

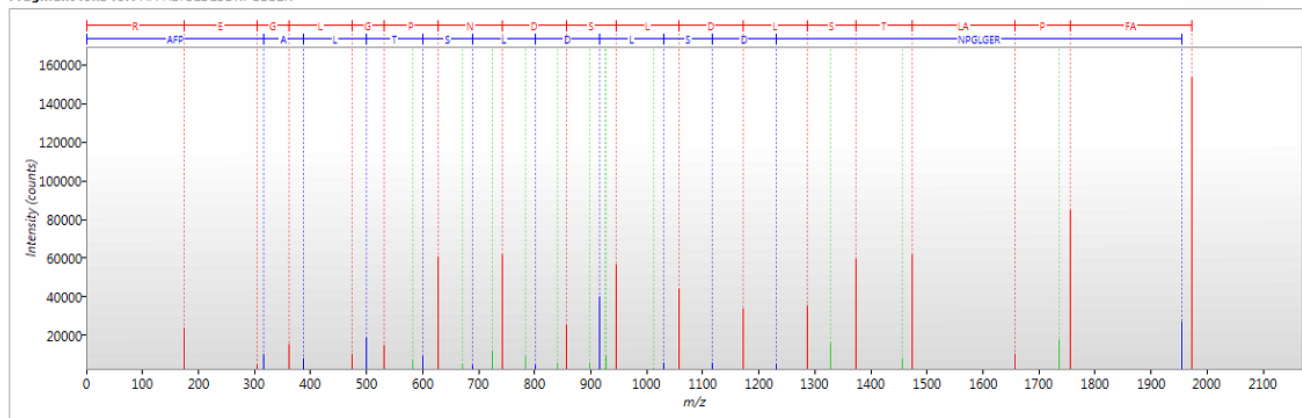
Supplementary document 2. Identification and quantification data of the 35 putative biomarkers for PCa in this study (proteins with statistically significant differential abundance in PCa in more than one group comparison (given in Table 1 and Figure 2) produced by Progenesis QI for proteomics V 3.0 (Nonlinear dynamics, Waters Corporation). The protein abundances in individual runs were normalized using the run that is least different from all other runs. Search settings included up to one missed cleavage, carbamidomethyl cysteine as a fixed modification and the methionine oxidation as variable modification. A minimum of 2 fragment ion matches were required per peptide identification and 5 fragment ion matches per protein identification with at least 2 peptide matches per protein identification. Quantification was done by Hi-N, using 3 most abundant peptides per protein. For each of the proteins, a table with the identified peptides as well as representative MS/MS spectra of peptides used to quantify protein expression levels is given. Peptide fragment annotation indicates the peaks that correspond to fragment ions from the peptide, and marks the positions of these ions within the peptide sequence. Peak colors legend: **Red** = y-series ion; **Blue** = b-series ion; **Green** = neutral loss ion.

P08571

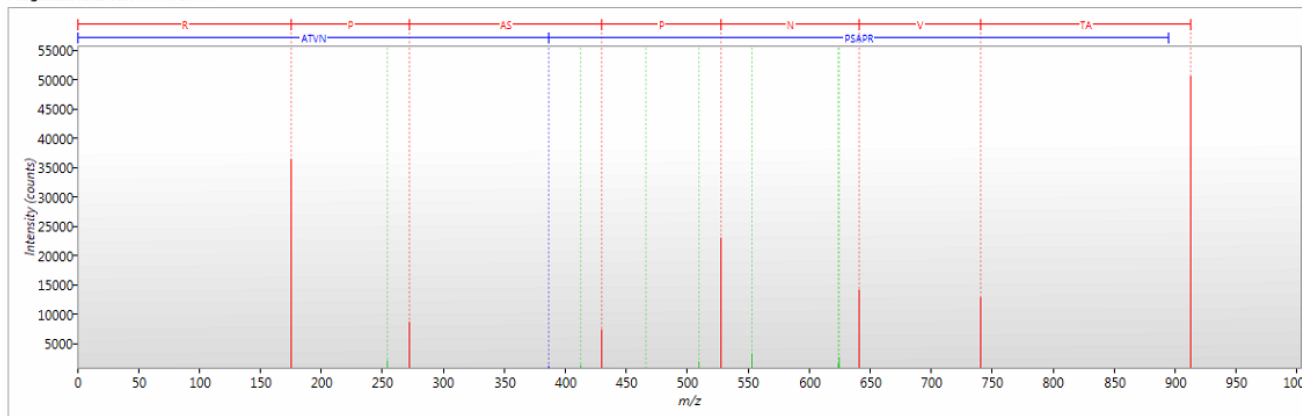
Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2
8 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Re
AFPALTSLDLSDNPGLGER	1607	9.60	22	1971.9901	2		0		yes	1.11e+006	4.58e+005	3.58e+005	6.19e+005
ATVNPSAPR	1193	8.35	17	911.4822	2		0		yes	3.90e+005	2.69e+005	1.55e+005	2.62e+005
CMVSSALNSLNSFAGLEQVPK	2586	6.97	9	2451.1047	3		1	[1] Carbamidomethyl C	no	5.59e+005	7.24e+005	2.66e+005	6.00e+005
CMVSSALNSLNSFAGLEQVPK	4104	---	---	2451.1066	2		1	[1] Carbamidomethyl C	no	1.74e+005	2.90e+004	1.37e+004	2.70e+005
LTVGAAQVPAQLLVGALR	13206	8.14	3	1776.0680	2		0		no	9041.84	1737.47	1314.00	1629.09
QYADTVK	3322	8.42	5	823.3974	2		0		no	2.60e+005	2.17e+005	2.58e+005	2.17e+005
QYADTVK	8861	8.42	5	823.3461	1		0		no	1.86e+005	1.06e+005	1.08e+005	1.67e+005
RVDADADPR	1529	8.23	19	1013.4823	2		0		no	8.47e+004	6.18e+004	3.12e+004	6.92e+004
RVDADADPR	1995	7.52	3	1013.4811	2		0		no	7.46e+004	2.67e+004	1.45e+004	2.69e+004
VLDLSNR	1266	8.82	15	975.4798	2		0	[6] Carbamidomethyl C	no	1.98e+005	1.01e+005	9.70e+004	1.22e+005
VLSIAQAHSPAFSCQVR	2033	8.50	17	1998.9711	3		0	[14] Carbamidomethyl C	yes	6.49e+005	4.78e+005	2.82e+005	4.54e+005
VLSIAQAHSPAFSCQVR	2973	8.70	2	1999.0043	3		0	[14] Carbamidomethyl C	no	2.46e+005	7.93e+004	4.71e+004	6.29e+004

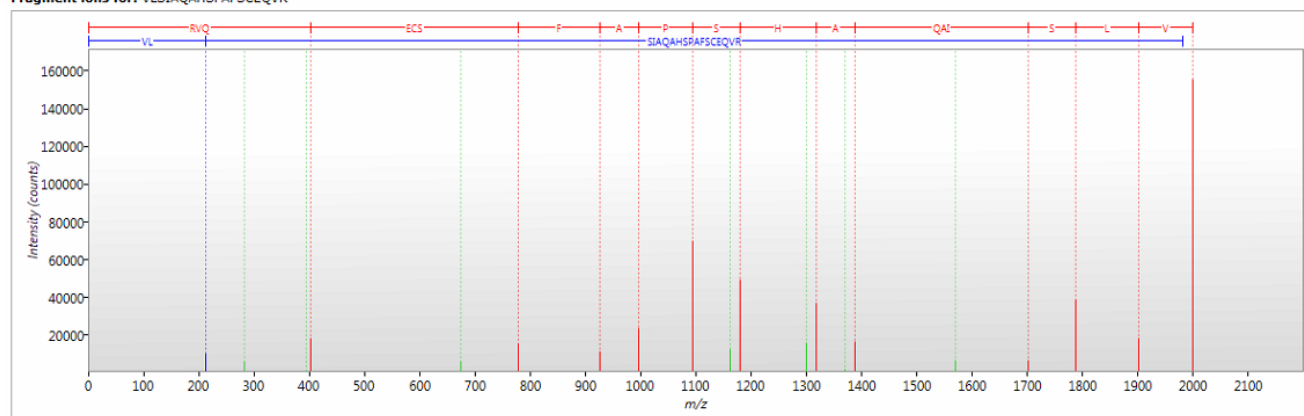
Fragment ions for: AFPALTSLDLSDNPGLGER



Fragment ions for: ATVNPSAPR



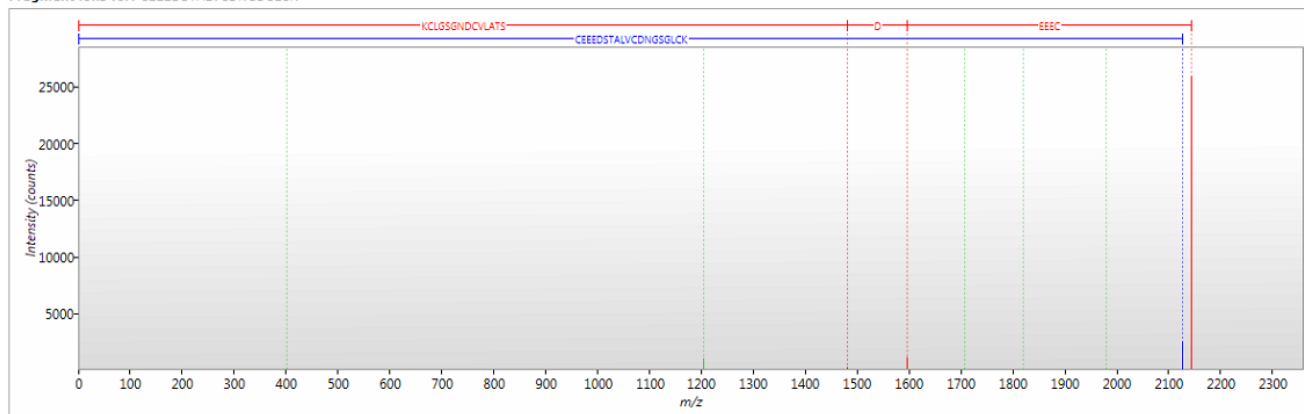
Fragment ions for: VLSIAQAHSPAFSCEQVR



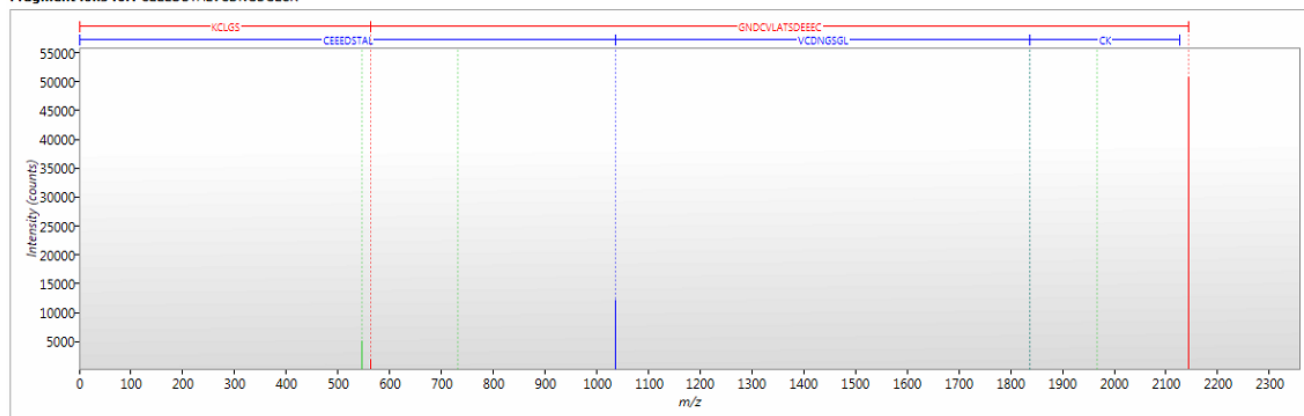
Actin_aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PcA	SPH	Bc	Rc
CEEDSTALVCDNGSGLCK	1150	5.58	2	2142.8759	3		0	[1] Carbamidomethyl C [11] Carbamidomethyl C [18] Carbamidomethyl C	yes	1.40e+005	8.33e+004	9.61e+005	7.53e+004
CEEDSTALVCDNGSGLCK	3717	6.34	2	2142.8534	2		0	[1] Carbamidomethyl C [11] Carbamidomethyl C [18] Carbamidomethyl C	yes	1.50e+005	6.25e+005	5.52e+005	3.26e+005
YPIEHGIIITNVDDMEKIVVHHSFYNELR	11856	6.28	2	3442.7453	5		0		yes	1.68e+005	4.49e+005	1.18e+006	6.37e+005
YSVIVIGGSILASLSTFQQMIIISKQYDEAGPSIVHR	35065	6.01	3	4082.8749	4		0		no	2.75e+005	3.62e+004	1548.87	5.06e+004

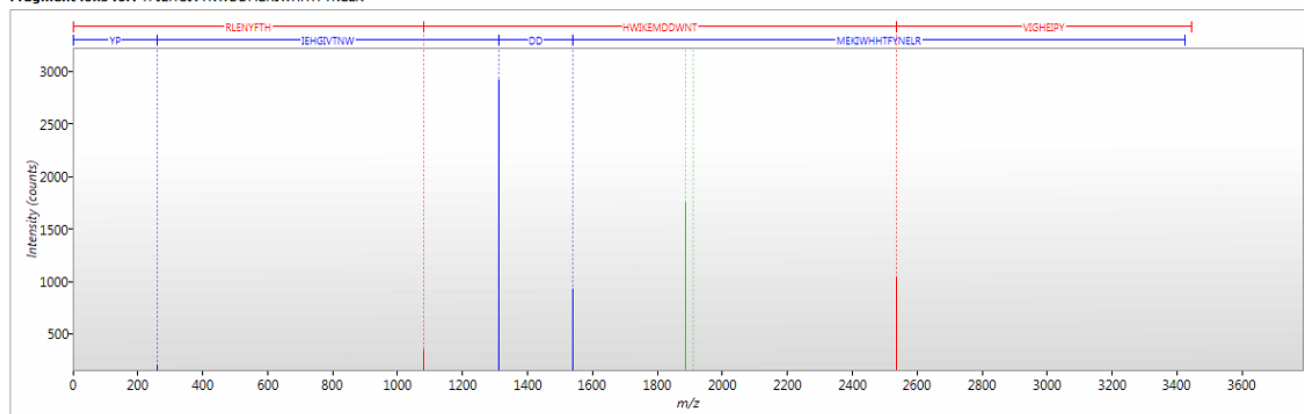
Fragment ions for: CEEEDSTALVCDNGSGLCK



Fragment ions for: CEEEDSTALVCDNGSGLCK



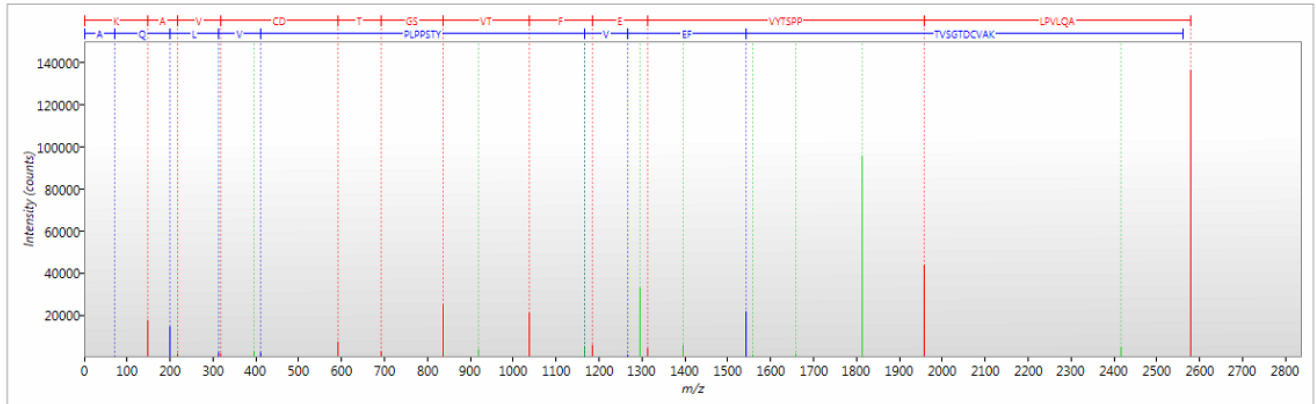
Fragment ions for: YPIEHGIVTNWDDMEKIWHHTFYNELR



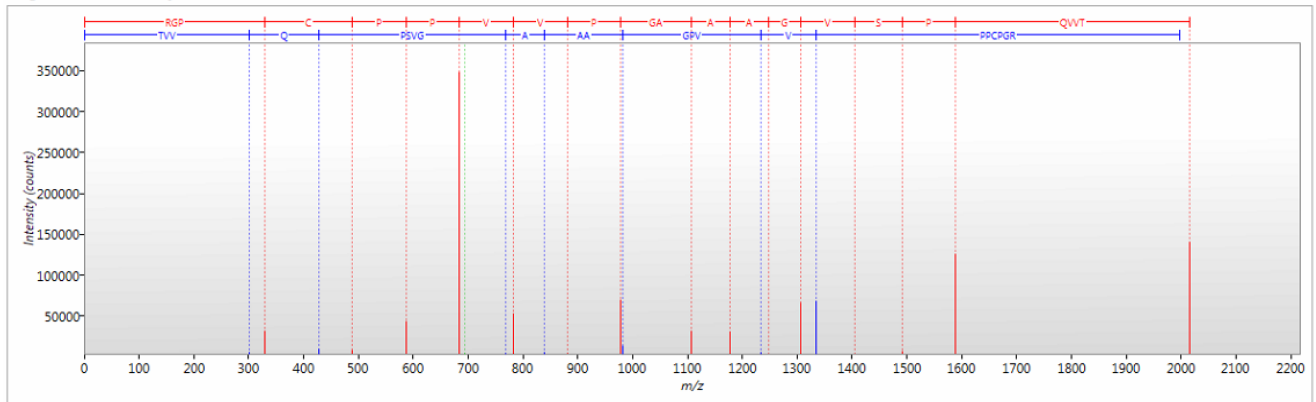
Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1
9 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
AQLVPLPPSTYVEFTVSGTDCVAK	7440	8.35	20	2578.2956	2		0	[21] Carbamidomethyl C	yes	1.03e+006	7.79e+004	9.75e+004	4.48e+005
AQLVPLPPSTYVEFTVSGTDCVAKEATEAAK	11451	7.74	6	3278.6310	3		0	[21] Carbamidomethyl C	no	1.44e+005	1.13e+004	7236.49	6.05e+004
CDSSPDSAEDEVIR	26963	7.96	2	1336.5567	3		0	[1] Carbamidomethyl C	no	1042.38	1289.09	396.14	369.53
EHAVEGDCDFQLLK	2392	6.48	2	1659.8029	3		0	[8] Carbamidomethyl C	no	1.62e+005	3.75e+005	1.74e+005	1.73e+005
EHAVEGDCDFQLLK	3226	9.08	9	1659.8030	3		0	[8] Carbamidomethyl C	no	6.87e+004	1.24e+005	1.28e+005	1.09e+005
EHAVEGDCDFQLLK	48117	7.57	2	1659.7538	1		0	[8] Carbamidomethyl C	no	13.40	0.00	1207.73	30.73
FSVYYAK	743	8.96	34	812.4408	2		0		no	3.65e+005	5.34e+005	2.97e+005	3.51e+005
FSVYYAK	1409	8.91	2	812.4034	2		0		no	3.61e+005	3.66e+005	3.38e+005	2.75e+005
HTLNQIDEVK	1367	9.49	6	1195.6177	2		0		no	1.46e+005	3.08e+004	6.92e+004	1.55e+004
QPNCDDEPETEEAALVAIDYINQNLPIVGYK	25585	10.01	16	3362.5197	2		0	[4] Carbamidomethyl C	no	1.48e+004	241.60	754.79	3927.96
QPNCDDEPETEEAALVAIDYINQNLPIVGYK	30935	9.86	2	3362.5106	2		0	[4] Carbamidomethyl C	no	1.33e+004	0.00	0.00	0.00
TVVQPSVGAAAGPVVPPCPGR	2193	9.48	35	2015.0521	3		0	[18] Carbamidomethyl C	yes	4.21e+005	2.60e+005	1.53e+005	2.91e+005
TVVQPSVGAAAGPVVPPCPGR	2286	9.48	34	2015.0407	2		0	[18] Carbamidomethyl C	yes	5.58e+005	2.10e+005	1.79e+005	4.63e+005
VCQDCPLLALNDTR	2683	6.51	2	1770.8115	2		0	[2] Carbamidomethyl C [5] Carbamidomethyl C	yes	4.45e+005	6.38e+005	4.79e+005	3.92e+005

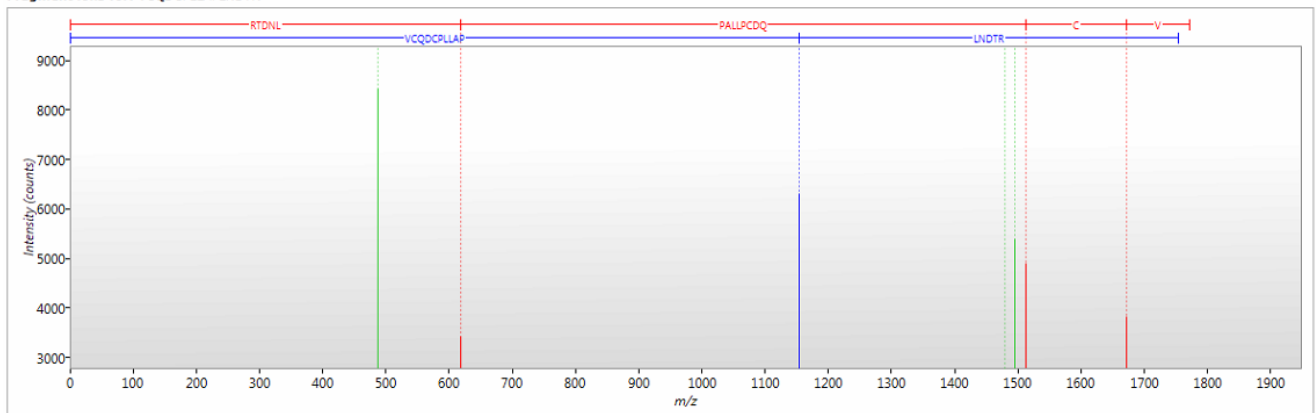
Fragment ions for: AQLVPLPPSTYVEFTVSGTDCVAK



Fragment ions for: TVVQPSVGAAAGPVVPPCPGR



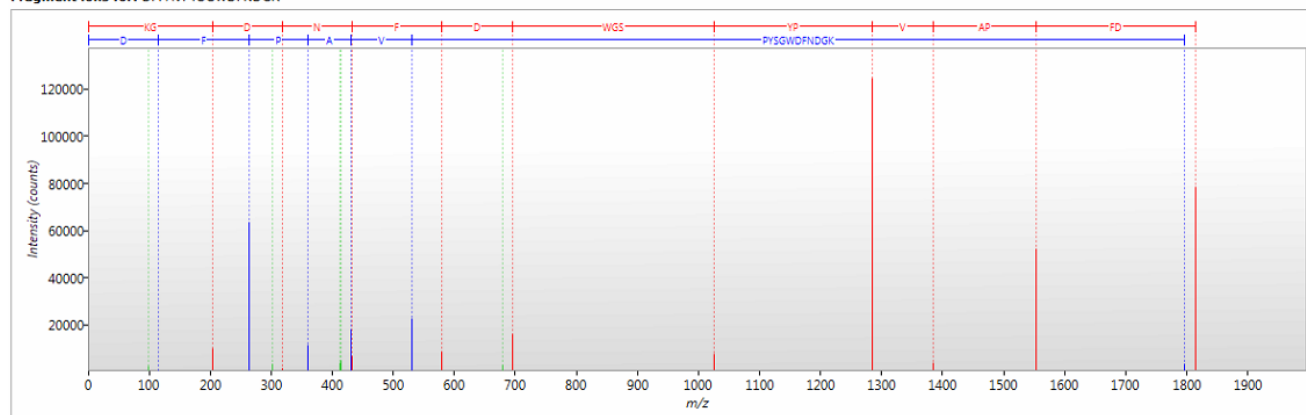
Fragment ions for: VCQDCPLLALNDTR



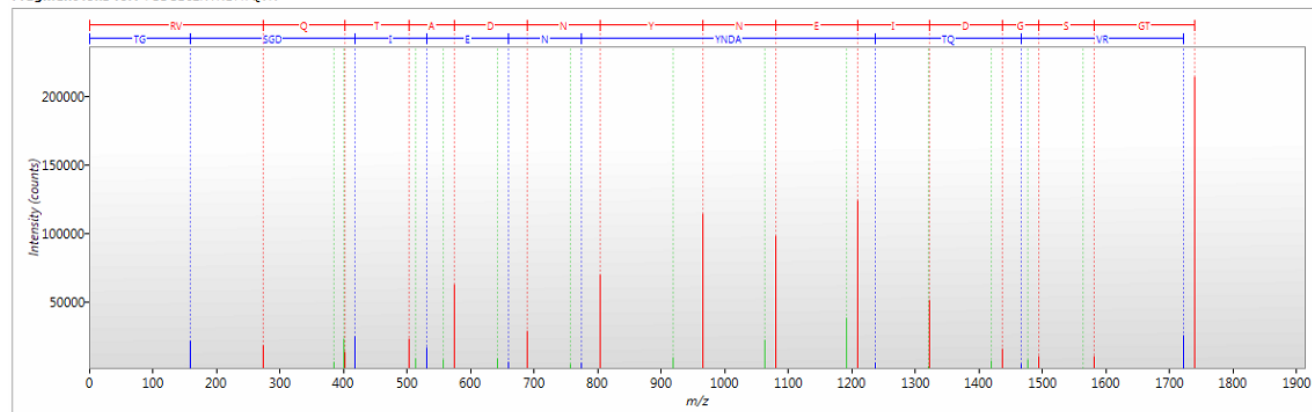
Alpha-amylase 1 O5=Homo sapiens GN=AMY1A PE=1 SV=2
9 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
ALVFV/DNHDNQR	3349	8.66	23	1426.6995	3		0		no	3.88e+004	3.08e+004	5147.43	6.14e+004
DFFAPVPSYGVDFNDGK	3244	9.05	24	1813.8456	2		1		yes	6.36e+005	3.06e+005	1.28e+005	4.56e+005
EVTINPDTT ¹⁶ CGNDVW ¹⁶ CEHR	4172	5.97	4	2302.0265	3		0	[10] Carbamidomethyl C [16] Carbamidomethyl C	no	1.52e+005	5.15e+004	2.66e+004	1.64e+005
EVTINPDTT ¹⁶ CGNDVW ¹⁶ CEHR	8041	8.53	5	2301.9755	2		0	[10] Carbamidomethyl C [16] Carbamidomethyl C	no	4.16e+004	1.41e+004	6300.43	6.08e+004
IYVSDGK	1405	9.15	24	895.4270	2		0		no	2.18e+005	1.99e+005	1.29e+005	2.29e+005
IYVSDGK	8308	9.15	23	895.4154	1		0		no	2.58e+004	1.20e+004	1.12e+004	3.31e+004
NVVDGQPFNTN ¹⁶ YDNGSNQVAFGR	4959	8.67	20	2584.1530	2		1		no	1.52e+005	1.06e+005	4.87e+004	2.84e+005
SGNEDEFR	1796	8.12	5	952.3979	2		0		no	3.83e+004	4.28e+004	2.72e+004	8.30e+004
TGSGDIENYNDATQVR	828	9.47	27	1738.7766	2		1		yes	5.69e+005	3.87e+005	1.83e+005	6.98e+005
TSIVHLFEVIR	12668	6.36	2	1286.6785	3		1		no	1082.51	2.10e+004	7.72	4.21e+004
WVDIALE ⁸ CER	1288	9.17	17	1289.6045	2		0	[8] Carbamidomethyl C	yes	4.74e+005	2.75e+005	1.74e+005	3.72e+005
WVDIALE ⁸ CER	12939	9.17	9	1289.5980	1		0	[8] Carbamidomethyl C	no	1.15e+004	368.54	298.47	7586.60

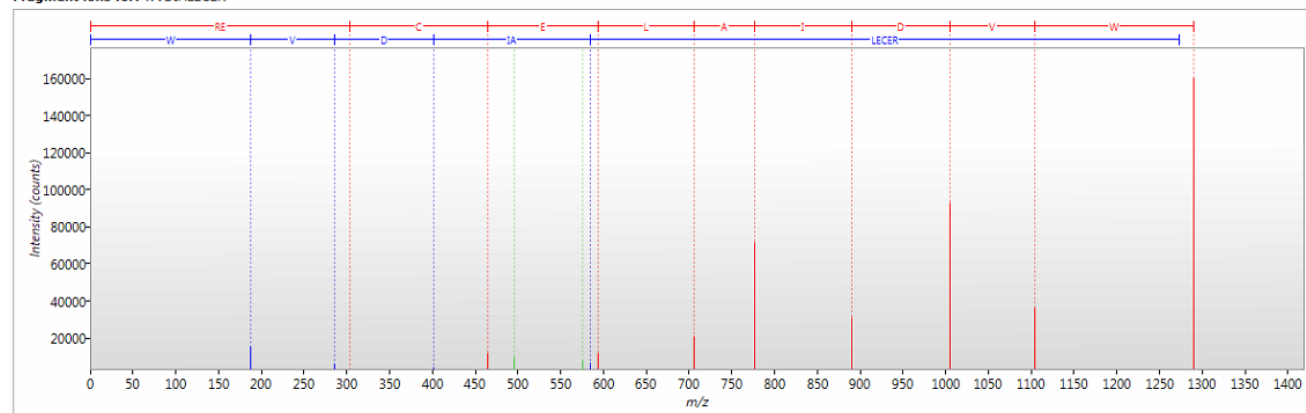
Fragment ions for: DFFAPVPSYGVDFNDGK



Fragment ions for: TGSGDIENYNDATQVR



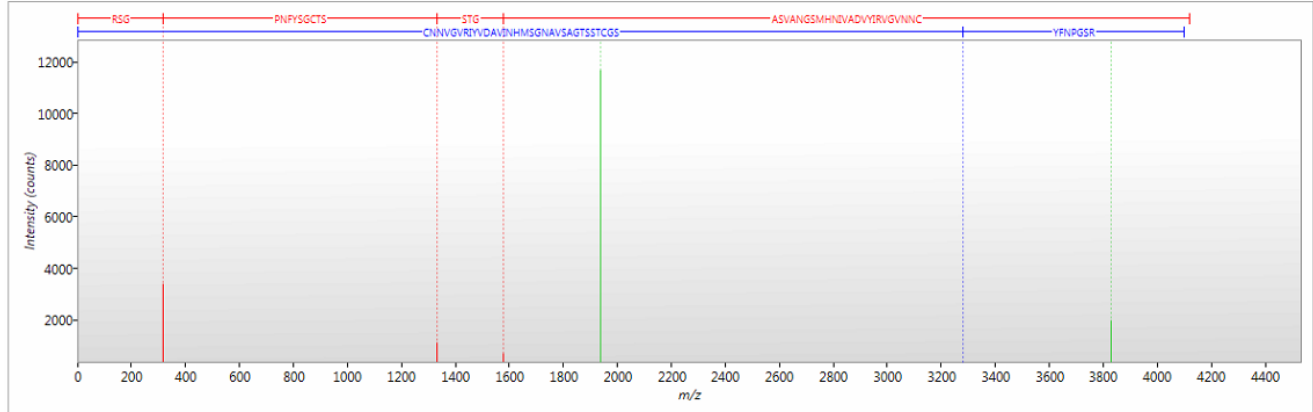
Fragment ions for: WVDIALE⁸CER



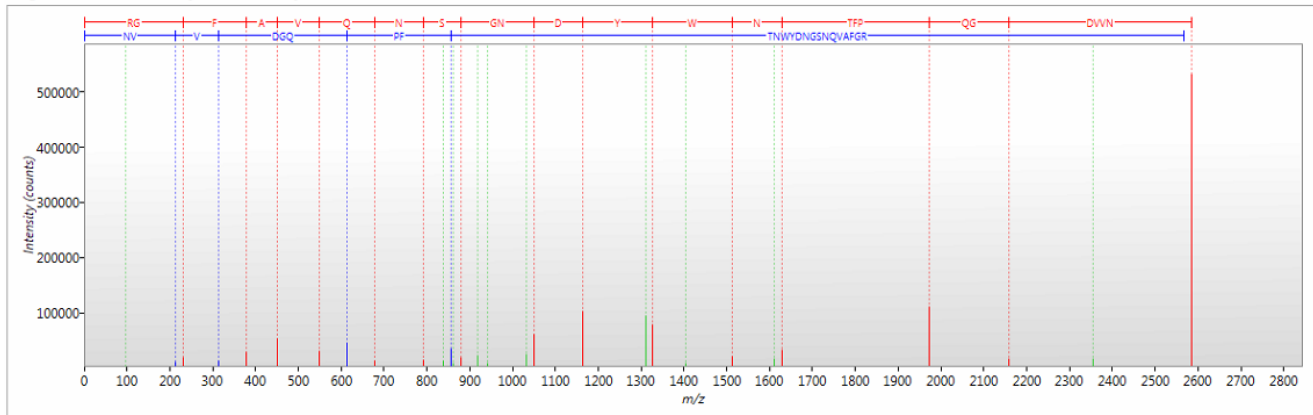
Alpha-amylase 2B OS=Homo sapiens GN=AMY2B PE=1 SV=1
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	QPH	Bc	Rc
NNVGVRIYVDVINHMSGNAVSGTSS ^{CT} SGSYFNPGR	25324	6.20	2	4117.8162	3		0	[1] Carbamidomethyl C [30] Carbamidomethyl C	yes	1.33e+004	754.84	126.46	9901.89
NVVDGQPF ^{NI} YDNGSNQVAFGR	4959	8.67	20	2584.1530	2		1		yes	1.52e+005	1.06e+005	4.87e+004	2.84e+005
TSIVHLFEV ^R	12668	6.36	2	1286.6785	3		1		yes	1082.51	2.10e+004	7.72	4.21e+004

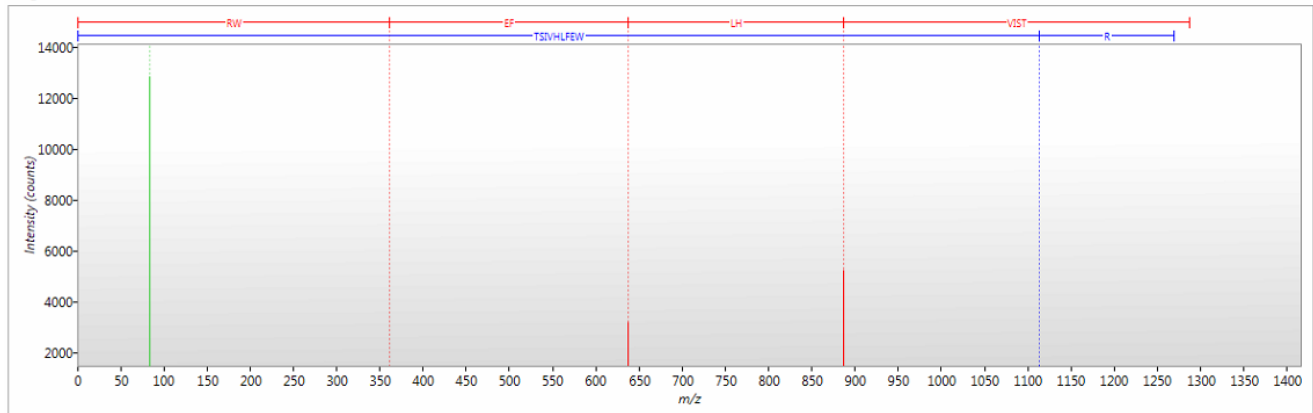
Fragment ions for: CNNVGVRIYVDVINHMSGNAVSGTSSCTSGSYFNPGR



Fragment ions for: NVVDGQPFNIYDNGSNQVAFGR



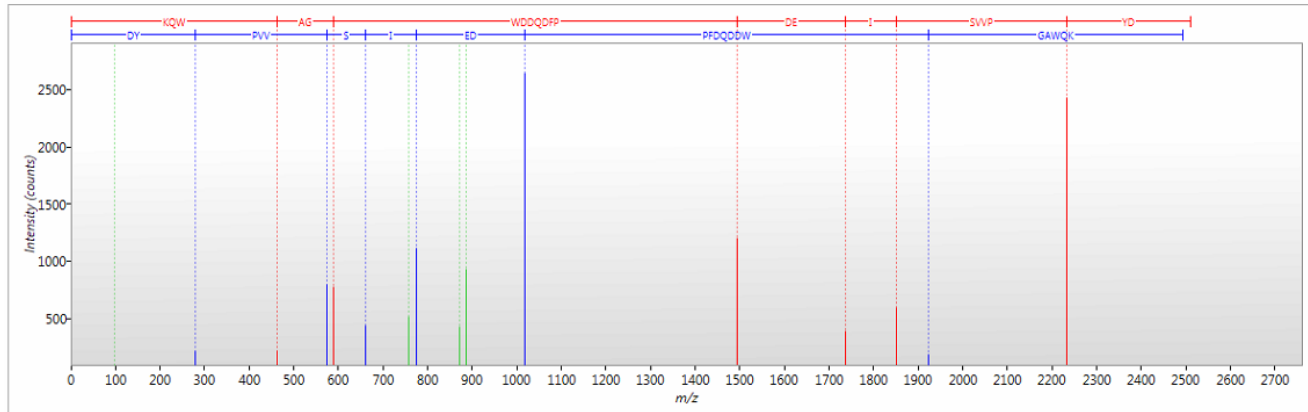
Fragment ions for: TSIVHLFEVR



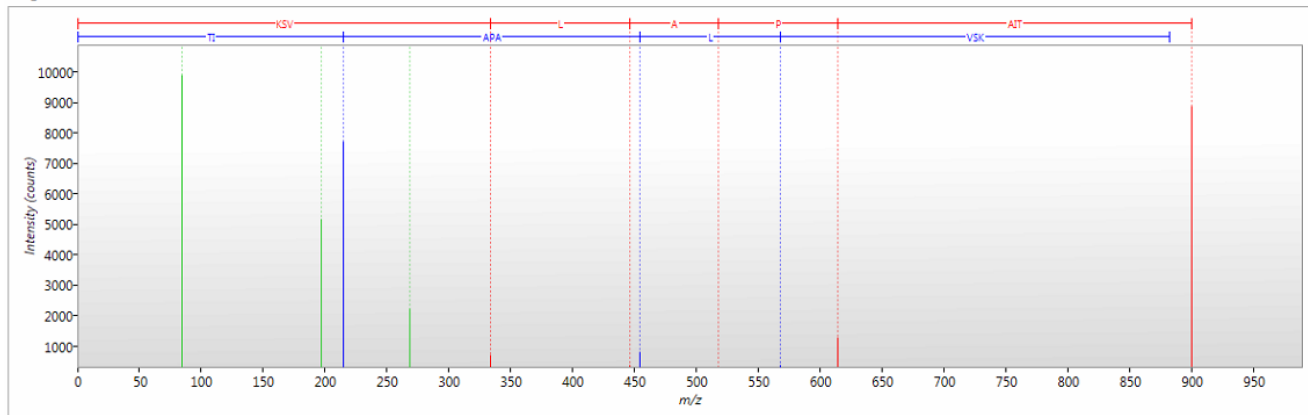
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
DYPVVSIEDPFDQDDWGAWQK	28693	7.37	5	2509.1077	2		0		yes	2356.92	3097.84	1849.30	4420.39
TIAPALVSK	3471	7.36	6	898.4641	2		0		yes	2.08e+005	3.72e+005	3.15e+005	2.24e+005

Fragment ions for: DYPVVSIEDPFDQDDWGAWQK



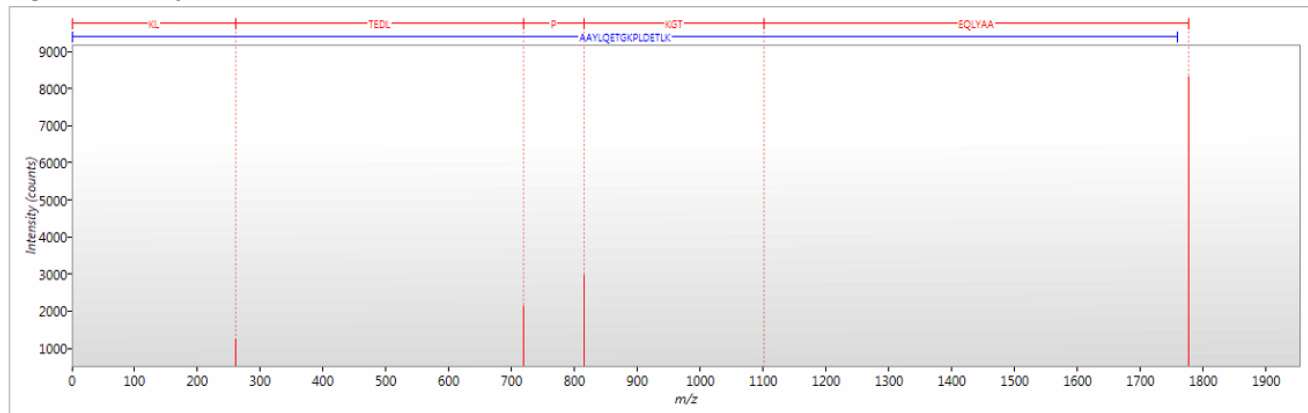
Fragment ions for: TIAPALVSK



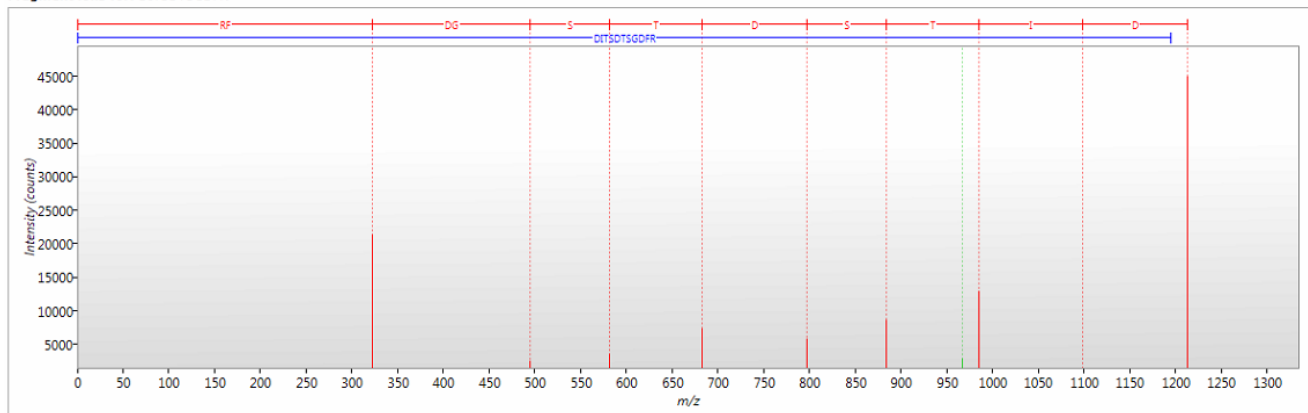
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
AAYLQETGKPLDETLK	4547	7.25	2	1775.8335	2		0		yes	5.74e+005	4.34e+005	3.06e+005	5.17e+005
DITSDTSGDFR	29302	8.71	2	1212.5313	1		0		yes	299.89	26.93	0.00	5007.30
GDRSEDFGVNEDLADSDAR	203	7.96	3	2066.8788	2		0		yes	1.99e+006	7.27e+005	3.72e+005	3.18e+006
GTDVNVFNTILTTR	53352	8.53	2	1549.6953	1		0		no	289.55	0.00	810.81	0.00
TPAQFDADLR	48550	8.57	2	1261.5912	1		0		no	599.28	24.91	628.43	1788.98

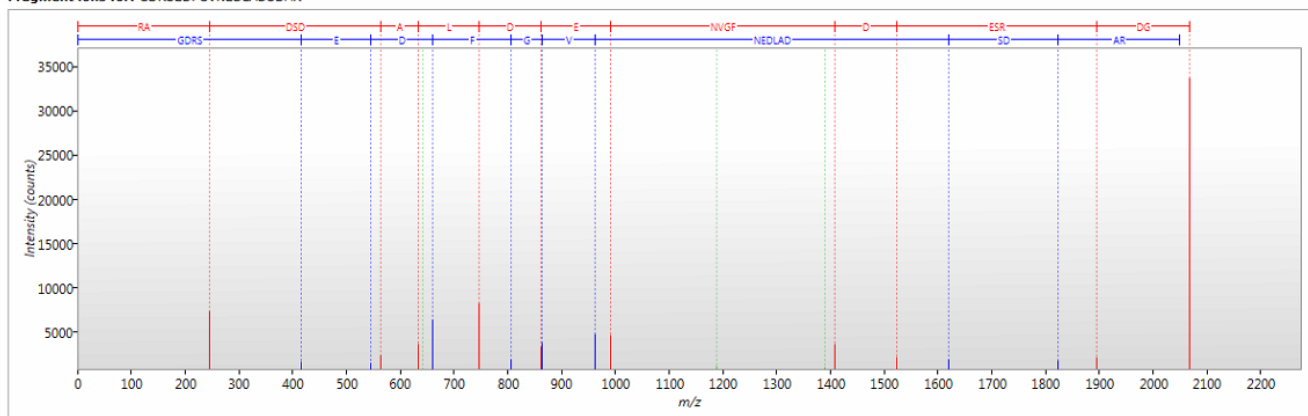
Fragment ions for: AAYLQETGKPLDETLK



Fragment ions for: DITSDTSGDFR



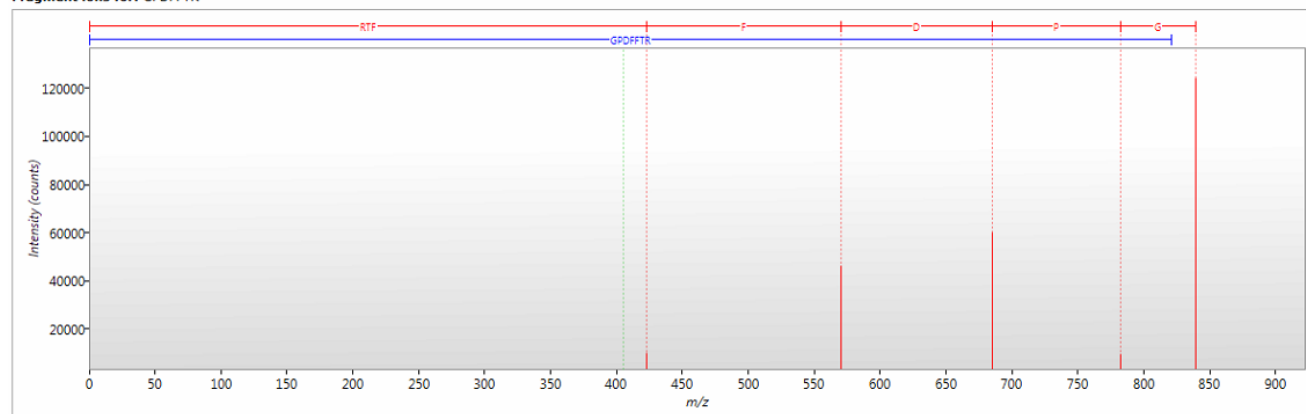
Fragment ions for: GDRSEDFGVNEDLADSDAR



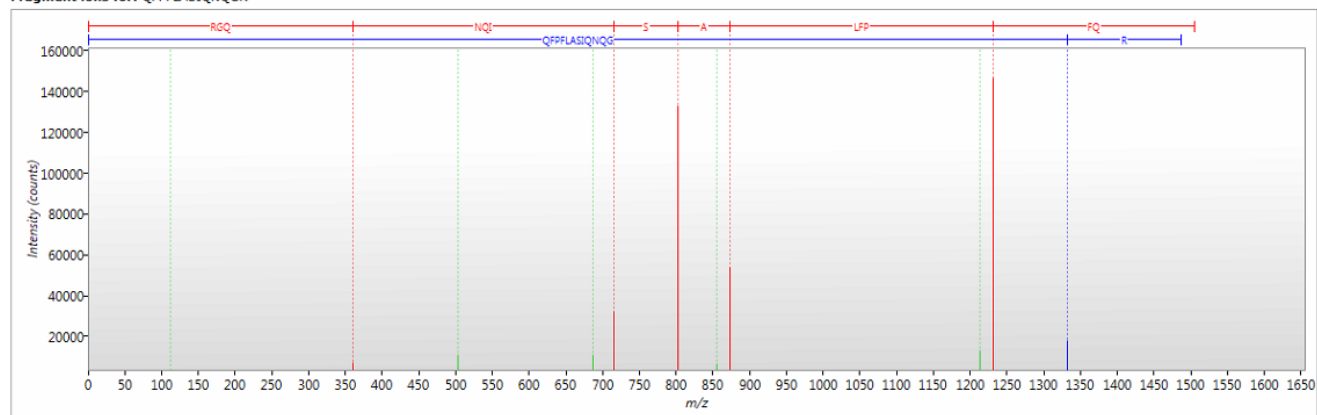
Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
GPDDFFTR	2261	7.02	5	838.4108	2		0		yes	6.48e+004	1.83e+005	1.15e+005	7.90e+004
QFPFLASIQNQGR	32351	6.74	2	1504.7693	1		0		yes	539.89	88.25	3340.67	502.05

Fragment ions for: GPDDFFTR



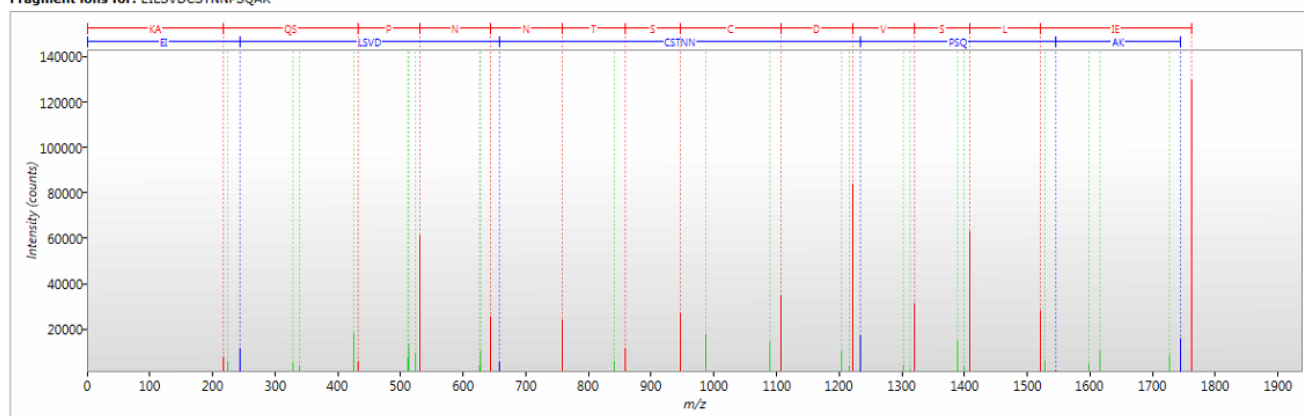
Fragment ions for: QFPFLASIQNQGR



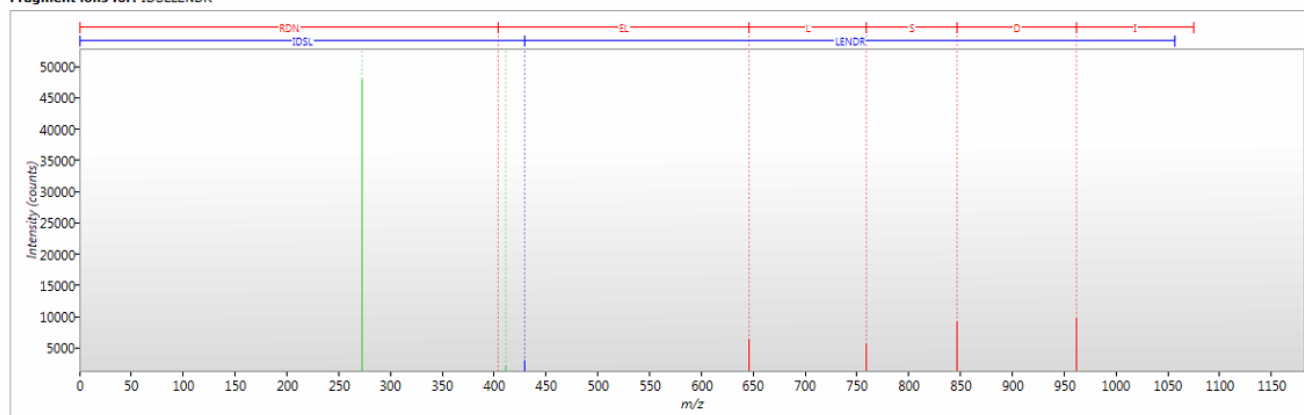
Clusterin O5=Homo sapiens GN=CLU PE=1 SV=1
10 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										P/CA	SPH	SE	RE
ALQEYR	8245	8.70	5	778.3929	1		0		no	7765.59	4141.64	4177.99	1.38e+004
ASSIDELFQDR	2351	8.61	30	1392.7006	2		0		no	3.93e+005	2.89e+005	2.59e+005	2.96e+005
ASSIDELFQDR	39635	8.40	7	1392.6822	1		0		no	18.26	57.08	0.00	1022.51
EILSVD ^{CS} TNNPSQAK	829	9.40	34	1761.8174	2		0	[7] Carbamidomethyl C	yes	4.89e+005	2.65e+005	2.29e+005	7.42e+005
EILSVD ^{CS} TNNPSQAK	46692	9.40	8	1761.8062	1		0	[7] Carbamidomethyl C	no	123.76	0.00	196.31	2321.54
EIQNAVNGVK	17391	7.93	9	1070.5611	1		0		no	6050.02	1917.85	4897.45	9389.06
HNSTG ^{CL} R	4833	6.66	4	943.4447	2		0	[6] Carbamidomethyl C	no	7.51e+004	1.21e+005	5.87e+004	8.67e+004
IDSLLNDR	142	8.49	2	1073.5498	2		0		yes	1.50e+006	4.48e+006	3.08e+006	1.91e+006
IDSLLNDR	2043	---	---	1073.5510	3		0		yes	2.20e+004	6.97e+004	7.77e+004	2.19e+004
IDSLLNDR	3602	---	---	1073.5449	1		0		yes	2.50e+004	7.76e+004	1.08e+005	5.04e+004
LKELPGV ^{CNET} MMALV ^{EE} CK ^{PK} CLK	7176	7.07	4	2967.3754	3		0	[8] Carbamidomethyl C [12] Oxidation M [13] Oxidation M [19] Carbamidomethyl C [22] Carbamidomethyl C	no	1.25e+005	4.09e+005	4.96e+004	5.47e+005
TLLIETNEER	21629	7.77	2	1231.6410	3		0		no	891.81	3.50	101.28	15.12
TLLSNLEEAK	1375	8.07	10	1116.5636	2		0		yes	3.43e+005	4.91e+005	3.43e+005	4.01e+005
VTTVASHTSDSDVPSGVTEV ^W VK	6455	8.75	35	2313.1640	2		0		no	7.56e+004	3.14e+004	3.55e+004	1.40e+005

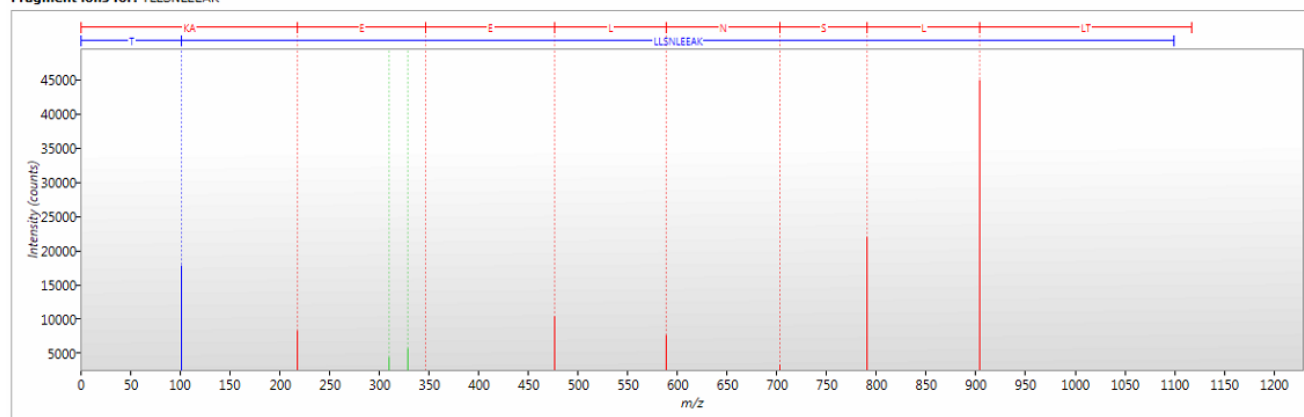
Fragment ions for: EILSVD^{CS}TNNPSQAK



Fragment ions for: IDSLLNDR



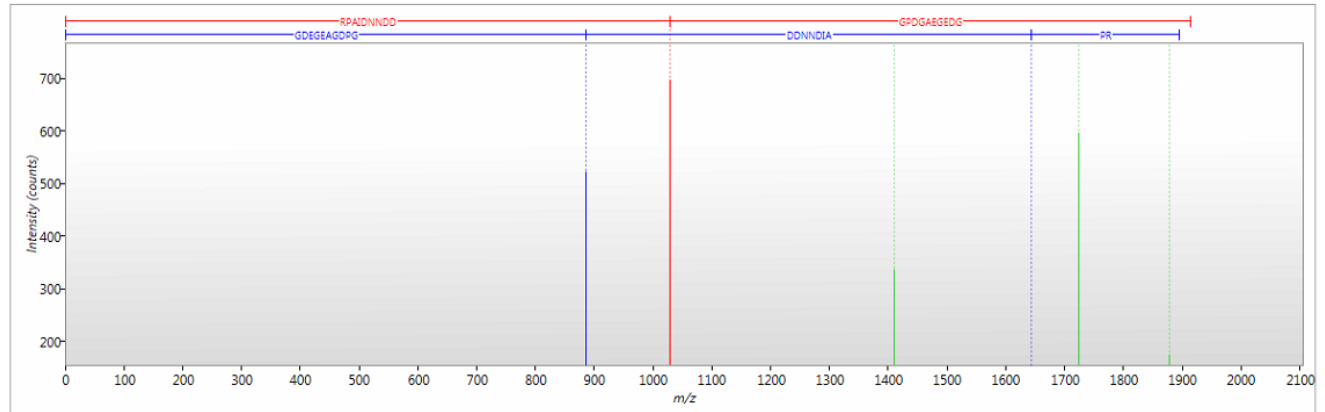
Fragment ions for: TLLSNLEEAK



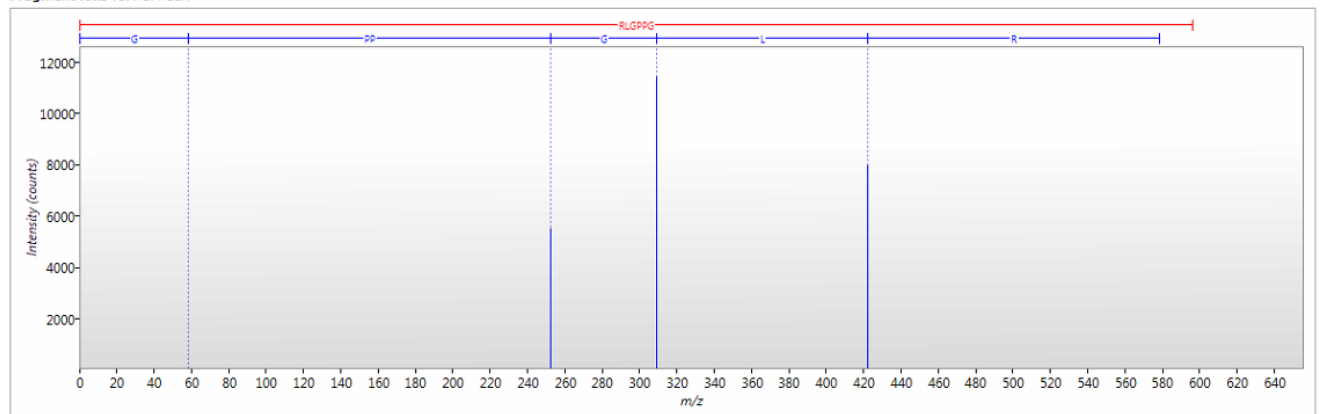
Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances				
										PCa	SPH	Be	Re	
GDEGEAGDPGDDNNDIAPR	27054	5.80	2	1912.7679	2		0		yes	3699.88	1426.31	514.70	2311.34	
GPPGLR	67	6.39	3	595.3453	1		0		yes	7.33e+005	2.87e+006	2.10e+006	1.30e+006	
GPPGLR	777	6.39	2	595.3451	2		0		yes	8.69e+004	2.17e+005	1.73e+005	1.24e+005	
LLLFSDGNSQGATPAAIEK	3617	7.87	12	1930.9723	2		1		no	3.25e+005	1.92e+005	3.01e+005	4.02e+005	
MCSCCECK	11508	6.88	3	1133.3556	2		0	[2] Carbamidomethyl C [4] Carbamidomethyl C [5] Carbamidomethyl C [7] Carbamidomethyl C	no	927.10	306.61	40.65	3517.94	
NFTAADVIGQSRDAEEAISQTDITVDMIK	3111	5.62	4	3224.5192	3		1		no	1.08e+006	1.38e+006	8.32e+005	9.63e+005	
VFSVAITPDHLEPR	2155	7.97	13	1579.8392	3		0		yes	9.86e+004	7.71e+004	7.23e+004	1.83e+005	

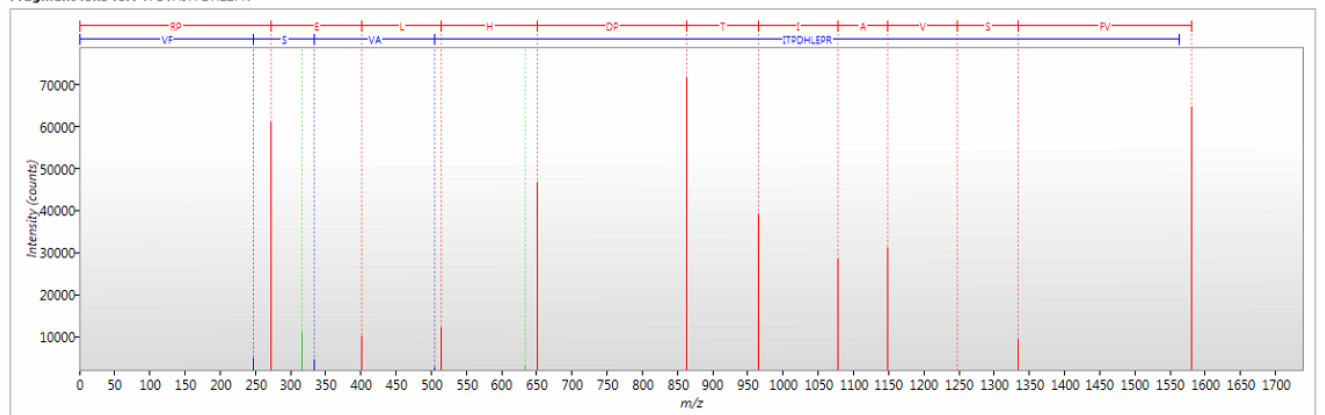
Fragment ions for: GDEGEAGDPGDDNNDIAPR



Fragment ions for: GPPGLR



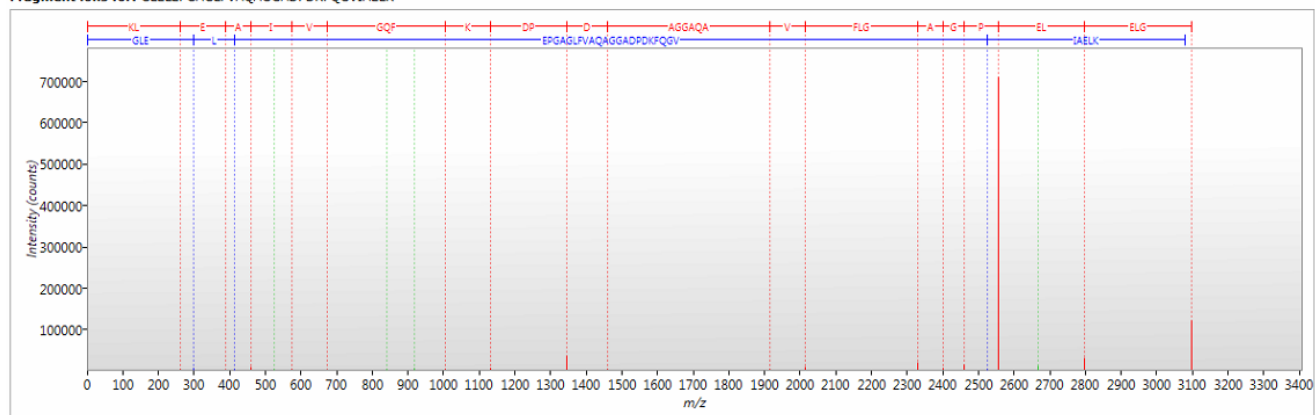
Fragment ions for: VFSVAITPDHLEPR



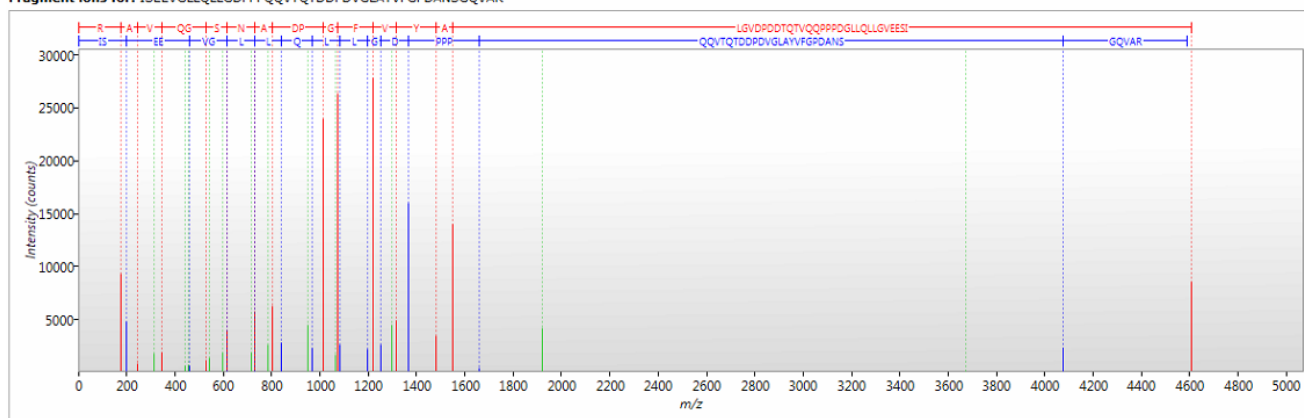
Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1 SV=5
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
GLELEPGAGLFVAQAGGADPKFQGVIAELK	5440	7.18	3	3096.6057	3		0		yes	2.26e+005	6.18e+004	3.72e+004	4.69e+005
ISEEVGLLQLLGDPQQVVTQTDDPDVGLAYVFGPDANSQGQVAR	8701	7.21	2	4605.2769	4		0		yes	4.87e+004	4454.71	1673.72	8.58e+004

Fragment ions for: GLELEPGAGLFVAQAGGADPKFQGVIAELK



Fragment ions for: ISEEVGLLQLLGDPQQVVTQTDDPDVGLAYVFGPDANSQGQVAR

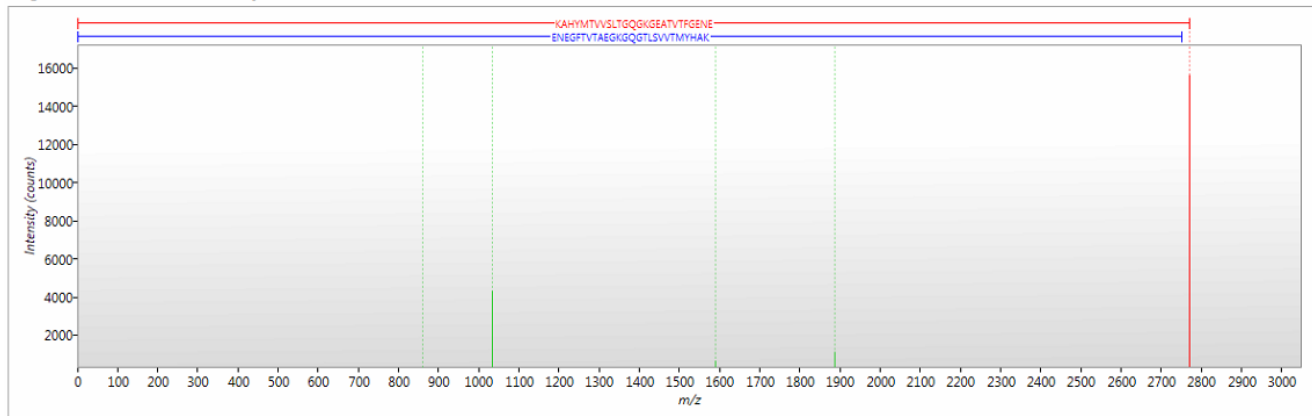


Complement C3 O5=Homo sapiens GN=C3 PE=1 SV=2
57 peptides

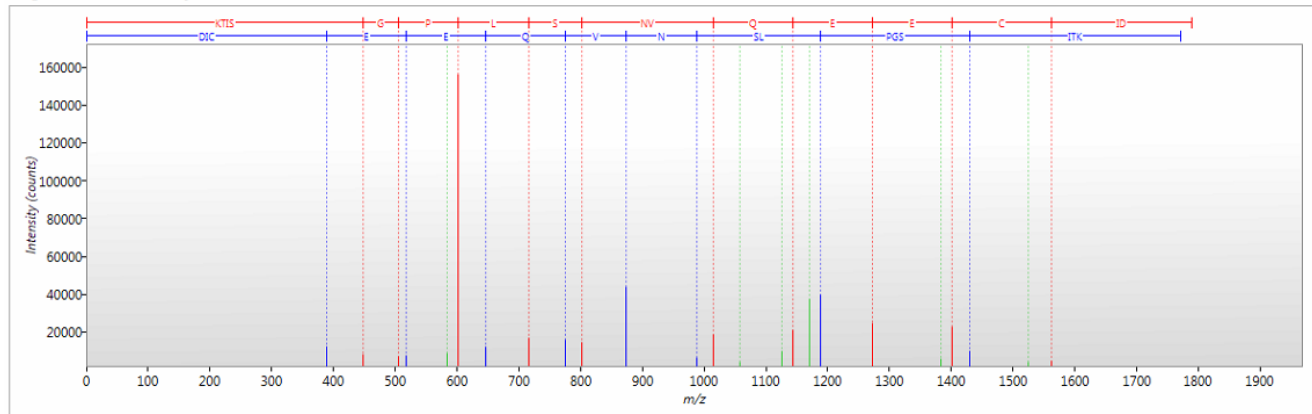
Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
AAVYHHFISDGV	1054	7.39	2	1470.6718	2		0		no	1.00e+005	4.63e+005	1.58e+005	2.01e+005
A ² CEPGVDYVYK	23229	8.39	8	1299.5776	1		0	[2] Carbamidomethyl C	no	2263.11	702.30	1.34e+004	403.57
A ² CEPGVDYVYK	2075	8.39	12	1299.5845	2		0	[2] Carbamidomethyl C	no	2.08e+005	3.60e+005	3.24e+005	1.36e+005
ADIG ² CTPGSGK	12236	8.51	15	1061.4852	1		0	[5] Carbamidomethyl C	no	5382.78	6817.20	1.47e+004	5624.23
ADIG ² CTPGSGK	26271	8.92	3	1061.4981	1		0	[5] Carbamidomethyl C	no	3729.79	2061.72	8840.33	1056.67
ADIG ² CTPGSGK	1819	8.92	20	1061.5094	2		0	[5] Carbamidomethyl C	no	2.42e+005	3.36e+005	3.02e+005	1.84e+005
AEDLVGK	2794	7.86	5	730.3692	2		0		no	3.46e+004	4.39e+004	3.32e+004	2.63e+004
ASHLGLAR	7339	7.08	8	823.3427	1		0		no	8.55e+004	3.47e+004	4.55e+004	6.13e+004
ASHLGLAR	22492	8.50	5	823.4525	1		0		no	145.83	167.71	4266.05	222.30
AYYENISQQVSTFEYK	3486	8.83	16	2164.9962	2		0		no	5.19e+004	2.59e+005	3.03e+005	7.70e+004
A ² AEEN ² CFIK	1496	8.07	18	1297.5481	2		0	[1] Carbamidomethyl C [6] Carbamidomethyl C	no	7.46e+004	1.52e+005	1.05e+005	4.06e+004
A ² AEEN ² CFIK	21137	8.07	17	1297.5408	1		0	[1] Carbamidomethyl C [6] Carbamidomethyl C	no	245.10	65.53	5461.23	221.13
DFDFVPPVVR	14369	7.84	7	1189.6088	1		0		no	2.04e+004	1.05e+004	2.26e+004	1.10e+004
D ² EEQVNSLPGSITK	2695	9.16	21	1788.8524	2		0	[3] Carbamidomethyl C	no	2.66e+005	4.13e+005	4.23e+005	2.40e+005
DTWVEHWPEEDE ² CQDEENQK	14299	8.75	14	2602.0218	2		0	[13] Carbamidomethyl C	no	369.72	2.98e+004	2.85e+004	3289.87
DTWVEHWPEEDE ² CQDEENQK	3195	8.75	18	2602.1485	3		0	[13] Carbamidomethyl C	no	2.63e+005	5.05e+005	3.32e+005	2.65e+005
DYAGVSDAGLTFTSSSGQQTAR	23139	7.21	4	2493.1010	2		0		no	9353.25	1184.98	9452.53	2939.02
EALKLEEK	2848	7.68	10	958.5011	2		0		no	9.57e+004	1.40e+005	1.35e+005	9.60e+004
EALKLEEK	22260	7.68	8	958.5123	1		0		no	872.20	1711.90	5876.29	821.42
ENEGFTVTAEGK	4229	7.34	2	1280.5991	2		0		no	2.09e+005	2.51e+005	2.22e+005	2.37e+005
ENEGFTVTAEGKGQGTLSVVT ² MYHAK	132	6.31	2	2769.3238	3		0	[22] Oxidation M	yes	5.42e+006	1.25e+006	1.85e+005	7.51e+006
EPGQDLVLLPLSITTD ² FIPSR	7403	9.32	16	2443.2950	2		0		no	1.45e+004	6.71e+004	8.36e+004	7650.72
EPGQDLVLLPLSITTD ² FIPSR	10044	9.22	8	2443.2961	2		0		no	4294.40	1.08e+004	9.48e+004	2464.64
EVVADSVWVDVK	13998	---	---	1344.7099	1		0		yes	436.24	116.53	2.39e+004	30.84
EVVADSVWVDVK	376	5.59	4	1344.6822	2		0		yes	4.85e+005	1.58e+006	2.06e+006	4.50e+005
EYVLPSFEVIVEPTK	3732	9.27	5	1877.9616	2		0		no	6.32e+004	5.21e+004	2.33e+005	4.14e+004
FISLGEA ² CK	990	8.33	19	1023.5139	2		0	[8] Carbamidomethyl C	no	1.95e+005	4.03e+005	2.22e+005	1.64e+005
FLTTAK	3715	---	---	679.3210	2		0		no	3.50e+004	4.01e+004	2.07e+004	3.16e+004
FLTTAK	1617	7.43	4	679.3094	1		0		no	3.94e+005	3.23e+005	3.35e+005	3.67e+005
FYHPEKEDGK	4678	7.62	2	1248.5856	3		0		no	6571.43	7655.15	1.46e+004	6498.34
FYYIYNEK	16820	8.24	10	1138.5271	1		0		no	9619.41	3972.55	1.25e+004	5521.69
GQGTLSVVTMYHAK	4736	5.17	2	1490.7028	2		0		no	2.00e+005	1.92e+005	1.14e+005	1.67e+005
ILLQGTPIVAQMTEDAVDAER	9525	9.03	2	2156.0803	3		0		no	1510.54	1386.59	9.23e+004	2399.86
ILLQGTPIVAQMTEDAVDAERLK	7046	7.59	3	2397.2055	3		0		no	2.52e+005	2.12e+005	2.90e+005	3.52e+005
ISLPESLK	3282	7.92	8	885.5116	2		0		no	5.75e+004	1.17e+005	1.10e+005	3.79e+004
IWDVVEK	1093	7.88	13	887.4759	2		0		no	8.31e+004	2.13e+005	2.10e+005	7.06e+004
KQELSEAEQATR	3117	8.51	22	1388.6509	2		0		no	1.80e+005	2.01e+005	2.11e+005	1.66e+005
KVLLDG ² VQNP	5976	7.18	2	1237.6135	3		0		no	1.14e+004	1.56e+004	4.80e+004	1.16e+004
L ² CRDEL ² CR	11136	6.95	4	1120.5147	3		0	[2] Carbamidomethyl C [7] Carbamidomethyl C	no	4547.84	6158.24	1797.00	1347.70
LMNIFLK	5510	8.03	3	877.5089	2		0		no	1586.40	7259.74	1.81e+004	2815.48
LPYSVVR	435	8.08	3	832.3271	1		0		no	5.81e+005	5.68e+005	5.53e+005	5.90e+005
LVAYYITLIGASQGR	12615	8.24	11	1510.9001	3		0		no	2.33e+004	4.09e+004	1.09e+004	1.20e+004
NTWILEI ² CTR	32337	7.80	4	1249.5955	1		0	[8] Carbamidomethyl C	no	3250.82	275.66	6679.33	2882.33
QDSLSSQNLGLVPLSWDIPELV ² MGQWK	16508	7.34	5	3297.6236	3		0	[25] Oxidation M	no	2093.24	2.57e+004	1.27e+004	4245.89

QGALELIK	8478	7.97	6	870.5048	1	0		no	6822.77	1.06e+004	1.81e+004	5642.67
QGALELIK	2381	7.97	7	870.4782	2	0		no	8.81e+004	1.27e+005	7.87e+004	8.81e+004
QKPDGVFQEDAPVHQE ¹⁸ IGGLR	3425	6.21	2	2579.2966	3	0	[18] Oxidation M	yes	1.57e+006	5.23e+005	2.85e+005	8.02e+005
QVREPGQDLVVLPLSITTDPIPSFR	25694	8.11	6	2826.5242	3	0		no	5360.94	3219.16	1.93e+004	1617.50
SDDKVTLEER	4966	7.56	2	1190.4161	2	0		no	3.64e+004	3.11e+004	4.79e+004	3.80e+004
SDDKVTLEER	4627	8.26	18	1190.5777	3	0		no	5.56e+004	1.03e+005	5.83e+004	4.54e+004
SGIPVITSPYQIHFTK	2097	8.95	22	1786.9619	3	0		no	2.41e+005	4.14e+005	2.04e+005	1.28e+005
SGQSEDRQVPVPGQQMTLK	15449	7.97	13	1984.9255	2	0		no	7766.89	1.48e+004	2.98e+004	8789.05
SGSDEVQVGGQR	29356	8.57	22	1288.5991	1	0		no	1689.48	2566.39	7107.69	368.79
SNLDEDIAEENIVSR	2669	9.21	20	1815.8837	2	0		no	4.73e+005	5.84e+005	4.19e+005	4.94e+005
SNLDEDIAEENIVSRSEPPESWLWNVEDLK	11194	6.28	4	3675.5742	3	0		no	4.35e+005	1.07e+005	1.77e+005	1.27e+005
SSLSPYIVIVPLK	42222	8.93	6	1400.8237	1	0		no	19.77	0.00	1805.09	1.64
TELRPGETLVNVELLR	2171	8.57	6	1871.0219	3	0		no	1.45e+005	1.82e+005	1.92e+005	1.38e+005
TFISPIK	2521	8.26	23	804.4666	2	0		no	5.14e+004	1.02e+005	7.25e+004	5.93e+004
TGLQEVVK	1428	8.24	15	1001.5355	2	0		no	2.49e+005	4.81e+005	3.67e+005	2.86e+005
TGLQEVVK	20706	7.70	9	1001.5253	1	0		no	1372.96	3497.63	2018.21	1146.75
TIYTPGSTVLVR	28024	8.91	12	1369.7248	1	0		no	54.58	211.94	5721.02	112.55
TLDPER	3026	7.44	2	729.3369	1	0		no	1.05e+005	8.90e+004	1.26e+005	8.11e+004
TMQALPYSTVGNSNNYLHLSVLR	8253	7.28	5	2577.2864	3	0		no	5.39e+004	1.14e+005	3.08e+004	6.36e+004
TMQALPYSTVGNSNNYLHLSVLR	14122	8.22	6	2577.1258	2	0		no	6875.11	8763.10	2.81e+004	1.39e+004
VFLDC ⁵ NYTELRL	1596	9.10	18	1701.7858	2	0	[5] Carbamidomethyl C [6] Carbamidomethyl C	no	5.89e+005	5.85e+005	5.82e+005	4.12e+005
VHQYFNVELIQPGAIVK	8988	9.14	9	1840.8846	2	0		no	6.72e+004	9.18e+004	1.22e+005	4.45e+004
VHQYFNVELIQPGAIVK	7824	7.77	3	1840.9197	3	0		no	3.64e+004	1.62e+005	5.52e+004	4.66e+004
VLLDGVQNPRL	2238	8.23	13	1109.5916	2	0		no	1.38e+005	1.83e+005	1.97e+005	1.08e+005
VLLDGVQNPRL	32669	8.23	10	1109.5973	1	0		no	648.26	1315.82	3549.55	459.40
VQLSNDFDEYIMAEQTIK	11629	9.12	15	2256.0959	2	0		no	2.70e+004	4.44e+004	7.00e+004	1.93e+004
VTIKPAPETEKRPQDAK	20668	6.82	5	1907.0749	3	0		no	2444.10	1.67e+004	2173.76	985.12
VVLVAVDK	10461	8.59	15	841.5103	1	0		no	1049.06	3533.92	2.28e+004	1706.13
VVPEGIR	4638	8.34	3	768.4349	2	0		no	2.81e+004	2.49e+004	2.74e+004	1.95e+004

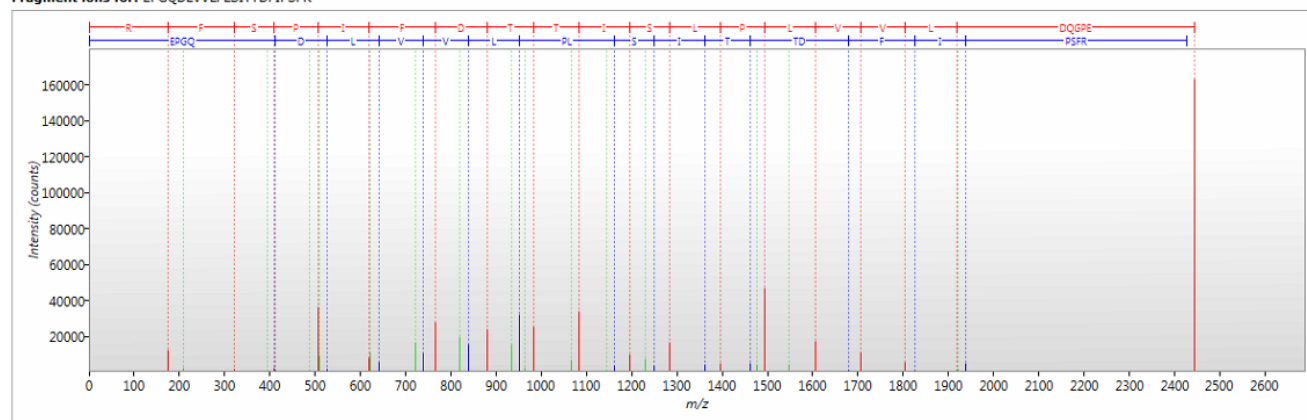
Fragment ions for: ENEGFTVTAEGKGQGLSVVTMYHAK



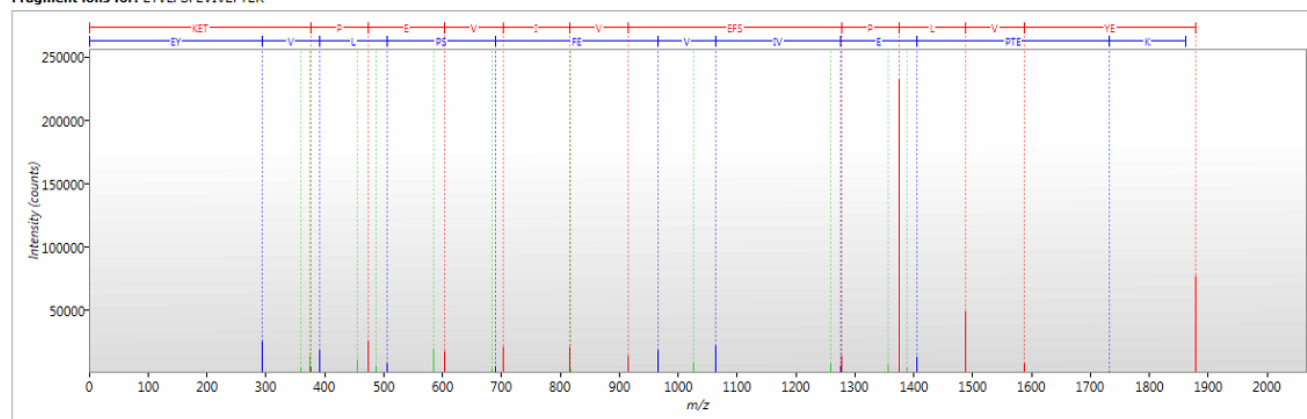
Fragment ions for: DICEEQVNSLPGSITK



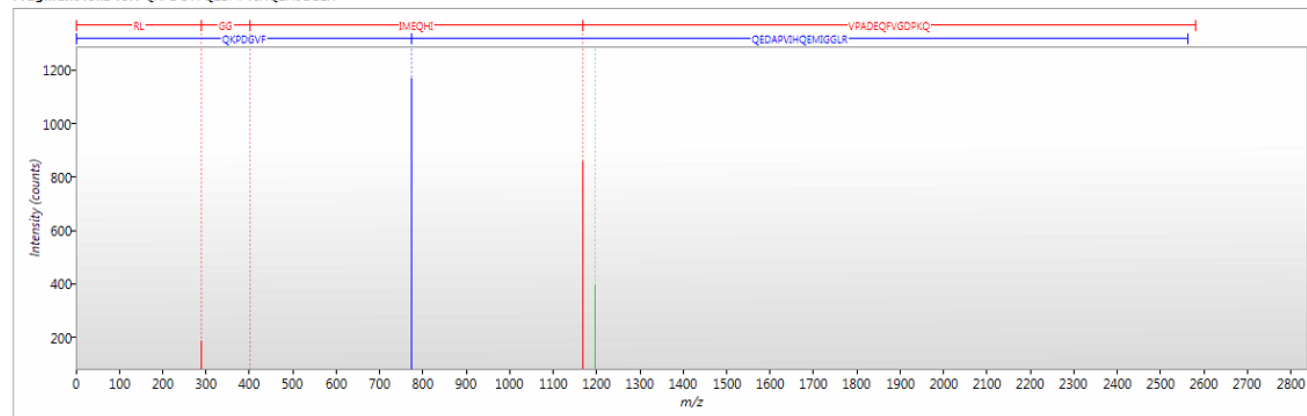
Fragment ions for: EPGQDLVVLLPSITTFIPSR



Fragment ions for: EYVLPSEFVIVEPTEK



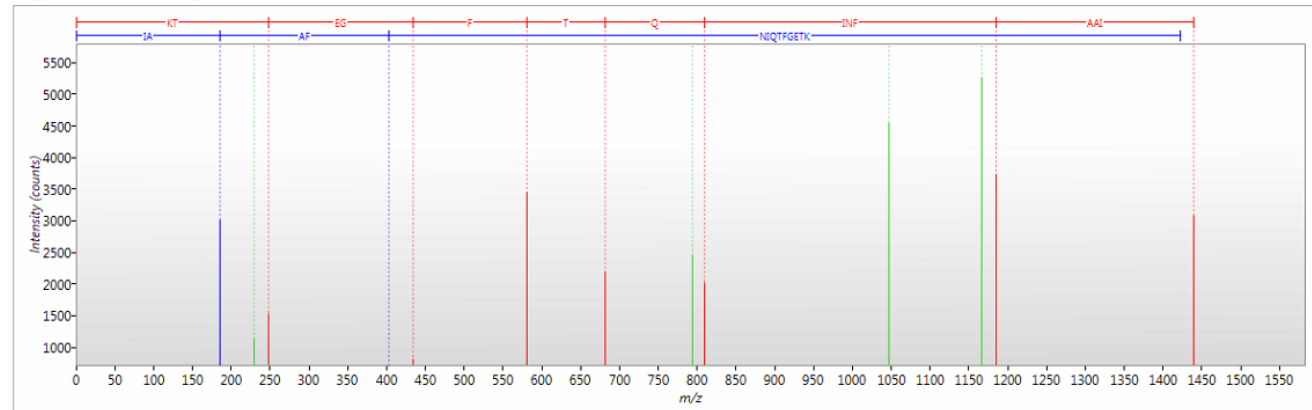
Fragment ions for: QKPDGVFQEDAPVIHQEMIGGLR



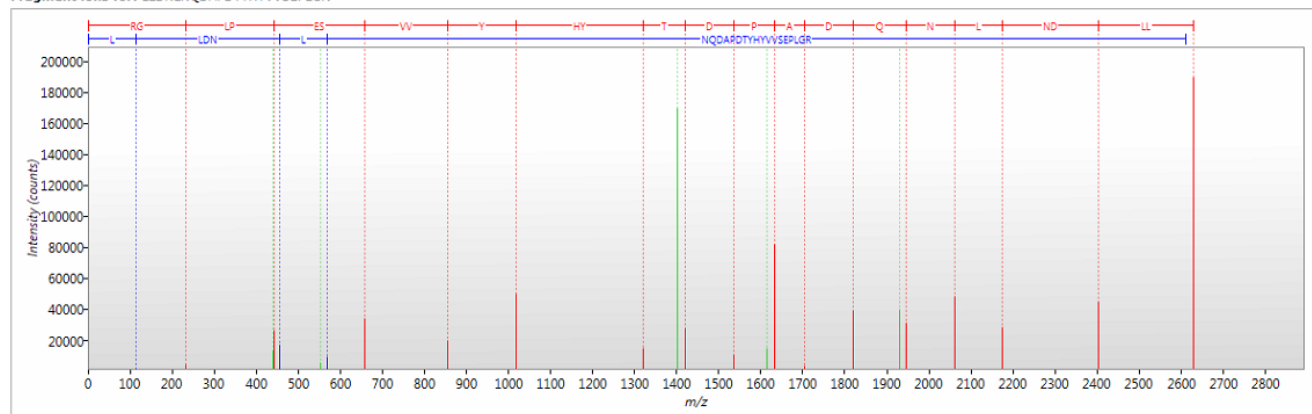
Deoxyribonuclease-1 OS=Homo sapiens GN=DNASE1 PE=1 SV=1
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Bc
IAAFNIQTFGETK	10667	7.17	3	1438.7837	3		0		yes	1379.25	7420.64	3645.24	2.84e+004
LLDNLNQDAPDTYHYVVEPLGR	1234	8.17	18	2628.2673	3		0		yes	7.03e+005	2.72e+005	1.97e+005	7.71e+005
LVWTSPTFQWLIPDSADTTATPTH ^C AYDR	7771	8.27	10	3250.5177	3		0	[24] Carbamidomethyl C	yes	1.49e+005	8.81e+004	3.51e+004	3.45e+005

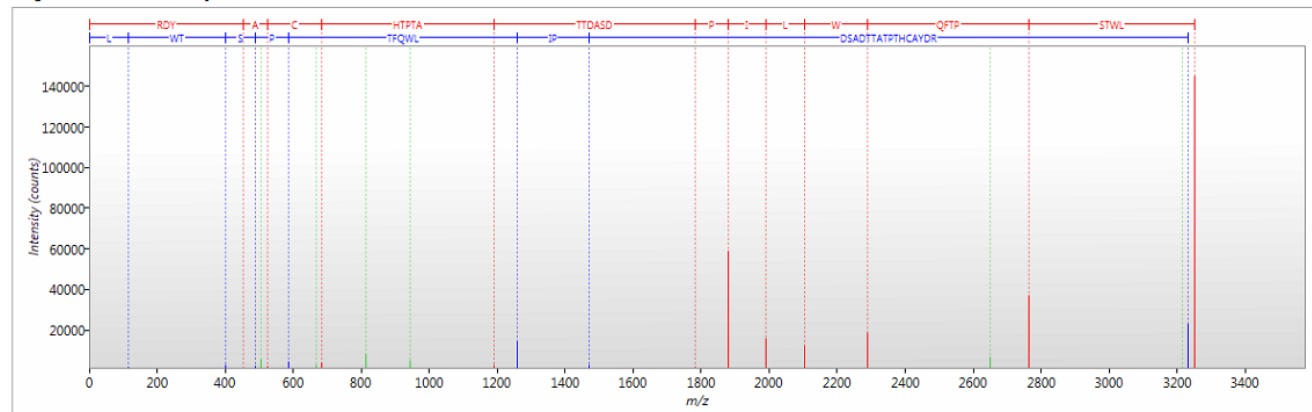
Fragment ions for: IAAFNITQTFGETK



Fragment ions for: LLDNLNQDAPDTYHYVVEPLGR



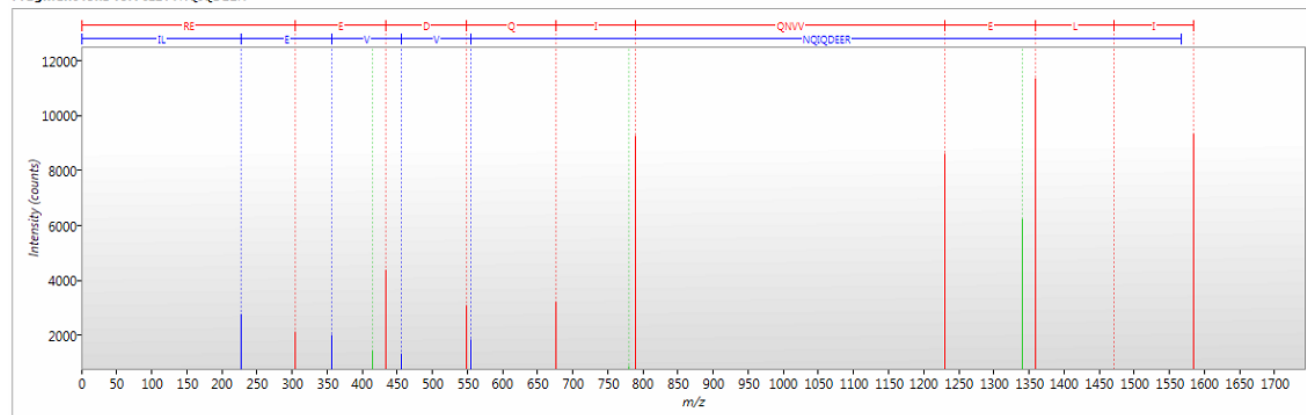
Fragment ions for: LVWTSPTFQWLIPDSADTTATPTHAYDR



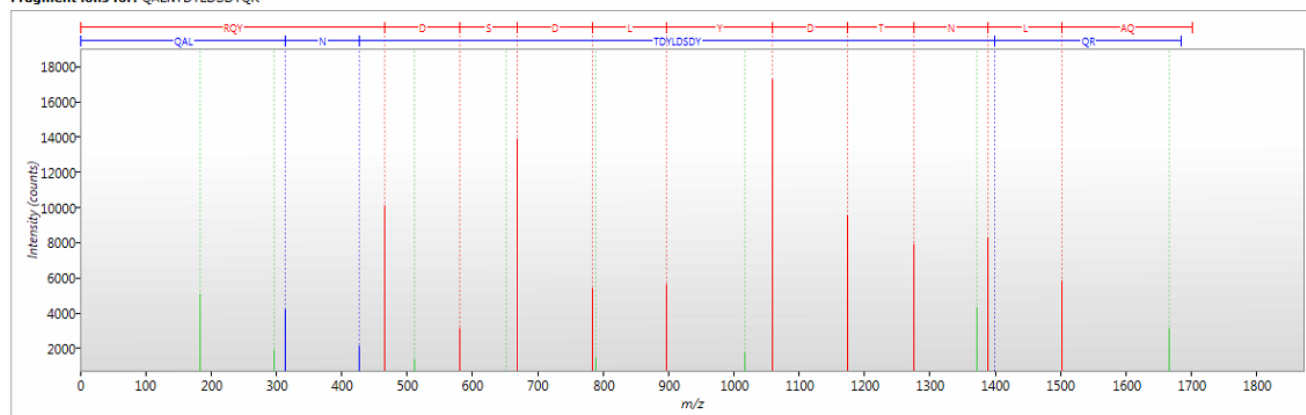
Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
ILEVNNQIQDEER	4000	8.04	12	1583.8087	2		0		yes	1.01e+005	5.47e+004	8.11e+004	9.50e+004
QALNTDYLDSDYQR	6468	8.26	17	1700.7903	2		0		yes	9.96e+004	5.80e+004	4.14e+004	8.25e+004
WLVEPQIDDPNSNLEEAEINEAEITSVNSLGSK	7639	8.21	7	3581.7292	3		0		yes	1.71e+005	2.12e+004	2606.47	7.35e+004

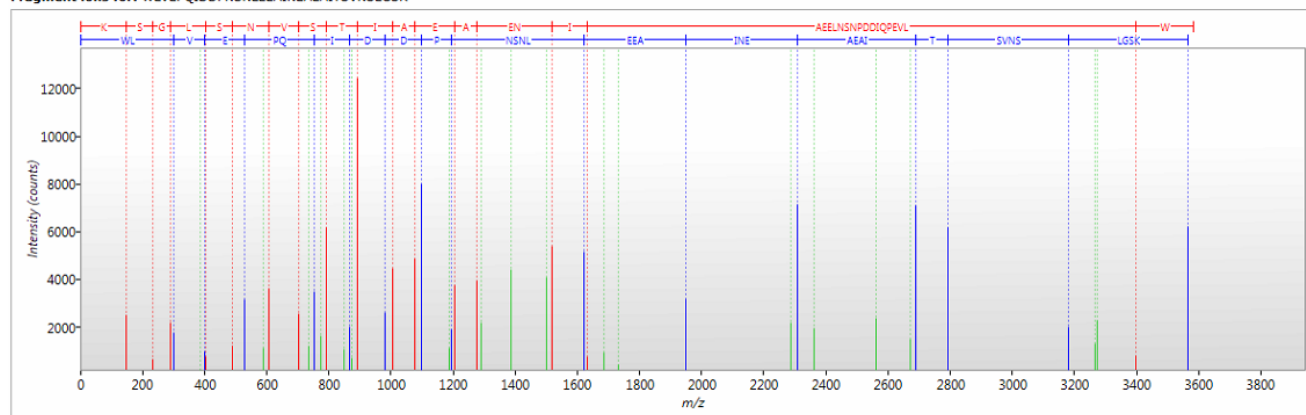
Fragment ions for: ILEVNNQIQDEER



Fragment ions for: QALNTDYLDSDYQR



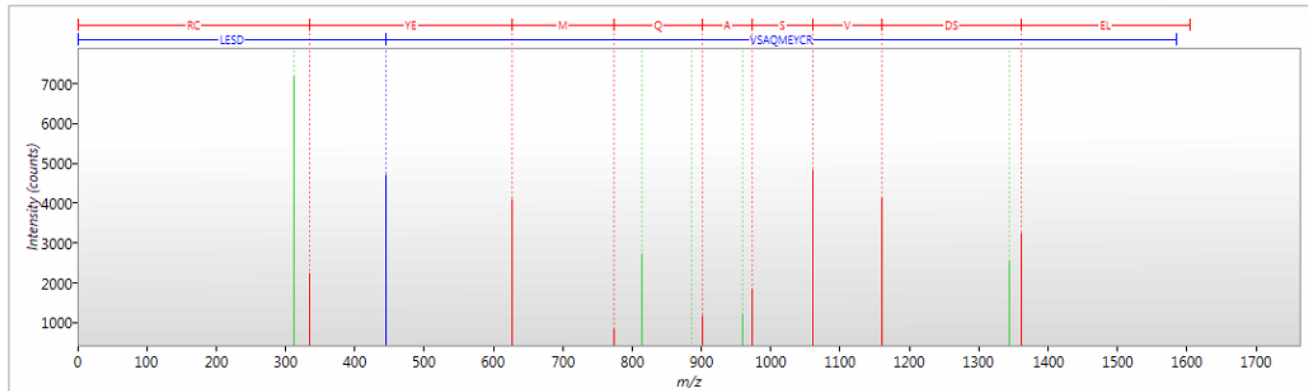
Fragment ions for: WLVEPQIDDPNSNLEEAEINEAEITSVNSLGSK



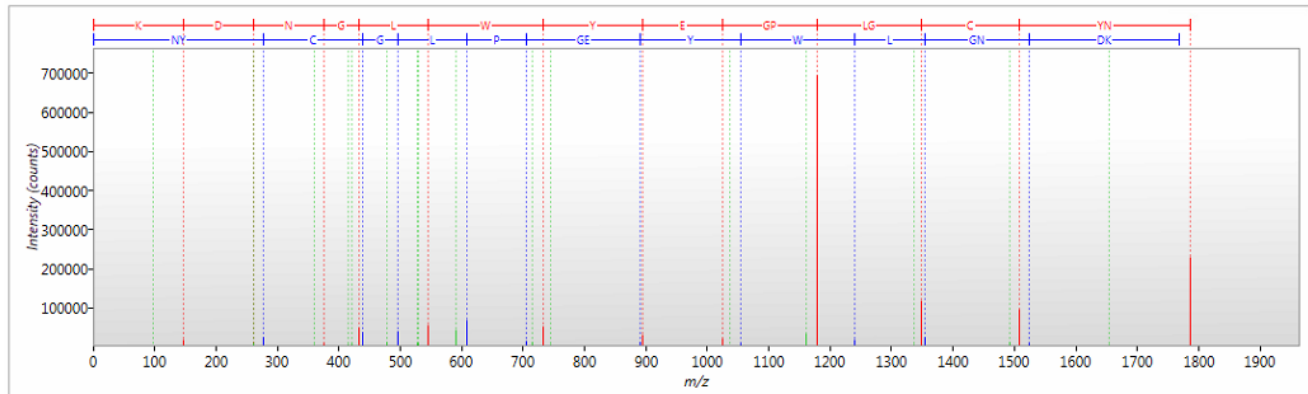
Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2
24 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances				
										PCA	SPH	DS	RS	
AHYGGFTVQIEANK	26759	---	---	1534.7131	1		0		no	0.00	0.00	6736.81		5.67
AHYGGFTVQIEANK	6345	9.11	9	1534.7004	2		0		no	1.60e+005	3.12e+005	1.91e+005	1.82e+005	
AHYGGFTVQIEANK	5298	8.45	6	1534.7356	3		0		no	8.09e+004	1.72e+005	4.90e+004	3.71e+004	
AHYGGFTVQIEANK	2963	9.39	9	1534.7014	2		0		no	5.57e+004	6.02e+004	3.91e+005	6.27e+004	
AHYGGFTVQIEANK	2609	9.39	9	1534.7267	3		0		no	3.55e+004	7.45e+004	1.68e+005	3.76e+004	
DNDGWLTSDFR	23995	8.56	9	1274.5567	1		0		no	846.34	229.50	7127.18	3503.90	
DNEHVNEYSSSELEK	40786	9.65	8	1767.7655	1		0		no	0.00	0.00	5031.72	0.00	
EDGGGWYYNR	25203	8.98	3	1238.5151	1		0		no	3089.72	409.98	7879.93	677.43	
EDGGGWYYNR	19106	9.24	17	1238.5177	1		0		no	5616.09	7282.33	1.91e+004	3633.92	
EDGGGWYYNR	1331	9.24	13	1238.5206	2		0		no	1.04e+005	1.55e+005	4.08e+005	6.40e+004	
EDGGGWYYNR	1203	9.16	10	1238.5543	2		0		no	2.03e+005	5.41e+005	4.24e+005	1.95e+005	
EDGGGWYYNRCHAAHPNGR	6398	6.48	2	2215.9327	2		0	[11] Carbamidomethyl C	no	2.29e+004	6.69e+004	1.42e+005	2.02e+004	
GHRPLDK	52290	8.53	3	821.4456	1		0		no	282.75	59.63	1343.78	335.40	
GHRPLDKK	12564	7.26	2	949.5454	3		0		no	793.45	2995.09	1.06e+004	2156.56	
GSWYSRRK	1650	6.34	2	1029.4818	3		0	[6] Oxidation M	no	6.13e+004	1.22e+005	7.45e+004	5.89e+004	
GSWYSRRK	3738	6.78	2	1029.4780	2		0	[6] Oxidation M	no	1.56e+005	1.68e+005	1.45e+005	1.43e+005	
HGTDGVTVMNHWK	7733	8.81	9	1543.7877	3		0		no	1.03e+004	5.67e+004	4.59e+004	2.70e+004	
IRPFFPQQ	928	8.91	18	1031.5651	2		0		no	2.02e+005	9.36e+005	6.08e+005	2.84e+005	
KAPDAGGCLHADPDLGVLCPTGQQLQALLQERPIR	8536	8.22	3	4083.0109	5		0	[8] Carbamidomethyl C [19] Carbamidomethyl C [23] Carbamidomethyl C	no	1.35e+005	1.22e+005	5.83e+004	1.64e+004	
KAPDAGGCLHADPDLGVLCPTGQQLQALLQERPIR	7897	8.75	5	4083.0729	4		0	[8] Carbamidomethyl C [19] Carbamidomethyl C [23] Carbamidomethyl C	no	5.10e+004	1.18e+005	7.21e+005	7.75e+004	
KAPDAGGCLHADPDLGVLCPTGQQLQALLQERPIR	5255	8.71	4	4083.0132	5		0	[8] Carbamidomethyl C [19] Carbamidomethyl C [23] Carbamidomethyl C	no	1.39e+005	1.02e+005	9.74e+005	9.98e+004	
KWDPIK	2637	7.80	2	835.4123	2		0		no	2.83e+005	4.43e+005	3.36e+005	2.45e+005	
LESQVSAQMEYCR	531	---	---	1602.8212	4		0	[9] Oxidation M [12] Carbamidomethyl C	yes	1.80e+006	2.81e+006	4.22e+005	8.34e+005	
LESQVSAQMEYCR	1387	8.06	2	1602.8075	2		0	[9] Oxidation M [12] Carbamidomethyl C	yes	1.34e+006	1.39e+006	3.43e+005	9.67e+005	
LESQVSAQMEYCR	185	---	---	1602.8120	3		0	[9] Oxidation M [12] Carbamidomethyl C	yes	6.02e+006	9.79e+006	1.44e+006	3.70e+006	
NYCGLPGEYWLGNLNDK	605	9.74	25	1784.8154	2		0	[3] Carbamidomethyl C	yes	8.15e+005	1.48e+006	1.41e+006	6.87e+005	
NYCGLPGEYWLGNLNDK	35896	9.74	7	1784.7651	1		0	[3] Carbamidomethyl C	no	0.00	0.00	3837.26	0.00	
NYCGLPGEYWLGNLNDKISQLTR	36967	7.64	3	2483.1826	2		0	[3] Carbamidomethyl C	no	1.03e+004	120.58	235.66	873.22	
NYCGLPGEYWLGNLNDKISQLTR	42747	7.78	3	2483.1518	2		0	[3] Carbamidomethyl C	no	3292.94	511.01	3560.50	721.47	
QCSKEDGGGWYYNR	4075	6.44	2	1741.8186	3		0	[2] Carbamidomethyl C	no	6.65e+004	2.51e+005	1.03e+005	1.35e+005	
QDGSVDFGR	764	8.92	19	979.4432	2		0		no	2.08e+005	5.42e+005	4.23e+005	1.16e+005	
QDGFHIVATNTDGG	401	9.14	22	1307.6124	2		0		no	3.76e+005	8.56e+005	6.99e+005	2.79e+005	
QDGFHIVATNTDGG	12333	9.14	17	1307.6038	1		0		no	1411.14	2772.24	2.00e+004	3442.53	
QDGFHIVATNTDGGNYCGLPGEYWLGNLNDK	8604	5.67	2	3074.4099	4		0	[16] Carbamidomethyl C	no	4131.41	4.18e+005	3.92e+004	4.09e+004	
QVKDNEHVNEYSSSELEK	925	---	---	2123.0597	4		0		yes	1.04e+005	1.57e+005	1.17e+006	1.09e+005	
QVKDNEHVNEYSSSELEK	1278	8.41	6	2123.0448	3		0		yes	2.77e+005	6.30e+005	1.47e+006	1.82e+005	
SILENLR	5026	8.68	9	843.4667	1		0		no	1.42e+004	1.50e+004	4.68e+004	5.71e+004	
TPCTVSCNIPVYSGK	595	9.67	24	1617.7759	2		0	[3] Carbamidomethyl C [7] Carbamidomethyl C	no	5.83e+005	1.03e+006	1.29e+006	4.64e+005	
TPCTVSCNIPVYSGK	31868	9.67	9	1617.7821	1		0	[3] Carbamidomethyl C [7] Carbamidomethyl C	no	68.51	0.00	5080.40	235.96	
TPCTVSCNIPVYSGKCEEIIR	27982	9.49	12	2547.2042	2		0	[3] Carbamidomethyl C [7] Carbamidomethyl C [17] Carbamidomethyl C	no	7513.94	373.97	6324.94	601.46	
TPCTVSCNIPVYSGKCEEIIR	2291	9.49	15	2547.2173	3		0	[3] Carbamidomethyl C [7] Carbamidomethyl C [17] Carbamidomethyl C	no	4.91e+005	3.66e+005	2.42e+005	1.71e+005	
YQISVHK	631	8.60	15	850.4506	2		0		no	5.22e+004	3.12e+005	1.84e+005	4.10e+004	

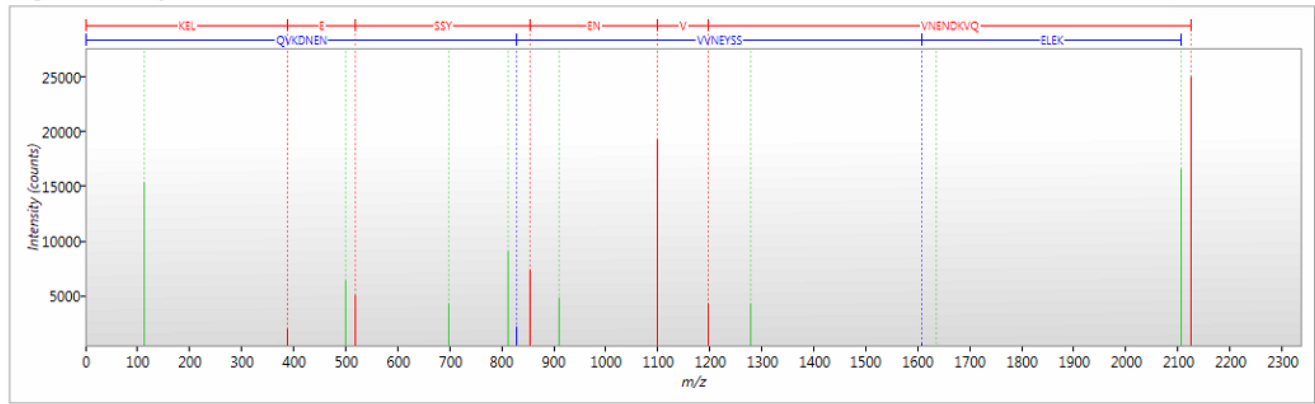
Fragment ions for: LESQVSAQMEYCR



Fragment ions for: NYCGLPGEYWLGNLNDK



Fragment ions for: QVKDNENVVNEYSSLEK

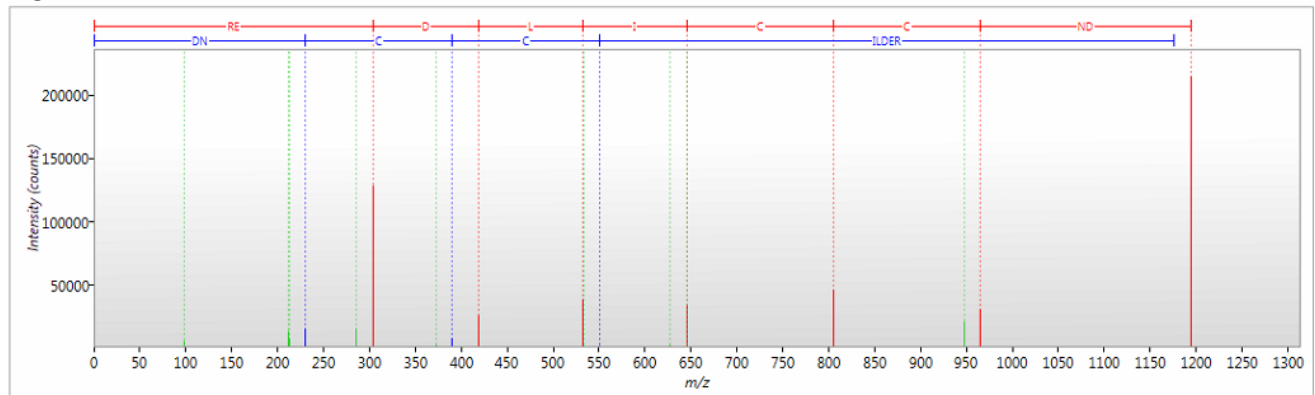


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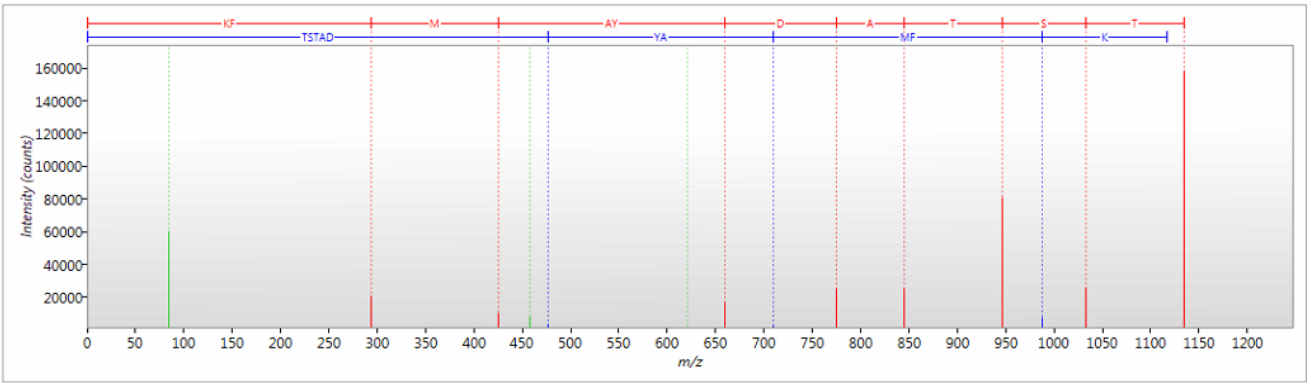
Fibrinogen gamma chain O5=Homo sapiens GN=FGG PE=1 SV=3
20 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										FCa	GFH	Le	ILc
AIQLTYNPDESSKPHMIDAAATLK	27009	8.97	10	2519.2055	2		0		no	3757.99	8057.03	2.56e+004	1093.73
AIQLTYNPDESSKPHMIDAAATLK	14222	8.74	11	2535.2477	2		0	[16] Oxidation M	no	1460.36	7973.94	3.81e+004	3319.80
ASTPNGYDNGIIVATWK	2447	8.79	13	1892.9153	2		0		no	3.27e+005	2.49e+005	3.40e+005	3.72e+005
DCQDIANK	303	9.44	18	962.4164	2		0	[2] Carbamidomethyl C	no	9.54e+004	3.58e+005	5.86e+005	8.10e+004
DCQDIANK	4698	9.44	18	962.4138	1		0	[2] Carbamidomethyl C	no	2.05e+004	2.18e+004	5.69e+004	1.93e+004
DNCCILDER	457	9.40	23	1193.4988	2		0	[3] Carbamidomethyl C [4] Carbamidomethyl C	yes	7.19e+005	1.05e+006	1.21e+006	5.77e+005
EGFGHLSPTGTTFWLGNEK	587	9.50	11	2206.0559	3		0		no	5.91e+005	3.55e+005	1.94e+006	5.32e+005
EGFGHLSPTGTTFWLGNEK	1708	9.19	11	2206.0540	3		0		no	3.42e+005	1.64e+006	4.47e+005	3.50e+005
FGSVCPPTCGIADFLSTYQTK	2135	9.45	16	2416.0723	2		0	[5] Carbamidomethyl C [9] Carbamidomethyl C	no	5.30e+004	4.90e+005	2.51e+005	1.98e+004
FGSVCPPTCGIADFLSTYQTK	2689	9.91	5	2416.0720	2		0	[5] Carbamidomethyl C [9] Carbamidomethyl C	no	2.24e+004	6491.52	4.93e+005	1.78e+004
FGSVCPPTCGIADFLSTYQTK	1325	9.64	17	2416.1137	3		0	[5] Carbamidomethyl C [9] Carbamidomethyl C	no	1.63e+005	7.71e+005	5.05e+005	9.22e+004
FGSVCPPTCGIADFLSTYQTK	1942	9.91	5	2416.1202	3		0	[5] Carbamidomethyl C [9] Carbamidomethyl C	no	4.25e+004	7.42e+004	5.82e+005	5.68e+004
IHLISTQSAIPYALR	6095	9.42	9	1681.9505	3		0		no	2774.25	1.21e+004	5.71e+004	3741.69
LTYAYFAGGDAGDAFGDFGDDPSDK	18948	8.99	8	2833.1673	2		0		no	946.28	5949.98	1.81e+004	80.38
LTYAYFAGGDAGDAFGDFGDDPSDK	20348	9.04	6	2833.1678	2		0		no	1185.79	45.13	2.61e+004	0.00
NWIQYK	2895	8.19	5	850.4384	2		0		no	4.18e+004	1.12e+005	5.82e+004	4.38e+004
QSGLYFIKPLK	3910	8.39	8	1292.7426	3		0		no	7.99e+004	2.15e+005	6.14e+004	7.75e+004
RLDGSVDFK	1145	8.42	13	1035.5264	2		0		no	2.43e+005	3.77e+005	4.84e+005	2.18e+005
RLDGSVDFK	18355	8.42	10	1035.4927	1		0		no	1.97e+004	7872.94	2.50e+004	1.73e+004
TSTADYAMFK	826	8.97	9	1133.5248	2		0		yes	1.46e+006	2.14e+006	1.20e+006	1.30e+006
TSTADYAMFK	27323	7.95	4	1149.5020	1		0	[8] Oxidation M	no	1409.49	1738.35	4734.46	349.00
VAQLEAQCEPCK	5012	8.72	4	1559.6897	2		0	[8] Carbamidomethyl C [12] Carbamidomethyl C	no	2.91e+004	6.25e+004	6.35e+004	3.25e+004
VAQLEAQCEPCK	55189	8.72	2	1559.6946	1		0	[8] Carbamidomethyl C [12] Carbamidomethyl C	no	0.00	12.43	422.33	0.00
VAQLEAQCEPCKDVTQIHDTGK	21287	---	---	2767.3241	2		0	[8] Carbamidomethyl C [12] Carbamidomethyl C	no	2028.62	1051.60	1.79e+004	9.35
VAQLEAQCEPCKDVTQIHDTGK	16917	---	---	2767.3236	2		0	[8] Carbamidomethyl C [12] Carbamidomethyl C	no	47.40	188.18	3.69e+004	6.84
VAQLEAQCEPCKDVTQIHDTGK	3479	9.45	5	2767.3063	3		0	[8] Carbamidomethyl C [12] Carbamidomethyl C	no	3.16e+004	1.25e+004	3.15e+005	1.65e+004
VAQLEAQCEPCKDVTQIHDTGK	3420	9.53	16	2767.3048	3		0	[8] Carbamidomethyl C [12] Carbamidomethyl C	no	1.39e+005	7.36e+005	4.93e+005	1.12e+005
VAQLEAQCEPCKDVTQIHDTGK	863	9.53	22	2767.3296	4		0	[8] Carbamidomethyl C [12] Carbamidomethyl C	yes	3.31e+005	1.89e+006	2.18e+006	3.12e+005
VAQLEAQCEPCKDVTQIHDTGKDCQDIANK	5155	7.86	7	3711.7830	5		0	[8] Carbamidomethyl C [12] Carbamidomethyl C [26] Carbamidomethyl C	no	2.51e+005	2.43e+005	5.54e+004	8.91e+004
VGPEADKYR	4682	8.26	9	1033.5211	3		0		no	1.41e+004	3.57e+004	3.61e+004	9128.42
VGPEADKYR	758	8.45	13	1033.5178	2		0		no	8.27e+004	2.46e+005	2.91e+005	4.17e+004
YEASILTHDSSIR	1298	9.10	5	1490.7410	3		0		no	3.81e+004	4.46e+004	3.64e+005	1.99e+004
YEASILTHDSSIR	1083	8.93	5	1490.7375	3		0		no	4.09e+004	5.62e+004	2.17e+005	2.99e+004
YEASILTHDSSIR	3519	8.93	5	1490.7156	2		0		no	3.30e+004	3.61e+004	1.28e+005	3.65e+004
YEASILTHDSSIR	3591	9.10	5	1490.7150	2		0		no	7.10e+004	5.18e+004	1.83e+005	4.04e+004
YLQEIYNSNNQK	14027	9.65	12	1512.7190	1		0		no	1420.01	718.99	2.87e+004	572.71
YLQEIYNSNNQK	610	9.65	24	1512.7213	2		0		no	3.81e+005	1.07e+006	1.28e+006	2.56e+005

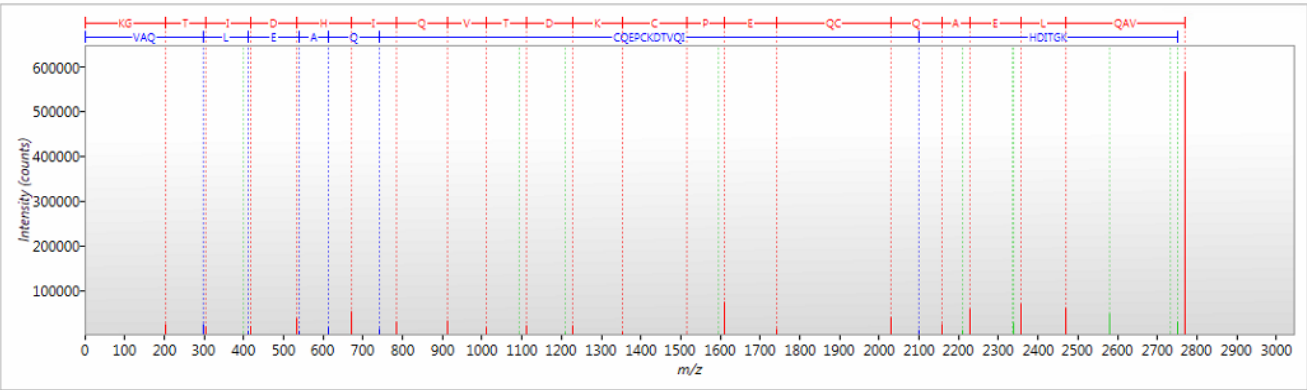
Fragment ions for: DNCCILDER



Fragment ions for: TSTADYAMFK



Fragment ions for: VAQLEAQCQEPCKDVTQIHDITGK

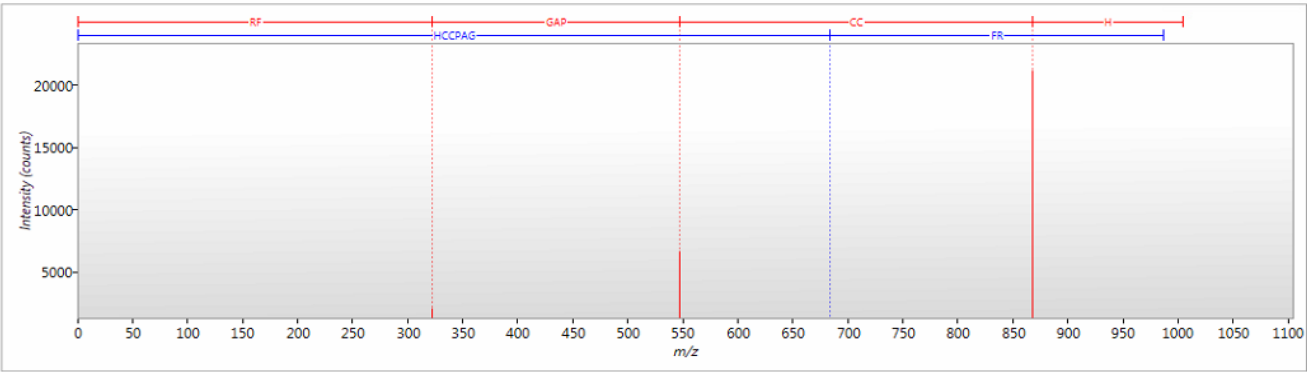


P28799

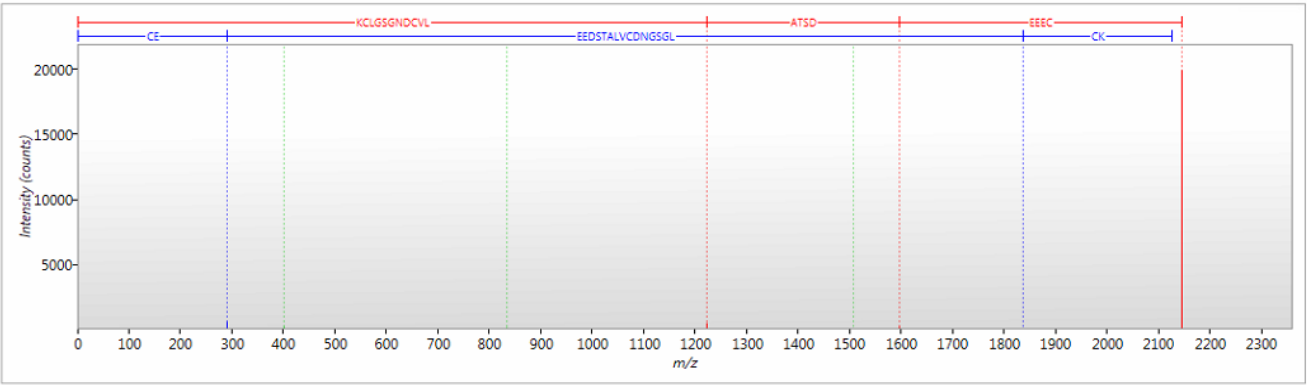
Granulins O5=Homo sapiens GN=GRN PE=1 SV=2
2 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances				
										PCa	BDH	Bc	Rc	
HCCPAGFR	632	6.29	4	1003.5125	2		0	[2] Carbamidomethyl C [3] Carbamidomethyl C	yes	5.23e+005	6.00e+005	4.37e+005	5.97e+005	
HCCPAGFR	7225	6.29	4	1003.5157	1		0	[2] Carbamidomethyl C [3] Carbamidomethyl C	yes	2.88e+004	3.28e+004	2.83e+004	3.03e+004	
QGVVACCPYRQGVCCADR	618	5.55	2	2142.8618	3		0	[5] Carbamidomethyl C [6] Carbamidomethyl C [13] Carbamidomethyl C [14] Carbamidomethyl C	yes	8.91e+005	5.02e+006	2.40e+006	1.55e+006	

Fragment ions for: HCCPAGFR



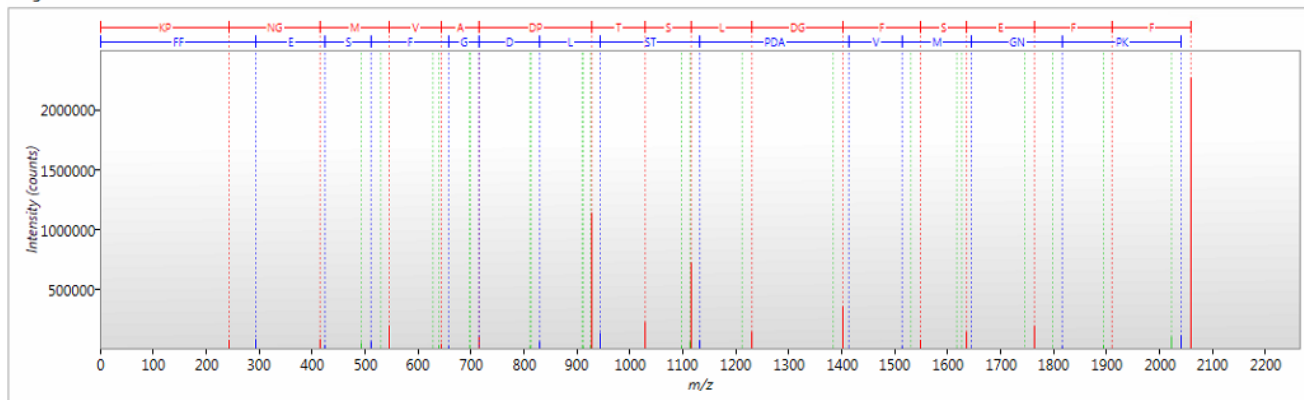
Fragment ions for: CEEEDSTALVCDNGSLGK



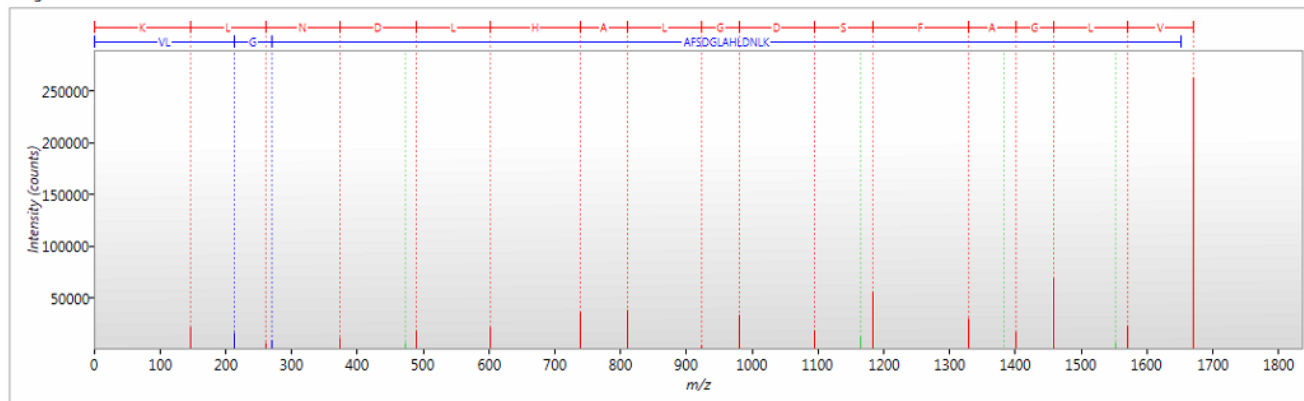
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2
10 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
EFTPPVQAAYQK	994	6.84	4	1377.6885	2		0		no	1.29e+005	2.95e+005	1.99e+005	1.08e+005
EFTPPVQAAYQK	13938	6.63	3	1377.6704	1		0		no	2775.17	3851.68	1.10e+004	1410.74
FFESFGDLSTPDAVMGNPK	158	10.32	15	2058.1039	3		0		yes	1.56e+006	5.92e+006	4.88e+006	3.67e+006
FFESFGDLSTPDAVMGNPK	316	10.32	16	2057.9433	2		0		yes	3.49e+005	9.33e+005	4.79e+006	2.49e+005
FFESFGDLSTPDAVMGNPK	1251	---	---	2058.1276	2		0		yes	6.45e+005	2.01e+006	1.19e+006	7.58e+005
FFESFGDLSTPDAVMGNPK	3168	9.82	5	2074.0015	3		0	[15] Oxidation M	no	3.20e+005	4.97e+005	2.09e+005	4.56e+005
FFESFGDLSTPDAVMGNPK	1824	9.82	12	2073.9398	2		0	[15] Oxidation M	no	1.19e+005	2.48e+005	7.77e+005	1.40e+005
FFESFGDLSTPDAVMGNPK	1400	9.98	9	2073.9406	2		0	[15] Oxidation M	no	1.40e+005	1.10e+005	8.78e+005	1.22e+005
GTFATLSELHCDK	15686	9.35	4	1477.7172	3		0	[11] Carbamidomethyl C	no	3826.31	1.68e+004	2.35e+004	5117.50
GTFATLSELHCDK	1302	9.35	5	1477.7077	2		0	[11] Carbamidomethyl C	no	6.21e+005	8.82e+005	6.79e+005	6.44e+005
MVHLTPEEKSAVTALVVGK	6367	6.82	2	1996.0066	3		0		no	8.20e+004	2.45e+005	1.68e+005	6.77e+004
SAVTALVVGK	1700	9.87	18	931.4917	1		0		no	2.19e+005	2.36e+005	1.16e+006	2.28e+005
SAVTALVVGK	4318	9.80	4	931.4826	1		0		no	9.51e+004	7.01e+004	1.24e+005	9.37e+004
VHLTPEEK	2846	9.43	10	951.4995	1		0		no	5870.63	1.11e+004	8.32e+004	4551.35
VHLTPEEK	256	9.71	5	951.5011	2		0		no	1.29e+005	4.39e+005	2.10e+006	1.19e+005
VHLTPEEK	157	9.43	10	951.5030	2		0		no	5.35e+004	1.96e+005	6.55e+005	5.29e+004
VLGAFSDGLAHLNLIK	673	9.94	13	1668.8576	3		0		yes	2.33e+005	6.89e+005	2.02e+006	2.82e+005
VNVDEVGGEALGR	3072	10.08	24	1313.6576	1		0		no	4611.70	3.43e+004	6.77e+005	6027.29
VVAGVANALAHK	6849	9.76	3	1148.6674	3		0		no	6779.42	5238.83	6.02e+004	4646.51

Fragment ions for: FFESFGDLSTPDAVMGNPK



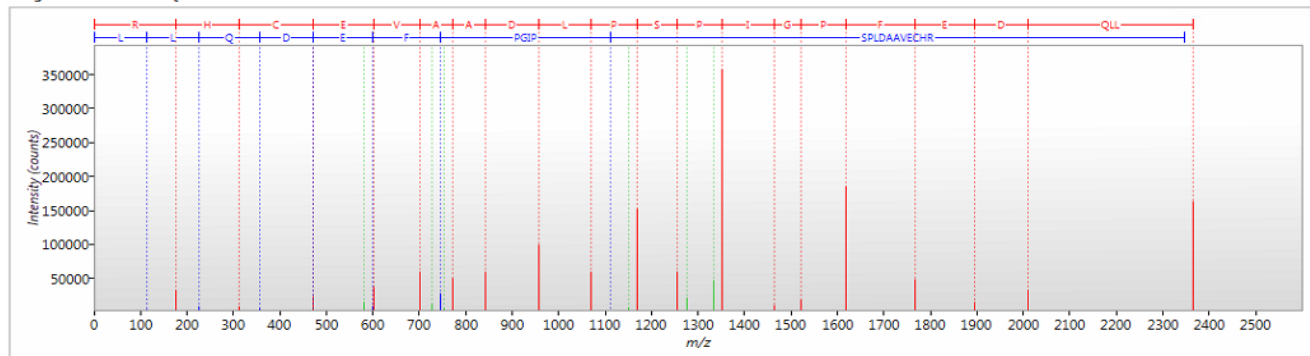
Fragment ions for: VLGAFSDGLAHLNLIK



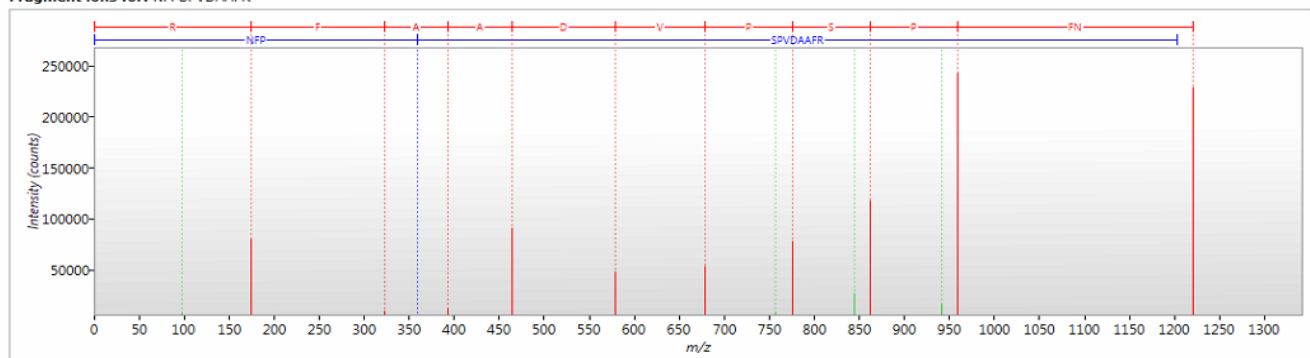
Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2
16 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PcA	BpH	Bc	Rc
DYFMP ^C GR	3126	8.50	14	1141.4899	2		0	[6] Carbamidomethyl C	no	1.30e+005	1.83e+005	9.31e+004	1.74e+005
ELISER	2354	7.83	5	745.3325	1		0		no	8.67e+004	1.27e+005	1.09e+005	8.58e+004
EVGTPHGILDSVDAAFI ^C PGSSR	1106	9.39	32	2497.2348	3		0	[19] Carbamidomethyl C	no	3.89e+005	9.97e+005	7.23e+005	4.25e+005
EVGTPHGILDSVDAAFI ^C PGSSR	2400	9.55	6	2497.2278	3		0	[19] Carbamidomethyl C	no	9.62e+004	3.84e+004	1.51e+005	4.28e+004
EVGTPHGILDSVDAAFI ^C PGSSR	9904	9.39	29	2497.1884	2		0	[19] Carbamidomethyl C	no	1.30e+004	5.88e+004	1.08e+005	3.04e+004
EVGTPHGILDSVDAAFI ^C PGSSR	16967	9.55	4	2497.2032	2		0	[19] Carbamidomethyl C	no	3192.02	6974.88	2.26e+004	4392.08
GEFVIVK	6956	8.25	13	764.4027	2		0		no	1.16e+004	1.76e+004	1.19e+004	1.32e+004
GGYTLVSGYPK	11643	7.83	14	1140.5579	1		0		no	3465.98	3620.22	1.52e+004	7280.19
LLQDEFPGIPSPDAAVE ^C HR	739	9.39	35	2363.1595	3		0	[19] Carbamidomethyl C	yes	3.76e+005	1.52e+006	1.42e+006	5.06e+005
LLQDEFPGIPSPDAAVE ^C HR	8642	9.39	30	2363.1061	2		0	[19] Carbamidomethyl C	yes	1.76e+004	5.85e+004	7.84e+004	4.84e+004
LVVIVLILK	4319	8.82	6	972.5371	2		0		no	1.16e+004	4.00e+004	3.20e+004	1.07e+004
NFPSPVDAAFR	359	8.52	36	1219.6052	2		0		yes	6.37e+005	1.52e+006	7.33e+005	5.55e+005
NFPSPVDAAFR	24032	8.78	2	1219.5919	1		0		no	1287.17	85.07	5659.54	1898.72
NFPSPVDAAFR	9513	8.52	33	1219.5866	1		0		yes	4.68e+004	2.63e+004	4.85e+004	4.06e+004
NFPSPVDAAFR	1793	8.78	2	1219.6012	2		0		no	1.20e+005	1.85e+005	2.64e+005	1.19e+005
QGHNSVFLIK	16115	6.73	4	1141.6258	3		0		no	1679.84	34.27	7580.48	53.81
QGHNSVFLIK	11917	7.33	7	1141.6286	3		0		no	821.83	2.47e+004	1.50e+004	4034.55
QGHNSVFLIK	12341	6.77	7	1141.6270	3		0		no	1.09e+004	1972.04	523.33	4470.92
QGHNSVFLIK	15415	7.32	3	1141.6235	3		0		no	0.00	0.00	6808.96	301.17
SGAQTAVITELPIVPIHEK	1734	8.70	11	1836.9075	3		0		no	1.91e+005	3.12e+005	7.79e+005	1.85e+005
SLGPN ^C CSANGPGLYLIHGPNLY ^C YSDVEK	1504	7.74	19	3281.5111	3		0	[7] Carbamidomethyl C [24] Carbamidomethyl C	yes	8.74e+005	1.64e+006	1.04e+006	8.12e+005
SLGPN ^C CSANGPGLYLIHGPNLY ^C YSDVEKLNAAK	3975	7.07	4	3778.8132	4		0	[7] Carbamidomethyl C [24] Carbamidomethyl C	no	9.43e+005	1.72e+005	8.50e+004	5.84e+005
SLGPN ^C CSANGPGLYLIHGPNLY ^C YSDVEKLNAAK	15749	7.07	2	3778.7897	3		0	[7] Carbamidomethyl C [24] Carbamidomethyl C	no	7.41e+004	2602.00	3356.97	3.18e+004
VDGAL ^C MEK	7902	7.46	10	1021.4457	1		0	[6] Carbamidomethyl C	no	7.07e+004	2.68e+004	5.24e+004	7.34e+004
VDGAL ^C MEKSLGPN ^C CSANGPGLYLIHGPNLY ^C YSDVEK	9894	6.13	3	4300.8817	3		0	[6] Carbamidomethyl C [7] Oxidation M [16] Carbamidomethyl C [33] Carbamidomethyl C	no	6.23e+004	1.53e+004	1992.79	6.79e+004
VVVVYPEKK	11511	6.87	3	1144.6236	3		0		no	1.03e+004	4.44e+004	1.43e+004	5445.52
YY ^C FQGNQFLR	24802	9.58	20	1494.6668	1		0	[3] Carbamidomethyl C	no	286.26	3638.62	5841.89	300.43

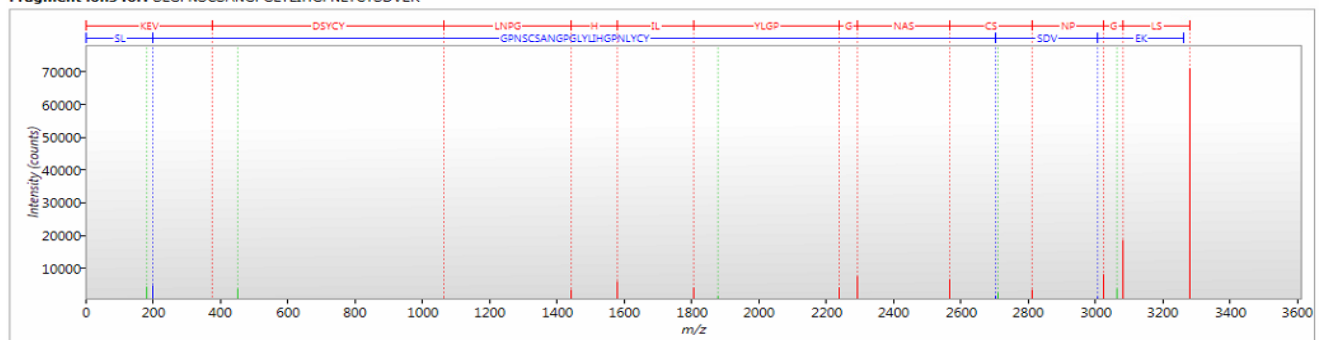
Fragment ions for: LLQDEFPGIPSPDAAVECHR



Fragment ions for: NFPSPVDAAFR



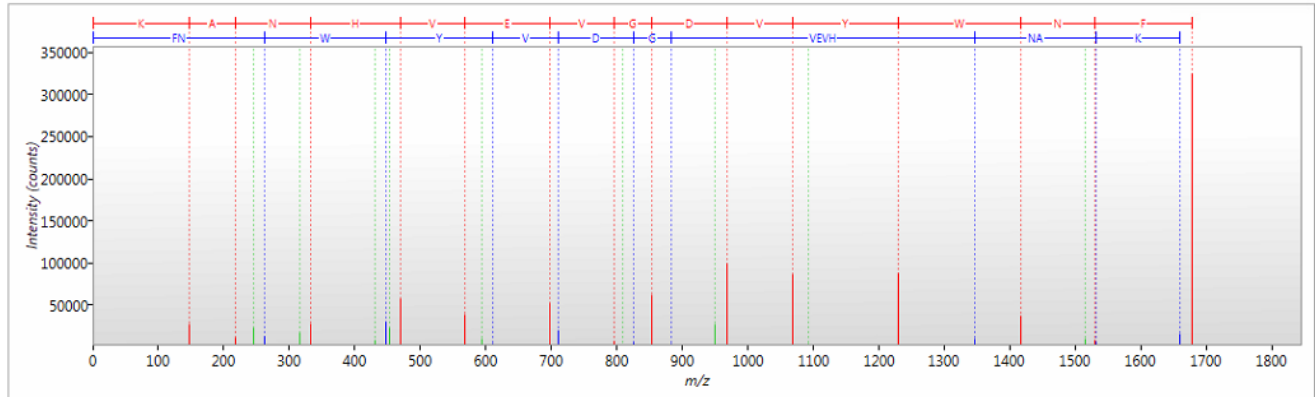
Fragment ions for: SLGPN^CCSANGPGLYLIHGPNLY^CYSDVEK



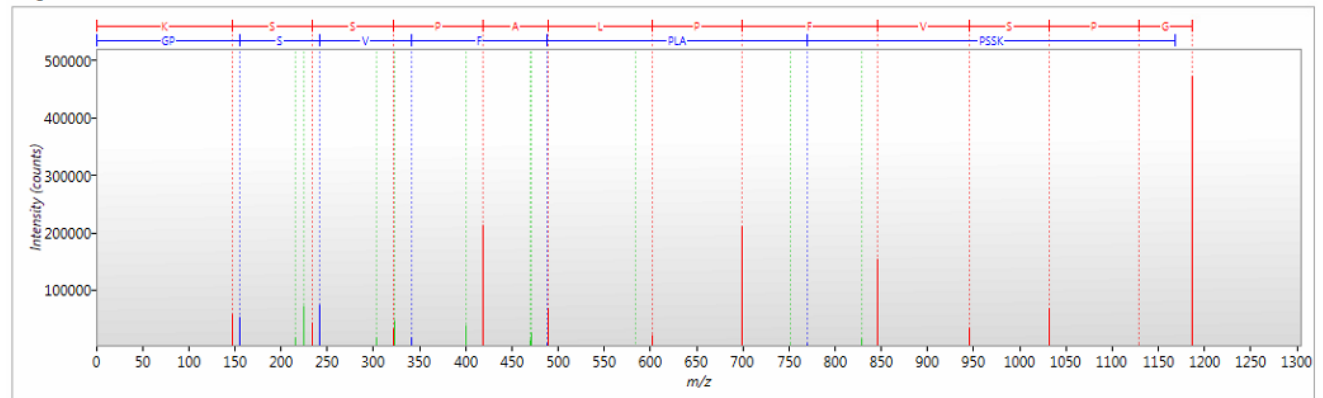
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1
6 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
FNWYVDGVEVHNAK	134	9.94	38	1676.7989	3		0		yes	1.37e+006	4.91e+006	2.79e+006	1.32e+006
FNWYVDGVEVHNAKTKPR	3105	7.42	9	2159.0944	3		0		no	4.41e+005	2.21e+005	1.36e+005	3.60e+005
GPSVFPLAPSSK	120	9.74	29	1185.6400	2		0		yes	1.57e+006	4.57e+006	2.73e+006	1.93e+006
GPSVFPLAPSSK	6495	9.74	22	1185.6390	1		0		yes	3.49e+004	7.79e+004	1.01e+005	5.23e+004
THTCPPCPAPELLGGPSVFLFPPKPK	6391	9.42	18	2843.4363	3		0	[4] Carbamidomethyl C.[7] Carbamidomethyl C	no	5.99e+005	1.45e+006	2.95e+005	4.45e+005
TPEVTCVVVDVSHEDPEVK	37	10.19	40	2138.0245	3		0	[6] Carbamidomethyl C	yes	3.86e+006	1.35e+007	8.12e+006	4.32e+006
TPEVTCVVVDVSHEDPEVK	975	10.19	40	2138.0098	2		0	[6] Carbamidomethyl C	yes	5.18e+005	1.10e+006	9.47e+005	5.63e+005
TTPPVLDSDGSFFLYSK	12563	9.44	6	1872.8941	1		0		no	200.07	4984.66	5.92e+004	2035.40

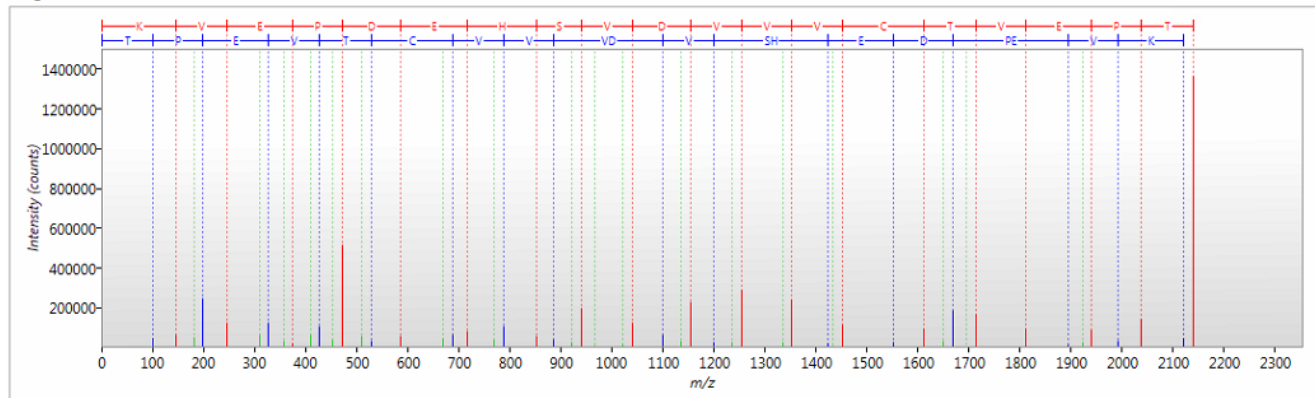
Fragment ions for: FNWYVDGVEVHNAK



Fragment ions for: GPSVFPLAPSSK



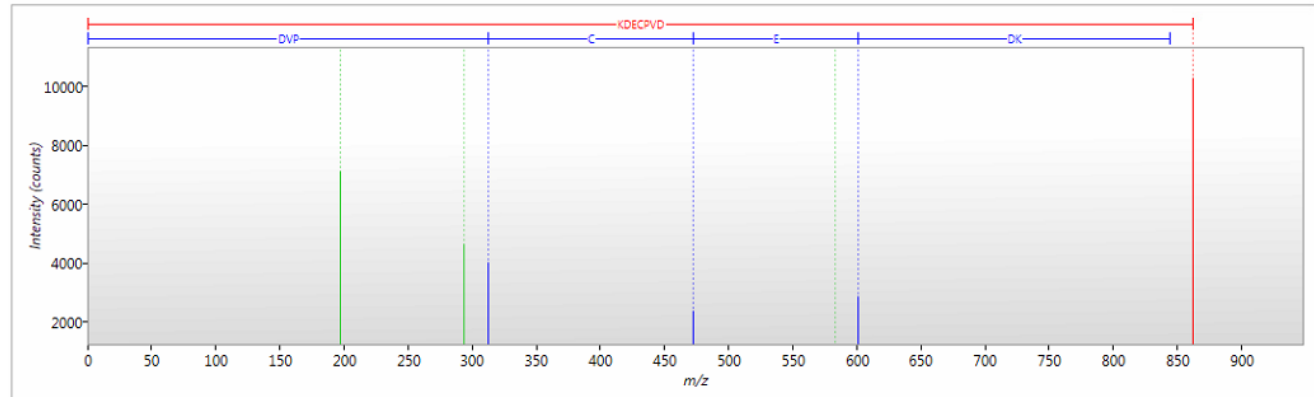
Fragment ions for: TPEVTCVVVDVSHEDPEVK



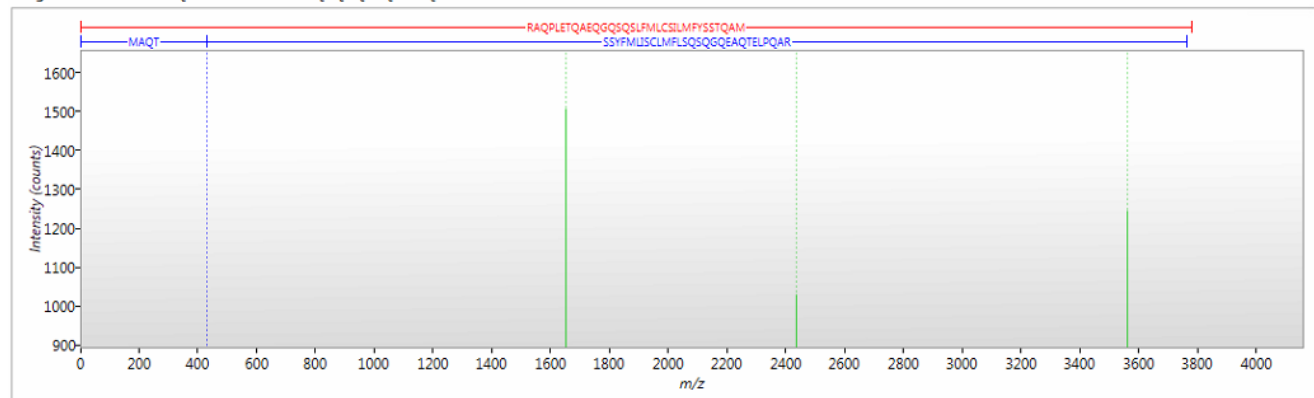
Lithostathine-1-alpha OS=Homo sapiens GN=REG1A PE=1 SV=3
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
DVP ^C EDK	8919	6.35	2	861.3525	1		0	[4] Carbamidomethyl C	yes	6.63e+004	4.49e+004	5.02e+004	5.85e+004
IS ^C PEGTNAYR	1730	8.51	10	1266.5851	2		1	[3] Carbamidomethyl C	no	3.43e+005	2.48e+005	1.56e+005	3.13e+005
MAQTSSYF ^C MLISCLMFLSQSQGQEAQTELPQAR	10493	5.55	2	3780.8949	4		0	[13] Carbamidomethyl C	yes	4.39e+005	1.20e+005	1.24e+005	3.24e+005
MAQTSSYF ^C MLISCLMFLSQSQGQEAQTELPQAR	14206	---	---	3780.9118	3		0	[13] Carbamidomethyl C	yes	2.12e+005	1.16e+004	2.95e+004	2.17e+005
SWIGIGAPSSVNP ^C GYCVSLTSSSTGFQK	12052	7.62	5	2686.2267	2		0	[15] Carbamidomethyl C	yes	1.06e+005	3.11e+004	1.35e+004	6.86e+004
SY ^C YFNEDR	36560	7.93	2	1415.6434	1		0	[3] Carbamidomethyl C	no	2589.29	626.70	2911.25	375.00

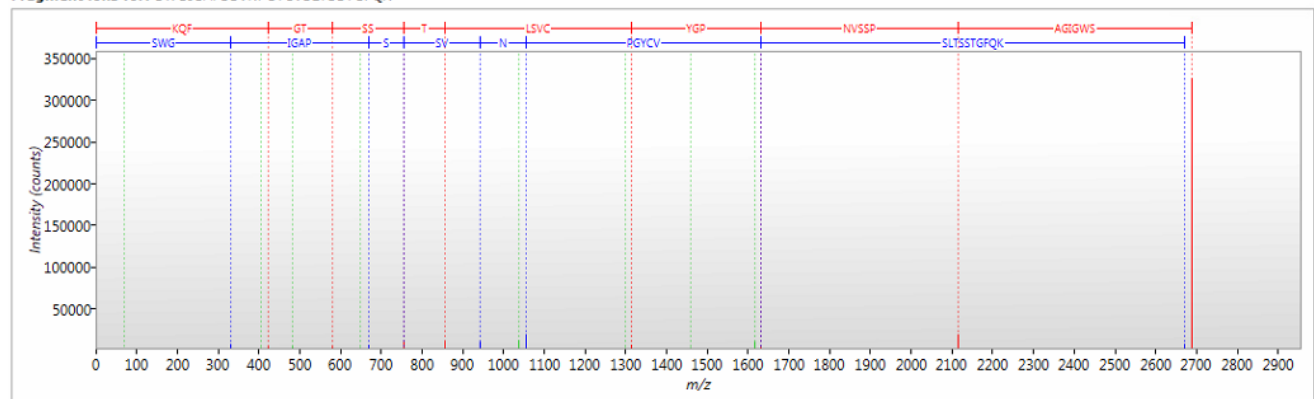
Fragment ions for: DVP^CEDK



Fragment ions for: MAQTSSYF^CMLISCLMFLSQSQGQEAQTELPQAR



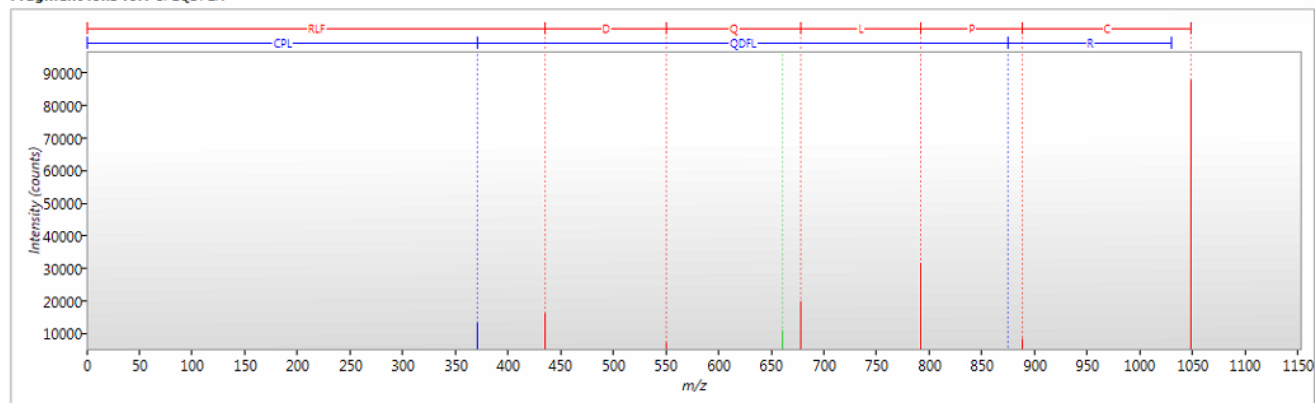
Fragment ions for: SWIGIGAPSSVNP^CGYCVSLTSSSTGFQK



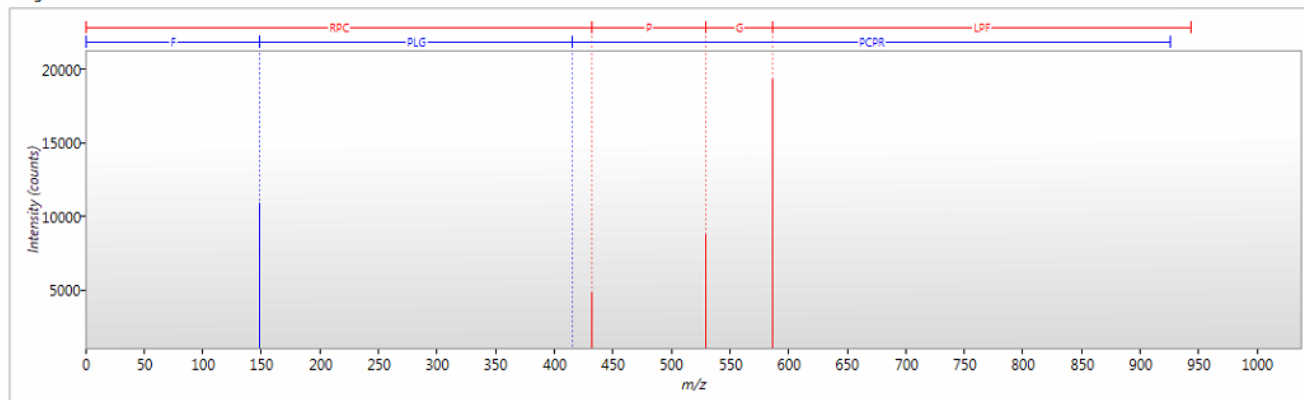
Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=1 SV=3
5 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
CPLQDFLR	3417	7.36	4	1047.5278	2		0	[1] Carbamidomethyl C	yes	7.69e+004	7.35e+004	4.03e+004	1.39e+005
DPYQEEV/PQGFQQLTK	6536	5.92	2	2051.0637	3		0		no	6.51e+004	4.78e+004	2.02e+004	2.86e+004
FPLGPCPR	226	6.55	3	942.5178	2		0	[6] Carbamidomethyl C	yes	6.51e+005	1.74e+006	1.31e+006	9.69e+005
QTPEYQNESSR	4272	6.17	2	1337.5738	2		1		no	1.72e+005	9.94e+004	7.31e+004	1.71e+005
QTPEYQNESSR	4291	6.17	2	1337.5693	3		1		no	1.31e+004	5440.79	2860.27	1.28e+004
TYPKDPYQEEV/PQGFQQLTK	4977	6.84	4	2540.1879	3		0		yes	1.96e+005	1.44e+005	1.27e+005	2.89e+005
TYPKDPYQEEV/PQGFQQLTK	28353	6.84	3	2540.1784	2		0		yes	879.82	113.84	181.07	1.30e+004

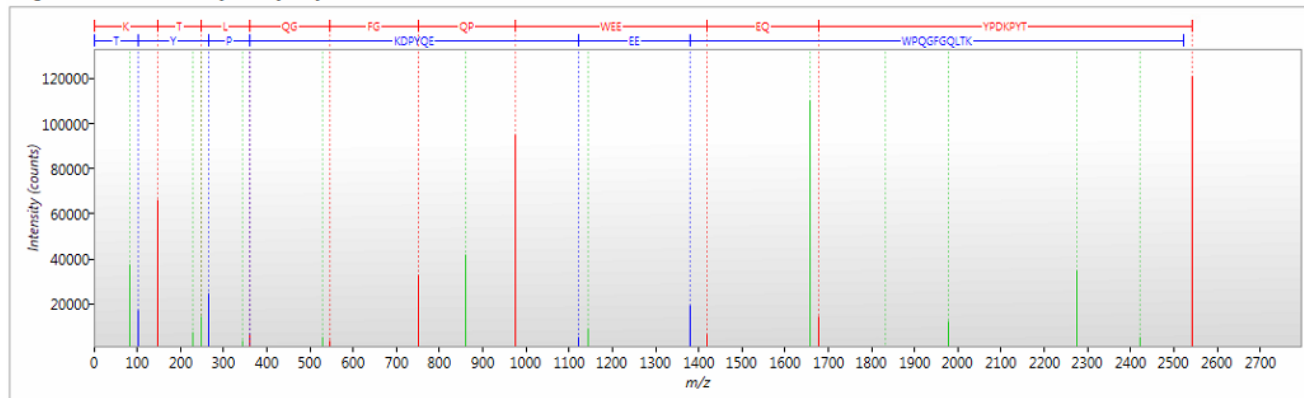
Fragment ions for: CPLQDFLR



Fragment ions for: FPLGPCPR



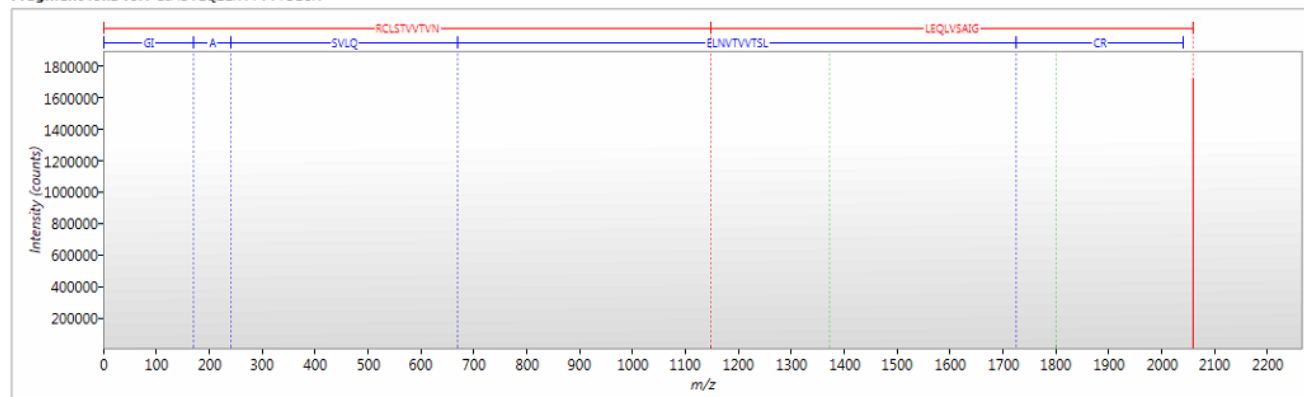
Fragment ions for: TYPKDPYQEEV/PQGFQQLTK



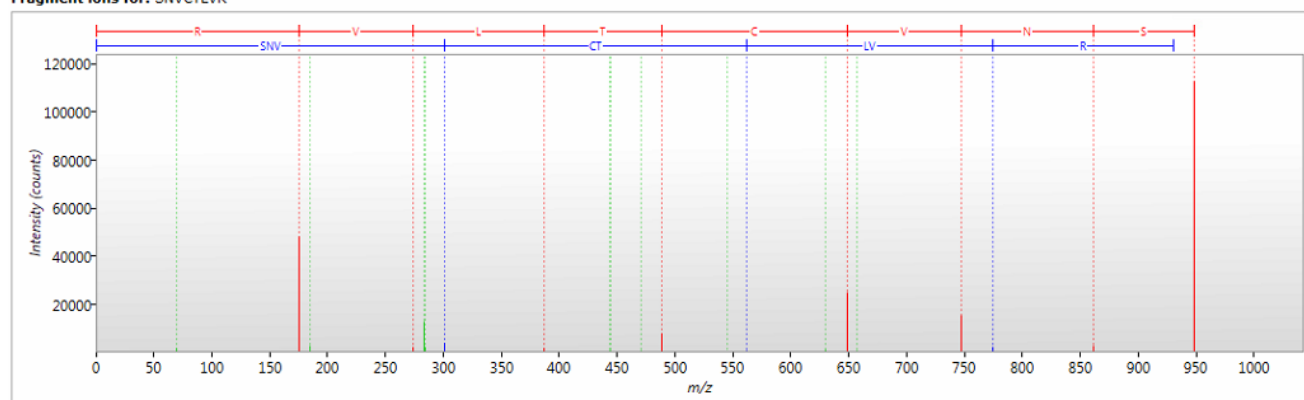
Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
GIASVLQELNVTVTSLCR	108	6.36	2	2058.1066	3		0	[18] Carbamidomethyl C	yes	3.06e+006	9.87e+006	5.81e+006	7.10e+006
SNVCTLVLR	774	8.50	7	947.4753	2		0	[4] Carbamidomethyl C	yes	7.52e+004	4.72e+005	2.14e+005	9.47e+004
SNVCTLVLR	8331	8.50	7	947.4689	1		0	[4] Carbamidomethyl C	no	1.00e+004	2.69e+004	2.93e+004	1.16e+004
VVLGAHNLSR	1378	7.85	2	1064.5671	2		0		yes	8.65e+004	1.44e+005	1.91e+005	8.67e+004
VVLGAHNLSR	21155	7.85	2	1064.5979	1		0		yes	948.68	399.85	4308.81	883.22

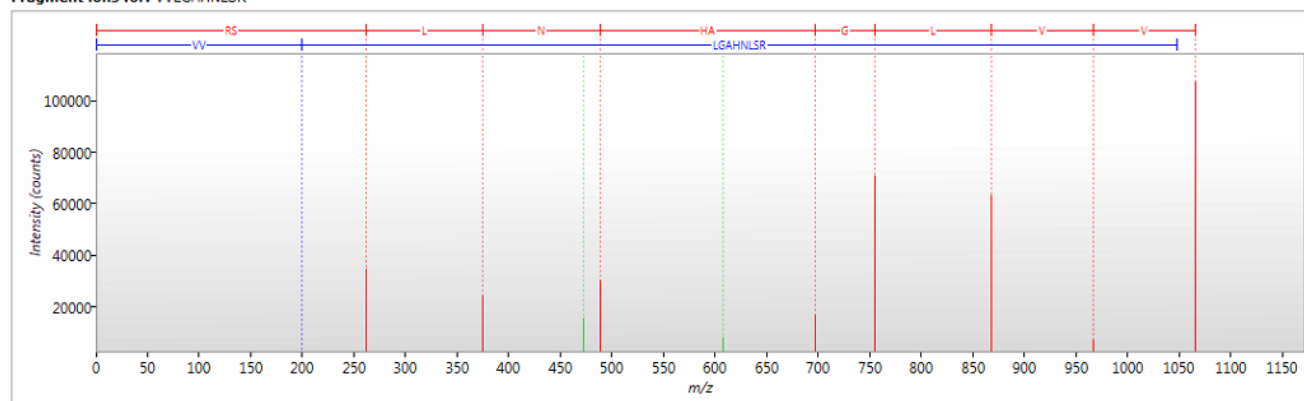
Fragment ions for: GIASVLQELNVTVTSLCR



Fragment ions for: SNVCTLVLR



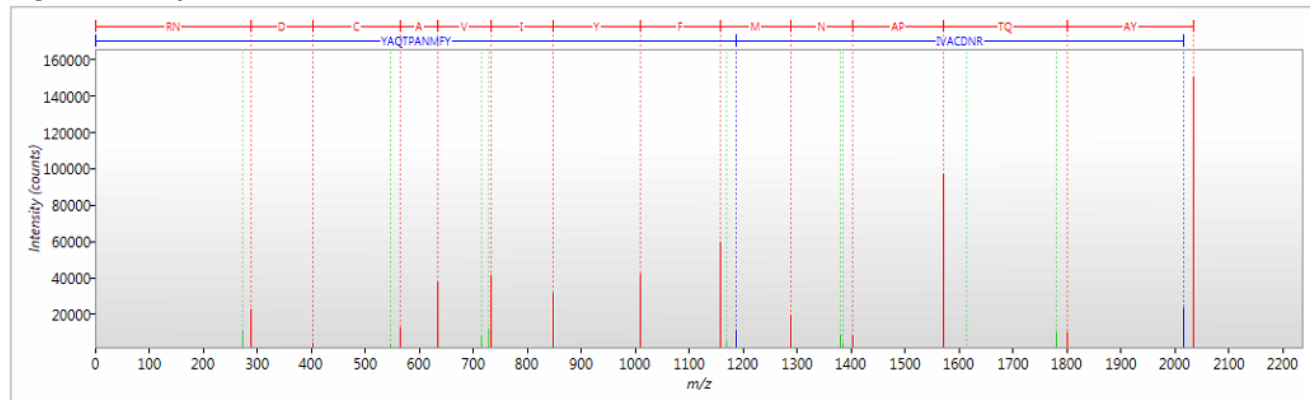
Fragment ions for: VVLGAHNLSR



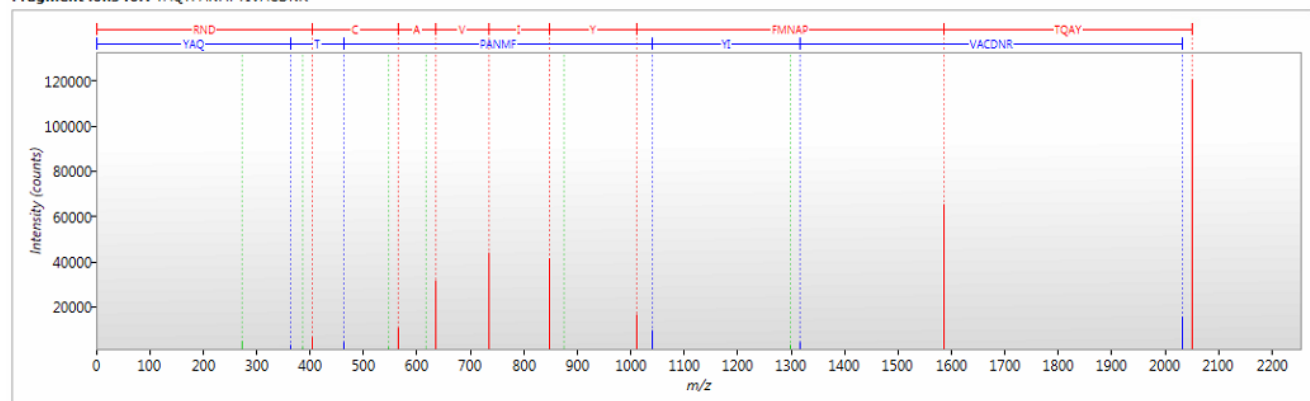
Non-secretory ribonuclease OS=Homo sapiens GN=RNASE2 PE=1 SV=2
4 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances				
										PCa	BPH	Bc	Rc	
NCHHSQSQPLIH ⁺ CNLTTPSQNISNCR	37114	6.28	2	3227.5388	4		0	[2] Carbamidomethyl C [14] Carbamidomethyl C [27] Carbamidomethyl C	no	1.52e+004	1520.83	552.59	4546.25	
RDPPQYPVVPVHLDR	1826	9.21	13	1786.9502	3		4		no	8.00e+005	7.19e+005	5.05e+005	1.12e+006	
RDPPQYPVVPVHLDR	1834	9.21	11	1786.8730	2		4		no	7.58e+005	4.67e+005	3.11e+005	7.08e+005	
YAQTANMFYIVACDNR	3357	9.22	18	2032.9330	2		0	[14] Carbamidomethyl C	yes	3.96e+005	9.64e+004	9.22e+004	3.96e+005	
YAQTANMFYIVACDNR	7697	9.22	3	2032.9203	3		0	[14] Carbamidomethyl C	yes	7.79e+004	2.44e+004	2.00e+004	4.83e+004	
YAQTANMFYIVACDNR	4203	8.65	9	2048.9156	2		0	[8] Oxidation M [14] Carbamidomethyl C	yes	2.63e+005	6.99e+004	2.92e+004	2.20e+005	

Fragment ions for: YAQTANMFYIVACDNR



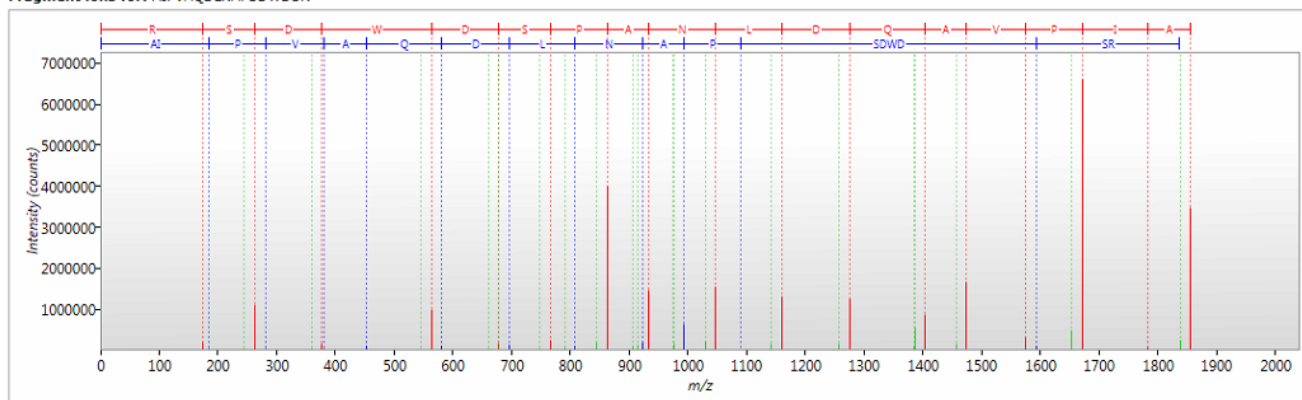
Fragment ions for: YAQTANMFYIVACDNR



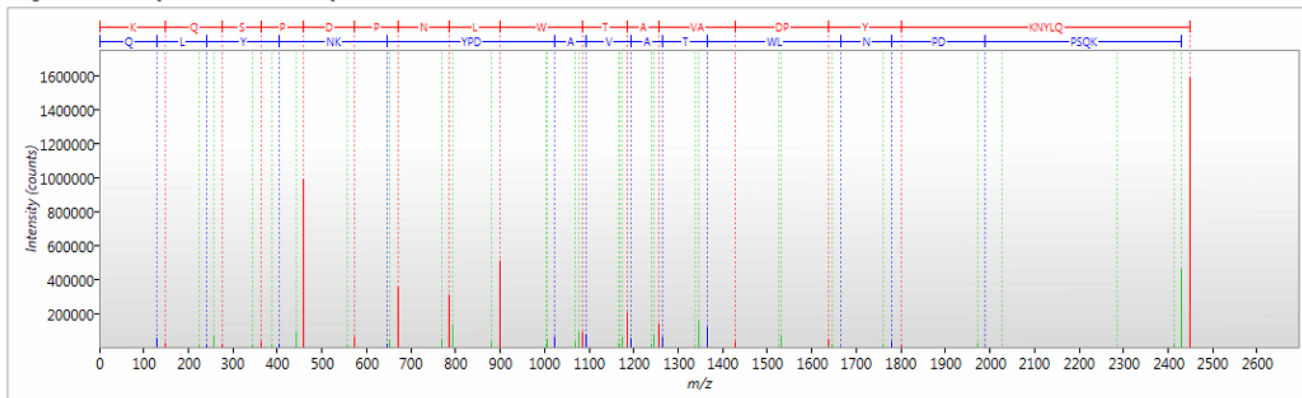
Osteopontin OS=Homo sapiens GN=SPP1 PE=1 SV=1
12 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
AIPVAQDLNAPSDVDSR	49	10.19	29	1853.8932	2		0		yes	4.91e+006	1.41e+006	2.94e+005	8.90e+006
AIPVAQDLNAPSDVDSR	12065	8.56	2	1853.8636	1		0		yes	2.10e+004	2349.36	38.11	5.26e+004
ANDESNEHSDVIDSQELSK	8148	9.02	19	2115.8263	2		1		no	6.43e+004	2.81e+004	8.19e+004	9.37e+004
DSYETSQLDDQSAETHSHK	15603	7.64	2	2176.9175	3		0		no	7767.28	20.15	0.00	12.49
GDSVYVGLR	883	9.36	27	964.4756	1		0		no	3.96e+005	3.11e+005	2.92e+005	7.03e+005
GKDSYETSQLDDQSAETHSHK	2773	9.70	12	2362.0429	4		0		no	1.21e+005	2.30e+004	1.41e+004	1.34e+005
GKDSYETSQLDDQSAETHSHK	18667	---	---	2362.0330	5		0		no	5575.23	1809.25	66.66	4217.73
GKDSYETSQLDDQSAETHSHK	13960	---	---	2362.0279	2		0		no	2.95e+004	6476.19	8218.69	5.87e+004
GKDSYETSQLDDQSAETHSHK	12532	---	---	2362.0287	2		1		no	3280.36	732.37	2933.33	3.50e+004
GKDSYETSQLDDQSAETHSHK	4598	9.56	5	2362.0252	3		0		no	9.44e+004	1.66e+004	2.21e+004	1.60e+004
GKDSYETSQLDDQSAETHSHK	3955	9.70	19	2362.0292	3		0		no	2.10e+005	7.52e+004	4.88e+004	2.80e+005
GKDSYETSQLDDQSAETHSHK	3829	8.50	2	2362.0276	3		0		no	1.27e+005	6.21e+004	6.42e+004	2.21e+005
GKDSYETSQLDDQSAETHSHK	22782	---	---	2362.0290	2		0		no	9947.65	20.17	299.55	726.90
GKDSYETSQLDDQSAETHSHK	2706	9.56	6	2362.0348	4		0		no	1.46e+005	2.86e+004	3.58e+004	4.06e+004
ISHELDSASSEVN	8146	8.98	16	1386.6102	1		0		no	2.39e+004	8453.70	1.26e+004	3.29e+004
ISHELDSASSEVN	223	8.98	18	1386.6220	2		0		no	7.87e+005	7.03e+005	2.46e+005	9.83e+005
KANDESNEHSDVIDSQELSK	12254	8.30	7	2244.0060	2		0		no	3.96e+004	8692.03	3355.67	6.88e+004
QETLPSK	3207	8.97	15	801.4198	1		0		no	1.94e+004	7762.62	3168.97	5.23e+004
QETLPSK	1769	9.24	4	801.4157	2		0		no	6.80e+004	4.41e+004	2.50e+004	9.14e+004
QETLPSK	750	8.97	16	801.4209	2		0		no	1.16e+005	1.17e+005	5.00e+004	1.85e+005
QLYNKYPDAVATV/LNPDPSQK	4022	9.67	26	2447.2022	2		0		yes	4.58e+005	1.07e+005	7.29e+004	6.74e+005
QLYNKYPDAVATV/LNPDPSQK	395	9.67	28	2447.2125	3		0		yes	3.46e+006	1.29e+006	3.70e+005	5.62e+006
QNLLAPQNAVSEETNDFKQETLPSK	15602	9.06	21	2887.4166	2		0		no	1.53e+004	1040.55	97.36	1.50e+004
QNLLAPQNAVSEETNDFKQETLPSK	726	9.06	29	2887.4055	3		0		no	1.09e+006	2.42e+005	2.49e+005	1.07e+006
RPDIQYPDATDEDTISHMESEELNGAYK	16392	7.96	2	3239.4217	3		0	[18] Oxidation M	no	1.01e+004	3175.95	3927.86	1.81e+004
YPDAVATV/LNPDPSQK	282	9.94	20	1800.8694	2		0		yes	1.57e+006	1.16e+006	5.08e+005	4.30e+006
YPDAVATV/LNPDPSQK	23471	---	---	1800.8552	1		0		yes	1917.48	50.20	306.93	2.78e+004

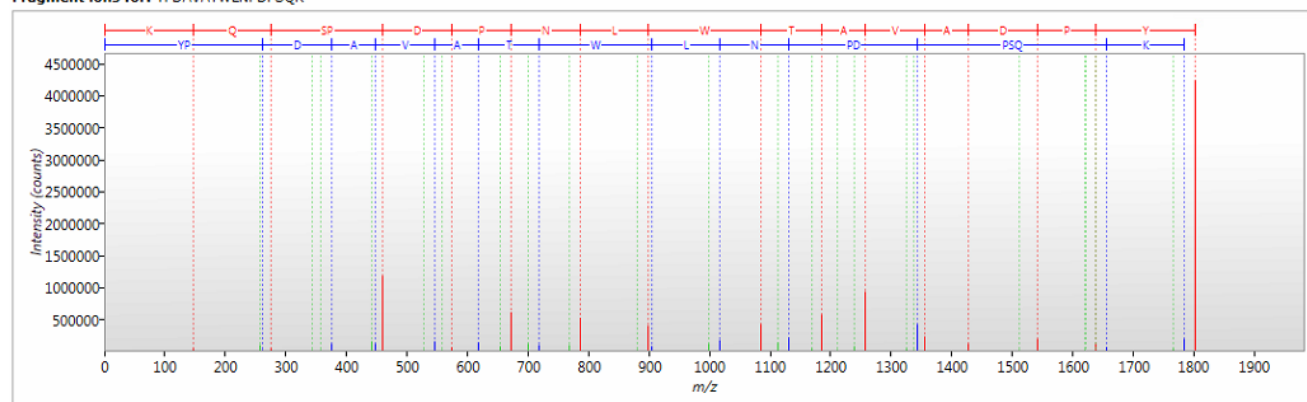
Fragment ions for: AIPVAQDLNAPSDVDSR



Fragment ions for: QLYNKYPDAVATV/LNPDPSQK



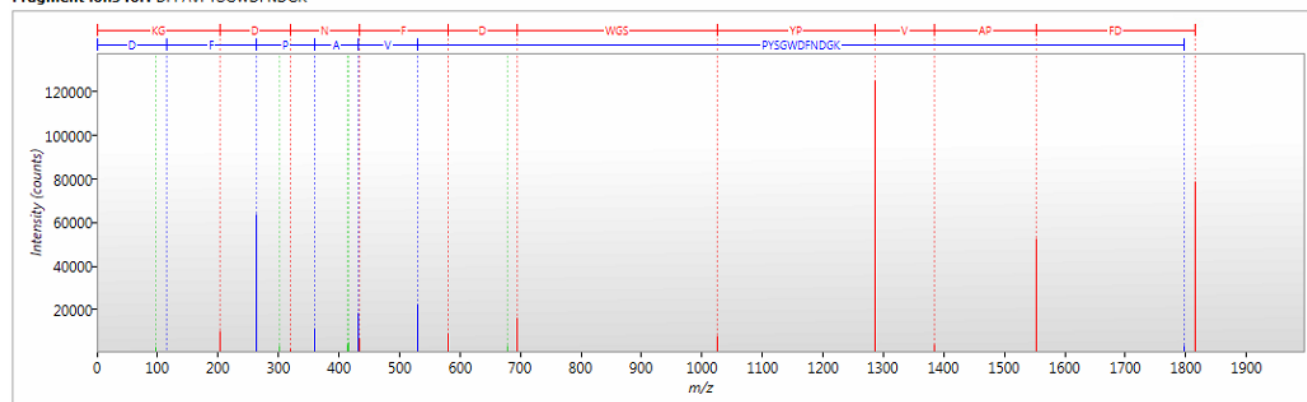
Fragment ions for: YPDAVATWLNPDPSQK



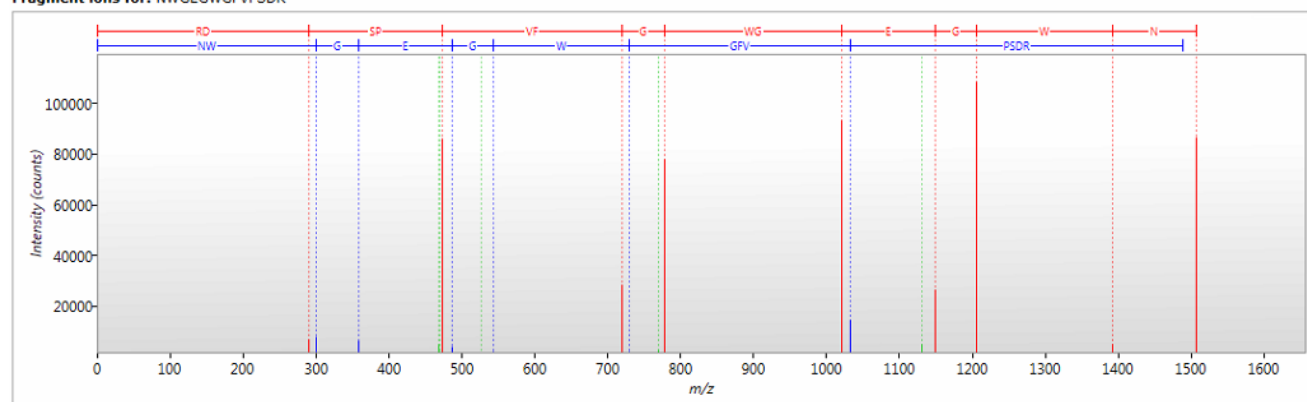
Pancreatic alpha-amylase OS=Homo sapiens GN=AMY2A PE=1 SV=2
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
DFPAVPYSGW/DFNDGK	3244	9.05	24	1813.8456	2		1		yes	6.36e+005	3.06e+005	1.28e+005	4.56e+005
NWGEGW/GFVPSDR	40574	8.92	4	1505.7445	1		0		yes	3908.80	198.28	149.71	3108.02
TGSGDIENYNDATQVR	828	9.47	27	1738.7766	2		1		yes	5.69e+005	3.87e+005	1.83e+005	6.98e+005

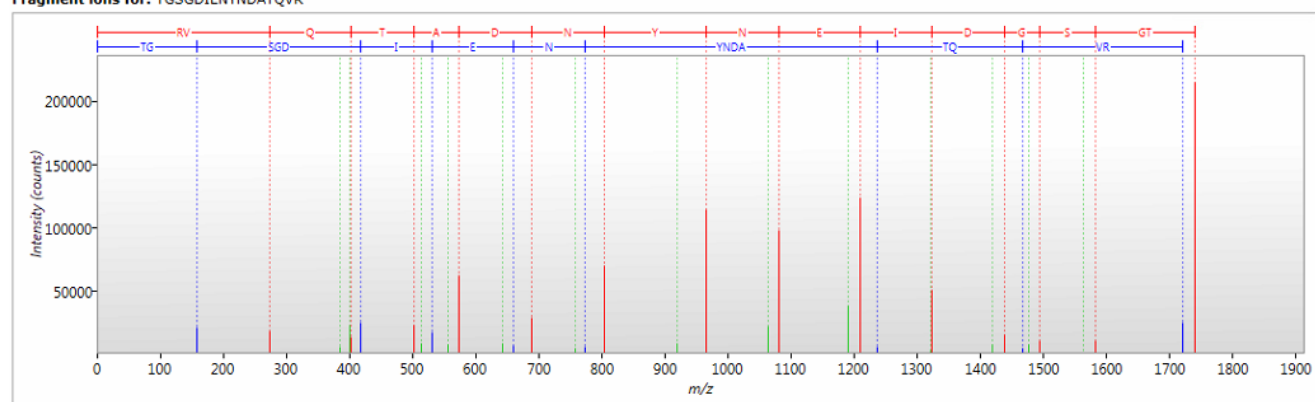
Fragment ions for: DFPAVPYSGWDFNDGK



Fragment ions for: NWGEGW/GFVPSDR



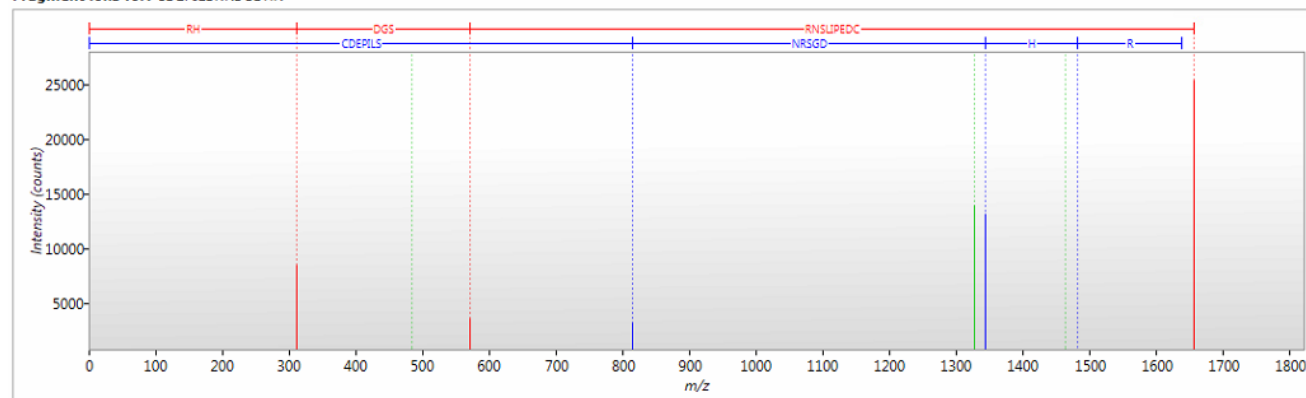
Fragment ions for: TGSGDIENYNDATQVR



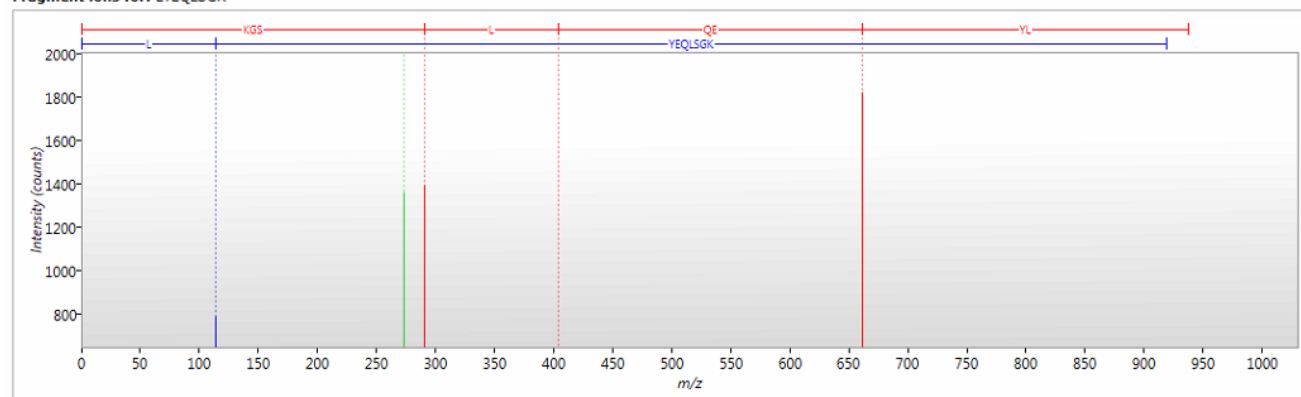
Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
ČDEPILSNRSGDHR	1506	6.48	2	1654.7567	3		0	[1] Carbamidomethyl C	yes	1.70e+005	8.96e+005	2.67e+005	3.94e+005
ČDEPILSNRSGDHR	4567	6.48	2	1654.7438	2		0	[1] Carbamidomethyl C	yes	6.62e+004	2.32e+005	9.78e+004	1.17e+005
LYEQLSGK	504	7.06	3	936.4529	1		0		yes	3.00e+005	6.88e+005	7.13e+005	3.37e+005
VLTPQTQVK	27675	7.13	3	884.5237	1		0		yes	210.67	0.96	45.33	945.23

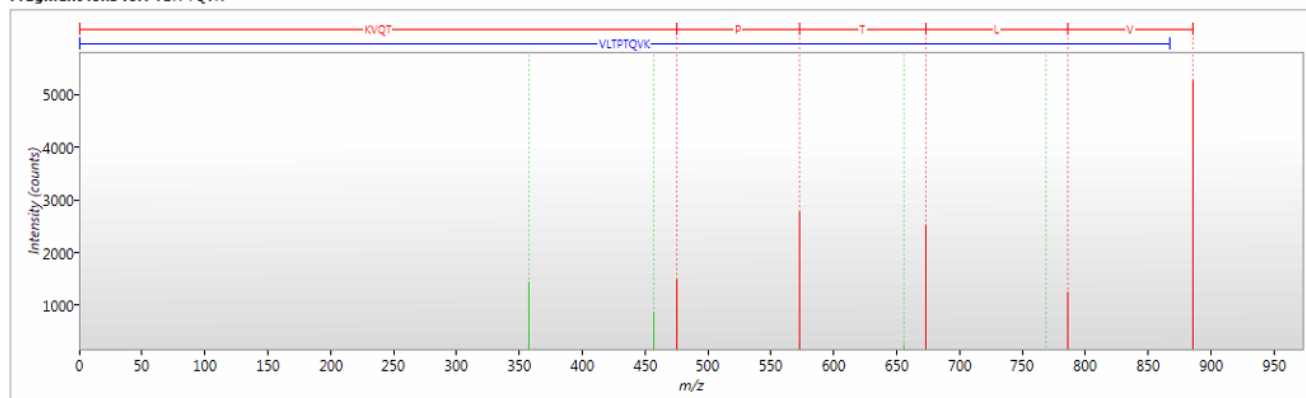
Fragment ions for: CDEPILSNRSGDHR



Fragment ions for: LYEQLSGK



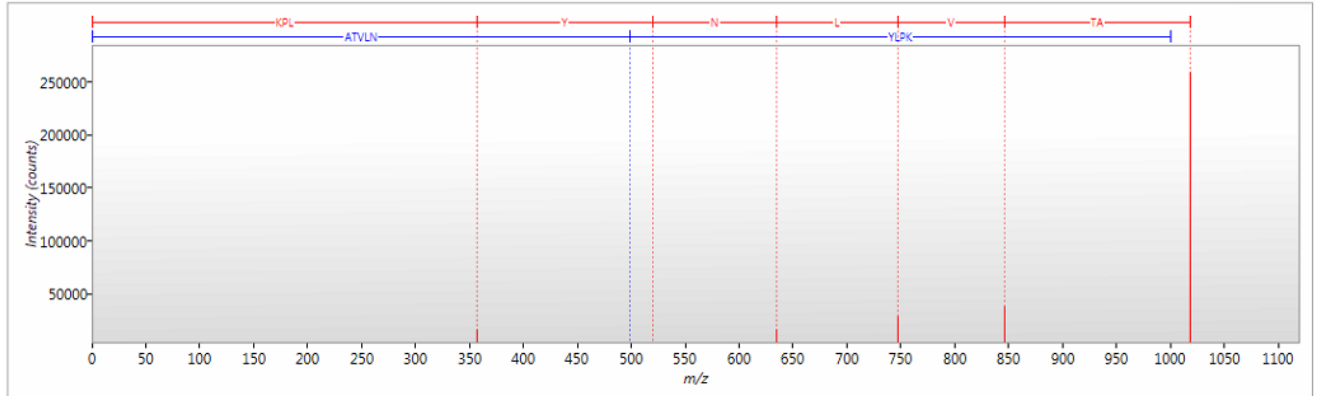
Fragment ions for: VLTPQTQVK



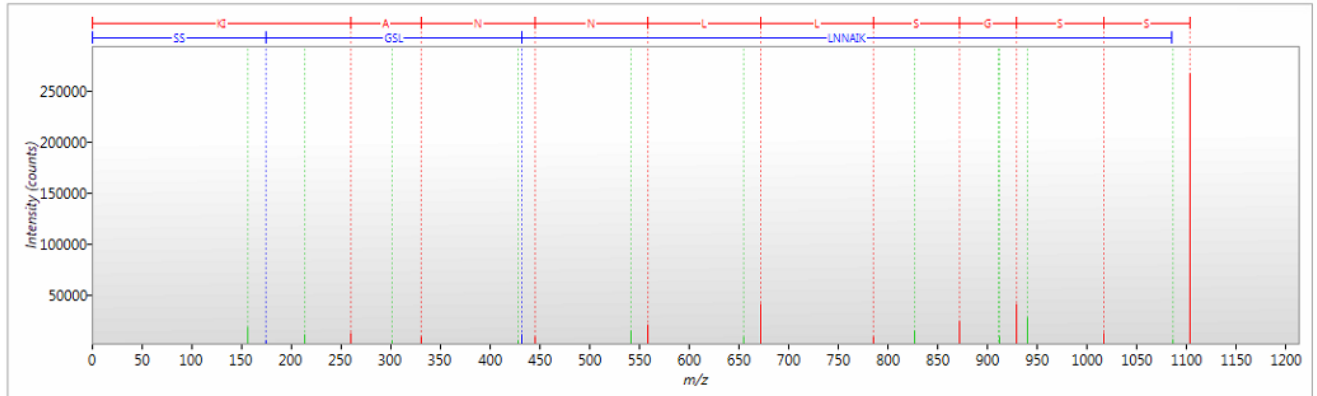
Pregnancy zone protein OS=Homo sapiens GN=PZP PE=1 SV=4
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances				
										PCa	BPH	Bc	Rc	
ATVLNLYPK	3454	8.16	2	1017.4788	2		0		yes	7.01e+004	1.59e+005	1.78e+005	7.47e+004	
ATVLNLYPK	6752	8.16	3	1017.4771	1		0		yes	1.81e+005	1.66e+005	2.07e+005	2.05e+005	
ATVLNLYPK	11989	7.65	2	1017.5664	1		0		no	1.43e+004	1.33e+004	2.54e+004	1.99e+004	
GEESYICGNER	3626	5.16	2	1472.5341	3		0	[6] Carbamidomethyl C.[8] Carbamidomethyl C	no	3.23e+004	4.41e+004	3.42e+004	1.97e+004	
NQGNTVLTAFVLK	59867	8.88	2	1490.7403	2		0		no	2.56e+004	6.78e+004	5.62e+004	5.52e+004	
NQGNTVLTAFVLKTFQAAR	33453	7.99	5	2165.0244	2		0		no	3.85e+004	2.15e+004	1.17e+004	1.38e+004	
SSGSLNNIAIK	1003	8.83	3	1102.6033	2		0		yes	2.86e+005	3.97e+005	6.70e+005	2.32e+005	
SSGSLNNIAIK	12251	8.83	2	1102.5911	1		0		yes	1.01e+004	4769.72	2.28e+004	5619.48	
VDSHFR	3010	8.71	5	759.3659	1		0		no	4.04e+004	5.40e+004	8.85e+004	3.70e+004	
VDSHFR	3391	8.71	5	759.3723	2		0		no	1.17e+004	4.55e+004	5.23e+004	1.97e+004	
YGAATFTR	1217	9.19	7	885.4315	2		0		yes	4.34e+004	1.73e+005	1.72e+005	3.39e+004	

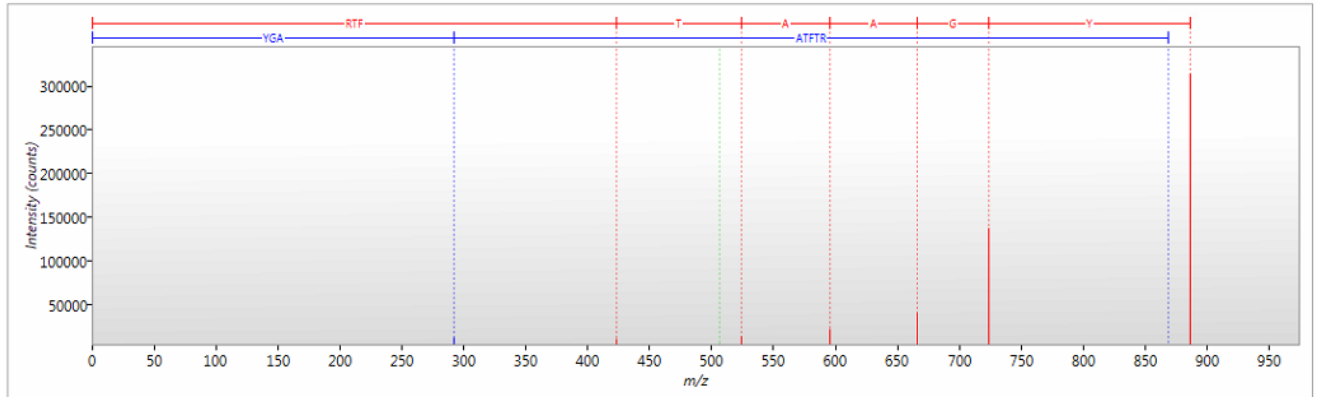
Fragment ions for: ATVLNLYPK



Fragment ions for: SSGSLNNIAIK



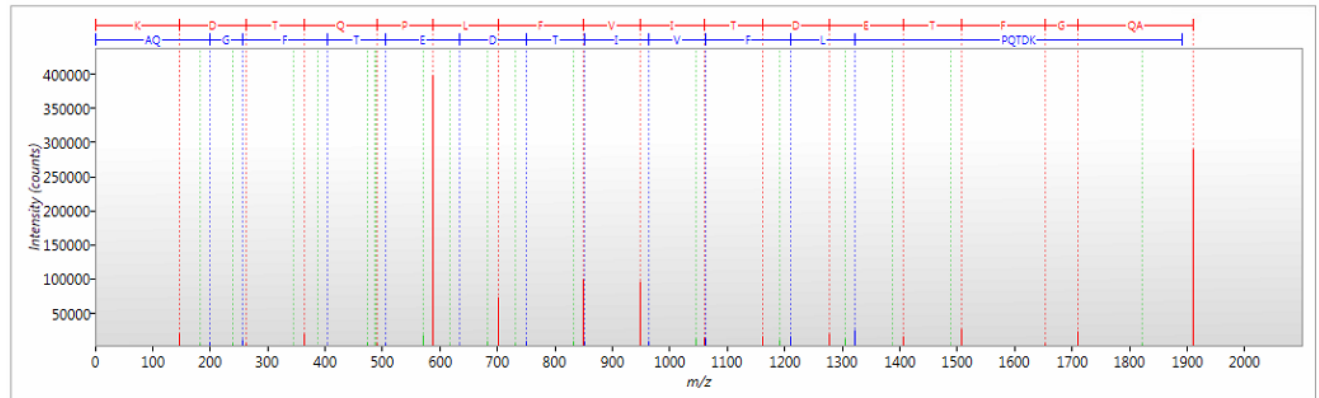
Fragment ions for: YGAATFTR



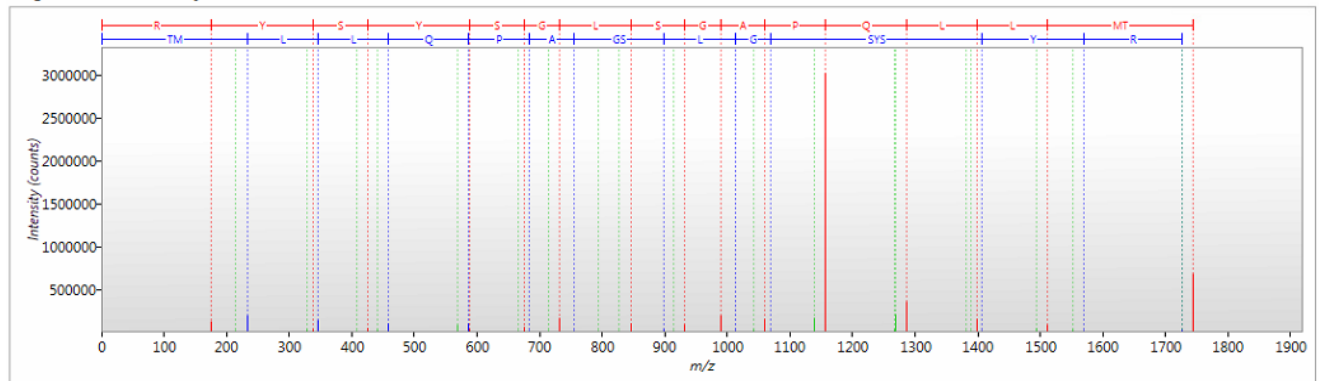
Prostaglandin-H2 D-isomerase O5=Homo sapiens GN=PTGDS PE=1 SV=1
9 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BRH	Sc	Rc
AQGFTEDTIVFLPQTDK	93	10.15	38	1908.9483	2		0		yes	6.98e+006	3.46e+006	8.58e+005	3.96e+006
AQGFTEDTIVFLPQTDK	625	10.15	38	1908.9242	3		0		yes	1.24e+006	8.88e+005	5.40e+005	6.90e+005
AQGFTEDTIVFLPQTDK	11612	---	---	1908.9079	1		0		yes	5.51e+004	9478.26	5261.12	2.48e+004
AQGFTEDTIVFLPQTDK ^{CM} TEQ	2544	9.64	11	2558.1465	2		1	[18] Carbamidomethyl C	no	3.08e+005	2.88e+005	2.34e+005	5.02e+005
AQGFTEDTIVFLPQTDK ^{CM} TEQ	913	9.64	11	2558.1419	3		1	[18] Carbamidomethyl C	no	1.06e+006	3.43e+005	2.11e+005	9.77e+005
AQGFTEDTIVFLPQTDK ^{CM} TEQ	2717	9.04	26	2574.1621	2		0	[18] Carbamidomethyl C; [19] Oxidation M	no	5.19e+005	6.63e+004	3.52e+004	1.87e+005
AQGFTEDTIVFLPQTDK ^{CM} TEQ	882	9.04	26	2574.1686	3		0	[18] Carbamidomethyl C; [19] Oxidation M	no	1.42e+006	4.78e+005	2.44e+005	6.60e+005
FTAF ^{CK}	1057	9.17	29	772.3566	1		0	[5] Carbamidomethyl C	no	6.44e+005	3.17e+005	1.82e+005	3.94e+005
FTAF ^{CK}	548	9.17	29	772.3619	2		0	[5] Carbamidomethyl C	no	5.64e+005	5.81e+005	2.23e+005	3.20e+005
GPGE ^{DFR}	280	9.01	26	776.3640	2		1		no	5.94e+005	6.92e+005	2.79e+005	4.99e+005
MATLYSR	949	9.26	29	840.4121	2		0		no	2.92e+005	2.37e+005	1.27e+005	2.37e+005
MATLYSR	3339	9.26	26	840.4057	1		0		no	9.29e+004	4.33e+004	4.02e+004	1.21e+005
^M MATLYSR	2152	8.75	4	856.4152	2		0	[1] Oxidation M	no	1.15e+005	8.90e+004	4.81e+004	4.99e+004
^M MATLYSR	10858	7.96	6	856.4169	2		0	[1] Oxidation M	no	1.23e+004	4688.58	1426.55	7352.22
TMLLQPAGSLGSYSYR	14880	8.95	8	1742.8515	1		0		yes	1.23e+004	1411.25	2841.06	2.69e+004
TMLLQPAGSLGSYSYR	156	9.98	35	1742.8614	2		0		yes	3.14e+006	1.50e+006	5.87e+005	3.15e+006
^T MLLQPAGSLGSYSYR	1709	9.19	4	1758.8468	2		0	[2] Oxidation M	no	8.75e+005	3.85e+005	3.46e+005	5.71e+005
^T MLLQPAGSLGSYSYR	388	9.37	32	1758.8416	2		0	[2] Oxidation M	yes	2.23e+006	1.88e+006	4.64e+005	1.33e+006

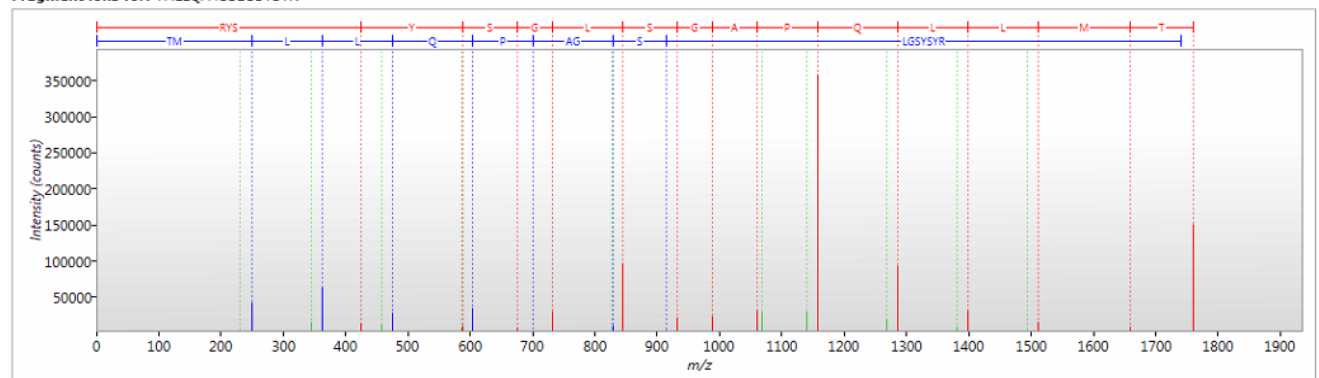
Fragment ions for: AQGFTEDTIVFLPQTDK



Fragment ions for: TMLLQPAGSLGSYSYR



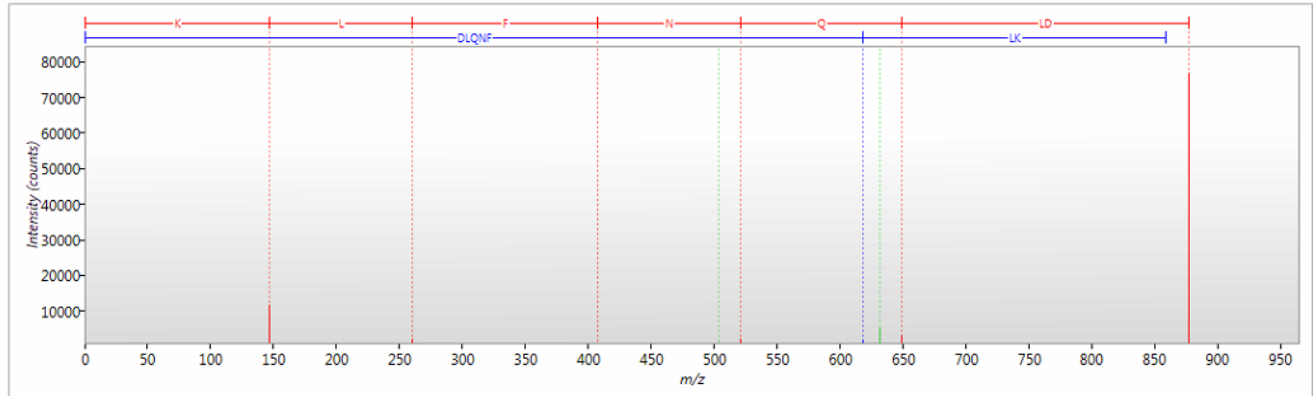
Fragment ions for: TMLLQPAGSLGSYSYR



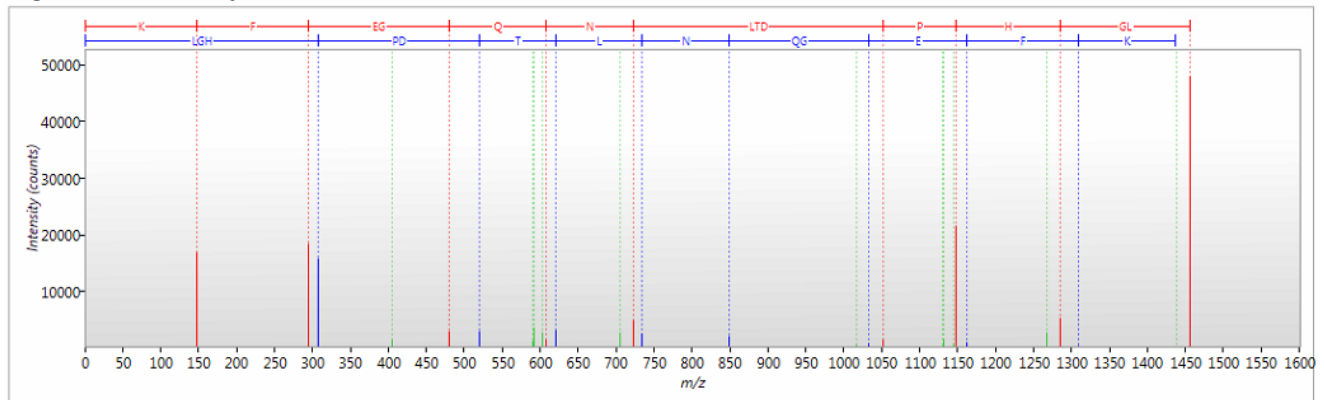
Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
DLQNFLK	2467	8.49	5	876.4655	2		0		yes	1.90e+004	1.13e+005	4.15e+004	3.72e+004
LGHPTLNQGEFK	3621	9.24	4	1454.7006	2		0		yes	3.02e+004	2.08e+005	2.24e+004	7.36e+004
LGHPTLNQGEFK	5004	6.41	2	1454.6958	2		0		yes	1.24e+004	7.77e+004	6.62e+004	2.11e+004
LTVASHEK	12038	8.88	2	970.4358	3		0		no	534.46	1360.21	4493.00	828.10

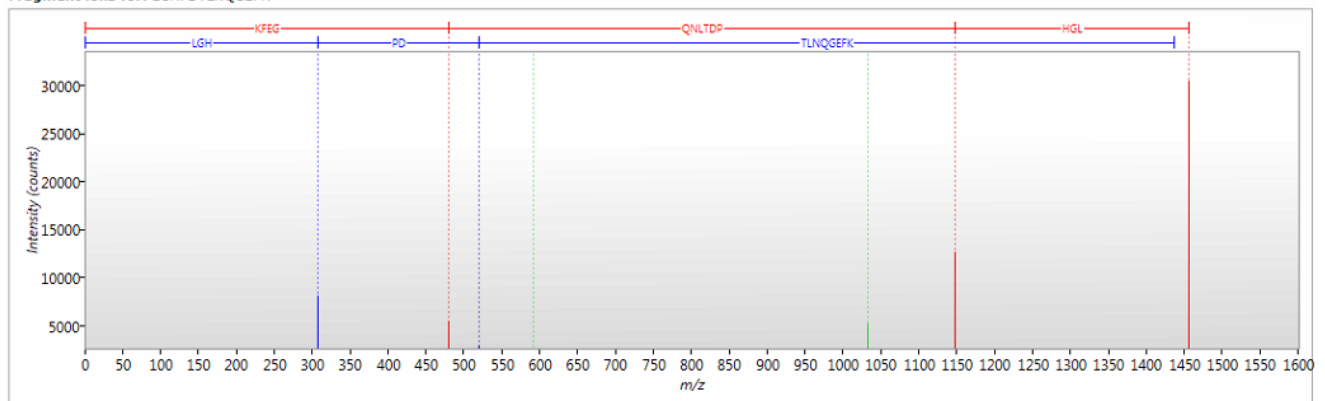
Fragment ions for: DLQNFLK



Fragment ions for: LGHPTLNQGEFK



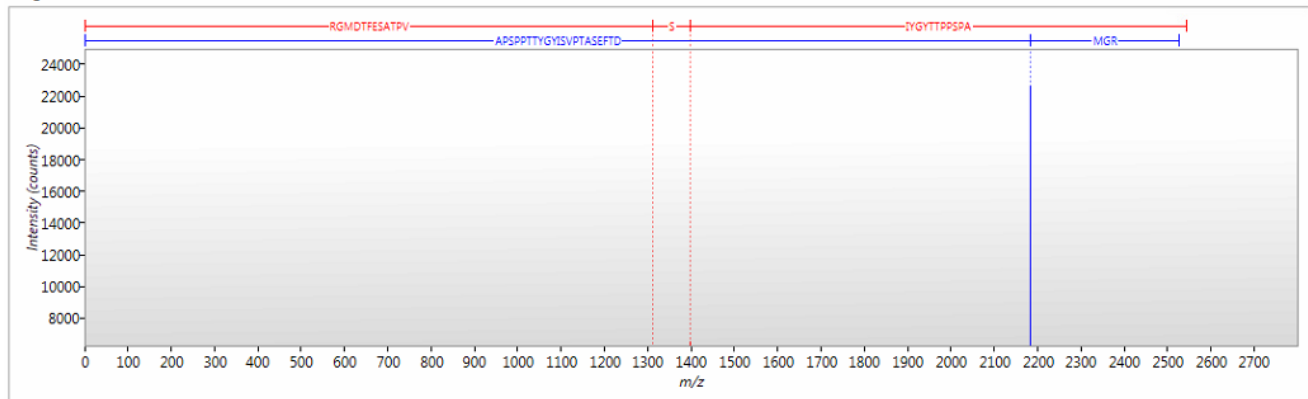
Fragment ions for: LGHPTLNQGEFK



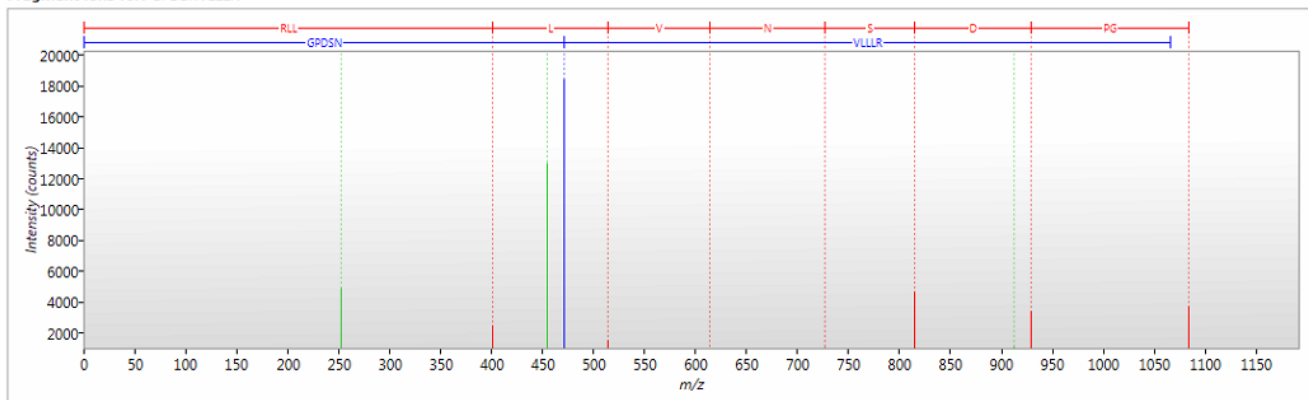
Roundabout homolog 4 OS=Homo sapiens GN=ROBO4 PE=1 SV=1
7 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Rc
APSPPTTYGYSVPTASEFTDMGR	390	5.64	2	2544.1176	2		0		yes	1.71e+006	4.42e+006	3.11e+006	2.26e+006
EADCVFIDASSPPSPRDEIFLTPNLSLPLVEV/RPDI/LEDMEVSHQTR	21052	6.15	2	5580.5106	4		0	[4] Carbamidomethyl C	no	1868.24	4.35e+004	0.00	8204.29
EDFQIQPR	17680	7.54	11	1031.4570	1		0		no	2.81e+004	1.46e+004	1.99e+004	3.63e+004
GPDSNVLLLR	2983	7.49	12	1082.5865	2		0		yes	5.62e+004	7.05e+004	9.01e+004	9.19e+004
LGTAIVSR	6941	6.90	7	702.3889	1		0		no	7990.78	6202.56	3313.03	1.63e+004
MDHSDSQV/LADTVVRSTSGSR	9600	5.58	2	2338.0510	3		0	[1] Oxidation M	no	5.36e+004	2.94e+004	2.95e+004	6.58e+004
VSIQEPQDYTEPVLLAVR	4592	8.20	16	2185.1077	2		0		yes	1.15e+005	2.51e+004	9606.89	1.68e+005
VSIQEPQDYTEPVLLAVR	4830	8.20	16	2185.0882	3		0		yes	1.58e+005	1.32e+005	1.44e+005	1.74e+005

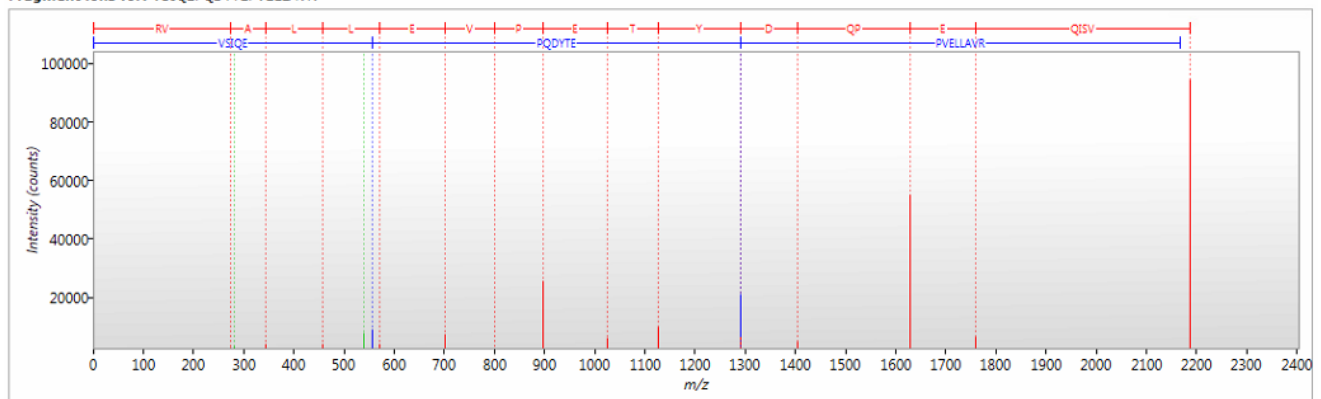
Fragment ions for: APSPPTTYGYSVPTASEFTDMGR



Fragment ions for: GPDSNVLLLR



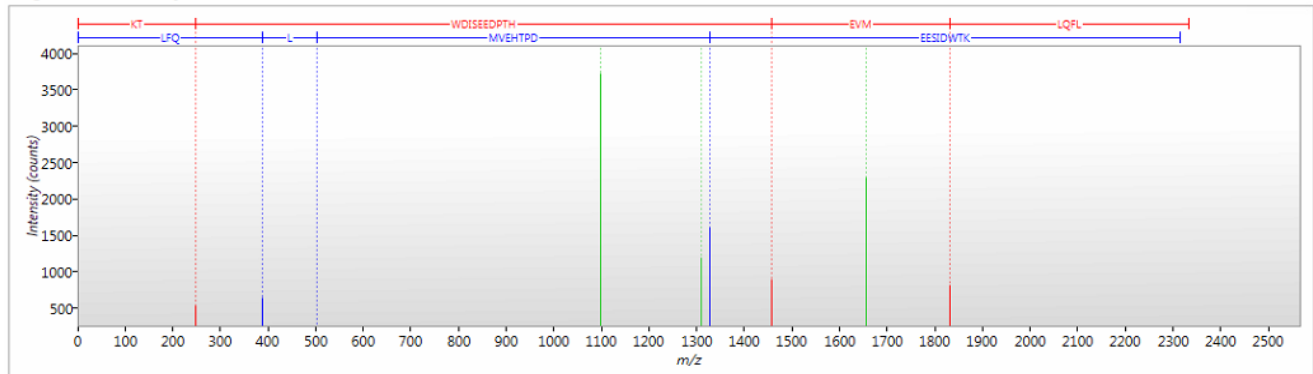
Fragment ions for: VSIQEPQDYTEPVLLAVR



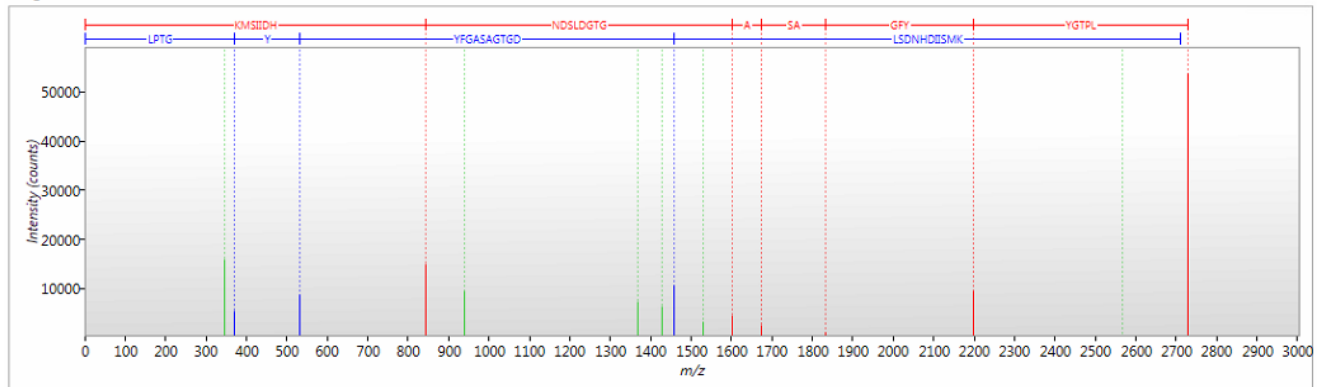
Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1 SV=1
9 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Re
AAEGVIV/R	3544	7.00	4	987.5068	2		0		no	1.34e+005	9.31e+004	7.22e+004	8.57e+004
DNFHGLAIFLDYTPNDETER	4549	8.20	15	2467.1506	3		0		no	1.48e+005	1.58e+005	7.10e+004	1.68e+005
DNFHGLAIFLDYTPNDETER	29751	8.20	16	2467.1240	2		0		no	4327.03	3706.71	1707.87	7300.71
DNFHGLAIFLDYTPNDETER	37431	7.83	2	2467.1291	2		0		no	4126.89	1783.71	1965.75	406.51
LFQLMVEHTPDEESIDWTK	3962	6.38	2	2333.0968	2		0	[5] Oxidation M	yes	1.15e+006	2.16e+005	1.85e+005	1.35e+006
LPTGYFFGASAGTGDLSDNHDIIISMK	4819	7.17	5	2729.2700	3		0		yes	2.45e+005	1.82e+005	8.35e+004	3.29e+005
LTPDER	3286	7.50	4	729.3533	1		1		no	5.56e+004	2.95e+004	2.29e+004	4.60e+004
LVPGPVFGSK	2711	8.52	24	999.5716	2		0		no	1.93e+005	2.16e+005	1.63e+005	2.04e+005
LVPGPVFGSK	9165	8.37	20	999.5691	1		0		no	1.44e+004	1.41e+004	8625.87	2.33e+004
NCIDITGVR	523	7.99	21	1046.5196	2		0	[2] Carbamidomethyl C	yes	1.24e+006	1.18e+006	7.86e+005	1.03e+006
NCIDITGVR	6622	7.99	21	1046.4685	1		0	[2] Carbamidomethyl C	yes	9.21e+004	3.85e+004	7.28e+004	7.59e+004
NRDHDFTLAVR	4224	8.35	3	1342.6747	3		0		no	4.65e+004	897.27	1.15e+004	1459.84
NRDHDFTLAVR	4641	8.46	2	1342.6746	3		0		no	5.60e+004	4795.46	354.47	1902.85
VTLAGCTADFR	19989	8.89	23	1425.6304	1		0	[7] Carbamidomethyl C	no	9051.30	1187.95	657.15	1.35e+004
VTLAGCTADFR	41394	7.84	3	1425.6358	1		0	[7] Carbamidomethyl C	no	5433.61	2859.72	1088.07	527.13

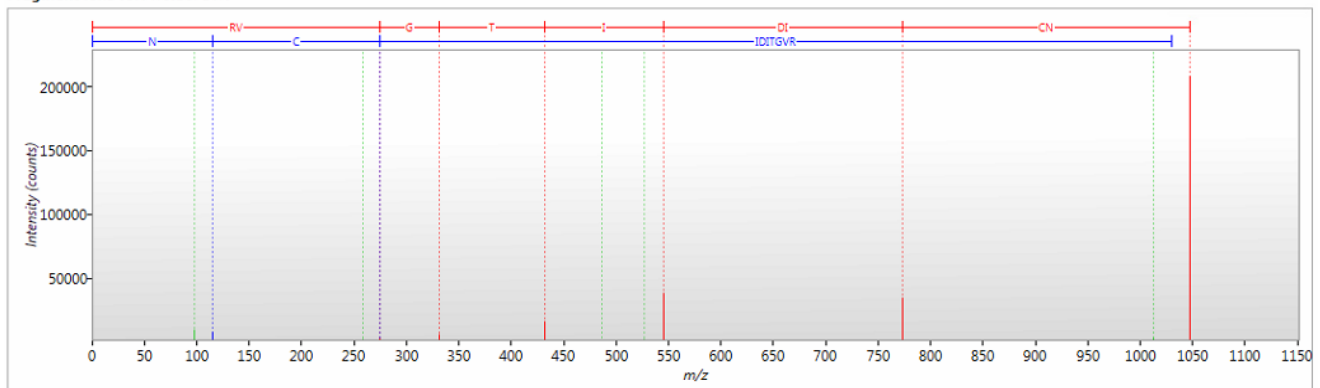
Fragment ions for: LFQLMVEHTPDEESIDWTK



Fragment ions for: LPTGYFFGASAGTGDLSDNHDIIISMK



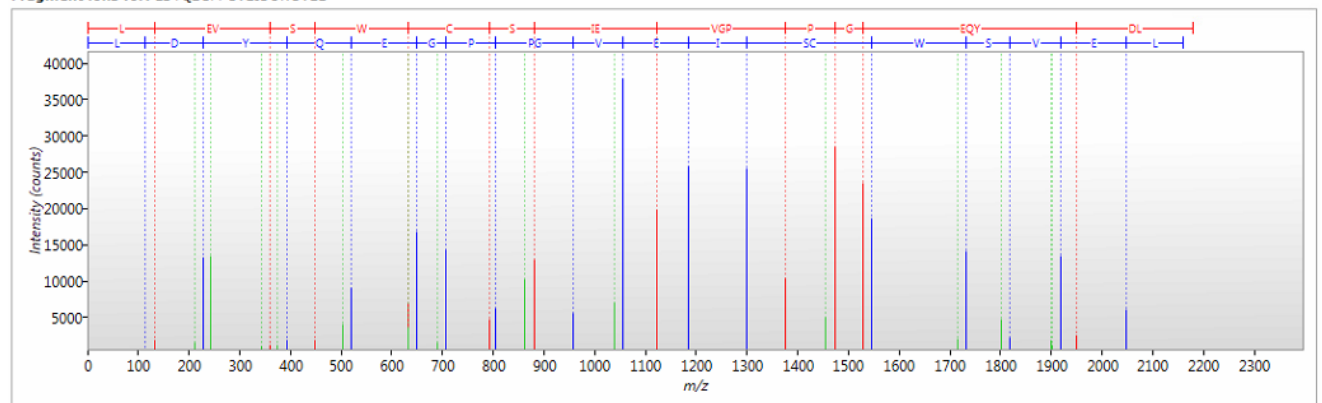
Fragment ions for: NCIDITGVR



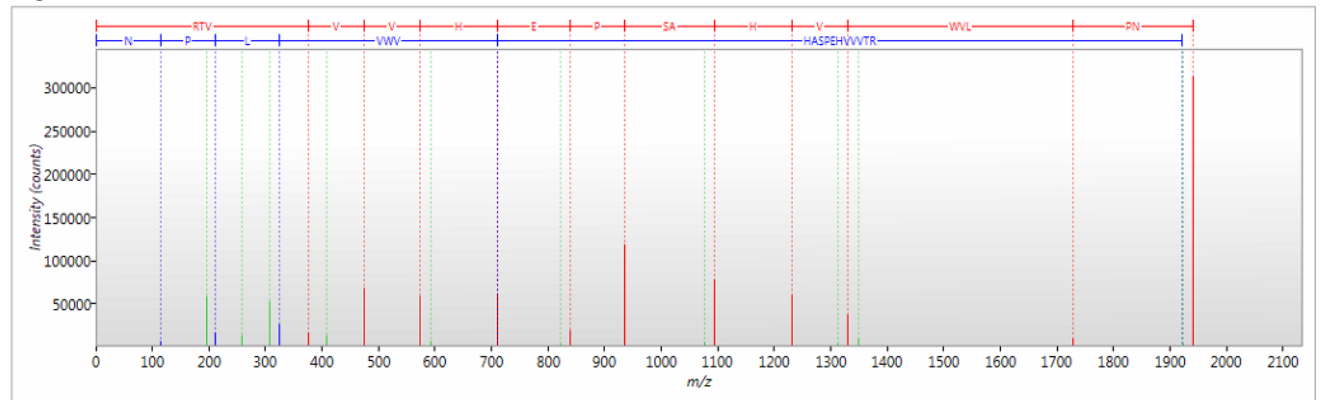
Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITI4 PE=1 SV=4
9 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	DPH	BC	TC
FKPTLSQQQK	5105	6.52	6	1203.5503	2		0		no	7.52e+004	1.21e+005	1.05e+005	6.72e+004
GPDVLVTATVSGK	5806	7.51	3	1143.5913	2		0		no	5.70e+004	5.00e+004	6.23e+004	4.76e+004
HLQMDIHIFEPQGISFLETSTFMTNQLVDALTTV/QNK	43407	6.00	2	4478.1712	4		0	[24] Oxidation M	no	836.93	2862.93	3077.83	868.01
LDYQEGPGPVEISCIVSEL	2346	9.21	28	2177.0087	2		0	[14] Carbamidomethyl C	yes	6.07e+005	1.89e+005	9.82e+004	6.71e+005
NMEQFYQVSIVAPNAK	7467	6.21	2	1747.8319	3		0		no	2.09e+004	2.81e+004	3.70e+004	1.48e+004
NPLVVVHASPEHVVVTR	1250	7.67	14	1939.0153	3		0		yes	8.85e+005	1.00e+006	3.51e+005	1.99e+006
NPLVVVHASPEHVVVTR	1539	7.28	2	1939.0350	3		0		no	7.17e+004	8.20e+004	4.29e+004	2.36e+005
NPLVVVHASPEHVVVTR	2112	7.74	6	1939.0320	3		0		no	4.19e+005	2.16e+005	1.97e+005	5.89e+004
NPLVVVHASPEHVVVTR	7043	7.28	3	1939.0176	4		0		no	4574.78	918.17	6930.64	2.79e+004
QGPVNLLSDPEQGVETGQYER	685	9.15	31	2414.1764	3		0		yes	9.57e+005	6.54e+005	3.56e+005	1.32e+006
QGPVNLLSDPEQGVETGQYER	1009	9.15	33	2414.1718	2		0		yes	9.24e+005	2.55e+005	1.68e+005	1.43e+006
QGPVNLLSDPEQGVETGQYEREK	1572	8.79	13	2671.2884	3		0		no	3.77e+005	1.00e+005	5.91e+004	6.62e+005
QGPVNLLSDPEQGVETGQYEREK	2676	8.88	3	2671.2618	3		0		no	2.87e+005	3.38e+004	3.72e+004	4.95e+004
QGPVNLLSDPEQGVETGQYEREK	19102	8.79	10	2671.2978	2		0		no	1.98e+004	5078.58	2823.05	2.72e+004
SPEQQTVDGNLIIR	6163	7.55	10	1810.9765	3		0		no	1.32e+005	3.86e+004	1.27e+005	2.58e+004

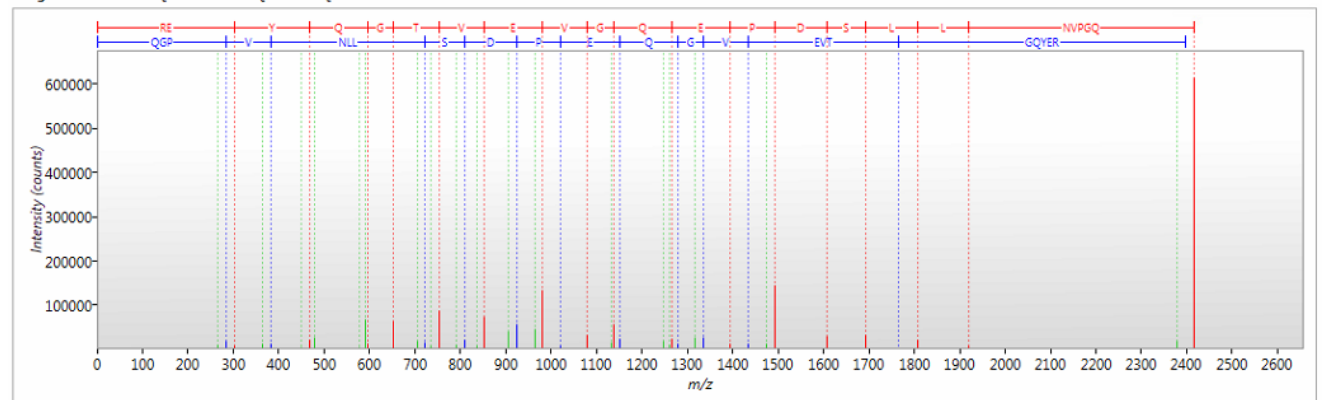
Fragment ions for: LDYQEGPPGVEISCWSVEL



Fragment ions for: NPLVWVHASPEHVVTR



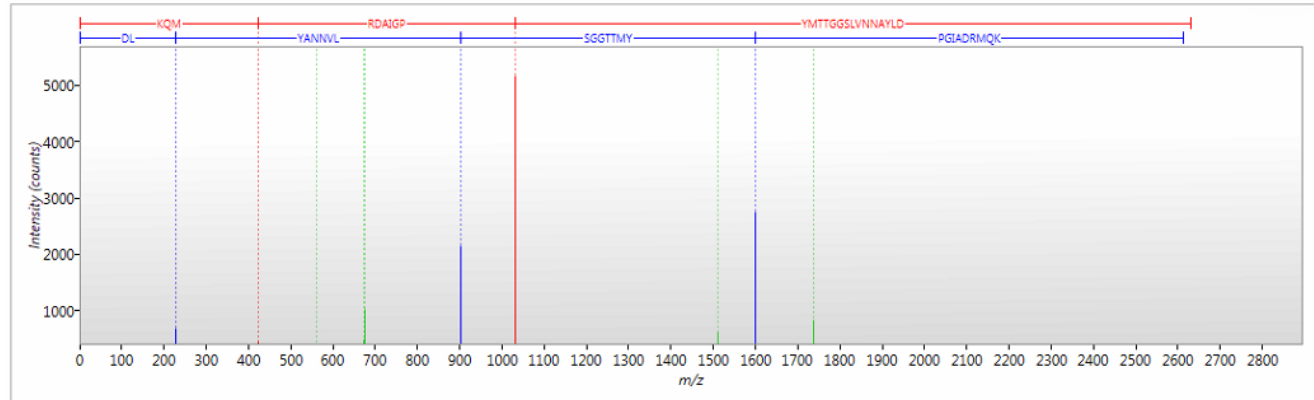
Fragment ions for: QGPVNLLSDPEQGVETGQYER



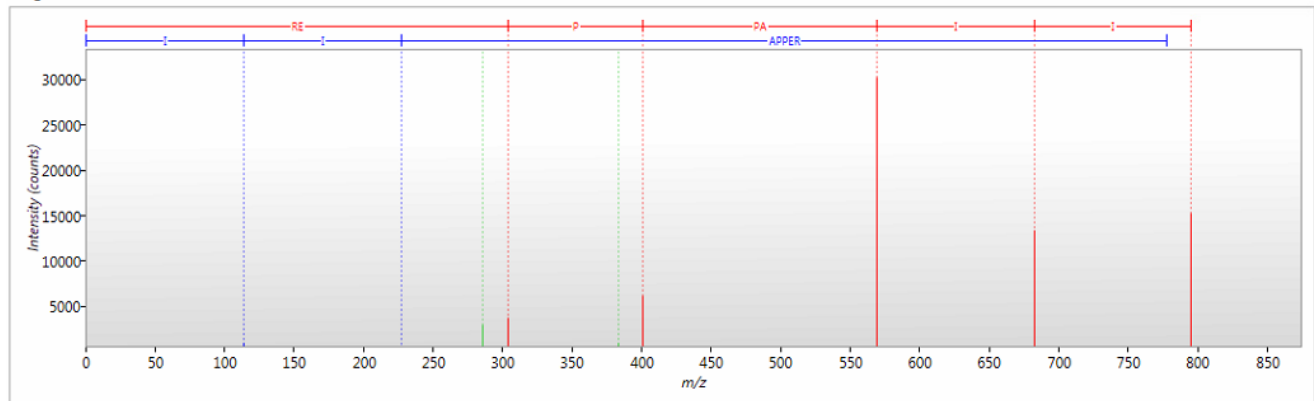
Actin_ gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										PCa	BPH	Bc	Bc
DLYANNVLSGGTTMYPGIADRMQK	3540	5.42	2	2630.2275	3		0	[14] Oxidation M	yes	2.62e+006	2.35e+006	1.66e+006	1.40e+006
IIAPPER	4810	7.87	5	794.4334	2		0		yes	1.92e+004	4.75e+004	1.73e+004	1.76e+004
YSVWIGGSILASLSTFQQMWISKPEYDEAGPSIVHR	19385	6.34	2	4052.0663	4		0		yes	2.17e+005	1.84e+004	1.45e+004	1.78e+005

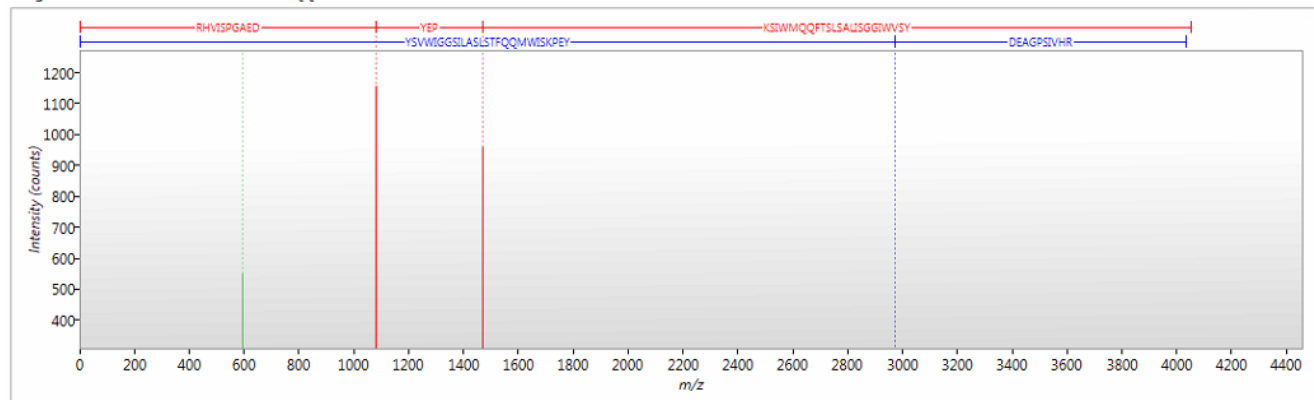
Fragment ions for: DLYANNVLSGGTTMYPGIADRMQK



Fragment ions for: IIAPPER



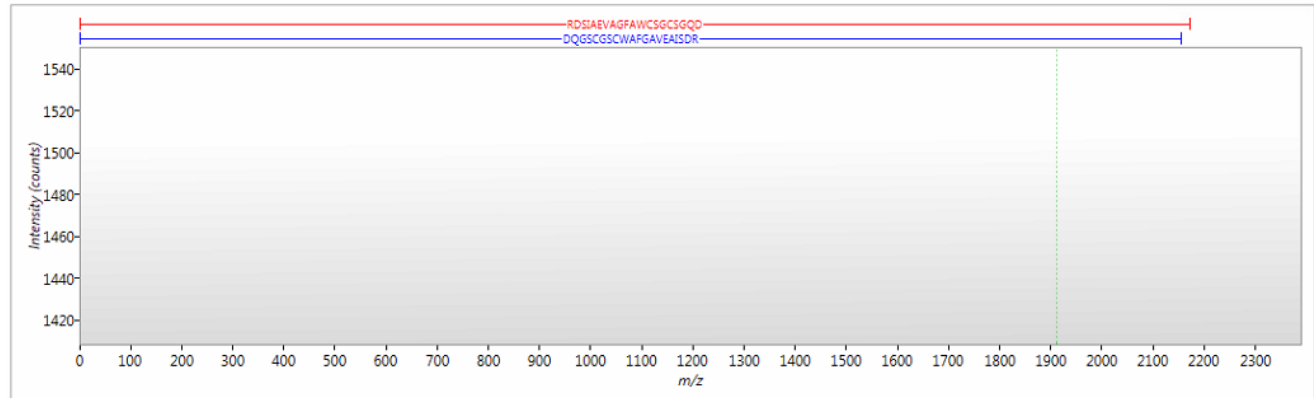
Fragment ions for: YSVWIGGSILASLSTFQQMWISKPEYDEAGPSIVHR



Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3
3 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances			
										pCa	BPH	Bc	Rc
DQGS C GS C WAFGAVEAISDR	13303	5.24	2	2172.1343	2		0	[5] Carbamidomethyl C; [8] Carbamidomethyl C	yes	2.55e+004	5.64e+004	7.73e+004	6.56e+004
EQWPQ C PTIK	28839	6.47	3	1285.6436	1		0	[6] Carbamidomethyl C	yes	501.68	835.09	4987.48	3536.74
i CEPGYSPTYK	62	7.34	4	1313.6574	2		1	[2] Carbamidomethyl C	no	1.61e+006	3.81e+006	1.63e+007	1.35e+006

Fragment ions for: DQGSGSCWAFGAVEAISDR



Fragment ions for: EQWPQCPTIK

