

PROTEOMICS

Supporting Information for Proteomics

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**High-throughput proteomic analysis of formalin-fixed paraffin-embedded
tissue microarrays using MALDI imaging mass spectrometry**

Table 1 Protein Identification

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Variable modifications : Acetyl (Protein N-term), Oxidation (M) (HW)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ± 200 ppm

Fragment Mass Tolerance: ± 0.4 Da

Max Missed Cleavages : 3

Instrument type : MALDI-TOF-TOF

Number of queries : 123

	SwissProt	Decoy	False discovery rate
Peptide matches above identity threshold	94	0	0
Peptide matches above homology or identity threshold	102	1	0.98

Keratin, type II cytoskeletal 6A	Macot Score (233)			ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	Mr(calc)						
1016.5420	1015.5347	1015.5298	4.83	0	41	0.0094		R.QLDSIVGER.G
1165.5830	1164.5757	1164.5775	-1.51	0	62	5.7e-05		K.YEELQVTAGR.H
1263.6915	1262.6842	1262.687	-2.22	0	81	9.2e-07		K.LALDVEIATYR.K
1407.7100	1406.7027	1406.7041	-1.01	0	34	0.044		K.ADTLTDEINFLR.A
1890.9550	1889.9477	1889.9635	-8.36	0	92	7.1e-08		R.QNLEPLFEQYINLNR.R
2047.0294	2046.0221	2046.0646	-20.77	1	21	0.88		R.QNLEPLFEQYINLNR.Q
2471.1831	2470.1758	2470.1798	-1.61	3	82	7.1e-07		R.GMQDLVEDFKNKYEDEINKR.T

Keratin, type II cytoskeletal 5	Macot Score (198)			ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	Mr(calc)						
1016.5420	1015.5347	1015.5298	4.83	0	41	0.0094		R.QLDSIVGER.G
1093.5220	1092.5147	1092.5199	-4.78	0	21	0.67		K.AQYEEIANR.S
1263.6915	1262.6842	1262.687	-2.22	0	81	9.2e-07		K.LALDVEIATYR.K
1410.7325	1409.7252	1409.7151	7.21	0	44	0.0042		R.SFSTASAITPSVSR.T
1439.7126	1438.7053	1438.7053	0.04	0	66	2.6e-05		R.GLVGVFGSGGGSSSSVK.F
1890.9550	1889.9477	1889.9635	-8.36	0	92	7.1e-08		R.QNLEPLFEQYINLNR.R
2047.0294	2046.0221	2046.0646	-20.77	1	21	0.88		R.QNLEPLFEQYINLNR.Q

Keratin, type II cytoskeletal 8	Macot Score (144)			ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	Mr(calc)						
1129.6152	1128.6079	1128.6138	-5.25	0	48	0.0019		K.LSELEAALQR.A
1277.6904	1276.6831	1276.7027	-15.31	0	22	0.7		K.LALDIEIATYR.K
1419.7931	1418.7858	1418.7405	31.9	0	64	4.7e-05		R.LEGLTDEINFLR.Q
1847.8475	1846.8402	1846.7978	23.0	0	83	5.8e-07		R.SNMDNMFESYINLNR.R
1863.8770	1862.8697	1862.7927	41.4	0	(49)	0.0013		R.SNMDNMFESYINLNR.R + Oxidation (M)

Histone H2A	Macot Score (146)			ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	Mr(calc)						
944.5400	943.5327	943.524	9.27	0	17	2.1		R.AGLQFPVGR.V
2915.5000	2914.4927	2914.5804	-30.07	0	146	2.8e-13		R.VGAGAPVYLAIVLEYLETAEILELAGNAAR.D

Alpha-enolase	Macot Score (122)			ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	Mr(calc)						
1129.6152	1128.6079	1128.6138	-5.25	0	48	0.0019		K.LSELEAALQR.A
1277.6904	1276.6831	1276.7027	-15.31	0	22	0.7		K.LALDIEIATYR.K
1419.7931	1418.7858	1418.7405	31.9	0	64	4.7e-05		R.LEGLTDEINFLR.Q
1847.8475	1846.8402	1846.7978	23.0	0	83	5.8e-07		R.SNMDNMFESYINLNR.R
1863.8770	1862.8697	1862.7927	41.4	0	(49)	0.0013		R.SNMDNMFESYINLNR.R + Oxidation (M)

Keratin, type I cytoskeletal 19	Macot Score (105)			ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	Mr(calc)						
1082.5175	1081.5102	1081.4829	25.3	0	27	0.16		K.DAEAWFTSR.T
1122.5560	1121.5487	1121.5717	-20.45	0	40	0.01		R.LEQEIATYR.S
1210.6031	1209.5958	1209.5778	14.9	1	32	0.06		R.KDAEAWFTSR.T
1222.6390	1221.6317	1221.6353	-2.95	1	55	0.00033		R.TKPFETEQLR.M
1354.6100	1353.6027	1353.5983	3.28	0	37	0.018		R.SQYEVMAEQNR.K
1554.7480	1553.7407	1553.7434	-1.74	0	42	0.0065		R.QSSATSSFGGLGGSVR.F
1674.8083	1673.8010	1673.7685	19.4	0	50	0.001		R.DYSHYTTIQDLR.D
2407.2258	2406.2185	2406.3019	-34.66	0	30	0.12		R.FGAQLAHQALISGIEAQLGDVR.A

Tubulin beta-2C chain	Macot Score (118)			ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	Mr(calc)						
1130.6021	1129.5948	1129.588	6.04	0	64	4.2e-05		R.FPQQLNADLR.K
1143.6100	1142.6027	1142.627	-21.27	0	29	0.15		K.LAVNMVFPRL
1601.8101	1600.8028	1600.8131	-6.40	0	75	3.8e-06		R.AVLVDLEPGTMDSVR.S
1620.8260	1619.8187	1619.8283	-5.89	0	31	0.086		R.LHFFMPGFAPLTSR.G
2798.4248	2797.4175	2797.3361	29.1	0	37	0.023		R.SGPFQIFRPNFVFGQSGAGNNWAK.G

Serum albumin precursor	Macot Score (113)			ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	Mr(calc)						
927.4923	926.4850	926.4861	-1.18	0	24	0.34		K.YLYEIAR.R
1467.8109	1466.8036	1466.8358	-21.92	1	33	0.051		R.RHPDYSVLLLR.L
1511.7955	1510.7882	1510.8355	-31.31	0	55	0.00038		K.VPQVSTPTLVEVSR.N
1623.7710	1622.7637	1622.7803	-10.21	0	59	0.00014		K.DVFLGMFLYEYAR.R
1639.7600	1638.7527	1638.7752	-13.72	0	(47)	0.0021		K.DVFLGMFLYEYAR.R + Oxidation (M)
1898.9000	1897.8927	1897.9879	-50.15	1	30	0.11		R.RHPYFYAPPELLFFAKR

Keratin, type II cytoskeletal 75	Macot Score (110)			ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	Mr(calc)						
1165.5830	1164.5757	1164.5775	-1.51	0	62	5.7e-05		K.YEELQVTAGR.H
1263.6915	1262.6842	1262.6870	-2.22	0	81	9.2e-07		K.LALDVEIATYR.K

Keratin, type II cytoskeletal 2 epidermal		Macot Score (103)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1263.6915	1262.6842	1262.687	-2.22	0	81	9.2e-07	K.LALDVEIATYR.K	
1320.6698	1319.6625	1319.5756	65.9	0	53	0.00057	R.HGGGGGGFGGGGFGSR.S	
1475.7600	1474.7527	1474.778	-17.13	0	21	0.83	R.FLEQQNQLVLTQK.W	

Keratin, type I cytoskeletal 16		Macot Score (94)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1036.5272	1035.5199	1035.525	-4.90	1	29	0.11	K.IRDWYQR.Q	
1122.5560	1121.5487	1121.5717	-20.45	0	40	0.01	R.LEQEIATYR.R	
1241.5970	1240.5897	1240.587	2.22	0	35	0.031	K.NHEEMLALR.G	
1259.6740	1258.6667	1258.6669	-0.18	1	41	0.0082	R.TKYEHELALR.Q	
1757.8680	1756.8607	1756.8784	-10.06	1	34	0.045	R.QRPSEIKDYSPTYFK.T	
2064.1130	2063.1057	2063.1375	-15.38	0	67	2.4e-05	K.IIAATIENAQPILQIDNAR.L	

Vimentin		Macot Score (88)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1428.7123	1427.7050	1427.7045	0.38	0	77	2.4e-06	R.SLYASSPGGVYATR.S	
2497.2173	2496.2100	2496.2496	-15.86	1	41	0.0089	R.LLQDSVDFSLADAINTEFKNTR.T	

Keratin, type I cytoskeletal 15		Macot Score (108)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1122.5560	1121.5487	1121.5717	-20.45	0	40	0.01	R.LEQEIATYR.S	
1248.6610	1247.6537	1247.6873	-26.94	1	45	0.0037	R.LKYENALR.Q	
1821.8787	1820.8714	1820.8766	-2.84	0	77	2.4e-06	R.GGSLLAGGGGFGGSLSGGGSR.S	
1877.8959	1876.8886	1876.8803	4.42	0	41	0.0079	M ₁ TTTFLQTSSTFGGGSTR.G + Acetyl (Protein N-term)	

Ferritin light chain		Macot Score (101)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1607.7820	1606.7747	1606.7991	-15.17	0	84	4.5e-07	R.LGGPEAGLGEYLFER.L	
1719.9220	1718.9147	1718.9791	-37.46	1	49	0.0014	K.KLNQALDLHALGSAR.T	

Protein S100-A9		Macot Score (72)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1455.7142	1454.7069	1454.7154	-5.82	0	18	1.6	K.LGHPTDLNQGFEK.E	
1614.7900	1613.7827	1613.7945	-7.32	0	53	0.00062	K.QLSFEEFIMLMAR.L	
1806.9113	1805.9040	1805.9312	-15.04	0	51	0.00087	R.NIETINTFHQYSVK.L	

Keratin, type I cytoskeletal 13		Macot Score (71)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1122.5560	1121.5487	1121.5717	-20.45	0	40	0.01	R.LEQEIATYR.S	
1248.6610	1247.6537	1247.6873	-26.94	1	45	0.0037	R.LKYENALR.Q	
1392.6880	1391.6807	1391.6867	-4.32	0	51	0.00082	K.MIGFPSSAGSVSPR.S	

78 kDa glucose-regulated protein precursor		Macot Score (78)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1566.7791	1565.7718	1565.7726	-0.48	0	51	0.00078	R.ITPSYVAFTPEGER.L	
1999.0770	1998.0697	1998.0786	-4.44	0	58	0.0002	R.GVPQIEVTFEIVDNGILR.	

Keratin, type I cytoskeletal 17		Macot Score (62)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1036.5272	1035.5199	1035.5250	-4.90	1	29	0.11	K.IRDWYQR.Q	
1122.5560	1121.5487	1121.5717	-20.45	0	40	0.01	R.LEQEIATYR.R	
1222.6390	1221.6317	1221.6353	-2.95	1	55	0.00033	R.TKFETEQALR.L	
2114.0249	2113.0176	2113.011	3.14	0	26	0.32	R.GQVGGIEVEMDAAPGVDLR.I	

Pulmonary surfactant-associated protein A1 precursor		Macot Score (103)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1447.7350	1446.7277	1446.699	19.8	0	52	0.00069	R.NPEENEAIASFVK.K	
1506.8000	1505.7927	1505.7759	11.1	0	23	0.51	R.GALSLQGSIMTVGEK.V + Oxidation (M)	
1984.0176	1983.0103	1983.0425	-16.22	1	37	0.023	R.IAVPRNPEENEAIASFVK.K	
2106.9856	2105.9783	2105.9694	4.22	0	48	0.002	K.YNTYAYVGLTEGSPGDFR.Y	
2329.1340	2328.1267	2328.1499	-9.94	0	61	8.4e-05	R.GPPGLPAHLDEELQATLHDFR.H + Oxidation (HW)	

Tubulin beta-2A chain		Macot Score (74)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
1130.6021	1129.5948	1129.588	6.04	0	64	4.2e-05	R.FPQQLNADLR.K	
1143.6100	1142.6027	1142.627	-21.27	0	29	0.15	K.LAVNMVFPFR.L	
1615.8186	1614.8113	1614.8287	-10.76	0	20	1.1	R.AILVDLEPGTMDSVR.S	
1620.8260	1619.8187	1619.8283	-5.89	0	31	0.086	R.LHFFMPGFAPLTSR.G	
2798.4248	2797.4175	2797.3361	29.1	0	37	0.023	R.SGPFQGFIRPDNFVGGSGAGNWNWAK.G	

Histone H4		Macot Score (57)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
989.5700	988.5627	988.5706	-7.91	0	36	0.025	K.VFLENVIR.D	
1325.7233	1324.7160	1324.7463	-22.84	0	54	0.00044	R.DNIQGITKPAIR.R	

Keratin, type I cytoskeletal 18		Macot Score (82)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
965.4800	964.4727	964.4614	11.7	0	36	0.024	R.AQYDELAR.K	
975.4492	974.4419	974.4458	-3.91	0	31	0.085	R.STFSTNYR.S	
2670.3108	2669.3035	2669.3846	-30.38	0	48	0.0018	R.YALQMEQLNGILLHESELAQTR.A	
2854.3882	2853.3809	2853.4005	-6.88	0	50	0.0012	R.SLGSVQAPSYGARPVSSAASVYAGAGGSGSR.I	

Actin, cytoplasmic		Macot Score (90)						Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		
976.4540	975.4467	975.441	5.84	0	30	0.1	K.AGFAGDDAPR.A	
1515.6600	1514.6527	1514.7419	-58.85	0	59	0.00014	K.IWHHTFYNELR.V	
1790.8907	1789.8834	1789.8846	-0.67	0	61	8.9e-05	K.SYELPDGQVITIGNER.F	
2215.0000	2213.9927	2214.0627	-31.60	0	28	0.19	K.DLYANTVLSGGTMMYPGIADR.M	

Proteins Identified with De Novo Sequencing

Vitronectin precursor		Macot Score (56)						Peptide	
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect			
1314.6980	1313.6907	1313.6728	13.6	1	29	0.14	R.RVDTVDPPYPR.S		
1646.8475	1645.8402	1645.81	18.3	0	54	0.00042	R.DVWGIEGPIAFAFR.I		
1666.7800	1665.7727	1665.7682	2.72	0	30	0.11	R.DWHGVPGQVDAAMAGR.I		

Glutathione S-transferase P		Macot Score (46)						Peptide	
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect			
1337.7000	1336.6927	1336.718	-18.89	0	29	0.13	M.PPYTVVYFPVR.G		
1883.9390	1882.9317	1882.9425	-5.72	0	46	0.0031	K.FQDGLTLYQSNILR.H		

Keratin, type II cytoskeletal 7		Macot Score (61)						Peptide	
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect			
1277.6904	1276.6831	1276.7027	-15.31	0	22	0.7	K.LALDIEIATYR.K		
1406.7100	1405.7027	1405.699	2.63	0	61	7.9e-05	M ₂ SIHFSSPVFTSR.S + Acetyl (Protein N-term)		
1442.7550	1441.7477	1441.7929	-31.33	0	21	0.89	R.LPDIFEAQIAGLR.G		
1453.8199	1452.8126	1452.83	-11.96	0	28	0.16	R.EVTINQSLAPLR.L		

Ig alpha chain C region		Macot Score (63)						Peptide	
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect			
1213.6259	1212.6186	1212.6251	-5.35	0	32	0.064	R.WLQGSQELPR.E		
1835.9080	1834.9007	1834.9425	-22.77	0	63	5.4e-05	R.QEPSQGTTFVAVTSILR.V		

Pyruvate kinase isozymes M1/M2		Macot Score (68)						Peptide	
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect			
1859.8700	1858.8627	1858.8924	-15.96	0	46	0.0026	K.FGVEQDQDMVFASFIR.K		
2465.2520	2464.2447	2464.2849	-16.32	0	55	0.00036	R.TATESFASDPILYRPAVALDTK.G		

Fibrinogen beta chain precursor		Macot Score (50)						Peptide	
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect			
980.4486	979.4413	979.4359	5.50	0	39	0.011	R.QDGSVDFGR.K		
1239.5300	1238.5227	1238.5105	9.88	0	25	0.26	K.EDGGGWYNR.C		
1950.9750	1949.9677	1949.9959	-14.45	0	39	0.015	R.EEAPSLRPAPPISGGGYR.A		

Fibrinogen gamma chain precursor		Macot Score (47)						Peptide	
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect			
1117.5070	1116.4997	1116.52	-18.14	0	38	0.019	R.VELEDWNGR.T		
1682.9268	1681.9195	1681.9515	-19.02	0	40	0.0099	K.IHLISTQSAIPYALR.V		

Heat shock protein beta-1		Mascot Score (50)						Peptide	
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect			
987.5430	986.5358	986.6025	-67.68	1	42	0.0069	R.RVPFSLLR.G		
1163.6035	1162.5962	1162.6135	-14.86	0	20	0.94	R.LFDQAFGLPR.L		
1905.9900	1904.9827	1904.9843	-0.85	0	41	0.0095	K.LATQSNEITIPVTFESR.A		

Collagen alpha-1(I) chain precursor							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	
1105.578	1104.570	1104.567	2.8	0			GVQGGPPGAGPR (Hydroxylated)
1459.711	1458.703	1458.759	38.4	0			GSAGPPGATGFPGAAGR (Hydroxylated)
898.484	897.476	897.502	29.5	0			GVVGLPGQR (Hydroxylated)
2705.260	2704.252	2704.247	1.9	0			GFSGLQGGPPGPGSGEQGSPGASGPAGPR (Hydroxylated)
2869.418	2868.410	2868.399	3.7	1			GLTGPIGPPGAGAGGDKGESGSPGAPGTGAR (Hydroxylated)

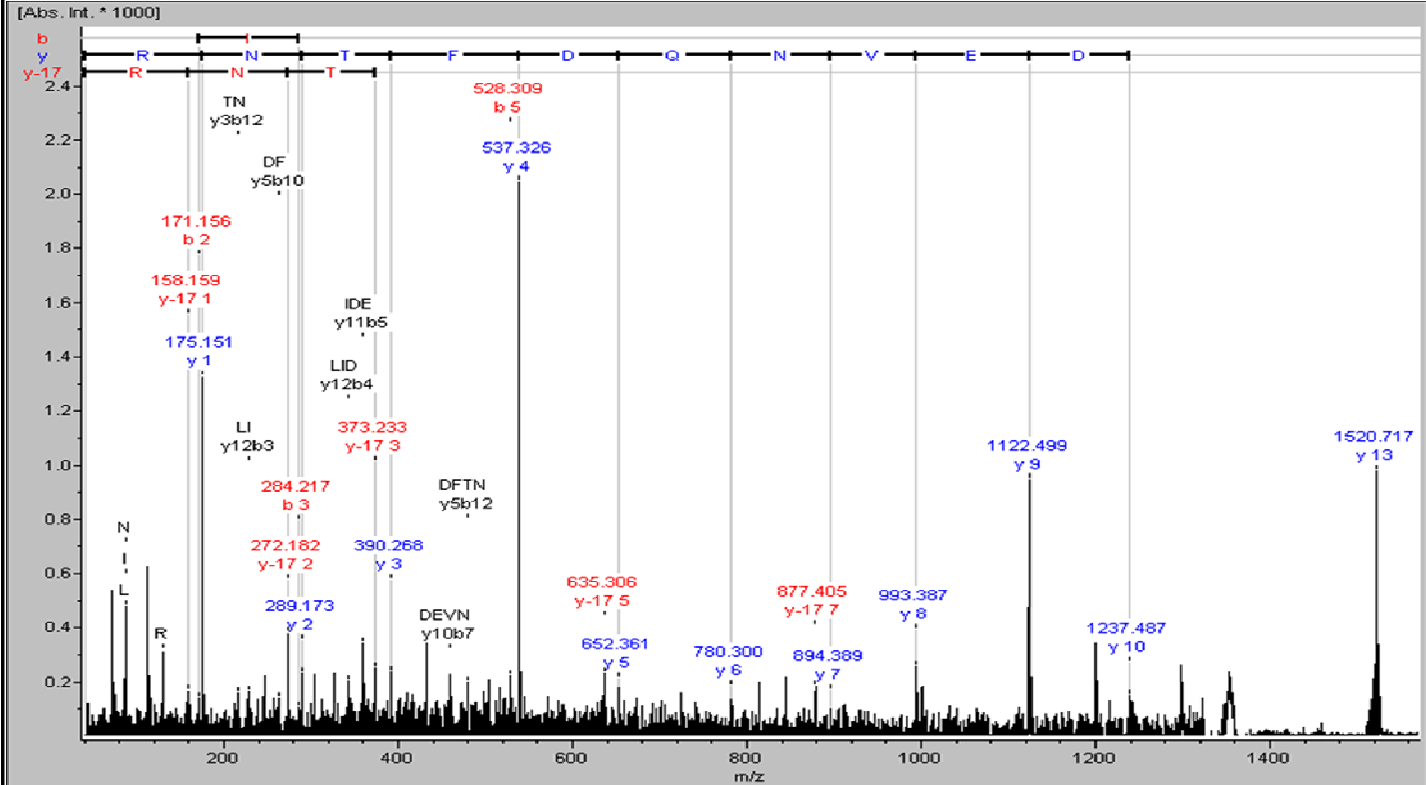
Collagen alpha-2(I) chain precursor							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	
1477.760	1476.752	1476.747	3.7	0			GLHGEFGLPGPAGPR (Hydroxylated)
1562.804	1561.796	1561.781	9.9	0			GETGSPGVPAGAVGPR
1493.771	1492.763	1492.742	14.4	0			GLHGEFGLPGPAGPR (Hydroxylated)
1533.719	1532.711	1532.667	28.7	0			GDGGPPGMTGFPGAAGR (Hydroxylated)
1655.823	1654.815	1654.806	5.7	1			GFPGADGVAGPKGPAGER (Hydroxylated)
2959.415	2958.407	2958.348	19.8	0			GPPGAAGAGPQQGFQGPAGEPGEPPQGTGPAGAR (Hydroxylated)

Tentative Protein Identifications

Protein disulfide-isomerase precursor	Mascot Score (50)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1780.8400	1779.8327	1779.8275	2.93	0	50	0.001	K.VDATEESDLAQYGVR.G	
Fibrinogen alpha chain precursor	Mascot Score (78)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1520.7173	1519.7100	1519.7267	-10.96	0	78	1.7e-06	K.GLIDEVNDQFTNR.I	
Aldo-keto reductase family 1 member C1	Mascot Score (85)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
2179.0750	2178.0677	2178.0817	-6.44	0	85	3.8e-07	R.HIDSAHLYNNEEQVGLAIR.S	
Glyceraldehyde-3-phosphate dehydrogenase	Mascot Score (79)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1763.8364	1762.8291	1762.7951	19.3	0	79	1.5e-06	K.LISWYDNEFGYSNR.V	
Carbonyl reductase [NADPH] 1	Mascot Score (72)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1652.8300	1651.8227	1651.8642	-25.09	0	72	8e-06	R.GQAAVQQLQAEGLSPR.F	
Hemoglobin subunit alpha	Mascot Score (69)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1833.9000	1832.8927	1832.8846	4.43	0	69	1.6e-05	K.TYFPHFDLSHGSAQVK.G	
Annexin A1	Mascot Score (63)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1702.8875	1701.8802	1701.8785	1.03	0	63	6e-05	K.GLGTDEDTLIEILASR.T	
Carcinoembryonic antigen-related cell adhesion molecule 5	Mascot Score (69)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
2177.0930	2176.0857	2176.1277	-19.28	0	69	1.4e-05	R.QIIQYVIGTQQATPGPAYSGR.E	
Apolipoprotein A-I precursor	Mascot Score (53)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1301.6510	1300.6437	1300.6411	1.98	0	53	0.00059	R.THLAPYSDELRL.Q	
Histone H2B	Mascot Score (47)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1759.8075	1758.8002	1758.8069	-3.80	0	47	0.0015	K.AMGIMNSFVNDIFER.I + Oxidation (M)	
Annexin A2	Mascot Score (47)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1111.5660	1110.5587	1110.5458	11.6	0	47	0.0019	R.QDIAFYQRR.R	
Macrophage migration inhibitory factor	Mascot Score (50)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1287.6816	1286.6743	1286.6805	-4.82	0	50	0.001	M.PMFIVNTNVPRL.A	
Serum amyloid P-component precursor	Mascot Score (45)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1156.5970	1155.5897	1155.5924	-2.32	0	45	0.0034	R.VGEYSLYIGR.H	
Tubulin alpha-1A chain	Mascot Score (45)							
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide	
1701.8616	1700.8543	1700.8985	-25.98	0	45	0.0037	R.AVFVDLEPTVIDEVR.T	

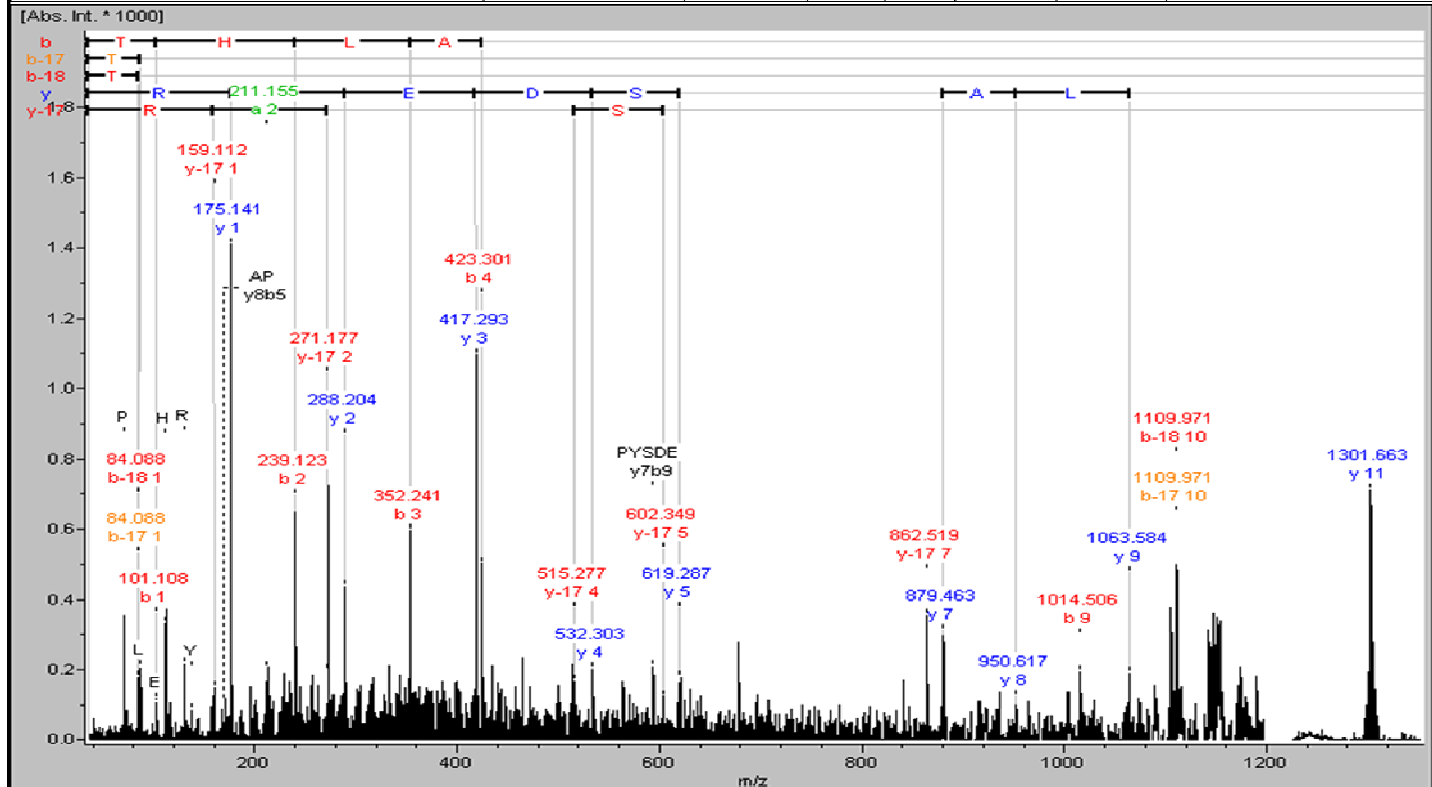
Stathmin	Mascot Score (49)							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		R.ASGQAFELISPR.S
1388.7150	1387.7077	1387.7459	-27.54	0	49	0.0012		
Peptidyl-prolyl cis-trans isomerase A	Mascot Score (46)							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		M_VNPTVFFDIAVDGEPLGR.V + Acetyl (Protein N-term)
1987.9899	1986.9826	1987.0051	-11.32	0	46	0.0029		
Protein disulfide-isomerase A3 precursor	Mascot Score (46)							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		R.ELSDFISYLQR.E
1370.7358	1369.7285	1369.6878	29.8	0	46	0.0024		
Histone H3-like	Mascot Score (45)							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		R.KLPFQR.L
788.4709	787.4636	787.4704	-8.67	1	45	0.0035		
Polymeric immunoglobulin receptor precursor	Mascot Score (48)							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		R.LVSLTLNLVTR.A
1228.7552	1227.7479	1227.7551	-5.82	0	48	0.0019		
Heterogeneous nuclear ribonucleoproteins A2/B1	Mascot Score (46)							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		R.GGGGNFGPGGSNFR.G
1377.6200	1376.6127	1376.6222	-6.88	0	46	0.0024		
Protein S100-P	Mascot Score (47)							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		M_TELETAMGMIIDVFSR.Y + Acetyl (Protein N-term)
1854.8900	1853.8827	1853.8903	-4.09	0	47	0.0023		
Myosin-9 - Homo sapiens (Human)	Mascot Score (43)							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		K.ANLQIDQINTDLNLR.S
1869.9500	1868.9427	1868.9592	-8.80	0	43	0.005		
Keratin, type II cytoskeletal 3	Mascot Score (81)							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		K.LALDVEIATYR.K
1263.6915	1262.6842	1262.6870	-2.22	0	81	9.2e-07		
Hemoglobin subunit beta	Mascot Score (66)							Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect		R.LLVVYPWTQR.F
1274.7000	1273.6927	1273.7183	-20.07	0	66	2.9e-05		

Fibrinogen alpha chain precursor	Mascot Score (61)	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide
Observed		1519.7100	1519.7267	-10.96	0	61	5.4e-05	K.GLIDEVNDFTNR.I
1520.7173								



		Fragment Ion Mass Errors (Da)												
		Gly	Leu	Ile	Asp	Glu	Val	Asn	Gln	Asp	Phe	Thr	Asn	Arg
Ion		1	2	3	4	5	6	7	8	9	10	11	12	13
a														
b			0.043	0.02		0.043								
b-17														
b-18														
b+18														-0.017
y		0.032	0.011	0.058	0.048	0.056	-0.064	-0.017	-0.088	-0.019	-0.058			-0.017
y-17		0.042	0.023	0.026		0.004		0.002						
i			0	0										0.036
		Arg	Asn	Thr	Phe	Asp	Gln	Asn	Val	Glu	Asp	Ile	Leu	Gly

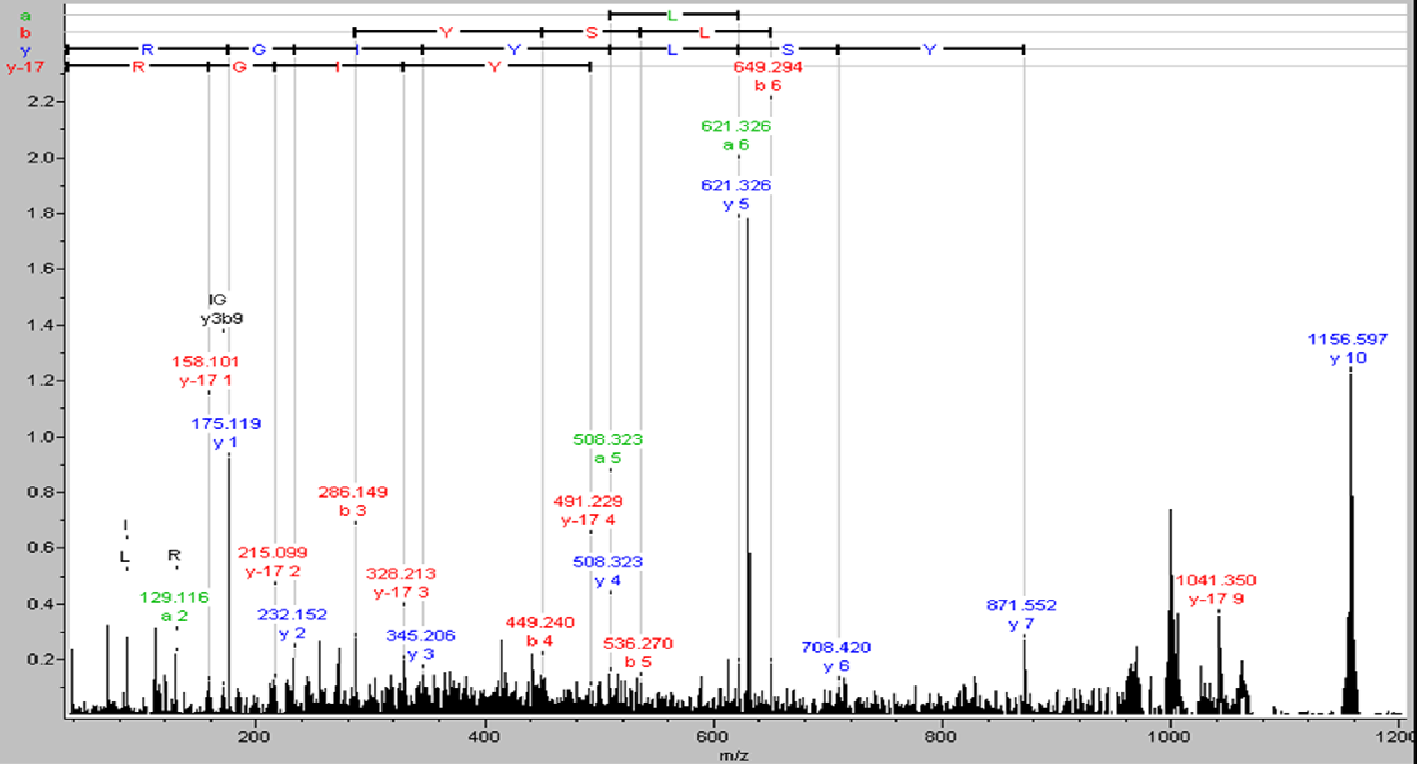
Apolipoprotein A-I precursor	Mascot Score (48)	Mr(calc)	ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	1300.6411	1.98	0	48	0.0013	R.THLAPYSDEL.R.Q
1301.6510	1300.6437						



Fragment Ion Mass Errors (Da)											
	Thr	His	Leu	Ala	Pro	Tyr	Ser	Asp	Glu	Leu	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11
a		0.036									
b		0.009	0.043	0.066					0.053		
b-17											
b-18	0.043										
b+18											
y	0.022	0.001	0.047	0.031	-0.017		0.043	0.159	0.042		0.015
y-17		-0.023		0.007	0.047		0.102				
i		0.021	0.057		0.01	0.014				0.057	0.012
	Arg	Leu	Glu	Asp	Ser	Tyr	Pro	Ala	Leu	His	Thr

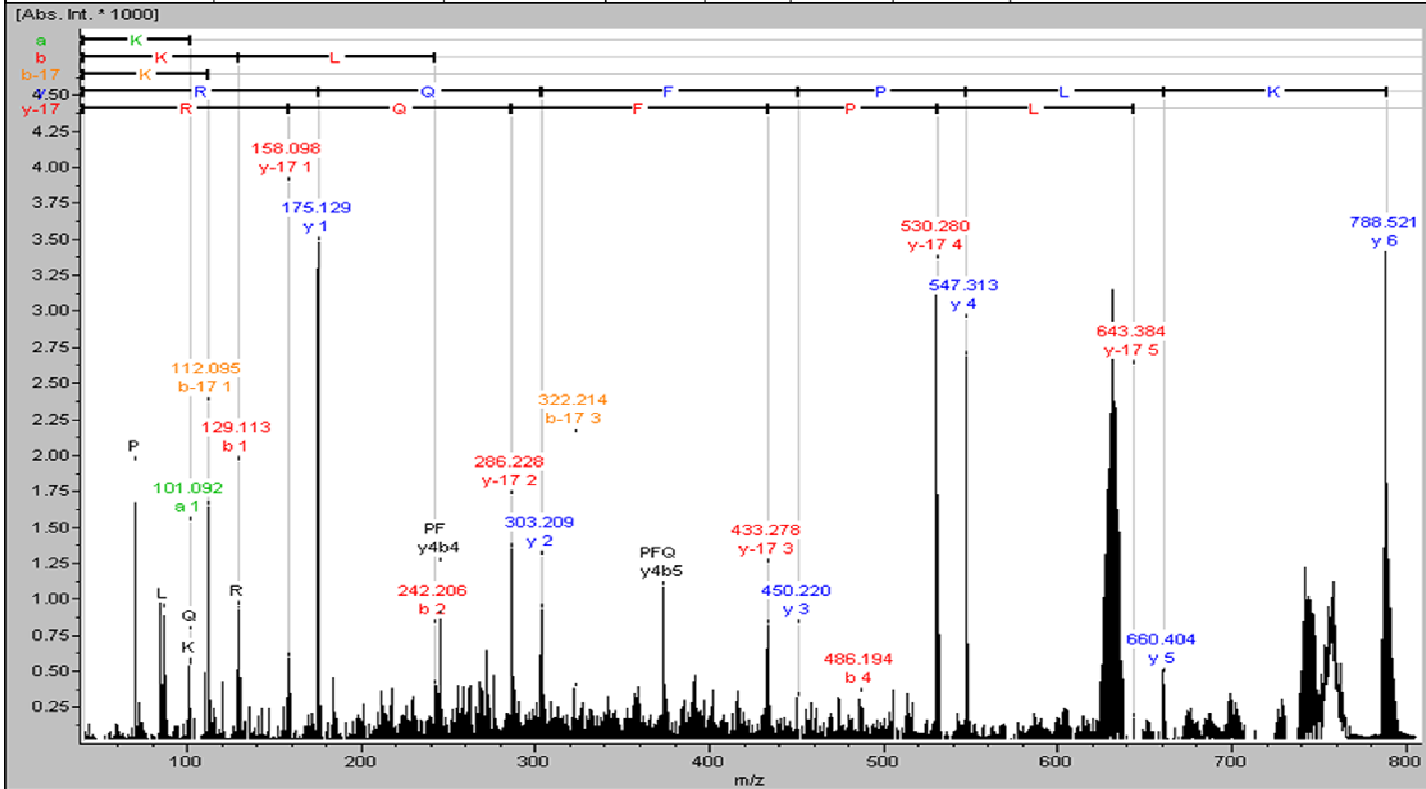
Serum amyloid P-component precursor	Mascot Score (43)	Mr(calc)	ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	1155.592	-2.32	0	43	0.0041	R.VGEYSLYIGR.H
1156.5970	1155.5897	1155.592	-2.32	0	43	0.0041	R.VGEYSLYIGR.H

[Abs. Int. * 1000]



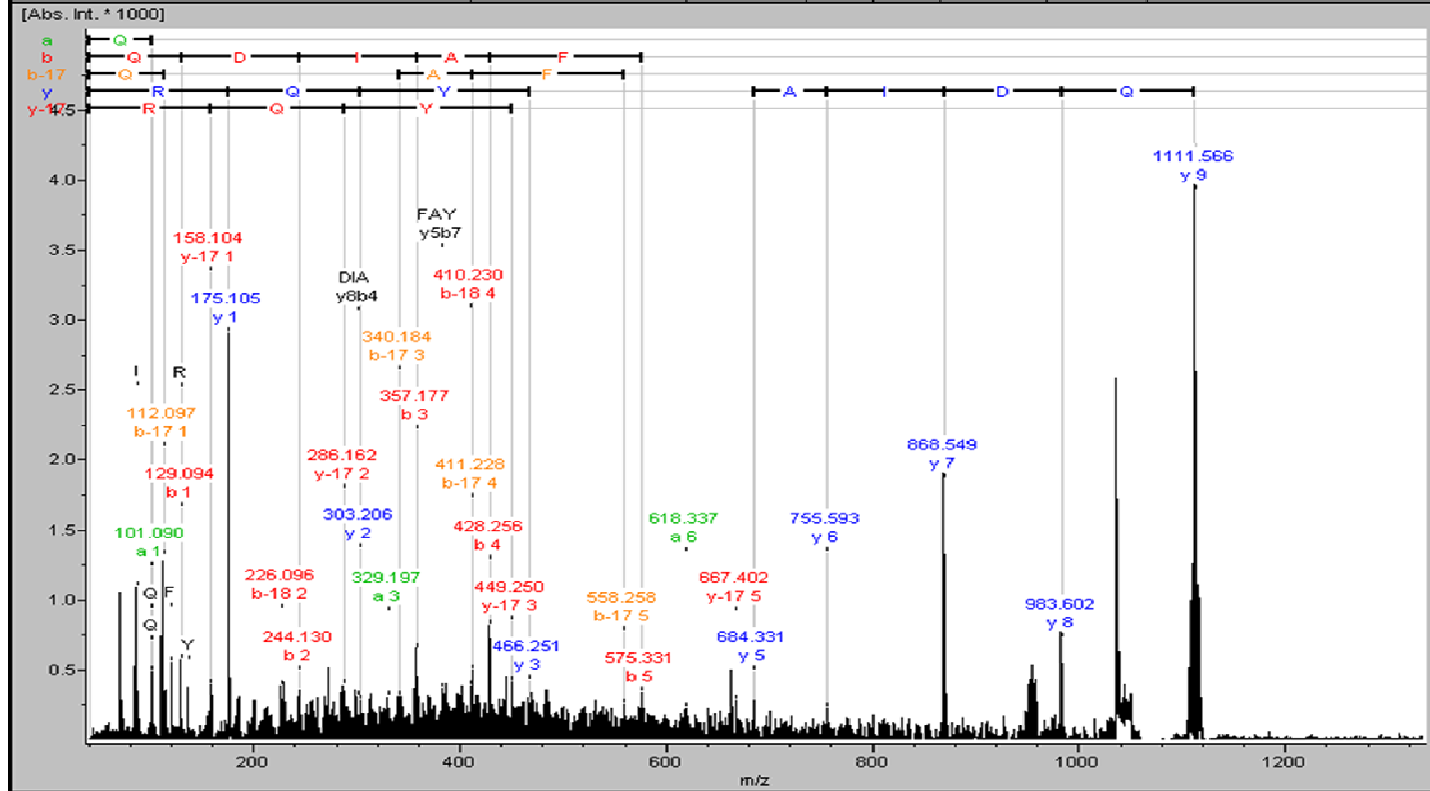
Ion	Val 1	Gly 2	Glu 3	Fragment Ion Mass Errors (Da)			Tyr 7	Ile 8	Gly 9	Arg 10
				Tyr 4	Ser 5	Leu 6				
a		0.014			0.082	0.002				
b			0.009	0.037	0.035	-0.025				
b-17										
b-18										
b+18		0.011								-0.003
y	0	0.012	-0.018	0.035	-0.046	0.016	0.085			-0.003
y-17	-0.015	-0.039	-0.009	-0.056						
i						-0.01		-0.01		0.003
	Arg	Gly	Ile	Tyr	Leu	Ser	Tyr	Glu	Gly	Val

Histone H3-like	Mascot Score37	Mr(calc)	ppm	Miss	Score	Expect	Peptide
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide
788.4709	787.4636	787.4704	-8.67	1	37	0.019	R.KLPFQR.L



Fragment Ion Mass Errors (Da)						
	Lys	Leu	Pro	Phe	Gln	Arg
Ion	1	2	3	4	5	6
a	-0.015					
b	0.011	0.02		-0.114		
b-17	0.019		0.002			
b-18						
b+18						0.044
y	0.01	0.032	-0.026	0.014	0.021	0.044
y-17	-0.019	0.053	0.034	-0.016	0.004	
i	-0.015	-0.001	-0.007		0.022	0
	Arg	Gln	Phe	Pro	Leu	Lys

Annexin A2	Mascot Score (46)						
Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Peptide
1111.5510	1110.5437	1110.5458	-1.86	0	46	0.0015	R.QDIAFAYQR.R



		Fragment Ion Mass Errors (Da)								
		Gln	Asp	Ile	Ala	Phe	Ala	Tyr	Gln	Arg
		1	2	3	4	5	6	7	8	9
Ion	a	0.019		0.015			0.012			
	b	0.028	0.037	0	0.042	0.049				
	b-17	0.058		0.034	0.041	0.002				
	b-18		0.013		0.026					
	b+18									0.013
	y	-0.014	0.029	0.011		-0.016	0.209	0.081	0.108	0.013
	y-17	-0.012	-0.013	0.012		0.058				
	i	0.019		0		0.015		0.02	0.019	-0.019
		Arg	Gln	Tyr	Ala	Phe	Ala	Ile	Asp	Gln