GFGFVCFSSPEEATK.A R.IVATKPLYVALAQR.K
267	PREDICTED: trifunctional enzyme subunit alpha, mitochondrial-like [Meleagris gallopavo] gi|326916634|ref|XP_003204611.1|	HADHA	23	209	83519/9.20	2063.1623 1226.6984 1901.8853	2062.1786 1225.6931 1900.9023	36 38 30	K.TILGTPEVLLGLLPGAGGTQR.L K.ALIGLYHGQVR.C K.LPAKPEVCTDEDIQMR.L
268	PREDICTED: heat shock protein beta-1 [Meleagris gallopavo] XP_003211746.1	HSPB1	32	388	21886/6.23	920.3991 1611.7372 1088.5177 1501.8282 1373.7335	919.3937 1610.7437 1087.5047 1500.8300 1372.7351	48 85 43 60 45	R.DWYHGSR.L K.HEEKQDEHGFISR.C K.QDEHGFISR.C R.KYTLPPGVEATAVR.S K.YTLPPGVEATAVR.S
269	PREDICTED: elongation factor 1-alpha 1-like [Meleagris gallopavo] gi|326916312|ref|XP_003204452.1|	EEF1A1	30	199	50467/ 9.10	1404.7298 975.5533	1403.7197 974.5437	43 52	K.YYVTIIDAPGHR.D R.LPLQDVYK.I
270	PREDICTED: plasminogen activator inhibitor 1 RNA-binding protein isoform X3 [Coturnix japonica] XP_015726260.1	SERBP1	20	538	46147/7.89	1670.7922 1511.7819 2007.9630 1229.5790 2111.8747	1669.7995 1510.7892 2006.9882 1228.5836 2110.9126	96 117 111 79 51	M.PGHLQEGFGCVVTNR.F R.KNPLPPFAASAGGER.R R.RPDQQQQQQGEGKPIDR.R R.KPNEGADGQWK.K K.SKSEEAHAEDSVMDHHFR.K
271	stress-induced-phosphoprotein 1, partial [Numida meleagris] XP_021238872.1	STIP1	12	92	22485/5.51	1002.5351 1912.9543	1001.5043 1911.9438	38 40	R.NHVLYSNR.S K.ATYEEGLKHEPGNAQLR.E
272	PREDICTED: 4-trimethylaminobutyraldehyde dehydrogenase [Meleagris gallopavo] XP_003208605.2	ALDH9A1	16	379	54953/6.31	2018.9022 966.4749 1024.5555 1185.6102	2017.9229 965.4719 1023.5502 1184.6077	161 38 37 81	R.VEPVDGGQTEDVYEPATGR.V K.AAFQTWSR.M K.FGLAGGVFTR.D R.AAIEYYSQLK.T

273	PREDICTED: lysosomal protective protein, partial [Meleagris gallopavo] XP_003212164.2	CTSA	17	394	52312/6.08	1509.7048	1508.7307	61	R.HFSGHLCIGPTQR.L
						1636.8027	1635.8621	85	K.EHGPFLVQPDGVTLK.Y
						1998.8730	1997.9483	85	R.YEGDYLVTHDLGNSFIR.M
						1446.6440	1445.6683	72	R.LYMQMNDQYLK.L
274	PREDICTED: cholesterol side-chain cleavage enzyme, mitochondrial [Meleagris gallopavo] XP_010715503.1	CYP11A1	21	399	58499/9.25	1408.6748	1407.6572	62	R.WTADFSHELFR.F
						1133.6946	1132.6717	56	R.LHPVAVTLQR.Y
						1035.5546	1034.5396	38	K.EVILQDYR.I
						1828.8891	1827.8791	106	R.DPEVFPKPEQFNPER.W
						937.4979	936.4818	67	K.GLSFGFGPR.Q
275	PREDICTED: cholesterol side-chain cleavage enzyme, mitochondrial [Meleagris gallopavo] XP_010715503.1	CYP11A1	31	829	58499/9.25	1540.7295	1539.7252	85	K.EGGFHNVHNIMASK.F
						1446.7926	1445.7878	77	K.LGVYESVNIISPR.D
						1221.6562	1220.6342	61	R.FSVPPWVAYR.D
						1408.6757	1407.6572	86	R.WTADFSHELFR.F
						1679.8341	1678.8137	96	R.FALESVCHVLYGER.L
						1753.8327	1752.8220	133	R.DHVHAWDAIFTQADK.C
						1133.6779	1132.6717	50	R.LHPVAVTLQR.Y
						1035.5482	1034.5396	36	K.EVILQDYR.I
						1828.9030	1827.8791	125	R.DPEVFPKPEQFNPER.W
276	PREDICTED: cholesterol side-chain cleavage enzyme, mitochondrial [Meleagris gallopavo] XP_010715503.1	CYP11A1	29	288	58499/9.25	1133.7215	1132.6717	33	R.LHPVAVTLQR.Y
						1828.9349	1827.8791	106	R.DPEVFPKPEQFNPER.W
						937.5321	936.4818	43	K.GLSFGFGPR.Q
277	PREDICTED: mitogen-activated protein kinase 1-like [Meleagris gallopavo] gi|326929501|ref|XP_003210902.1|	MAPK1	22	347	42701/6.81	1565.7161	1564.7093	71	K.ISPFEHQTYCQR.T
						1209.6529	1208.6414	71	K.YIHSANVLHR.D
						2143.9770	2142.9971	56	R.VADPDHDHTGFLTEYVATR.W
						913.4674	912.4930	40	K.NKVPWNR.L
						1107.5701	1106.5608	46	K.ELIFEETAR.F
278	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo]	ZP3	15	236	48706/5.58	1590.6788	1589.6859	67	R.GDPSAWSYGAEAHSR.A
						1666.8212	1665.8297	42	R.TNPAVIPIECHYPR.R
						2111.7917	2110.8177	73	R.DVCSCCETGNCEPPALSR.R
279	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	23	162	48706/5.58	1590.6713	1589.6859	48	R.GDPSAWSYGAEAHSR.A
						1666.8167	1665.8297	37	R.TNPAVIPIECHYPR.R

280	PREDICTED: collagen alpha-2(VI) chain isoform X1 [Meleagris gallopavo] XP_003207399.1	COL6A2	15	354	110229/5.55	1793.8546	1792.8996	76	K.LFAVAPSEDVYEQGLR.E
						1297.6274	1296.6462	35	R.EIASPPHDLYR.S
						1425.6639	1424.6895	60	K.DALHIDENTIER.I
						1033.5370	1032.5716	32	K.NFVVNVVSR.L
						1000.4638	999.4886	36	R.IGEQNFHR.A
						1847.7881	1846.8373	58	R.EKDYESLSQPSFFDR.F
281	PREDICTED: collagen alpha-2(VI) chain-like [Meleagris gallopavo] gi|326922323|ref|XP_003207399.1|	COL6A2	9	424	110229/5.55	1793.8700	1792.8996	50	K.LFAVAPSEDVYEQGLR.E
						1297.6545	1296.6462	61	R.EIASPPHDLYR.S
						1170.4908	1169.4811	71	K.HEAYAECYK.M
						1763.8688	1762.8890	67	R.VGVVQYSHEGTFEAIK.L
						1847.8290	1846.8373	63	R.EKDYESLSQPSFFDR.F
282	PREDICTED: collagen alpha-1(VI) chain [Meleagris gallopavo] XP_010711460.1	COL6A1	16	321	109009/5.63	1702.8954	1701.8475	67	K.WIAGGTHTGEALQFSK.E
						1448.7774	1447.7307	39	R.FLEASKPAEDSVR.V
						1563.8560	1562.8053	36	K.VLVFSDGNSQGITAR.A
						1286.6707	1285.5939	45	K.TANYDVVYGER.H
283	PREDICTED: collagen alpha-1(VI) chain [Meleagris gallopavo] XP_010711460.1	COL6A1	16	164	109009/5.63	1448.8213	1447.7307	48	R.FLEASKPAEDSVR.V
						1563.9032	1562.8053	40	K.VLVFSDGNSQGITAR.A
284	PREDICTED: collagen alpha-1(VI) chain [Meleagris gallopavo] XP_010711460.1	COL6A1	15	403	109009/5.63	1605.9093	1604.8423	49	K.VFSVAISPHHLDQR.L
						1702.9021	1701.8475	65	K.WIAGGTHTGEALQFSK.E
						1448.8018	1447.7307	52	R.FLEASKPAEDSVR.V
						1563.8728	1562.8053	31	K.VLVFSDGNSQGITAR.A
						1286.6825	1285.5939	54	K.TANYDVVYGER.H
						1056.5978	1055.5400	31	R.GVFYQTVSR.K
285	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	30	746	48706/5.58	1590.7098	1589.6859	126	R.GDPSAWSYGAEAHSR.A
						2456.2775	2455.2754	57	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1870.0179	1868.9996	98	R.TLINYDPSPASNPVIIR.T
						1666.8587	1665.8297	101	R.TNPAVIPIECHYPR.R
						1366.6764	1365.6525	67	K.VTPADQGPDPQNK.A
						1144.5960	1143.5673	77	R.NTWVPVEGSR.D

286	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	30	891	48706/5.58	1590.7150	1589.6859	126	R.GDPSAWSYGAEAHSR.A
						2456.3046	2455.2754	126	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1870.0343	1868.9996	158	R.TLINYDPSPASNPVIIR.T
						1666.8638	1665.8297	99	R.TNPAVIPIECHYPR.R
						1366.6774	1365.6525	67	K.VTPADQGPDPQNK.A
						1144.5973	1143.5673	86	R.NTWVPVEGSR.D
287	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	30	788	48706/5.58	1590.6416	1589.6859	119	R.GDPSAWSYGAEAHSR.A
						2456.1809	2455.2754	131	R.AVAGSHPVAVQCQEAQLVVTVHR.D
						1869.9426	1868.9996	125	R.TLINYDPSPASNPVIIR.T
						1666.7863	1665.8297	97	R.TNPAVIPIECHYPR.R
						1144.5355	1143.5673	91	R.NTWVPVEGSR.D
288	PREDICTED: cytochrome c oxidase subunit 5A, mitochondrial-like [Meleagris gallopavo]	COX5A	18	98	15982/5.21	1148.6516	1147.6098	34	R.RLNDFASAVR.I
						992.5543	991.5087	41	R.LNDFASAVR.I
289	PREDICTED: lactoylglutathione lyase [Meleagris gallopavo] XP_010705220.1	TPI1	39	287	20610/5.82	1298.7171	1297.6489	34	K.DFIFQQTMLR.V
						1314.7125	1313.6438	39	K.DFIFQQTMLR.V + Oxidation (M)
						1986.0230	1984.9490	84	R.KATLELTHNWGTENDEK.O
290	PREDICTED: calponin-3-like [Meleagris gallopavo] gi|326925093|ref|XP_003208756.1|	CNN3	52	292	34871/ 5.76	781.4047	780.3654	39	R.DIYDQK.H
						939.5244	938.4644	32	K.GMSVYGLGR.Q
						1560.6784	1559.6165	106	R.DYHGQYSDQGIDY.-
291	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	23	202	48706/5.58	1590.6510	1589.6859	85	R.GDPSAWSYGAEAHSR.A
						1869.9534	1868.9996	39	R.TLINYDPSPASNPVIIR.T
						1666.7733	1665.8297	48	R.TNPAVIPIECHYPR.R
292	PREDICTED: proteasome subunit alpha type-1 [Coturnix japonica] XP_015719573.1	PSMA1	22	190	29592/6.08	1778.8104	1777.8020	67	R.NQYDNDVTVWSPQGR.I
						2104.9652	2103.9782	66	R.KPALPADEPAEKAEEPMEH.- + Oxidation
293	mitochondrial translation elongation factor Tu [Gallus gallus] ARS01456.1	TUFM	21	227	47363/6.79	1838.1012	1836.9344	55	R.DRPHVNVGTIGHVDHGK.T
						1185.7235	1184.6149	45	R.AEAGDNVGALLR.G
						1172.6633	1171.5656	74	R.QPMVVEEGQR.F

294	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	28	500	48706/5.58	1590.6679 1869.9707 1666.8082 2111.7707	1589.6859 1868.9996 1665.8297 2110.8177	136 114 85 106	R.GDPSAWSYGAEAHSR.A R.TLINYDPSPASNPVIIR.T R.TNPAVIPIECHYPR.R R.DVCSCCETGNCEPPALSR.R
295	PREDICTED: alcohol dehydrogenase [NADP(+)] [Meleagris gallopavo] XP_003208849.1	AKR1A1	24	223	40306/8.77	1299.6627 1497.6682 1529.6619	1298.6367 1496.6460 1528.6371	34 50 42	K.HHPEDVEPALR.K R.YDYTDYKDTWK.A R.DAGHPHYPFNDPY.-
296	PREDICTED: non-POU domain-containing octamer-binding protein isoform X2 [Meleagris gallopavo] XP_010713300.1	NONO	29	153	53144/9.00	1248.5884 1229.5775	1247.6081 1228.5949	33 33	R.FACHSASLTVR.N R.GNPGGEFGPNKR.R
297	PREDICTED: polypyrimidine tract-binding protein 1-like [Meleagris gallopavo] gi|326934420|ref|XP_003213288.1|	PTBP1	11	212	56850/9.35	1461.7589 1897.8863 978.5568	1460.7412 1896.8822 977.5407	85 33 46	R.SQPIYIQFSNHK.E K.LSLDGQNIYNACCTLR.I K.HQTVQLPR.E
298	polypyrimidine tract-binding protein 1 isoform X3 [Columba livia] XP_021152653.1	PTBP1	10	239	64204/9.30	1461.7785 1897.9275 978.5790	1460.7412 1896.8822 977.5407	76 64 35	R.SQPIYIQFSNHK.E K.LSLDGQNIYNACCTLR.I K.HQTVQLPR.D
299	PREDICTED: phosphatidylinositol transfer protein alpha isoform [Meleagris gallopavo] XP_010720029.1	PITPNA	56	313	31443/5.80	2047.9452 1200.5353 1391.7309 934.4965	2046.9494 1199.5182 1390.7092 933.4821	90 34 44 30	K.NETGGGEGVEVLVNEPYER.D K.AWNAYPYCR.T K.NVEAIYIDIADR.S R.LFTNFHR.Q
300	PREDICTED: zona pellucida sperm-binding protein 3 [Meleagris gallopavo] XP_010715515.1	ZP3	10	188	48706/5.58	1590.6859 1666.8900	1589.6859 1665.8297	99 48	R.GDPSAWSYGAEAHSR.A R.TNPAVIPIECHYPR.R

301	PREDICTED: electron transfer flavoprotein subunit alpha, mitochondrial-like [Meleagris gallopavo]	ETFA	48	404	36666/6.25	820.4006 2040.9357 1750.9091	819.4239 2039.9656 1749.9301	35 115 91	K.SPNTFVR.T R.TIYAGNVLCTVQCDEAVK.V K.VTPPAPVGLSEWIEQK.L
302	stathmin [Gallus gallus] NP_001001858.1	STMN1	18	241	17072/6.18	1358.8133 1497.8453 1282.7173	1357.7354 1496.7875 1281.6605	76 73 67	R.ASGQAFELILGPR.S R.SKEAAPEFPLSPPK.K K.EAAPEFPLSPPK.K
303	PREDICTED: translocon-associated protein subunit delta [Gallus gallus] XP_015129111.1	SSR4	20	337	18551/5.67	1304.7254 1363.7042 1491.8080 1439.9011	1303.6309 1362.6092 1490.7041 1438.8045	64 85 79 65	R.YQVSWSLEHR.S K.FFDEESYSALR.K K.FFDEESYSALRK.A R.IRPLFTVSVDHR.G
304	PREDICTED: epididymal secretory protein E1, partial [Meleagris gallopavo] XP_010710061.1		21	246	16360/7.11	1557.8099 1030.5988 1068.5664	1556.7253 1029.5277 1067.5036	122 30 74	K.DGSIQEVNVSPCPR.Q K.SGIQCPIQK.G K.GHSYSYLNK.L
305	PREDICTED: hypothetical protein LOC100549033 [Meleagris gallopavo] gi|326934995|ref|XP_003213567.1|		23	129	15326/6.14	1660.8240 1676.8150 1785.9510	1659.7709 1675.7658 1784.8846	59 41 87	K.QQSVLGPEMEQMQR.S K.QQSVLGPEMEQMQR.S K.GGEGIAAPIGPSSYPWAR.N
306	PREDICTED: actin-related protein 2/3 complex subunit 5, partial [Meleagris gallopavo] XP_003208573.2	ARPC5	26	138	12973/9.81	2131.1362	2130.0018	116	K.GFESPSDNSSAVLLQWHEK.A
307	PREDICTED: LOW QUALITY PROTEIN: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] gi|326919872|ref|XP_003206201.1|	ZP1	19	618	96950/ 8.00	2190.9666 1803.6671 1419.7257 2523.3231 1073.5899 1358.7808	2189.9663 1802.6658 1418.7154 2522.3129 1072.5665 1357.7718	80 75 89 81 70 47	R.YHYDCGDFGMQLLAFPTR.G R.DACLQAGCCFDDTDR.A R.GLSAQPYNLDSVR.L R.LVYENQLISTIDVQPGPHGSVTR.D R.DSVYILHAR.C K.VLRDPIYVEVR.L

308	PREDICTED: LOW QUALITY PROTEIN: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] gi|326919872|ref|XP_00320620	ZP1	19	519	96950/ 8.00	1803.6644	1802.6658	84	R.DACLQAGCCFDDTDR.A
						1419.7218	1418.7154	97	R.GLSAQPYNLDSVR.L
						2523.3372	2522.3129	69	R.LVYENQLISTIDVQPGPHGSVTR.D
						1073.5806	1072.5665	44	R.DSVYILHAR.C
						1358.7777	1357.7718	35	K.VLRDPIYVEVR.L
309	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo]	ZP1	8	141	98702/7.62	1803.7341	1802.6658	68	R.DACLQAGCCFDDTDR.A
						1419.7754	1418.7154	61	R.GLSAQPYNLDSVR.L
310	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	8	317	98702/7.62	1803.8056	1802.6658	55	R.DACLQAGCCFDDTDR.A
						1419.8356	1418.7154	61	R.GLSAQPYNLDSVR.L
						1073.6648	1072.5665	40	R.DSVYILHAR.C
						2301.1904	2300.0485	92	R.IATDESYSSYHPDTDYPLVK.V
311	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	7	256	98702/7.62	1803.7678	1802.6658	34	R.DACLQAGCCFDDTDR.A
						1419.7968	1418.7154	59	R.GLSAQPYNLDSVR.L
						1073.6354	1072.5665	30	R.DSVYILHAR.C
						2301.1534	2300.0485	98	R.IATDESYSSYHPDTDYPLVK.V
312	PREDICTED: plastin-3-like [Meleagris gallopavo] gi|326924289|ref|XP_003208362.1|	PLS3	19	218	71267/5.51	2785.3732	2784.2032	79	K.EGICAIGGTSELSSEGTQHSYSEEEK.Y
						1458.8700	1457.7515	53	R.QFVTPADVVSGNPK.L
	Plastin-3, partial [Chelonia mydas] EMP39187.1	PLS3	18	191	68813/5.35	2785.3732	2784.2032	79	K.EGICAIGGTSELSSEGTQHSYSEEEK.Y
						1458.8700	1457.7515	53	R.QFVTPADVVSGNPK.L
313	PREDICTED: transketolase [Meleagris gallopavo] XP_010716778.1	TKT	23	206	64056/7.25	1446.7977	1445.7991	41	R.KIDSVLEGHPVPR.Q
						2060.0227	2059.0487	71	R.LGQSDPAPLQHHVEIYQK.R
						2543.1868	2542.2200	31	R.TSRPENPVIYNNNEDFHIGQAK.V
314	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	7	145	98702/7.62	1419.7957	1418.7154	58	R.GLSAQPYNLDSVR.L
						1073.6389	1072.5665	31	R.DSVYILHAR.C
						1358.8457	1357.7718	42	K.VLRDPIYVEVR.L
315	PREDICTED: zona pellucida sperm-binding protein 1 [Meleagris gallopavo] XP_003206201.2	ZP1	7	204	98702/7.62	1419.8206	1418.7154	58	R.GLSAQPYNLDSVR.L
						2301.1835	2300.0485	60	R.IATDESYSSYHPDTDYPLVK.V
316	PREDICTED: calcium-binding protein p22-like [Meleagris gallopavo]		56	151	21800/ 4.90	1885.9705	1884.9006	59	R.IINAFFSEGEDQVNFR.G
						790.4439	789.4286	32	K.LHFAFR.L

	gi|326920476|ref|XP_003206498.1|								
317	PREDICTED: phosphatidylethanolamine-binding protein 1-like, partial [Meleagris gallopavo] gi|326929994|ref|XP_003211138.1|	PEBP1	31	178	20406/9.44	1560.8224 1324.6955 1414.7185	1559.8195 1323.6863 1413.7034	35 46 46	K.LYTLVLTDPDAPSR.K R.YVWLVYEQPK.Q K.QLACNEPILSNR.S
318	PREDICTED: thioredoxin [Calidris pugnax] XP_014811930.1	TXN	20	170	12000/5.12	1395.7329 1221.5580	1394.6929 1220.5358	110 41	K.SVGSLSEFEAELK.S K.CMPTFQFYK.S
319	PREDICTED: enhancer of rudimentary homolog [Meleagris gallopavo] gi|326920608|ref|XP_003206561.1|	ERH	41	290	12896/5.63	2054.8910 1105.6255 1328.6927	2053.8067 1104.5386 1327.6044	144 44 60	R.TYADYESVNECMEGVCK.M K.MYEEHLKR.M R.ADTQTYQPYNK.D
320	PREDICTED: glutaredoxin-related protein 5, mitochondrial-like [Meleagris gallopavo] gi|326921012|ref|XP_003206758.1|	GLRX5	20	161	10413/5.21	988.5679 1278.7351	987.4774 1277.6364	57 91	R.LHGVEDYR.A R.AHDVLQDPDLR.Q
321	ATP synthase subunit e, mitochondrial [Gallus gallus] NP_001091003.1	ATP5ME	18	147	8334/7.93	1525.8044 1681.8997	1524.7460 1680.8471	86 46	R.YDYLKPIAEEER.R R.YDYLKPIAEEERR.I
322	PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP1A-like [Meleagris gallopavo] gi|326932031|ref|XP_003212125.1|	FKBP1A	13	86	11872/5.66	1533.7312	1532.7042	78	R.GWEEGVAQMSVGQR.A
323	PREDICTED: pterin-4-alpha-carbinolamine dehydratase-like, partial [Meleagris gallopavo] gi|326923467|ref|XP_003207957.1|	PCBD1	38	253	11916/6.06	1695.0286 1116.6188 1239.6832 829.4431	1693.9111 1115.5360 1238.5833 828.3952	41 79 39 40	R.LNAEEREQLLPNLR.A R.AVGWNEVEGR.D K.EFHFKDFNR.A R.AFGFMTR.V

324	PREDICTED: galectin-1 [Meleagris gallopavo] XP_003202288.1	LGALS1	22	226	15211/6.58	1393.6974 1293.5911 995.5196	1392.6898 1292.5819 994.5124	103 48 32	K.DSTHLGLHFNPR.F K.KMEEWGTEQR.E R.ETVFPFQK.G
325	PREDICTED: 40S ribosomal protein S12-like [Meleagris gallopavo] gi|326915903|ref|XP_003204251.1|	RPS12	52	370	15967/8.82	1066.6346 2135.0869 1061.5892 970.5774 1585.8282	1065.5931 2133.9646 1060.5376 969.5356 1584.7671	42 44 36 33 84	K.TALIHDGLAR.G R.QAHLCVLASNCDEPMYVK.L K.LGEWVGLCK.I K.IDREGKPR.K K.ESQAKDVIEEYFK.C
326	PREDICTED: ATPase inhibitor, mitochondrial [Picoides pubescens] XP_009909816.1	ATP5IF1	30	244	8772/9.46	1438.8282 1966.1161	1437.6385 1964.9089	84 132	K.HHEEEIDHHQK.E K.HHEEEIDHHQKEIER.L
327	glutathione S-transferase alpha class A2 [Meleagris gallopavo] gi|356640670|gb|AET31409.1|	GSTA2	27	293	25540/8.45	945.4869 1557.8365 932.5192	944.4644 1556.7947 931.4876	39 109 31	R.YFPVYEK.A K.ALKDHGQDYLVGNK.L K.FLQPGSQR.K
328	PREDICTED: glutathione S-transferase alpha class A1.3 isoform X2 [Meleagris gallopavo] XP_010706101.1		32	235	25379/8.76	1238.5459 979.5285	1237.5840 978.5538	67 46	K.DHGHDFLVGNK.L K.FPLLQSFK.A
329	PREDICTED: superoxide dismutase [Mn], mitochondrial-like [Meleagris gallopavo] gi|326915675|ref|XP_003204139.1|	SOD2	17	183	26336/8.58	1032.5219 1687.9135	1031.4713 1686.8478	50 86	R.DFGSFANFK.E K.AIWNVINWENVSSR.Y
330	glutathione S-transferase alpha class A1.2 [Meleagris gallopavo] gi|290874551|gb|ADD65348.1|	GSTA4	28	105	25269/8.75	1490.7860 979.6023	1489.7565 978.5538	45 42	R.WLLAAAGVEFEER.I K.FPLLQSFK.A
331	glutathione S-transferase alpha class A4 [Meleagris gallopavo] gi|356640658|gb|AET31403.1|	GSTA4	11	109	26343/9.05	1257.5656	1256.5898	95	K.DHGQDFLVGNR.L
332	PREDICTED: proteasome activator complex subunit 3-like [Meleagris gallopavo] gi|326934185|ref|XP_003213174.1|	PSME3	48	272	28383/ 5.84	1155.6943 1668.8178 1078.5098	1154.6634 1667.8002 1077.4879	32 39 53	K.MWVQLLIPR.I R.TVESEAASYLDQISR.Y K.YPHVEDYR.R

333	PREDICTED: 3-mercaptopyruvate sulfurtransferase isoform X2 [Meleagris gallopavo] XP_010709815.1	MPST	27	224	33453/5.66	1876.9032 2489.2345 1590.7543	1875.8574 2488.1983 1589.7321	45 44 48	R.HIPGAVFFDIDQCSDR.T K.LGVGNDSHVVVYDGSDQGLFSAPR.V K.TYEDILDNLDSHR.F
334	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial-like, partial [Meleagris gallopavo] gi|326923625|ref|XP_003208035.1|	NDUFB8	50	152	16408/5.67	2680.1913 1618.7110	2679.1475 1617.7212	38 68	R.VEDYQPYPDDGFGYGDYPMLPNK.S R.DPWYQWDQPDLR.R
335	PREDICTED: retinol-binding protein 4-like [Meleagris gallopavo] gi|326923741|ref|XP_003208093.1|	RBP4	25	118	22856/6.30	1198.6618 2702.1578	1197.6182 2701.1140	45 51	K.YWGVASFLQK.G K.GNDDHWVVDTDYDTYALHYSCR.E
336	PREDICTED: enoyl-CoA hydratase, mitochondrial [Meleagris gallopavo] XP_003207855.3	ECHS1	52	519	30017/8.55	1893.8731 2111.1736 1336.7083 1352.6991 1447.7738	1892.8152 2110.1171 1335.6526 1351.6476 1446.7143	103 143 60 44 75	K.TFQECYSGGFLAGWDR.V K.AQFGQPEILLGTIPGAGGTQR.L K.SLAMEMVLTGER.I K.SLAMEMVLTGER.I + Oxidation (M) R.LFYATFATDDRK.E
337	PREDICTED: eukaryotic translation initiation factor 4E-like [Meleagris gallopavo] gi|326919063|ref|XP_003205803.1|	EIF4E	33	224	26051/5.49	1887.9206 1503.7832	1886.9261 1502.7729	36 62	K.TEPAPTQEVASPEQYIK.H K.IVIGYQSHADTATK.S
338	PREDICTED: platelet-activating factor acetylhydrolase IB subunit beta [Meleagris gallopavo] XP_003212802.1	PAFAH1B2	37	294	25636/5.66	2377.9428 958.4013 1140.6099	2376.9989 957.4239 1139.6299	99 42 34	-.MSHGDSNPAAVPHAAEDTQGDDR.W R.WMSQHNR.F R.LINTQQPQAK.V
339	PREDICTED: cytochrome b-c1 complex subunit Rieske, mitochondrial [Meleagris gallopavo] XP_003209829.2	UQCRFS1	20	214	27012/6.38	816.4752 1660.7676 1264.6213	815.5018 1659.7951 1263.6320	44 60 46	R.GKPLFVR.H R.TQAEINQEAEVDVSK.L K.LRDPQHDLDR.V
340	PREDICTED: thioredoxin-dependent peroxide reductase,	PRDX3	36	208	25810/7.60	1220.6849 3443.6948	1219.6673 3442.6140	56 94	K.HLSINDLPVGR.S K.AFQYVETHGEVCPANWTPDSPTIKPSPEASK.E

	mitochondrial, partial [Meleagris gallopavo] XP_010713240.1								
341	PREDICTED: proteasome subunit beta type-2 [Meleagris gallopavo] XP_010721633.2	PSMB2	24	203	33249/9.65	1281.6970 1952.0243	1280.6877 1951.0415	77 58	R.FVLNLTSFNAR.F R.FIDKDGIHEVDNVPLLK.A
342	10 kDa heat shock protein, mitochondrial [Gallus gallus] NP_990398.1	HSPE1	56	305	11133/8.68	1035.6277 1327.8027 1076.6287 1573.8694	1034.5913 1326.7620 1075.5914 1572.8188	39 44 56 87	R.KFLPLFDR.V K.VLQATVVAVGSGAR.G K.VLLPEYGGTK.I K.IVLEDKDYYLFR.D
343	PREDICTED: ATP synthase subunit d, mitochondrial-like [Meleagris gallopavo] gi|326931068|ref|XP_003211658.1|	ATP5F1D	67	198	14109/ 5.64	1249.6507 1726.8919	1248.6350 1725.8879	72 63	R.IAEYEQQLQK.L R.EKYPFWPHKPVADL.-
344	PREDICTED: vitellogenin-2-like [Meleagris gallopavo] XP_019473941.1	VTG2	6	162	194504/8.71	1576.9400 1605.7752	1575.8620 1604.7617	114 32	K.IVLQPVHTDANIEK.I R.GNAPDIPMQSYGSLR.Y
345	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 [Numida meleagris] XP_021230868.1	NDUFS5	56	160	12903/8.38	1979.8518 1528.6607	1978.8956 1527.6889	50 58	R.QSTTQPYGVAGACHAFER.E R.EWVECGHGLGQTR.A
346	PREDICTED: dihydropteridine reductase [Mesitornis unicolor] gi|704559850|ref|XP_010182378.1|	QDPR	21	175	25113/6.89	1631.6818 1645.7030	1630.8137 1644.8471	55 66	K.VDAILCVAGGWAGGSAK.A K.QSVWTSTISSHLATK.H
347	phosphoglycerate mutase 1 [Gallus gallus] NP_001026727.1	PGAM1	57	494	29051/7.03	1312.5937 2070.8862 2375.1154 1683.8940	1311.5956 2069.8901 2374.1304 1682.9032	93 115 48 73	R.HGESAWNLENR.F R.FCGWYDADLSPAGQQEAR.R R.SFDIPPPPMQSDHPFFSTISK.D R.ALPFWNEEIVPQIK.E
348	PREDICTED: BAG family molecular chaperone regulator 2 [Meleagris gallopavo] XP_019468781.1	BAG2	44	325	18359/5.32	1467.7582 2105.0342 1593.7956 1721.8908	1466.7477 2104.0511 1592.7868 1720.8818	66 36 70 70	R.NAQQQESLLHATK.M R.LLSLYGACTSDVPAGPIDQK.F K.FQSVVIGCAIEDQK.K K.FQSVVIGCAIEDQKK.I

349	calpain small subunit, partial [Gallus gallus] BAA22638.1	CAPNS1	38	243	24014/5.05	1906.9676 1236.7130	1905.9585 1235.7026	83 88	R.SGTIGVQELPGAFEAAGFR.L R.LPPELWGVLGR.R
350	PREDICTED: apolipoprotein A-I [Meleagris gallopavo] XP_010722021.1	APOA1	51	412	30593/5.58	1741.7869 1285.6193 1351.7326 1253.5727 1057.6049 1120.5786	1740.7856 1284.6172 1350.7296 1252.5724 1056.5927 1119.5747	50 35 43 74 41 33	R.SFWQHDDPQTPLDR.I K.LREDMAPYYK.E K.IRPFLDQFSTK.W K.WTEELEQYR.Q K.VVEQLSNLR.E K.MTPLVQEFR.E
351	thioredoxin domain-containing protein 17 [Numida meleagris] XP_021271377.1	TXNDC17	49	277	14474/5.46	1255.6750 1675.8387	1254.5993 1674.7494	88 95	R.GYGEFVQTAQR.Y R.SWCPDCVTAEPVVR.K
352	PREDICTED: fatty acid-binding protein, brain-like [Meleagris gallopavo] gi|326915985|ref|XP_003204292.1|	FABP7	64	281	13504/6.13	1523.5097 1251.4959	1522.6423 1250.6044	109 49	K.LGEEFDETTPDDR.N K.WDGKETNFVR.E
353	PREDICTED: hypothetical protein LOC100549033, partial [Meleagris gallopavo] gi|326934995|ref|XP_003213567.1|		30	150	15326/6.14	1660.7835 1785.9060	1659.7709 1784.8846	47 79	K.QQSVLGPEMEQMQR.S K.GGEGIAAPIGPSSYPWAR.N
354	PREDICTED: membrane-associated progesterone receptor component 1-like [Meleagris gallopavo] gi|326924618|ref|XP_003208522.1|	PGRMC1	31	166	11527/ 4.56	2553.2021 1187.5464	2552.1878 1186.5295	75 68	K.EALKDDYDDLSDLNATQQETLR.D R.DWESQFTFK.Y
355	PREDICTED: cytochrome b5 [Meleagris gallopavo] XP_003204966.1	CYB5A	63	472	15513/4.96	1205.5707 1705.8472 1497.7371 2205.9208 2038.0335	1204.5473 1704.8444 1496.7260 2204.9207 2037.0531	46 118 107 49 72	M.VGSSEAGGEAWR.G K.HNNSQSTWIIVHNR.I K.FLDEHPGGEEVLR.E R.EQAGGDATENFEDVGHSTDAR.A R.ALSETFIIGELHPDDRPK.L
356	PREDICTED: sorcin [Meleagris gallopavo] XP_010711000.2	SRI	27	182	20870/5.37	1237.5389 1504.6590	1236.5524 1503.6738	63 59	K.QHFVSFDSDR.S K.ITFDDYIACCVK.L

357	cytochrome b5 [Numida meleagris] XP_021263894.1	CYB5A	31	253	1080.6066	1079.5876 2010.0029 1505.7112	1079.5876 2008.9854 1504.6946	57 93 49	R.EAWLVIHGR.V R.FLEEHPGGEEVLLEQAGR.D K.QYYIGEIHPDDR.K
358	PREDICTED: 60S acidic ribosomal protein P2-like [Meleagris gallopavo] gi|326920193|ref|XP_003206359.1|	RPLP2	43	231	11835/4.42	1589.9076 1461.8223 1817.0459 2808.5160	1588.7944 1460.6995 1815.9214 2807.4123	31 49 34 69	K.KILDSVGIETDDER.L K.ILDSVGIETDDER.L K.ILDSVGIETDDERLNK.V K.LASMPAGGAVAVST-GGVSAAPAAGAAPAAAEEK.K
359	PREDICTED: chloride intracellular channel protein 2-like [Meleagris gallopavo] gi|326924230|ref|XP_003208334.1|	CLIC2	41	144	28476/5.39	1807.8108 1605.7930	1806.7778 1604.7722	41 36	K.AGLDGENIGNCPFCQR.L K.YKESFDVGSDIFAK.F
360	chloride intracellular channel protein 4 [Numida meleagris] XP_021231376.1	CLIC4	22	155	28675/5.44	1681.7643 1371.7017	1680.7162 1370.6538	65 33	K.AGSDGESIGNCPFSQR.L K.NSRPEANEGLER.G
361	PREDICTED: glutamate--cysteine ligase regulatory subunit, partial [Meleagris gallopavo] XP_010714156.1	GCLM	20	122	24394/5.20	1265.7083 1568.8375	1264.6776 1567.7995	30 65	K.LFIVGSNSSSVR.D K.QFDIQLLTHNDPK.G
362	Ran-specific GTPase-activating protein, partial [Nestor notabilis] KFQ44929.1	RANBP1	42	179	22752/5.19	1381.6730 1335.6511 1034.5484	1380.6296 1334.6143 1033.5192	61 39 33	K.TLEEDEEELFK.M R.FASENDLPEWK.E R.FLNAENAQK.F
363	PREDICTED: SH3 domain-binding glutamic acid-rich-like protein-like [Meleagris gallopavo] gi|326924407|ref|XP_003208419.1|	SH3BGRL	41	262	12787/5.07	1161.6553 1480.6857 1848.9555	1160.6414 1479.6670 1847.9417	38 92 87	R.RPASGNPLPPR.L R.YLGDYEAFFEAR.E R.ENNAVYAFLGLTAPPGSK.E
364	OVA, partial [Gallus gallus] AUD54558.1		20	136	43181/5.13	1687.9458 1860.0579	1686.8325 1858.9425	53 37	R.GGLEPINFQTAADQAR.E R.ELINSWVESQTDGIIR.N

365	PREDICTED: hypothetical protein LOC100549033, partial [Meleagris gallopavo] gi|326934995|ref|XP_003213567.1|		47	232	15326/6.14	1660.7397 1785.8595	1659.7709 1784.8846	68 126	K.QQSVLGPEMEQMQR.S K.GGEGIAAPIGPSSYPWAR.N
366	PREDICTED: hypothetical protein LOC100549033, partial [Meleagris gallopavo] gi|326934995|ref|XP_003213567.1|		37	294	15326/ 6.14	1692.7969 970.5961 2913.4852 1785.9228	1691.7607 969.5495 2912.4304 1784.8846	38 43 100 80	K.QQSVLGPEMEQMQR.S 2 Oxidation (M) R.SNPLLGLEK.R R.QLEEVAQSDKGGEGIAAPIGPSSY-PWAR.N K.GGEGIAAPIGPSSYPWAR.N
367	PREDICTED: apolipoprotein B-100 [Meleagris gallopavo] XP_010706280.1	APOB	6	185	525494/8.32	1519.6970 1416.6382	1518.6779 1415.6317	77 39	K.ALFDYFGYSHDGK.Q K.EYSASANYDLQR.E
368	PREDICTED: apolipoprotein B-100 [Meleagris gallopavo] XP_010706280.1	APOB	8	309	525494/8.32	1519.6430 1416.6014	1518.6779 1415.6317	78 69	K.ALFDYFGYSHDGK.Q K.EYSASANYDLQR.E
369	PREDICTED: apolipoprotein B-100 [Meleagris gallopavo] XP_010706280.1	APOB	3	144	525494/8.32	1519.7238 1416.6754	1518.6779 1415.6317	55 31	K.ALFDYFGYSHDGK.Q K.EYSASANYDLQR.E
370	PREDICTED: heterogeneous nuclear ribonucleoprotein K isoform X3 [Gallus gallus] XP_004949259.1	HNRNPK	45	504	47467/5.64	1579.6742 1780.7662 1533.7567 1098.4290 1340.7714 1194.6739 1259.5516	1578.6984 1779.7911 1532.7875 1097.4448 1339.7962 1193.6921 1258.5677	46 81 70 42 52 71 34	K.RPAEDMEEEQAFK.R R.TDYNASVSVPDSSGPER.I K.IIPTLEEYQHYK.G K.GSDFDCELR.L K.IILDLISESPIK.G R.NLPLPPPPPPR.G K.IDEPLEGSEDR.I
371	PREDICTED: bleomycin hydrolase [Meleagris gallopavo] XP_003211808.1	bleomycin hydrolase	31	212	53449/5/64	1417.7794 1091.4875	1416.7613 1090.4679	44 58	K.TLYNNQPIDVLK.K R.VENSWGEDR.G
372	PREDICTED: rho GDP-dissociation inhibitor 1-like [Meleagris gallopavo] gi|326930769|ref|XP_003211514.1|	ARHGDIA	34	378	23305/5.04	1917.9837 964.5172 1615.8190	1916.9327 963.4926 1614.7712	114 53 93	K.SIQEIQELDKDDESLR.K K.YIQHTFR.K K.IDKTEYMVGSYGPR.A

373	probable global transcription activator SNF2L2 isoform X7 [Strigops habroptila] XP_030327249.1	SMARCA2	17	286	36925/6.36	1762.7771 1416.7977 1324.6945	1761.7727 1415.7773 1323.6710	77 105 83	K.AIEDGNLEEMEEEVR.L R.QLSEVFIQLPSR.K K.ELPEYYELIR.K
374	PREDICTED: proteasome subunit alpha type-3-like [Meleagris gallopavo] gi|326921206|ref|XP_003206853.1|	PSMA3	39	187	31756/ 5.10	1095.5953 1380.7945	1094.5356 1379.7343	35 74	K.LYEEGSNKR.L R.HVGMAVAGLLADAR.S
375	RecName: Full=Cathepsin B; AltName: Full=Cathepsin B1; Contains: RecName: Full=Cathepsin B light chain; Contains: RecName: Full=Cathepsin B heavy chain; Flags: Precursor P43233.1		23	281	38475/5.74	1324.5953 1880.9661 1824.8836	1323.5554 1879.9289 1823.8472	38 70 87	R.HCEPGYSPSYK.E K.SGVYQHVSGEQVGGHAIR.I R.GEDHCGIESEIVAGVPR.M
376	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial, partial [Anas platyrhynchos] EOB01155.1	HADH	32	193	31796/6.62	1551.7304 1018.5104	1550.7616 1017.5244	99 46	K.FADKPEAGAEFIEK.T K.DTPGFIVNR.L
377	PREDICTED: 3,2-trans-enoyl-CoA isomerase, mitochondrial-like [Meleagris gallopavo] gi|326929302|ref|XP_003210806.1|		35	205	34322/8.93	1325.5806 1032.5158	1324.5836 1031.5222	66 45	K.STEHYAEFWR.A R.AVQEMWLR.L
378	PREDICTED: phosphatidylethanolamine-binding protein 1 [Meleagris gallopavo] XP_003211138.2	PEBP1	58	519	20406/9.44	1560.8364 1457.7019 1977.9661 1324.6922 1414.7159	1559.8195 1456.6922 1976.9327 1323.6863 1413.7034	69 36 181 75 68	K.LYTLVLTDPDAPSR.K R.EWHHFLVTNMK.G + Oxidation (M) K.GNDVESGTVLSDYVGSGPPK.G R.YVWLVYEQPK.Q K.QLACNEPILSNR.S
379	PREDICTED: FAS-associated death domain protein [Meleagris gallopavo] XP_003206412.1	FADD	11	128	23246/6.23	1386.8307 1300.7838	1385.7337 1299.6783	58 54	K.VVIEVICENVGR.D R.DLQEQLAQSLR.E

380	hypothetical protein ASZ78_002096 [Callipepla squamata] OXB64166.1 endoplasmic reticulum resident protein 29 [Meleagris gallopavo]	ERP29	24	278	28274/7.63	1340.7273 1247.5745 1703.8933	1339.7024 1246.5506 1702.8526	53 74 106	K.GSVPLDTITFYK.V K.FDTQYPYGEK.Q K.ILEQGEEFAANEVVR.I
381	PREDICTED: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 [Meleagris gallopavo] XP_003210738.1	NDUFB10	25	179	20748/6.22	988.4619 1311.7803 1158.5787	987.4450 1310.7558 1157.5578	30 34 55	K.SYYYHQK.F R.LVDQQIVEIVR.E R.YGDLGVHGNAR.T
382	PREDICTED: ovalbumin isoform X1 [Meleagris gallopavo] XP_010706723.1	SERPINB14	24	340	43274/5.18	1677.8007 1537.7484 1848.9033	1676.8118 1536.7572 1847.9166	104 70 94	R.GGLESINFQTAADQAR.G K.AFKDEDTQAIPFR.V K.ISQAVHAAYAEIYEAGR.E
383	PREDICTED: peptidyl-prolyl cis-trans isomerase B, partial [Fulmarus glacialis] XP_009572727.1	PPIB	53	396	18298/9.63	1378.7031 1286.5718 1587.7398	1377.7140 1285.5761 1586.7365	87 97 38	K.TVENFVALATGEK.G K.DFMIQGGDFTR.G K.SIYGDRFPDENFK.L
384	PREDICTED: ovalbumin isoform X1 [Meleagris gallopavo] XP_010706723.1	SERPINB14	23	207	43274/5.18	1677.8262 1537.7670 1848.9336	1676.8118 1536.7572 1847.9166	80 54 33	R.GGLESINFQTAADQAR.G K.AFKDEDTQAIPFR.V K.ISQAVHAAYAEIYEAGR.E