Supplementary Table 2. Human epididymal proteins identified by MALDI-TOF MS and MALDI-TOF/TOF MS

Part I: Proteins identified by Voyager DE－STR biospectrometry workstation (not include keratins)

Part II: Proteins identified by 4800 MALDI TOF/TOF Analyzer (not include single-peptide identified proteins and keratins)

Part III: The observed precursor mass , charge and the labeled MS/MS spectrum of the 32 single-peptide identified proteins.

Part IV: Presentation of PMF spectrum

Criteria for acceptance:

For PMF:

All identified proteins had a significance threshold of at least $p \leqslant 0.05$, Score$\geqslant$60 and at least four masses matched.

If more than one protein was identified in a spot, the single protein member with the highest score (top rank) was chosen from the muti-protein family.

For MS/MS:

Individual ions scores $\geqslant$ 37 (Significance level, $p \leqslant 0.05$)

Part I: **Proteins identified by Voyager DE－STR biospectrometry workstation**

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
1	EF2_HUMAN	94	15	95146	6.42	9	8	Elongation factor 2
2	IREB1_HUMAN	141	17	98337	6.23	11	11	Iron-responsive element-binding protein 1
3	VINC_HUMAN	105	14	123591	5.51	14	12	Vinculin
4	GANAB_HUMAN	89	13	106807	5.74	15	10	Neutral alpha-glucosidase AB precursor
5	CBX5_HUMAN	61	32	22211	5.71	15	5	Chromobox protein homolog 5
6	HS90A_HUMAN	81	13	84607	4.94	12	9	Heat shock protein HSP 90-alpha
7	TGM2_HUMAN	77	15	77280	5.11	11	8	Protein-glutamine gamma-glutamyltransferase 2
8	TRFE_HUMAN	123	23	77000	6.81	16	13	Serotransferrin precursor
9	CO3_HUMAN	134	12	187030	6.02	17	15	Complement C3 precursor
10	WDR1_HUMAN	120	37	66152	6.17	24	12	WD repeat protein 1
11	PUR9_HUMAN	118	27	64575	6.27	15	11	Bifunctional purine biosynthesis protein PURH
12	KPYM_HUMAN	146	26	57900	7.96	13	12	Pyruvate kinase isozymes M1/M2
13	APOA1_HUMAN	86	19	30759	5.56	9	6	Apolipoprotein A-I precursor
14	HBB_HUMAN	109	62	15988	6.75	9	7	Hemoglobin subunit beta
15	UBIQ_HUMAN,	98	61	8560	6.56	7	5	Ubiquitin
16	UCP3_HUMAN	185	20	34193	9.31	16	5	Mitochondrial uncoupling protein 3
17	MOES_HUMAN	67	14	67778	6.08	11	7	Moesin

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
18	IGHG1_HUMAN	97	29	36083	8.46	7	6	Ig gamma-1 chain C region
19	ILEU_HUMAN,	63	17	42715	5.9	12	6	Leukocyte elastase inhibitor
20	ACY1_HUMAN	146	41	45856	5.77	20	13	Aminoacylase-1
21	SBP1_HUMAN	103	26	52280	6.13	19	10	Selenium-binding protein 1
22	CNDP2_HUMAN	126	29	52845	5.66	18	11	Cytosolic nonspecific dipeptidase
23	ALBU_HUMAN	118	23	69321	5.92	18	13	Serum albumin
24	1433Z_HUMAN	97	31	27728	4.73	15	9	14-3-3 protein zeta/delta
25	TAGL_HUMAN	130	45	22596	8.87	16	12	Transgelin
26	ANXA5_HUMAN	76	18	35914	4.94	6	5	Annexin A5
27	ACTB_HUMAN	127	20	41710	5.29	13	6	Actin, cytoplasmic 1
28	ACTG_HUMAN	95	29	41766	5.31	12	8	Actin, cytoplasmic 2
29	KCRB_HUMAN	107	26	42617	5.34	11	8	Creatine kinase B-type
30	DDAH1_HUMAN	79	29	31102	5.53	10	6	NG,NG-dimethylarginine dimethylaminohydrolase 1
31	IPYR_HUMAN,	124	41	32639	5.54	13	9	Inorganic pyrophosphatase
32	BHMT1_HUMAN	70	19	44942	6.41	10	6	Betaine--homocysteine S-methyltransferase 1
33	AL1A1_HUMAN	62	13	54827	6.3	7	5	Retinal dehydrogenase 1
34	GP73_HUMAN	61	13	45306	4.91	8	5	Golgi phosphoprotein 2
35	ADHX_HUMAN	74	20	39698	7.45	6	5	Alcohol dehydrogenase class 3 chi chain
36	IDHC_HUMAN	79	17	46630	6.53	11	7	Isocitrate dehydrogenase

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
37	ALDOA_HUMAN	104	34	39395	8.3	9	7	Fructose-bisphosphate aldolase A
38	G3P_HUMAN	73	25	36030	8.57	7	5	Glyceraldehyde-3-phosphate dehydrogenase
39	MDHC_HUMAN	77	20	36403	6.91	8	6	Malate dehydrogenase
40	PNPH_HUMAN	84	28	32097	6.45	9	7	Purine nucleoside phosphorylase
41	TPIS_HUMAN	105	34	26653	6.45	9	7	Triosephosphate isomerase
42	PEBP1_HUMAN	71	36	21044	7.01	9	5	Phosphatidylethanolamine-binding protein 1
43	ALDR_HUMAN	82	22	35830	6.51	9	6	Aldose reductase
44	PPIA_HUMAN	99	36	18001	7.68	11	9	Peptidyl-prolyl cis-trans isomerase A
45	HINT1_HUMAN	61	30	13793	6.43	9	4	Histidine triad nucleotide-binding protein 1
46	LDHB_HUMAN	72	20	36615	5.71	11	6	L-lactate dehydrogenase B chain
47	TTHY_HUMAN	112	53	15877	5.52	8	6	Transthyretin precursor
48	6PGL_HUMAN	74	30	27530	5.7	13	6	6-phosphogluconolactonase
49	GRP78_HUMAN	123	0	72288	5.07	15	11	78 kDa glucose-regulated protein
50	IPYR_HUMAN	124	41	32639	5.54	13	9	Inorganic pyrophosphatase
51	TTHY_HUMAN	104	48	15877	5.52	5	5	Transthyretin precursor
52	GALK1_HUMAN	127	26	42246	6.04	11	9	Galactokinase
53	NADC_HUMAN,	61	21	30796	5.81	11	5	Nicotinate-nucleotide pyrophosphorylase
54	CRYL1_HUMAN	114	30	35396	5.81	10	8	Lambda-crystallin homolog
55	PSME1_HUMAN	144	48	28705	5.78	20	12	Proteasome activator complex subunit 1

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
56	GALM_HUMAN	144	40	37742	6.18	13	10	Aldose 1-epimerase
57	AK1A1_HUMAN	138	37	36550	6.32	8	8	Alcohol dehydrogenase
58	ARK72_HUMAN	61	17	39564	6.7	9	5	Aflatoxin B1 aldehyde reductase member 2
59	MDHC_HUMAN	69	23	36403	6.91	12	7	Malate dehydrogenase,
60	PGAM1_HUMAN	102	37	28786	6.67	11	8	Phosphoglycerate mutase 1
61	CAH1_HUMAN	63	31	28852	6.59	13	6	Carbonic anhydrase 1
62	TPIS_HUMAN	149	48	26653	6.45	8	8	Triosephosphate isomerase
63	PPIA_HUMAN	71	32	18001	7.68	11	6	Peptidyl-prolyl cis-trans isomerase A
64	PRDX1_HUMAN	98	37	22096	8.27	8	6	Peroxiredoxin-1
65	BLVRB_HUMAN	85	49	22105	7.13	14	7	Flavin reductase
66	KAD1_HUMAN	102	43	21621	8.73	11	8	Adenylate kinase isoenzyme 1
67	SPTB2_HUMAN	61	4	274439	5.39	7	7	Spectrin beta chain, brain 1
68	PEBP1_HUMAN	66	32	21044	7.01	6	4	Phosphatidylethanolamine-binding protein 1
69	COF1_HUMAN	105	42	18491	8.22	8	6	Cofilin-1
70	UBIQ_HUMAN	98	61	8560	6.56	7	5	Ubiquitin
71	ENPL_HUMAN	117	14	92411	4.76	11	11	Endoplasmin precursor
72	HS90A_HUMAN	81	13	83212	4.97	12	8	Heat shock protein HSP 90-beta
73	A1BG_HUMAN	67	16	54239	5.58	11	7	Alpha-1B-glycoprotein precursor
74	PLSL_HUMAN	133	24	70245	5.2	16	12	Plastin-2

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
75	ACON_HUMAN	157	20	85372	7.36	12	12	Aconitate hydratase
76	ENOA_HUMAN	73	19	47139	7.01	9	8	Alpha-enolase
77	IDHC_HUMAN	149	31	46630	6.53	14	12	Isocitrate dehydrogenase
78	TIGD2_HUMAN	62	16	59586	9.12	10	6	Tigger transposable element-derived protein 2
79	PGAM1_HUMAN	171	54	28786	6.67	12	11	Phosphoglycerate mutase 1
80	MAWBP_HUMAN	65	22	31765	6.06	10	6	Probable isomerase MAWBP
81	XTP3B_HUMAN	67	16	54823	5.88	10	6	XTP3-transactivated gene B protein precursor
82	CAH3_HUMAN	110	38	29553	6.86	9	7	Carbonic anhydrase 3
83	TPIS_HUMAN	160	46	26653	6.45	12	9	Triosephosphate isomerase
84	ACTS_HUMAN	68	25	42024	5.23	11	6	Actin, alpha skeletal muscle
84	PRDX6_HUMAN	111	36	25019	6	9	7	Peroxiredoxin-6
85	NT5C_HUMAN	98	432	23368	6.18	13	7	5'-deoxyribonucleotidase, cytosolic type
86	SAMP_HUMAN	72	20	25371	6.1	4	4	Serum amyloid P-component precursor
87	KHL15_HUMAN	61	7	69730	5.98	6	5	Kelch-like protein 15
88	GDIR_HUMAN	85	25	23193	5.02	6	5	Rho GDP-dissociation inhibitor 1
89	PRDX2_HUMAN	62	26	21878	5.66	7	4	Peroxiredoxin-2
90	CART1_HUMAN	68	20	36938	8.8	10	6	Cartilage homeoprotein 1
91	6PGL_HUMAN	74	30	27530	5.7	13	6	6-phosphogluconolactonase
92	HSPB1_HUMAN	114	37	22768	5.98	9	7	Heat-shock protein beta-1

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
93	M4K4_HUMAN	62	5	142013	7.09	7	6	Mitogen-activated protein kinase kinase kinase kinase 4
94	PHP14_HUMAN	61	47	13824	5.65	10	5	14 kDa phosphohistidine phosphatase
95	TBA3_HUMAN	102	30	50104	4.94	12	8	Tubulin alpha-3 chain
96	TBAK_HUMAN	102	30	50120	4.94	12	8	Tubulin alpha-ubiquitous chain
97	S10AB_HUMAN	60	42	11733	6.56	9	5	Protein S100-A11
98	A1AT_HUMAN	124	28	46707	5.37	15	10	Alpha-1-antiproteinase
99	VIME_HUMAN	120	20	53619	5.06	14	11	Vimentin
101	ANXA5_HUMAN	99	30	35914	4.94	10	7	Annexin A5
102	1433E_HUMAN	68	19	29155	4.63	8	6	14-3-3 protein epsilon
103	TBA6_HUMAN	96	29	49863	4.96	14	8	Tubulin alpha-6 chain
104	TBAK_HUMAN	136	34	50120	4.94	16	11	Tubulin alpha-ubiquitous chain
105	GRP78_HUMAN	191	27	72288	5.07	19	16	78 kDa glucose-regulated protein precursor
106	A1AG1_HUMAN	78	22	23497	4.93	9	5	Alpha-1-acid glycoprotein 1 precursor
107	TRFE_HUMAN	190	26	77000	6.81	10	18	Serotransferrin precursor
108	TKT_HUMAN	65	10	67835	7.58	4	4	Transketolase
109	KPYM_HUMAN	149	30	57900	7.96	18	14	Pyruvate kinase isozymes M1/M2
110	PRDX1_HUMAN	70	35	22096	8.27	10	5	Peroxiredoxin-1
111	BLVRB_HUMAN	78	37	22105	7.13	9	6	Flavin reductase
112	PPIB_HUMAN	125	42	22728	9.33	9	9	Peptidyl-prolyl cis-trans isomerase B precursor

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
113	PARK7_HUMAN	61	29	19878	6.33	8	5	Protein DJ-1
114	PYR_HUMAN	103	20	32639	5.54	8	5	Inorganic pyrophosphatase
115	IGHG1_HUMAN	62	20	36083	8.46	10	5	Ig gamma-1 chain C region
116	FBN1_HUMAN	61	4	312098	4.81	11	10	Fibrillin-1
117	BTBD6_HUMAN	61	16	45896	5.45	8	5	BTB/POZ domain-containing protein 6
118	AGR2_HUMAN	74	42	19967	9.03	10	5	Anterior gradient protein 2
119	PDXK_HUMAN	84	24	35080	5.75	9	6	Pyridoxal kinase
120	FGD2_HUMAN	61	14	74845	6.51	6	5	RhoGEF and PH domain-containing protein 2
121	CNDP2_HUMAN	65	10	52845	5.66	4	4	Cytosolic nonspecific dipeptidase
122	PLXA4_HUMAN	66	6	212318	6.42	7	7	Plexin-A4 precursor
123	PRKDC_HUMAN	64	4	468788	6.75	16	14	NA-dependent protein kinase catalytic subunit
124	CF152_HUMAN	64	9	80505	7.31	5	5	Uncharacterized protein C6orf152
125	3BP2_HUMAN	63	11	62204	7.67	7	5	SH3 domain-binding protein 2
126	IQEC1_HUMAN	70	8	108247	6.49	9	6	IQ motif and Sec7 domain-containing protein 1
127	CSHL_HUMAN	68	19	22634	5.57	5	4	Chorionic somatomammotropin hormone-like 1
128	TEKT4_HUMAN	74	10	50617	6.01	4	4	Tektin-4
129	KLF5_HUMAN	71	11	50759	8.86	5	4	Krueppel-like factor 5
130	CC74A_HUMAN	65	15	41580	10.52	5	5	Coiled-coil domain-containing protein 74A
131	THUM2_HUMAN	61	12	53333	8.2	4	4	THUMP domain-containing protein 2

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
132	VDAC1_HUMAN	82	25	30754	8.62	6	4	Voltage-dependent anion-selective channel protein 1
133	KBTB3_HUMAN	61	8	69350	5.22	6	5	Kelch repeat and BTB domain-containing protein 3
134	ZN484_HUMAN	69	8	98158	8.68	6	6	Zinc finger protein 484
135	WISP1_HUMAN	62	15	40304	6.84	5	4	WNT1-inducible-signaling pathway protein 1
136	ROA2_HUMAN	60	12	37407	8.97	5	4	Heterogeneous nuclear ribonucleoproteins A2/B1
137	GRP75_HUMAN	76	14	73635	5.87	10	7	Stress-70 protein
138	PANK3_HUMAN	63	15	41068	6.13	6	4	Pantothenate kinase 3
139	LDH6A_HUMAN	65	12	36484	6.51	5	4	L-lactate dehydrogenase A-like 6A
140	SOLH2_HUMAN	62	12	46911	6.79	4	3	Spermatogenesis- and oogenesis-specific basic helix-loop-helix-containing protein 2
141	B1AN51_HUMAN	75	18	54014	8.6	6	5	spermatogenesis associated 6
142	RL13A_HUMAN	66	31	18509	10.51	5	4	60S ribosomal protein L13a
143	SALL1_HUMAN	65	27	15646	8.15	4	4	SALL1 protein
144	KAD4_HUMAN	65	27	22073	5.38	7	5	Adenylate kinase isoenzyme 4
145	WFDC2_HUMAN	84	36	14337	6.79	6	5	WAP four-disulfide core domain protein 2 precursor
146	CPNS1_HUMAN	61	12	57948	6.41	5	4	Calpain small subunit 1
147	C1GLT_HUMAN	65	17	42176	6.17	7	5	Glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1
148	RG9D2_HUMAN	66	20	39694	7.29	7	6	RNA methyltransferase domain containing 2

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
149	SPA4L_HUMAN	67	14	43053	8.61	5	4	Sperm-associated antigen 4-like protein
150	ENOG_HUMAN	62	17	47239	4.91	9	5	Gamma-enolase
151	GDIR1_HUMAN	85	25	23193	5.02	6	5	Rho GDP-dissociation inhibitor 1
152	FABPH_HUMAN		35	14849	6.29	7	5	Fatty acid-binding protein
153	PAPS2_HUMAN	63	12	69457	8.18	6	5	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 2
154	HINT1_HUMAN	64	52	13793	6.43	10	5	Histidine triad nucleotide-binding protein 1
155	UBE2N_HUMAN	72	26	17127	6.13	10	5	Ubiquitin-conjugating enzyme E2 N
156	TBCA_HUMAN	62	25	12847	5.25	7	6	Tubulin-specific chaperone A
157	MLRN_HUMAN	73	29	19814	4.8	5	5	Myosin regulatory light chain 2
158	CYB5_HUMAN	68	42	15321	4.88	7	4	Cytochrome b5
159	NDKA_HUMAN	95	42	17138	5.83	7	7	Nucleoside diphosphate kinase A
160	NPC2_HUMAN	66	37	16559	7.56	7	4	Epididymal secretory protein E1 precursor
161	COF1_HUMAN	88	48	18491	8.22	9	5	Cofilin-1
162	PEBP1_HUMAN	106	56	21044	7.01	8	6	Phosphatidylethanolamine-binding protein 1
163	CRYAB_HUMAN	65	33	20146	6.76	10	4	Alpha crystallin B chain
164	SODM_HUMAN	62	20	24707	8.35	7	4	Superoxide dismutase [Mn], mitochondrial precursor
165	APT_HUMAN	62	30	19595	5.78	7	4	Adenine phosphoribosyltransferase
166	CAYP1_HUMAN	97	30	20954	4.74	8	7	Calcyphosin

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
167	ARFRP_HUMAN	61	20	22599	7.49	5	4	ARF-related protein 1
168	RANB3_HUMAN	62	17	60173	4.7	9	6	Ran-binding protein 3
169	PHP14_HUMAN	77	47	13824	5.56	8	6	14 kDa phosphohistidine phosphatase
170	WNT5A_HUMAN	60	18	40860	8.72	5	5	Protein Wnt-5a
171	PRDX5_HUMAN	116	41	22012	8.85	8	7	Peroxiredoxin-5, mitochondrial precursor
172	MYL6_HUMAN	71	33	16919	4.56	7	5	Myosin light polypeptide 6
173	MLRN_HUMAN	69	29	19814	4.8	5	5	Myosin regulatory light chain 2
174	SODC_HUMAN	68	38	15926	5.7	7	4	Superoxide dismutase [Cu-Zn]
175	PRDX3_HUMAN	71	38	27675	7.67	7	5	Thioredoxin-dependent peroxide reductase
176	AB14B_HUMAN	65	28	22332	5.94	7	5	Abhydrolase domain-containing protein 14B
177	TAGL_HUMAN	131	41	22465	8.88	11	39	Transgelin
178	CNN1_HUMAN	69	16	33150	9.16	8	6	Calponin-1
179	HBA_HUMAN	66	34	15117	8.73	6	4	Hemoglobin subunit alpha
180	EP3B_HUMAN	62	36	17573	6.51	6	4	Epididymal secretory protein E3 beta precursor
181	COF1_HUMAN	60	32	18360	8.26	6	4	Cofilin-1
182	PPIA_HUMAN	119	50	17870	7.82	13	10	Peptidyl-prolyl cis-trans isomerase A
183	NDKB_HUMAN	76	41	17287	8.52	8	5	Nucleoside diphosphate kinase B
184	WDR1_HUMAN	93	21	66152	6.17	12	8	WD repeat protein 1
185	IGHG1_HUMAN	123	34	36083	8.46	7	7	Ig gamma-1 chain C region

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
186	GDIB_HUMAN	120	26	50631	6.11	10	9	Rab GDP dissociation inhibitor beta
187	SBP1_HUMAN	64	15	52280	6.13	11	6	Selenium-binding protein 1
188	ARP3_HUMAN	148	31	47341	5.61	11	10	Actin-like protein 3
189	GSHB_HUMAN	114	25	52352	5.67	12	9	Glutathione synthetase
189	GSHB_HUMAN	114	25	52352	5.67	12	9	Glutathione synthetase
190	PLSL_HUMAN	114	27	70245	5.2	13	10	Plastin-2
191	VTDB_HUMAN	75	23	52929	5.4	11	7	Vitamin D-binding protein precursor
192	TBA3_HUMAN	71	17	50104	4.94	6	5	Tubulin alpha-3 chain
193	A1AT_HUMAN	62	15	46707	5.37	8	5	Alpha-1-antitrypsin precursor
194	TBB5_HUMAN	62	10	49639	4.78	8	5	Tubulin beta chain
195	A1AT_HUMAN	64	19	46707	5.37	13	6	Alpha-1-antitrypsin precursor
196	TBB2C_HUMAN	60	15	49799	4.79	13	6	Tubulin beta-2C chain
197	TBB4_HUMAN	60	13	49554	4.78	17	6	Tubulin beta-4 chain
198	TPM2_HUMAN	71	19	32831	4.66	15	7	Tropomyosin beta chain
200	BLK_HUMAN	61	10	57702	7.98	6	5	Tyrosine-protein kinase BLK
201	TPM4_HUMAN	62	8	28504	4.67	4	4	Tropomyosin alpha-4 chain
202	ACTH_HUMAN	65	17	41850	5.31	10	5	Actin, gamma-enteric smooth muscle
203	ACTC_HUMAN	60	16	41992	5.23	10	5	Actin, alpha cardiac muscle 1
204	ACTS_HUMAN	61	16	42024	5.23	10	5	Actin, alpha skeletal muscle

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
205	ACTA_HUMAN	60	16	41982	5.23	10	5	Actin, aortic smooth muscle
206	KCRB_HUMAN	65	19	42617	5.34	13	6	Creatine kinase B-type
207	LDHB_HUMAN	121	33	36615	5.71	10	8	L-lactate dehydrogenase B chain
208	DDAH1_HUMAN	60	20	31102	5.53	6	4	NG,NG-dimethylarginine dimethylaminohydrolase 1
209	BPNT1_HUMAN	60	22	33371	5.46	6	4	3',5'-bisphosphate nucleotidase 1
210	ANXA5_HUMAN	104	30	35914	4.94	9	7	Annexin A5
211	1433E_HUMAN	81	27	29155	4.63	9	6	14-3-3 protein epsilon
212	1433Z_HUMAN	61	24	27728	4.73	7	4	14-3-3 protein zeta/delta
213	1433B_HUMAN	61	21	28065	4.76	7	5	14-3-3 protein beta/alpha
214	NU160_HUMAN	63	6	148905	5.41	7	6	Nuclear pore complex protein Nup160
215	GDIR_HUMAN	105	34	23193	5.02	7	6	Rho GDP-dissociation inhibitor 1
216	KHL15_HUMAN	60	7	69730	5.98	7	5	Kelch-like protein 15
217	HSPB1_HUMAN	116	47	22768	5.98	6	6	Heat-shock protein beta-1
218	GSTP1_HUMAN	64	26	23341	5.43	4	4	Glutathione S-transferase P
219	GSTO1_HUMAN	60	22	27548	6.23	11	5	Glutathione transferase omega-1
220	PNPH_HUMAN	129	35	32097	6.45	9	8	Purine nucleoside phosphorylase
221	PIPNA_HUMAN	65	20	31786	6.11	7	5	Phosphatidylinositol transfer protein alpha isoform
222	GALM_HUMAN	109	36	37742	6.18	12	8	Aldose 1-epimerase
223	FBX25_HUMAN	60	16	43285	8.35	12	5	F-box only protein 25

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
224	ARK72_HUMAN	60	15	39564	6.7	5	4	Aflatoxin B1 aldehyde reductase member 2
225	AK1A1_HUMAN	62	19	36550	6.32	5	4	Alcohol dehydrogenase [NADP+]
226	IDHC_HUMAN	125	27	46630	6.53	10	9	Isocitrate dehydrogenase [NADP] cytoplasmic
227	PGK1_HUMAN	87	25	44586	8.3	7	6	Phosphoglycerate kinase 1
228	ALDOA_HUMAN	104	33	39395	8.3	9	7	Fructose-bisphosphate aldolase A
229	LDHA_HUMAN		10	36665	8.44	5	4	L-lactate dehydrogenase A chain
230	MDHC_HUMAN	62	16	36403	6.91	5	4	Malate dehydrogenase
231	PGAM1_HUMAN	141	51	28786	6.67	9	8	Phosphoglycerate mutase 1
232	CAH3_HUMAN	165	56	29553	6.86	10	10	Carbonic anhydrase 3
233	CSRP1_HUMAN	82	54	20554	8.9	10	6	Cysteine and glycine-rich protein 1
234	PRDX1_HUMAN	61	20	22096	8.27	7	4	Peroxiredoxin-1
235	PEBP1_HUMAN	111	40	21044	7.01	8	7	Phosphatidylethanolamine-binding protein 1
236	PARK7_HUMAN	68	31	19878	6.33	6	5	Protein DJ-1
237	PRDX2_HUMAN	99	31	21878	5.66	9	6	Peroxiredoxin-2
238	HSPB6_HUMAN	110	78	17125	5.95	9	6	Heat-shock protein beta-6
239	KC1A_HUMAN	62	16	38890	9.59	9	5	Casein kinase I isoform alpha
240	HINT1_HUMAN	99	71	13793	6.43	13	6	Histidine triad nucleotide-binding protein 1
241	DEST_HUMAN	99	48	18493	8.06	9	7	Destrin
242	ALBU_HUMAN	177	23	69321	5.92	13	11	Serum albumin precursor

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
243	LMNA_HUMAN	72	13	74095	6.57	14	8	Lamin-A/C
244	PRELP_HUMAN	61	15	43782	9.47	10	5	Prolargin precursor
245	PUR9_HUMAN	110	24	64575	6.27	12	9	Bifunctional purine biosynthesis protein PURH
246	STIP1_HUMAN	133	22	62599	6.4	13	12	Stress-induced-phosphoprotein 1
247	LMNA_HUMAN	144	21	74095	6.57	15	13	Lamin-A/C
248	ACON_HUMAN	164	25	85372	7.36	13	13	Aconitate hydratase, mitochondrial precursor
249	LMNA_HUMAN	107	20	74095	6.57	13	10	Lamin-A/C
250	IREB1_HUMAN	142	16	98337	6.23	17	15	Iron-responsive element-binding protein 1
251	PPIB_HUMAN	142	42	22728	9.33	8	8	Peptidyl-prolyl cis-trans isomerase B precursor
252	ALDOA_HUMAN	125	34	39395	8.3	9	8	Fructose-bisphosphate aldolase A
253	TRFE_HUMAN	115	20	77000	6.81	11	10	Serotransferrin precursor (
254	KAD1_HUMAN	110	32	21621	8.73	8	7	Adenylate kinase isoenzyme 1
255	PPIA_HUMAN	109	43	18001	7.68	11	7	Peptidyl-prolyl cis-trans isomerase A
256	PEBP1_HUMAN	98	49	21044	7.01	9	6	Phosphatidylethanolamine-binding protein 1
257	PGK1_HUMAN	89	21	44586	8.3	6	6	Phosphoglycerate kinase 1
258	WDR1_HUMAN	87	18	66152	6.17	16	9	WD repeat protein 1
259	ACON_HUMAN	83	12	85372	7.36	8	7	Aconitate hydratase, mitochondrial precursor
260	CO6A1_HUMAN	82	10	108462	5.26	11	9	Collagen alpha-1 chain precursor
261	HNRPL_HUMAN	81	17	60149	6.65	14	8	Heterogeneous nuclear ribonucleoprotein L

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
262	KAD3_HUMAN	80	31	25550	9.15	10	6	GTP:AMP phosphotransferase mitochondrial
263	PRDX1_HUMAN	79	25	22096	8.27	7	5	Peroxiredoxin-1
264	WDR17_HUMAN	62	7	147638	6.01	9	7	WD repeat protein 17
265	CH10_HUMAN	62	29	10925	8.89	8	4	10 kDa heat shock protein, mitochondrial
266	LEG3_HUMAN	60	19	26172	8.58	5	4	Galectin-3
267	TDRD7_HUMAN	63	8	123522	6.84	14	9	Tudor domain-containing protein 7
268	ATPA_HUMAN	60	12	59714	9.16	8	5	ATP synthase subunit alpha, mitochondrial precursor
269	COF1_HUMAN	63	26	18491	8.22	6	4	Cofilin-1
270	CO6A1_HUMAN	70	9	108462	5.26	6	6	Collagen alpha-1 chain precursor
271	PPAC3_HUMAN	61	28	29429	9.98	6	4	Probable lipid phosphate phosphatase PPAPDC3
272	KIF14_HUMAN	60	5	186375	8.06	9	8	Kinesin-like protein KIF14
273	PSD3_HUMAN	64	10	60156	8.83	7	5	PH and SEC7 domain-containing protein 3
274	TRFE_HUMAN	135	23	77000	6.81	13	13	Serotransferrin precursor
275	LMNA_HUMAN	62	14	74095	6.57	14	7	Lamin-A/C (70 kDa lamin
276	CAND2_HUMAN	60	10	122604	5.58	10	7	Cullin-associated NEDD8-dissociated protein 2
277	WDR1_HUMAN	100	31	66152	6.17	18	10	WD repeat protein 1
278	ALDOC_HUMAN	65	18	39431	6.41	9	5	Fructose-bisphosphate aldolase C
279	NMBR_HUMAN	60	10	43424	8.93	8	5	Neuromedin-B receptor
280	PS1C1_HUMAN	63	42	16568	6.28	10	4	Psoriasis susceptibility 1 candidate gene 1 protein

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
281	CA163_HUMAN	61	19	25720	5.66	6	4	Hcp beta-lactamase-like protein C1orf163
282	TCPZ_HUMAN	65	16	57988	6.23	11	6	T-complex protein 1 subunit zeta
283	A1AT_HUMAN	60	13	46707	5.37	5	4	Alpha-1-antitrypsin precursor
284	CALR_HUMAN	60	20	48112	4.29	11	5	Calreticulin precursor
285	CALR_HUMAN	91	28	48112	4.29	13	8	Calreticulin precursor
286	ENPL_HUMAN	63	9	92411	4.76	9	7	Endoplasmin precursor
287	DESM_HUMAN	83	28	53503	5.21	15	8	Desmin
288	TBB2B_HUMAN	100	24	49921	4.78	17	11	Tubulin beta-2B chain
289	TBB2A_HUMAN	100	24	49875	4.78	17	11	Tubulin beta-2A chain
290	ECHM_HUMAN	123	33	31367	8.34	13	9	Enoyl-CoA hydratase, mitochondrial precursor
291	PIMT_HUMAN	71	30	24635	6.7	9	5	Protein-L-isoaspartate O-methyltransferase
292	TPIS_HUMAN	210	72	26653	6.45	16	13	Triosephosphate isomerase
293	DCXR_HUMAN	64	19	25897	8.33	7	4	L-xylulose reductase
295	PRDX1_HUMAN	80	34	22096	8.27	13	6	Peroxiredoxin-1
296	MAR1_HUMAN	64	23	13149	8.29	10	4	Melanoma antigen recognized by T-cells 1
297	GDIR_HUMAN	85	22	23193	5.02	11	7	Rho GDP-dissociation inhibitor 1
298	VIME_HUMAN	72	21	53619	5.06	17	7	Vimentin
299	DESM_HUMAN	109	31	53503	5.21	14	9	Desmin
300	PDIA3_HUMAN	70	13	56747	5.98	10	6	Protein disulfide-isomerase A3 precursor

No.	**Entry name**	**Score**	**Coverage %**	**Mr**	**pI**	**Searched**	**Matched**	**Protein description**
301	PDIA3_HUMAN	96	21	56747	5.98	13	9	Protein disulfide-isomerase A3 precursor
302	SBP1_HUMAN	89	23	52280	6.13	16	9	Selenium-binding protein 1
303	SYWC_HUMAN	61	15	53132	5.83	12	6	Tryptophanyl-tRNA synthetase, cytoplasmic
304	SBP1_HUMAN	108	22	52280	6.13	17	10	Selenium-binding protein 1
305	TCPB_HUMAN	124	28	57452	6.01	14	10	T-complex protein 1 subunit beta
306	SCOT_HUMAN	114	33	56122	7.14	12	9	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor
307	APOA1_HUMAN	90	25	30759	5.56	12	7	Apolipoprotein A-I precursor
308	APOA1_HUMAN	120	37	30759	5.56	14	10	Apolipoprotein A-I precursor
309	ITPA_HUMAN	85	54	21432	5.5	7	5	Inosine triphosphate pyrophosphatase
310	TGM2_HUMAN	65	10	77280	5.11	11	6	Protein-glutamine gamma-glutamyltransferase 2
311	PARK7_HUMAN	88	38	19878	6.33	19	9	Protein DJ-1
312	HEBP1_HUMAN	108	55	21084	5.71	14	9	Heme-binding protein 1
313	PRDX2_HUMAN	101	35	21878	5.66	8	6	Peroxiredoxin-2
314	GSTP1_HUMAN	92	47	23341	5.43	11	7	Glutathione S-transferase P
315	ANXA2_HUMAN	61	25	38580	7.57	15	6	Annexin A2
316	HSPB1_HUMAN	139	38	22768	5.98	9	8	Heat-shock protein beta-1
317	GRB2_HUMAN	71	20	25190	5.89	13	7	Growth factor receptor-bound protein 2
318	CRSP6_HUMAN	65	9	72831	7.05	13	7	CRSP complex subunit 6

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
319	HSPB1_HUMAN	85	28	22768	5.98	11	6	Heat-shock protein beta-1
320	PSB3_HUMAN	74	33	22933	6.14	12	7	Proteasome subunit beta type 3
321	NT5C_HUMAN	64	21	23368	6.18	18	6	5'-deoxyribonucleotidase, cytosolic type
322	HSPB1_HUMAN	94	39	22768	5.98	14	7	Heat-shock protein beta-1
323	PSA2_HUMAN	68	33	25882	6.92	13	6	Proteasome subunit alpha type 2
324	PIMT_HUMAN	95	43	24635	6.7	15	8	Protein-L-isoaspartate O-methyltransferase
325	ES1_HUMAN	89	44	28153	8.5	12	7	ES1 protein homolog, mitochondrial precursor
326	HCD2_HUMAN	118	47	26906	7.66	13	10	3-hydroxyacyl-CoA dehydrogenase type-2
327	BLVRB_HUMAN	98	46	22105	7.13	16	9	Flavin reductase
328	BLVRB_HUMAN	72	51	22105	7.13	18	7	Flavin reductase
329	PRDX1_HUMAN	117	49	22096	8.27	14	8	Peroxiredoxin-1
330	G3P_HUMAN	69	25	36030	8.57	14	6	Glyceraldehyde-3-phosphate dehydrogenase
331	WDR25_HUMAN	60	11	60123	9.21	10	6	WD repeat protein 25 - Homo sapiens
332	G3P_HUMAN	69	25	36030	8.57	14	6	Glyceraldehyde-3-phosphate dehydrogenase
333	MTAP_HUMAN	62	30	31230	6.75	13	6	S-methyl-5-thioadenosine phosphorylase
334	PGAM1_HUMAN	148	51	28786	6.67	11	10	Phosphoglycerate mutase 1
335	TPIS_HUMAN	187	55	26653	6.45	12	11	Triosephosphate isomerase
336	TPIS_HUMAN	66	20	26653	6.45	11	5	Triosephosphate isomerase
337	ALBU_HUMAN	119	17	69321	5.92	14	12	Serum albumin precursor - Homo sapiens

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
338	PNPH_HUMAN	151	47	32097	6.45	16	13	Purine nucleoside phosphorylase
339	PGAM1_HUMAN	141	49	28786	6.67	13	10	Phosphoglycerate mutase 1
340	ECHM_HUMAN	95	32	31367	8.34	12	8	Enoyl-CoA hydratase, mitochondrial precursor
341	ANXA1_HUMAN	119	34	38690	6.57	14	9	Annexin A1
342	BDH_HUMAN	60	20	38132	9.11	11	5	D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor
343	GSTO1_HUMAN	65	19	27548	6.23	10	5	Glutathione transferase omega-1
344	PSME1_HUMAN	62	22	28705	5.78	8	5	Proteasome activator complex subunit 1
345	PSB7_HUMAN	61	20	29946	7.57	12	6	Proteasome subunit beta type 7 precursor
346	6PGL_HUMAN	60	25	27530	5.7	12	5	6-phosphogluconolactonase
347	DDAH2_HUMAN	99	35	29625	5.66	11	7	NG,NG-dimethylarginine dimethylaminohydrolase 2
348	CATD_HUMAN	62	8	44524	6.1	5	5	Cathepsin D precursor
349	CAPZB_HUMAN	125	34	31331	5.36	15	11	F-actin capping protein subunit beta
350	PHB_HUMAN	93	31	29786	5.57	12	7	Prohibitin - Homo sapiens
351	NET1_HUMAN	65	11	67690	9.13	9	6	Netrin-1 precursor - Homo sapiens
352	HSPB1_HUMAN	84	32	22768	5.98	11	6	Heat-shock protein beta-1
353	GDIR_HUMAN	94	34	23193	5.02	10	7	Rho GDP-dissociation inhibitor 1
354	HEBP2_HUMAN	91	32	22861	4.58	9	6	Heme-binding protein 2
355	TPM4_HUMAN	97	24	28504	4.67	15	8	Tropomyosin alpha-4 chain

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
356	GNA15_HUMAN	62	24	43480	8.71	14	7	Guanine nucleotide-binding protein alpha-15 subunit
357	HS90B_HUMAN	77	13	83212	4.97	12	8	Heat shock protein HSP 90-bet
358	KPTN_HUMAN	123	28	57900	7.96	18	14	Kaptin
359	NADC_HUMAN	65	21	30796	5.81	11	5	Nicotinate-nucleotide pyrophosphorylase
360	ILK_HUMAN	61	13	51386	8.3	13	6	Integrin-linked protein kinase
361	KLH15_HUMAN	61	7	69730	5.98	7	5	Kelch-like protein 15
362	PSME3_HUMAN	61	29	29488	5.69	23	6	Proteasome activator complex subunit
363	RHG25_HUMAN	60	13	72385	5.83	19	8	Rho GTPase-activating protein 25
364	RHOQ_HUMAN	60	32	22645	5.94	7	4	Rho-related GTP-binding protein RhoQ
365	CSRP1_HUMAN	82	54	20554	8.9	10	6	Cysteine and glycine-rich protein 2
366	SAHH_HUMAN	118	20	47685	5.92	10	9	Adenosylhomocysteinase
367	ADCY5_HUMAN	141	19	140757	6.9	17	14	Adenylate cyclase type 5
368	D104A_HUMAN	60	36	8520	9.41	3	3	Beta-defensin 104
369	D105A_HUMAN	69	29	8916	8.71	5	4	Beta-defensin 105
370	DB118_HUMAN	65	20	13605	6.88	5	4	Beta-defensin 118
371	DB121_HUMAN	66	40	8450	8.99	4	3	Beta-defensin 121
372	DB129_HUMAN	139	30	20285	9.04	7	7	Beta-defensin 129
373	DB132_HUMAN	69	53	10603	9.72	4	3	Beta-defensin 132
374	CADH1_HUMAN	60	6	97396	4.58	6	4	Cadherin-1

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
375	AKAP4_HUMAN	80	14	95842	6.56	9	7	A-kinase anchor protein 4
376	CST8_HUMAN	61	34	16265	9.05	6	3	Cystatin-8
377	CST11_HUMAN	92	56	16495	6.51	5	4	Cystatin-11
378	CYTC_HUMAN	90	38	15789	9	4	4	Cystatin-C
379	CRIS1_HUMAN	69	21	28462	5.57	6	4	Cysteine-rich secretory protein 1
380	ADA28_HUMAN	104	15	87123	6.38	11	8	Disintegrin and metalloproteinase domain-containing protein 28
381	ADAM7_HUMAN	155	22	85613	6.08	13	11	Disintegrin and metalloproteinase domain-containing protein 7
382	SAT1_HUMAN	102	42	20011	5.09	6	5	Diamine acetyltransferase 1
383	LCN6_HUMAN	84	47	18033	4.84	6	4	Epididymal-specific lipocalin-6
384	LCN8_HUMAN	92	41	19068	6.84	7	5	Epididymal-specific lipocalin-8
385	MA2B2_HUMAN	159	21	113908	6.74	15	12	Epididymis-specific alpha-mannosidase
386	EPPI_HUMAN	62	34	15273	8.52	4	3	Eppin
387	ESPB1_HUMAN	125	43	26089	6.2	10	7	Epididymal sperm-binding protein 1
388	LCN12_HUMAN	111	42	21486	5.48	5	5	Epididymal-specific lipocalin-12
389	CAZA3_HUMAN	129	37	35002	7.61	8	7	F-actin-capping protein subunit alpha-3
390	TXND3_HUMAN	125	19	67227	4.9	11	9	Thioredoxin domain-containing protein 3
391	TXND5_HUMAN	148	36	47599	5.63	12	9	Thioredoxin domain-containing protein 5

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
392	WDR8_HUMAN	162	33	51555	6.37	12	10	WD repeat-containing protein 8
393	WFDC8_HUMAN	90	29	27805	8.43	6	5	WAP four-disulfide core domain protein 8
394	WFDC6_HUMAN	62	30	14616	8.64	6	4	WAP four-disulfide core domain protein 6
395	RNAS9_HUMAN	86	35	24291	6.18	8	5	Ribonuclease-like protein 9
396	RNS12_HUMAN	60	25	17166	6.64	5	3	Ribonuclease-like protein 12
397	RNS13_HUMAN	79	30	17833	8.87	5	4	Ribonuclease-like protein 13
398	RNAS4_HUMAN	68	31	16829	9.3	7	4	Ribonuclease 4
399	SPAG1_HUMAN	100	15	103574	6.46	11	8	Sperm-associated antigen 1
400	GSTP1_HUMAN	75	40	23341	5.43	9	5	Glutathione S-transferase P
401	GSTP1_HUMAN	97	48	23341	5.43	15	8	Glutathione S-transferase P
402	PA1B3_HUMAN	67	17	25718	6.33	12	5	Platelet-activating factor acetylhydrolase IB subunit gamma
403	UCRI_HUMAN	66	27	29633	8.55	10	5	Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor
404	CATB_HUMAN	61	22	37797	5.88	12	6	Cathepsin B precursor
405	SFRS3_HUMAN	93	41	19318	11.64	10	6	Splicing factor, arginine/serine-rich 3
406	RAN_HUMAN	62	17	24408	7.01	10	5	GTP-binding nuclear protein Ran
407	HAP1_HUMAN	61	9	75467	4.68	10	9	Huntingtin-associated protein 1
408	BLVRB_HUMAN	111	56	22105	7.13	11	7	Flavin reductase
409	ANXA5_HUMAN	167	42	35914	4.94	14	11	Annexin A5

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
410	MIME_HUMAN	69	13	33901	5.46	11	6	Mimecan precursor
411	NADC_HUMA	62	18	30796	5.81	10	5	Nicotinate-nucleotide pyrophosphorylase [carboxylating]
412	ANXA4_HUMAN	135	36	35860	5.84	10	9	Annexin A4
413	ECH1_HUMAN	62	18	35793	8.16	11	5	Delta-Delta-dienoyl-CoA isomerase, mitochondrial precursor
414	SIAS_HUMAN	83	20	40281	6.29	7	6	Sialic acid synthase
415	TXNL1_HUMAN	62	29	32231	4.4	8	4	Thioredoxin-like protein 1
416	DCPS_HUMAN	63	12	38585	5.93	6	4	Scavenger mRNA decapping enzyme DcpS
417	ALDR_HUMAN	69	17	35830	6.51	7	5	Aldose reductase
418	ANXA2_HUMAN	77	17	38580	7.57	8	6	Annexin A2
419	ALDOA_HUMAN	146	37	39395	8.3	13	10	Fructose-bisphosphate aldolase A
420	IPYR_HUMAN	86	29	32639	5.54	8	6	Inorganic pyrophosphatase
421	APOH_HUMAN	64	21	38273	8.34	8	5	Beta-2-glycoprotein 1 precursor
422	FIBB_HUMAN	62	18	55892	8.54	9	6	Fibrinogen beta chain precursor
423	EXTL3_HUMAN	62	8	104682	6.08	6	5	Exostosin-like 3
424	ASSY_HUMAN	63	16	46501	8.08	6	4	Argininosuccinate synthase
425	TOR3A_HUMAN	57	12	46169	5.67	5	4	Torsin-3A precursor
426	GDIB_HUMAN	99	30	50631	6.11	15	9	Rab GDP dissociation inhibitor beta
427	SEP11_HUMAN	80	17	49367	6.36	11	7	Septin-11
428	ACTZ_HUMAN	60	13	42587	6.19	5	4	Alpha-centractin

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
429	NRAP_HUMAN	62	5	196950	9.24	8	8	Nebulin-related-anchoring protein
430	CD5_HUMAN	64	13	54590	8.66	5	4	T-cell surface glycoprotein CD5 precursor
431	ACY1_HUMAN	148	30	45856	5.77	12	10	Aminoacylase-1
432	SEPT2_HUMAN	100	23	41461	6.15	11	8	Septin-2
433	IDHC_HUMAN	75	14	46630	6.53	8	6	Isocitrate dehydrogenase [NADP] cytoplasmic
434	EFTU_HUMAN	154	27	49510	7.26	14	12	Elongation factor Tu, mitochondrial precursor
435	IDHC_HUMAN	117	29	46630	6.53	12	9	Isocitrate dehydrogenase [NADP] cytoplasmic
436	PGK1_HUMAN	61	22	44586	8.3	12	6	Phosphoglycerate kinase 1
437	ZN559_HUMAN	65	14	62277	8.9	6	5	Zinc finger protein 559
438	LZTR1_HUMAN	60	12	94658	6.12	6	5	Leucine-zipper-like transcriptional regulator 1
439	DDAH1_HUMAN	105	36	31102	5.53	11	8	NG,NG-dimethylarginine dimethylaminohydrolase 1
440	ECH1_HUMAN	60	15	35793	8.16	5	4	Delta-Delta-dienoyl-CoA isomerase, mitochondrial precursor
441	HSP71_HUMAN	121	19	69995	5.48	12	10	Heat shock 70 kDa protein 1
442	HSP7C_HUMAN	79	17	70854	5.37	12	8	Heat shock cognate 71 kDa protein
443	GRP78_HUMAN	108	18	72288	5.07	11	9	78 kDa glucose-regulated protein precursor
444	G3P_HUMAN	85	26	36030	8.57	10	7	Glyceraldehyde-3-phosphate dehydrogenase
445	VDAC2_HUMAN	94	31	38069	65.32	11	7	Voltage-dependent anion-selective channel protein 2
446	GBLP_HUMAN	60	23	35055	7.6	11	5	Guanine nucleotide-binding protein subunit beta 2-like 1
447	ATP4A_HUMAN	64	10	114017	5.58	11	7	Potassium-transporting ATPase alpha chain 1

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
448	ROA2_HUMAN	115	31	37407	8.97	10	8	Heterogeneous nuclear ribonucleoproteins A2/B1
449	PDIA3_HUMAN	70	16	56747	5.98	11	8	Protein disulfide-isomerase A3 precursor
450	GRHPR_HUMAN	89	31	35646	7.01	11	7	Glyoxylate reductase/hydroxypyruvate reductase
451	IREB1_HUMAN	87	13	98337	6.23	17	11	Iron-responsive element-binding protein 1
452	LMNA_HUMAN	115	23	74095	6.57	16	11	Lamin-A/C
453	WDR1_HUMAN	81	17	66152	6.17	14	8	WD repeat protein 1
454	O10X1_HUMAN	61	15	34416	8.71	11	6	Olfactory receptor 10X1
455	TPM4_HUMAN	62	12	28504	4.67	14	6	Tropomyosin alpha-4 chain
456	ZNF57_HUMAN	61	19	64439	9.11	14	8	Zinc finger protein 57
457	ACTC_HUMAN	71	20	41992	5.23	11	6	Actin, alpha cardiac muscle 1
458	RCN1_HUMAN	91	30	38866	4.86	12	7	Reticulocalbin-1 precursor
459	SCRN2_HUMAN	95	25	46535	5.44	14	8	Secernin-2
460	ACY1_HUMAN	126	28	45856	5.77	11	9	Aminoacylase-1
461	AK1A1_HUMAN	137	41	36550	6.32	14	10	Alcohol dehydrogenase [NADP+]
463	PDIA1_HUMAN	113	24	57480	4.76	12	9	Protein disulfide-isomerase
464	TBB2C_HUMAN	87	17	50255	4.79	11	7	Tubulin beta-2C chain
465	TCPE_HUMAN	81	17	60089	5.45	10	8	T-complex protein 1 subunit epsilon
466	ALDH2_HUMAN	70	15	56859	6.63	9	6	Aldehyde dehydrogenase
467	HNRH1_HUMAN	127	29	49484	5.89	9	9	Heterogeneous nuclear ribonucleoprotein H

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
468	HNRH2_HUMAN	120	33	49517	5.89	14	11	Heterogeneous nuclear ribonucleoprotein H2
469	NLTP_HUMAN	97	25	59640	6.44	14	10	Non-specific lipid-transfer protein
470	SCOT1_HUMAN	88	24	56578	7.14	13	9	3-ketoacid-coenzyme A transferase 1
471	AL1B1_HUMAN	94	20	57658	6.36	13	8	Aldehyde dehydrogenase X
472	SERA_HUMAN	95	18	57356	6.29	12	8	D-3-phosphoglycerate dehydrogenase
473	IMDH2_HUMAN	98	22	56226	6.44	11	8	Inosine-5'-monophosphate dehydrogenase 2
474	RUVB1_HUMAN	139	30	50538	6.02	12	10	RuvB-like 1
475	RLA2_HUMAN	72	32	11649	4.33	7	4	60S acidic ribosomal protein
476	GLNA_HUMAN	137	26	42037	6.43	14	11	Glutamine synthetase
477	AN13B_HUMAN	61	10	70162	6.47	9	6	Ankyrin repeat domain-containing protein 13B
478	TDRD7_HU	60	7	123506	6.84	9	7	Tudor domain-containing protein 7
479	AMPL_HUMAN	66	24	56131	8.03	17	8	aminopeptidase
480	FSCN1_HUMAN	103	21	54496	6.84	12	9	Fascin
481	ANX11_HUMAN	92	18	54355	7.53	13	9	Annexin A11
482	AL7A1_HUMAN	103	21	58450	8.21	12	9	Alpha-aminoadipic semialdehyde dehydrogenase
483	YBOX2_HUMAN	62	16	38495	10.82	12	5	Y-box-binding protein 2
484	DLDH_HUMA	79	15	54143	7.95	9	7	Dihydrolipoyl dehydrogenase
485	AL4A1_HUMAN	116	18	61681	8.25	12	9	Delta-1-pyrroline-5-carboxylate dehydrogenase
486	DHE3_HUMAN	116	22	61359	7.66	14	12	Glutamate dehydrogenase 1

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
487	CV028_HUMAN	77	18	55175	6.77	11	9	UPF0027 protein C22orf28
488	FUMH_HUMAN	62	11	54602	8.85	8	5	Fumarate hydratase
489	TXND5_HUMAN	70	22	47599	5.63	14	7	Thioredoxin domain-containing protein 5
490	NDUS1_HUMAN	74	11	79417	5.89	8	7	NADH-ubiquinone oxidoreductase 75 kDa
491	LMNB2_HUMAN	60	12	67647	5.29	10	7	Lamin-B2
492	LEG1_HUMAN	84	58	14706	5.34	8	5	Galectin-1
493	CLCN6_HUMAN	62	7	97153	6.49	7	6	Chloride transport protein 6
494	CO6A2_HUMAN	103	11	108512	5.85	11	10	Collagen alpha-2
495	RAB3D_HUMAN	61	26	24252	4.76	7	4	Ras-related protein Rab-3D
496	PRS10_HUMAN	71	17	44145	7.1	12	7	26S protease regulatory subunit S10B
497	ARK73_HUMAN	88	30	37183	6.67	14	8	Aflatoxin B1 aldehyde reductase member 3
498	CK054_HUMAN	111	39	35095	6.23	14	9	Ester hydrolase C11orf54
499	GALE_HUMAN	62	20	38257	6.26	11	5	UDP-glucose 4-epimerase
500	THTR_HUMAN	84	29	33408	6.77	12	7	Thiosulfate sulfurtransferase
501	ODPB_HUMAN	78	28	39208	6.2	13	7	Pyruvate dehydrogenase E1 component subunit beta
502	GPDA_HUMAN	117	31	37543	5.81	13	10	Glycerol-3-phosphate dehydrogenase
503	HDGF_HUMAN	63	20	26772	4.7	7	4	Hepatoma-derived growth factor
504	CAPZB_HUMAN	78	25	31331	5.36	13	7	F-actin-capping protein
505	CATD_HUMAN	60	10	44524	6.1	9	5	Cathepsin D

No.	Entry name	Score	Coverage %	Mr	pI	Searched	Matched	Protein description
506	PEF1_HUMAN	64	17	30361	6.1	12	6	Peflin
507	MYL9_HUMAN	92	29	19814	4.8	6	5	Myosin regulatory light polypeptide 9
508	OFD1_HUMAN	62	8	116599	5.82	10	7	Oral-facial-digital syndrome 1 protein
509	BTBDA_HUMAN	61	13	53746	7.66	9	5	BTB/POZ domain-containing protein 10
510	FLNA_HUMAN	60	5	280564	5.7	12	9	Filamin-A

Part II: Proteins identified by 4800 MALDI TOF/TOF Analyzer （not include single-peptide identified proteins）

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
511	mitochondrial ATP synthase beta subunit precursor	gi|32189394	10	2	DQEGQDVLLFIDNIFR	64
					IVAVIGAVVDVQFDEGLPPILNALEVQGR	107
512	GRP78 precursor	gi|386758	12	6	SDIDEIVLVGGSTR	103
					ITPSYVAFTPEGER	110
					KSDIDEIVLVGGSTR	48
					VTHAVVTVPAYFNDAQR	125
					DNHLLGTFDLTGIPPAPR	144
					IEIESFYEGEDFSETLTR	155
513	beta-trace protein, prostaglandin D synthase, PGD	gi|404390	36	2	AQGFTEDSIVFLPQTDK	59
					SPHWGSTYSVSVVETDYDHYALLYSQGSK	137
514	Tubulin, beta 2C	gi|23958133	10	3	FPGQLNADLR	71
					AVLVDLEPGTMDSVR	37
					GHYTEGAELVDSVLDVVR	94

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
515	serine proteinase inhibitor, clade A, member 1	gi|50363217	7	2	DTVFALVNYIFFK	40
					ELDRDTVFALVNYIFFK	42
516	Niemann-Pick disease, type C2 precursor variant	gi|62896507	22	2	LVVEWQLQDDK	49
					AVVHGILMGVPVPFPIPEPDGCK	60
517	glutathione S-transferase Mu 3	gi|23065552	13	2	LLLEFTDTSYEEK	56
					LTFVDFLTYDILDQNR	102
518	aldehyde dehydrogenase 1A1	gi|21361176	12	3	TIPIDGNFFTYTR	96
					IFVEESIYDEFVR	85
					SPCIVLADADLDNAVEFAHHGVFYHQGQCCIAASR	57
519	Unknown (protein for IMAGE:3934797)	gi|15679996	4	3	FQNALLVR	45
					VPQVSTPTLVEVSR	53
					KVPQVSTPTLVEVSR	38
520	Protein disulfide-isomerase A3 precursor	gi|220702506	10	3	ELSDFISYLQR	88
					SDVLELTDDNFESR	106

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					TFSHELSDFGLESTAGEIPVVAIR	223
521	Protein disulfide-isomerase A3 precursor	gi|220702506	12	4	FLQDYFDGNLK	37
					ELSDFISYLQR	81
					SDVLELTDDNFESR	79
					TFSHELSDFGLESTAGEIPVVAIR	207
522	glutathione S-transferase P	gi|4504183	15	2	PPYTVVYFPVR	78
					ALPGQLKPFETLLSQNQGGK	72
523	ubiquitin and ribosomal protein S27a precursor	gi|4506713	33	2	EGIPPDQQR	67
					TITLEVEPSDTIENVK	54
524	peroxiredoxin-4	gi|5453549	16	3	QITLNDLPVGR	40
					DYGVYLEDSGHTLR	85
					EEECHFYAGGQVYPGEASR	63
525	albumin preproprotein	gi|4502027	3	2	FQNALLVR	37
					DVFLGMFLYEYAR	38
526	albumin preproprotein	gi|4502027	3	3	FQNALLVR	53

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					DVFLGMFLYEYAR	60
					DVFLGMFLYEYAR	41
527	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	38
					SYELPDGQVITIGNER	94
528	actin, cytoplasmic 2	gi|4501887	13	3	QEYDESGPSIVHR	100
					SYELPDGQVITIGNER	145
					VAPEEHPVLLTEAPLNPK	66
529	Transferrin	gi|37747855	5	2	EGYYGYTGAFR	54
					DQYELLCLDNTR	41
530	peroxiredoxin-2 isoform a	gi|32189392	15	3	QITVNDLPVGR	77
					EGGLGPLNIPLLADVTR	172
					KEGGLGPLNIPLLADVTR	171
531	apolipoprotein A-I preproprotein	gi|4557321	9	2	THLAPYSDELR	82
					VSFLSALEEYTK	69
532	Carbonic anhydrase 2	gi|157830746	21	4	GGPLDGTYR	51
					SADFTNFDPR	85

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					AVQQPDGLAVLGIFLK	110
					YDPSLKPLSVSYDQATSLR	110
533	peptidylprolyl isomerase A	gi|10863927	19	2	IIPGFMCQGGDFTR	40
					VNPTVFFDIAVDGEPLGR	138
534	tubulin beta-2C chain	gi|5174735	8	3	YLTVAAVFR	46
					FPGQLNADLR	86
					GHYTEGAELVDSVLDVVR	174
535	Transferrin	gi|37747855	3	2	EGYYGYTGAFR	80
					DQYELLCLDNTR	70
536	TSA	gi|1617118	18	2	EGGLGPLNIPLLADVTR	75
					KEGGLGPLNIPLLADVTR	53
537	albumin preproprotein	gi|4502027	3	2	FQNALLVR	56
					DVFLGMFLYEYAR	76
538	Transferrin	gi|37747855	6	4	EGYYGYTGAFR	83
					DQYELLCLDNTR	91
					ADRDQYELLCLDNTR	89

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					SAGWNIPIGLLYCDLPEP	128
539	biliverdin-IX beta reductase isozyme I	gi|544759	28	2	TVAGQDAVIVLLGTR	96
					IAIFGATGQTGLTTLAQAVQAGYEVTVLVR	157
540	albumin preproprotein	gi|4502027	6	3	FQNALLVR	59
					DVFLGMFLYEYAR	67
					KVPQVSTPTLVEVSR	47
541	TAGLN	gi|49168456	11	3	YDEELEER	40
					KYDEELEER	54
					TDMFQTVDLFEGK	50
542	PGK1	gi|48145549	16	4	LGDVYVNDAFGTAHR	142
					ALESPERPFLAILGGAK	68
					VLNNMEIGTSLFDEEGAK	114
					ITLPVDFVTADKFDENAK	88
543	Unknown (protein for IMAGE:3934797)	gi|15679996	4	3	FQNALLVR	38
					VPQVSTPTLVEVSR	64
					KVPQVSTPTLVEVSR	39

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
544	Carbonic anhydrase 2	gi|157830746	17	3	SADFTNFDPR	67
					AVQQPDGLAVLGIFLK	85
					YDPSLKPLSVSYDQATSLR	88
545	aldehyde dehydrogenase 1	gi|2183299	5	2	TIPIDGNFFTYTR	88
					IFVEESIYDEFVR	107
546	Beta-hexosaminidase subunit beta precursor	gi|30749651	6	2	GSYSLSHVYTPNDVR	49
					EISEVFPDQFIHLGGDEVEFK	88
547	actin, alpha cardiac muscle 1 proprotein	gi|4885049	7	2	IWHHTFYNELR	59
					SYELPDGQVITIGNER	139
548	Triosephosphate isomerase	gi|999892	11	2	HVFGESDELIGQK	80
					DCGATWVVLGHSER	63
549	unnamed protein product	gi|34526803	6	2	LQFPLPTAQR	39
					QPQVAELLAEAR	38
550	Unknown (protein for IMAGE:3934797)	gi|15679996	4	3	FQNALLVR	56
					VPQVSTPTLVEVSR	55

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					KVPQVSTPTLVEVSR	61
551	GRP78 precursor	gi|386758	8	4	SDIDEIVLVGGSTR	77
					KSDIDEIVLVGGSTR	47
					DNHLLGTFDLTGIPPAPR	106
					IEIESFYEGEDFSETLTR	78
552	glutathione S-transferase Mu 3	gi|23065552	12	2	VDIIENQVMDFR	52
					LTFVDFLTYDILDQNR	165
553	albumin preproprotein	gi|4502027	2	2	DVFLGMFLYEYAR	118
					DVFLGMFLYEYAR	43
554	phosphoglycerate kinase 2	gi|31543397	8	2	LGDVYVNDAFGTAHR	99
					ALENPVRPFLAILGGAK	46
555	endoplasmin precursor	gi|4507677	5	3	SILFVPTSAPR	37
					GVVDSDDLPLNVSR	56
					EEEAIQLDGLNASQIR	79
556	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	75
					IFVEESIYDEFVR	76

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
557	heat shock protein 27	gi|662841	21	3	LFDQAFGLPR	65
					VSLDVNHFAPDELTVK	64
					LATQSNEITIPVTFESR	111
558	aldehyde dehydrogenase 1	gi|2183299	7	3	QAFQIGSPWR	47
					TIPIDGNFFTYTR	107
					IFVEESIYDEFVR	103
559	actin, cytoplasmic 2	gi|4501887	7	2	IWHHTFYNELR	70
					SYELPDGQVITIGNER	128
560	chaperonin containing TCP1, subunit 2 (beta), isoform	gi|119617636	11	3	QVLLSAAEAAEVILR	86
					LIHFSGVALGEACTIVLR	101
					VQDDEVGDGTTSVTVLAAELLR	178
561	albumin preproprotein	gi|4502027	6	3	FQNALLVR	62
					DVFLGMFLYEYAR	83
					KVPQVSTPTLVEVSR	47
562	Nitrilase family, member 2	gi|18088311	9	2	FAELAQIYAQR	66

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					AVDNQVYVATASPAR	100
563	heat shock cognate 71 kDa protein isoform 1 [Homo	gi|5729877	13	5	FEELNADLFR	56
					TTPSYVAFTDTER	74
					STAGDTHLGGEDFDNR	75
					TVTNAVVTVPAYFNDSQR	106
					TLSSSTQASIEIDSLYEGIDFYTSITR	140
564	creatine kinase B-type	gi|21536286	25	6	DLFDPIIEDR	55
					VLTPELYAELR	58
					LAVEALSSLDGDLAGR	115
					TFLVWVNEEDHLR	63
					GTGGVDTAAVGGVFDVSNADR	151
					TDLNPDNLQGGDDLDPNYVLSSR	175
565	ezrin	gi|21614499	6	3	ALQLEEER	41
					QLLTLSSELSQAR	74
					SQEQLAAELAEYTAK	47

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
566	Epididymal secretory glutathione peroxidase precursor	gi|116667974	11	3	FLVGPDGIPVMR	41
					FLVGPDGIPVMR	41
					GTIYDYEAIALNK	78
567	Fatty acid-binding protein, adipocyte	gi|52695841	20	2	LVSSENFDDYMK	80
					STITLDGGVLVHVQK	63
568	albumin preproprotein	gi|4502027	2	2	DVFLGMFLYEYAR	87
					DVFLGMFLYEYAR	58
569	Triosephosphate isomerase	gi|999892	11	3	HVFGESDELIGQK	103
					TATPQQAQEVHEK	47
					RHVFGESDELIGQK	41
570	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	16	3	VPTANVSVVDLTCR	98
					LISWYDNEFGYSNR	137
					VIHDNFGIVEGLMTTVHAITATQK	73
571	methylthioadenosine phosphorylase	gi|847724	12	2	IGIIGGTGLDDPEILEGR	50

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EEIQPGDIVIIDQFIDR	96
572	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	86
					IFVEESIYDEFVR	73
573	hypothetical protein	gi|31873302	7	2	VVIGMDVAASEFFR	48
					AAVPSGASTGIYEALELR	101
574	albumin preproprotein	gi|4502027	2	2	DVFLGMFLYEYAR	70
					DVFLGMFLYEYAR	45
575	TAGLN	gi|49168456	11	2	KYDEELEER	58
					TDMFQTVDLFEGK	48
576	hypothetical protein	gi|31873302	10	3	YISPDQLADLYK	61
					VVIGMDVAASEFFR	64
					AAVPSGASTGIYEALELR	168
577	hypothetical protein	gi|31873302	10	3	YISPDQLADLYK	45
					VVIGMDVAASEFFR	48
					AAVPSGASTGIYEALELR	142
578	Proteasome (prosome, macropain) subunit,	gi|13543551	13	2	NQYDNDVTVWSPQGR	87

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
	alpha type					
					ILHVDNHIGISIAGLTADA	138
579	hypothetical protein	gi|31873439	7	2	LISQIVSSITASLR	54
					FDGALNVDLTEFQTNLVP	95
580	beta globin chain variant	gi|13549112	17	2	VNVDEVGGEALGR	38
					EFTQPVQAAYQK	54
581	Human Muscle Pyruvate Kinase	gi|67464392	6	2	FGVEQDVDMVFASFIR	53
					EAEAAIYHLQLFEELR	104
582	T-complex protein 1 subunit eta isoform b	gi|58331185	8	2	CQVFEETQIGGER	60
					LPIGDVATQYFADR	41
583	albumin preproprotein	gi|4502027	11	5	FQNALLVR	40
					HPDYSVVLLLR	40
					KVPQVSTPTLVEVSR	42
					RPCFSALEVDETYVPK	47
					VFDEFKPLVEEPQNLIK	64
584	Transferrin	gi|37747855	6	3	EGYYGYTGAFR	67

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					KPVEEYANCHLAR	60
					ADRDQYELLCLDNTR	58
585	Oxy-Human Hemoglobin	gi|37928140	42	3	VGAHAGEYGAEALER	119
					TYFPHFDLSHGSAQVK	126
					VADALTNAVAHVDDMPNALSALSDLHAHK	104
586	Transferrin	gi|37747855	8	4	EGYYGYTGAFR	78
					KPVEEYANCHLAR	64
					ADRDQYELLCLDNTR	59
					NLNEKDYELLCLDGTR	57
587	Adenylate kinase isoenzyme 1	gi|66361358	19	3	EVQQGEEFER	83
					YGYTHLSTGDLLR	104
					GQLVPLETVLDMLR	50
588	Chain A, Human Peroxiredoxin 5	gi|15826629	23	3	THLPGFVEQAEALK	82
					VGDAIPAVEVFEGEPGNK	81
					ETDLLLDDSLVSIFGNR	173
589	Transthyretin precursor	gi|230651	31	2	YTIAALLSPYSYSTTAVVTNPK	82

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					ALGISPFHEHAEVVFTANDSGPR	147
590	SH3 domain-binding glutamic acid-rich-like protein	gi|4506925	47	3	GDYDAFFEAR	78
					ENNAVYAFLGLTAPPGSK	63
					ENVPENSRPATGYPLPPQIFNESQYR	82
591	Nm23 protein	gi|35068	14	2	DRPFFAGLVK	50
					TFIAIKPDGVQR	49
592	nucleoside phosphorylase	gi|157168362	25	4	DHINLPGFSGQNPLR	71
					LGADAVGMSTVPEVIVAR	48
					LTQAQIFDYGEIPNFPR	99
					ELQEGTYVMVAGPSFETVAECR	46
593	phenazine biosynthesis-like domain-containing protein	gi|62177133	15	2	GEPGGQTQAFDFYSR	115
					RAEDGIVLDLPLYPAHPQDFHEVEDLIK	50
594	heat shock protein 27	gi|662841	21	3	LFDQAFGLPR	79
					VSLDVNHFAPDELTVK	90

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					LATQSNEITIPVTFESR	120
595	Transferrin	gi|37747855	8	4	EGYYGYTGAFR	64
					KPVEEYANCHLAR	52
					ADRDQYELLCLDNTR	44
					NLNEKDYELLCLDGTR	57
596	albumin preproprotein	gi|4502027	13	6	FQNALLVR	41
					AVMDDFAAFVEK	43
					RHPDYSVVLLLR	45
					KVPQVSTPTLVEVSR	58
					RPCFSALEVDETYVPK	56
					VFDEFKPLVEEPQNLIK	78
597	Hemoglobin subunit beta	gi|3660145	41	4	VNVDEVGGEALGR	47
					EFTPPVQAAYQK	58
					VLGAFSDGLAHLDNLK	111
					FFESFGDLSTPDAVMGNPK	112
598	Hemoglobin subunit beta	gi|3660145	48	5	LLVVYPWTQR	41

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VNVDEVGGEALGR	39
					EFTPPVQAAYQK	39
					VLGAFSDGLAHLDNLK	85
					FFESFGDLSTPDAVMGNPK	65
599	Transferrin	gi|37747855	8	4	EGYYGYTGAFR	86
					KPVEEYANCHLAR	69
					ADRDQYELLCLDNTR	77
					NLNEKDYELLCLDGTR	107
600	TAGLN	gi|49168456	13	2	KYDEELEER	53
					LVEWIIVQCGPDVGRPDR	52
601	peroxiredoxin 1	gi|55959887	11	2	TIAQDYGVLK	50
					QITVNDLPVGR	73
602	Hemoglobin subunit beta	gi|3660145	41	4	VNVDEVGGEALGR	74
					EFTPPVQAAYQK	69
					VLGAFSDGLAHLDNLK	105
					FFESFGDLSTPDAVMGNPK	110

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
603	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	93
					LISWYDNEFGYSNR	111
604	Protein DJ-1	gi|33358055	36	3	GPGTSFEFALAIVEALNGK	52
					GLIAAICAGPTALLAHEIGFGSK	96
					EGPYDVVVLPGGNLGAQNLSESAAVK	141
605	Human Serum Albumin	gi|157830361	14	6	FQNALLVR	59
					AVMDDFAAFVEK	45
					KVPQVSTPTLVEVSR	60
					RPCFSALEVDETYVPK	69
					VFDEFKPLVEEPQNLIK	112
					EFNAETFTFHADICTLSEK	76
606	Human Serum Albumin	gi|157830361	12	5	FQNALLVR	45
					KVPQVSTPTLVEVSR	57
					RPCFSALEVDETYVPK	70
					VFDEFKPLVEEPQNLIK	73

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EFNAETFTFHADICTLSEK	82
607	ABHD14B protein	gi|30047108	33	5	EALPGSGQAR	45
					FSVLLLHGIR	70
					EGTIQVQGQALFFR	109
					FSSETWQNLGTLHR	85
					TPALIVYGDQDPMGQTSFEHLK	59
608	glutathione S-transferase	gi|4504183	13	2	PPYTVVYFPVR	54
					FQDGDLTLYQSNTILR	105
609	serine proteinase inhibitor, clade A, member 1	gi|50363217	8	2	LQHLENELTHDIITK	69
					VFSNGADLSGVTEEAPLK	64
610	hemoglobin subunit alpha	gi|4504345	42	3	VGAHAGEYGAEALER	122
					TYFPHFDLSHGSAQVK	131
					VADALTNAVAHVDDMPNALSALSDLHAHK	118
611	mammary-derived growth inhibitor	gi|1869803	18	3	WDGQETTLVR	71
					LGVEFDETTADDR	101

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					LGVEFDETTADDRK	56
612	Haloacid dehalogenase-like hydrolase domain-containing protein 2	gi|251837027	19	3	TFFLEALR	49
					DGLALGPGPFVTALEYATDTK	40
					KLEFDISEDEIFTSLTAAR	173
613	nucleoside phosphorylase	gi|157168362	11	2	DHINLPGFSGQNPLR	38
					LTQAQIFDYGEIPNFPR	37
614	actin, cytoplasmic 2	gi|4501887	13	3	QEYDESGPSIVHR	78
					SYELPDGQVITIGNER	109
					VAPEEHPVLLTEAPLNPK	75
615	aflatoxin B1 aldehyde reductase member 2	gi|41327764	8	2	QVETELFPCLR	40
					ALQAAYGASAPSVTSAALR	121
616	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	119
					LISWYDNEFGYSNR	101
617	Valosin-containing protein	gi|111305821	5	2	LIVDEAINEDNSVVSLSQPK	101

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EDEEESLNEVGYDDIGGCR	44
618	nucleoside phosphorylase	gi|157168362	17	3	DHINLPGFSGQNPLR	99
					LGADAVGMSTVPEVIVAR	61
					LTQAQIFDYGEIPNFPR	119
619	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	96
					LISWYDNEFGYSNR	88
620	Human Serum Albumin	gi|157830361	12	5	FQNALLVR	37
					KVPQVSTPTLVEVSR	57
					RPCFSALEVDETYVPK	56
					VFDEFKPLVEEPQNLIK	65
					EFNAETFTFHADICTLSEK	42
621	Transferrin	gi|37747855	8	4	EGYYGYTGAFR	76
					KPVEEYANCHLAR	51
					ADRDQYELLCLDNTR	85
					NLNEKDYELLCLDGTR	86

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
622	ALB protein	gi|23241675	17	4	KVPQVSTPTLVEVSR	72
					RPCFSALEVDETYVPK	37
					VFDEFKPLVEEPQNLIK	104
					EFNAETFTFHADICTLSEK	50
623	peroxiredoxin-2 isoform a	gi|32189392	15	3	QITVNDLPVGR	62
					EGGLGPLNIPLLADVTR	147
					KEGGLGPLNIPLLADVTR	171
624	Human Serum Albumin	gi|157830361	7	3	HPDYSVVLLLR	49
					KVPQVSTPTLVEVSR	45
					VFDEFKPLVEEPQNLIK	63
625	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	43
					LISWYDNEFGYSNR	54
626	Adenylate kinase isoenzyme 1	gi|66361358	12	2	EVQQGEEFER	80
					YGYTHLSTGDLLR	108
627	enolase 1 variant	gi|62896593	15	4	YISPDQLADLYK	49

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VVIGMDVAASEFFR	56
					AAVPSGASTGIYEALELR	131
					FTASAGIQVVGDDLTVTNPK	79
628	albumin preproprotein	gi|4502027	8	3	AVMDDFAAFVEK	75
					RPCFSALEVDETYVPK	108
					EFNAETFTFHADICTLSEK	118
629	Tubulin, beta 2C	gi|23958133	12	4	FPGQLNADLR	60
					INVYYNEATGGK	37
					AVLVDLEPGTMDSVR	50
					GHYTEGAELVDSVLDVVR	103
630	actin, cytoplasmic 2	gi|4501887	15	4	GYSFTTTAER	45
					QEYDESGPSIVHR	94
					SYELPDGQVITIGNER	118
					VAPEEHPVLLTEAPLNPK	68
631	hypothetical protein	gi|31873302	7	2	YISPDQLADLYK	49
					AAVPSGASTGIYEALELR	131

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
632	Prostaglandin reductase 2	gi|208435567	5	2	MEEVYLPDNINEGQVQVR	65
					MEEVYLPDNINEGQVQVR	116
633	ALB protein	gi|23241675	22	6	FQNALLVR	61
					AVMDDFAAFVEK	63
					KVPQVSTPTLVEVSR	92
					RPCFSALEVDETYVPK	95
					VFDEFKPLVEEPQNLIK	123
					EFNAETFTFHADICTLSEK	106
634	Tubulin, beta 2C	gi|23958133	6	2	FPGQLNADLR	58
					GHYTEGAELVDSVLDVVR	118
635	serine proteinase inhibitor, clade A, member 1	gi|50363217	8	2	LQHLENELTHDIITK	78
					VFSNGADLSGVTEEAPLK	92
636	unnamed protein product	gi|35440	17	2	MPFPVNHGASSEDTLLK	40
					VNFHFILFNNVDGHLYELDGR	73
637	Protein DJ-1	gi|42543006	24	2	GPGTSFEFALAIVEALNGK	45

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EGPYDVVVLPGGNLGAQNLSESAAVK	140
638	heat shock protein 27	gi|662841	21	3	LFDQAFGLPR	60
					VSLDVNHFAPDELTVK	51
					LATQSNEITIPVTFESR	107
639	TSA	gi|1617118	9	2	EGGLGPLNIPLLADVTR	84
					KEGGLGPLNIPLLADVTR	106
640	Superoxide dismutase [Cu-Zn]	gi|31615344	32	3	GDGPVQGIINFEQK	60
					DGVADVSIEDSVISLSGDHCIIGR	105
					HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR	83
641	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	88
					LISWYDNEFGYSNR	63
642	Human Serum Albumin	gi|157830361	5	2	KVPQVSTPTLVEVSR	49
					VFDEFKPLVEEPQNLIK	70
643	biliverdin-IX beta reductase isozyme I	gi|544759	25	2	TVAGQDAVIVLLGTR	86
					YVAVMPPHIGDQPLTGAYTVTLDGR	67

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
644	Triosephosphate isomerase	gi|999892	13	2	HVFGESDELIGQK	85
					VPADTEVVCAPPTAYIDFAR	66
645	actin, cytoplasmic 2	gi|4501887	15	4	GYSFTTTAER	54
					QEYDESGPSIVHR	90
					SYELPDGQVITIGNER	131
					VAPEEHPVLLTEAPLNPK	100
646	ALB protein	gi|23241675	12	3	KVPQVSTPTLVEVSR	59
					RPCFSALEVDETYVPK	41
					VFDEFKPLVEEPQNLIK	56
647	hypothetical protein	gi|51476390	9	4	YLYEIAR	41
					LVNEVTEFAK	51
					QEPERNECFLQHK	58
					LVRPEVDVMCTAFHDNEETFLK	39
648	hypothetical protein	gi|51476390	4	3	YLYEIAR	41
					LVNEVTEFAK	49
					FKDLGEENFK	41

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
649	peroxiredoxin-6	gi|4758638	27	5	NFDEILR	50
					LPFPIIDDR	81
					LSILYPATTGR	49
					DFTPVCTTELGR	77
					PGGLLLGDVAPNFEANTTVGR	158
650	hypothetical protein	gi|31873302	10	4	YISPDQLADLYK	54
					VVIGMDVAASEFFR	75
					VVIGMDVAASEFFR	72
					AAVPSGASTGIYEALELR	148
651	ALB protein	gi|23241675	22	6	FQNALLVR	59
					AVMDDFAAFVEK	48
					KVPQVSTPTLVEVSR	65
					RPCFSALEVDETYVPK	76
					VFDEFKPLVEEPQNLIK	78
					EFNAETFTFHADICTLSEK	81
652	Triosephosphate isomerase	gi|999892	13	2	HVFGESDELIGQK	90

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VPADTEVVCAPPTAYIDFAR	75
653	Apolipoprotein A-I precursor	gi|90108664	12	3	DEPPQSPWDR	57
					THLAPYSDELR	82
					VSFLSALEEYTK	56
654	actin, cytoplasmic 2	gi|4501887	13	3	QEYDESGPSIVHR	86
					SYELPDGQVITIGNER	103
					VAPEEHPVLLTEAPLNPK	90
655	hypothetical protein	gi|51476390	7	4	YLYEIAR	44
					LVNEVTEFAK	51
					FKDLGEENFK	39
					QEPERNECFLQHK	41
656	unnamed protein product	gi|194389712	11	3	GPEEEHPSVTLFR	84
					TVQPKPDYGAAVAFFEETAR	129
					AGFALDEGIANPTDAFTVFYSER	128
657	unnamed protein product	gi|16552261	9	3	EEAENTLQSFR	51
					TNEKVELQELNDR	53

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EMEENFAVEAANYQDTIGR	98
658	unnamed protein product	gi|21757082	12	3	EPQVYTLPPSR	59
					EPQVYTLPPSRDELTK	52
					TPEVTCVVVDVSHEDPEVK	101
659	unnamed protein product	gi|21757082	8	2	EPQVYTLPPSR	59
					TPEVTCVVVDVSHEDPEVK	56
660	ALB protein	gi|23241675	22	6	FQNALLVR	61
					AVMDDFAAFVEK	69
					KVPQVSTPTLVEVSR	78
					RPCFSALEVDETYVPK	89
					VFDEFKPLVEEPQNLIK	87
					EFNAETFTFHADICTLSEK	64
661	aldehyde dehydrogenase 1	gi|2183299	10	4	QAFQIGSPWR	46
					TIPIDGNFFTYTR	101
					IFVEESIYDEFVR	90
					ELGEYGFHEYTEVK	43

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
662	Protein disulfide-isomerase A3 precursor	gi|220702506	15	5	ELSDFISYLQR	54
					DLLIAYYDVDYEK	53
					SDVLELTDDNFESR	64
					MDATANDVPSPYEVR	53
					TFSHELSDFGLESTAGEIPVVAIR	130
663	phosphoglycerate kinase 1	gi|4505763	16	4	LGDVYVNDAFGTAHR	100
					ALESPERPFLAILGGAK	61
					VLNNMEIGTSLFDEEGAK	65
					ITLPVDFVTADKFDENAK	65
664	Tubulin, beta 2C	gi|23958133	10	3	FPGQLNADLR	93
					AVLVDLEPGTMDSVR	41
					GHYTEGAELVDSVLDVVR	170
665	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	128
					LISWYDNEFGYSNR	94
666	actin, cytoplasmic 2	gi|4501887	18	5	AGFAGDDAPR	68

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					GYSFTTTAER	51
					QEYDESGPSIVHR	111
					SYELPDGQVITIGNER	154
					VAPEEHPVLLTEAPLNPK	89
667	HSP70-1	gi|4529893	6	2	AQIHDLVLVGGSTR	82
					QTQIFTTYSDNQPGVLIQVYEGER	126
668	Human Serum Albumin	gi|157830361	14	6	FQNALLVR	42
					AVMDDFAAFVEK	48
					KVPQVSTPTLVEVSR	37
					RPCFSALEVDETYVPK	58
					VFDEFKPLVEEPQNLIK	88
					EFNAETFTFHADICTLSEK	101
669	hypothetical protein	gi|31873302	10	3	YISPDQLADLYK	52
					VVIGMDVAASEFFR	53
					AAVPSGASTGIYEALELR	128
670	unnamed protein product	gi|21757082	11	3	EPQVYTLPPSR	56

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					FNWYVDGVEVHNAK	48
					TPEVTCVVVDVSHEDPEVK	57
671	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	54
					IFVEESIYDEFVR	75
672	PGK1	gi|48145549	16	4	LGDVYVNDAFGTAHR	111
					ALESPERPFLAILGGAK	45
					VLNNMEIGTSLFDEEGAK	74
					ITLPVDFVTADKFDENAK	77
673	fructose-bisphosphate aldolase A	gi|4557305	16	3	FSHEEIAMATVTALR	66
					IGEHTPSALAIMENANVLAR	49
					YTPSGQAGAAASESLFVSNHAY	81
674	Chain A, Aldehyde Reductase	gi|157834561	9	2	DAGHPLYPFNDPY	41
					GLEVTAYSPLGSSDR	101
675	ALB protein	gi|23241675	18	5	FQNALLVR	62
					AVMDDFAAFVEK	70
					RPCFSALEVDETYVPK	92

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VFDEFKPLVEEPQNLIK	115
					EFNAETFTFHADICTLSEK	116
676	ALB protein	gi|23241675	17	5	FQNALLVR	48
					AVMDDFAAFVEK	38
					KVPQVSTPTLVEVSR	86
					RPCFSALEVDETYVPK	67
					VFDEFKPLVEEPQNLIK	52
677	aldehyde dehydrogenase 1	gi|2183299	5	2	TIPIDGNFFTYTR	77
					IFVEESIYDEFVR	103
678	Human Muscle Pyruvate Kinase	gi|67464392	7	2	FGVEQDVDMVFASFIR	40
					TATESFASDPILYRPVAVALDTK	63
679	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	gi|134104755	13	3	ALPESLGQHALR	95
					DENATLDGGDVLFTGR	62
					LQLNIVEMKDENATLDGGDVLFTGR	116
680	hypothetical protein	gi|31873302	10	4	YISPDQLADLYK	63

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VVIGMDVAASEFFR	52
					VVIGMDVAASEFFR	65
					AAVPSGASTGIYEALELR	146
681	phosphoglycerate kinase 1	gi|4505763	12	3	LGDVYVNDAFGTAHR	122
					ALESPERPFLAILGGAK	56
					VLNNMEIGTSLFDEEGAK	69
682	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	45
					LISWYDNEFGYSNR	66
683	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	13	3	VPTANVSVVDLTCR	120
					LVINGNPITIFQER	99
					LISWYDNEFGYSNR	137
684	albumin, isoform CRA_t	gi|119626083	7	3	FQNALLVR	46
					KVPQVSTPTLVEVSR	70
					VFDEFKPLVEEPQNLIK	70

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
685	Protein disulfide-isomerase A3 precursor	gi|220702506	15	5	ELSDFISYLQR	41
					DLLIAYYDVDYEK	38
					SDVLELTDDNFESR	76
					MDATANDVPSPYEVR	51
					TFSHELSDFGLESTAGEIPVVAIR	136
686	unnamed protein product	gi|37403	9	3	IQLVEEELDR	52
					IQVLQQQADDAEER	65
					KIQVLQQQADDAEER	73
687	6-phosphogluconolactonase	gi|6912586	18	3	ELPAAVAPAGPASLAR	59
					IVAPISDSPKPPPQR	41
					LVPFDHAESTYGLYR	79
688	endoplasmic reticulum protein 29, isoform CRA_b	gi|119618398	10	2	ESYPVFYLFR	52
					ILDQGEDFPASEMTR	48
689	heat shock protein 27	gi|662841	25	4	QDEHGYISR	41
					LFDQAFGLPR	98

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VSLDVNHFAPDELTVK	93
					LATQSNEITIPVTFESR	131
690	Human Serum Albumin	gi|157830361	9	4	YLYEIAR	40
					KVPQVSTPTLVEVSR	56
					RPCFSALEVDETYVPK	50
					VFDEFKPLVEEPQNLIK	57
691	aldehyde dehydrogenase 1	gi|2183299	10	4	QAFQIGSPWR	43
					TIPIDGNFFTYTR	96
					IFVEESIYDEFVR	122
					ELGEYGFHEYTEVK	40
692	carbonyl reductase 3 variant	gi|62898419	15	3	AFENCSEDLQER	37
					FHQLDIDDLQSIR	60
					GQAAVQQLQAEGLSPR	82
693	Protein disulfide-isomerase A3 precursor	gi|220702506	10	3	DLLIAYYDVDYEK	43
					SDVLELTDDNFESR	71
					DASIVGFFDDSFSEAHSEFLK	63

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
694	Alpha-1-antitrypsin precursor	gi|28948408	12	3	TDTSHHDQDHPTFNK	84
					DTEEEDFHVDQVTTVK	93
					LYHSEAFTVNFGDTEEAK	47
695	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	66
					IFVEESIYDEFVR	61
696	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	LVINGNPITIFQER	74
					LISWYDNEFGYSNR	67
697	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	13	3	VPTANVSVVDLTCR	79
					LVINGNPITIFQER	61
					LISWYDNEFGYSNR	98
698	Human Serum Albumin	gi|157830361	14	6	FQNALLVR	45
					HPDYSVVLLLR	67
					KVPQVSTPTLVEVSR	51
					RPCFSALEVDETYVPK	64

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VFDEFKPLVEEPQNLIK	101
					EFNAETFTFHADICTLSEK	63
699	unnamed protein product	gi|16552261	14	4	ISLPLPNFSSLNLR	46
					TNEKVELQELNDR	40
					EMEENFAVEAANYQDTIGR	103
					QVQSLTCEVDALKGTNESLER	66
700	galactokinase 1	gi|119609722	16	5	LQFPLPTAQR	49
					EVQLEELEAAR	42
					QPQVAELLAEAR	48
					EEFGAEPELAVSAPGR	63
					KDGLVSLLTTSEGADEPQR	88
701	heat shock 70kDa protein 8 isoform 1 variant	gi|62897129	6	3	FEELNADLFR	54
					ARFEELNADLFR	47
					QTQTFTTYSDNQPGVLIQVYEGER	153
702	actin, gamma-enteric smooth muscle	gi|4501889	12	3	GYSFVTTAER	43

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
	propeptide					
					SYELPDGQVITIGNER	145
					VAPEEHPTLLTEAPLNPK	49
703	prepro-alpha2(I) collagen	gi|1418930	2	2	GEAGAAGPAGPAGPR	52
					GETGPSGPVGPAGAVGPR	131
704	trifunctional enzyme subunit alpha, mitochondrial	gi|20127408	4	2	ADMVIEAVFEDLSLK	40
					DSIFSNLTGQLDYQGFEK	65
705	collagen, type VI, alpha 3, isoform CRA_f	gi|119591514	2	3	VNHFVPEAGSR	50
					SVEDAQDVSLALTQR	86
					VVIHFTDGADGDLADLHR	53
706	protein disulfide isomerase-related protein 5	gi|1710248	7	2	TGEAIVDAALSALR	91
					LYSSSDDVIELTPSNFNR	90
707	heat shock protein 27	gi|662841	13	2	LFDQAFGLPR	91
					LATQSNEITIPVTFESR	91

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
708	collagen, type VI, alpha 1 precursor	gi|87196339	2	2	DQLLPPSPNNR	43
					VFSVAITPDHLEPR	59
709	albumin preproprotein	gi|4502027	6	3	FQNALLVR	54
					DVFLGMFLYEYAR	74
					KVPQVSTPTLVEVSR	55
710	phosphoglycerate kinase 1	gi|4505763	12	3	LGDVYVNDAFGTAHR	75
					ALESPERPFLAILGGAK	52
					ITLPVDFVTADKFDENAK	41
711	Tubulin, beta 2C	gi|23958133	6	2	FPGQLNADLR	61
					GHYTEGAELVDSVLDVVR	78
712	hypothetical protein	gi|31873270	6	2	LTGFHETSNINDFSAGVANR	79
					RLTGFHETSNINDFSAGVANR	37
713	phosphoglycerate kinase 1	gi|4505763	8	2	LGDVYVNDAFGTAHR	77
					ALESPERPFLAILGGAK	53
714	heat shock protein 27	gi|662841	13	2	LFDQAFGLPR	66
					LATQSNEITIPVTFESR	71

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
715	lamin A/C isoform 1 precursor	gi|27436946	7	4	NIYSEELR	39
					TLEGELHDLR	56
					LQEKEDLQELNDR	73
					NSNLVGAAHEELQQSR	103
716	hypothetical protein	gi|11276938	4	4	IGFPWSEIR	45
					IQVWHAEHR	48
					APDFVFYAPR	71
					KAPDFVFYAPR	70
717	unknown	gi|62988748	2	4	VNHFVPEAGSR	40
					SVEDAQDVSLALTQR	103
					VAVVTYNNEVTTEIR	67
					VVIHFTDGADGDLADLHR	60
718	peroxiredoxin-2 isoform a	gi|32189392	15	3	QITVNDLPVGR	46
					EGGLGPLNIPLLADVTR	80
					KEGGLGPLNIPLLADVTR	53
719	Unknown	gi|15679996	13	2	FQNALLVR	40

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					KVPQVSTPTLVEVSR	39
720	smooth muscle myosin heavy chain	gi|4417214	6	4	IAQLEEQVEQEAR	59
					LQQELDDLVVDLDNQR	112
					ELEGHISDLQEDLDSER	58
					DVASLSSQLQDTQELLQEETR	99
721	peptidylprolyl isomerase A	gi|10863927	30	4	VSFELFADK	48
					FEDENFILK	42
					IIPGFMCQGGDFTR	48
					VNPTVFFDIAVDGEPLGR	153
722	apolipoprotein A-I preproprotein	gi|4557321	10	2	THLAPYSDELR	60
					EQLGPVTQEFWDNLEK	80
723	Hemoglobin subunit delta	gi|56553723	20	2	LLVVYPWTQR	63
					FFESFGDLSTPDAVMGNPK	127
724	medium-chain specific acyl-CoA dehydrogenase	gi|4557231	7	2	IYQIYEGTSQIQR	72
					AFTGFIVEADTPGIQIGR	74

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
725	alpha 2 type VI collagen isoform 2C2 precursor	gi|115527062	4	2	YGGLHFSDQVEVFSPPGSDR	93
					NDYATMLPDSTEIDQDTINR	62
726	HSPA9 protein	gi|21040386	4	2	AQFEGIVTDLIR	54
					LLGQFTLIGIPPAPR	37
727	outer dense fiber protein 2/2	gi|2996006	6	4	NIDLTAIISDLR	53
					KNIDLTAIISDLR	56
					LAECQDQLQGYER	43
					QTAEYSAFKLENER	78
728	ubiquitin and ribosomal protein S27a precursor	gi|4506713	19	2	IQDKEGIPPDQQR	59
					TITLEVEPSDTIENVK	44
729	hypothetical protein	gi|31873270	6	2	LTGFHETSNINDFSAGVANR	151
					RLTGFHETSNINDFSAGVANR	90
730	aldehyde dehydrogenase 1	gi|2183299	5	2	QAFQIGSPWR	64
					IAKEEIFGPVQQIMK	53

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
731	methylmalonate semialdehyde dehydrogenase	gi|188696	9	2	AISFVGSNKAGEYIFER	188
					NHGVVMPDANKENTLNQLVGAAFGAAGQR	125
732	Peptidyl-prolyl cis-trans isomerase A	gi|2981743	14	2	FEDENFILK	41
					IIPGFXCQGGDFTR	60
733	nucleoside diphosphate kinase B	gi|4505409	26	3	DRPFFPGLVK	49
					TFIAIKPDGVQR	55
					VMLGETNPADSKPGTIR	38
734	Nm23 protein	gi|35068	19	2	TFIAIKPDGVQR	108
					VMLGETNPADSKPGTIR	46
735	peroxiredoxin 1	gi|55959887	15	2	GLFIIDDKGILR	61
					TIAQDYGVLKADEGISFR	105
736	Peptidyl-prolyl cis-trans isomerase A	gi|1633054	18	3	IIPGFMCQGGDFTR	64
					IIPGFMCQGGDFTR	51
					SIYGEKFEDENFILK	62
737	unnamed protein product	gi|189054552	7	3	FQNALLVR	57

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					KVPQVSTPTLVEVSR	59
					VHTECCHGDLLECADDR	65
738	Unknown	gi|15679996	11	2	FQNALLVR	56
					KVPQVSTPTLVEVSR	68
739	hypothetical protein	gi|51476390	4	2	FQNALLVR	41
					KVPQVSTPTLVEVSR	66
740	PGK1	gi|48145549	16	4	LGDVYVNDAFGTAHR	117
					ALESPERPFLAILGGAK	66
					VLNNMEIGTSLFDEEGAK	100
					ITLPVDFVTADKFDENAK	57
741	Valosin-containing protein	gi|111305821	5	2	LIVDEAINEDNSVVSLSQPK	84
					EDEEESLNEVGYDDIGGCR	87
742	hypothetical protein	gi|51476390	4	2	LVNEVTEFAK	42
					QEPERNECFLQHK	54
743	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	16	3	VPTANVSVVDLTCR	123

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					LISWYDNEFGYSNR	102
					VIHDNFGIVEGLMTTVHAITATQK	47
744	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	57
					IFVEESIYDEFVR	67
745	chaperonin containing TCP1, subunit 2 (beta), isoform	gi|119617636	8	2	QVLLSAAEAAEVILR	58
					VQDDEVGDGTTSVTVLAAELLR	181
746	neuropolypeptide h3	gi|913159	18	2	LYTLVLTDPDAPSR	65
					GNDISSGTVLSDYVGSGPPK	39
747	Transferrin	gi|37747855	4	2	EGYYGYTGAFR	93
					ADRDQYELLCLDNTR	82
748	Glutathione S-transferase P	gi|23200510	10	2	PPYTVVYFPVR	75
					ALPGQLKPFETLLSQNQGGK	81
749	Protein disulfide-isomerase A3 precursor	gi|220702506	15	5	FLQDYFDGNLK	41
					ELSDFISYLQR	86
					SDVLELTDDNFESR	66

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					MDATANDVPSPYEVR	66
					TFSHELSDFGLESTAGEIPVVAIR	253
750	albumin preproprotein	gi|4502027	3	3	FQNALLVR	42
					DVFLGMFLYEYAR	84
					DVFLGMFLYEYAR	38
751	sorbitol dehydrogenase	gi|1583520	9	2	LENYPIPEPGPNEVLLR	91
					LPDNVTFEEGALIEPLSVGIHACR	61
752	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	75
					LISWYDNEFGYSNR	76
753	tubulin beta-2C chain	gi|5174735	6	2	FPGQLNADLR	51
					GHYTEGAELVDSVLDVVR	84
754	Proteasome (prosome, macropain) subunit, alpha type,	gi|13543551	15	2	NQYDNDVTVWSPQGR	60
					DLEFTIYDDDDVSPFLEGLEERPQR	99
755	biliverdin-IX beta reductase isozyme I	gi|544759	20	2	TVAGQDAVIVLLGTR	90

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					YVAVMPPHIGDQPLTGAYTVTLDGR	57
756	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	59
					LISWYDNEFGYSNR	53
757	Chain A, Human Guanidinoacetate N-Methyltransferase	gi|71042532	14	2	TEVMALVPPADCR	54
					VQEAPIDEHWIIECNDGVFQR	62
758	catechol-O-methyltransferase	gi|179955	14	3	YLPDTLLLEECGLLR	87
					GTVLLADNVICPGAPDFLAHVR	101
					KGTVLLADNVICPGAPDFLAHVR	124
759	Nitrilase family, member 2	gi|18088311	9	2	FAELAQIYAQR	75
					AVDNQVYVATASPAR	113
760	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	39
					LISWYDNEFGYSNR	55
761	Glyceraldehyde-3-phosphate	gi|67464043	8	2	VPTANVSVVDLTCR	66

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
	dehydrogenase					
					LISWYDNEFGYSNR	72
762	PGAM1	gi|49456447	16	3	VLIAAHGNSLR	39
					HGESAWNLENR	51
					NLKPIKPMQFLGDEETVR	56
763	peroxiredoxin-6	gi|4758638	13	3	NFDEILR	48
					LSILYPATTGR	82
					DFTPVCTTELGR	77
764	Carbonic anhydrase 2	gi|157830746	17	3	SADFTNFDPR	49
					AVQQPDGLAVLGIFLK	56
					YDPSLKPLSVSYDQATSLR	133
765	heat shock cognate 71 kDa protein isoform 1	gi|5729877	5	2	TTPSYVAFTDTER	76
					TVTNAVVTVPAYFNDSQR	105
766	Triosephosphate isomerase	gi|999892	25	3	DCGATWVVLGHSER	90
					VPADTEVVCAPPTAYIDFAR	156

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					ELASQPDVDGFLVGGASLKPEFVDIINAK	117
767	Glutathione S-transferase P	gi|23200510	23	3	PPYTVVYFPVR	78
					ALPGQLKPFETLLSQNQGGK	50
					YISLIYTNYEAGKDDYVK	49
768	hypothetical protein	gi|31873302	10	4	YISPDQLADLYK	51
					VVIGMDVAASEFFR	72
					VVIGMDVAASEFFR	41
					AAVPSGASTGIYEALELR	138
769	aldehyde dehydrogenase 1	gi|2183299	10	4	QAFQIGSPWR	53
					EEIFGPVQQIMK	43
					TIPIDGNFFTYTR	95
					IFVEESIYDEFVR	106
770	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	gi|134104755	13	3	ALPESLGQHALR	68
					DENATLDGGDVLFTGR	107
					LQLNIVEMKDENATLDGGDVLFTGR	143

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
771	Unknown	gi|15679996	11	2	FQNALLVR	41
					KVPQVSTPTLVEVSR	80
772	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	43
					LISWYDNEFGYSNR	58
773	glutathione S-transferase P	gi|4504183	15	2	PPYTVVYFPVR	42
					ALPGQLKPFETLLSQNQGGK	48
774	aldehyde dehydrogenase 1	gi|2183299	13	5	QAFQIGSPWR	50
					TIPIDGNFFTYTR	111
					IFVEESIYDEFVR	110
					ELGEYGFHEYTEVK	40
					GYFVQPTVFSNVTDEMR	39
775	Transferrin	gi|37747855	4	2	EGYYGYTGAFR	79
					ADRDQYELLCLDNTR	67
776	heat shock protein 27	gi|662841	26	4	QLSSGVSEIR	51
					LFDQAFGLPR	83

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VSLDVNHFAPDELTVK	80
					LATQSNEITIPVTFESR	100
777	Carbonic anhydrase 2	gi|157830746	17	3	SADFTNFDPR	51
					AVQQPDGLAVLGIFLK	45
					YDPSLKPLSVSYDQATSLR	94
778	peroxiredoxin-4	gi|5453549	9	2	QITLNDLPVGR	63
					DYGVYLEDSGHTLR	128
779	Heat-Shock 70kd Protein 42kd Atpase	gi|6729803	9	4	AQIHDLVLVGGSTR	72
					TTPSYVAFTDTER	60
					ATAGDTHLGGEDFDNR	68
					IINEPTAAAIAYGLDR	59
780	phosphatidylethanolamine binding protein [Homo	gi|14585855	22	2	IQGQELSAYQAPSPPAHSGFHR	85
					FHLGEPEASTQFMTQNYQDSPTLQAPR	79
781	calreticulin precursor variant	gi|62897681	7	2	EQFLDGDGWTSR	68
					IKDPDASKPEDWDER	79

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
782	creatine kinase B-type	gi|21536286	21	5	DLFDPIIEDR	50
					VLTPELYAELR	50
					LAVEALSSLDGDLAGR	93
					GTGGVDTAAVGGVFDVSNADR	80
					TDLNPDNLQGGDDLDPNYVLSSR	156
783	unnamed protein product	gi|189054552	7	4	FQNALLVR	51
					VPQVSTPTLVEVSR	47
					KVPQVSTPTLVEVSR	76
					VHTECCHGDLLECADDR	55
784	VCP protein	gi|48257098	7	3	EVDIGIPDATGR	47
					ELQELVQYPVEHPDK	37
					QTNPSAMEVEEDDPVPEIR	84
785	heat shock cognate 71 kDa protein isoform 1	gi|5729877	7	3	FEELNADLFR	39
					STAGDTHLGGEDFDNR	57
					TVTNAVVTVPAYFNDSQR	83

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
786	GRP78 precursor	gi|386758	8	4	SDIDEIVLVGGSTR	103
					KSDIDEIVLVGGSTR	101
					DNHLLGTFDLTGIPPAPR	138
					IEIESFYEGEDFSETLTR	138
787	Niemann-Pick disease, type C2 precursor variant	gi|62896507	26	2	EVNVSPCPTQPCQLSK	39
					AVVHGILMGVPVPFPIPEPDGCK	76
789	heat shock cognate 71 kDa protein isoform 1	gi|5729877	11	4	FEELNADLFR	52
					STAGDTHLGGEDFDNR	79
					TVTNAVVTVPAYFNDSQR	90
					QTQTFTTYSDNQPGVLIQVYEGER	161
791	glutathione S-transferase Mu 3	gi|23065552	13	2	LKPQYLEELPGQLK	41
					LTFVDFLTYDILDQNR	87
792	tropomyosin 2 (beta) isoform 2 variant	gi|62898077	14	3	IQLVEEELDR	62
					KLVILEGELER	61

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EENVEIHQTLDQTLLELNNL	162
793	unnamed protein product	gi|221039588	8	2	EQFNEFR	55
					IDNDGDGFVTTEELK	81
794	Tubulin, beta 2C	gi|23958133	6	2	FPGQLNADLR	72
					GHYTEGAELVDSVLDVVR	154
795	unnamed protein product	gi|35655	6	2	VDATEESDLAQQYGVR	89
					ILFIFIDSDHTDNQR	53
796	GRP78 precursor	gi|386758	10	5	SDIDEIVLVGGSTR	78
					KSDIDEIVLVGGSTR	61
					VTHAVVTVPAYFNDAQR	68
					DNHLLGTFDLTGIPPAPR	64
					IEIESFYEGEDFSETLTR	115
797	hypothetical protein	gi|31873439	7	2	QLFHPEQLITGK	63
					FDGALNVDLTEFQTNLVP	56
798	actin, cytoplasmic 2	gi|4501887	18	4	QEYDESGPSIVHR	101
					SYELPDGQVITIGNER	128

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VAPEEHPVLLTEAPLNPK	72
					DLYANTVLSGGTTMYPGIADR	45
799	proteasome (prosome, macropain) subunit, alpha type	gi|54696300	25	4	GVNTFSPEGR	47
					LFQVEYAIEAIK	72
					AIGSASEGAQSSLQEVYHK	89
					GPQLFHMDPSGTFVQCDAR	40
800	actin, cytoplasmic 2	gi|4501887	18	4	QEYDESGPSIVHR	87
					SYELPDGQVITIGNER	131
					VAPEEHPVLLTEAPLNPK	57
					DLYANTVLSGGTTMYPGIADR	43
801	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	61
					LISWYDNEFGYSNR	64
802	hypothetical protein	gi|31873302	10	4	YISPDQLADLYK	54
					VVIGMDVAASEFFR	55

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VVIGMDVAASEFFR	43
					AAVPSGASTGIYEALELR	141
803	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	68
					IFVEESIYDEFVR	64
804	Chain A, Aldehyde Reductase	gi|157834561	8	2	HHPEDVEPALR	39
					GLEVTAYSPLGSSDR	91
805	Unknown	gi|15679996	11	2	FQNALLVR	38
					KVPQVSTPTLVEVSR	75
806	GRP78 precursor	gi|386758	8	4	SDIDEIVLVGGSTR	52
					KSDIDEIVLVGGSTR	39
					DNHLLGTFDLTGIPPAPR	44
					IEIESFYEGEDFSETLTR	77
807	peroxiredoxin-2 isoform a	gi|32189392	15	3	QITVNDLPVGR	62
					EGGLGPLNIPLLADVTR	161
					KEGGLGPLNIPLLADVTR	146
808	heat shock 70kDa protein 8 isoform 1	gi|62897129	7	3	FEELNADLFR	87

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
	variant					
					NQTAEKEEFEHQQK	59
					QTQTFTTYSDNQPGVLIQVYEGER	131
809	heat shock protein 27	gi|662841	21	3	LFDQAFGLPR	70
					VSLDVNHFAPDELTVK	51
					LATQSNEITIPVTFESR	84
810	peptidylprolyl isomerase A	gi|10863927	25	3	FEDENFILK	46
					IIPGFMCQGGDFTR	51
					VNPTVFFDIAVDGEPLGR	104
811	Serum albumin precursor	gi|157830361	4	2	FQNALLVR	49
					VHTECCHGDLLECADDR	95
812	Unknown	gi|15679996	11	2	FQNALLVR	62
					KVPQVSTPTLVEVSR	51
813	Triosephosphate isomerase	gi|999892	13	2	HVFGESDELIGQK	76
					VPADTEVVCAPPTAYIDFAR	106
814	Human Carbonic Anhydrase Ii	gi|157834071	24	4	SADFTNFDPR	62

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					AVQQPDGLAVLGIFLK	70
					ILNNGHSFNVEFDDSQDK	109
					YDPSLKPLSVSYDQATSLR	112
815	Unknown	gi|15679996	11	2	FQNALLVR	41
					KVPQVSTPTLVEVSR	45
816	Protein disulfide-isomerase A3 precursor	gi|220702506	12	4	FLQDYFDGNLK	49
					ELSDFISYLQR	67
					SDVLELTDDNFESR	76
					TFSHELSDFGLESTAGEIPVVAIR	212
817	AGR2	gi|68012756	23	3	HLSPDGQYVPR	38
					LYAYEPADTALLLDNMK	50
					LAEQFVLLNLVYETTDK	75
818	endoplasmin precursor	gi|4507677	13	7	GLFDEYGSK	47
					FAFQAEVNR	66
					SILFVPTSAPR	47
					GVVDSDDLPLNVSR	82

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EEEAIQLDGLNASQIR	88
					ESDDPMAYIHFTAEGEVTFK	40
					TDDEVVQREEEAIQLDGLNASQIR	125
819	galactokinase 1	gi|119609722	16	5	LQFPLPTAQR	39
					EVQLEELEAAR	50
					QPQVAELLAEAR	58
					EEFGAEPELAVSAPGR	68
					KDGLVSLLTTSEGADEPQR	69
820	dynactin subunit 2	gi|5453629	8	2	VSALDLAVLDQVEAR	76
					ENLATVEGNFASIDER	96
821	beta globin chain variant	gi|13549112	15	2	LLVVYPWTQR	54
					EFTQPVQAAYQK	52
822	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	62
					SYELPDGQVITIGNER	128
823	Chain A, Native Human Lysosomal	gi|30749651	6	2	GSYSLSHVYTPNDVR	71
					EISEVFPDQFIHLGGDEVEFK	96

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
824	Vitamin D-binding protein	gi|139641	7	2	EDFTSLSLVLYSR	49
					HQPQEFPTYVEPTNDEICEAFR	72
825	phosphoglycerate mutase 2	gi|50593010	11	2	VLIAAHGNSLR	40
					ELKPTKPMQFLGDEETVR	39
826	Unknown	gi|15679996	11	2	FQNALLVR	42
					KVPQVSTPTLVEVSR	55
827	lamin-A/C isoform 2	gi|5031875	7	3	AAYEAELGDAR	41
					LQEKEDLQELNDR	76
					NSNLVGAAHEELQQSR	63
828	heat shock protein 60	gi|77702086	11	3	AAVEEGIVLGGGCALLR	75
					KPLVIIAEDVDGEALSTLVLNR	138
					LVQDVANNTNEEAGDGTTTATVLAR	119
829	protein disulfide isomerase-related protein 5	gi|1710248	11	3	TGEAIVDAALSALR	91
					LAAVDATVNQVLASR	75
					LYSSSDDVIELTPSNFNR	136

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
830	mutant desmin	gi|71011128	15	5	VAELYEEELR	69
					FASEASGYQDNIAR	106
					RIESLNEEIAFLK	48
					FLEQQNAALAAEVNR	146
					LQEEIQLKEEAENNLAAFR	114
831	actin, alpha cardiac muscle 1 proprotein	gi|4885049	15	4	GYSFVTTAER	51
					QEYDEAGPSIVHR	61
					SYELPDGQVITIGNER	131
					VAPEEHPTLLTEAPLNPK	59
832	Protein disulfide-isomerase A3 precursor	gi|220702506	5	2	DLLIAYYDVDYEK	53
					SDVLELTDDNFESR	89
833	unnamed protein product	gi|189054552	4	2	FQNALLVR	62
					VHTECCHGDLLECADDR	74
834	ACO2	gi|49168620	4	2	SQFTITPGSEQIR	42
					NAVTQEFGPVPDTAR	53
835	mutant desmin	gi|71011128	8	3	VAELYEEELR	54

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					FASEASGYQDNIAR	58
					FLEQQNAALAAEVNR	137
836	tropomyosin alpha-4 chain isoform 1	gi|223555975	8	2	IQLVEEELDR	66
					KLVILEGELER	45
837	unnamed protein product	gi|16552261	9	3	VELQELNDR	38
					ISLPLPNFSSLNLR	56
					EMEENFAVEAANYQDTIGR	86
838	actin, cytoplasmic 2	gi|4501887	13	3	QEYDESGPSIVHR	86
					SYELPDGQVITIGNER	141
					VAPEEHPVLLTEAPLNPK	48
839	actin, gamma-enteric smooth muscle propeptide	gi|4501889	7	2	GYSFVTTAER	39
					SYELPDGQVITIGNER	130
840	heat shock cognate 71 kDa protein isoform 1	gi|5729877	11	5	DAGTIAGLNVLR	64
					VEIIANDQGNR	46

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					TTPSYVAFTDTER	95
					STAGDTHLGGEDFDNR	57
					TVTNAVVTVPAYFNDSQR	97
841	Unknown	gi|15679996	11	2	FQNALLVR	43
					KVPQVSTPTLVEVSR	58
842	mitochondrial ATP synthase	gi|89574029	17	5	AHGGYSVFAGVGER	82
					VALTGLTVAEYFR	48
					LVLEVAQHLGESTVR	83
					DQEGQDVLLFIDNIFR	93
					AIAELGIYPAVDPLDSTSR	60
843	GRP78 precursor	gi|386758	7	3	SDIDEIVLVGGSTR	98
					ITPSYVAFTPEGER	79
					IEIESFYEGEDFSETLTR	132
844	Unknown	gi|15679996	11	2	FQNALLVR	42
					KVPQVSTPTLVEVSR	48
845	AGR2	gi|68012756	24	3	HLSPDGQYVPR	38

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					LAEQFVLLNLVYETTDK	39
					LYAYEPADTALLLDNMKK	46
846	peptidylprolyl isomerase A	gi|10863927	19	2	IIPGFMCQGGDFTR	44
					VNPTVFFDIAVDGEPLGR	93
847	mutant desmin	gi|71011128	7	2	FLEQQNAALAAEVNR	86
					LQEEIQLKEEAENNLAAFR	57
848	mutant desmin	gi|71011128	8	3	VAELYEEELR	41
					FASEASGYQDNIAR	69
					FLEQQNAALAAEVNR	121
849	GRP78 precursor	gi|386758	8	4	SDIDEIVLVGGSTR	89
					KSDIDEIVLVGGSTR	85
					DNHLLGTFDLTGIPPAPR	110
					IEIESFYEGEDFSETLTR	111
850	beta globin chain variant	gi|13549112	17	2	VNVDEVGGEALGR	65
					EFTQPVQAAYQK	49
851	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	68

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					SYELPDGQVITIGNER	110
852	aldehyde dehydrogenase 1A1	gi|21361176	8	3	EEIFGPVQQIMK	47
					TIPIDGNFFTYTR	88
					IFVEESIYDEFVR	101
853	peroxiredoxin-2 isoform a	gi|32189392	15	3	QITVNDLPVGR	49
					EGGLGPLNIPLLADVTR	134
					KEGGLGPLNIPLLADVTR	140
854	Carbonic anhydrase 2	gi|157830746	17	3	SADFTNFDPR	44
					AVQQPDGLAVLGIFLK	37
					YDPSLKPLSVSYDQATSLR	120
855	Triosephosphate isomerase	gi|999892	13	2	HVFGESDELIGQK	89
					VPADTEVVCAPPTAYIDFAR	107
856	Protein disulfide-isomerase A3 precursor	gi|220702506	5	2	DLLIAYYDVDYEK	46
					SDVLELTDDNFESR	87
857	protein disulfide isomerase	gi|860986	17	6	FVMQEEFSR	37
					FLQDYFDGNLK	43

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					ELSDFISYLQR	64
					MDATANDVPSPYEVR	75
					VVVAENFDEIVNNENK	58
					TFSHELSDFGLESTAGEIPVVAIR	208
858	peptidylprolyl isomerase A	gi|10863927	25	3	FEDENFILK	38
					IIPGFMCQGGDFTR	49
					VNPTVFFDIAVDGEPLGR	157
859	neuropolypeptide h3	gi|913159	18	2	LYTLVLTDPDAPSR	61
					GNDISSGTVLSDYVGSGPPK	68
860	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	86
					SYELPDGQVITIGNER	118
861	Protein disulfide-isomerase A3 precursor	gi|220702506	14	5	FVMQEEFSR	54
					FLQDYFDGNLK	50
					ELSDFISYLQR	77
					SDVLELTDDNFESR	78
					TFSHELSDFGLESTAGEIPVVAIR	180

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
862	GRP78 precursor	gi|386758	12	6	SDIDEIVLVGGSTR	96
					AKFEELNMDLFR	38
					KSDIDEIVLVGGSTR	97
					DNHLLGTFDLTGIPPAPR	110
					GVPQIEVTFEIDVNGILR	58
					IEIESFYEGEDFSETLTR	124
863	ATP5A1 protein	gi|13938339	10	3	EAYPGDVFYLHSR	126
					QGQYSPMAIEEQVAVIYAGVR	63
					EVAAFAQFGSDLDAATQQLLSR	67
864	Protein disulfide-isomerase A3 precursor	gi|220702506	8	3	LAPEYEAAATR	45
					DLLIAYYDVDYEK	48
					SDVLELTDDNFESR	92
865	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	74
					IFVEESIYDEFVR	92
866	actin, alpha cardiac muscle 1 proprotein	gi|4885049	10	3	GYSFVTTAER	66
					QEYDEAGPSIVHR	64

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					SYELPDGQVITIGNER	131
867	hypothetical protein	gi|51476390	4	2	LVNEVTEFAK	70
					QEPERNECFLQHK	43
868	Unknown	gi|15679996	11	2	FQNALLVR	42
					KVPQVSTPTLVEVSR	72
869	unnamed protein product	gi|37403	9	3	IQLVEEELDR	40
					IQVLQQQADDAEER	39
					KIQVLQQQADDAEER	49
870	unnamed protein product	gi|189054552	7	3	FQNALLVR	58
					KVPQVSTPTLVEVSR	59
					VHTECCHGDLLECADDR	51
871	hypothetical protein	gi|51476390	5	3	LCTVATLR	46
					LVNEVTEFAK	67
					QEPERNECFLQHK	59
873	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	gi|134104755	10	2	ALPESLGQHALR	94

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					DENATLDGGDVLFTGR	83
875	Chain A, Structure Of Human Muscle Pyruvate Kinase	gi|67464392	7	2	FGVEQDVDMVFASFIR	54
					TATESFASDPILYRPVAVALDTK	42
876	protein disulfide isomerase	gi|860986	10	3	ELSDFISYLQR	45
					MDATANDVPSPYEVR	66
					TFSHELSDFGLESTAGEIPVVAIR	189
877	Glutathione S-transferase P	gi|23200510	10	2	PPYTVVYFPVR	78
					ALPGQLKPFETLLSQNQGGK	68
878	protein disulfide isomerase-related protein 5	gi|1710248	11	3	TGEAIVDAALSALR	117
					LAAVDATVNQVLASR	60
					LYSSSDDVIELTPSNFNR	111
879	protein disulfide isomerase	gi|860986	12	4	GFPTIYFSPANK	37
					ELSDFISYLQR	61
					MDATANDVPSPYEVR	53

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					TFSHELSDFGLESTAGEIPVVAIR	177
880	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	99
					LISWYDNEFGYSNR	78
881	lamin A/C isoform 1 precursor	gi|27436946	4	2	LQEKEDLQELNDR	47
					NSNLVGAAHEELQQSR	47
882	heat shock protein 27	gi|662841	13	2	LFDQAFGLPR	42
					LATQSNEITIPVTFESR	90
883	peroxiredoxin-4	gi|5453549	9	2	QITLNDLPVGR	55
					DYGVYLEDSGHTLR	90
884	peroxiredoxin-6	gi|4758638	10	2	LSILYPATTGR	59
					DFTPVCTTELGR	74
885	heat shock protein 27	gi|662841	21	3	LFDQAFGLPR	76
					VSLDVNHFAPDELTVK	83
					LATQSNEITIPVTFESR	102
886	unnamed protein product	gi|16552261	8	3	VELQELNDR	46

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EEAENTLQSFR	50
					EMEENFAVEAANYQDTIGR	129
887	heat shock protein 27	gi|662841	21	3	LFDQAFGLPR	63
					VSLDVNHFAPDELTVK	53
					LATQSNEITIPVTFESR	92
888	lipoprotein Gln I	gi|229479	8	2	DEPPQSPWDR	43
					THLAPYSDELR	66
889	Tubulin, beta 2C	gi|23958133	10	3	FPGQLNADLR	93
					AVLVDLEPGTMDSVR	44
					GHYTEGAELVDSVLDVVR	163
890	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	68
					LISWYDNEFGYSNR	53
891	peroxiredoxin-6	gi|4758638	17	4	NFDEILR	37
					LPFPIIDDR	76
					LSILYPATTGR	41

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					DFTPVCTTELGR	56
892	PGK1	gi|48145549	12	3	LGDVYVNDAFGTAHR	126
					ALESPERPFLAILGGAK	49
					VLNNMEIGTSLFDEEGAK	76
893	Annexin A2	gi|73909156	9	3	GVDEVTIVNILTNR	94
					AEDGSVIDYELIDQDAR	73
					RAEDGSVIDYELIDQDAR	83
894	tropomyosin alpha-4 chain isoform 1	gi|223555975	8	2	IQLVEEELDR	39
					KLVILEGELER	42
895	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	46
					LISWYDNEFGYSNR	44
896	unnamed protein product	gi|16552261	6	2	EEAENTLQSFR	46
					EMEENFAVEAANYQDTIGR	149
897	ALB protein	gi|23241675	19	5	FQNALLVR	57
					KVPQVSTPTLVEVSR	72

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					RPCFSALEVDETYVPK	70
					VFDEFKPLVEEPQNLIK	67
					EFNAETFTFHADICTLSEK	44
898	tubulin beta-2C chain	gi|5174735	6	2	FPGQLNADLR	41
					GHYTEGAELVDSVLDVVR	49
899	PGK1	gi|48145549	16	4	LGDVYVNDAFGTAHR	121
					ALESPERPFLAILGGAK	55
					VLNNMEIGTSLFDEEGAK	62
					ITLPVDFVTADKFDENAK	64
900	Triosephosphate isomerase	gi|999892	20	2	VPADTEVVCAPPTAYIDFAR	70
					ELASQPDVDGFLVGGASLKPEFVDIINAK	55
901	unnamed protein product	gi|16552261	7	2	ISLPLPNFSSLNLR	52
					EMEENFAVEAANYQDTIGR	103
902	actin, cytoplasmic 2	gi|4501887	13	3	QEYDESGPSIVHR	47
					SYELPDGQVITIGNER	133
					VAPEEHPVLLTEAPLNPK	49

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
903	TSA	gi|1617118	9	2	EGGLGPLNIPLLADVTR	152
					KEGGLGPLNIPLLADVTR	84
904	dimethylarginine dimethylaminohydrolase 2 [Homo	gi|123279699	16	2	DFAVSTVPVSGPSHLR	70
					IVEIGDENATLDGTDVLFTGR	102
905	hypothetical protein	gi|51476390	3	2	YLYEIAR	44
					QEPERNECFLQHK	54
906	unnamed protein product	gi|16552261	7	2	ISLPLPNFSSLNLR	37
					EMEENFAVEAANYQDTIGR	90
907	beta actin	gi|4501885	13	3	QEYDESGPSIVHR	45
					SYELPDGQVITIGNER	125
					VAPEEHPVLLTEAPLNPK	44
908	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	60
					SYELPDGQVITIGNER	128
909	actin, cytoplasmic 2	gi|4501887	12	3	AGFAGDDAPR	51
					SYELPDGQVITIGNER	133

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VAPEEHPVLLTEAPLNPK	56
910	beta-actin-like protein 2	gi|63055057	9	2	SYELPDGQVITIGNER	133
					VAPDEHPILLTEAPLNPK	41
911	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	65
					SYELPDGQVITIGNER	150
912	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	gi|134104755	13	3	ALPESLGQHALR	49
					DENATLDGGDVLFTGR	38
					LQLNIVEMKDENATLDGGDVLFTGR	104
913	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	40
					IFVEESIYDEFVR	75
914	heat shock protein 60	gi|77702086	14	4	AAVEEGIVLGGGCALLR	103
					ISSIQSIVPALEIANAHR	90
					KPLVIIAEDVDGEALSTLVLNR	193
					LVQDVANNTNEEAGDGTTTATVLAR	119
915	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	68

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					SYELPDGQVITIGNER	148
916	hypothetical protein	gi|31873302	7	2	VVIGMDVAASEFFR	49
					AAVPSGASTGIYEALELR	128
917	actin, cytoplasmic 2	gi|4501887	13	3	QEYDESGPSIVHR	60
					SYELPDGQVITIGNER	150
					VAPEEHPVLLTEAPLNPK	76
918	mutant desmin	gi|71011128	9	3	FASEASGYQDNIAR	59
					INLPIQTYSALNFR	44
					FLEQQNAALAAEVNR	106
919	TapasinERP57 HETERODIMER	gi|220702506	10	3	ELSDFISYLQR	75
					SDVLELTDDNFESR	70
					TFSHELSDFGLESTAGEIPVVAIR	180
920	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	45
					SYELPDGQVITIGNER	146
921	protein disulfide isomerase	gi|860986	9	2	DASIVGFFDDSFSEAHSEFLK	77
					TFSHELSDFGLESTAGEIPVVAIR	123

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
922	heat shock protein 60	gi|77702086	14	4	AAVEEGIVLGGGCALLR	47
					ISSIQSIVPALEIANAHR	46
					KPLVIIAEDVDGEALSTLVLNR	187
					LVQDVANNTNEEAGDGTTTATVLAR	141
923	albumin preproprotein	gi|4502027	8	3	KVPQVSTPTLVEVSR	40
					RPCFSALEVDETYVPK	40
					VFDEFKPLVEEPQNLIK	64
924	HSPA9 protein	gi|21040386	6	3	AQFEGIVTDLIR	63
					LLGQFTLIGIPPAPR	47
					NAVITVPAYFNDSQR	66
925	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	49
					IFVEESIYDEFVR	89
926	SPTAN1 protein	gi|31565122	1	2	ELPTAFDYVEFTR	46
					SSLSSAQADFNQLAELDR	42
927	unnamed protein product	gi|189065555	19	5	EGIAQTVFLGLNR	107
					LFVDGQEIAVVYFR	118

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					QIEINTISASFGGLASR	129
					IEPEPFENCLLRPGSPAR	76
					ATFAGLYSLDVGEEGDQAIAEALAAPSR	166
928	TapasinERP57 HETERODIMER	gi|220702506	12	4	FLQDYFDGNLK	58
					ELSDFISYLQR	67
					SDVLELTDDNFESR	88
					TFSHELSDFGLESTAGEIPVVAIR	219
929	aldehyde dehydrogenase 1A1	gi|21361176	8	3	TIPIDGNFFTYTR	87
					IFVEESIYDEFVR	122
					ELGEYGFHEYTEVK	41
930	enolase 1 variant	gi|62896593	19	5	YISPDQLADLYK	82
					VVIGMDVAASEFFR	63
					AAVPSGASTGIYEALELR	158
					LAMQEFMILPVGAANFR	44
					FTASAGIQVVGDDLTVTNPK	136
931	Human Serum Albumin	gi|157830361	19	5	YLYEIAR	43

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					FQNALLVR	45
					KVPQVSTPTLVEVSR	43
					RPCFSALEVDETYVPK	69
					VFDEFKPLVEEPQNLIK	116
932	unnamed protein product	gi|189054101	10	2	QAALQVAEGFISR	69
					MQYAPNTQVEILPQGHESPIFK	53
933	heat shock protein 27	gi|662841	13	2	LFDQAFGLPR	58
					LATQSNEITIPVTFESR	114
934	Triosephosphate isomerase	gi|999892	20	2	VPADTEVVCAPPTAYIDFAR	165
					ELASQPDVDGFLVGGASLKPEFVDIINAK	117
935	mutant desmin	gi|71011128	11	4	VAELYEEELR	60
					EEAENNLAAFR	49
					FASEASGYQDNIAR	112
					FLEQQNAALAAEVNR	127
936	mitochondrial ATP synthase	gi|89574029	17	5	AHGGYSVFAGVGER	84
					VALTGLTVAEYFR	51

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					LVLEVAQHLGESTVR	67
					DQEGQDVLLFIDNIFR	129
					AIAELGIYPAVDPLDSTSR	81
937	heat shock protein 60	gi|77702086	14	4	AAVEEGIVLGGGCALLR	88
					ISSIQSIVPALEIANAHR	89
					KPLVIIAEDVDGEALSTLVLNR	212
					LVQDVANNTNEEAGDGTTTATVLAR	92
938	TapasinERP57 HETERODIMER	gi|220702506	8	3	FLQDYFDGNLKR	39
					DLLIAYYDVDYEK	77
					SDVLELTDDNFESR	83
939	heterogeneous nuclear ribonucleoproteins A2/B1	gi|14043072	18	4	DYFEEYGK	43
					GGGGNFGPGPGSNFR	88
					LFIGGLSFETTEESLR	126
					NMGGPYGGGNYGPGGSGGSGGYGGR	51
940	Protein DJ-1	gi|42543006	22	2	GAEEMETVIPVDVMR	59

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EGPYDVVVLPGGNLGAQNLSESAAVK	151
941	nucleoside phosphorylase	gi|157168362	21	4	FEVGDIMLIR	38
					DHINLPGFSGQNPLR	44
					LGADAVGMSTVPEVIVAR	64
					LTQAQIFDYGEIPNFPR	135
942	smooth muscle mysosin heavy chain	gi|36507	4	2	LQQELDDLVVDLDNQR	64
					DVASLSSQLQDTQELLQEETR	52
943	mutant desmin	gi|71011128	12	4	VAELYEEELR	50
					FASEASGYQDNIAR	88
					FLEQQNAALAAEVNR	110
					LQEEIQLKEEAENNLAAFR	100
944	myosin light polypeptide 6 isoform 1	gi|17986258	10	2	DQGTYEDYVEGLR	41
					NKDQGTYEDYVEGLR	37
945	Hemoglobin subunit beta	gi|3660145	47	5	LHVDPENFR	47
					VNVDEVGGEALGR	45
					EFTPPVQAAYQK	68

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VLGAFSDGLAHLDNLK	100
					FFESFGDLSTPDAVMGNPK	124
946	peptidylprolyl isomerase A	gi|10863927	19	2	IIPGFMCQGGDFTR	40
					VNPTVFFDIAVDGEPLGR	140
947	neuropolypeptide h3	gi|913159	19	2	LYTLVLTDPDAPSR	68
					GNDISSGTVLSDYVGSGPPK	97
948	Hemoglobin subunit alpha	gi|37928140	42	3	VGAHAGEYGAEALER	118
					TYFPHFDLSHGSAQVK	140
					VADALTNAVAHVDDMPNALSALSDLHAHK	61
949	Hemoglobin subunit beta	gi|61679604	27	3	LHVDPENFR	51
					EFTPPVQAAYQK	42
					FFESFGDLSTPDAVMGNPK	108
950	albumin preproprotein	gi|4502027	8	3	AVMDDFAAFVEK	41
					RPCFSALEVDETYVPK	81
					EFNAETFTFHADICTLSEK	41
951	heterogeneous nuclear ribonucleoprotein H	gi|5031753	7	2	HTGPNSPDTANDGFVR	42

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					STGEAFVQFASQEIAEK	77
952	ATP5A1 protein	gi|13938339	10	3	EAYPGDVFYLHSR	72
					QGQYSPMAIEEQVAVIYAGVR	78
					EVAAFAQFGSDLDAATQQLLSR	86
953	Hemoglobin subunit beta	gi|3660145	32	3	EFTPPVQAAYQK	42
					VLGAFSDGLAHLDNLK	67
					FFESFGDLSTPDAVMGNPK	126
954	unnamed protein product	gi|194388088	4	2	FEELCSDLFR	42
					AQIHDLVLVGGSTR	68
955	fructose-bisphosphate aldolase A	gi|4557305	7	2	ADDGRPFPQVIK	51
					FSHEEIAMATVTALR	42
956	Alpha-1-antitrypsin precursor	gi|28948408	18	5	GKWERPFEVK	48
					ITPNLAEFAFSLYR	122
					TDTSHHDQDHPTFNK	93
					DTEEEDFHVDQVTTVK	57
					LYHSEAFTVNFGDTEEAK	152

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
957	antitrypsin alpha1 mutant	gi|224224	21	6	GKWERPFEVK	46
					ITPNLAEFAFSLYR	94
					LQHLENELTHDIITK	110
					FNKPFVFLMIEQNTK	67
					DTEEEDFHVDQVTTVK	60
					LYHSEAFTVNFGDTEEAK	147
958	actin, cytoplasmic 2	gi|4501887	24	6	GYSFTTTAER	66
					AVFPSIVGRPR	63
					QEYDESGPSIVHR	93
					SYELPDGQVITIGNER	150
					VAPEEHPVLLTEAPLNPK	104
					DLYANTVLSGGTTMYPGIADR	48
959	hypothetical protein	gi|51476390	9	4	FQNALLVR	41
					AVMDDFAAFVEK	40
					KVPQVSTPTLVEVSR	67
					VFDEFKPLVEEPQNLIK	81

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
960	hypothetical protein	gi|51476390	15	7	YLYEIAR	44
					FQNALLVR	45
					LVNEVTEFAK	43
					KVPQVSTPTLVEVSR	68
					RPCFSALEVDETYVPK	76
					VFDEFKPLVEEPQNLIK	115
					EFNAETFTFHADICTLSEK	68
961	antitrypsin alpha1 mutant	gi|224224	19	5	ITPNLAEFAFSLYR	112
					LQHLENELTHDIITK	83
					FNKPFVFLMIEQNTK	77
					DTEEEDFHVDQVTTVK	62
					LYHSEAFTVNFGDTEEAK	145
962	Horf6 A Novel Human Peroxidase Enzyme	gi|3318841	30	5	LPFPIIDDR	74
					VVFVFGPDKK	38
					LSILYPATTGR	38
					ELAILLGMLDPAEKDEK	38

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					PGGLLLGDVAPNFEANTTVGR	174
963	unnamed protein product	gi|16552261	17	5	KVESLQEEIAFLK	46
					ISLPLPNFSSLNLR	77
					TNEKVELQELNDR	110
					LLQDSVDFSLADAINTEFK	116
					EMEENFAVEAANYQDTIGR	103
964	KRT8 protein	gi|62913980	10	3	LSELEAALQR	42
					ASLEAAIADAEQR	69
					LEGLTDEINFLR	89
965	hypothetical protein	gi|51476390	13	6	FQNALLVR	40
					LVNEVTEFAK	43
					AVMDDFAAFVEK	55
					KVPQVSTPTLVEVSR	61
					RPCFSALEVDETYVPK	43
					VFDEFKPLVEEPQNLIK	106
966	Alpha-1-acid glycoprotein 1	gi|112877	11	2	TEDTIFLR	44

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					YVGGQEHFAHLLILR	106
967	Apolipoprotein A-I precursor	gi|90108664	22	5	AKPALEDLR	59
					DEPPQSPWDR	55
					THLAPYSDELR	74
					VSFLSALEEYTK	59
					DSGRDYVSQFEGSALGK	115
968	Apolipoprotein A-I precursor	gi|90108664	17	4	DEPPQSPWDR	48
					THLAPYSDELR	76
					VSFLSALEEYTK	74
					DYVSQFEGSALGK	100
969	beta tropomyosin	gi|6573280	7	2	IQLVEEELDR	71
					KLVILEGELER	93
970	unnamed protein product	gi|28590	5	2	RHPDYSVVLLLR	37
					VFDEFKPLVEEPQNLIK	100
971	Tubulin, beta 2C	gi|23958133	20	6	IREEYPDR	37
					FPGQLNADLR	93

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					INVYYNEATGGK	63
					AVLVDLEPGTMDSVR	37
					GHYTEGAELVDSVLDVVR	174
					FWEVISDEHGIDPTGTYHGDSDLQLER	99
972	Aldehyde Reductase	gi|157834561	20	4	GLVQALGLSNFNSR	102
					DAGHPLYPFNDPY	37
					GLEVTAYSPLGSSDR	116
					AWRDPDEPVLLEEPVVLALAEK	73
973	TapasinERP57 HETERODIMER	gi|220702506	13	4	LAPEYEAAATR	66
					DLLIAYYDVDYEK	68
					SDVLELTDDNFESR	100
					FISDKDASIVGFFDDSFSEAHSEFLK	113
974	Human Muscle Pyruvate Kinase	gi|67464392	15	5	LDIDSPPITAR	54
					IYVDDGLISLQVK	68
					GADFLVTEVENGGSLGSK	41
					FGVEQDVDMVFASFIR	63

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					TATESFASDPILYRPVAVALDTK	98
975	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	gi|134104755	17	3	ALPESLGQHALR	47
					QHQLYVGVLGSK	48
					LQLNIVEMKDENATLDGGDVLFTGR	46
976	Protein DJ-1	gi|42543006	24	2	GPGTSFEFALAIVEALNGK	89
					EGPYDVVVLPGGNLGAQNLSESAAVK	99
977	unnamed protein product	gi|37403	13	4	IQLVEEELDR	69
					KLVIIEGDLER	68
					IQVLQQQADDAEER	76
					KIQVLQQQADDAEER	106
978	unnamed protein product	gi|16552261	7	2	ISLPLPNFSSLNLR	87
					EMEENFAVEAANYQDTIGR	94
979	serine proteinase inhibitor, clade A, member 1	gi|50363217	14	4	GKWERPFEVK	42
					ITPNLAEFAFSLYR	91

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					ELDRDTVFALVNYIFFK	91
					LYHSEAFTVNFGDTEEAK	95
980	beta tropomyosin	gi|6573280	12	3	IQLVEEELDR	81
					KLVILEGELER	102
					IQLVEEELDRAQER	64
981	Human Serum Albumin	gi|157830361	13	3	FQNALLVR	52
					RPCFSALEVDETYVPK	74
					VFDEFKPLVEEPQNLIK	97
982	tropomyosin 2 (beta) isoform 2 variant	gi|62898077	23	5	LVILEGELER	61
					IQLVEEELDR	83
					KLVILEGELER	102
					IQLVEEELDRAQER	64
					EENVEIHQTLDQTLLELNNL	148
983	heat shock protein 27	gi|662841	30	6	VPFSLLR	37
					RVPFSLLR	38
					QLSSGVSEIR	84

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					LFDQAFGLPR	97
					VSLDVNHFAPDELTVK	120
					LATQSNEITIPVTFESR	149
984	Human Serum Albumin	gi|157830361	25	6	FQNALLVR	45
					AVMDDFAAFVEK	56
					RHPDYSVVLLLR	72
					KVPQVSTPTLVEVSR	67
					RPCFSALEVDETYVPK	134
					VFDEFKPLVEEPQNLIK	106
985	hypothetical protein	gi|51476390	5	3	YLYEIAR	43
					LVNEVTEFAK	47
					QEPERNECFLQHK	63
986	unnamed protein product	gi|16552261	12	4	EEAENTLQSFR	48
					KVESLQEEIAFLK	75
					ISLPLPNFSSLNLR	88
					EMEENFAVEAANYQDTIGR	138

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
987	Alpha-1-acid glycoprotein 1	gi|112877	14	2	EQLGEFYEALDCLR	59
					YVGGQEHFAHLLILR	96
988	Tubulin, beta 2C	gi|23958133	7	2	AVLVDLEPGTMDSVR	39
					GHYTEGAELVDSVLDVVR	171
989	albumin preproprotein	gi|4502027	3	2	YLYEIAR	45
					QEPERNECFLQHK	39
990	unnamed protein product	gi|28590	5	3	LVNEVTEFAK	56
					FKDLGEENFK	58
					HPDYSVVLLLR	52
991	ALB protein	gi|23241675	10	3	FQNALLVR	38
					KVPQVSTPTLVEVSR	81
					VFDEFKPLVEEPQNLIK	100
992	antitrypsin alpha1 mutant	gi|224224	8	2	LQHLENELTHDIITK	112
					VFSNGADLSGVTEEAPLK	106
993	beta globin chain	gi|66473265	33	2	VLGAFSDGLAHLDNLK	66
					FFESFGDLSTPDAVMGNPK	99

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
994	hypothetical protein	gi|51476390	5	2	YICENQDSISSK	55
					VHTECCHGDLLECADDR	97
995	albumin preproprotein	gi|4502027	3	2	YLYEIAR	37
					HPYFYAPELLFFAK	77
996	hypothetical protein	gi|51476390	6	3	LVNEVTEFAK	65
					FKDLGEENFK	69
					RPCFSALEVDETYVPK	39
997	Tubulin, beta 2C	gi|23958133	7	2	INVYYNEATGGK	43
					GHYTEGAELVDSVLDVVR	170
998	Triosephosphate isomerase	gi|999892	17	2	HVFGESDELIGQK	69
					ELASQPDVDGFLVGGASLKPEFVDIINAK	86
999	Triosephosphate isomerase	gi|999892	17	2	HVFGESDELIGQK	92
					ELASQPDVDGFLVGGASLKPEFVDIINAK	92
1000	albumin preproprotein	gi|4502027	8	3	AVMDDFAAFVEK	54
					RPCFSALEVDETYVPK	96
					EFNAETFTFHADICTLSEK	102

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1001	mammary-derived growth inhibitor	gi|1869803	18	3	WDGQETTLVR	72
					LGVEFDETTADDR	101
					LGVEFDETTADDRK	64
1002	hypothetical protein	gi|51476390	4	3	YLYEIAR	42
					LVNEVTEFAK	54
					FKDLGEENFK	65
1003	hypothetical protein	gi|31873324	6	2	FKDIFQEIYDK	57
					SDYLNTFEFMDK	52
1004	Transthyretin precursor	gi|2098257	68	6	GSPAINVAVHVFR	96
					AADDTWEPFASGK	79
					KAADDTWEPFASGK	74
					YTIAALLSPYSYSTTAVVTNPK	153
					ALGISPFHEHAEVVFTANDSGPR	133
					TSESGELHGLTTEEEFVEGIYKVEIDTK	102
1005	Superoxide dismutase [Cu-Zn]	gi|31615344	32	2	GDGPVQGIINFEQK	94
					HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR	93

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1006	albumin preproprotein	gi|4502027	6	2	RPCFSALEVDETYVPK	88
					EFNAETFTFHADICTLSEK	99
1007	ALB protein	gi|23241675	22	6	FQNALLVR	64
					AVMDDFAAFVEK	78
					KVPQVSTPTLVEVSR	104
					RPCFSALEVDETYVPK	79
					VFDEFKPLVEEPQNLIK	108
					EFNAETFTFHADICTLSEK	84
1008	calreticulin precursor variant	gi|62897681	6	2	EQFLDGDGWTSR	110
					FYALSASFEPFSNK	72
1009	antitrypsin alpha1 mutant	gi|224224	11	3	LQHLENELTHDIITK	71
					VFSNGADLSGVTEEAPLK	117
					FNKPFVFLMIEQNTK	55
1010	peroxiredoxin-2 isoform a	gi|32189392	15	3	QITVNDLPVGR	68
					EGGLGPLNIPLLADVTR	138
					KEGGLGPLNIPLLADVTR	166

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1011	TAGLN	gi|49168456	14	2	KYDEELEER	43
					TDMFQTVDLFEGKDMAAVQR	43
1012	Horf6 A Novel Human Peroxidase Enzyme	gi|3318841	29	5	NFDEILR	37
					LPFPIIDDR	73
					LSILYPATTGR	66
					ELAILLGMLDPAEKDEK	82
					PGGLLLGDVAPNFEANTTVGR	169
1013	serine proteinase inhibitor, clade A, member 1	gi|50363217	8	3	DTEEEDFHVDQVTTVK	86
					LYHSEAFTVNFGDTEEAK	98
					LYHSEAFTVNFGDTEEAK	132
1014	Triosephosphate isomerase	gi|999892	25	3	DCGATWVVLGHSER	135
					VPADTEVVCAPPTAYIDFAR	144
					ELASQPDVDGFLVGGASLKPEFVDIINAK	106
1015	albumin preproprotein	gi|4502027	3	2	YLYEIAR	41
					HPYFYAPELLFFAK	99

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1016	TAGLN	gi|49168456	19	4	KYDEELEER	66
					QMEQVAQFLK	39
					TDMFQTVDLFEGK	69
					TDMFQTVDLFEGKDMAAVQR	50
1017	Triosephosphate isomerase	gi|999892	17	2	HVFGESDELIGQK	90
					ELASQPDVDGFLVGGASLKPEFVDIINAK	64
1018	Heat-Shock 70kd Protein 42kd Atpase	gi|6729803	12	6	DAGVIAGLNVLR	99
					VEIIANDQGNR	69
					LVNHFVEEFKR	84
					TTPSYVAFTDTER	128
					ATAGDTHLGGEDFDNR	79
					IINEPTAAAIAYGLDR	63
1019	albumin preproprotein	gi|4502027	8	3	AVMDDFAAFVEK	70
					RPCFSALEVDETYVPK	90
					EFNAETFTFHADICTLSEK	86
1020	albumin preproprotein	gi|4502027	5	2	AVMDDFAAFVEK	54

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EFNAETFTFHADICTLSEK	117
1021	albumin preproprotein	gi|4502027	6	2	RPCFSALEVDETYVPK	111
					EFNAETFTFHADICTLSEK	71
1022	protein disulfide isomerase	gi|860986	15	6	GFPTIYFSPANK	48
					ELSDFISYLQR	80
					FLQDYFDGNLKR	67
					MDATANDVPSPYEVR	72
					TFSHELSDFGLESTAGEIPVVAIR	238
					KTFSHELSDFGLESTAGEIPVVAIR	190
1023	albumin preproprotein	gi|4502027	6	2	RPCFSALEVDETYVPK	114
					EFNAETFTFHADICTLSEK	128
1024	TAGLN	gi|49168456	23	3	KYDEELEER	49
					LVEWIIVQCGPDVGRPDR	45
					TDMFQTVDLFEGKDMAAVQR	61
1025	Protein DJ-1	gi|42543006	32	3	GAEEMETVIPVDVMR	54
					GPGTSFEFALAIVEALNGK	66

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EGPYDVVVLPGGNLGAQNLSESAAVK	149
1026	albumin preproprotein	gi|4502027	8	3	AVMDDFAAFVEK	69
					RPCFSALEVDETYVPK	56
					EFNAETFTFHADICTLSEK	74
1027	TapasinERP57 HETERODIMER	gi|220702506	15	5	ELSDFISYLQR	88
					FLQDYFDGNLKR	47
					DLLIAYYDVDYEK	43
					SDVLELTDDNFESR	47
					KTFSHELSDFGLESTAGEIPVVAIR	117
1028	Apolipoprotein A-I precursor	gi|90108664	22	5	AKPALEDLR	48
					DEPPQSPWDR	57
					THLAPYSDELR	80
					VSFLSALEEYTK	47
					LREQLGPVTQEFWDNLEK	74
1029	aldehyde dehydrogenase 1	gi|2183299	7	3	QAFQIGSPWR	43
					TIPIDGNFFTYTR	72

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					IFVEESIYDEFVR	92
1030	6-phosphogluconolactonase	gi|6912586	17	3	VTLTLPVLNAAR	43
					ELPAAVAPAGPASLAR	112
					LVPFDHAESTYGLYR	84
1031	aldehyde dehydrogenase 1	gi|2183299	10	4	QAFQIGSPWR	60
					TIPIDGNFFTYTR	94
					IFVEESIYDEFVR	92
					ELGEYGFHEYTEVK	42
1032	hypothetical protein	gi|31873302	14	5	YISPDQLADLYK	73
					VVIGMDVAASEFFR	81
					VVIGMDVAASEFFR	60
					AAVPSGASTGIYEALELR	169
					LAMQEFMILPVGAANFR	54
1033	unnamed protein product	gi|16552261	7	2	ISLPLPNFSSLNLR	62
					EMEENFAVEAANYQDTIGR	94
1034	TPM4-ALK fusion oncoprotein type 2	gi|10441386	19	5	LVILEGELER	62

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					IQLVEEELDR	73
					KLVILEGELER	102
					IQALQQQADEAEDR	94
					KIQALQQQADEAEDR	74
1035	albumin preproprotein	gi|4502027	5	2	AVMDDFAAFVEK	68
					EFNAETFTFHADICTLSEK	68
1036	Human Serum Albumin	gi|157830361	21	5	FQNALLVR	51
					AVMDDFAAFVEK	54
					KVPQVSTPTLVEVSR	86
					RPCFSALEVDETYVPK	56
					VFDEFKPLVEEPQNLIK	104
1037	albumin, isoform CRA_n	gi|119626077	35	6	YLYEIAR	48
					LVNEVTEFAK	76
					QEPERNECFLQHK	83
					HPYFYAPELLFFAK	102
					RHPYFYAPELLFFAK	84

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					ALVLIAFAQYLQQCPFEDHVK	119
1038	Transferrin	gi|37747855	8	4	EGYYGYTGAFR	87
					KPVEEYANCHLAR	64
					EDPQTFYYAVAVVK	69
					NLNEKDYELLCLDGTR	102
1039	albumin preproprotein	gi|4502027	4	6	RHPDYSVVLLLR	59
					DVFLGMFLYEYAR	71
					DVFLGMFLYEYAR	66
					RPCFSALEVDETYVPK	80
					VFDEFKPLVEEPQNLIK	104
					EFNAETFTFHADICTLSEK	46
1040	TapasinERP57 HETERODIMER	gi|220702506	12	5	ELSDFISYLQR	62
					FLQDYFDGNLKR	78
					SDVLELTDDNFESR	58
					TFSHELSDFGLESTAGEIPVVAIR	160
					KTFSHELSDFGLESTAGEIPVVAIR	180

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1041	LAP3	gi|48146373	14	5	TLIEFLLR	41
					GVLFASGQNLAR	60
					GSDEPPVFLEIHYK	83
					TFYGLHQDFPSVVLVGLGK	60
					AAGIDEQENWHEGKENIR	85
1042	Human Serum Albumin	gi|157830361	9	2	RHPDYSVVLLLR	39
					VFDEFKPLVEEPQNLIK	63
1043	hypothetical protein	gi|51476390	9	5	YLYEIAR	45
					LVNEVTEFAK	61
					FKDLGEENFK	56
					QEPERNECFLQHK	54
					HPYFYAPELLFFAK	105
1044	Human Serum Albumin	gi|168988718	12	6	YLYEIAR	45
					LVNEVTEFAK	64
					FKDLGEENFK	71
					QEPERNECFLQHK	80

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					HPYFYAPELLFFAK	108
					ALVLIAFAQYLQQCPFEDHVK	120
1045	albumin, isoform CRA_t	gi|119626083	9	5	FQNALLVR	47
					HPDYSVVLLLR	98
					RHPDYSVVLLLR	58
					KVPQVSTPTLVEVSR	64
					VFDEFKPLVEEPQNLIK	105
1046	hypothetical protein	gi|51476390	9	5	YLYEIAR	45
					LVNEVTEFAK	55
					FKDLGEENFK	55
					QEPERNECFLQHK	47
					HPYFYAPELLFFAK	89
1047	albumin, isoform CRA_n	gi|119626077	13	6	YLYEIAR	44
					LVNEVTEFAK	85
					QEPERNECFLQHK	89
					HPYFYAPELLFFAK	101

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					RHPYFYAPELLFFAK	73
					ALVLIAFAQYLQQCPFEDHVK	132
1048	albumin preproprotein	gi|4502027	7	4	HPDYSVVLLLR	63
					DVFLGMFLYEYAR	63
					DVFLGMFLYEYAR	53
					VFDEFKPLVEEPQNLIK	80
1049	albumin, isoform CRA_t	gi|119626083	9	4	FQNALLVR	48
					HPDYSVVLLLR	67
					KVPQVSTPTLVEVSR	67
					VFDEFKPLVEEPQNLIK	114
1050	78 kDa glucose-regulated protein	gi|16507237	9	4	TWNDPSVQQDIK	65
					TFAPEEISAMVLTK	48
					ITPSYVAFTPEGER	76
					VTHAVVTVPAYFNDAQR	72
1051	TSA	gi|1617118	9	2	EGGLGPLNIPLLADVTR	106
					KEGGLGPLNIPLLADVTR	106

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1052	oxygen regulated protein precursor variant	gi|62897071	5	3	AHFNLDESGVLSLDR	59
					LYQPEYQEVSTEEQR	53
					YSHDFNFHINYGDLGFLGPEDLR	48
1053	smooth muscle myosin heavy chain	gi|4417214	4	2	LQQELDDLVVDLDNQR	50
					DVASLSSQLQDTQELLQEETR	65
1054	TAGLN	gi|49168456	4	2	YDEELEER	39
					KYDEELEER	54
1055	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	101
					IFVEESIYDEFVR	107
1056	protein disulfide isomerase-related protein 5	gi|1710248	16	4	TGEAIVDAALSALR	76
					LAAVDATVNQVLASR	39
					LYSSSDDVIELTPSNFNR	53
					ALDLFSDNAPPPELLEIINEDIAK	82
1057	3-oxoacyl-CoA thiolase	gi|22796316	10	2	AEELGLPILGVLR	49
					IAQFLSDIPETVPLSTVNR	71

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1058	unnamed protein product	gi|189054552	4	3	FQNALLVR	44
					VPQVSTPTLVEVSR	39
					KVPQVSTPTLVEVSR	84
1059	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	39
					SYELPDGQVITIGNER	120
1060	ATP5A1 protein	gi|13938339	6	2	EAYPGDVFYLHSR	88
					QGQYSPMAIEEQVAVIYAGVR	73
1061	HSPA2 protein	gi|23271312	9	4	VEIIANDQGNR	51
					TTPSYVAFTDTER	124
					STAGDTHLGGEDFDNR	72
					VHSAVITVPAYFNDSQR	120
1062	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	60
					SYELPDGQVITIGNER	110
1063	Human Muscle Pyruvate Kinase	gi|67464392	9	3	LDIDSPPITAR	49
					FGVEQDVDMVFASFIR	45
					TATESFASDPILYRPVAVALDTK	39

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1064	aldehyde dehydrogenase 1	gi|2183299	7	3	QAFQIGSPWR	49
					TIPIDGNFFTYTR	94
					IFVEESIYDEFVR	115
1065	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	49
					IFVEESIYDEFVR	58
1066	chaperonin containing TCP1, subunit 2 (beta), isoform	gi|119617636	15	4	GATQQILDEAER	44
					QVLLSAAEAAEVILR	87
					VQDDEVGDGTTSVTVLAAELLR	183
					MLPTIIADNAGYDSADLVAQLR	45
1067	lamin A/C isoform 1 precursor	gi|27436946	4	2	SLETENAGLR	48
					NSNLVGAAHEELQQSR	91
1068	heat shock 70kDa protein 8 isoform 1 variant	gi|62897129	7	3	FEELNADLFR	62
					NQTAEKEEFEHQQK	48
					QTQTFTTYSDNQPGVLIQVYEGER	88

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1069	aldehyde dehydrogenase 1A1	gi|21361176	5	2	TIPIDGNFFTYTR	51
					IFVEESIYDEFVR	69
1070	glutathione S-transferase Mu 3	gi|23065552	13	2	LLLEFTDTSYEEK	72
					LTFVDFLTYDILDQNR	153
1071	fructose-bisphosphate aldolase A	gi|4557305	7	2	ADDGRPFPQVIK	40
					FSHEEIAMATVTALR	51
1072	alpha 3 type VI collagen isoform 2 precursor	gi|240255542	3	2	DVVFLLDGSEGVR	51
					IEDGVLQFLVLLVAGR	40
1073	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	40
					SYELPDGQVITIGNER	121
1074	GRP78 precursor	gi|386758	13	6	SDIDEIVLVGGSTR	117
					ITPSYVAFTPEGER	97
					KSDIDEIVLVGGSTR	106
					VTHAVVTVPAYFNDAQR	134
					DNHLLGTFDLTGIPPAPR	165
					IEIESFYEGEDFSETLTR	156

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1075	actin, cytoplasmic 2	gi|4501887	13	3	QEYDESGPSIVHR	94
					SYELPDGQVITIGNER	153
					VAPEEHPVLLTEAPLNPK	71
1076	protein disulfide isomerase	gi|860986	7	2	ELSDFISYLQR	62
					TFSHELSDFGLESTAGEIPVVAIR	88
1077	endoplasmic reticulum protein 29, isoform CRA_b	gi|119618398	9	2	ESYPVFYLFR	71
					ILDQGEDFPASEMTR	37
1078	albumin preproprotein	gi|4502027	6	3	FQNALLVR	53
					DVFLGMFLYEYAR	62
					KVPQVSTPTLVEVSR	45
1079	mutant desmin	gi|71011128	8	3	VAELYEEELR	69
					FASEASGYQDNIAR	79
					FLEQQNAALAAEVNR	147
1080	ACO2	gi|49168620	4	2	SQFTITPGSEQIR	68
					NAVTQEFGPVPDTAR	46

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1081	prepro-alpha2(I) collagen	gi|1418930	2	2	GEAGAAGPAGPAGPR	45
					GETGPSGPVGPAGAVGPR	94
1082	actin, cytoplasmic 2	gi|4501887	8	2	QEYDESGPSIVHR	90
					SYELPDGQVITIGNER	130
1083	mutant desmin	gi|71011128	5	2	VAELYEEELR	54
					FLEQQNAALAAEVNR	79
1084	smooth muscle mysosin heavy chain	gi|36507	1	2	QLHEYETELEDER	50
					LQQELDDLVVDLDNQR	57
1085	filamin-A isoform 2	gi|160420317	2	4	YGGDEIPFSPYR	51
					AFGPGLQGGSAGSPAR	44
					VANPSGNLTETYVQDR	76
					EGPYSISVLYGDEEVPR	67
1086	FLJ00119 protein	gi|18676444	2	2	YGGDEIPFSPYR	38
					EGPYSISVLYGDEEVPR	47
1087	aldehyde dehydrogenase 1	gi|2183299	7	3	QAFQIGSPWR	42
					TIPIDGNFFTYTR	77

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					IFVEESIYDEFVR	90
1088	heat shock protein 27	gi|662841	21	3	LFDQAFGLPR	65
					VSLDVNHFAPDELTVK	43
					LATQSNEITIPVTFESR	92
1089	outer dense fiber protein 2/2	gi|2996006	4	2	LEADEVAAQLER	44
					KEELEEVAHELAETEHENTVLR	143
1090	heat shock cognate 71 kDa protein isoform 1	gi|5729877	8	4	DAGTIAGLNVLR	101
					VEIIANDQGNR	66
					TTPSYVAFTDTER	119
					TVTNAVVTVPAYFNDSQR	120
1091	tubulin beta-2C chain	gi|5174735	6	2	FPGQLNADLR	58
					GHYTEGAELVDSVLDVVR	95
1092	creatine kinase B-type	gi|21536286	16	4	DLFDPIIEDR	60
					VLTPELYAELR	80
					LAVEALSSLDGDLAGR	84

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					TDLNPDNLQGGDDLDPNYVLSSR	139
1093	neuropolypeptide h3	gi|913159	17	2	LYTLVLTDPDAPSR	90
					GNDISSGTVLSDYVGSGPPK	69
1094	protein disulfide isomerase-related protein 5	gi|1710248	7	2	TGEAIVDAALSALR	94
					LYSSSDDVIELTPSNFNR	110
1095	heat shock cognate 71 kDa protein isoform 1	gi|5729877	13	5	FEELNADLFR	51
					TTPSYVAFTDTER	50
					STAGDTHLGGEDFDNR	75
					TVTNAVVTVPAYFNDSQR	41
					QTQTFTTYSDNQPGVLIQVYEGER	77
1096	TapasinERP57 HETERODIMER	gi|220702506	13	5	ELSDFISYLQR	89
					SDVLELTDDNFESR	95
					MDATANDVPSPYEVR	57
					TFSHELSDFGLESTAGEIPVVAIR	193

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					KTFSHELSDFGLESTAGEIPVVAIR	139
1097	smooth muscle myosin heavy chain	gi|4417214	4	2	LQQELDDLVVDLDNQR	97
					DVASLSSQLQDTQELLQEETR	82
1098	TAGLN	gi|49168456	11	2	KYDEELEER	60
					TDMFQTVDLFEGK	39
1099	actin, aortic smooth muscle	gi|4501883	8	2	QEYDEAGPSIVHR	38
					SYELPDGQVITIGNER	132
1100	fructose-bisphosphate aldolase A	gi|4557305	11	3	ADDGRPFPQVIK	44
					LQSIGTENTEENR	43
					FSHEEIAMATVTALR	38
1101	rapamycin-binding protein	gi|182640	9	2	LVIPSELGYGER	48
					KLVIPSELGYGER	44
1102	GRP78 precursor	gi|386758	10	5	SDIDEIVLVGGSTR	91
					KSDIDEIVLVGGSTR	83
					VTHAVVTVPAYFNDAQR	76
					DNHLLGTFDLTGIPPAPR	112

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					IEIESFYEGEDFSETLTR	126
1103	actin, alpha cardiac muscle 1 proprotein	gi|4885049	8	2	QEYDEAGPSIVHR	46
					SYELPDGQVITIGNER	100
1104	filamin A	gi|190192184	3	4	DAPQDFHPDR	59
					LPQLPITNFSR	51
					SAGQGEVLVYVEDPAGHQEEAK	123
					SADFVVEAIGDDVGTLGFSVEGPSQAK	123
1105	heat shock protein gp96 precursor	gi|15010550	4	3	EAESSPFVER	60
					KEAESSPFVER	59
					FQSSHHPTDITSLDQYVER	142
1106	collagen type VI, alpha 3 chain	gi|3127926	3	5	ALILVGLER	39
					SVEDAQDVSLALTQR	100
					VAVVTYNNEVTTEIR	91
					VVIHFTDGADGDLADLHR	79
					GAQGPAGPAGPPGLIGEQGISGPR	98
1107	mutant desmin	gi|71011128	15	5	VAELYEEELR	64

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					FASEASGYQDNIAR	96
					RIESLNEEIAFLK	47
					FLEQQNAALAAEVNR	143
					LQEEIQLKEEAENNLAAFR	111
1108	TapasinERP57 HETERODIMER	gi|220702506	10	3	SDVLELTDDNFESR	80
					MDATANDVPSPYEVR	39
					TFSHELSDFGLESTAGEIPVVAIR	133
1109	ACO2	gi|49168620	6	3	SQFTITPGSEQIR	54
					NAVTQEFGPVPDTAR	78
					WVVIGDENYGEGSSR	43
1110	ACO2	gi|49168620	4	2	SQFTITPGSEQIR	42
					NAVTQEFGPVPDTAR	47
1111	heat shock protein 60	gi|77702086	14	4	AAVEEGIVLGGGCALLR	107
					IQEIIEQLDVTTSEYEK	95
					KPLVIIAEDVDGEALSTLVLNR	162
					LVQDVANNTNEEAGDGTTTATVLAR	150

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1112	protein disulfide isomerase	gi|860986	12	4	ELSDFISYLQR	49
					DLLIAYYDVDYEK	56
					MDATANDVPSPYEVR	53
					TFSHELSDFGLESTAGEIPVVAIR	120
1113	GRP78 precursor	gi|386758	8	3	SDIDEIVLVGGSTR	61
					DNHLLGTFDLTGIPPAPR	98
					IEIESFYEGEDFSETLTR	75
1114	Collagen, type VI, alpha 2	gi|41350923	3	2	DIASTPHELYR	53
					YGGLHFSDQVEVFSPPGSDR	134
1115	lipoamide dehydrogenase precursor old gene name	gi|307137	6	2	NLGLEELGIELDPR	48
					AEVITCDVLLVCIGR	72
1116	glutathione S-transferase Mu 3	gi|23065552	13	2	LLLEFTDTSYEEK	38
					LTFVDFLTYDILDQNR	116
1117	mitochondrial ATP synthase	gi|89574029	21	6	AHGGYSVFAGVGER	116
					VALTGLTVAEYFR	63

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					LVLEVAQHLGESTVR	100
					IMDPNIVGSEHYDVAR	55
					DQEGQDVLLFIDNIFR	147
					AIAELGIYPAVDPLDSTSR	93
1118	actin, gamma-enteric smooth muscle propeptide	gi|4501889	7	2	GYSFVTTAER	43
					SYELPDGQVITIGNER	132
1119	ubiquitin and ribosomal protein S27a precursor	gi|4506713	16	2	EGIPPDQQR	38
					TITLEVEPSDTIENVK	60
1120	3-oxoacyl-CoA thiolase	gi|22796316	10	2	AEELGLPILGVLR	54
					IAQFLSDIPETVPLSTVNR	76
1121	heat shock protein 60	gi|77702086	14	4	AAVEEGIVLGGGCALLR	72
					IQEIIEQLDVTTSEYEK	92
					KPLVIIAEDVDGEALSTLVLNR	165
					LVQDVANNTNEEAGDGTTTATVLAR	94

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1122	alpha 3 type VI collagen isoform 2 precursor	gi|240255542	6	3	IEDGVLQFLVLLVAGR	63
					DILFLFDGSANLVGQFPVVR	54
					GADQAELEEIAFDSSLVFIPAEFR	94
1123	Tubulin, beta 2C	gi|23958133	6	2	FPGQLNADLR	69
					GHYTEGAELVDSVLDVVR	157
1124	endoplasmin precursor	gi|4507677	11	7	GLFDEYGSK	66
					FAFQAEVNR	69
					SILFVPTSAPR	59
					GVVDSDDLPLNVSR	84
					EEEAIQLDGLNASQIR	112
					ESDDPMAYIHFTAEGEVTFK	42
					TDDEVVQREEEAIQLDGLNASQIR	79
1125	Collagen, type I, alpha 1	gi|22328092	3	2	GETGPAGPAGPVGPVGAR	96
					DGEAGAQGPPGPAGPAGER	85
1126	Triosephosphate isomerase	gi|999892	26	3	VVLAYEPVWAIGTGK	55
					VPADTEVVCAPPTAYIDFAR	94

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					ELASQPDVDGFLVGGASLKPEFVDIINAK	100
1127	hypothetical protein	gi|52545928	2	2	DVVFLLDGSEGVR	74
					LVDYLDVGFDTTR	95
1128	transketolase	gi|388891	5	2	LDNLVAILDINR	49
					ILATPPQEDAPSVDIANIR	84
1129	albumin preproprotein	gi|4502027	6	3	FQNALLVR	39
					DVFLGMFLYEYAR	58
					KVPQVSTPTLVEVSR	74
1130	FLJ00119 protein	gi|18676444	4	3	YGGDEIPFSPYR	49
					EGPYSISVLYGDEEVPR	71
					FNEEHIPDSPFVVPVASPSGDAR	48
1131	CKB	gi|49457530	14	3	VLTPELYAELR	72
					GTGGVDTAAVGGVFDVSNADR	38
					TDLNPDNLQGGDDLDPNYVLSSR	129
1132	heterogeneous nuclear ribonucleoprotein A3, isoform	gi|119631468	19	4	GFAFVTFDDHDTVDK	80

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					LFIGGLSFETTDDSLR	58
					IFVGGIKEDTEEYNLR	50
					SSGSPYGGGYGSGGGSGGYGSR	75
1133	TapasinERP57 HETERODIMER	gi|220702506	10	4	LAPEYEAAATR	64
					DGEEAGAYDGPR	79
					DLLIAYYDVDYEK	45
					SDVLELTDDNFESR	81
1134	Glutathione S-transferase P	gi|23200510	23	3	PPYTVVYFPVR	68
					ALPGQLKPFETLLSQNQGGK	87
					YISLIYTNYEAGKDDYVK	49
1135	Annexin A2	gi|73909156	15	5	AYTNFDAER	45
					QDIAFAYQR	52
					GVDEVTIVNILTNR	90
					AEDGSVIDYELIDQDAR	107
					RAEDGSVIDYELIDQDAR	80
1136	collagen, type VI, alpha 3, isoform CRA_f	gi|119591514	1	2	SVEDAQDVSLALTQR	56

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VVIHFTDGADGDLADLHR	46
1137	collagen, type VI, alpha 3, isoform CRA_f	gi|119591514	1	2	SVEDAQDVSLALTQR	110
					VVIHFTDGADGDLADLHR	62
1138	mutant desmin	gi|71011128	17	6	DNLLDDLQR	56
					VAELYEEELR	84
					FASEASGYQDNIAR	136
					RIESLNEEIAFLK	44
					FLEQQNAALAAEVNR	139
					LQEEIQLKEEAENNLAAFR	102
1139	lamin B2, isoform CRA_a	gi|119589784	4	2	ALYESELADAR	56
					DVMQQQLAEYQELLDVK	51
1140	collagen, type VI, alpha 3, isoform CRA_d	gi|119591512	3	4	DVVFLLDGSEGVR	93
					ALNLGYALDYAQR	56
					LVDYLDVGFDTTR	85
					GADQAELEEIAFDSSLVFIPAEFR	161
1141	Transferrin	gi|37747855	4	3	EGYYGYTGAFR	87

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					DQYELLCLDNTR	69
					ADRDQYELLCLDNTR	99
1142	ubiquinol-cytochrome c reductase core I protein	gi|515634	9	2	NALVSHLDGTTPVCEDIGR	55
					YIYDQCPAVAGYGPIEQLPDYNR	91
1143	mutant desmin	gi|71011128	6	2	FASEASGYQDNIAR	37
					FLEQQNAALAAEVNR	85
1144	unnamed protein product	gi|194389904	8	2	VLTPELYAELR	44
					LAVEALSSLDGDLAGR	55
1145	actin, alpha cardiac muscle 1 proprotein	gi|4885049	8	2	QEYDEAGPSIVHR	42
					SYELPDGQVITIGNER	104
1146	Tubulin, beta 2C	gi|23958133	10	3	FPGQLNADLR	89
					AVLVDLEPGTMDSVR	51
					GHYTEGAELVDSVLDVVR	157
1147	heterogeneous nuclear ribonucleoproteins A2/B1	gi|14043072	9	2	GGGGNFGPGPGSNFR	60

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					LFIGGLSFETTEESLR	47
1148	actin, aortic smooth muscle	gi|4501883	12	3	IWHHSFYNELR	57
					SYELPDGQVITIGNER	133
					VAPEEHPTLLTEAPLNPK	37
1149	smooth muscle mysosin heavy chain	gi|36507	3	3	QLHEYETELEDER	38
					LQQELDDLVVDLDNQR	81
					DVASLSSQLQDTQELLQEETR	64
1150	calreticulin precursor variant	gi|62897681	9	2	IKDPDASKPEDWDER	65
					CKDDEFTHLYTLIVRPDNTYEVK	55
1151	Cathepsin B precursor	gi|157833437	9	2	HYGYNSYSVSNSEK	61
					GQDHCGIESEVVAGIPR	117
1152	PGK1	gi|48145549	8	2	LGDVYVNDAFGTAHR	65
					ALESPERPFLAILGGAK	52
1153	aldehyde dehydrogenase 1A1	gi|21361176	8	3	EEIFGPVQQIMK	37
					TIPIDGNFFTYTR	76
					IFVEESIYDEFVR	93

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1154	enolase 1 variant	gi|62896593	15	5	YISPDQLADLYK	60
					VVIGMDVAASEFFR	58
					VVIGMDVAASEFFR	58
					AAVPSGASTGIYEALELR	134
					FTASAGIQVVGDDLTVTNPK	45
1155	hypothetical protein	gi|31873302	10	3	YISPDQLADLYK	38
					VVIGMDVAASEFFR	43
					AAVPSGASTGIYEALELR	114
1156	vinculin	gi|7669550	4	2	GILSGTSDLLLTFDEAEVR	53
					LLAVAATAPPDAPNREEVFDER	58
1157	MTHSP75	gi|292059	6	3	VQQTVQDLFGR	45
					AQFEGIVTDLIR	56
					NAVITVPAYFNDSQR	44
1158	heat shock protein 70 testis variant	gi|3461866	4	2	DAGVIAGLNVLR	39
					TTPSYVAFTDTER	120
1159	ALB protein	gi|23241675	17	5	FQNALLVR	43

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					AVMDDFAAFVEK	47
					KVPQVSTPTLVEVSR	56
					RPCFSALEVDETYVPK	45
					VFDEFKPLVEEPQNLIK	79
1160	unnamed protein product	gi|28590	9	4	FQNALLVR	43
					AVMDDFAAFVEK	47
					RPCFSALEVDETYVPK	45
					VFDEFKPLVEEPQNLIK	79
1161	KH-type splicing regulatory protein	gi|154355000	6	2	AINQQTGAFVEISR	50
					GGGGPGGGGPGGGSAGGPSQPPGGGGPGIR	37
1162	TapasinERP57 HETERODIMER	gi|220702506	15	4	SDVLELTDDNFESR	81
					MDATANDVPSPYEVR	49
					DASIVGFFDDSFSEAHSEFLK	114
					TFSHELSDFGLESTAGEIPVVAIR	149
1163	aldehyde dehydrogenase 1A1	gi|21361176	10	4	EEIFGPVQQIMK	46
					TIPIDGNFFTYTR	74

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					IFVEESIYDEFVR	93
					ELGEYGFHEYTEVK	55
1164	3-phosphoglycerate dehydrogenase	gi|5771523	5	2	DLPLLLFR	51
					EELIAELQDCEGLIVR	83
1165	Hemoglobin subunit beta	gi|3660145	41	4	VNVDEVGGEALGR	47
					EFTPPVQAAYQK	46
					VLGAFSDGLAHLDNLK	62
					FFESFGDLSTPDAVMGNPK	75
1166	albumin preproprotein	gi|4502027	5	2	AVMDDFAAFVEK	60
					RPCFSALEVDETYVPK	63
1167	ALB protein	gi|23241675	10	3	FQNALLVR	46
					KVPQVSTPTLVEVSR	84
					VFDEFKPLVEEPQNLIK	42
1168	protein disulfide isomerase	gi|860986	8	2	MDATANDVPSPYEVR	42
					KTFSHELSDFGLESTAGEIPVVAIR	103
1169	fructose-bisphosphate aldolase A	gi|4557305	7	2	ADDGRPFPQVIK	47

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					FSHEEIAMATVTALR	50
1170	Chain A, Uncleaved Alpha-1-Antitrypsin	gi|157830080	9	2	LQHLENELTHDIITK	110
					GTEAAGAMFLEAIPMSIPPEVK	51
1171	ALB protein	gi|23241675	8	2	KVPQVSTPTLVEVSR	66
					VFDEFKPLVEEPQNLIK	55
1172	Similar to Elongation factor 2b	gi|19353009	5	2	YEWDVAEAR	51
					AYLPVNESFGFTADLR	111
1173	ALB protein	gi|23241675	17	5	FQNALLVR	45
					AVMDDFAAFVEK	59
					KVPQVSTPTLVEVSR	107
					RPCFSALEVDETYVPK	50
					VFDEFKPLVEEPQNLIK	107
1174	fructose-bisphosphate aldolase A	gi|4557305	10	2	FSHEEIAMATVTALR	66
					IGEHTPSALAIMENANVLAR	47
1175	actin, alpha cardiac muscle 1 proprotein	gi|4885049	8	2	QEYDEAGPSIVHR	44
					SYELPDGQVITIGNER	127

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1176	unnamed protein product	gi|194388088	10	4	LLQDFFDGR	53
					FEELCSDLFR	55
					AQIHDLVLVGGSTR	128
					QTQIFTTYSDNQPGVLIQVYEGER	114
1177	heat shock cognate 71 kDa protein isoform 1	gi|5729877	7	3	FEELNADLFR	72
					SQIHDIVLVGGSTR	60
					QTQTFTTYSDNQPGVLIQVYEGER	140
1178	unnamed protein product	gi|189054552	7	3	FQNALLVR	66
					KVPQVSTPTLVEVSR	80
					VFDEFKPLVEEPQNLIK	78
1179	Human Muscle Pyruvate Kinase	gi|67464392	10	3	LDIDSPPITAR	50
					GADFLVTEVENGGSLGSK	45
					TATESFASDPILYRPVAVALDTK	68
1180	albumin preproprotein	gi|4502027	13	6	FQNALLVR	54
					RHPDYSVVLLLR	55

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					DVFLGMFLYEYAR	54
					KVPQVSTPTLVEVSR	85
					VFDEFKPLVEEPQNLIK	104
					QNCELFEQLGEYKFQNALLVR	58
1181	actin, cytoplasmic 2	gi|4501887	13	3	QEYDESGPSIVHR	67
					SYELPDGQVITIGNER	117
					VAPEEHPVLLTEAPLNPK	48
1182	mutant desmin	gi|71011040	5	2	EEAENNLAAFR	55
					FASEASGYQDNIAR	96
1183	actin, alpha cardiac muscle 1 proprotein	gi|4885049	8	2	QEYDEAGPSIVHR	74
					SYELPDGQVITIGNER	127
1184	actin, cytoplasmic 2	gi|4501887	13	3	QEYDESGPSIVHR	99
					SYELPDGQVITIGNER	109
					VAPEEHPVLLTEAPLNPK	67
1185	mutant desmin	gi|71011128	15	6	VAELYEEELR	70
					EEAENNLAAFR	62

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					FASEASGYQDNIAR	129
					RIESLNEEIAFLK	50
					FLEQQNAALAAEVNR	113
					LQEEIQLKEEAENNLAAFR	117
1186	albumin preproprotein	gi|4502027	9	4	CCTESLVNR	48
					AVMDDFAAFVEK	62
					RPCFSALEVDETYVPK	140
					EFNAETFTFHADICTLSEK	52
1187	peptidylprolyl isomerase A	gi|10863927	28	3	IIPGFMCQGGDFTR	40
					SIYGEKFEDENFILK	54
					VNPTVFFDIAVDGEPLGR	139
1188	peroxiredoxin-2	gi|32189392	15	3	QITVNDLPVGR	46
					EGGLGPLNIPLLADVTR	124
					KEGGLGPLNIPLLADVTR	112
1189	albumin preproprotein	gi|4502027	8	3	AVMDDFAAFVEK	76
					RPCFSALEVDETYVPK	129

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					EFNAETFTFHADICTLSEK	100
1190	Annexin A2	gi|73909156	23	6	AYTNFDAER	55
					QDIAFAYQR	61
					TNQELQEINR	42
					GVDEVTIVNILTNR	99
					AEDGSVIDYELIDQDAR	121
					RAEDGSVIDYELIDQDAR	71
1191	ATP5A1 protein	gi|13938339	10	3	EAYPGDVFYLHSR	75
					EVAAFAQFGSDLDAATQQLLSR	73
					FENAFLSHVVSQHQALLGTIR	82
1192	ALB protein	gi|23241675	17	5	FQNALLVR	61
					AVMDDFAAFVEK	39
					KVPQVSTPTLVEVSR	122
					RPCFSALEVDETYVPK	53
					VFDEFKPLVEEPQNLIK	44
1193	Unknown	gi|15679996	20	3	FQNALLVR	46

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					KVPQVSTPTLVEVSR	80
					RPCFSALEVDETYVPK	44
1194	hypothetical protein	gi|51476390	4	3	YLYEIAR	45
					LVNEVTEFAK	56
					FKDLGEENFK	66
1195	hypothetical protein	gi|31873324	6	2	FKDIFQEIYDK	44
					SDYLNTFEFMDK	52
1196	hypothetical protein	gi|51476390	4	2	YLYEIAR	38
					RHPYFYAPELLFFAK	44
1197	Human Serum Albumin	gi|157830361	10	4	RHPDYSVVLLLR	51
					KVPQVSTPTLVEVSR	47
					RPCFSALEVDETYVPK	73
					VFDEFKPLVEEPQNLIK	95
1198	albumin, isoform CRA_t	gi|119626083	6	2	KVPQVSTPTLVEVSR	68
					VFDEFKPLVEEPQNLIK	66
1199	galectin-1	gi|4504981	28	3	DGGAWGTEQR	44

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					DSNNLCLHFNPR	85
					LNLEAINYMAADGDFK	68
1200	lamin A/C isoform 1 precursor	gi|27436946	5	3	NIYSEELR	42
					SLETENAGLR	40
					NSNLVGAAHEELQQSR	105
1201	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	15	3	VPTANVSVVDLTCR	118
					LISWYDNEFGYSNR	78
					VIISAPSADAPMFVMGVNHEK	39
1202	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	37
					LISWYDNEFGYSNR	61
1203	Glyceraldehyde-3-phosphate dehydrogenase	gi|67464043	8	2	VPTANVSVVDLTCR	105
					LISWYDNEFGYSNR	97
1204	protein disulfide isomerase	gi|860986	13	4	FLQDYFDGNLK	37

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					MDATANDVPSPYEVR	61
					VVVAENFDEIVNNENK	44
					TFSHELSDFGLESTAGEIPVVAIR	182
1205	heat shock protein 27	gi|662841	21	3	LFDQAFGLPR	65
					VSLDVNHFAPDELTVK	57
					LATQSNEITIPVTFESR	61
1206	dimethylarginine dimethylaminohydrolase 2	gi|123279699	25	3	DFAVSTVPVSGPSHLR	82
					GVPESLASGEGAGAGLPALDLAK	96
					IVEIGDENATLDGTDVLFTGR	140
1207	6-phosphogluconolactonase	gi|6912586	18	3	ELPAAVAPAGPASLAR	82
					IVAPISDSPKPPPQR	40
					LVPFDHAESTYGLYR	90
1208	endoplasmic reticulum protein 29	gi|119618398	10	2	ESYPVFYLFR	67
					ILDQGEDFPASEMTR	39
1209	unnamed protein product	gi|194384036	16	3	ALESPERPFLAILGGAK	58
					VLNNMEIGTSLFDEEGAK	56

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					ITLPVDFVTADKFDENAK	79
1210	Annexin A2	gi|73909156	12	4	QDIAFAYQR	44
					GVDEVTIVNILTNR	80
					AEDGSVIDYELIDQDAR	83
					RAEDGSVIDYELIDQDAR	72
1211	Superoxide dismutase [Cu-Zn]	gi|31615344	25	2	GDGPVQGIINFEQK	83
					DGVADVSIEDSVISLSGDHCIIGR	126
1212	albumin preproprotein	gi|4502027	8	3	AVMDDFAAFVEK	56
					RPCFSALEVDETYVPK	83
					EFNAETFTFHADICTLSEK	64
1213	Human Serum Albumin	gi|157830361	11	5	FQNALLVR	46
					HPDYSVVLLLR	70
					KVPQVSTPTLVEVSR	47
					RPCFSALEVDETYVPK	73
					VFDEFKPLVEEPQNLIK	85
1214	peptidylprolyl isomerase A	gi|10863927	20	2	SIYGEKFEDENFILK	59

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VNPTVFFDIAVDGEPLGR	128
1215	mutant desmin	gi|71011128	18	6	VELQELNDR	46
					VAELYEEELR	60
					EEAENNLAAFR	71
					FASEASGYQDNIAR	101
					FLEQQNAALAAEVNR	153
					TPSSYGAGELLDFSLADAVNQEFLTTR	136
1216	Tubulin, beta 2C	gi|23958133	12	4	FPGQLNADLR	54
					INVYYNEATGGK	38
					AVLVDLEPGTMDSVR	47
					GHYTEGAELVDSVLDVVR	118
1217	unnamed protein product	gi|35655	12	4	YKPESEELTAER	88
					VDATEESDLAQQYGVR	103
					ILFIFIDSDHTDNQR	94
					HNQLPLVIEFTEQTAPK	66
1218	mutant desmin	gi|71011128	24	7	VAELYEEELR	72

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					FASEASGYQDNIAR	123
					RIESLNEEIAFLK	48
					INLPIQTYSALNFR	92
					FLEQQNAALAAEVNR	132
					LQEEIQLKEEAENNLAAFR	142
					TPSSYGAGELLDFSLADAVNQEFLTTR	126
1219	beta-subunit (AA 1-312)	gi|28931	9	3	AHGGYSVFAGVGER	53
					DQEGQDVLLFIDNIFR	131
					AIAELGIYPAVDPLDSTSR	64
1220	ALB protein	gi|23241675	10	3	FQNALLVR	37
					KVPQVSTPTLVEVSR	48
					VFDEFKPLVEEPQNLIK	82
1221	albumin, isoform CRA_t	gi|119626083	7	3	FQNALLVR	43
					HPDYSVVLLLR	77
					VFDEFKPLVEEPQNLIK	65
1222	Apolipoprotein A-I precursor	gi|90108664	21	5	AKPALEDLR	44

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					DEPPQSPWDR	64
					THLAPYSDELR	76
					VSFLSALEEYTK	49
					DYVSQFEGSALGK	49
1223	albumin, isoform CRA_t	gi|119626083	8	4	HPDYSVVLLLR	45
					RHPDYSVVLLLR	54
					KVPQVSTPTLVEVSR	72
					VFDEFKPLVEEPQNLIK	95
1224	albumin, isoform CRA_t	gi|119626083	7	3	FQNALLVR	51
					KVPQVSTPTLVEVSR	76
					VFDEFKPLVEEPQNLIK	85
1225	actin, cytoplasmic 2	gi|4501887	13	3	QEYDESGPSIVHR	86
					SYELPDGQVITIGNER	130
					VAPEEHPVLLTEAPLNPK	77
1226	Splicing factor proline/glutamine-rich	gi|29881667	4	2	FGQGGAGPVGGQGPR	90
					FAQHGTFEYEYSQR	63

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1227	Human Serum Albumin	gi|157830361	11	6	FQNALLVR	48
					HPDYSVVLLLR	79
					RHPDYSVVLLLR	55
					KVPQVSTPTLVEVSR	84
					RPCFSALEVDETYVPK	70
					VFDEFKPLVEEPQNLIK	54
1228	Human Serum Albumin	gi|157830361	11	6	FQNALLVR	38
					HPDYSVVLLLR	37
					VPQVSTPTLVEVSR	42
					KVPQVSTPTLVEVSR	70
					RPCFSALEVDETYVPK	38
					VFDEFKPLVEEPQNLIK	74
1229	lipoamide dehydrogenase precursor old gene name	gi|307137	6	2	VCHAHPTLSEAFR	65
					AEVITCDVLLVCIGR	82
1230	LAP3	gi|48146373	4	2	TLIEFLLR	48

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					GVLFASGQNLAR	65
1231	LAP3	gi|48146373	7	3	TLIEFLLR	64
					GVLFASGQNLAR	90
					LILADALCYAHTFNPK	88
1232	aconitase precursor	gi|3600098	9	4	SQFTITPGSEQIR	91
					FKLEAPDADELPR	118
					NAVTQEFGPVPDTAR	93
					WVVIGDENYGEGSSR	74
1233	aconitase precursor	gi|3600098	11	5	EGWPLDIR	60
					SQFTITPGSEQIR	88
					FKLEAPDADELPR	101
					NAVTQEFGPVPDTAR	117
					WVVIGDENYGEGSSR	129
1234	outer dense fiber protein 2/2	gi|2996006	7	5	NIDLTAIISDLR	60
					KNIDLTAIISDLR	68
					TRLEADEVAAQLER	89

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					LAECQDQLQGYER	74
					KEELEEVAHELAETEHENTVLR	208
1235	oxygen regulated protein precursor variant	gi|62897071	6	4	AHFNLDESGVLSLDR	106
					LYQPEYQEVSTEEQR	90
					LYQPEYQEVSTEEQREEISGK	80
					YSHDFNFHINYGDLGFLGPEDLR	86
1236	mitochondrial ATP synthase	gi|89574029	17	5	AHGGYSVFAGVGER	97
					VALTGLTVAEYFR	46
					LVLEVAQHLGESTVR	94
					DQEGQDVLLFIDNIFR	85
					AIAELGIYPAVDPLDSTSR	102
1237	calreticulin precursor variant	gi|62897681	8	2	KVHVIFNYK	54
					CKDDEFTHLYTLIVRPDNTYEVK	85
1238	actin, cytoplasmic 2	gi|4501887	15	4	AGFAGDDAPR	51
					QEYDESGPSIVHR	100
					SYELPDGQVITIGNER	135

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					VAPEEHPVLLTEAPLNPK	95
1239	calreticulin precursor variant	gi|62897681	8	2	KVHVIFNYK	53
					CKDDEFTHLYTLIVRPDNTYEVK	111
1240	protein disulfide isomerase-related protein 5	gi|1710248	16	4	TGEAIVDAALSALR	88
					LAAVDATVNQVLASR	62
					LYSSSDDVIELTPSNFNR	128
					ALDLFSDNAPPPELLEIINEDIAK	56
1241	outer dense fiber protein 2/2	gi|2996006	5	4	NIDLTAIISDLR	78
					KNIDLTAIISDLR	88
					TRLEADEVAAQLER	51
					LAECQDQLQGYER	81
1242	hypothetical protein	gi|31873302	9	2	AAVPSGASTGIYEALELR	131
					AGYTDKVVIGMDVAASEFFR	63
1243	Aldehyde dehydrogenase, mitochondrial precursor	gi|6137677	4	2	TIEEVVGR	46

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					TIPIDGDFFSYTR	98
1244	endoplasmin precursor	gi|4507677	5	3	FAFQAEVNR	42
					SILFVPTSAPR	47
					TDDEVVQREEEAIQLDGLNASQIR	70
1245	actin, aortic smooth muscle	gi|4501883	16	4	GYSFVTTAER	47
					QEYDEAGPSIVHR	101
					SYELPDGQVITIGNER	153
					DLYANNVLSGGTTMYPGIADR	50
1246	malate dehydrogenase 1	gi|119620368	11	2	FVEGLPINDFSR	84
					NVIIWGNHSSTQYPDVNHAK	82
1247	Aldehyde Reductase	gi|157834561	14	3	DAGHPLYPFNDPY	81
					GLEVTAYSPLGSSDR	68
					ILQNIKVFDFTFSPEEMK	48
1248	PGK1	gi|48145549	23	5	LGDVYVNDAFGTAHR	72
					ALESPERPFLAILGGAK	62
					ITLPVDFVTADKFDENAK	71

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					QIVWNGPVGVFEWEAFAR	62
					DCVGPEVEKACANPAAGSVILLENLR	63
1249	pyruvate dehydrogenase E1-beta subunit	gi|189762	11	2	IMEGPAFNFLDAPAVR	72
					TNHLVTVEGGWPQFGVGAEICAR	90
1250	calmodulin	gi|825635	46	4	DTDSEEEIREAFR	73
					VFDKDGNGYISAAELR	135
					EAFSLFDKDGDGTITTK	143
					EADIDGDGQVNYEEFVQMMTAK	97
1251	actin, alpha cardiac muscle 1 proprotein	gi|4885049	15	4	AVFPSIVGRPR	52
					QEYDEAGPSIVHR	101
					SYELPDGQVITIGNER	130
					VAPEEHPTLLTEAPLNPK	79
1252	MYL6 protein	gi|113812151	33	4	EAFQLFDR	47
					NKDQGTYEDYVEGLR	77
					MTEEEVEMLVAGHEDSNGCINYEELVR	64
					MTEEEVEMLVAGHEDSNGCINYEELVR	67

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
1253	hypothetical protein	gi|11276938	6	3	FYPEDVAEELIQDITQK	77
					VTTMDAELEFAIQPNTTGK	42
					AKFYPEDVAEELIQDITQK	51
1254	Tubulin, beta 2C	gi|23958133	7	3	INVYYNEATGGK	46
					GHYTEGAELVDSVLDVVR	139
					GHYTEGAELVDSVLDVVRK	44
1255	tropomyosin 2 (beta) isoform 2 variant	gi|62898077	14	4	LVILEGELER	41
					IQLVEEELDR	80
					KLVILEGELER	86
					EENVEIHQTLDQTLLELNNL	164
1256	chaperonin containing TCP1	gi|119617636	20	5	QVLLSAAEAAEVILR	84
					LIHFSGVALGEACTIVLR	40
					LALVTGGEIASTFDHPELVK	76
					VQDDEVGDGTTSVTVLAAELLR	163
					MLPTIIADNAGYDSADLVAQLR	93
1257	actin, alpha skeletal muscle	gi|4501881	6	2	AGFAGDDAPR	41

No.	Protein description	NCBI accession no.	Sequence coverage%	Matched peptide number	Peptide sequence	Ion score
					AVFPSIVGRPR	51
1258	actin, aortic smooth muscle	gi|4501883	8	2	QEYDEAGPSIVHR	86
					SYELPDGQVITIGNER	132
1259	heat shock cognate 71 kDa protein isoform 1	gi|5729877	7	2	SINPDEAVAYGAAVQAAILSGDK	115
					QTQTFTTYSDNQPGVLIQVYEGER	155
1260	unnamed protein product	gi|37403	14	5	IQLVEEELDR	39
					KLVIIEGDLER	44
					IQVLQQQADDAEER	56
					IQLVEEELDRAQER	47
					KIQVLQQQADDAEER	75

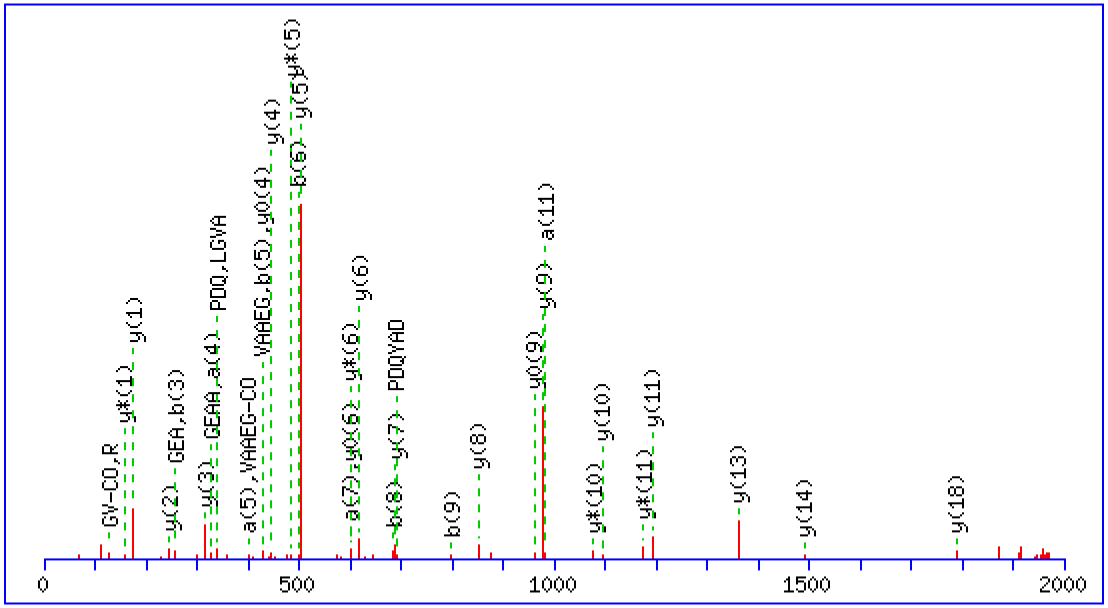
Part III: The observed precursor mass , charge and the labeled MS/MS spectrum of the 32 single-peptide identified proteins.

1261

MS/MS Fragmentation of SLGVAAEGLPDQYADGEAAR

Found in gi|55669632, Chain A, Crystal Structure Of Human Glycine N-Methyltransferase, (1990.0756,1+)

Ions Score: 135



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		70.0287	**S**						**20**
2	86.0964	173.1285		155.1179	201.1234		183.1128	**L**	1844.8409	1843.8457	1902.9192	1885.8927	1884.9086	**19**
3	30.0338	230.1499		212.1394	**258.1448**		240.1343	**G**			**1789.8351**	1772.8086	1771.8246	**18**
4	72.0808	**329.2183**		311.2078	357.2132		339.2027	**V**	1688.751	1701.771	1732.813	1715.787	1714.803	**17**

									1	5	7	1	1	
5	44.0495	**400.2554**		382.2449	**428.2504**		410.2398	**A**	1617.7140		1633.7453	1616.7187	1615.7347	**16**
6	44.0495	471.2926		453.2820	**499.2875**		481.2769	**A**	1546.6768		1562.7081	1545.6816	1544.6976	**15**
7	102.0550	**600.3352**		582.3246	628.3301		610.3195	**E**	1417.6343	1416.6390	**1491.6710**	1474.6445	1473.6605	**14**
8	30.0338	657.3566		639.3461	**685.3515**		667.3410	**G**			**1362.6284**	1345.6019	1344.6179	**13**
9	86.0964	770.4407		752.4301	**798.4356**		780.4250	**L**	1247.5287	1246.5335	1305.6070	1288.5804	1287.5964	**12**
10	70.0651	867.4934		849.4829	895.4884		877.4778	**P**	1150.4760	1149.4807	**1192.5229**	**1175.4964**	1174.5123	**11**
11	88.0393	**982.5204**		964.5098	1010.5153		992.5047	**D**	1035.4490	1034.4538	**1095.4701**	**1078.4436**	1077.4596	**10**
12	101.0709	1110.5790	1093.5524	1092.5684	1138.5739	1121.5473	1120.5633	**Q**	907.3904	906.3952	**980.4432**	963.4167	**962.4326**	**9**
13	136.0757	1273.6423	1256.6157	1255.6317	1301.6372	1284.6107	1283.6266	**Y**	744.3271		**852.3846**	835.3581	834.3741	**8**
14	44.0495	1344.6794	1327.6529	1326.6688	1372.6743	1355.6478	1354.6638	**A**	673.2900		**689.3213**	672.2947	671.3107	**7**
15	88.0393	1459.7064	1442.6798	1441.6958	1487.7013	1470.6747	1469.6907	**D**	558.2631	557.2678	**618.2842**	**601.2576**	**600.2736**	**6**
16	30.0338	1516.7278	1499.7013	1498.7173	1544.7227	1527.6962	1526.7122	**G**			**503.2572**	**486.2307**	485.2467	**5**
17	102.0550	1645.7704	1628.7439	1627.7598	1673.7653	1656.7388	1655.7548	**E**	372.1990	371.2037	**446.2358**	429.2092	**428.2252**	**4**

18	44.0495	1716.8075	1699.7810	1698.7970	1744.8024	1727.7759	1726.7919	**A**	301.1619		**317.1932**	300.1666		**3**
19	44.0495	1787.8446	1770.8181	1769.8341	1815.8396	1798.8130	1797.8290	**A**	230.1248		**246.1561**	229.1295		**2**
20	**129.1135**							**R**	74.0237	73.0284	**175.1190**	**158.0924**		**1**

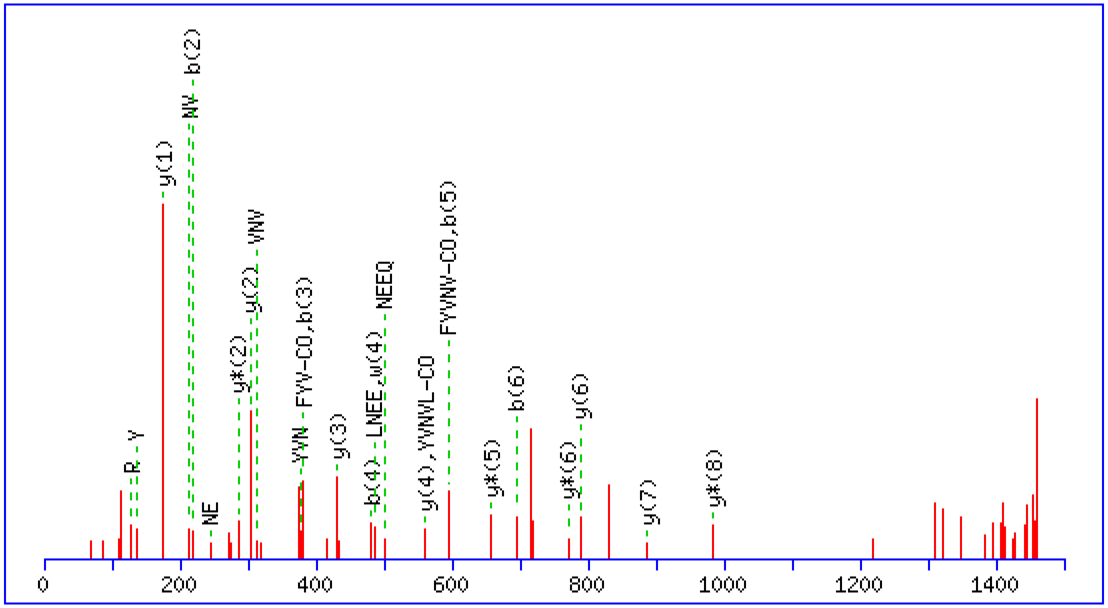
1262

MS/MS Fragmentation of AFYVNVLNEEQR

Found in gi|7245756, Chain A, Human Erythrocyte Catalase,

(1481.7946,1+)

Ions Score: 40



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	y	y*	y^0	#

1	44.0495	44.0495			72.0444			**A**						**12**
2	120.0808	191.1179			**219.1128**			**F**	1318.6386		1410.7012	1393.6747	1392.6906	**11**
3	**136.0757**	354.1812			**382.1761**			**Y**	1155.5753		1263.6328	1246.6062	1245.6222	**10**
4	72.0808	453.2496			**481.2445**			**V**	1056.5069	1069.5273	1100.5695	1083.5429	1082.5589	**9**
5	87.0553	567.2926	550.2660		**595.2875**	578.2609		**N**	942.4639	941.4687	1001.5010	**984.4745**	983.4905	**8**
6	72.0808	666.3610	649.3344		**694.3559**	677.3293		**V**	843.3955	856.4159	**887.4581**	870.4316	869.4476	**7**
7	86.0964	779.4450	762.4185		807.4400	790.4134		**L**	730.3115	729.3162	**788.3897**	**771.3632**	770.3791	**6**
8	87.0553	893.4880	876.4614		921.4829	904.4563		**N**	616.2685	615.2733	675.3056	**658.2791**	657.2951	**5**
9	102.0550	1022.5306	1005.5040	1004.5200	1050.5255	1033.4989	1032.5149	**E**	487.2259	**486.2307**	**561.2627**	544.2362	543.2522	**4**
10	102.0550	1151.5732	1134.5466	1133.5626	1179.5681	1162.5415	1161.5575	**E**	358.1833	357.1881	**432.2201**	415.1936	414.2096	**3**
11	101.0709	1279.6317	1262.6052	1261.6212	1307.6266	1290.6001	1289.6161	**Q**	230.1248	229.1295	**303.1775**	**286.1510**		**2**
12	**129.1135**							**R**	74.0237	73.0284	**175.1190**	158.0924		**1**

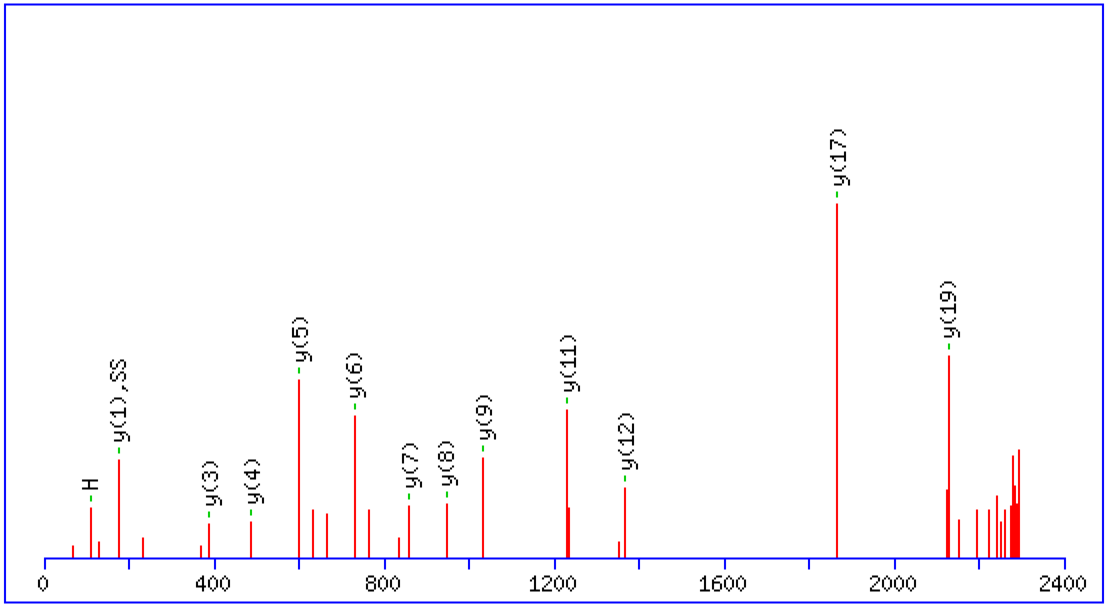
1263

MS/MS Fragmentation of ADFDNTVAIHPTSSEELVTLR

Found in gi|157830846, Chain A, Human Glutathione Reductase,

(2315.2935,1+)

Ions Score: 113



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	44.0495	44.0495			72.0444			**A**							**21**
2	88.0393	159.0764		141.0659	187.0713		169.0608	**D**	2184.0931	2183.0979		2244.1143	2227.0877	2226.1037	**20**
3	120.0808	306.1448		288.1343	334.1397		316.1292	**F**	2037.0247			**2129.0873**	2112.0608	2111.0768	**19**
4	88.0393	421.1718		403.1612	449.1667		431.1561	**D**	1921.9978	1921.0025		1982.0189	1964.9924	1964.0083	**18**
5	87.0553	535.2147	518.1882	517.2041	563.2096	546.1831	545.1991	**N**	1807.9549	1806.9596		**1866.9920**	1849.9654	1848.9814	**17**
6	74.0600	636.2624	619.2358	618.2518	664.2573	647.2307	646.2467	**T**	1706.9072	1719.9276	1721.9068	1752.9490	1735.9225	1734.9385	**16**

7	72.0808	735.3308	718.3042	717.3202	763.3257	746.2992	745.3151	**V**	1607.8388	1620.8592		1651.9014	1634.8748	1633.8908	**15**
8	44.0495	806.3679	789.3414	788.3573	834.3628	817.3363	816.3523	**A**	1536.8016			1552.8329	1535.8064	1534.8224	**14**
9	86.0964	919.4520	902.4254	901.4414	947.4469	930.4203	929.4363	**I**	1423.7176	1436.7380	1450.7536	1481.7958	1464.7693	1463.7853	**13**
10	**110.0713**	1056.5109	1039.4843	1038.5003	1084.5058	1067.4793	1066.4952	**H**	1286.6587			**1368.7118**	1351.6852	1350.7012	**12**
11	70.0651	1153.5636	1136.5371	1135.5531	1181.5586	1164.5320	1163.5480	**P**	1189.6059	1188.6107		**1231.6529**	1214.6263	1213.6423	**11**
12	74.0600	1254.6113	1237.5848	1236.6008	1282.6062	1265.5797	1264.5957	**T**	1088.5582	1101.5786	1103.5579	1134.6001	1117.5735	1116.5895	**10**
13	60.0444	1341.6434	1324.6168	1323.6328	1369.6383	1352.6117	1351.6277	**S**	1001.5262	1000.5310		**1033.5524**	1016.5259	1015.5419	**9**
14	60.0444	1428.6754	1411.6488	1410.6648	1456.6703	1439.6438	1438.6597	**S**	914.4942	913.4989		**946.5204**	929.4938	928.5098	**8**
15	102.0550	1557.7180	1540.6914	1539.7074	1585.7129	1568.6863	1567.7023	**E**	785.4516	784.4563		**859.4884**	842.4618	841.4778	**7**
16	102.0550	1686.7606	1669.7340	1668.7500	1714.7555	1697.7289	1696.7449	**E**	656.4090	655.4137		**730.4458**	713.4192	712.4352	**6**
17	86.0964	1799.8446	1782.8181	1781.8341	1827.8395	1810.8130	1809.8290	**L**	543.3249	542.3297		**601.4032**	584.3766	583.3926	**5**
18	72.0808	1898.9130	1881.8865	1880.9025	1926.9080	1909.8814	1908.8974	**V**	444.2565	457.2769		**488.3191**	471.2926	470.3085	**4**
19	74.0600	1999.9607	1982.9342	1981.9502	2027.9556	2010.9291	2009.9451	**T**	343.2088	356.2292	358.2085	**389.2507**	372.2241	371.2401	**3**

20	86.0964	2113.0448	2096.0182	2095.0342	2141.0397	2124.0132	2123.0291	**L**	230.1248	229.1295		288.2030	271.1765		**2**
21	129.1135							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

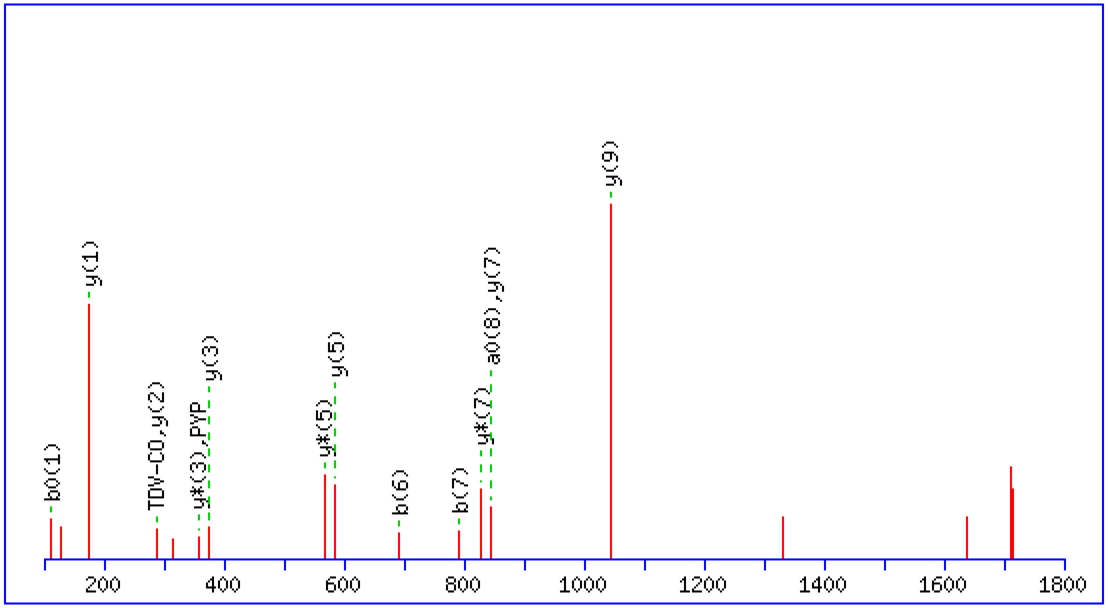
1264

MS/MS Fragmentation of EFSITDVVPYPISLR

Found in gi|4579909, apg-2,

(1735.9844,1+)

Ions Score: 41



#	**Immon.**	**a**	**a^0**	**b**	**b^0**	**Seq.**	**v**	**w**	**w'**	**y**	**y***	**y^0**	**#**
1	102.0550	102.0550	84.0444	130.0499	**112.0393**	**E**							**15**
2	120.0808	249.1234	231.1128	277.1183	259.1077	**F**	1514.8213			1606.8839	1589.8574	1588.8734	**14**
3	60.0444	336.1554	318.1448	364.1503	346.1397	**S**	1427.7893	1426.7940		1459.8155	1442.7890	1441.8049	**13**
4	86.0964	449.2395	431.2289	477.2344	459.2238	**I**	1314.7052	1327.7256	1341.7413	1372.7835	1355.7569	1354.7729	**12**
5	74.0600	550.2871	532.2766	578.2821	560.2715	**T**	1213.6575	1226.6780	1228.6572	1259.6994	1242.6729	1241.6888	**11**
6	88.0393	665.3141	647.3035	**693.3090**	675.2984	**D**	1098.6306	1097.6354		1158.6517	1141.6252	1140.6412	**10**
7	72.0808	764.3825	746.3719	**792.3774**	774.3668	**V**	999.5622	1012.5826		**1043.6248**	1026.5982	1025.6142	**9**
8	72.0808	863.4509	**845.4403**	891.4458	873.4353	**V**	900.4938	913.5142		944.5564	927.5298	926.5458	**8**
9	70.0651	960.5037	942.4931	988.4986	970.4880	**P**	803.4410	802.4458		**845.4880**	**828.4614**	827.4774	**7**
10	136.0757	1123.5670	1105.5564	1151.5619	1133.5514	**Y**	640.3777			748.4352	731.4087	730.4246	**6**
11	70.0651	1220.6198	1202.6092	1248.6147	1230.6041	**P**	543.3249	542.3297		**585.3719**	**568.3453**	567.3613	**5**
12	86.0964	1333.7038	1315.6933	1361.6987	1343.6882	**I**	430.2409	443.2613	457.2769	488.3191	471.2926	470.3085	**4**
13	60.0444	1420.73	1402.72	1448.73	1430.72	**S**	343.208	342.213		**375.235**	**358.208**	357.224	**3**

		59	53	08	02		8	6		**0**	**5**	5	
14	86.0964	1533.8199	1515.8094	1561.8148	1543.8043	**L**	230.1248	229.1295		**288.2030**	271.1765		**2**
15	129.1135					**R**	74.0237	73.0284		**175.1190**	158.0924		

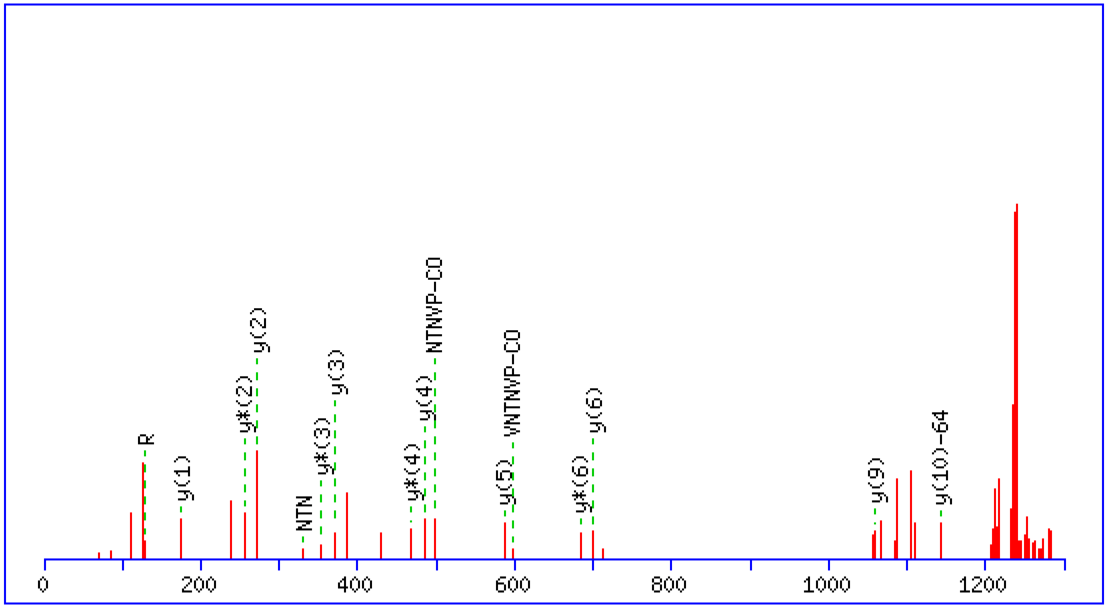
1265

MS/MS Fragmentation of PMFIVNTNVPR

Found in gi|5542151, Chain A, Macrophage Migration Inhibitory Factor,

(1303.7183,1+)

Ions Score: 48



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	70.0651	70.0651			98.0600			**P**							**11**
2	56.0495	153.1022			181.0972			**M**	1114.6004	1113.6051		**1142.6317**	1125.6051	1124.6211	**10**
3	120.0808	300.1707			328.1656			**F**	967.5320			**1059.5946**	1042.5680	1041.5840	**9**
4	86.0964	413.2547			441.2496			**I**	854.4479	867.4683	881.4839	912.5261	895.4996	894.5156	**8**
5	72.0808	512.3231			540.3181			**V**	755.3795	768.3999		799.4421	782.4155	781.4315	**7**
6	87.0553	626.3661	609.3395		654.3610	637.3344		**N**	641.3365	640.3413		**700.3737**	**683.3471**	682.3631	**6**
7	74.0600	727.4137	710.3872	709.4032	755.4087	738.3821	737.3981	**T**	540.2889	553.3093	555.2885	**586.3307**	569.3042	568.3202	**5**
8	87.0553	841.4567	824.4301	823.4461	869.4516	852.4250	851.4410	**N**	426.2459	425.2507		**485.2831**	**468.2565**		**4**
9	72.0808	940.5251	923.4985	922.5145	968.5200	951.4934	950.5094	**V**	327.1775	340.1979		**371.2401**	**354.2136**		**3**
10	70.0651	1037.5778	1020.5513	1019.5673	1065.5728	1048.5462	1047.5622	**P**	230.1248	229.1295		**272.1717**	**255.1452**		**2**
11	**129.1135**							**R**	74.0237	73.0284		**175.1190**	158.0924		

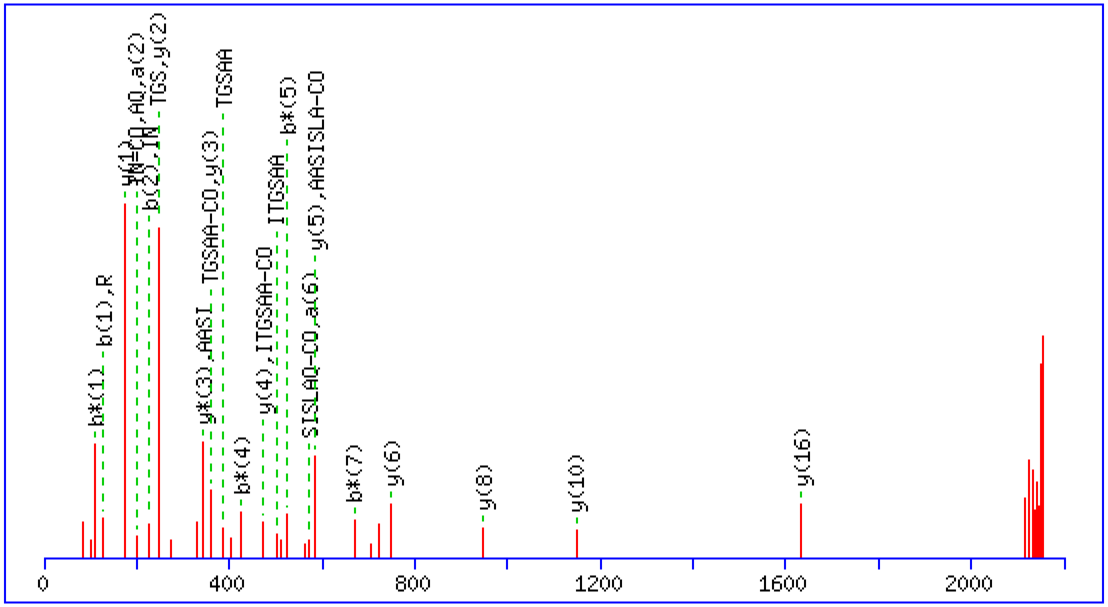
1266

MS/MS Fragmentation of QVTITGSAASISLAQYLINAR

Found in gi|460771, hnRNP-E1,

(2177.2593,1+)

Ions Score: 65



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	101.0709	101.0709	84.0444		**129.0659**	**112.0393**		**Q**							**21**
2	72.0808	**200.1394**	183.1128		**228.1343**	211.1077		**V**	2005.0713	2018.0917		2049.1339	2032.1073	2031.1233	**20**
3	74.060	301.18	284.16	283.17	329.18	312.15	311.17	**T**	1904.0	1917.0	1919.0	1950.0	1933.0	1932.0	**19**

	0	70	05	65	19	54	14		236	440	233	655	389	549	
4	86.0964	414.2711	397.2445	396.2605	442.2660	**425.2395**	424.2554	**I**	1790.9395	1803.9599	1817.9756	1849.0178	1831.9912	1831.0072	**18**
5	74.0600	515.3188	498.2922	497.3082	543.3137	**526.2871**	525.3031	**T**	1689.8919	1702.9123	1704.8915	1735.9337	1718.9072	1717.9232	**17**
6	30.0338	**572.3402**	555.3137	554.3297	600.3352	583.3086	582.3246	**G**				**1634.8860**	1617.8595	1616.8755	**16**
7	60.0444	659.3723	642.3457	641.3617	687.3672	**670.3406**	669.3566	**S**	1545.8384	1544.8431		1577.8646	1560.8380	1559.8540	**15**
8	44.0495	730.4094	713.3828	712.3988	758.4043	741.3777	740.3937	**A**	1474.8013			1490.8326	1473.8060	1472.8220	**14**
9	44.0495	801.4465	784.4199	783.4359	829.4414	812.4149	811.4308	**A**	1403.7641			1419.7954	1402.7689	1401.7849	**13**
10	60.0444	888.4785	871.4520	870.4680	916.4734	899.4469	898.4629	**S**	1316.7321	1315.7369		1348.7583	1331.7318	1330.7478	**12**
11	86.0964	1001.5626	984.5360	983.5520	1029.5575	1012.5310	1011.5469	**I**	1203.6480	1216.6684	1230.6841	1261.7263	1244.6997	1243.7157	**11**
12	60.0444	1088.5946	1071.5681	1070.5840	1116.5895	1099.5630	1098.5790	**S**	1116.6160	1115.6208		**1148.6422**	1131.6157	1130.6317	**10**
13	86.0964	1201.6787	1184.6521	1183.6681	1229.6736	1212.6470	1211.6630	**L**	1003.5320	1002.5367		1061.6102	1044.5837		**9**
14	44.0495	1272.7158	1255.6892	1254.7052	1300.7107	1283.6842	1282.7001	**A**	932.4948			**948.5261**	931.4996		**8**
15	101.0709	1400.7744	1383.7478	1382.7638	1428.7693	1411.7427	1410.7587	**Q**	804.4363	803.4410		877.4890	860.4625		**7**
16	136.0757	1563.8377	1546.8112	1545.8271	1591.8326	1574.8061	1573.8221	**Y**	641.3729			**749.4305**	732.4039		**6**

17	86.0964	1676.9218	1659.8952	1658.9112	1704.9167	1687.8901	1686.9061	**L**	528.2889	527.2936		**586.3671**	569.3406		**5**
18	86.0964	1790.0058	1772.9793	1771.9953	1818.0007	1800.9742	1799.9902	**I**	415.2048	428.2252	442.2409	**473.2831**	456.2565		**4**
19	87.0553	1904.0488	1887.0222	1886.0382	1932.0437	1915.0171	1914.0331	**N**	301.1619	300.1666		**360.1990**	**343.1724**		**3**
20	44.0495	1975.0859	1958.0593	1957.0753	2003.0808	1986.0542	1985.0702	**A**	230.1248			**246.1561**	229.1295		**2**
21	**129.1135**							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

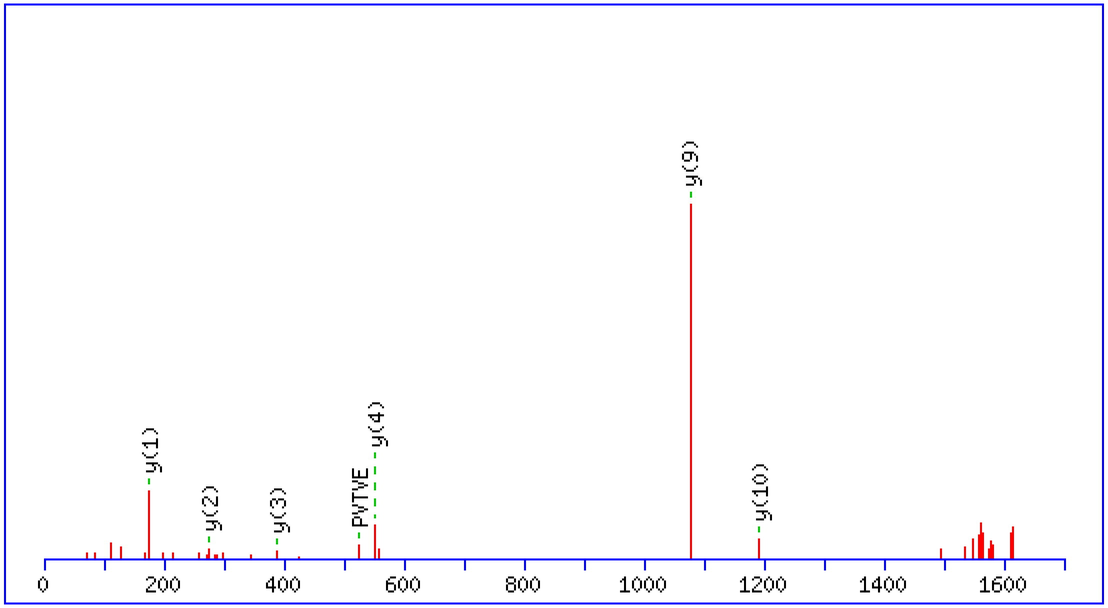
1267

MS/MS Fragmentation of LTVEDPVTVEYITR

Found in gi|12314029, proteasome subunit,

(1634.9735,1+)

Ions Score: 44



#	Immon.	a	a^0	b	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964		114.0913		**L**							**14**
2	74.0600	187.1441	169.1335	215.1390	197.1285	**T**	1475.7377	1488.7581	1490.7373	1521.7795	1504.7530	1503.7690	**13**
3	72.0808	286.2125	268.2020	314.2074	296.1969	**V**	1376.6692	1389.6896		1420.7318	1403.7053	1402.7213	**12**
4	102.0550	415.2551	397.2445	443.2500	425.2395	**E**	1247.6266	1246.6314		1321.6634	1304.6369	1303.6529	**11**
5	88.0393	530.2821	512.2715	558.2770	540.2664	**D**	1132.5997	1131.6045		**1192.6208**	1175.5943	1174.6103	**10**
6	70.0651	627.3348	609.3243	655.3297	637.3192	**P**	1035.5469	1034.5517		**1077.5939**	1060.5673	1059.5833	**9**
7	72.0808	726.403	708.392	754.398	736.387	**V**	936.478	949.498		980.541	963.514	962.530	**8**

		2	7	1	6		5	9		1	6	6	
8	74.0600	827.4509	809.4403	855.4458	837.4353	**T**	835.4308	848.4512	850.4305	881.4727	864.4462	863.4621	**7**
9	72.0808	926.5193	908.5088	954.5142	936.5037	**V**	736.3624	749.3828		780.4250	763.3985	762.4145	**6**
10	102.0550	1055.5619	1037.5514	1083.5568	1065.5463	**E**	607.3198	606.3246		681.3566	664.3301	663.3461	**5**
11	136.0757	1218.6252	1200.6147	1246.6202	1228.6096	**Y**	444.2565			**552.3140**	535.2875	534.3035	**4**
12	86.0964	1331.7093	1313.6987	1359.7042	1341.6937	**I**	331.1724	344.1928	358.2085	**389.2507**	372.2241	371.2401	**3**
13	74.0600	1432.7570	1414.7464	1460.7519	1442.7413	**T**	230.1248	243.1452	245.1244	**276.1666**	259.1401	258.1561	**2**
14	129.1135					**R**	74.0237	73.0284		**175.1190**	158.0924		

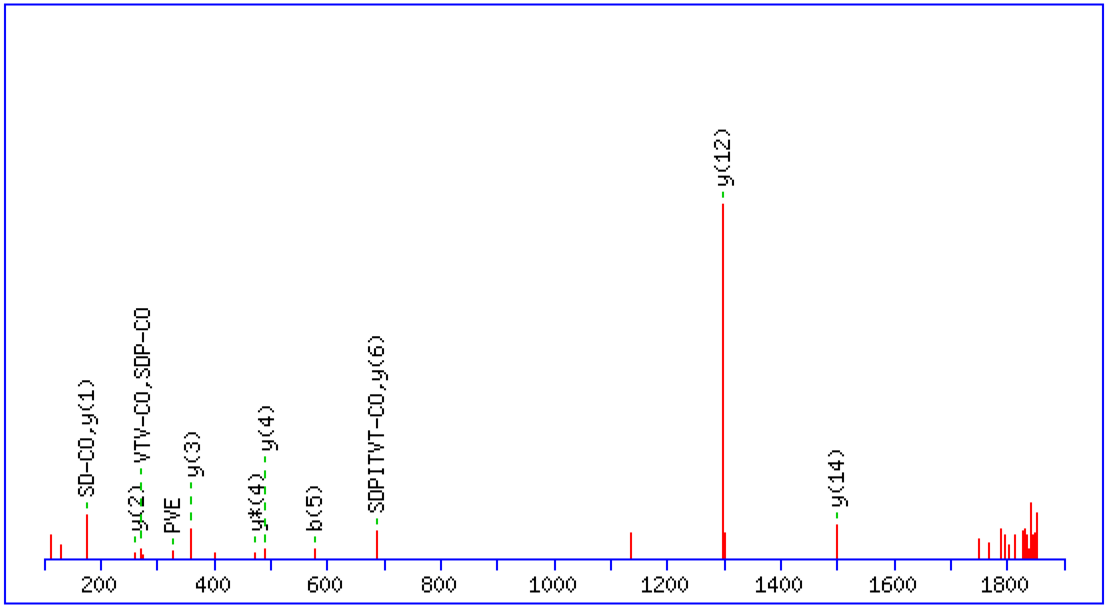
1268

MS/MS Fragmentation of LFDSDPITVTVPVEVSR

Found in gi|338305, SP40,40,

(1873.964,1+)

Ions Score: 41



#	Immon.	a	a^0	b	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964		114.0913		**L**							**17**
2	120.0808	233.1648		261.1598		**F**	1668.8439			1760.9065	1743.8800	1742.8959	**16**
3	88.0393	348.1918	330.1812	376.1867	358.1761	**D**	1553.8170	1552.8217		1613.8381	1596.8115	1595.8275	**15**
4	60.0444	435.2238	417.2132	463.2187	445.2082	**S**	1466.7849	1465.7897		**1498.8112**	1481.7846	1480.8006	**14**
5	88.0393	550.2508	532.2402	**578.2457**	560.2351	**D**	1351.7580	1350.7627		1411.7791	1394.7526	1393.7686	**13**
6	70.0651	647.3035	629.2930	675.2984	657.2879	**P**	1254.7052	1253.7100		**1296.7522**	1279.7256	1278.7416	**12**
7	86.0964	760.387	742.377	788.382	770.371	**I**	1141.62	1154.64	1168.65	1199.69	1182.67	1181.68	**11**

		6	0	5	9		12	16	72	94	29	89	
8	74.0600	861.4353	843.4247	889.4302	871.4196	**T**	1040.5735	1053.5939	1055.5732	1086.6154	1069.5888	1068.6048	**10**
9	72.0808	960.5037	942.4931	988.4986	970.4880	**V**	941.5051	954.5255		985.5677	968.5411	967.5571	**9**
10	74.0600	1061.5514	1043.5408	1089.5463	1071.5357	**T**	840.4574	853.4778	855.4571	886.4993	869.4727	868.4887	**8**
11	72.0808	1160.6198	1142.6092	1188.6147	1170.6041	**V**	741.3890	754.4094		785.4516	768.4250	767.4410	**7**
12	70.0651	1257.6725	1239.6620	1285.6674	1267.6569	**P**	644.3362	643.3410		**686.3832**	669.3566	668.3726	**6**
13	72.0808	1356.7409	1338.7304	1384.7359	1366.7253	**V**	545.2678	558.2882		589.3304	572.3039	571.3198	**5**
14	102.0550	1485.7835	1467.7730	1513.7785	1495.7679	**E**	416.2252	415.2300		**490.2620**	**473.2354**	472.2514	**4**
15	72.0808	1584.8520	1566.8414	1612.8469	1594.8363	**V**	317.1568	330.1772		**361.2194**	344.1928	343.2088	**3**
16	60.0444	1671.8840	1653.8734	1699.8789	1681.8683	**S**	230.1248	229.1295		**262.1510**	245.1244	244.1404	**2**
17	129.1135					**R**	74.0237	73.0284		**175.1190**	158.0924		

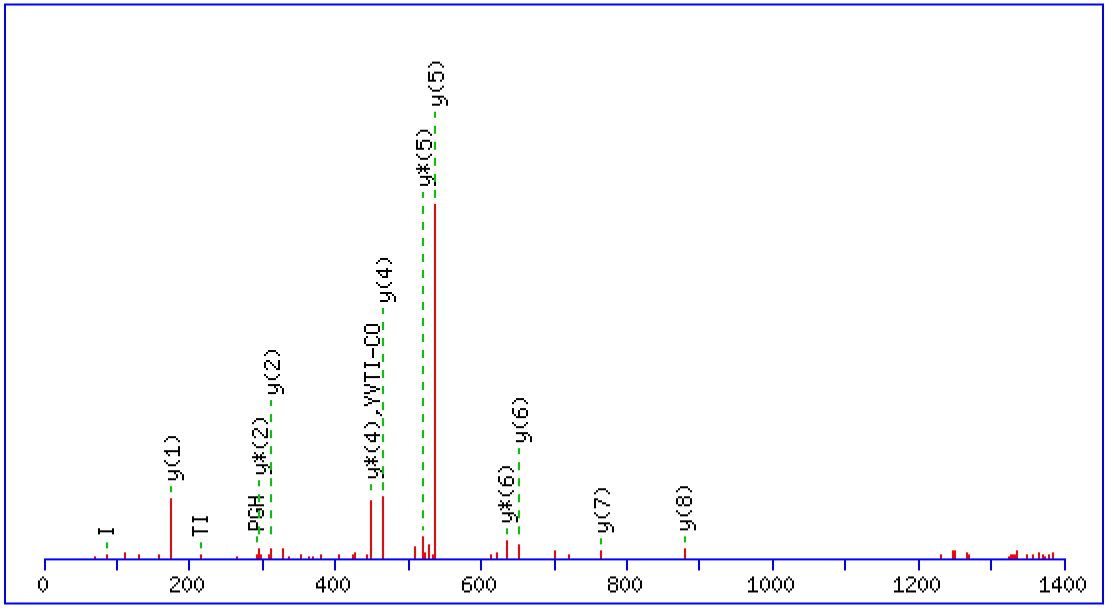
1269

MS/MS Fragmentation of YYVTIIDAPGHR

Found in gi|31092, unnamed protein product,

(1404.6914,1+)

Ions Score: 49



#	Immon.	a	a^0	b	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	136.0757	136.0757		164.0706		**Y**							**12**
2	136.0757	299.1390		327.1339		**Y**	1133.6062			1241.6637	1224.6371	1223.6531	**11**
3	72.0808	398.2074		426.2023		**V**	1034.5378	1047.5582		1078.6004	1061.5738	1060.5898	**10**
4	74.0600	499.2551	481.2445	527.2500	509.2395	**T**	933.4901	946.5105	948.4898	979.5320	962.5054	961.5214	**9**
5	**86.0964**	612.3392	594.3286	640.3341	622.3235	**I**	820.4060	833.4264	847.4421	**878.4843**	861.4577	860.4737	**8**
6	**86.0964**	725.4232	707.4127	753.4182	735.4076	**I**	707.3220	720.3424	734.3580	**765.4002**	748.3737	747.3896	**7**

7	88.0393	840.4502	822.4396	868.4451	850.4345	**D**	592.2950	591.2998		**652.3161**	**635.2896**	634.3056	**6**
8	44.0495	911.4873	893.4767	939.4822	921.4716	**A**	521.2579			**537.2892**	**520.2627**		**5**
9	70.0651	1008.5401	990.5295	1036.5350	1018.5244	**P**	424.2051	423.2099		**466.2521**	**449.2255**		**4**
10	30.0338	1065.5615	1047.5510	1093.5564	1075.5459	**G**				369.1993	352.1728		**3**
11	110.0713	1202.6204	1184.6099	1230.6154	1212.6048	**H**	230.1248			**312.1779**	**295.1513**		**2**
12	129.1135					**R**	74.0237	73.0284		**175.1190**	158.0924		

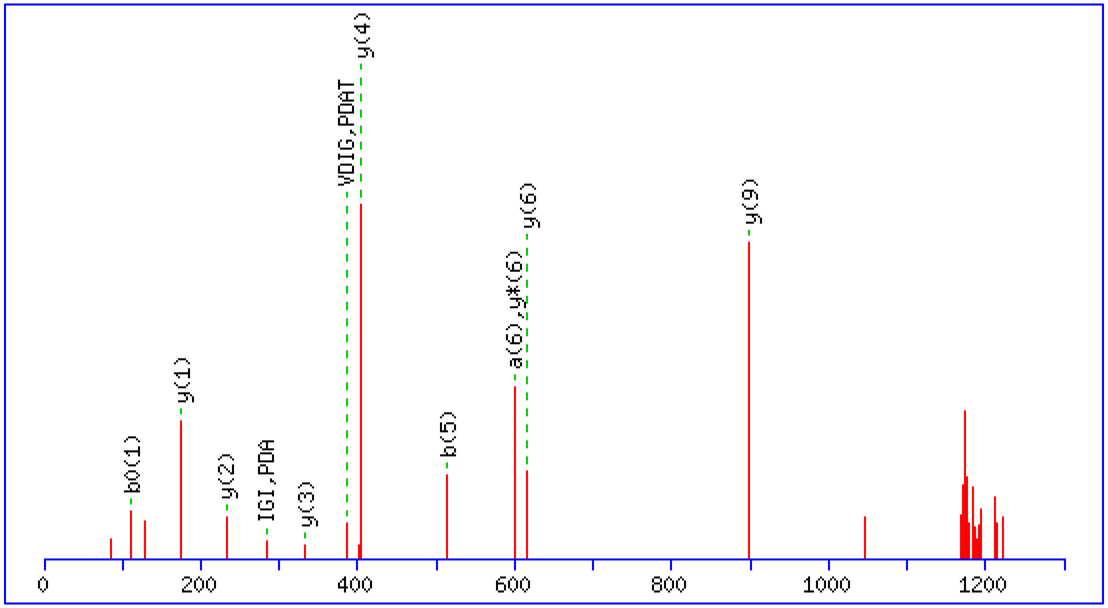
1270

MS/MS Fragmentation of EVDIGIPDATGR

Found in gi|48257098, VCP protein,

(1242.6382,1+)

Ions Score: 37



#	Immon.	a	a^0	b	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	102.0550	102.0550	84.0444	130.0499	**112.0393**	E							12
2	72.0808	201.1234	183.1128	229.1183	211.1077	V	1069.5273	1082.5477		1113.5899	1096.5633	1095.5793	11
3	88.0393	316.1503	298.1397	344.1452	326.1347	D	954.5003	953.5051		1014.5215	997.4949	996.5109	10
4	86.0964	429.2344	411.2238	457.2293	439.2187	I	841.4163	854.4367	868.4523	**899.4945**	882.4680	881.4839	9
5	30.0338	486.2558	468.2453	**514.2508**	496.2402	G				786.4104	769.3839	768.3999	8
6	86.0964	**599.3399**	581.3293	627.3348	609.3243	I	671.3107	684.3311	698.3468	729.3890	712.3624	711.3784	7
7	70.0651	696.392	678.382	724.387	706.377	P	574.258	573.262		**616.304**	**599.278**	598.294	6

		7	1	6	0		0	7		**9**	**4**	4	
8	88.0393	811.4196	793.4090	839.4145	821.4040	**D**	459.2310	458.2358		519.2522	502.2256	501.2416	**5**
9	44.0495	882.4567	864.4462	910.4516	892.4411	**A**	388.1939			**404.2252**	387.1987	386.2146	**4**
10	74.0600	983.5044	965.4938	1011.4993	993.4888	**T**	287.1462	300.1666	302.1459	**333.1881**	316.1615	315.1775	**3**
11	30.0338	1040.5259	1022.5153	1068.5208	1050.5102	**G**				**232.1404**	215.1139		**2**
12	129.1135					**R**	74.0237	73.0284		**175.1190**	158.0924		

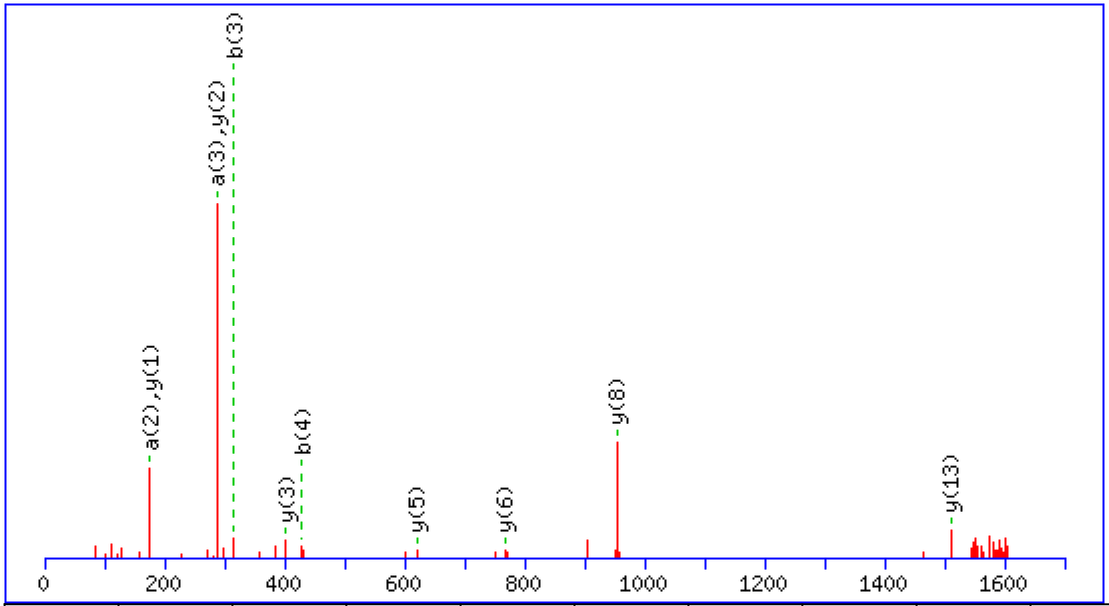
1271

MS/MS Fragmentation of DSLLQDGEFSMDLR

Found in gi|5822002, Chain A, Profilin Binds Proline-Rich Ligands In Two Distinct Amide Backbone Orientations,

(1625.7438,1+)

Ions Score: 55



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	y	y*	y^0	#
1	88.0393	88.0393		70.0287	116.0342		98.0237	D						14
2	60.0444	175.0713		157.0608	203.0662		185.0557	S	1478.6944	1477.6992	1510.7206	1493.6941	1492.7101	13
3	86.0964	288.1554		270.1448	316.1503		298.1397	L	1365.6103	1364.6151	1423.6886	1406.6620	1405.6780	12
4	86.0964	401.2395		383.2289	429.2344		411.2238	L	1252.5263	1251.5310	1310.6045	1293.5780	1292.5940	11
5	101.0709	529.2980	512.2715	511.2875	557.2930	540.2664	539.2824	Q	1124.4677	1123.4725	1197.5205	1180.4939	1179.5099	10
6	88.0393	644.3250	627.2984	626.3144	672.3199	655.2933	654.3093	D	1009.4408	1008.4455	1069.4619	1052.4353	1051.4513	9
7	30.0338	701.346	684.319	683.335	729.341	712.314	711.330	G			954.434	937.408	936.424	8

		4	9	9	4	8	8				**9**	4	4	
8	102.0550	830.3890	813.3625	812.3785	858.3840	841.3574	840.3734	**E**	823.3767	822.3815	897.4135	880.3869	879.4029	**7**
9	120.0808	977.4575	960.4309	959.4469	1005.4524	988.4258	987.4418	**F**	676.3083		**768.3709**	751.3443	750.3603	**6**
10	60.0444	1064.4895	1047.4629	1046.4789	1092.4844	1075.4578	1074.4738	**S**	589.2763	588.2810	**621.3025**	604.2759	603.2919	**5**
11	104.0528	1195.5300	1178.5034	1177.5194	1223.5249	1206.4983	1205.5143	**M**	458.2358	457.2405	534.2704	517.2439	516.2599	**4**
12	88.0393	1310.5569	1293.5304	1292.5463	1338.5518	1321.5253	1320.5413	**D**	343.2088	342.2136	**403.2300**	386.2034	385.2194	**3**
13	86.0964	1423.6410	1406.6144	1405.6304	1451.6359	1434.6093	1433.6253	**L**	230.1248	229.1295	**288.2030**	271.1765		**2**
14	129.1135							**R**	74.0237	73.0284	**175.1190**	158.0924		

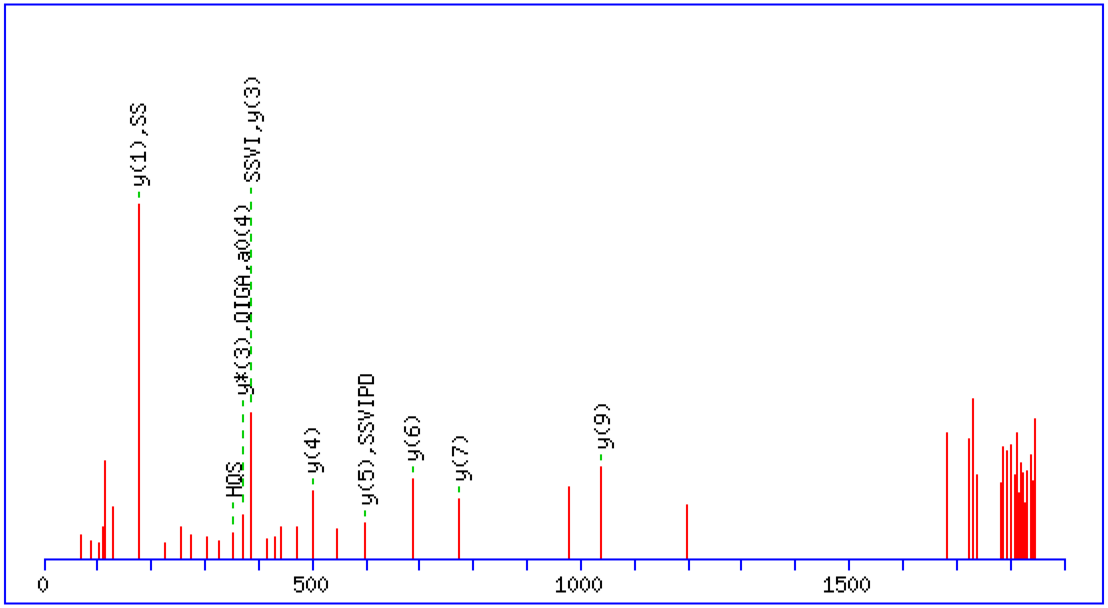
1272

MS/MS Fragmentation of SSQIGAVVSHQSSVIPDR

Found in gi|62898045, pyridoxine 5'-phosphate oxidase variant,

(1866.901,1+)

Ions Score: 46



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		70.0287	S							18
2	60.0444	147.0764		129.0659	175.0713		157.0608	S	1747.9086	1746.9133		1779.9348	1762.9082	1761.9242	17
3	101.0709	275.1350	258.1084	257.1244	303.1299	286.1034	285.1193	Q	1619.8500	1618.8547		1692.9028	1675.8762	1674.8922	16
4	86.0964	388.2191	371.1925	370.2085	416.2140	399.1874	398.2034	I	1506.7659	1519.7863	1533.8020	1564.8442	1547.8176	1546.8336	15
5	30.0338	445.2405	428.2140	427.2300	473.2354	456.2089	455.2249	G				1451.7601	1434.7336	1433.7496	14
6	44.0495	516.2776	499.2511	498.2671	544.2726	527.2460	526.2620	A	1378.7074			1394.7387	1377.7121	1376.7281	13

7	72.0808	615.3461	598.3195	597.3355	643.3410	626.3144	625.3304	**V**	1279.6389	1292.6593		1323.7015	1306.6750	1305.6910	**12**
8	72.0808	714.4145	697.3879	696.4039	742.4094	725.3828	724.3988	**V**	1180.5705	1193.5909		1224.6331	1207.6066	1206.6226	**11**
9	60.0444	801.4465	784.4199	783.4359	829.4414	812.4149	811.4308	**S**	1093.5385	1092.5432		1125.5647	1108.5382	1107.5541	**10**
10	110.0713	938.5054	921.4789	920.4948	966.5003	949.4738	948.4898	**H**	956.4796			**1038.5327**	1021.5061	1020.5221	**9**
11	101.0709	1066.5640	1049.5374	1048.5534	1094.5589	1077.5323	1076.5483	**Q**	828.4210	827.4258		901.4738	884.4472	883.4632	**8**
12	60.0444	1153.5960	1136.5695	1135.5854	1181.5909	1164.5644	1163.5804	**S**	741.3890	740.3937		**773.4152**	756.3886	755.4046	**7**
13	60.0444	1240.6280	1223.6015	1222.6175	1268.6230	1251.5964	1250.6124	**S**	654.3570	653.3617		**686.3832**	669.3566	668.3726	**6**
14	72.0808	1339.6965	1322.6699	1321.6859	1367.6914	1350.6648	1349.6808	**V**	555.2885	568.3089		**599.3511**	582.3246	581.3406	**5**
15	86.0964	1452.7805	1435.7540	1434.7700	1480.7754	1463.7489	1462.7649	**I**	442.2045	455.2249	469.2405	**500.2827**	483.2562	482.2722	**4**
16	70.0651	1549.8333	1532.8067	1531.8227	1577.8282	1560.8016	1559.8176	**P**	345.1517	344.1565		**387.1987**	**370.1721**	369.1881	**3**
17	88.0393	1664.8602	1647.8337	1646.8497	1692.8551	1675.8286	1674.8446	**D**	230.1248	229.1295		290.1459	273.1193	272.1353	**2**
18	129.1135							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

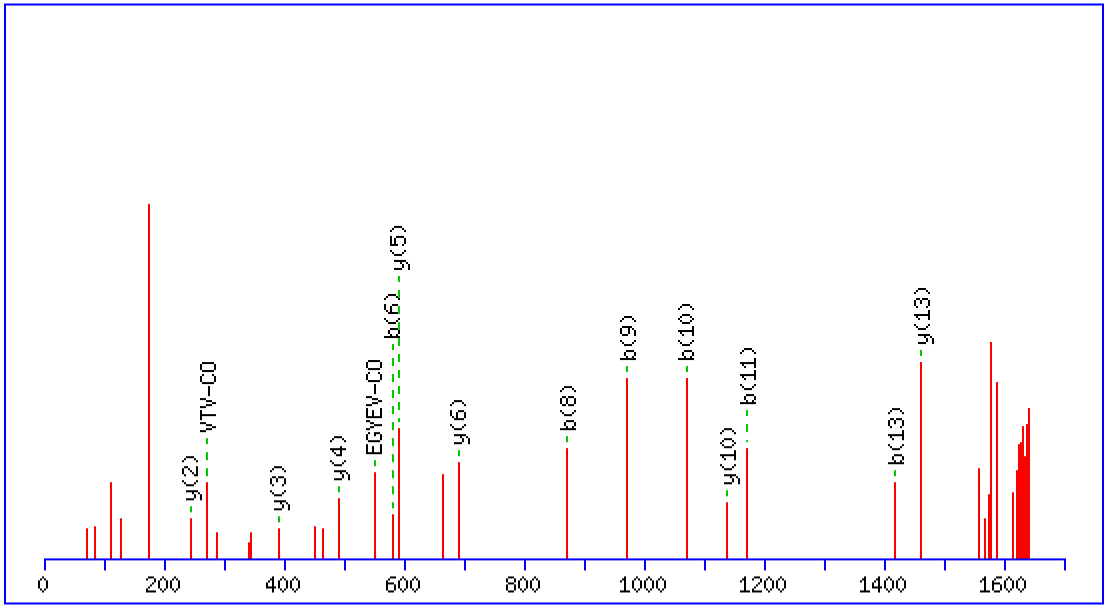
1273

MS/MS Fragmentation of VTPPEGYEVVTVFPK

Found in gi|1905874, carboxyl terminal LIM domain protein,

(1661.808,1+)

Ions Score: 39



#	Immon.	a	a^0	b	b^0	Seq.	y	y*	y^0	#
1	72.0808	72.0808		100.0757		**V**				**15**
2	74.0600	173.1285	155.1179	201.1234	183.1128	**T**	1562.8101	1545.7835	1544.7995	**14**
3	70.0651	270.1812	252.1707	298.1761	280.1656	**P**	**1461.7624**	1444.7359	1443.7518	**13**
4	70.0651	367.2340	349.2234	395.2289	377.2183	**P**	1364.7096	1347.6831	1346.6991	**12**
5	102.0550	496.2766	478.2660	524.2715	506.2609	**E**	1267.6569	1250.6303	1249.6463	**11**

6	30.0338	553.2980	535.2875	**581.2930**	563.2824	**G**	**1138.6143**	1121.5877	1120.6037	**10**
7	136.0757	716.3614	698.3508	744.3563	726.3457	**Y**	1081.5928	1064.5663	1063.5823	**9**
8	102.0550	845.4040	827.3934	**873.3989**	855.3883	**E**	918.5295	901.5029	900.5189	**8**
9	72.0808	944.4724	926.4618	**972.4673**	954.4567	**V**	789.4869	772.4604	771.4763	**7**
10	72.0808	1043.5408	1025.5302	**1071.5357**	1053.5251	**V**	**690.4185**	673.3919	672.4079	**6**
11	74.0600	1144.5885	1126.5779	**1172.5834**	1154.5728	**T**	**591.3501**	574.3235	573.3395	**5**
12	72.0808	1243.6569	1225.6463	1271.6518	1253.6412	**V**	**490.3024**	473.2758		**4**
13	120.0808	1390.7253	1372.7147	**1418.7202**	1400.7096	**F**	**391.2340**	374.2074		**3**
14	70.0651	1487.7781	1469.7675	1515.7730	1497.7624	**P**	**244.1656**	227.1390		**2**
15	101.1073					**K**	147.1128	130.0863		**1**

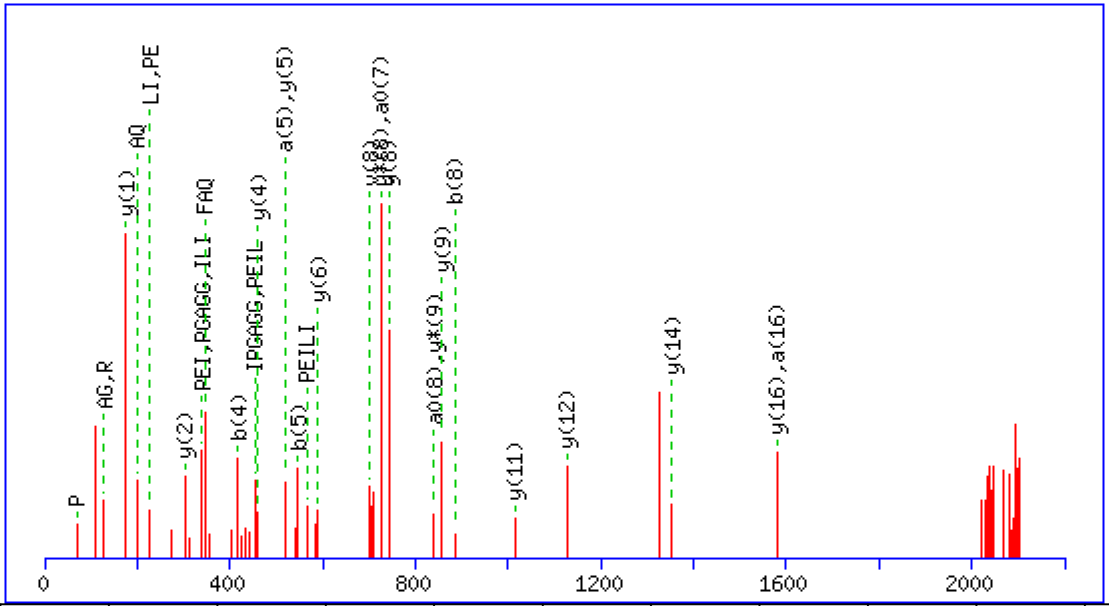
1274

MS/MS Fragmentation of AQFAQPEILIGTIPGAGGTQR

Found in gi|1922287, enoyl-CoA hydratase,

(2125.177,1+)

Ions Score: 80



#	**Immon.**	**a**	**a***	**a⁰**	**b**	**b***	**b⁰**	**Seq.**	**v**	**w**	**w'**	**y**	**y***	**y⁰**	**#**
1	44.0495	44.0495			72.0444			**A**							**21**
2	101.0709	172.1081	155.0815		**200.1030**	183.0764		**Q**	1981.0502	1980.0549		2054.1029	2037.0764	2036.0924	**20**
3	120.0808	319.1765	302.1499		**347.1714**	330.1448		**F**	1833.9817			1926.0443	1909.0178	1908.0338	**19**
4	44.0495	390.2136	373.1870		**418.2085**	401.1819		**A**	1762.9446			1778.9759	1761.9494	1760.9654	**18**
5	101.0709	**518.2722**	501.2456		**546.2671**	529.2405		**Q**	1634.8860	1633.8908		1707.9388	1690.9123	1689.9282	**17**
6	**70.0651**	615.3249	598.2984		643.3198	626.2933		**P**	1537.8333	1536.8380		**1579.8802**	1562.8537	1561.8697	**16**
7	102.05	744.36	727.34	**726.35**	772.36	755.33	754.35	**E**	1408.7	1407.7		1482.8	1465.8	1464.8	**15**

	50	75	10	**70**	24	59	19		907	954		275	009	169	
8	86.0964	857.4516	840.4250	**839.4410**	**885.4465**	868.4199	867.4359	**I**	1295.7066	1308.7270	1322.7427	**1353.7849**	1336.7583	1335.7743	**14**
9	86.0964	970.5356	953.5091	952.5251	998.5306	981.5040	980.5200	**L**	1182.6226	1181.6273		1240.7008	1223.6743	1222.6902	**13**
10	86.0964	1083.6197	1066.5932	1065.6091	1111.6146	1094.5881	1093.6041	**I**	1069.5385	1082.5589	1096.5746	**1127.6167**	1110.5902	1109.6062	**12**
11	30.0338	1140.6412	1123.6146	1122.6306	1168.6361	1151.6095	1150.6255	**G**				**1014.5327**	997.5061	996.5221	**11**
12	74.0600	1241.6889	1224.6623	1223.6783	1269.6838	1252.6572	1251.6732	**T**	911.4694	924.4898	926.4690	957.5112	940.4847	939.5007	**10**
13	86.0964	1354.7729	1337.7464	1336.7624	1382.7678	1365.7413	1364.7573	**I**	798.3853	811.4057	825.4213	**856.4635**	**839.4370**	838.4530	**9**
14	**70.0651**	1451.8257	1434.7991	1433.8151	1479.8206	1462.7940	1461.8100	**P**	**701.3325**	700.3373		**743.3795**	**726.3529**	725.3689	**8**
15	30.0338	1508.8471	1491.8206	1490.8366	1536.8421	1519.8155	1518.8315	**G**				646.3267	629.3002	628.3161	**7**
16	44.0495	**1579.8843**	1562.8577	1561.8737	1607.8792	1590.8526	1589.8686	**A**	573.2740			**589.3053**	572.2787	571.2947	**6**
17	30.0338	1636.9057	1619.8792	1618.8952	1664.9006	1647.8741	1646.8901	**G**				**518.2681**	501.2416	500.2576	**5**
18	30.0338	1693.9272	1676.9006	1675.9166	1721.9221	1704.8956	1703.9115	**G**				**461.2467**	444.2201	443.2361	**4**
19	74.0600	1794.9749	1777.9483	1776.9643	1822.9698	1805.9432	1804.9592	**T**	358.1833	371.2037	373.1830	404.2252	387.1987	386.2146	**3**
20	101.0709	1923.0334	1906.0069	1905.0229	1951.0284	1934.0018	1933.0178	**Q**	230.1248	229.1295		**303.1775**	286.1510		**2**

21	129.1135							R	74.0237	73.0284		175.1190	158.0924		1

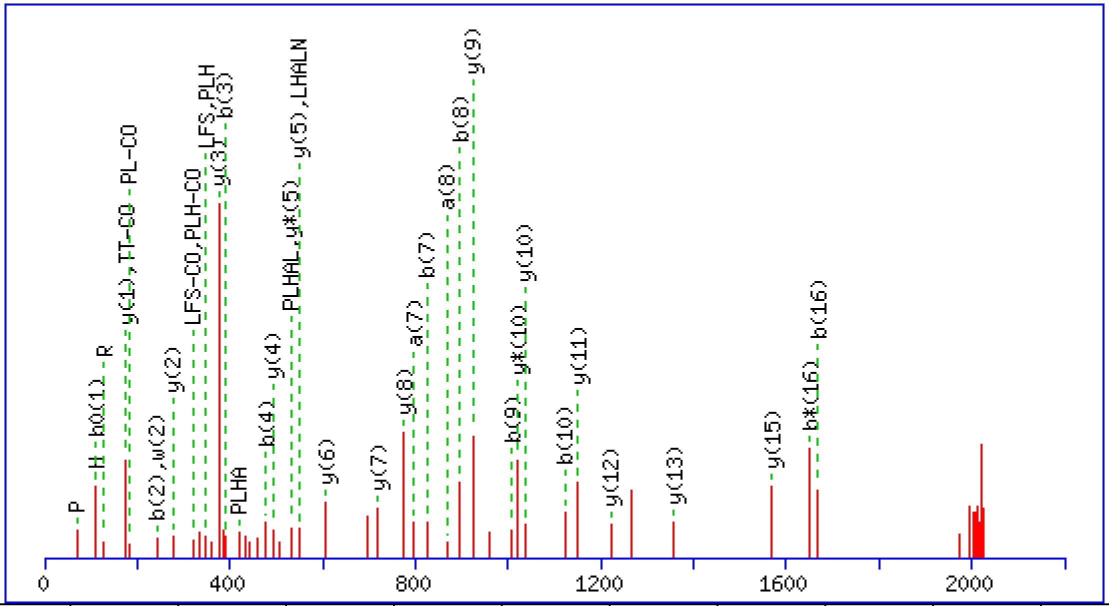
1275

MS/MS Fragmentation of ELFSPLHALNFGIGGDTTR

Found in gi|4505585, platelet-activating factor acetylhydrolase,

(2045.0693,1+)

Ions Score: 122



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	102.05	102.05		84.044	130.04		112.03	E							19

	50	50		4	99		**93**							
2	86.0964	215.1390		197.1285	**243.1339**		225.1234	**L**	1857.9242	1856.9290		1916.0025	1898.9759	1897.9919	**18**
3	120.0808	362.2074		344.1969	**390.2023**		372.1918	**F**	1710.8558			1802.9184	1785.8919	1784.9078	**17**
4	60.0444	449.2395		431.2289	**477.2344**		459.2238	**S**	1623.8238	1622.8285		1655.8500	1638.8234	1637.8394	**16**
5	**70.0651**	546.2922		528.2817	574.2871		556.2766	**P**	1526.7710	1525.7758		**1568.8180**	1551.7914	1550.8074	**15**
6	86.0964	659.3763		641.3657	687.3712		669.3606	**L**	1413.6870	1412.6917		1471.7652	1454.7387	1453.7546	**14**
7	**110.0713**	**796.4352**		778.4246	**824.4301**		806.4195	**H**	1276.6280			**1358.6811**	1341.6546	1340.6706	**13**
8	44.0495	**867.4723**		849.4617	**895.4672**		877.4567	**A**	1205.5909			**1221.6222**	1204.5957	1203.6117	**12**
9	86.0964	980.5564		962.5458	**1008.5513**		990.5407	**L**	1092.5069	1091.5116		**1150.5851**	1133.5586	1132.5745	**11**
10	87.0553	1094.5993	1077.5728	1076.5887	**1122.5942**	1105.5677	1104.5837	**N**	978.4639	977.4687		**1037.5010**	**1020.4745**	1019.4905	**10**
11	120.0808	1241.6677	1224.6412	1223.6572	1269.6626	1252.6361	1251.6521	**F**	831.3955			**923.4581**	906.4316	905.4476	**9**
12	30.0338	1298.6892	1281.6626	1280.6786	1326.6841	1309.6575	1308.6735	**G**				**776.3897**	759.3632	758.3791	**8**
13	86.0964	1411.7732	1394.7467	1393.7627	1439.7682	1422.7416	1421.7576	**I**	661.2900	674.3104	688.3260	**719.3682**	702.3417	701.3577	**7**
14	30.0338	1468.7947	1451.7682	1450.7841	1496.7896	1479.7631	1478.7791	**G**				**606.2842**	589.2576	588.2736	**6**

15	30.0338	1525.8162	1508.7896	1507.8056	1553.8111	1536.7845	1535.8005	**G**				**549.2627**	**532.2362**	531.2522	**5**
16	88.0393	1640.8431	1623.8166	1622.8326	**1668.8380**	**1651.8115**	1650.8275	**D**	432.2201	431.2249		**492.2413**	475.2147	474.2307	**4**
17	74.0600	1741.8908	1724.8642	1723.8802	1769.8857	1752.8592	1751.8751	**T**	331.1724	344.1928	346.1721	**377.2143**	360.1878	359.2037	**3**
18	74.0600	1842.9385	1825.9119	1824.9279	1870.9334	1853.9068	1852.9228	**T**	230.1248	**243.1452**	245.1244	**276.1666**	259.1401	258.1561	**2**
19	**129.1135**							**R**	74.0237	73.0284		**175.1190**	158		

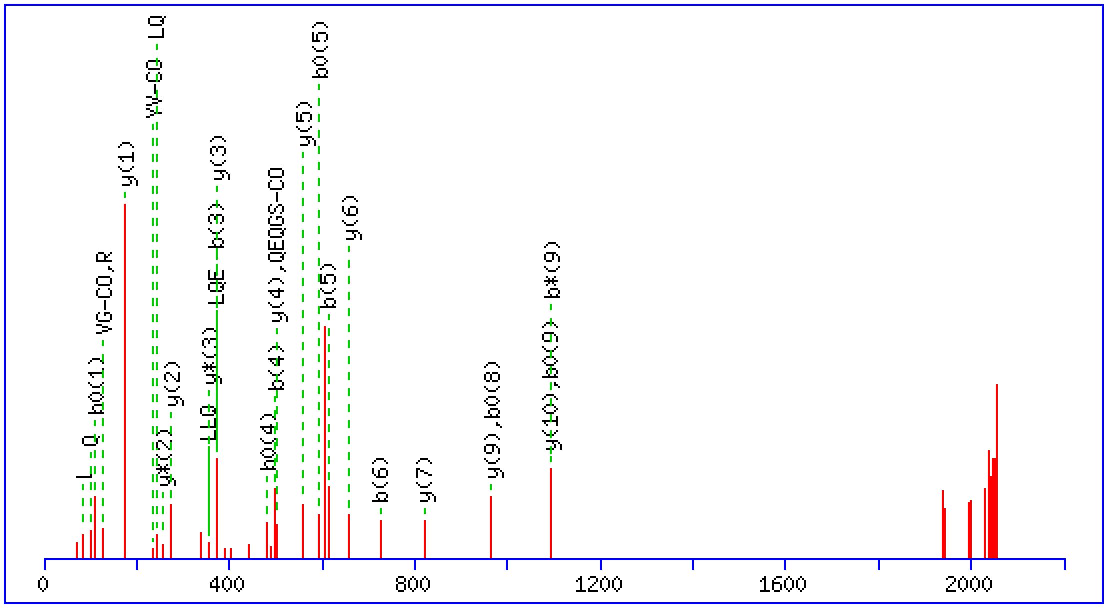
1276

MS/MS Fragmentation of EELQLLQEQGSYVGEVVR

Found in gi|62087652, proteasome 26S ATPase,

(2076.1179,1+)

Ions Score: 66



#	Immon.	a	a*	a⁰	b	b*	b⁰	Seq.	v	w	y	y*	y⁰	#
1	102.0550	102.0550		84.0444	130.0499		**112.0393**	**E**						**18**
2	102.0550	231.0975		213.0870	259.0925		241.0819	**E**	1872.9814	1871.9862	1947.0182	1929.9916	1929.0076	**17**
3	**86.0964**	344.1816		326.1710	**372.1765**		354.1660	**L**	1759.8973	1758.9021	1817.9756	1800.9490	1799.9650	**16**
4	**101.0709**	472.2402	455.2136	454.2296	**500.2351**	483.2086	**482.2245**	**Q**	1631.8388	1630.8435	1704.8915	1687.8650	1686.8810	**15**
5	**86.0964**	585.3243	568.2977	567.3137	**613.3192**	596.2926	**595.3086**	**L**	1518.7547	1517.7595	1576.8329	1559.8064	1558.8224	**14**
6	**86.0964**	698.4083	681.3818	680.3978	**726.4032**	709.3767	708.3927	**L**	1405.6706	1404.6754	1463.7489	1446.7223	1445.7383	**13**

7	**101.0709**	826.4669	809.4403	808.4563	854.4618	837.4353	836.4512	**Q**	1277.6121	1276.6168	1350.6648	1333.6383	1332.6543	**12**
8	102.0550	955.5095	938.4829	937.4989	983.5044	966.4779	**965.4938**	**E**	1148.5695	1147.5742	1222.6062	1205.5797	1204.5957	**11**
9	**101.0709**	1083.5681	1066.5415	1065.5575	1111.5630	**1094.5364**	**1093.5524**	**Q**	1020.5109	1019.5156	**1093.5637**	1076.5371	1075.5531	**10**
10	30.0338	1140.5895	1123.5630	1122.5790	1168.5844	1151.5579	1150.5739	**G**			**965.5051**	948.4785	947.4945	**9**
11	60.0444	1227.6216	1210.5950	1209.6110	1255.6165	1238.5899	1237.6059	**S**	876.4574	875.4621	908.4836	891.4571	890.4730	**8**
12	136.0757	1390.6849	1373.6583	1372.6743	1418.6798	1401.6533	1400.6692	**Y**	713.3941		**821.4516**	804.4250	803.4410	**7**
13	72.0808	1489.7533	1472.7268	1471.7427	1517.7482	1500.7217	1499.7377	**V**	614.3257	627.3461	**658.3883**	641.3617	640.3777	**6**
14	30.0338	1546.7748	1529.7482	1528.7642	1574.7697	1557.7431	1556.7591	**G**			**559.3198**	542.2933	541.3093	**5**
15	102.0550	1675.8174	1658.7908	1657.8068	1703.8123	1686.7857	1685.8017	**E**	428.2616	427.2663	**502.2984**	485.2718	484.2878	**4**
16	72.0808	1774.8858	1757.8592	1756.8752	1802.8807	1785.8541	1784.8701	**V**	329.1932	342.2136	**373.2558**	**356.2292**		**3**
17	72.0808	1873.9542	1856.9276	1855.9436	1901.9491	1884.9226	1883.9385	**V**	230.1248	243.1452	**274.1874**	**257.1608**		**2**
18	**129.1135**							**R**	74.0237	73.0284	**175.1190**	158.0924		**1**

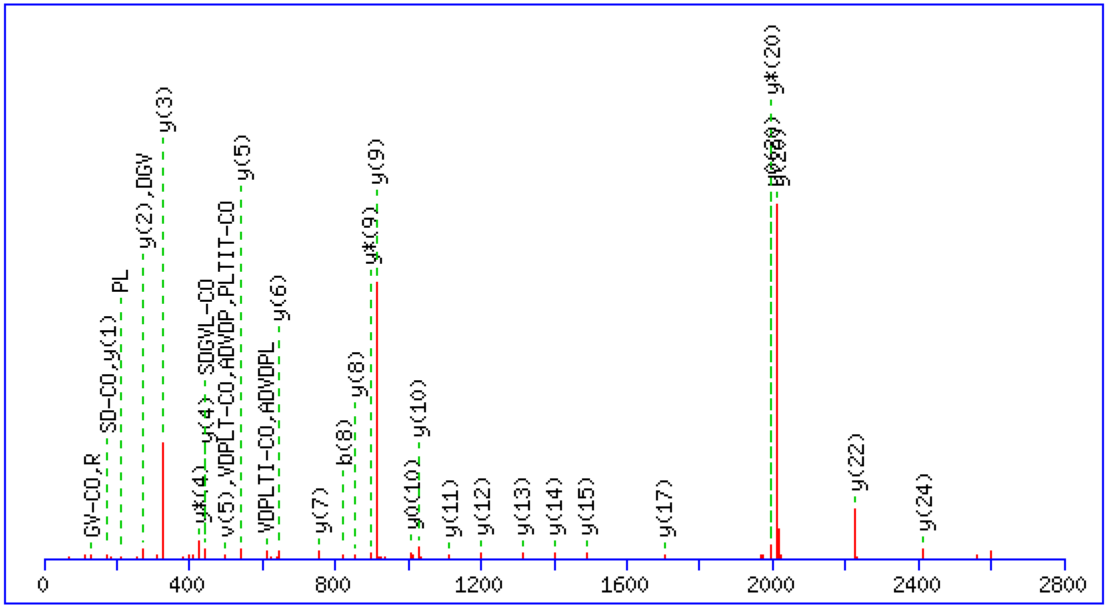
1277

MS/MS Fragmentation of IPADVDPLTITSSLSSDGVLTVNGPR

Found in gi|537532, alpha-B-crystallin,

(2624.4412,1+)

Ions Score: 172



#	Immon.	a	a*	a⁰	b	b*	b⁰	Seq.	v	w	w'	y	y*	y⁰	#
1	86.0964	86.0964			114.0913			**I**							**26**
2	70.0651	183.1492			**211.1441**			**P**	2469.2467	2468.2515		2511.2937	2494.2671	2493.2831	**25**
3	44.049	254.18			282.18			**A**	2398.2			**2414.2**	2397.2	2396.2	**24**

	5	63			12				096			**409**	144	304	
4	88.0393	369.2132		351.2027	397.2082		379.1976	**D**	2283.1827	2282.1874		2343.2038	2326.1773	2325.1932	**23**
5	72.0808	468.2817		450.2711	496.2766		478.2660	**V**	2184.1143	2197.1347		**2228.1769**	2211.1503	2210.1663	**22**
6	88.0393	583.3086		565.2980	**611.3035**		593.2930	**D**	2069.0873	2068.0921		2129.1085	2112.0819	2111.0979	**21**
7	70.0651	680.3614		662.3508	708.3563		690.3457	**P**	1972.0346	1971.0393		**2014.0815**	**1997.0550**	**1996.0709**	**20**
8	86.0964	793.4454		775.4349	**821.4403**		803.4298	**L**	1858.9505	1857.9552		1917.0287	1900.0022	1899.0182	**19**
9	74.0600	894.4931		876.4825	922.4880		904.4775	**T**	1757.9028	1770.9232	1772.9025	1803.9447	1786.9181	1785.9341	**18**
10	86.0964	1007.5772		989.5666	1035.5721		1017.5615	**I**	1644.8188	1657.8392	1671.8548	**1702.8970**	1685.8705	1684.8864	**17**
11	74.0600	1108.6249		1090.6143	1136.6198		1118.6092	**T**	1543.7711	1556.7915	1558.7707	1589.8129	1572.7864	1571.8024	**16**
12	60.0444	1195.6569		1177.6463	1223.6518		1205.6412	**S**	1456.7390	1455.7438		**1488.7653**	1471.7387	1470.7547	**15**
13	60.0444	1282.6889		1264.6783	1310.6838		1292.6733	**S**	1369.7070	1368.7118		**1401.7332**	1384.7067	1383.7227	**14**
14	86.0964	1395.7730		1377.7624	1423.7679		1405.7573	**L**	1256.6230	1255.6277		**1314.7012**	1297.6747	1296.6906	**13**
15	60.0444	1482.8050		1464.7944	1510.7999		1492.7894	**S**	1169.5909	1168.5957		**1201.6171**	1184.5906	1183.6066	**12**
16	60.0444	1569.8370		1551.8265	1597.8319		1579.8214	**S**	1082.5589	1081.5636		**1114.5851**	1097.5586	1096.5745	**11**

17	88.0393	1684.8640		1666.8534	1712.8589		1694.8483	**D**	967.5320	966.5367		**1027.5531**	1010.5265	**1009.5425**	**10**
18	30.0338	1741.8854		1723.8749	1769.8804		1751.8698	**G**				**912.5261**	**895.4996**	894.5156	**9**
19	72.0808	1840.9539		1822.9433	1868.9488		1850.9382	**V**	811.4421	824.4625		**855.5047**	838.4781	837.4941	**8**
20	86.0964	1954.0379		1936.0273	1982.0328		1964.0223	**L**	698.3580	697.3628		**756.4363**	739.4097	738.4257	**7**
21	74.0600	2055.0856		2037.0750	2083.0805		2065.0699	**T**	597.3103	610.3307	612.3100	**643.3522**	626.3257	625.3416	**6**
22	72.0808	2154.1540		2136.1434	2182.1489		2164.1384	**V**	**498.2419**	511.2623		**542.3045**	525.2780		**5**
23	87.0553	2268.1969	2251.1704	2250.1864	2296.1918	2279.1653	2278.1813	**N**	384.1990	383.2037		**443.2361**	**426.2096**		**4**
24	30.0338	2325.2184	2308.1918	2307.2078	2353.2133	2336.1868	2335.2027	**G**				**329.1932**	312.1666		**3**
25	70.0651	2422.2712	2405.2446	2404.2606	2450.2661	2433.2395	2432.2555	**P**	230.1248	229.1295		**272.1717**	255.1452		**2**
26	**129.1135**							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

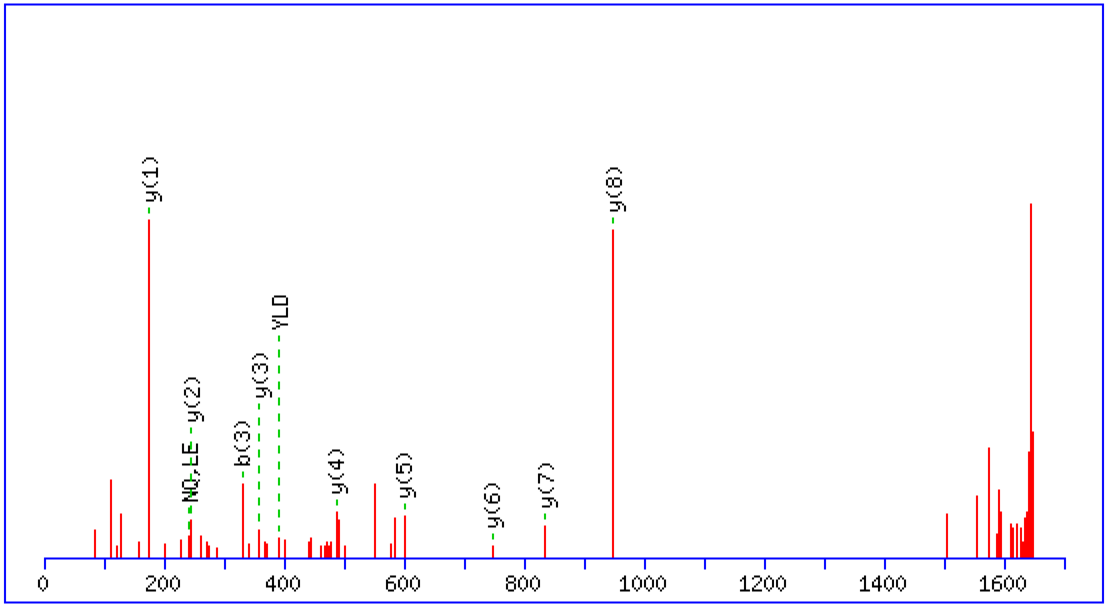
1278

MS/MS Fragmentation of SLEYLDLSFNQIAR

Found in gi|642534, lumican,

(1668.8555,1+)

Ions Score: 50



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		70.0287	**S**							**14**
2	86.0964	173.1285		155.1179	201.1234		183.1128	**L**	1523.7489	1522.7536		1581.8271	1564.8006	1563.8166	**13**
3	102.0550	302.1710		284.1605	**330.1660**		312.1554	**E**	1394.7063	1393.7110		1468.7431	1451.7165	1450.7325	**12**
4	136.0757	465.2344		447.2238	493.2293		475.2187	**Y**	1231.6430			1339.7005	1322.6739	1321.6899	**11**

5	86.0964	578.3184		560.3079	606.3134		588.3028	**L**	1118.5589	1117.5636		1176.6371	1159.6106	1158.6266	**10**
6	88.0393	693.3454		675.3348	721.3403		703.3297	**D**	1003.5320	1002.5367		1063.5531	1046.5265	1045.5425	**9**
7	86.0964	806.4294		788.4189	834.4244		816.4138	**L**	890.4479	889.4526		**948.5261**	931.4996	930.5156	**8**
8	60.0444	893.4615		875.4509	921.4564		903.4458	**S**	803.4159	802.4206		**835.4421**	818.4155	817.4315	**7**
9	120.0808	1040.5299		1022.5193	1068.5248		1050.5142	**F**	656.3474			**748.4100**	731.3835		**6**
10	87.0553	1154.5728	1137.5463	1136.5622	1182.5677	1165.5412	1164.5572	**N**	542.3045	541.3093		**601.3416**	584.3151		**5**
11	101.0709	1282.6314	1265.6048	1264.6208	1310.6263	1293.5998	1292.6157	**Q**	414.2459	413.2507		**487.2987**	470.2722		**4**
12	86.0964	1395.7155	1378.6889	1377.7049	1423.7104	1406.6838	1405.6998	**I**	301.1619	314.1823	328.1979	**359.2401**	342.2136		**3**
13	44.0495	1466.7526	1449.7260	1448.7420	1494.7475	1477.7209	1476.7369	**A**	230.1248			**246.1561**	229.1295		**2**
14	129.1135							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

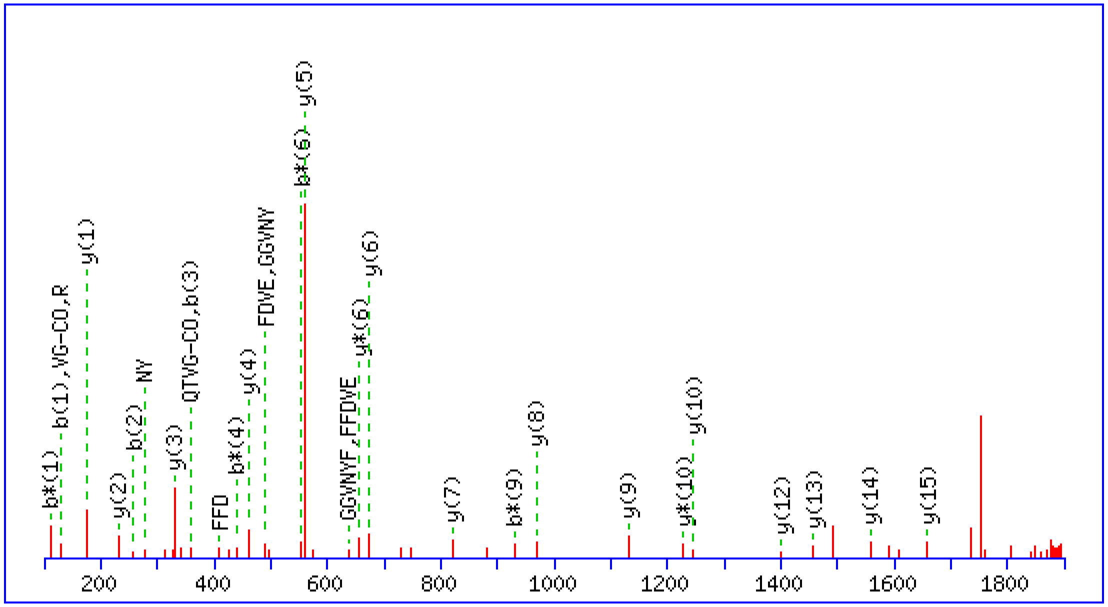
1279

MS/MS Fragmentation of QQTVGGVNYFFDVEVGR

Found in gi|118188, Cystatin-SN,

(1914.9723,1+)

Ions Score: 116



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	101.0709	101.0709	84.0444		**129.0659**	**112.0393**		**Q**							**17**
2	101.0709	229.1295	212.1030		**257.1244**	240.0979		**Q**	1713.8231	1712.8279		1786.8759	1769.8493	1768.8653	**16**
3	74.0600	330.1772	313.1506	312.1666	**358.1721**	341.1456	340.1615	**T**	1612.7754	1625.7958	1627.7751	**1658.8173**	1641.7908	1640.8067	**15**
4	72.0808	429.2456	412.2191	411.2350	457.2405	**440.2140**	439.2300	**V**	1513.7070	1526.7274		**1557.7696**	1540.7431	1539.7591	**14**
5	30.0338	486.2671	469.2405	468.2565	514.2620	497.2354	496.2514	**G**				**1458.7012**	1441.6747	1440.6906	**13**

6	30.0338	543.2885	526.2620	525.2780	571.2835	**554.2569**	553.2729	**G**				**1401.6797**	1384.6532	1383.6692	**12**
7	72.0808	642.3570	625.3304	624.3464	670.3519	653.3253	652.3413	**V**	1300.5957	1313.6161		1344.6583	1327.6317	1326.6477	**11**
8	87.0553	756.3999	739.3733	738.3893	784.3948	767.3682	766.3842	**N**	1186.5528	1185.5575		**1245.5899**	**1228.5633**	1227.5793	**10**
9	136.0757	919.4632	902.4367	901.4526	947.4581	**930.4316**	929.4476	**Y**	1023.4894			**1131.5469**	1114.5204	1113.5364	**9**
10	120.0808	1066.5316	1049.5051	1048.5211	1094.5265	1077.5000	1076.5160	**F**	876.4210			**968.4836**	951.4571	950.4730	**8**
11	120.0808	1213.6000	1196.5735	1195.5895	1241.5950	1224.5684	1223.5844	**F**	729.3526			**821.4152**	804.3886	803.4046	**7**
12	88.0393	1328.6270	1311.6004	1310.6164	1356.6219	1339.5953	1338.6113	**D**	614.3257	613.3304		**674.3468**	**657.3202**	656.3362	**6**
13	72.0808	1427.6954	1410.6688	1409.6848	1455.6903	1438.6638	1437.6797	**V**	515.2572	528.2776		**559.3198**	542.2933	541.3093	**5**
14	102.0550	1556.7380	1539.7114	1538.7274	1584.7329	1567.7064	1566.7223	**E**	386.2146	385.2194		**460.2514**	443.2249	442.2409	**4**
15	72.0808	1655.8064	1638.7799	1637.7958	1683.8013	1666.7748	1665.7908	**V**	287.1462	300.1666		**331.2088**	314.1823		**3**
16	30.0338	1712.8279	1695.8013	1694.8173	1740.8228	1723.7962	1722.8122	**G**				**232.1404**	215.1139		**2**
17	**129.1135**							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

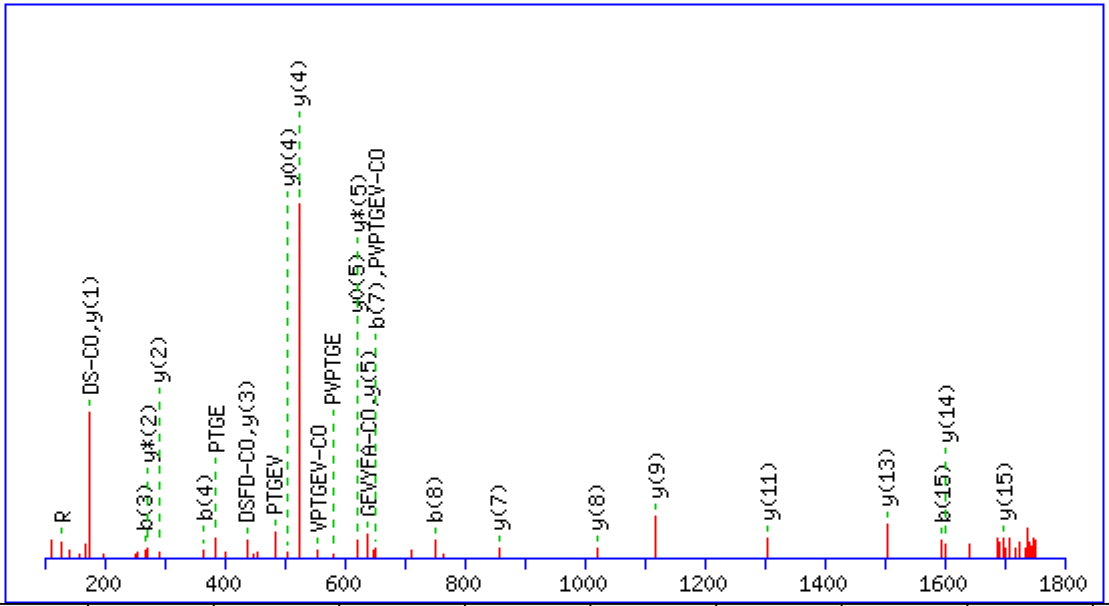
1280

MS/MS Fragmentation of APVPTGEVYFADSFDR

Found in gi|7709904, calnexin,

(1770.7988,1+)

Ions Score: 107



#	Immon.	a	a^0	b	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	44.0495	44.0495		72.0444		**A**							**16**
2	70.0651	141.1022		169.0972		**P**	1657.7493	1656.7540		**1699.7962**	1682.7697	1681.7857	**15**
3	72.0808	240.1707		**268.1656**		**V**	1558.6809	1571.7013		**1602.7435**	1585.7169	1584.7329	**14**
4	70.0651	337.2234		**365.2183**		**P**	1461.6281	1460.6329		**1503.6751**	1486.6485	1485.6645	**13**

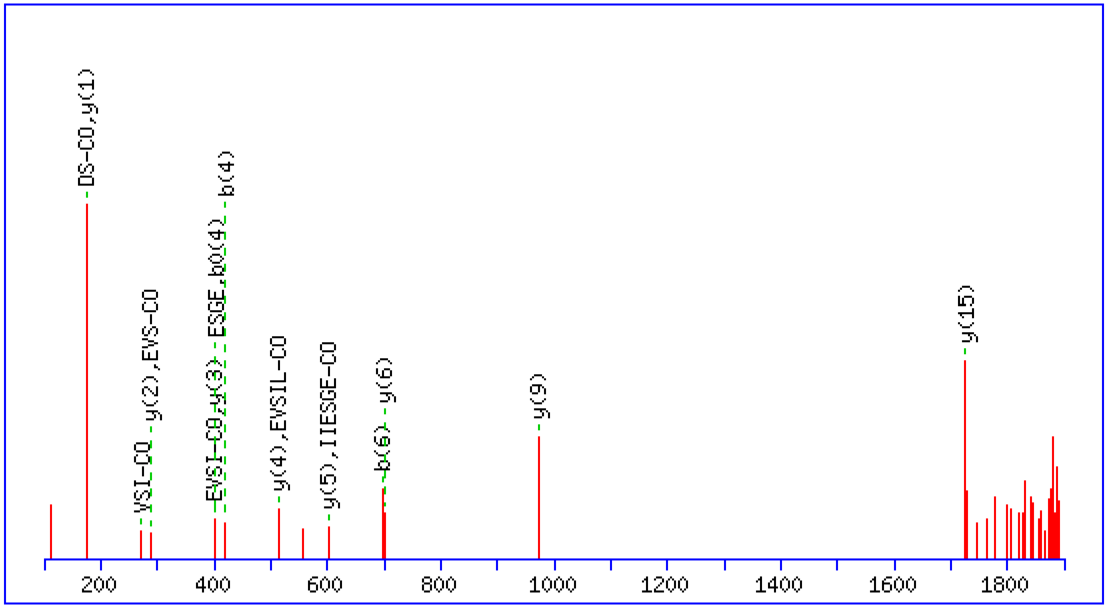
5	74.0600	438.2711	420.2605	466.2660	448.2554	**T**	1360.5804	1373.6008	1375.5801	1406.6223	1389.5957	1388.6117	**12**
6	30.0338	495.2926	477.2820	523.2875	505.2769	**G**				**1305.5746**	1288.5481	1287.5640	**11**
7	102.0550	624.3352	606.3246	**652.3301**	634.3195	**E**	1174.5164	1173.5211		1248.5531	1231.5266	1230.5426	**10**
8	72.0808	723.4036	705.3930	**751.3985**	733.3879	**V**	1075.4480	1088.4684		**1119.5106**	1102.4840	1101.5000	**9**
9	136.0757	886.4669	868.4563	914.4618	896.4512	**Y**	912.3846			**1020.4421**	1003.4156	1002.4316	**8**
10	120.0808	1033.5353	1015.5247	1061.5302	1043.5197	**F**	765.3162			**857.3788**	840.3523	839.3682	**7**
11	44.0495	1104.5724	1086.5619	1132.5673	1114.5568	**A**	694.2791			710.3104	693.2838	692.2998	**6**
12	88.0393	1219.5994	1201.5888	1247.5943	1229.5837	**D**	579.2522	578.2569		**639.2733**	**622.2467**	**621.2627**	**5**
13	60.0444	1306.6314	1288.6208	1334.6263	1316.6157	**S**	492.2201	491.2249		**524.2463**	507.2198	**506.2358**	**4**
14	120.0808	1453.6998	1435.6892	1481.6947	1463.6842	**F**	345.1517			**437.2143**	420.1878	419.2037	**3**
15	88.0393	1568.7268	1550.7162	**1596.7217**	1578.7111	**D**	230.1248	229.1295		**290.1459**	**273.1193**	272.1353	**2**
16	**129.1135**					**R**	74.0237	73.0284		**175.1190**	158.0924		

MS/MS Fragmentation of ADSFYIIESGEVSILIR

Found in gi|4758958, cAMP-dependent protein kinase type II-alpha regulatory subunit,

(1911.9822,1+)

Ions Score: 60



#	Immon.	a	a^0	b	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	44.0495	44.0495		72.0444		A							17
2	88.0393	159.0764	141.0659	187.0713	169.0608	D	1780.9480	1779.9527		1840.9691	1823.9426	1822.9585	16
3	60.0444	246.1084	228.0979	274.1034	256.0928	S	1693.9159	1692.9207		1725.9422	1708.9156	1707.9316	15

4	120.0808	393.1769	375.1663	**421.1718**	**403.1612**	**F**	1546.8475			1638.9101	1621.8836	1620.8996	**14**
5	136.0757	556.2402	538.2296	584.2351	566.2245	**Y**	1383.7842			1491.8417	1474.8152	1473.8312	**13**
6	86.0964	669.3243	651.3137	**697.3192**	679.3086	**I**	1270.7001	1283.7205	1297.7362	1328.7784	1311.7518	1310.7678	**12**
7	86.0964	782.4083	764.3978	810.4032	792.3927	**I**	1157.6161	1170.6365	1184.6521	1215.6943	1198.6678	1197.6838	**11**
8	102.0550	911.4509	893.4403	939.4458	921.4353	**E**	1028.5735	1027.5782		1102.6103	1085.5837	1084.5997	**10**
9	60.0444	998.4829	980.4724	1026.4779	1008.4673	**S**	941.5415	940.5462		**973.5677**	956.5411	955.5571	**9**
10	30.0338	1055.5044	1037.4938	1083.4993	1065.4888	**G**				886.5356	869.5091	868.5251	**8**
11	102.0550	1184.5470	1166.5364	1212.5419	1194.5313	**E**	755.4774	754.4822		829.5142	812.4876	811.5036	**7**
12	72.0808	1283.6154	1265.6048	1311.6103	1293.5998	**V**	656.4090	669.4294		**700.4716**	683.4450	682.4610	**6**
13	60.0444	1370.6474	1352.6369	1398.6424	1380.6318	**S**	569.3770	568.3817		**601.4032**	584.3766	583.3926	**5**
14	86.0964	1483.7315	1465.7209	1511.7264	1493.7159	**I**	456.2929	469.3133	483.3289	**514.3711**	497.3446		**4**
15	86.0964	1596.8156	1578.8050	1624.8105	1606.7999	**L**	343.2088	342.2136		**401.2871**	384.2605		**3**
16	86.0964	1709.8996	1691.8891	1737.8945	1719.8840	**I**	230.1248	243.1452	257.1608	**288.2030**	271.1765		**2**

17	129.1135					**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

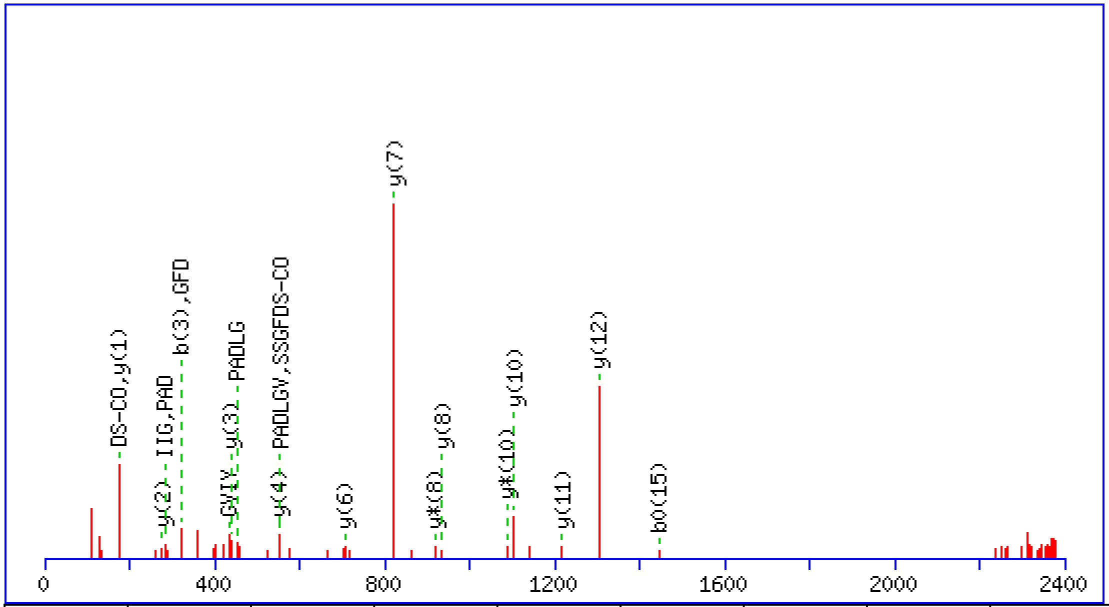
1282

MS/MS Fragmentation of GVYIIGSSGFDSIPADLGVIYTR

Found in gi|4929567, CGI-49 protein,

(2400.2207,1+)

Ions Score: 65



#	Immon.	a	a^0	b	b^0	Seq.	v	w	w'	y	y*	y^0	#

1	30.0338	30.0338		58.0287		**G**							**23**
2	72.0808	129.1022		157.0972		**V**	2299.1605	2312.1809		2343.2231	2326.1965	2325.2125	**22**
3	136.0757	292.1656		**320.1605**		**Y**	2136.0972			2244.1547	2227.1281	2226.1441	**21**
4	86.0964	405.2496		**433.2445**		**I**	2023.0131	2036.0335	2050.0491	2081.0913	2064.0648	2063.0808	**20**
5	86.0964	518.3337		546.3286		**I**	1909.9290	1922.9494	1936.9651	1968.0073	1950.9807	1949.9967	**19**
6	30.0338	575.3552		603.3501		**G**				1854.9232	1837.8967	1836.9127	**18**
7	60.0444	662.3872	644.3766	690.3821	672.3715	**S**	1765.8755	1764.8803		1797.9018	1780.8752	1779.8912	**17**
8	60.0444	749.4192	731.4087	777.4141	759.4036	**S**	1678.8435	1677.8483		1710.8697	1693.8432	1692.8592	**16**
9	30.0338	806.4407	788.4301	834.4356	816.4250	**G**				1623.8377	1606.8112	1605.8271	**15**
10	120.0808	953.5091	935.4985	981.5040	963.4934	**F**	1474.7536			1566.8162	1549.7897	1548.8057	**14**
11	88.0393	1068.5360	1050.5255	1096.5310	1078.5204	**D**	1359.7267	1358.7314		1419.7478	1402.7213	1401.7373	**13**
12	60.0444	1155.5681	1137.5575	1183.5630	1165.5524	**S**	1272.6947	1271.6994		**1304.7209**	1287.6943	1286.7103	**12**
13	86.0964	1268.6521	1250.6416	1296.6470	1278.6365	**I**	1159.6106	1172.6310	1186.6467	**1217.6889**	1200.6623	1199.6783	**11**
14	70.0651	1365.70	1347.69	1393.69	1375.68	**P**	1062.55	1061.56		**1104.60**	**1087.57**	1086.59	**10**

		49	43	98	92		78	26		**48**	**82**	42	
15	44.0495	1436.7420	1418.7314	1464.7369	**1446.7264**	**A**	991.5207			1007.5520	990.5255	989.5415	**9**
16	88.0393	1551.7690	1533.7584	1579.7639	1561.7533	**D**	876.4938	875.4985		**936.5149**	**919.4884**	918.5043	**8**
17	86.0964	1664.8530	1646.8424	1692.8479	1674.8374	**L**	763.4097	762.4145		**821.4880**	804.4614	803.4774	**7**
18	30.0338	1721.8745	1703.8639	1749.8694	1731.8588	**G**				**708.4039**	691.3774	690.3933	**6**
19	72.0808	1820.9429	1802.9323	1848.9378	1830.9272	**V**	607.3198	620.3402		651.3824	634.3559	633.3719	**5**
20	86.0964	1934.0270	1916.0164	1962.0219	1944.0113	**I**	494.2358	507.2562	521.2718	**552.3140**	535.2875	534.3035	**4**
21	136.0757	2097.0903	2079.0797	2125.0852	2107.0746	**Y**	331.1724			**439.2300**	422.2034	421.2194	**3**
22	74.0600	2198.1380	2180.1274	2226.1329	2208.1223	**T**	230.1248	243.1452	245.1244	**276.1666**	259.1401	258.1561	**2**
23	129.1135					**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

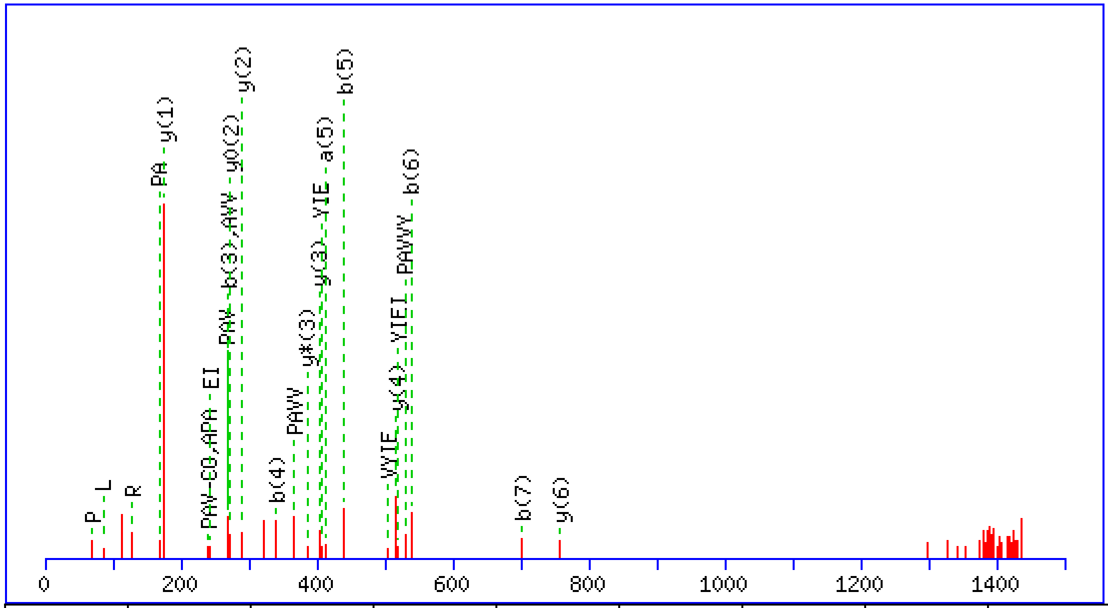
1283

MS/MS Fragmentation of TAPAVVYIEILDR

Found in gi|21466051, Chain A, Crystal Structure Of The Mitochondrial Serine Protease Htra2,

(1459.7542,1+)

Ions Score: 39



#	Immon.	a	a⁰	b	b⁰	Seq.	v	w	w'	y	y*	y⁰	#
1	74.0600	74.0600	56.0495	102.0550	84.0444	T							13
2	44.0495	145.0972	127.0866	173.0921	155.0815	A	1342.7365			1358.7678	1341.7413	1340.7573	12
3	**70.0651**	242.1499	224.1394	**270.1448**	252.1343	P	1245.6838	1244.6885		1287.7307	1270.7042	1269.7201	11
4	44.0495	313.1870	295.1765	**341.1819**	323.1714	A	1174.6467			1190.6780	1173.6514	1172.6674	10
5	72.0808	**412.2554**	394.2449	**440.2504**	422.2398	V	1075.5782	1088.5986		1119.6408	1102.6143	1101.6303	9
6	72.0808	511.3239	493.3133	**539.3188**	521.3082	V	976.5098	989.5302		1020.5724	1003.5459	1002.5619	8

7	136.0757	674.3872	656.3766	**702.3821**	684.3715	**Y**	813.4465			921.5040	904.4775	903.4934	**7**
8	**86.0964**	787.4713	769.4607	815.4662	797.4556	**I**	700.3624	713.3828	727.3985	**758.4407**	741.4141	740.4301	**6**
9	102.0550	916.5138	898.5033	944.5088	926.4982	**E**	571.3198	570.3246		645.3566	628.3301	627.3461	**5**
10	**86.0964**	1029.5979	1011.5873	1057.5928	1039.5823	**I**	458.2358	471.2562	485.2718	**516.3140**	499.2875	498.3035	**4**
11	**86.0964**	1142.6820	1124.6714	1170.6769	1152.6663	**L**	345.1517	344.1565		**403.2300**	**386.2034**	385.2194	**3**
12	88.0393	1257.7089	1239.6984	1285.7038	1267.6933	**D**	230.1248	229.1295		**290.1459**	273.1193	**272.1353**	**2**
13	**129.1135**					**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

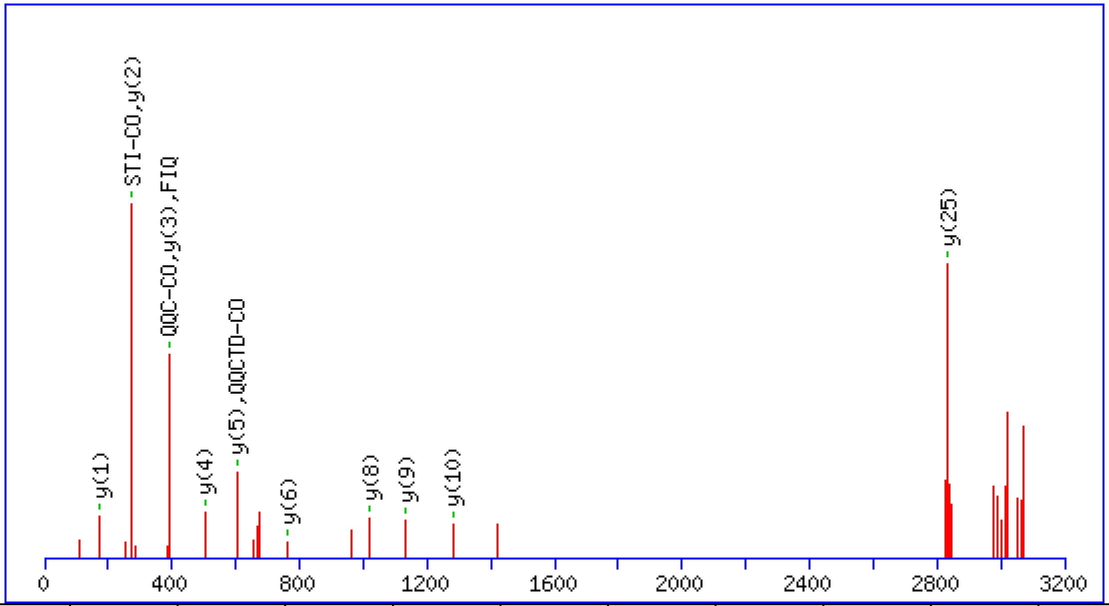
1284

MS/MS Fragmentation of YDGSTIVPGEQGAEYQHFIQQCTDDVR

Found in gi|52696274, Chain A, Nmr Structure Of Human Coactosin-Like Protein,

(3113.4163,1+)

Ions Score: 68



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	136.0757	136.0757			164.0706			Y							27
2	88.0393	251.1026		233.0921	279.0975		261.0870	D	2890.3061	2889.3108		2950.3272	2933.3006	2932.3166	26
3	30.0338	308.1241		290.1135	336.1190		318.1084	G				2835.3003	2818.2737	2817.2897	25
4	60.0444	395.1561		377.1456	423.1510		405.1405	S	2746.2526	2745.2573		2778.2788	2761.2522	2760.2682	24
5	74.0600	496.2038		478.1932	524.1987		506.1882	T	2645.2049	2658.2253	2660.2046	2691.2468	2674.2202	2673.2362	23
6	86.0964	609.2879		591.2773	637.2828		619.2722	I	2532.1208	2545.1412	2559.1569	2590.1991	2573.1725	2572.1885	22
7	72.080	708.35		690.34	736.35		718.34	V	2433.0	2446.0		2477.1	2460.0	2459.1	21

	8	63		57	12		06		524	728		150	885	045	
8	70.0651	805.4090		787.3985	833.4040		815.3934	**P**	2335.9997	2335.0044		2378.0466	2361.0201	2360.0360	**20**
9	30.0338	862.4305		844.4199	890.4254		872.4149	**G**				2280.9938	2263.9673	2262.9833	**19**
10	102.0550	991.4731		973.4625	1019.4680		1001.4575	**E**	2149.9356	2148.9403		2223.9724	2206.9458	2205.9618	**18**
11	101.0709	1119.5317	1102.5051	1101.5211	1147.5266	1130.5000	1129.5160	**Q**	2021.8770	2020.8818		2094.9298	2077.9032	2076.9192	**17**
12	30.0338	1176.5531	1159.5266	1158.5426	1204.5481	1187.5215	1186.5375	**G**				1966.8712	1949.8447	1948.8606	**16**
13	44.0495	1247.5903	1230.5637	1229.5797	1275.5852	1258.5586	1257.5746	**A**	1893.8184			1909.8497	1892.8232	1891.8392	**15**
14	102.0550	1376.6329	1359.6063	1358.6223	1404.6278	1387.6012	1386.6172	**E**	1764.7758	1763.7806		1838.8126	1821.7861	1820.8021	**14**
15	136.0757	1539.6962	1522.6696	1521.6856	1567.6911	1550.6645	1549.6805	**Y**	1601.7125			1709.7700	1692.7435	1691.7595	**13**
16	101.0709	1667.7548	1650.7282	1649.7442	1695.7497	1678.7231	1677.7391	**Q**	1473.6539	1472.6587		1546.7067	1529.6802	1528.6961	**12**
17	110.0713	1804.8137	1787.7871	1786.8031	1832.8086	1815.7820	1814.7980	**H**	1336.5950			1418.6481	1401.6216	1400.6376	**11**
18	120.0808	1951.8821	1934.8555	1933.8715	1979.8770	1962.8505	1961.8664	**F**	1189.5266			**1281.5892**	1264.5627	1263.5786	**10**
19	86.0964	2064.9661	2047.9396	2046.9556	2092.9611	2075.9345	2074.9505	**I**	1076.4425	1089.4630	1103.4786	**1134.5208**	1117.4943	1116.5102	**9**
20	101.0709	2193.0247	2175.9982	2175.0142	2221.0196	2203.9931	2203.0091	**Q**	948.3840	947.3887		**1021.4367**	1004.4102	1003.4262	**8**

21	101.0709	2321.0833	2304.0568	2303.0727	2349.0782	2332.0517	2331.0677	**Q**	820.3254	819.3301		893.3782	876.3516	875.3676	**7**
22	133.0430	2481.1140	2464.0874	2463.1034	2509.1089	2492.0823	2491.0983	**C**	660.2947	659.2995		**765.3196**	748.2930	747.3090	**6**
23	74.0600	2582.1616	2565.1351	2564.1511	2610.1565	2593.1300	2592.1460	**T**	559.2471	572.2675	574.2467	**605.2889**	588.2624	587.2784	**5**
24	88.0393	2697.1886	2680.1620	2679.1780	2725.1835	2708.1569	2707.1729	**D**	444.2201	443.2249		**504.2413**	487.2147	486.2307	**4**
25	88.0393	2812.2155	2795.1890	2794.2050	2840.2104	2823.1839	2822.1999	**D**	329.1932	328.1979		**389.2143**	372.1878	371.2037	**3**
26	72.0808	2911.2839	2894.2574	2893.2734	2939.2788	2922.2523	2921.2683	**V**	230.1248	243.1452		**274.1874**	257.1608		**2**
27	129.1135							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

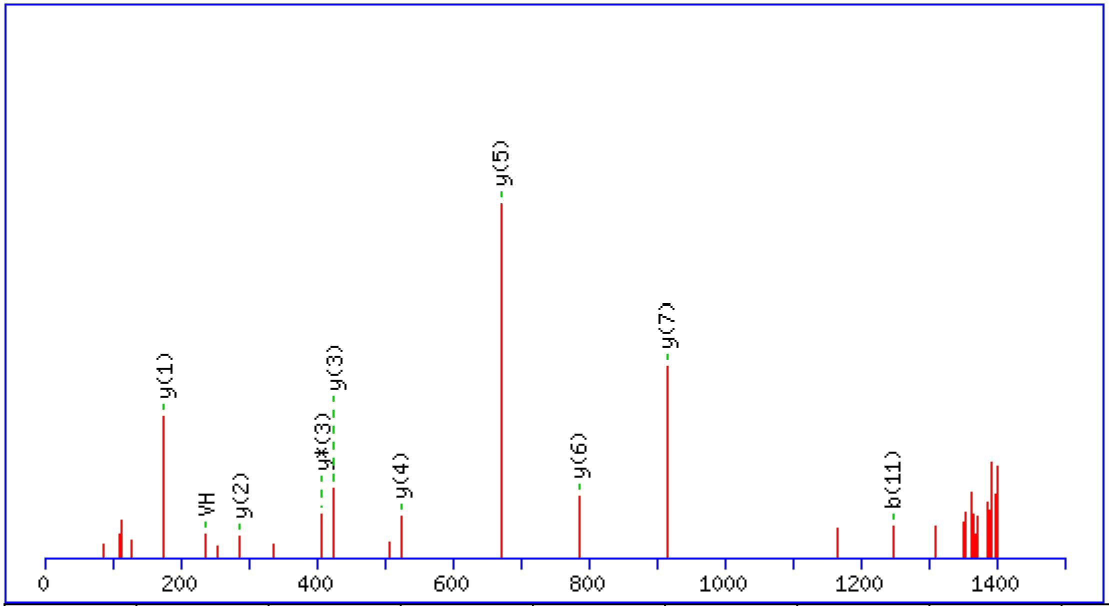
1285

MS/MS Fragmentation of VHVGDEDFVHLR

Found in gi|145579988, Chain A, Stefin B (Cystatin B) Tetramer,

(1422.7471,1+)

Ions Score: 58



#	Immon.	a	a^0	b	b^0	Seq.	v	w	y	y*	y^0	#
1	72.0808	72.0808		100.0757		**V**						**12**
2	110.0713	209.1397		**237.1346**		**H**	1241.5909		1323.6440	1306.6175	1305.6335	**11**
3	72.0808	308.2081		336.2030		**V**	1142.5225	1155.5429	1186.5851	1169.5586	1168.5745	**10**
4	30.0338	365.2296		393.2245		**G**			1087.5167	1070.4902	1069.5061	**9**
5	88.0393	480.2565	462.2459	508.2514	490.2409	**D**	970.4741	969.4789	1030.4952	1013.4687	1012.4847	**8**
6	102.0550	609.2991	591.2885	637.2940	619.2835	**E**	841.4315	840.4363	**915.4683**	898.4417	897.4577	**7**
7	88.0393	724.3260	706.3155	752.3210	734.3104	**D**	726.4046	725.4093	**786.4257**	769.3991	768.4151	**6**
8	120.0808	871.3945	853.3839	899.3894	881.3788	**F**	579.3362		**671.3988**	654.3722		**5**

9	72.0808	970.4629	952.4523	998.4578	980.4472	**V**	480.2677	493.2881	**524.3303**	507.3038		**4**
10	110.0713	1107.5218	1089.5112	1135.5167	1117.5061	**H**	343.2088		**425.2619**	**408.2354**		**3**
11	86.0964	1220.6058	1202.5953	**1248.6008**	1230.5902	**L**	230.1248	229.1295	**288.2030**	271.1765		**2**
12	129.1135					**R**	74.0237	73.0284	**175.1190**	158.0924		

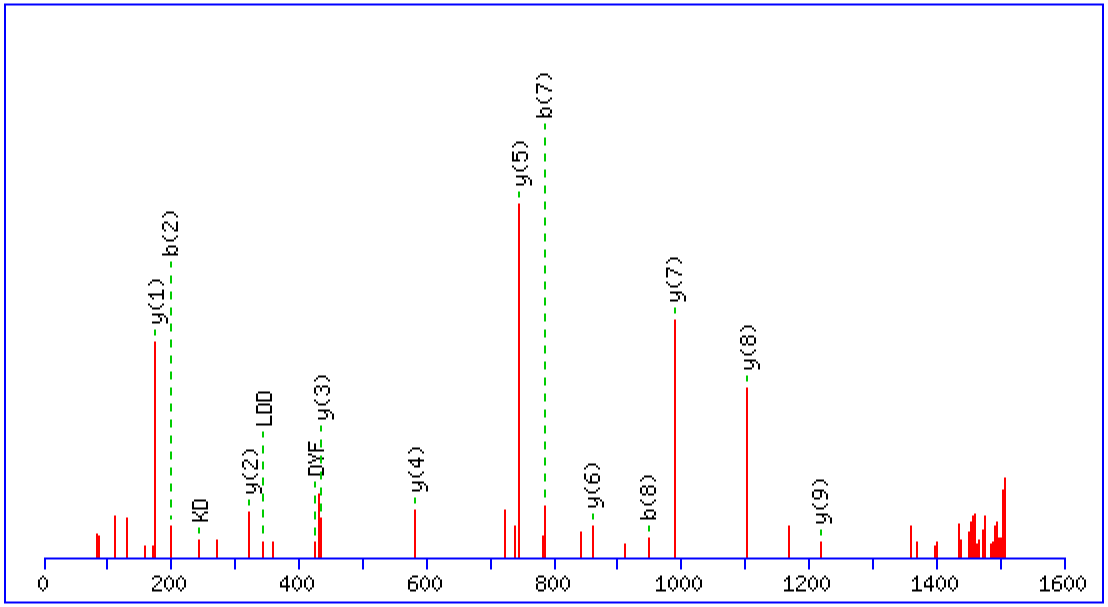
1286

MS/MS Fragmentation of VVLDDKDYFLFR

Found in gi|4008131, chaperonin 10,

(1529.7937,1+)

Ions Score: 62



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	y	y*	y^0	#
1	72.0808	72.0808			100.0757			**V**						**12**
2	72.0808	171.1492			**199.1441**			**V**	1386.6688	1399.6892	1430.7314	1413.7049	1412.7209	**11**
3	86.0964	284.2333			312.2282			**L**	1273.5848	1272.5895	1331.6630	1314.6365	1313.6525	**10**
4	88.0393	399.2602		381.2496	427.2551		409.2445	**D**	1158.5578	1157.5626	**1218.5790**	1201.5524	1200.5684	**9**
5	88.0393	514.2871		496.2766	542.2821		524.2715	**D**	1043.5309	1042.5356	**1103.5520**	1086.5255	1085.5415	**8**
6	101.1073	642.3821	625.3556	624.3715	670.3770	653.3505	652.3665	**K**	915.4359	914.4407	**988.5251**	971.4985	970.5145	**7**
7	88.0393	757.4090	740.3825	739.3985	**785.4040**	768.3774	767.3934	**D**	800.4090	799.4137	**860.4301**	843.4036	842.4196	**6**
8	136.0757	920.4724	903.4458	902.4618	**948.4673**	931.4407	930.4567	**Y**	637.3457		**745.4032**	728.3766		**5**
9	120.0808	1067.5408	1050.5142	1049.5302	1095.5357	1078.5092	1077.5251	**F**	490.2772		**582.3398**	565.3133		**4**
10	86.0964	1180.6249	1163.5983	1162.6143	1208.6198	1191.5932	1190.6092	**L**	377.1932	376.1979	**435.2714**	418.2449		**3**
11	120.0808	1327.6933	1310.6667	1309.6827	1355.6882	1338.6616	1337.6776	**F**	230.1248		**322.1874**	305.1608		**2**
12	129.1135							**R**	74.0237	73.0284	**175.1190**	158.0924		

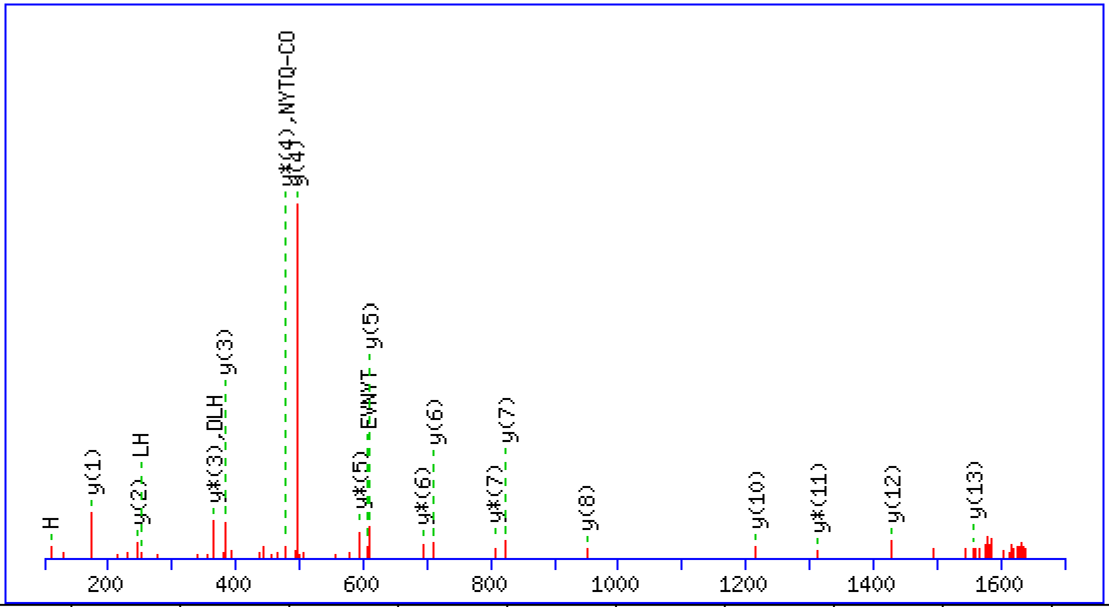
1287

MS/MS Fragmentation of TEVNYTQLVDLHAR

Found in gi|75709200, phospholipid hydroperoxide glutathione peroxidase, mitochondrial isoform A precursor,

(1658.8502,1+)

Ions Score: 89



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	74.0600	74.0600		56.0495	102.0550		84.0444	**T**							**14**
2	102.0550	203.1026		185.0921	231.0975		213.0870	**E**	1483.7652	1482.7700		**1557.8020**	1540.7754	1539.7914	**13**
3	72.0808	302.1710		284.1605	330.1660		312.1554	**V**	1384.6968	1397.7172		**1428.7594**	1411.7328	1410.7488	**12**
4	87.055	416.21	399.18	398.20	444.20	427.18	426.19	**N**	1270.6	1269.6		1329.6	**1312.6**	1311.6	**11**

	3	40	74	34	89	23	83		539	586		910	**644**	804	
5	136.0757	579.2773	562.2508	561.2667	**607.2722**	590.2457	589.2617	**Y**	1107.5905			**1215.6480**	1198.6215	1197.6375	**10**
6	74.0600	680.3250	663.2984	662.3144	708.3199	691.2933	690.3093	**T**	1006.5429	1019.5633	1021.5425	1052.5847	1035.5582	1034.5742	**9**
7	101.0709	808.3836	791.3570	790.3730	836.3785	819.3519	818.3679	**Q**	878.4843	877.4890		**951.5370**	934.5105	933.5265	**8**
8	86.0964	921.4676	904.4411	903.4571	949.4625	932.4360	931.4520	**L**	765.4002	764.4050		**823.4785**	**806.4519**	805.4679	**7**
9	72.0808	1020.5360	1003.5095	1002.5255	1048.5310	1031.5044	1030.5204	**V**	666.3318	679.3522		**710.3944**	**693.3678**	692.3838	**6**
10	88.0393	1135.5630	1118.5364	1117.5524	1163.5579	1146.5313	1145.5473	**D**	551.3049	550.3096		**611.3260**	**594.2994**	593.3154	**5**
11	86.0964	1248.6470	1231.6205	1230.6365	1276.6420	1259.6154	1258.6314	**L**	438.2208	437.2255		**496.2990**	**479.2725**		**4**
12	**110.0713**	1385.7060	1368.6794	1367.6954	1413.7009	1396.6743	1395.6903	**H**	301.1619			**383.2150**	**366.1884**		**3**
13	44.0495	1456.7431	1439.7165	1438.7325	1484.7380	1467.7114	1466.7274	**A**	230.1248			**246.1561**	229.1295		**2**
14	129.1135							**R**	74.0237	73.0284		**175.1190**	158.0924		

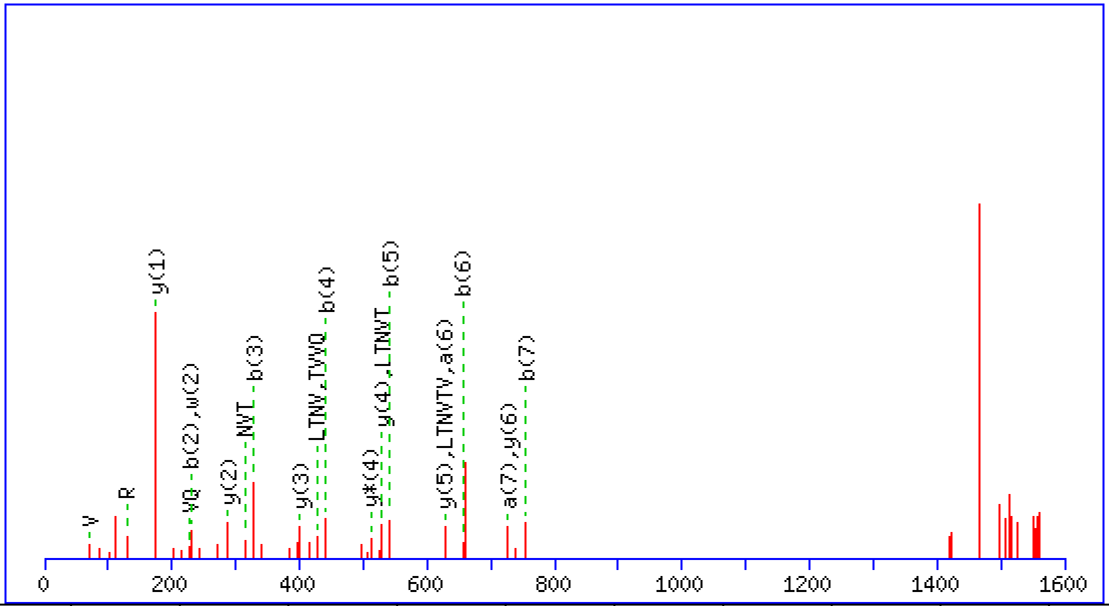
1288

MS/MS Fragmentation of DIVLTNVTVVQLLR

Found in gi|9502072, spermatogenic cell-specific glyceraldehyde 3-phosphate dehydrogenase-2,

(1582.9894,1+)

Ions Score: 51



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	88.0393	88.0393		70.0287	116.0342		98.0237	D							14
2	86.0964	201.1234		183.1128	**229.1183**		211.1077	I	1409.8475	1422.8679	1436.8835	1467.9257	1450.8992	1449.9152	13
3	**72.0808**	300.1918		282.1812	**328.1867**		310.1761	V	1310.7791	1323.7995		1354.8417	1337.8151	1336.8311	12
4	86.0964	413.2758		395.2653	**441.2708**		423.2602	L	1197.6950	1196.6998		1255.7732	1238.7467	1237.7627	11
5	74.0600	514.3235		496.3130	**542.3184**		524.3079	T	1096.6473	1109.6677	1111.6470	1142.6892	1125.6626	1124.6786	10
6	87.055	**628.36**	611.33	610.35	**656.36**	639.33	638.35	N	982.60	981.60		1041.6	1024.6	1023.6	9

	3	**65**	99	59	**14**	48	08		44	91		415	150	309	
7	**72.0808**	**727.4349**	710.4083	709.4243	**755.4298**	738.4032	737.4192	**V**	883.5360	896.5564		927.5986	910.5720	909.5880	**8**
8	74.0600	828.4825	811.4560	810.4720	856.4775	839.4509	838.4669	**T**	782.4883	795.5087	797.4880	828.5302	811.5036	810.5196	**7**
9	**72.0808**	927.5510	910.5244	909.5404	955.5459	938.5193	937.5353	**V**	683.4199	696.4403		**727.4825**	710.4559		**6**
10	**72.0808**	1026.6194	1009.5928	1008.6088	1054.6143	1037.5877	1036.6037	**V**	584.3515	597.3719		**628.4141**	611.3875		**5**
11	101.0709	1154.6780	1137.6514	1136.6674	1182.6729	1165.6463	1164.6623	**Q**	456.2929	455.2976		**529.3457**	**512.3191**		**4**
12	86.0964	1267.7620	1250.7355	1249.7515	1295.7569	1278.7304	1277.7464	**L**	343.2088	342.2136		**401.2871**	384.2605		**3**
13	86.0964	1380.8461	1363.8195	1362.8355	1408.8410	1391.8144	1390.8304	**L**	230.1248	**229.1295**		**288.2030**	271.1765		**2**
14	**129.1135**							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

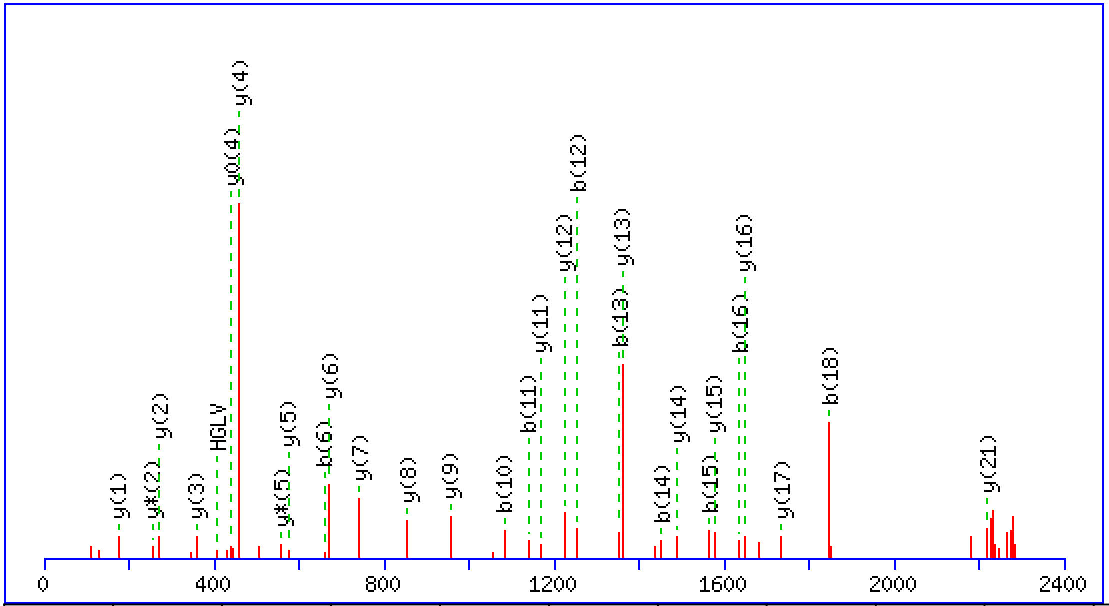
1289

MS/MS Fragmentation of SGYHQSASEHGLVVIAPDTSPR

Found in gi|55957281, esterase D/formylglutathione hydrolase,

(2308.0579,1+)

Ions Score:149



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		70.0287	S							22
2	30.0338	117.0659		99.0553	145.0608		127.0502	G				**2221.0996**	2204.0731	2203.0891	21
3	136.0757	280.1292		262.1186	308.1241		290.1135	Y	2056.0206			2164.0782	2147.0516	2146.0676	20
4	110.0713	417.1881		399.1775	445.1830		427.1724	H	1918.9617			2001.0148	1983.9883	1983.0043	19
5	101.0709	545.2467	528.2201	527.2361	573.2416	556.2150	555.2310	Q	1790.9032	1789.9079		1863.9559	1846.9294	1845.9454	18
6	60.0444	632.2787	615.2522	614.2681	**660.2736**	643.2471	642.2631	S	1703.8711	1702.8759		**1735.8973**	1718.8708	1717.8868	17
7	44.049	703.31	686.28	685.30	731.31	714.28	713.30	A	1632.8			**1648.8**	1631.8	1630.8	16

	5	58	93	52	07	42	02		340			**653**	388	547	
8	60.0444	790.3478	773.3213	772.3373	818.3428	801.3162	800.3322	**S**	1545.8020	1544.8067		**1577.8282**	1560.8016	1559.8176	**15**
9	102.0550	919.3904	902.3639	901.3799	947.3854	930.3588	929.3748	**E**	1416.7594	1415.7641		**1490.7962**	1473.7696	1472.7856	**14**
10	110.0713	1056.4493	1039.4228	1038.4388	**1084.4443**	1067.4177	1066.4337	**H**	1279.7005			**1361.7536**	1344.7270	1343.7430	**13**
11	30.0338	1113.4708	1096.4443	1095.4602	**1141.4657**	1124.4392	1123.4552	**G**				**1224.6947**	1207.6681	1206.6841	**12**
12	86.0964	1226.5549	1209.5283	1208.5443	**1254.5498**	1237.5232	1236.5392	**L**	1109.5950	1108.5997		**1167.6732**	1150.6467	1149.6626	**11**
13	72.0808	1325.6233	1308.5967	1307.6127	**1353.6182**	1336.5917	1335.6076	**V**	1010.5265	1023.5469		1054.5891	1037.5626	1036.5786	**10**
14	72.0808	1424.6917	1407.6652	1406.6811	**1452.6866**	1435.6601	1434.6761	**V**	911.4581	924.4785		**955.5207**	938.4942	937.5102	**9**
15	86.0964	1537.7758	1520.7492	1519.7652	**1565.7707**	1548.7441	1547.7601	**I**	798.3741	811.3945	825.4101	**856.4523**	839.4258	838.4417	**8**
16	44.0495	1608.8129	1591.7863	1590.8023	**1636.8078**	1619.7812	1618.7972	**A**	727.3369			**743.3682**	726.3417	725.3577	**7**
17	70.0651	1705.8656	1688.8391	1687.8551	1733.8606	1716.8340	1715.8500	**P**	630.2842	629.2889		**672.3311**	655.3046	654.3206	**6**
18	88.0393	1820.8926	1803.8660	1802.8820	**1848.8875**	1831.8610	1830.8769	**D**	515.2572	514.2620		**575.2784**	**558.2518**	557.2678	**5**
19	74.0600	1921.9403	1904.9137	1903.9297	1949.9352	1932.9086	1931.9246	**T**	414.2096	427.2300	429.2092	**460.2514**	443.2249	**442.2409**	**4**
20	60.0444	2008.9723	1991.9457	1990.9617	2036.9672	2019.9407	2018.9566	**S**	327.1775	326.1823		**359.2037**	342.1772	341.1932	**3**

21	70.0651	2106.0251	2088.9985	2088.0145	2134.0200	2116.9934	2116.0094	**P**	230.1248	229.1295		**272.1717**	**255.1452**		**2**
22	129.1135							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

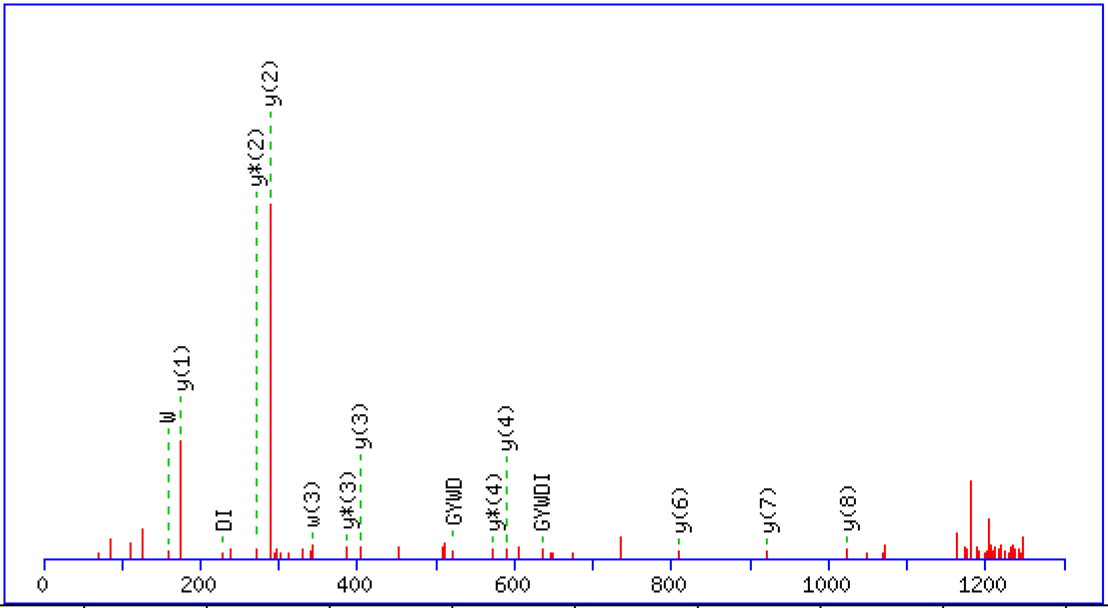
1290

MS/MS Fragmentation of PMTLGYWDIR

Found in gi|468260, glutathione S-transferase GSTM5-5,

(1267.601,1+)

Ions Score:39



#	Immon.	a	a^0	b	b^0	Seq.	v	w	w'	y	y*	y^0	#

1	70.0651	70.0651		98.0600		**P**							**10**
2	56.0495	153.1022		181.0972		**M**	1078.5316	1077.5364		1106.5629	1089.5364	1088.5524	**9**
3	74.0600	254.1499	236.1394	282.1448	264.1343	**T**	977.4839	990.5043	992.4836	**1023.5258**	1006.4993	1005.5152	**8**
4	86.0964	367.2340	349.2234	395.2289	377.2183	**L**	864.3999	863.4046		**922.4781**	905.4516	904.4676	**7**
5	30.0338	424.2555	406.2449	452.2504	434.2398	**G**				**809.3941**	792.3675	791.3835	**6**
6	136.0757	587.3188	569.3082	615.3137	597.3031	**Y**	644.3151			752.3726	735.3461	734.3620	**5**
7	**159.0917**	773.3981	755.3875	801.3930	783.3824	**W**	458.2358			**589.3093**	**572.2827**	571.2987	**4**
8	88.0393	888.4250	870.4145	916.4200	898.4094	**D**	343.2088	**342.2136**		**403.2300**	**386.2034**	385.2194	**3**
9	86.0964	1001.5091	983.4985	1029.5040	1011.4935	**I**	230.1248	243.1452	257.1608	**288.2030**	**271.1765**		**2**
10	129.1135					**R**	74.0237	73.0284		**175.1190**	158.0924		

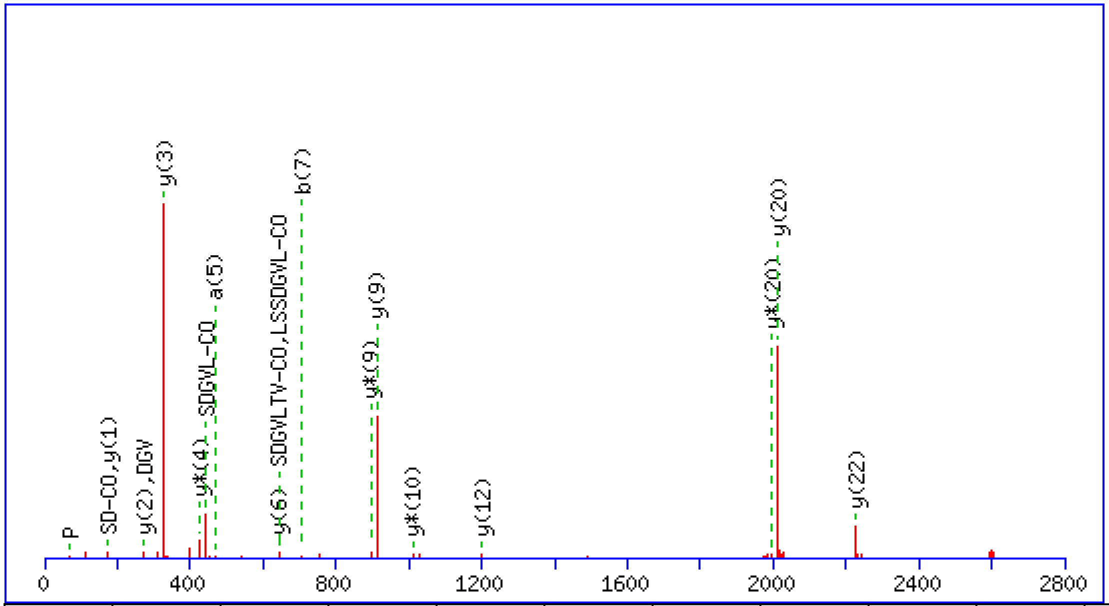
1291

MS/MS Fragmentation of IPADVDPLTITSSLSSDGVLTVNGPR

Found in gi|2852648, unknown,

(2624.271,1+)

Ions Score:42



#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964			114.0913			I							26
2	70.0651	183.1492			211.1441			P	2469.2467	2468.2515		2511.2937	2494.2671	2493.2831	25
3	44.0495	254.1863			282.1812			A	2398.2096			2414.2409	2397.2144	2396.2304	24
4	88.0393	369.2132		351.2027	397.2082		379.1976	D	2283.1827	2282.1874		2343.2038	2326.1773	2325.1932	23
5	72.0808	468.2817		450.2711	496.2766		478.2660	V	2184.1143	2197.1347		2228.1769	2211.1503	2210.1663	22
6	88.0393	583.3086		565.2980	611.3035		593.2930	D	2069.0873	2068.0921		2129.1085	2112.0819	2111.0979	21
7	70.065	680.36		662.35	708.35		690.34	P	1972.0	1971.0		2014.0	1997.0	1996.0	20

	1	14		08	**63**		57		346	393		**815**	**550**	709	
8	86.0964	793.4454		775.4349	821.4403		803.4298	**L**	1858.9505	1857.9552		1917.0287	1900.0022	1899.0182	**19**
9	74.0600	894.4931		876.4825	922.4880		904.4775	**T**	1757.9028	1770.9232	1772.9025	1803.9447	1786.9181	1785.9341	**18**
10	86.0964	1007.5772		989.5666	1035.5721		1017.5615	**I**	1644.8188	1657.8392	1671.8548	1702.8970	1685.8705	1684.8864	**17**
11	74.0600	1108.6249		1090.6143	1136.6198		1118.6092	**T**	1543.7711	1556.7915	1558.7707	1589.8129	1572.7864	1571.8024	**16**
12	60.0444	1195.6569		1177.6463	1223.6518		1205.6412	**S**	1456.7390	1455.7438		1488.7653	1471.7387	1470.7547	**15**
13	60.0444	1282.6889		1264.6783	1310.6838		1292.6733	**S**	1369.7070	1368.7118		1401.7332	1384.7067	1383.7227	**14**
14	86.0964	1395.7730		1377.7624	1423.7679		1405.7573	**L**	1256.6230	1255.6277		1314.7012	1297.6747	1296.6906	**13**
15	60.0444	1482.8050		1464.7944	1510.7999		1492.7894	**S**	1169.5909	1168.5957		**1201.6171**	1184.5906	1183.6066	**12**
16	60.0444	1569.8370		1551.8265	1597.8319		1579.8214	**S**	1082.5589	1081.5636		1114.5851	1097.5586	1096.5745	**11**
17	88.0393	1684.8640		1666.8534	1712.8589		1694.8483	**D**	967.5320	966.5367		1027.5531	**1010.5265**	1009.5425	**10**
18	30.0338	1741.8854		1723.8749	1769.8804		1751.8698	**G**				**912.5261**	**895.4996**	894.5156	**9**
19	72.0808	1840.9539		1822.9433	1868.9488		1850.9382	**V**	811.4421	824.4625		855.5047	838.4781	837.4941	**8**
20	86.0964	1954.0379		1936.0273	1982.0328		1964.0223	**L**	698.3580	697.3628		756.4363	739.4097	738.4257	**7**

21	74.0600	2055.0856		2037.0750	2083.0805		2065.0699	**T**	597.3103	610.3307	612.3100	**643.3522**	626.3257	625.3416	**6**
22	72.0808	2154.1540		2136.1434	2182.1489		2164.1384	**V**	498.2419	511.2623		542.3045	525.2780		**5**
23	87.0553	2268.1969	2251.1704	2250.1864	2296.1918	2279.1653	2278.1813	**N**	384.1990	383.2037		443.2361	**426.2096**		**4**
24	30.0338	2325.2184	2308.1918	2307.2078	2353.2133	2336.1868	2335.2027	**G**				**329.1932**	312.1666		**3**
25	**70.0651**	2422.2712	2405.2446	2404.2606	2450.2661	2433.2395	2432.2555	**P**	230.1248	229.1295		**272.1717**	255.1452		**2**
26	129.1135							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

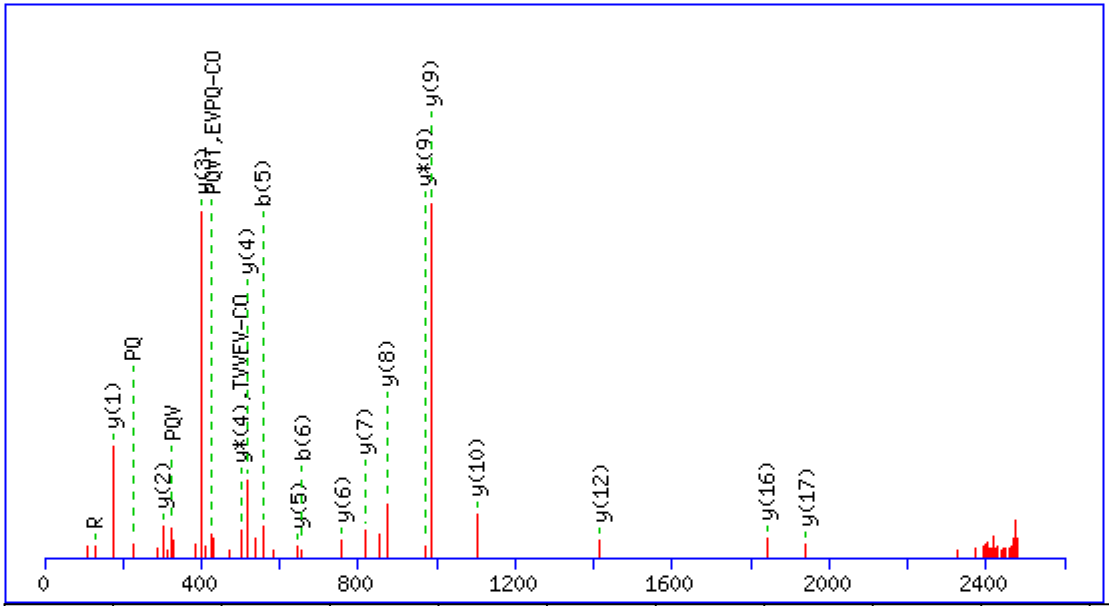
1292

MS/MS Fragmentation of ETVVEVPQVTWEDIGGLEDVKR

Found in gi|11095437, valosin-containing protein,

(2498.2822,1+)

Ions Score:117



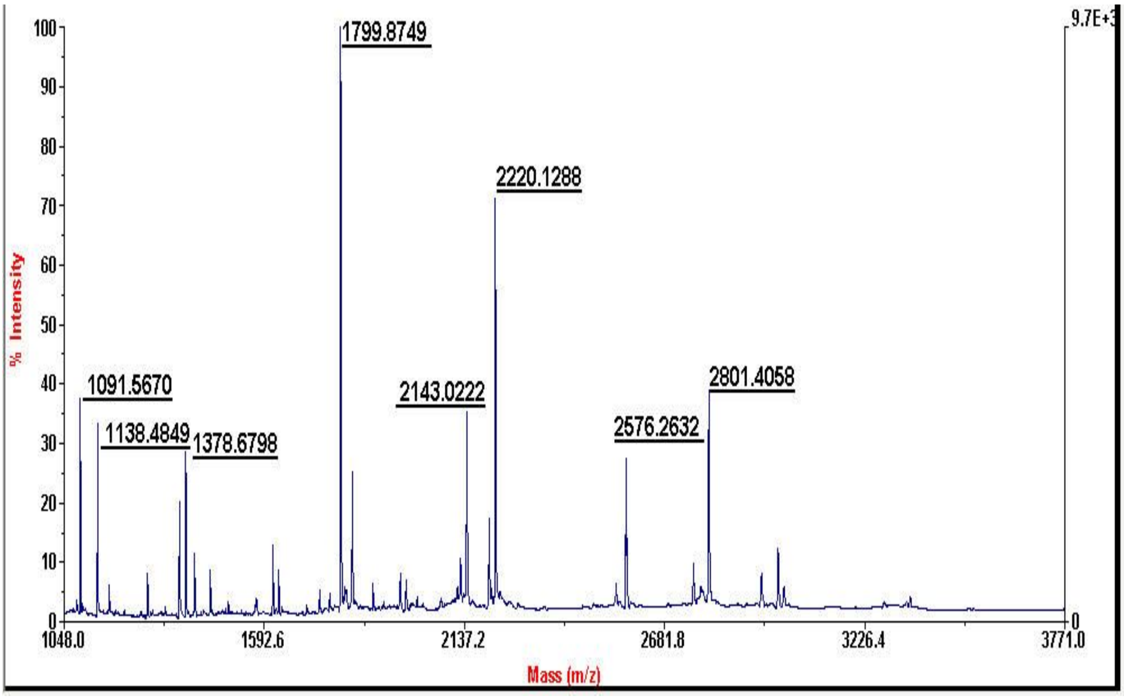
#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	w	w'	y	y*	y^0	#
1	102.0550	102.0550		84.0444	130.0499		112.0393	E							22
2	74.0600	203.1026		185.0921	231.0975		213.0870	T	2323.1929	2336.2133	2338.1925	2369.2347	2352.2082	2351.2242	21
3	72.0808	302.1710		284.1605	330.1660		312.1554	V	2224.1244	2237.1448		2268.1870	2251.1605	2250.1765	20
4	72.0808	401.2395		383.2289	429.2344		411.2238	V	2125.0560	2138.0764		2169.1186	2152.0921	2151.1081	19
5	102.0550	530.2821		512.2715	558.2770		540.2664	E	1996.0134	1995.0182		2070.0502	2053.0237	2052.0396	18
6	72.0808	629.3505		611.3399	657.3454		639.3348	V	1896.9450	1909.9654		1941.0076	1923.9811	1922.9971	17
7	70.065	726.40		708.39	754.39		736.38	P	1799.8	1798.8		1841.9	1824.9	1823.9	16

	1	32		27	81		76		923	970		**392**	127	286	
8	101.0709	854.4618	837.4353	836.4512	882.4567	865.4302	864.4462	**Q**	1671.8337	1670.8384		1744.8864	1727.8599	1726.8759	**15**
9	72.0808	953.5302	936.5037	935.5197	981.5251	964.4986	963.5146	**V**	1572.7653	1585.7857		1616.8279	1599.8013	1598.8173	**14**
10	74.0600	1054.5779	1037.5514	1036.5673	1082.5728	1065.5463	1064.5623	**T**	1471.7176	1484.7380	1486.7172	1517.7594	1500.7329	1499.7489	**13**
11	159.0917	1240.6572	1223.6307	1222.6467	1268.6521	1251.6256	1250.6416	**W**	1285.6383			**1416.7118**	1399.6852	1398.7012	**12**
12	102.0550	1369.6998	1352.6733	1351.6892	1397.6947	1380.6682	1379.6842	**E**	1156.5957	1155.6004		1230.6325	1213.6059	1212.6219	**11**
13	88.0393	1484.7268	1467.7002	1466.7162	1512.7217	1495.6951	1494.7111	**D**	1041.5687	1040.5735		**1101.5899**	1084.5633	1083.5793	**10**
14	86.0964	1597.8108	1580.7843	1579.8003	1625.8057	1608.7792	1607.7952	**I**	928.4847	941.5051	955.5207	**986.5629**	**969.5364**	968.5524	**9**
15	30.0338	1654.8323	1637.8057	1636.8217	1682.8272	1665.8006	1664.8166	**G**				**873.4789**	856.4523	855.4683	**8**
16	30.0338	1711.8537	1694.8272	1693.8432	1739.8487	1722.8221	1721.8381	**G**				**816.4574**	799.4308	798.4468	**7**
17	86.0964	1824.9378	1807.9113	1806.9272	1852.9327	1835.9062	1834.9222	**L**	701.3577	700.3624		**759.4359**	742.4094	741.4254	**6**
18	102.0550	1953.9804	1936.9539	1935.9698	1981.9753	1964.9488	1963.9648	**E**	572.3151	571.3198		**646.3519**	629.3253	628.3413	**5**
19	88.0393	2069.0073	2051.9808	2050.9968	2097.0023	2079.9757	2078.9917	**D**	457.2881	456.2929		**517.3093**	**500.2827**	499.2987	**4**
20	72.0808	2168.0758	2151.0492	2150.0652	2196.0707	2179.0441	2178.0601	**V**	358.2197	371.2401		**402.2823**	385.2558		**3**

21	101.1073	2296.1707	2279.1442	2278.1602	2324.1656	2307.1391	2306.1551	**K**	230.1248	229.1295		**303.2139**	286.1874		**2**
22	**129.1135**							**R**	74.0237	73.0284		**175.1190**	158.0924		**1**

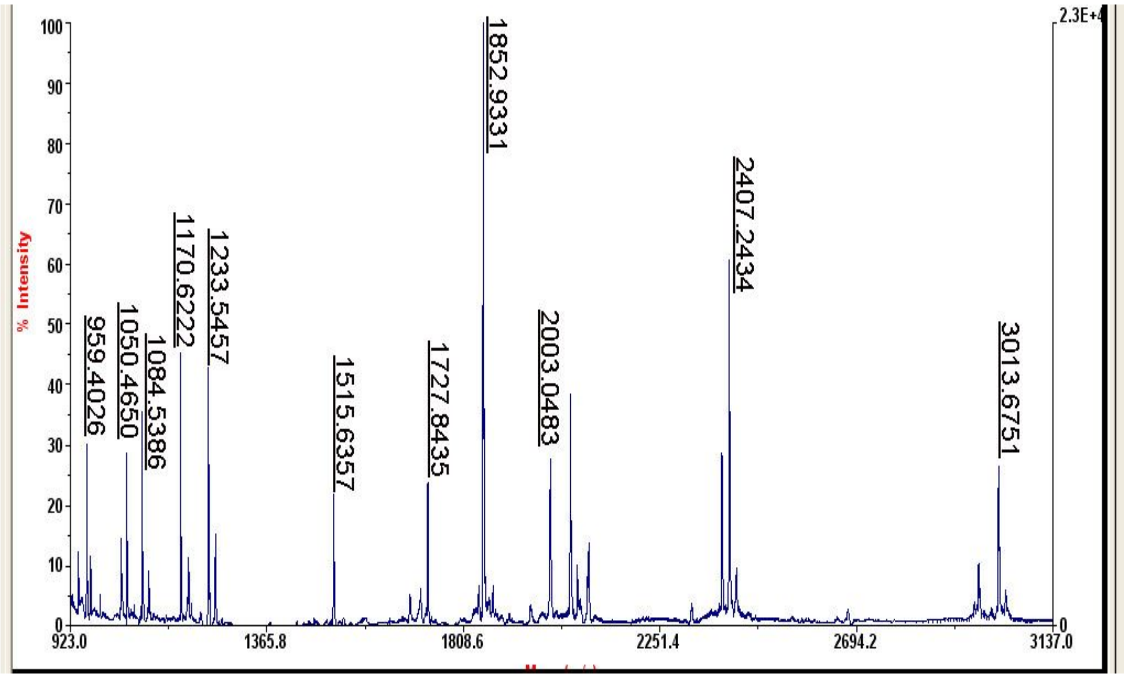
Part IV: Presentation of PMF spectrum

1 ） Elongation factor 2



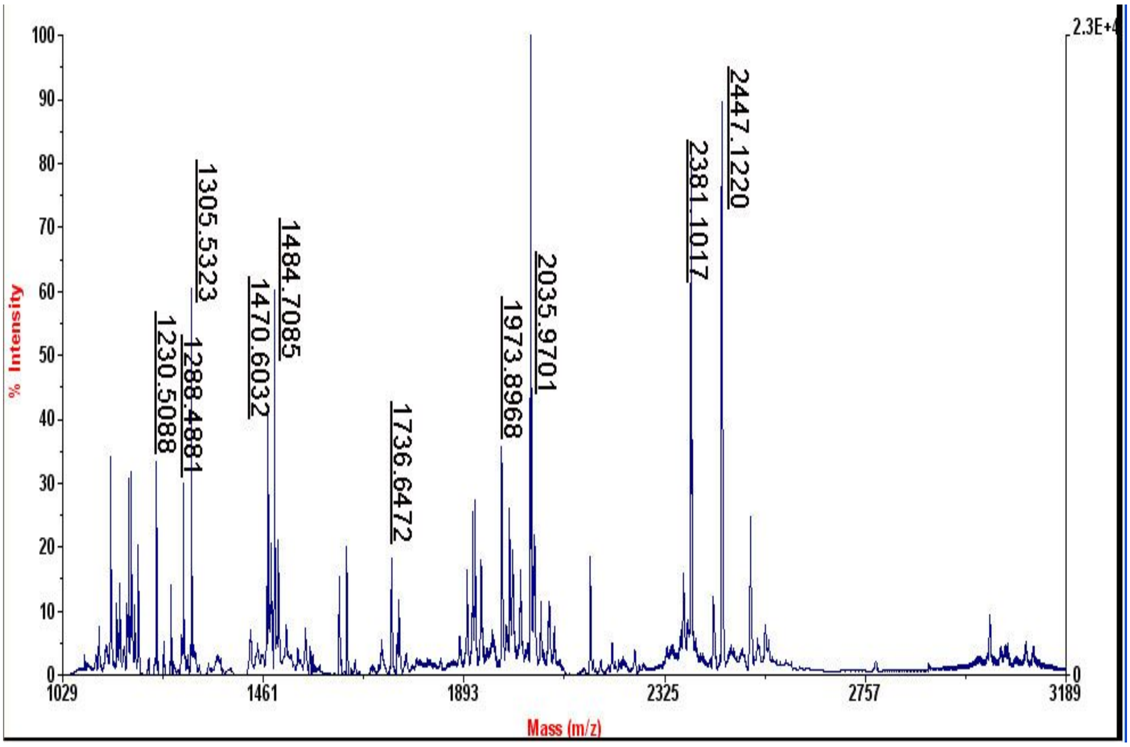
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 9	1091.5670	1090.5598	1090.5771	-0.0173	0	-.VNFTVDQIR.A
93 - 119	2801.4058	2800.3985	2800.4031	-0.0046	0	K.DGAGFLINLIDSPGHVDFSSEVTAALR.V
120 - 143	2576.2632	2575.2559	2575.2985	-0.0426	0	R.VTDGALVVVDCVSGVCVQTETVLR.Q
2						
162 - 179	2220.1288	2219.1216	2219.1473	-0.0258	0	R.ALLELQLEPEELYQTFQR.I
605 - 624	2143.0222	2142.0149	2142.0705	-0.0555	1	K.ARPFPDGLAEDIDKGEVSAR.Q
638 - 646	1138.4849	1137.4776	1137.5090	-0.0314	0	K.YEWDVAEAR.K
727 - 738	1378.6798	1377.6725	1377.7074	-0.0349	0	R.CLYASVLTAQPR.L
785 - 800	1799.8749	1798.8676	1798.8889	-0.0213	0	K.AYLPVNESFGFTADLR.S

2) Iron-responsive element-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
57 - 72	2003.0483	2002.0411	2002.0384	0.0026	1	K.KQDIENILHWNVTQHK.N
73 - 82	1170.6222	1169.6149	1169.6556	-0.0407	0	K.NIEVPFKPAR.V
142 - 149	1050.4650	1049.4577	1049.4778	-0.0201	0	K.NQDLEFER.N
159 - 168	1233.5457	1232.5385	1232.5509	-0.0124	0	K.WGSQAFHNMR.I
277 - 293	1852.9331	1851.9258	1851.9518	-0.0260	0	K.FVEFFGPGVAQLSIADR.A
336 - 344	1084.5386	1083.5313	1083.5535	-0.0222	0	K.YLQAVGMFR.D
401 - 413	1515.6357	1514.6284	1514.7014	-0.0730	0	K.GFQVAPEHHNDHK.T
588 - 601	1727.8435	1726.8363	1726.8638	-0.0276	1	K.DIWPTRDEIQAVER.Q
705 - 712	959.4026	958.3954	958.4144	-0.0191	0	R.EFNSYGSR.R
737 - 758	2407.2434	2406.2361	2406.2179	0.0182	0	K.QAPQTIHLPSGEILDVFDAAER.Y
806 - 834	3013.6751	3012.6678	3012.5225	0.1453	0	R.SNLVGMGVIPLEYLPGENADALGLTGQER.Y

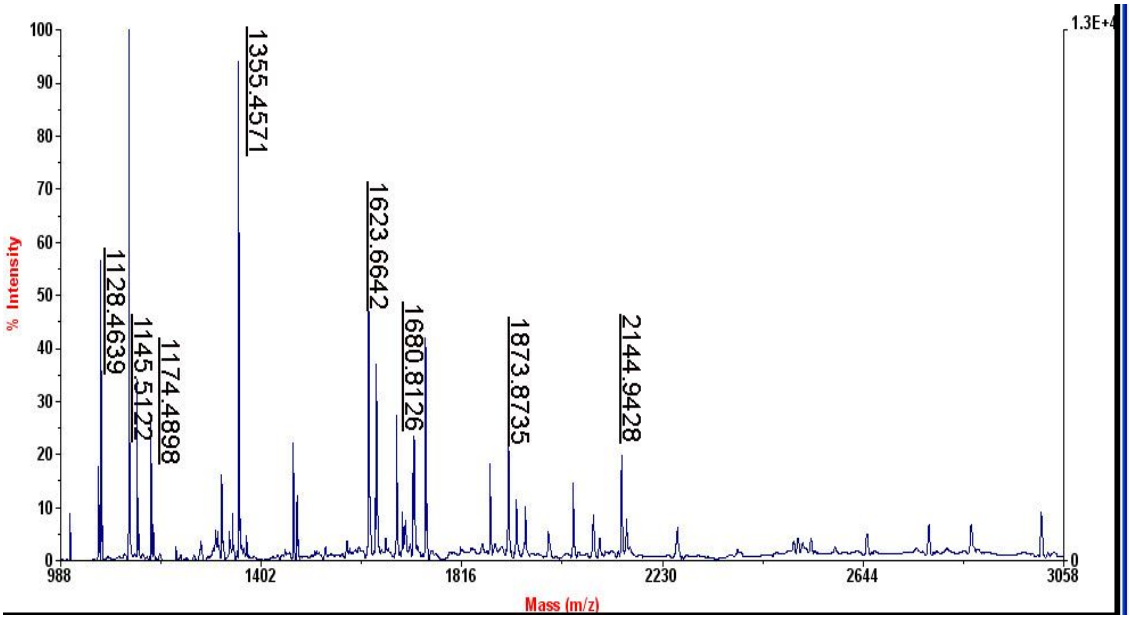
3) Vinculin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
87 - 104	1973.8968	1972.8895	1973.0040	-0.1145	0	K.LVQAAQMLQSDPYSVPAR.D
87 - 104	1989.8969	1988.8896	1988.9989	-0.1093	0	K.LVQAAQMLQSDPYSVPAR.D
Oxidation (M)						
113 - 131	2035.9701	2034.9629	2035.0473	-0.0844	0	R.GILSGTSDLLLTFDEAEVR.K
178 - 187	1305.5325	1304.5252	1304.6221	-0.0970	0	R.QQELTHQEHR.V
285 - 299	1470.6032	1469.5959	1469.6746	-0.0787	0	R.DPSASPGDAGEQAIR.Q
417 - 427	1288.4881	1287.4808	1287.6129	-0.1320	1	K.IAELCDDPKER.D
502 - 511	1230.5088	1229.5016	1229.5677	-0.0661	0	R.WIDNPTVDDR.G
547 - 560	1484.7085	1483.7012	1483.7994	-0.0982	0	R.VDQLTAQLADLAAR.G
607 - 628	2381.1017	2380.0945	2380.2022	-0.1077	1	K.LLAVAATAPPDAPNREEVFDER.A
684 - 698	1736.6472	1735.6399	1735.7624	-0.1225	0	R.NPGNQAAYEHFETMK.N
832 - 852	2447.1220	2446.1148	2446.1804	-0.0657	0	R.EAFQPQEPDFPPPPPDLEQLR.L
1046 - 1054	1132.4917	1131.4844	1131.5706	-0.0862	0	R.TNLLQVCER.I

No match to: 927.4225, 1639.7833

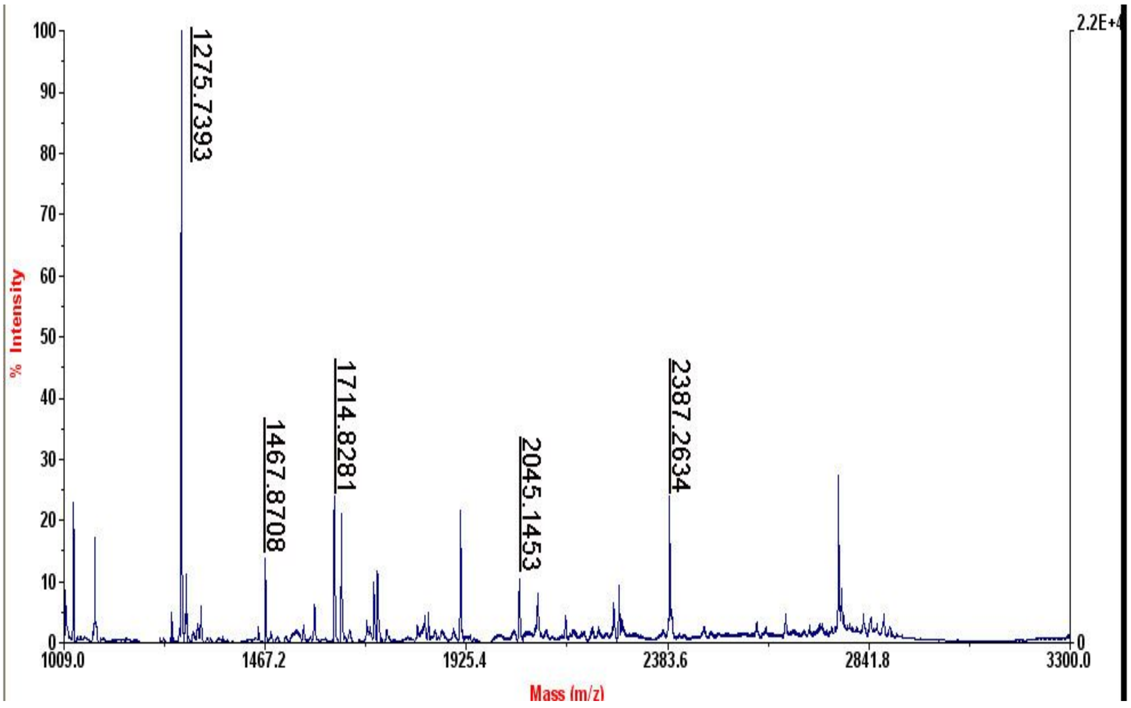
4) Neutral alpha-glucosidase AB precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
36 - 48	1623.6642	1622.6570	1622.6705	-0.0135	1	R.SNFKTCEESSFCK.R 2
52 - 61	1145.5122	1144.5049	1144.6353	-0.1303	0	R.SIRPGLSPYR.A
101 - 109	1174.4898	1173.4825	1173.6142	-0.1317	1	R.FRIDELEPR.R
113 - 127	1680.8126	1679.8053	1679.9358	-0.1305	1	R.YRVPDVLVADPPIAR.L
174 - 182	1128.4639	1127.4566	1127.5723	-0.1157	0	R.GLLEFEHQR.A
438 - 445	1071.3772	1070.3700	1070.4821	-0.1122	0	R.YFTWDPSR.F
559 - 569	1355.4571	1354.4498	1354.5803	-0.1305	0	K.DAQHYGGWEHR.D
570 - 588	2144.9428	2143.9356	2144.0472	-0.1117	0	R.DVHNIYGLYVHMATADGLR.Q
684 - 698	1873.8735	1872.8662	1872.9958	-0.1297	1	R.REPWLLPSQHNDIIR.D
915 - 929	1740.7860	1739.7787	1739.9206	-0.1419	0	R.LSFQHDPETSVLVLR.K

No match to: 927.3888, 960.4500, 1639.7869, 1714.6822, 1910.8136

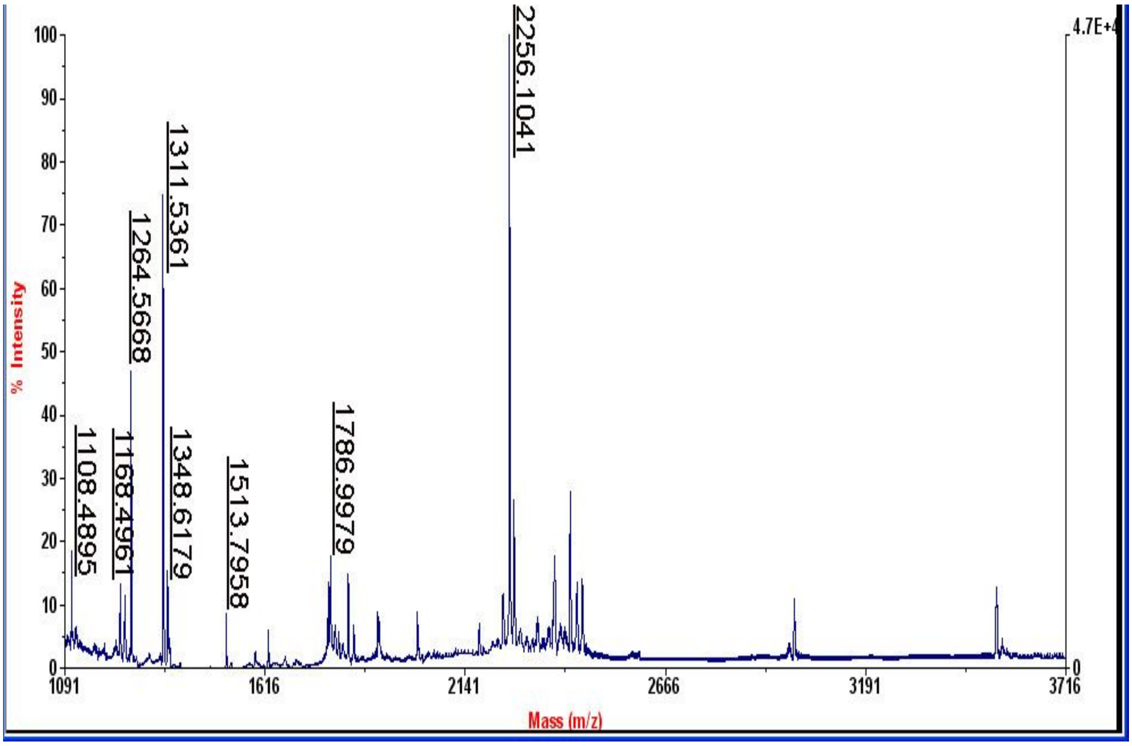
5) Chromobox protein homolog 5



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 28	2387.2634	2386.2562	2386.0659	0.1903	1	R.TADSSSSEDEEEYVVEKVLDR.R
30 - 40	1275.7393	1274.7320	1274.7597	-0.0277	1	R.VVKGQVEYLLK.W
126 - 141	1714.8281	1713.8209	1713.8139	0.0069	0	K.IIGATDSCGDLMFLMK.W
126 - 143	2045.1453	2044.1380	2043.9831	0.1549	1	K.IIGATDSCGDLMFLMKWK.D
Oxidation (M)						
160 - 171	1467.8708	1466.8635	1466.7227	0.1407	0	K.CPQIVIAFYEER.L

No match to: 927.4930, 960.5775, 998.5335, 1030.5621, 1078.5164, 1623.8529, 1639.9163, 1722.8988, 1911.0120, 2771.5753

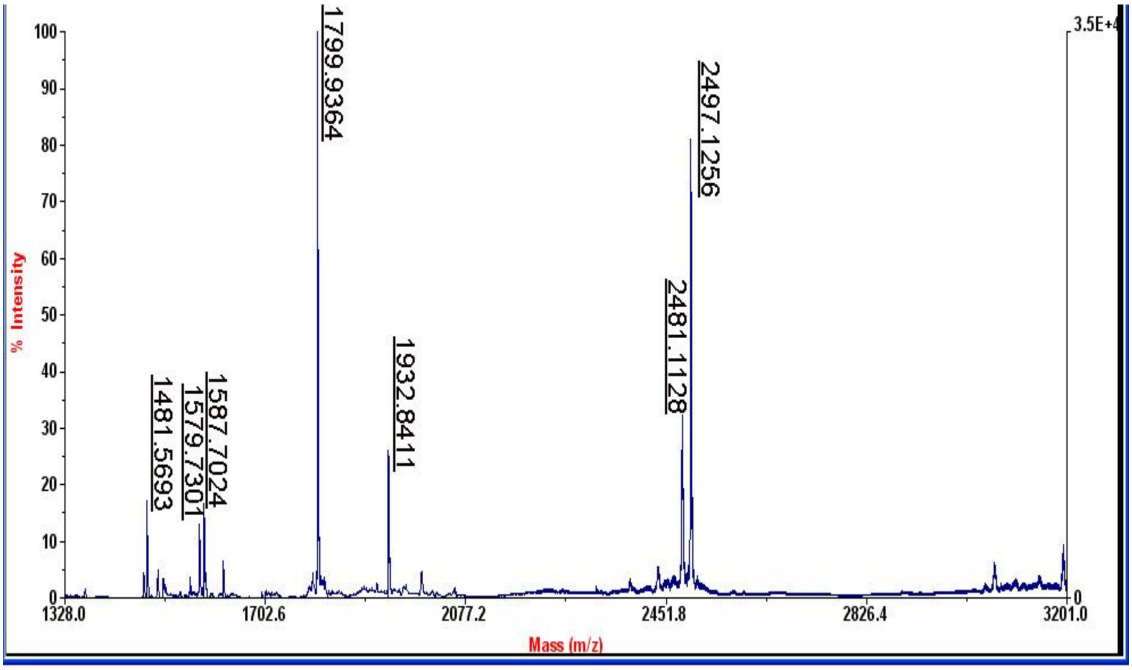
6) Heat shock protein HSP 90-alpha



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
154 - 173	2256.1041	2255.0968	2254.9515	0.1453	0	K.HNDDEQYAWESSAGGSFTVR.T	
192 - 201	1311.5361	1310.5289	1310.5626	-0.0338	0	K.EDQTEYLEER.R	
346 - 355	1264.5668	1263.5595	1263.6360	-0.0765	1	R.RAPFDLFENR.K	
347 - 355	1108.4895	1107.4822	1107.5349	-0.0527	0	R.APFDLFENR.K	
387 - 400	1513.7958	1512.7885	1512.7783	0.0102	0	R.GVVDSEDLPLNISR.E	
447 - 456	1168.4961	1167.4888	1167.5632	-0.0744	0	K.LGIHEDSQNR.K	
500 - 510	1235.5470	1234.5397	1234.5942	-0.0544	0	K.DQVANSAFVER.L	
621 - 632	1348.6179	1347.6106	1347.5798	0.0308	1	R.DNSTMGYMAAKK.H	2 Oxidation (M)
633 - 647	1786.9979	1785.9907	1785.9373	0.0534	0	K.HLEINPDHSIIETLR.Q	

No match to: 1782.9945, 1911.0963, 2177.1023

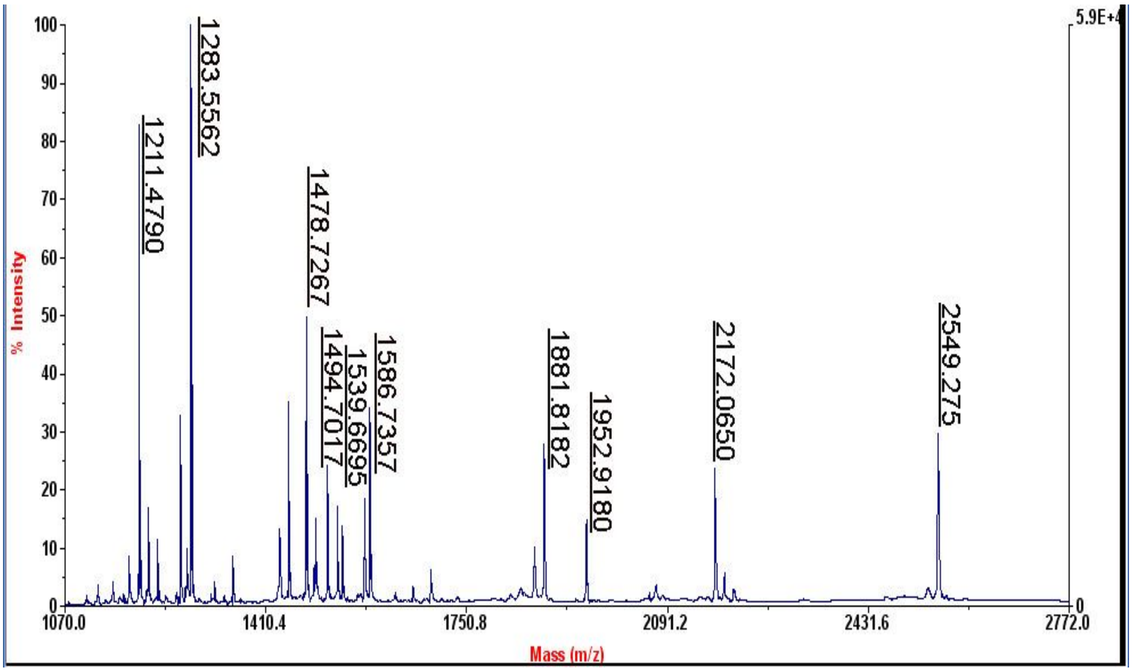
7) Protein-glutamine gamma-glutamyltransferase 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
36 - 48	1587.7024	1586.6951	1586.7993	-0.1042	0	R.GQPFWLTLHFEGR.N	
223 - 240	1932.8411	1931.8338	1931.9192	-0.0854	0	R.VVSGMVNCNDDQGVLLGR.W	
241 - 262	2481.1128	2480.1056	2480.1430	-0.0374	0	R.WDNNYGDGVSPMSWIGSVDILR.R	
241 - 262	2497.1256	2496.1183	2496.1379	-0.0196	0	R.WDNNYGDGVSPMSWIGSVDILR.R	
Oxidation (M)							
365 - 377	1481.5693	1480.5620	1480.6438	-0.0818	0	K.SEGTYCCGPVPVR.A	2
528 - 540	1579.7301	1578.7228	1578.8293	-0.1065	0	K.YLLNLNLEPFSEK.S	
551 - 562	1511.6695	1510.6622	1510.7449	-0.0827	1	K.YRDCLTESNLIK.V	
565 - 580	1799.9364	1798.9291	1799.0192	-0.0901	0	R.ALLVEPVINSYLLAER.D	

No match to: 1000.4327, 1623.7011, 1993.8471

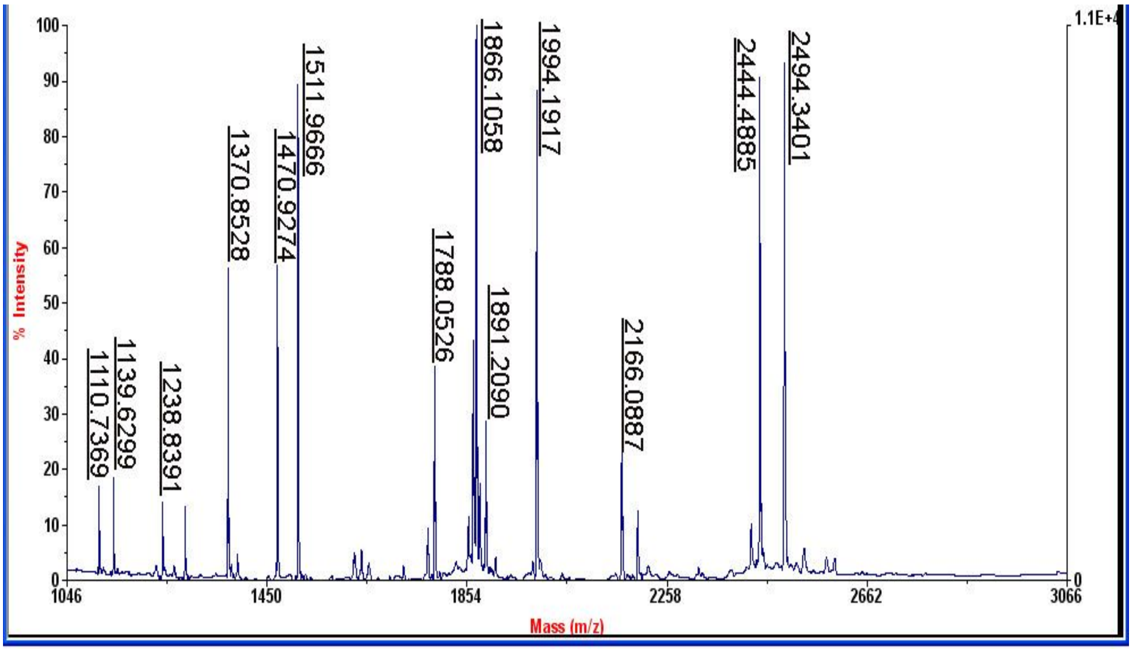
8) Serotransferrin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
27 - 42	1881.8182	1880.8109	1880.8297	-0.0188	1	R.WCAVSEHEATKCQSFR.D	
123 - 132	1211.4790	1210.4717	1210.5400	-0.0683	0	K.DSGFQMNQLR.G	Oxidation (M)
144 - 162	2171.0650	2170.0578	2170.0881	-0.0303	0	R.SAGWNIPIGLLYCDLPEPR.K	
240 - 251	1539.6695	1538.6622	1538.7035	-0.0413	0	R.DQYELLCLDNTR.K	
252 - 273	2549.2753	2548.2680	2548.2856	-0.0176	1	R.KPVDEYKDCHLAQVPSHTVVAR.S	
332 - 343	1478.7267	1477.7194	1477.7275	-0.0081	0	K.MYLGYEYVTAIR.N	
332 - 343	1494.7017	1493.6944	1493.7224	-0.0280	0	K.MYLGYEYVTAIR.N	Oxidation (M)
363 - 371	1195.5088	1194.5015	1194.5352	-0.0337	0	K.WCALSHHER.L	
495 - 508	1577.6446	1576.6373	1576.6503	-0.0130	0	R.FDEFFSEGCAPGSK.K	
531 - 541	1283.5562	1282.5489	1282.5618	-0.0128	0	K.EGYYGYTGAFR.C	
572 - 587	1952.9180	1951.9107	1951.9309	-0.0202	1	K.NLNEKDYELLCLDGTR.K	
588 - 600	1586.7357	1585.7284	1585.7671	-0.0387	0	R.KPVEEYANCHLAR.A	
684 - 696	1531.6387	1530.6314	1530.6806	-0.0493	0	K.CSTSSLLEACTFR.R	2

No match to: 1265.5383, 1448.6324, 1514.6284

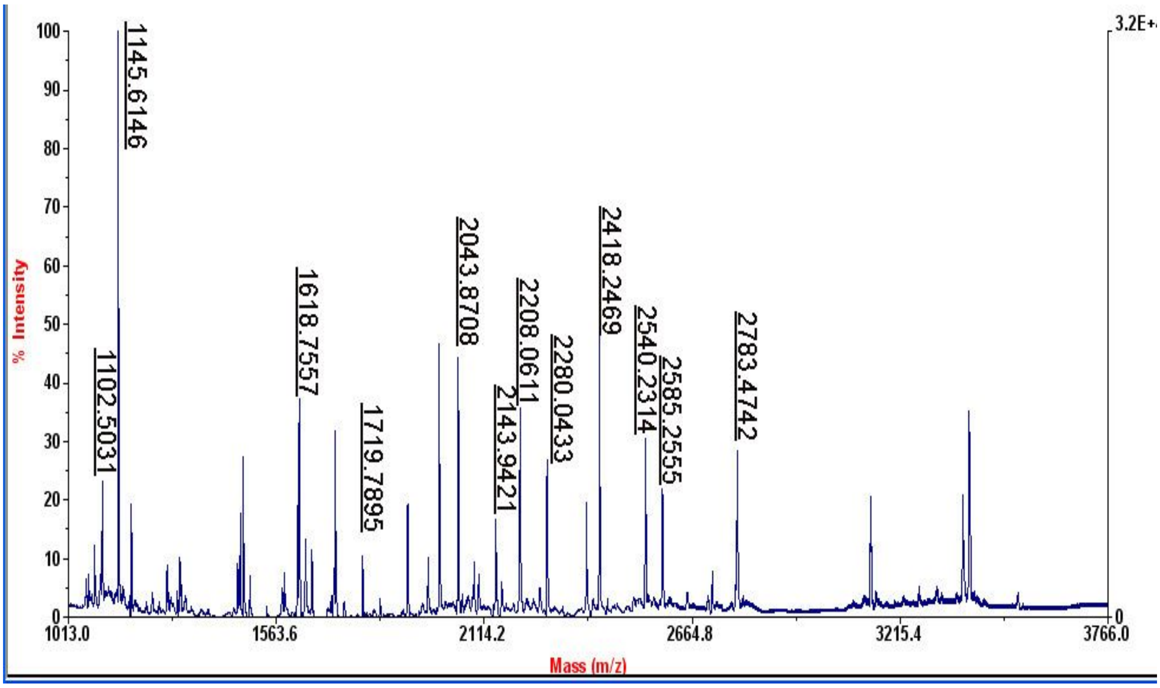
9) Complement C3 precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
137 - 148	1370.8528	1369.8455	1369.7241	0.1214	0	K.TIYTPGSTVLYR.I
208 - 225	2166.0887	2165.0814	2164.9952	0.0862	0	R.AYYENSPQQVFSTEFEVK.E
242 - 249	1139.6299	1138.6226	1138.5335	0.0891	0	K.FYYIYNEK.G
264 - 281	1994.1917	1993.1844	1993.0268	0.1576	1	K.KVEGTAFVIFGIQDGEQR.I
265 - 281	1866.1058	1865.0986	1864.9318	0.1667	0	K.VEGTAFVIFGIQDGEQR.I
291 - 304	1470.9274	1469.9201	1469.7725	0.1476	0	R.IPIEDGSGEVVLSR.K
305 - 315	1238.8391	1237.8318	1237.7142	0.1176	1	R.KVLLDGVQNPR.A
306 - 315	1110.7369	1109.7297	1109.6193	0.1104	0	K.VLLDGVQNPR.A
344 - 359	1788.0526	1787.0453	1786.9617	0.0836	0	R.SGIPIVTSPYQIHFTK.T
409 - 425	1891.2090	1890.2017	1890.0687	0.1331	0	K.LSINTHPSQKPLSITVR.T
463 - 478	1872.1579	1871.1506	1871.0264	0.1241	0	R.TELRPGETLNVNFLLR.M
509 - 530	2444.4885	2443.4812	2443.2998	0.1814	0	R.EPGQDLVVLPLSITTDFIPSFR.L
531 - 544	1511.9666	1510.9594	1510.8143	0.1451	0	R.LVAYYTLIGASGQR.E
634 - 657	2494.3401	2493.3329	2493.1407	0.1921	0	K.DYAGVFSDAGLTFTSSSGQQTAQR.A
1321 - 1337	1855.9711	1854.9638	1854.8482	0.1155	1	R.SEETKENEGFTVTAEGK.G

No match to: 1283.7769, 1774.0859

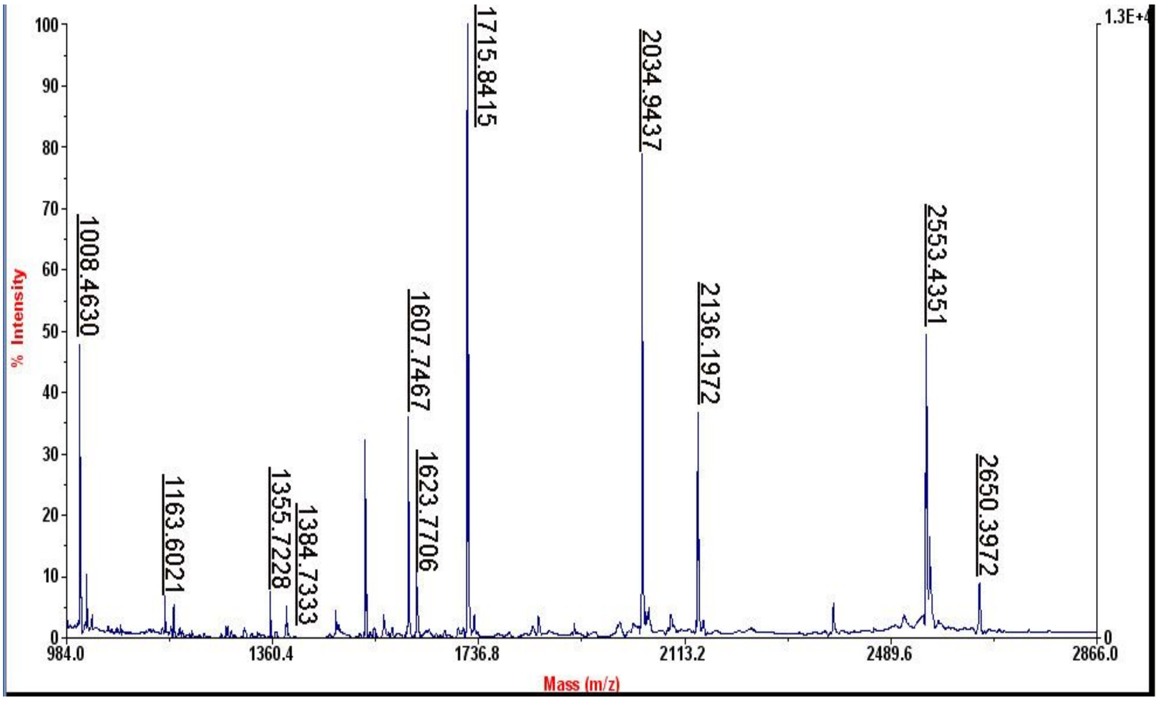
10) WD repeat protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 17	1145.6146	1144.6073	1144.6240	-0.0167	0	K.VFASLPQVER.G
44 - 65	2418.2469	2417.2396	2417.2339	0.0057	0	R.NIDNPALADIYTEHAHQVVVAK.Y
66 - 81	1618.7557	1617.7485	1617.7674	-0.0189	0	K.YAPSGFYIASGDVSGK.L
96 - 104	1102.5031	1101.4958	1101.5131	-0.0173	0	K.YEYQPFAGK.I
127 - 147	2208.0611	2207.0538	2207.0646	-0.0108	0	K.FGAVFLWDSGSSVGEITGHNK.V
162 - 180	2043.8708	2042.8635	2042.9043	-0.0408	0	R.LATGSDDNCAAFFEGPPFK.F
204 - 219	1719.7895	1718.7822	1718.8151	-0.0329	0	R.FATASADGQIYIYDGK.T
232 - 256	2585.2555	2584.2483	2584.2193	0.0289	0	K.AHDGGIYAISWSPDSTHLLSASGDK.T
371 - 389	2143.9421	2142.9349	2142.9231	0.0117	0	R.MTVDESGQLISCSMDDTVR.Y
490 - 511	2280.0433	2279.0360	2279.0528	-0.0168	0	K.GPVTDVAYSHDGAFLAVCDASK.V
512 - 534	2540.2314	2539.2241	2539.2131	0.0110	0	K.VVTVFSVADGYSENNVFYGHHAK.I
576 - 600	2783.4742	2782.4670	2782.4038	0.0632	0	R.LHHVSSLAWLDEHTLVTTSHDASVK.E

No match to: 909.0530, 927.4831, 1179.5894, 1307.6612, 1467.8058, 1475.7335, 1623.7880, 1639.8635, 1791.6941, 1910.9125, 1993.9741, 2383.9698

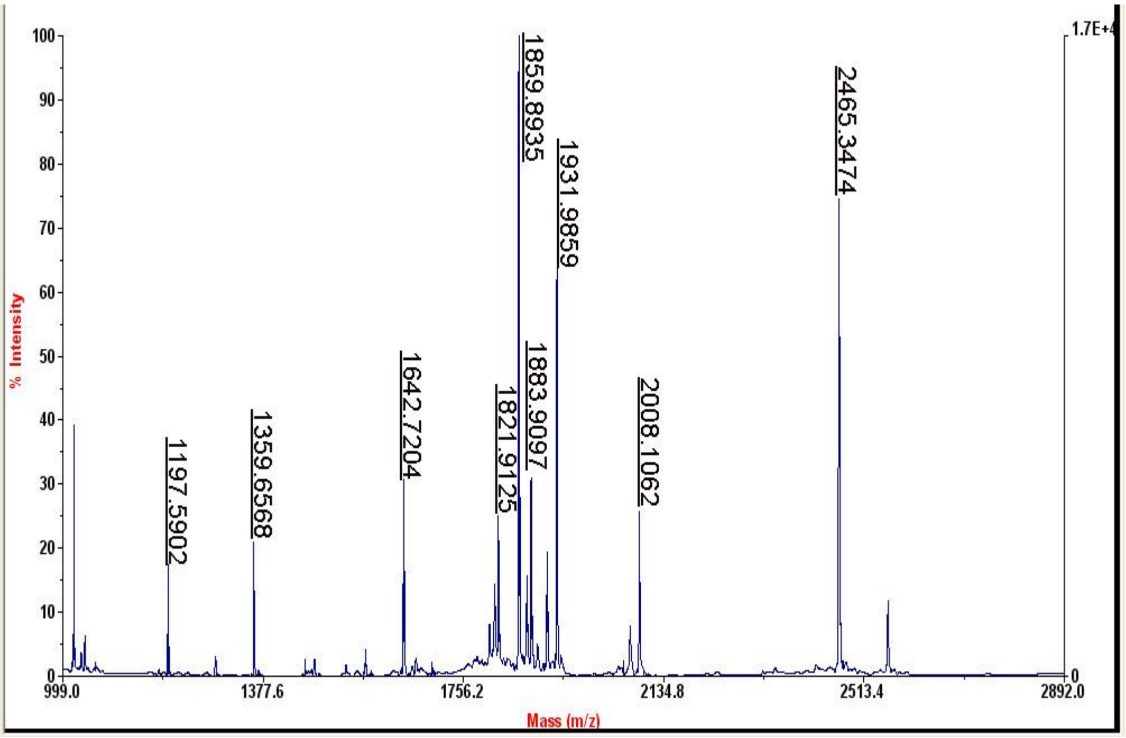
11) Bifunctional purine biosynthesis protein PURH



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
50 - 64	1607.7467	1606.7395	1606.7660	-0.0266	0	R.DVSELTGFPEMLGGR.V
50 - 64	1623.7706	1622.7633	1622.7610	0.0024	0	R.DVSELTGFPEMLGGR.V Oxidation (M)
67 - 79	1355.7228	1354.7155	1354.7833	-0.0678	0	K.TLHPAVHAGILAR.N
109 - 133	2553.4351	2552.4278	2552.3696	0.0582	0	K.TVASPGVTVEEAVEQIDIGGVTLLR.A
178 - 194	2034.9437	2033.9364	2033.9119	0.0245	0	K.AFTHTAQYDEAISDYFR.K
295 - 305	1163.6021	1162.5949	1162.6346	-0.0397	0	K.TLTPISAAYAR.A
438 - 451	1384.7333	1383.7261	1383.7218	0.0043	0	K.NGQVIGIGAGQQSR.I
462 - 468	1008.4630	1007.4557	1007.4977	-0.0420	0	K.ANYWWLR.H
484 - 507	2650.3972	2649.3899	2649.3133	0.0767	1	K.RAEISNAIDQYVTGTIGEDEDLIK.W
531 - 545	1715.8415	1714.8343	1714.8566	-0.0223	0	K.LTEVSISSDAFFPFR.D
570 - 588	2136.1972	2135.1899	2135.1408	0.0491	0	K.VVIEACDELGIILAHTNLR.L

No match to: 909.3013, 1475.7153, 1529.7265, 2560.1923

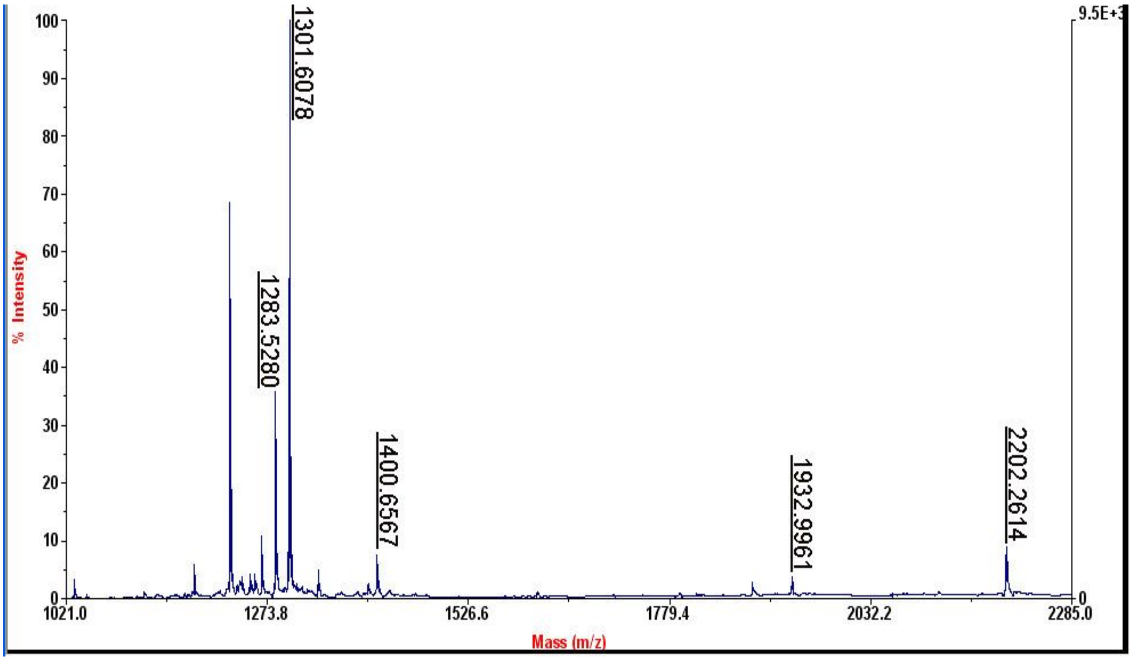
12) Pyruvate kinase isozymes M1/M2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 56	1359.6568	1358.6496	1358.6976	-0.0480	0	R.NTGIICTIGPASR.S
74 - 89	1883.9097	1882.9024	1882.8962	0.0062	0	R.LNFSHGTHEYHAETIK.N
93 - 115	2465.3474	2464.3401	2464.2849	0.0552	0	R.TATESFASDPILYRPVAVALDTK.G
142 - 151	1197.5902	1196.5829	1196.5747	0.0082	0	K.ITLDNAYMEK.C
231 - 246	1859.8935	1858.8863	1858.8923	-0.0060	0	K.FGVEQDVDMVFASFIR.K
231 - 246	1875.8567	1874.8495	1874.8872	-0.0377	0	K.FGVEQDVDMVFASFIR.K Oxidation (M)
271 - 278	953.4430	952.4357	952.4726	-0.0369	0	K.IENHEGVR.R
279 - 294	1821.9125	1820.9053	1820.9090	-0.0037	1	R.RFDEILEASDGIMVAR.G
368 - 376	1019.4767	1018.4694	1018.5083	-0.0389	0	K.GDYPLEAVR.M
384 - 399	1931.9859	1930.9786	1930.9788	-0.0002	0	R.EAEAAIYHLQLFEELR.R
384 - 400	2088.1062	2087.0990	2087.0799	0.0191	1	R.EAEAAIYHLQLFEELRR.L
476 - 489	1642.7204	1641.7131	1641.7634	-0.0503	0	K.DPVQEAWAEDVDLR.V

No match to: 1913.9643

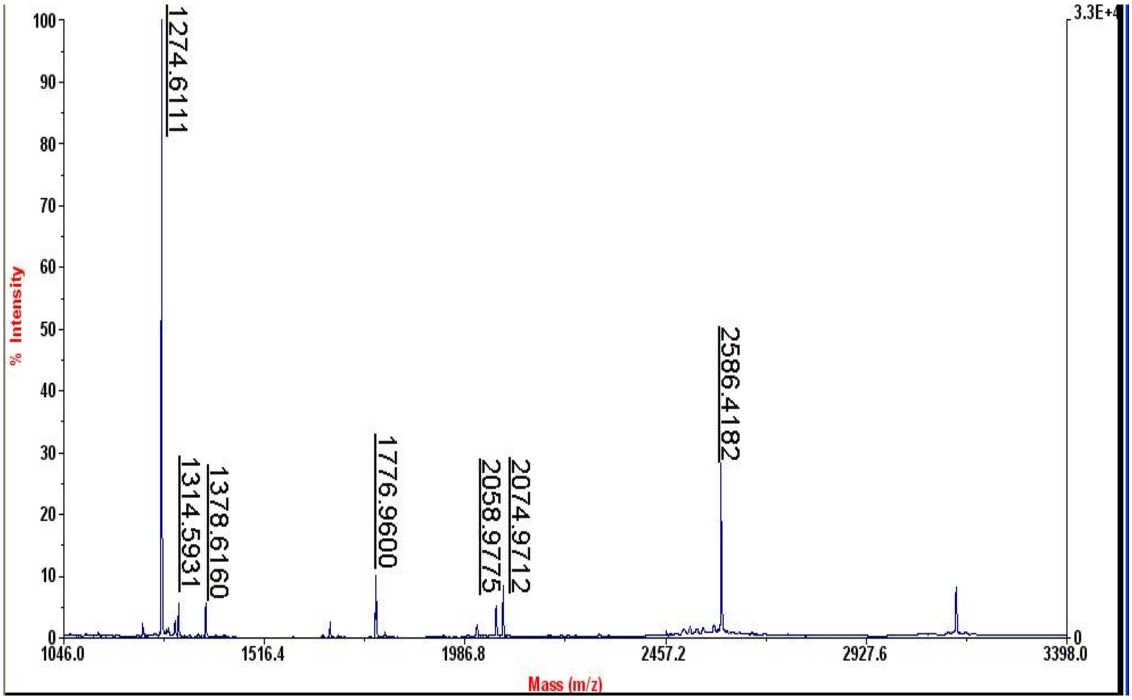
13) Apolipoprotein A-I precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
52 - 64	1400.6567	1399.6494	1399.6619	-0.0125	0	R.DYVSQFEGSALGK.Q
84 - 101	2202.2614	2201.2541	2201.1116	0.1425	1	K.LREQLGPVTQEFWDNLEK.E
86 - 101	1932.9961	1931.9888	1931.9265	0.0624	0	R.EQLGPVTQEFWDNLEK.E
131 - 140	1411.6451	1410.6378	1410.6601	-0.0223	1	K.KWQEEMELYR.Q
132 - 140	1283.5280	1282.5207	1282.5652	-0.0445	0	K.WQEEMELYR.Q
185 - 195	1301.6078	1300.6005	1300.6411	-0.0406	0	R.THLAPYSDELR.Q

No match to: 1226.4871, 1266.5214, 1337.7339

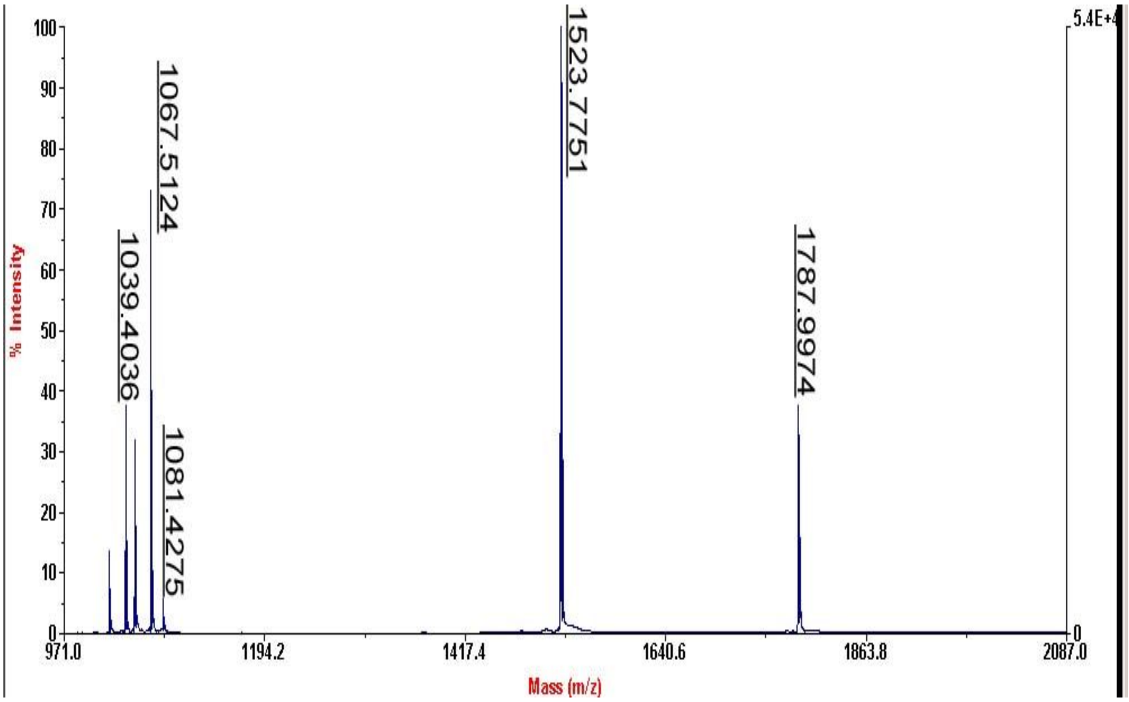
14) Hemoglobin subunit beta



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
19 - 31	1314.5931	1313.5858	1313.6575	-0.0716	0	K.VNVDEVGGEALGR.L
32 - 41	1274.6111	1273.6039	1273.7183	-0.1144	0	R.LLVVYPWTQR.F
42 - 60	2058.9775	2057.9702	2057.9404	0.0299	0	R.FFESFGDLSTPDAVMGNPK.V
42 - 60	2074.9712	2073.9639	2073.9353	0.0286	0	R.FFESFGDLSTPDAVMGNPK.V
Oxidation (M)						
84 - 105	2586.4182	2585.4110	2585.2332	0.1778	1	K.GTFATLSELHCDKLHVDPENFR.L
106 - 121	1776.9600	1775.9527	1775.9868	-0.0341	0	R.LLGNVLVCVLAHHFGK.E
122 - 133	1378.6160	1377.6087	1377.6928	-0.0841	0	K.EFTPPVQAAYQK.V

No match to: 2585.3451, 3137.1133

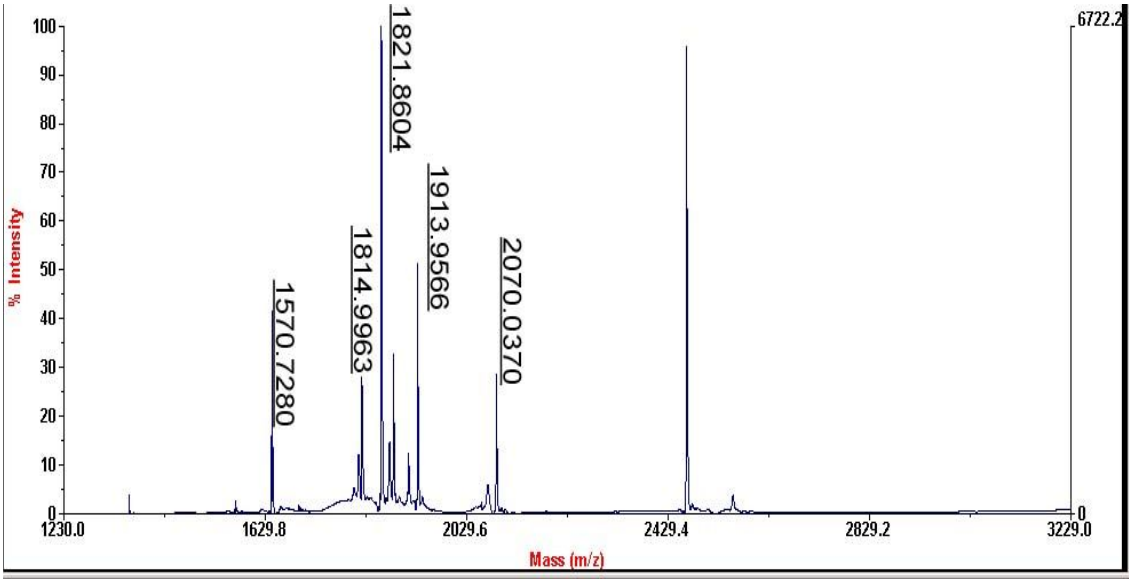
15） Ubiquitin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
12 - 27	1787.9974	1786.9901	1786.9200	0.0702	0	K.TITLEVEPSDTIENVK.A
30 - 42	1523.7751	1522.7678	1522.7739	-0.0061	1	K.IQDKEGIPPDQQR.L
34 - 42	1039.4036	1038.3963	1038.5094	-0.1131	0	K.EGIPPDQQR.L
55 - 63	1081.4275	1080.4202	1080.5451	-0.1249	0	R.TLSDYNIQK.E
64 - 72	1067.5124	1066.5051	1066.6135	-0.1084	0	K.ESTLHLVLR.L

No match to: 1021.3893, 1049.4933

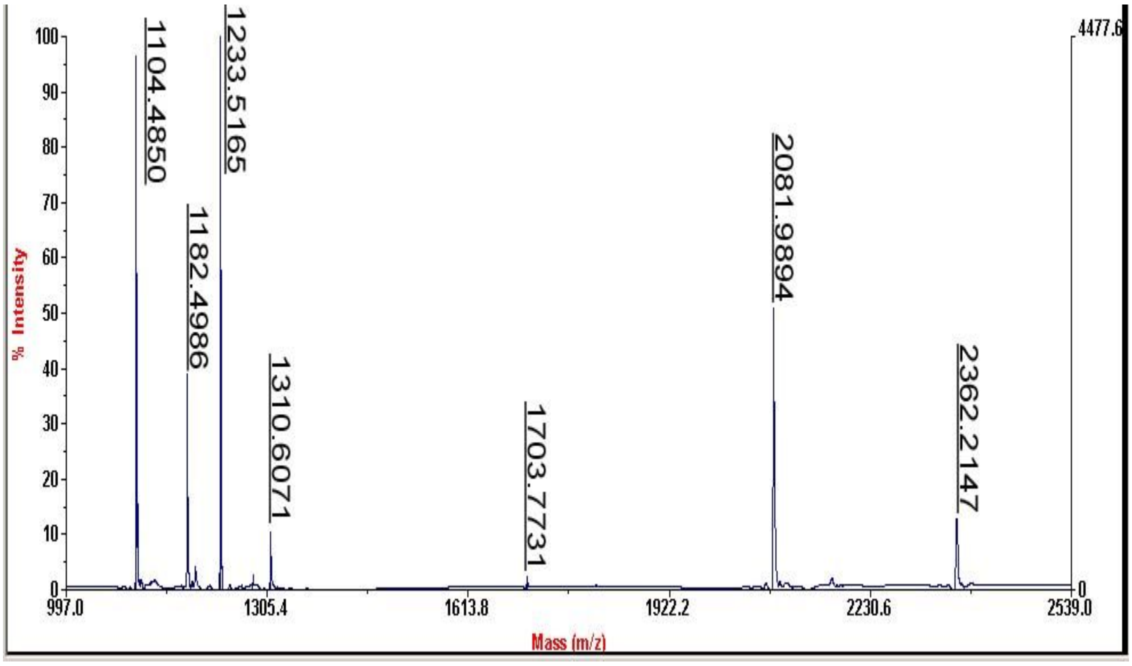
16） Mitochondrial uncoupling protein 3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
88 - 103	1814.9963	1813.9890	1813.9396	0.0494	1	R.QMSFASIRIGLYDSVK.Q
144 - 157	1570.7280	1569.7207	1569.8011	-0.0804	1	R.FQASIHLGPSRSDR.K
189 - 204	1821.8604	1820.8532	1820.9342	-0.0810	0	R.NAIVNCAEVVTYDILK.E
283 - 298	1913.9566	1912.9493	1912.9756	-0.0264	0	R.LGSWNVVMFVTYEQLK.R
283 - 299	2070.0370	2069.0297	2069.0767	-0.0470	1	R.LGSWNVVMFVTYEQLKR.A

No match to: 1019.4447, 1197.5840, 1359.6379, 1642.7134, 1859.8784, 1875.8612, 1883.8560, 1931.9683, 2088.0823, 2465.3227, 2557.3513

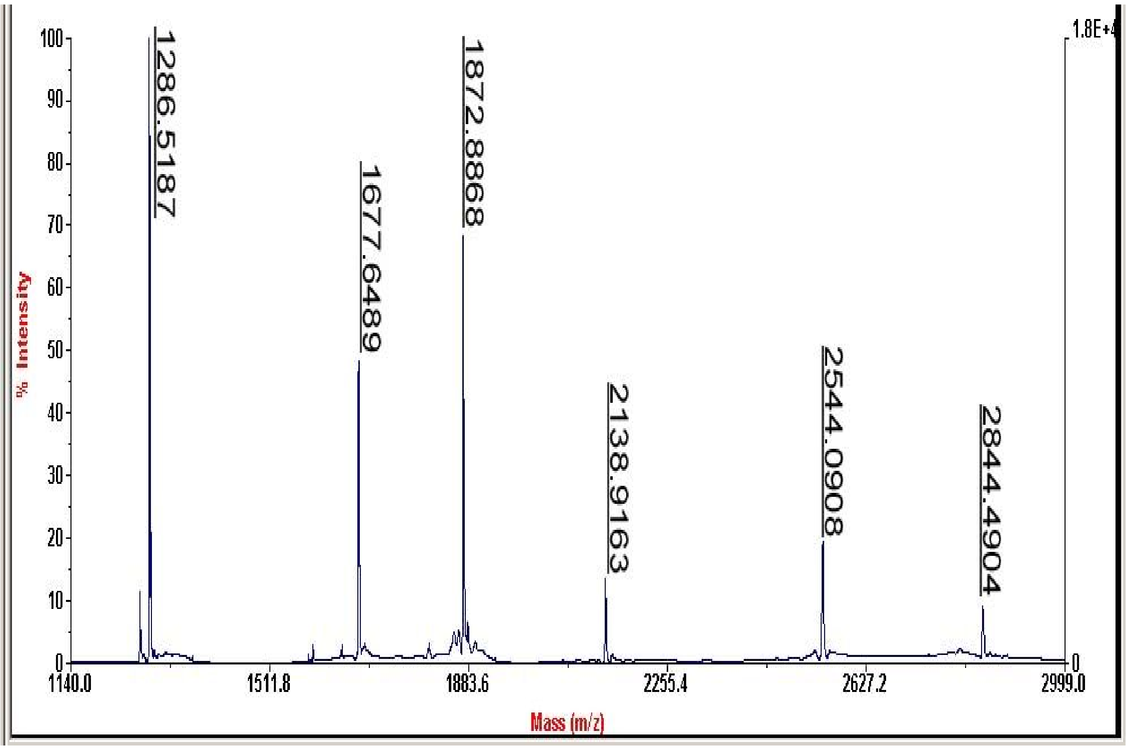
17） Moesin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
84 - 100	2081.9894	2080.9821	2080.9953	-0.0132	0	K.FYPEDVSEELIQDITQR.L
213 - 233	2362.2147	2361.2074	2361.1600	0.0474	0	K.GSELWLGVDALGLNIYEQNDR.L
238 - 246	1104.4850	1103.4777	1103.5763	-0.0986	0	K.IGFPWSEIR.N
263 - 273	1310.6071	1309.5998	1309.6819	-0.0821	1	K.KAPDFVFYAPR.L
264 - 273	1182.4986	1181.4913	1181.5869	-0.0956	0	K.APDFVFYAPR.L
413 - 427	1703.7731	1702.7658	1702.8559	-0.0902	0	K.TQEQLALEMAELTAR.I
439 - 448	1233.5165	1232.5092	1232.5673	-0.0581	0	K.ESEAVEWQQK.A

No match to: 1195.4795, 1478.6859, 1623.7354, 2171.1001

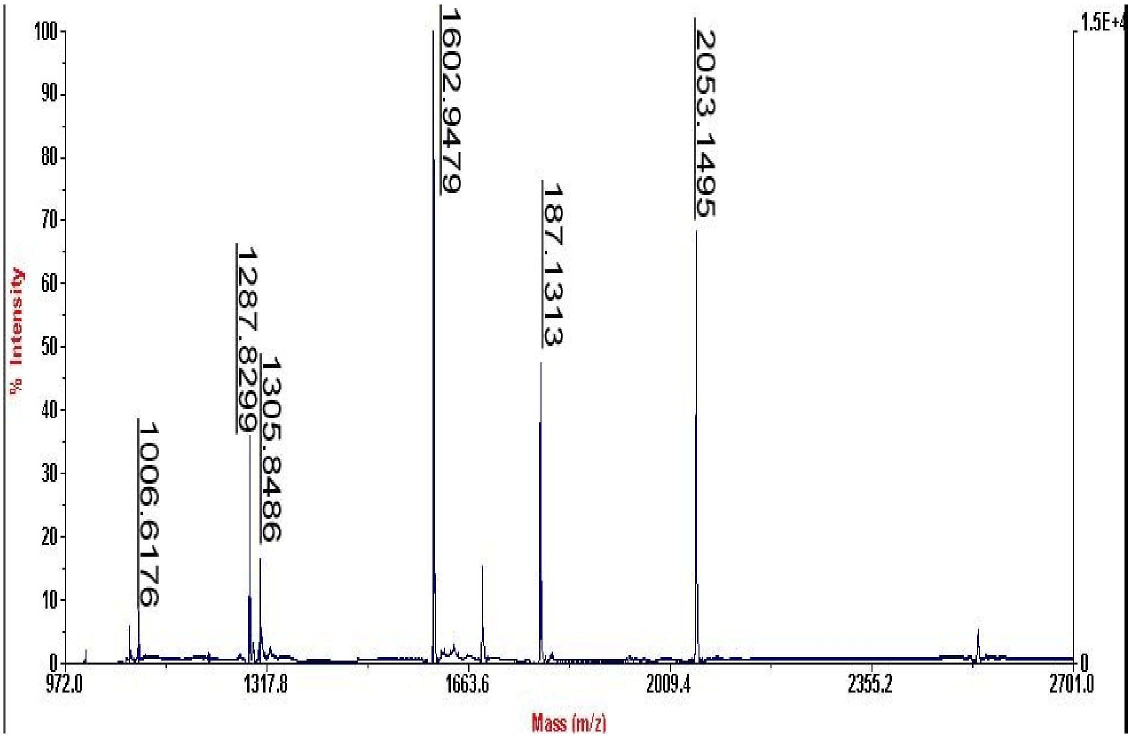
18） Ig gamma-1 chain C region



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
106 - 131	2844.4904	2843.4831	2843.4502	0.0329	0	K.THTCPPCPAPELLGGPSVFLFPPKPK.D 2
139 - 157	2138.9163	2137.9090	2138.0201	-0.1111	0	R.TPEVTCVVVDVSHEDPEVK.F
158 - 171	1677.6489	1676.6416	1676.7946	-0.1530	0	K.FNWYVDGVEVHNAK.T
228 - 238	1286.5187	1285.5114	1285.6666	-0.1552	0	R.EPQVYTLPPSR.D
228 - 243	1872.8868	1871.8796	1871.9629	-0.0833	1	R.EPQVYTLPPSRDELTK.N
254 - 275	2544.0908	2543.0836	2543.1240	-0.0404	0	K.GFYPSDIAVEWESNGQPENNYK.T

No match to: 1268.5175

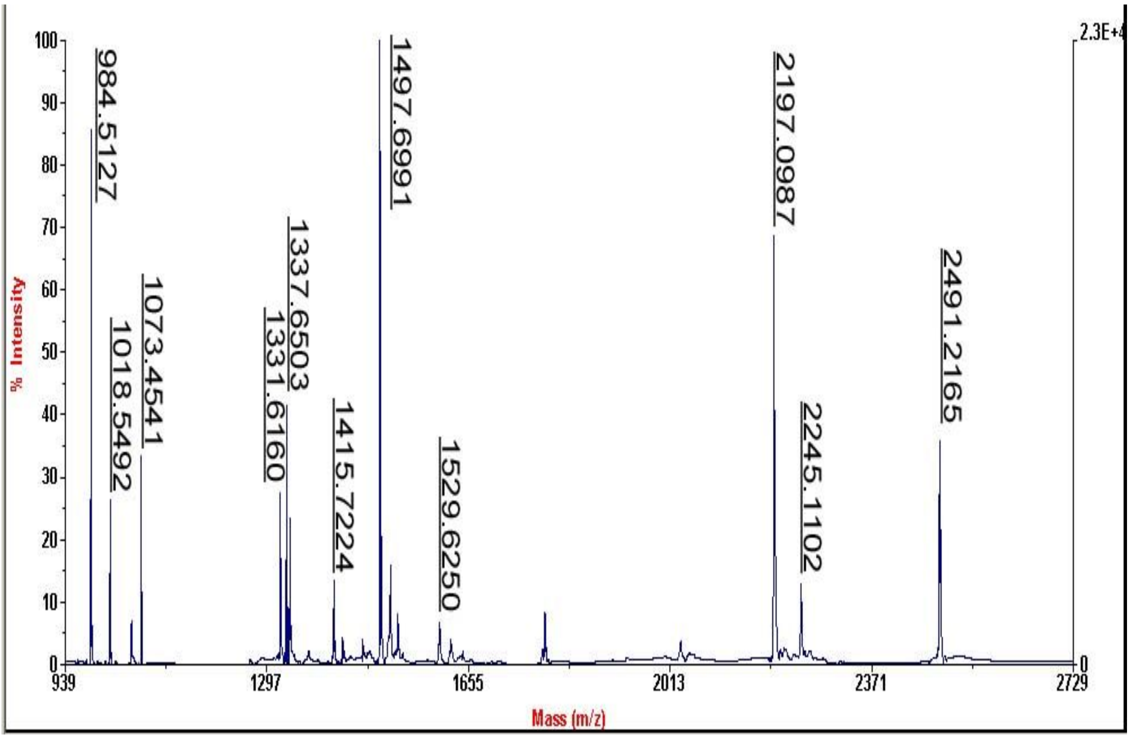
19） Leukocyte elastase inhibitor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
57 - 69	1602.9479	1601.9406	1601.7586	0.1820	0	K.TFHFNTVEEVHSR.F
70 - 80	1305.8486	1304.8413	1304.6837	0.1577	1	R.FQSLNADINKR.G
178 - 186	1006.6176	1005.6104	1005.4879	0.1224	0	K.EATTNAPFR.L
204 - 213	1218.7256	1217.7184	1217.5968	0.1216	0	K.FAYGYIEDLK.C
291 - 301	1207.7816	1206.7743	1206.6244	0.1499	0	R.LGVQDLFNSSK.A
364 - 375	1287.8299	1286.8226	1286.6731	0.1495	0	R.HNSSGSILFLGR.F

No match to: 909.1137, 925.1257, 1687.0810, 1786.1058, 2053.1495, 2536.6373

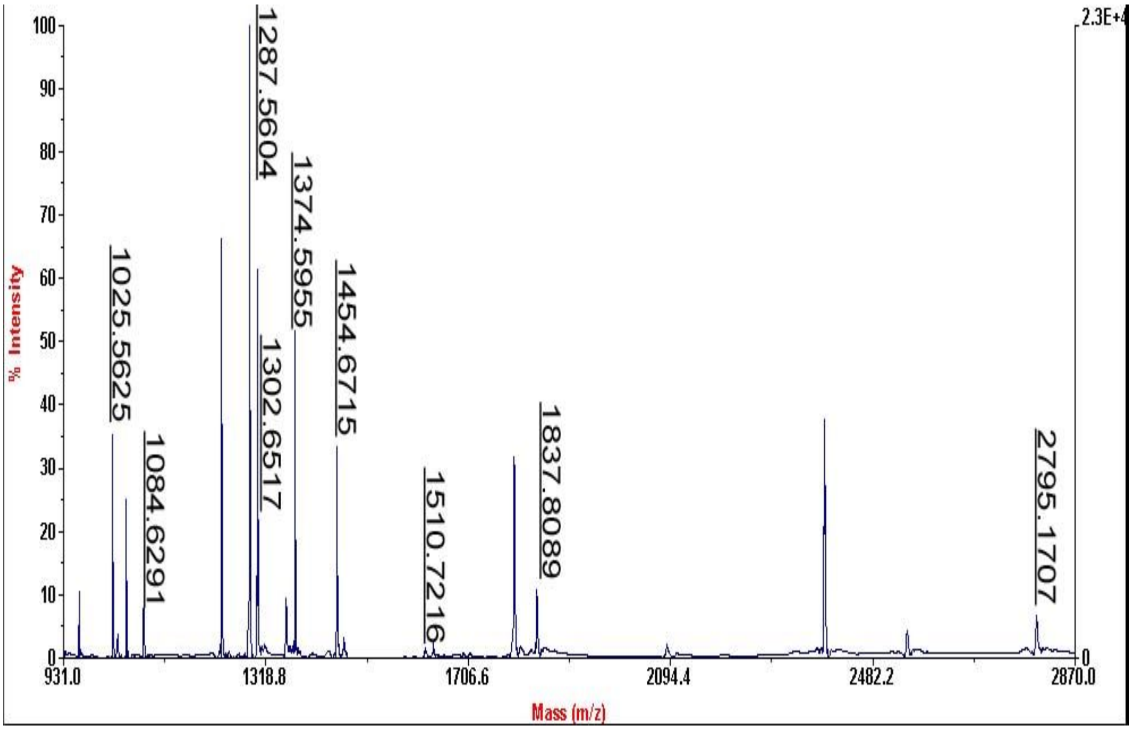
20） Aminoacylase-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
5 - 17	1497.6991	1496.6919	1496.7259	-0.0340	0	K.GPEEEHPSVTLFR.Q	
24 - 43	2197.0987	2196.0915	2196.0851	0.0064	0	R.TVQPKPDYGAAVAFFEETAR.Q	
89 - 100	1529.6250	1528.6177	1528.6735	-0.0558	0	K.EHWSHDPFEAFK.D	
101 - 109	1073.4541	1072.4468	1072.4825	-0.0357	0	K.DSEGYIYAR.G	
116 - 126	1337.6503	1336.6430	1336.6809	-0.0378	0	K.CVSIQYLEAVR.R	
169 - 191	2491.2165	2490.2092	2490.1702	0.0390	0	R.AGFALDEGIANPTDAFTVFYSER.S	
222 - 230	1018.5492	1017.5419	1017.5971	-0.0552	0	K.VVNSILAFR.E	
256 - 276	2245.1102	2244.1029	2244.0884	0.0145	0	K.LEGGVAYNVIPATMSASFDFR.V	
333 - 350	2030.9467	2029.9394	2029.9448	-0.0054	0	K.DMNLTLEPEIMPAATDNR.Y	
354 - 367	1415.7224	1414.7152	1414.7390	-0.0239	0	R.AVGVPALGFSPMNR.T	
354 - 367	1431.6684	1430.6611	1430.7339	-0.0728	0	R.AVGVPALGFSPMNR.T	Oxidation (M)
368 - 378	1331.6160	1330.6088	1330.6629	-0.0542	0	R.TPVLLHDHDER.L	
379 - 386	984.5127	983.5054	983.5552	-0.0498	0	R.LHEAVFLR.G	

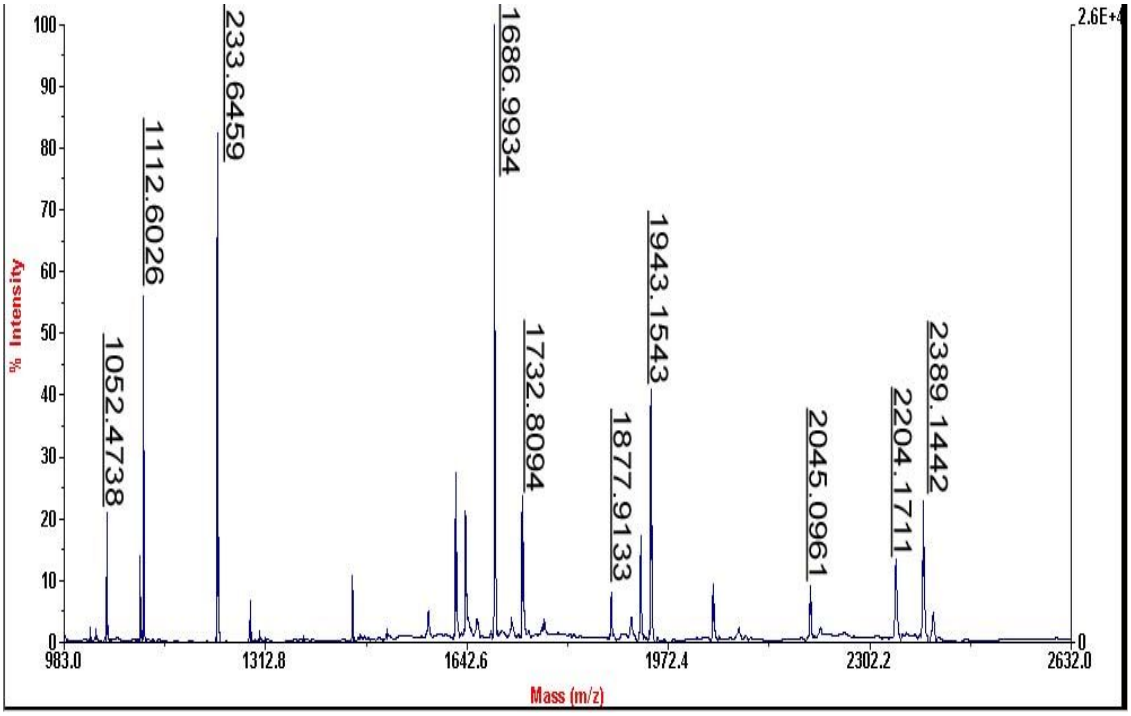
No match to: 1056.5522, 1320.6186, 1467.7877, 1515.7160, 1602.7270, 1623.7644, 1790.8780

21） Selenium-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
24 - 34	1454.6715	1453.6642	1453.7275	-0.0633	0	R.EEIVYLPCIYR.N
53 - 62	1287.5604	1286.5531	1286.6190	-0.0658	0	K.SPQYCQVIHR.L
94 - 103	1084.6291	1083.6219	1083.6652	-0.0433	0	K.LVLPSLISSR.I
161 - 174	1510.7216	1509.7143	1509.7714	-0.0571	0	K.GGFVLLDGETFEVK.G
196 - 211	1837.8089	1836.8016	1836.9304	-0.1288	0	R.HNVMISTEWAAPNVLR.D
212 - 235	2795.1707	2794.1634	2794.2775	-0.1141	0	R.DGFNPADVEAGLYGSHLYVWDWQR.H
246 - 254	1025.5625	1024.5552	1024.5917	-0.0365	0	K.DGLIPLEIR.F
334 - 344	1374.5955	1373.5882	1373.6688	-0.0806	0	R.QYDISDPQRPR.L
412 - 419	1051.4933	1050.4861	1050.5498	-0.0638	0	K.QFYPDLIR.E
449 - 460	1302.6517	1301.6444	1301.7091	-0.0647	0	K.EPLGPALAHELR.Y

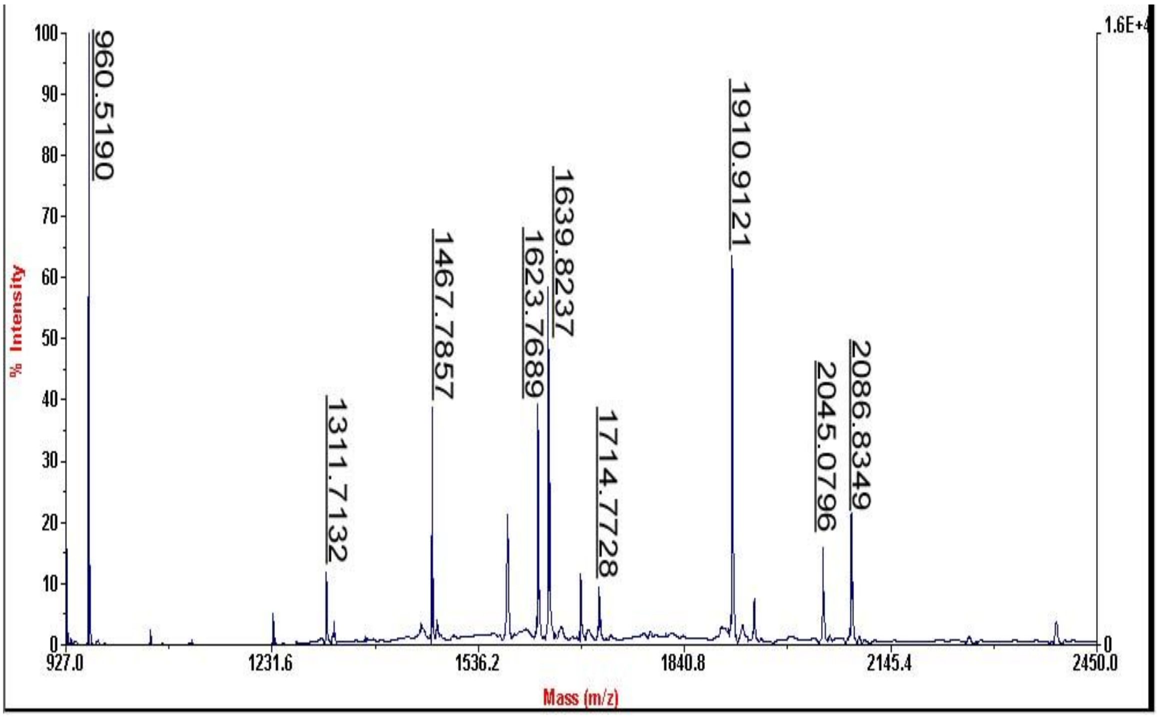
22） Cytosolic nonspecific dipeptidase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 17	2045.0961	2044.0888	2043.9935	0.0953	1	-.MAALTTLFKYIDENQDR.Y
Oxidation (M)						
10 - 17	1052.4738	1051.4665	1051.4570	0.0095	0	K.YIDENQDR.Y
67 - 84	1943.1543	1942.1470	1942.1251	0.0219	1	K.QKLPDGSEIPLPPILLGR.L
69 - 84	1686.9934	1685.9861	1685.9716	0.0145	0	K.LPDGSEIPLPPILLGR.L
150 - 159	1112.6026	1111.5954	1111.5985	-0.0032	0	K.TGQEIPVNVR.F
160 - 180	2389.1442	2388.1370	2388.0613	0.0757	0	R.FCLEGMEESGSEGLDELIFAR.K
203 - 211	1107.6072	1106.5999	1106.5906	0.0093	0	K.KPCITYGLR.G
255 - 275	2204.1711	2203.1639	2203.1484	0.0155	0	R.GNILIPGINEAVAAVTEEEHK.L
276 - 289	1732.8094	1731.8021	1731.7879	0.0142	0	K.LYDDIDFDIEEFAK.D
311 - 329	1877.9133	1876.9060	1876.9318	-0.0258	0	R.YPSLSLHGIEGAFSGSGAK.T
403 - 413	1233.6459	1232.6386	1232.6401	-0.0015	0	K.TVFGVEPDLTR.E

No match to: 927.4822, 960.5557, 1454.7310, 1623.8088, 1639.9018, 1926.1182, 2344.1555

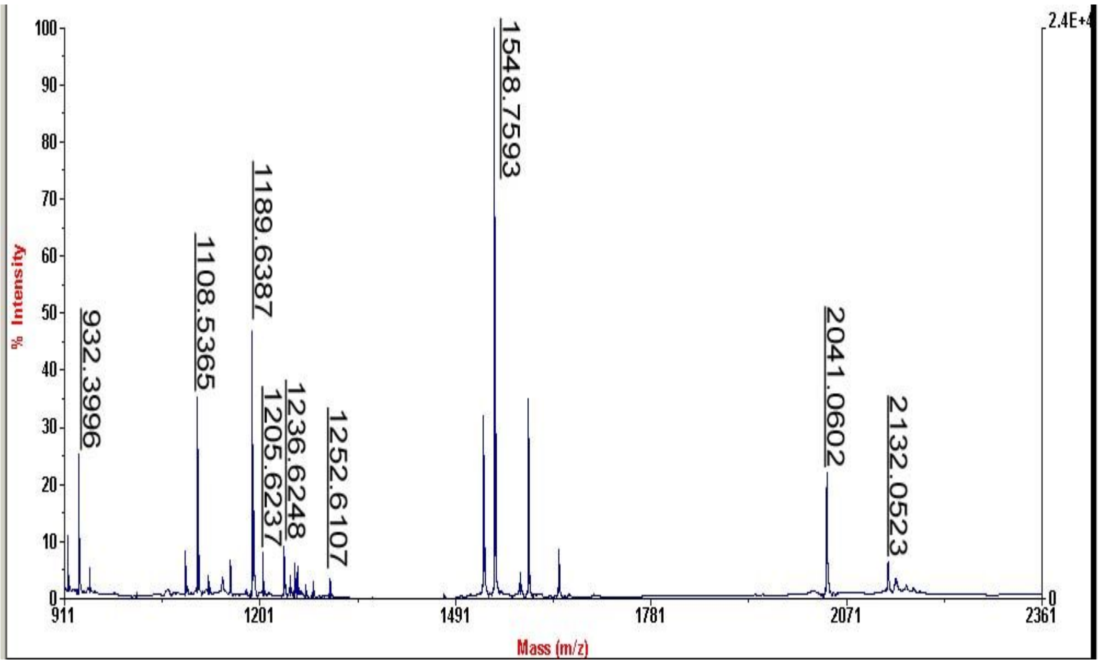
23） Serum albumin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
118 - 130	1714.7728	1713.7655	1713.7893	-0.0238	1	K.QEPERNECFLQHK.D	
139 - 160	2650.3839	2649.3766	2649.2566	0.1199	0	R.LVRPEVDVMCTAFHDNEETFLK.K	
139 - 161	2778.4458	2777.4386	2777.3516	0.0870	1	R.LVRPEVDVMCTAFHDNEETFLKK.Y	
162 - 168	927.4607	926.4534	926.4861	-0.0327	0	K.YLYEIAR.R	
265 - 281	2086.8349	2085.8277	2085.8302	-0.0026	0	K.VHTECCHGDLLECADDR.A	3
348 - 360	1623.7689	1622.7616	1622.7802	-0.0186	0	K.DVFLGMFLYEYAR.R	
348 - 360	1639.8237	1638.8164	1638.7751	0.0412	0	K.DVFLGMFLYEYAR.R	Oxidation (M)
361 - 372	1467.7857	1466.7784	1466.8357	-0.0573	1	R.RHPDYSVVLLLR.L	
362 - 372	1311.7132	1310.7059	1310.7346	-0.0287	0	R.HPDYSVVLLLR.L	
397 - 413	2045.0795	2044.0722	2044.0880	-0.0158	0	K.VFDEFKPLVEEPQNLIK.Q	
427 - 434	960.5190	959.5117	959.5552	-0.0435	0	K.FQNALLVR.Y	
509 - 524	1910.9121	1909.9049	1909.9243	-0.0195	0	R.RPCFSALEVDETYVPK.E	
525 - 543	2260.0009	2258.9936	2259.0154	-0.0218	0	K.EFNAETFTFHADICTLSEK.E	

No match to: 1579.0358, 1686.9558, 1943.1181, 2141.0920, 2389.1214

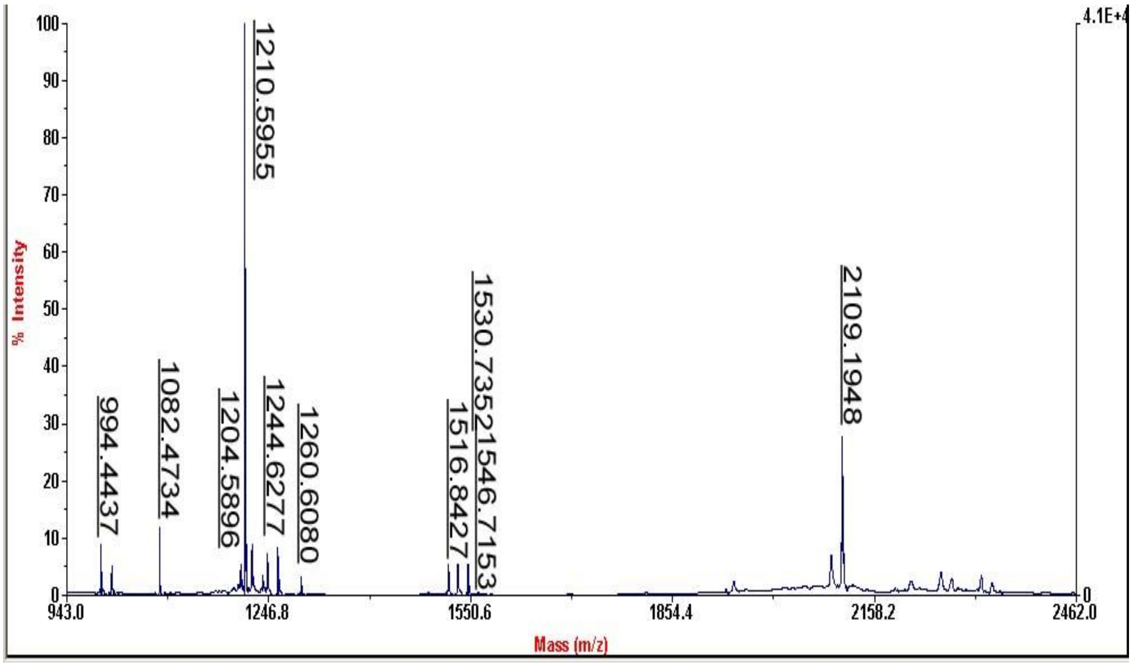
24）14-3-3 protein zeta/delta



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
28 - 41	1548.7593	1547.7520	1547.7063	0.0458	0	K.SVTEQGAELSNEER.N	
121 - 127	932.3996	931.3923	931.4221	-0.0298	1	K.MKGDYYR.Y	
140 - 157	2041.0602	2040.0529	2039.9799	0.0730	0	K.GIVDQSQQAYQEAFEISK.K	
158 - 167	1236.6248	1235.6175	1235.6445	-0.0269	1	K.KEMQPTHPIR.L	
158 - 167	1252.6107	1251.6035	1251.6394	-0.0359	1	K.KEMQPTHPIR.L	Oxidation (M)
159 - 167	1108.5365	1107.5292	1107.5495	-0.0203	0	K.EMQPTHPIR.L	
194 - 212	2132.0523	2131.0451	2130.9844	0.0606	0	K.TAFDEAIAELDTLSEESYK.D	
213 - 222	1189.6387	1188.6315	1188.6536	-0.0222	0	K.DSTLIMQLLR.D	
213 - 222	1205.6237	1204.6165	1204.6485	-0.0321	0	K.DSTLIMQLLR.D	Oxidation (M)

No match to: 916.4048, 1090.5343, 1156.5971, 1532.7557, 1598.7675, 1643.8528

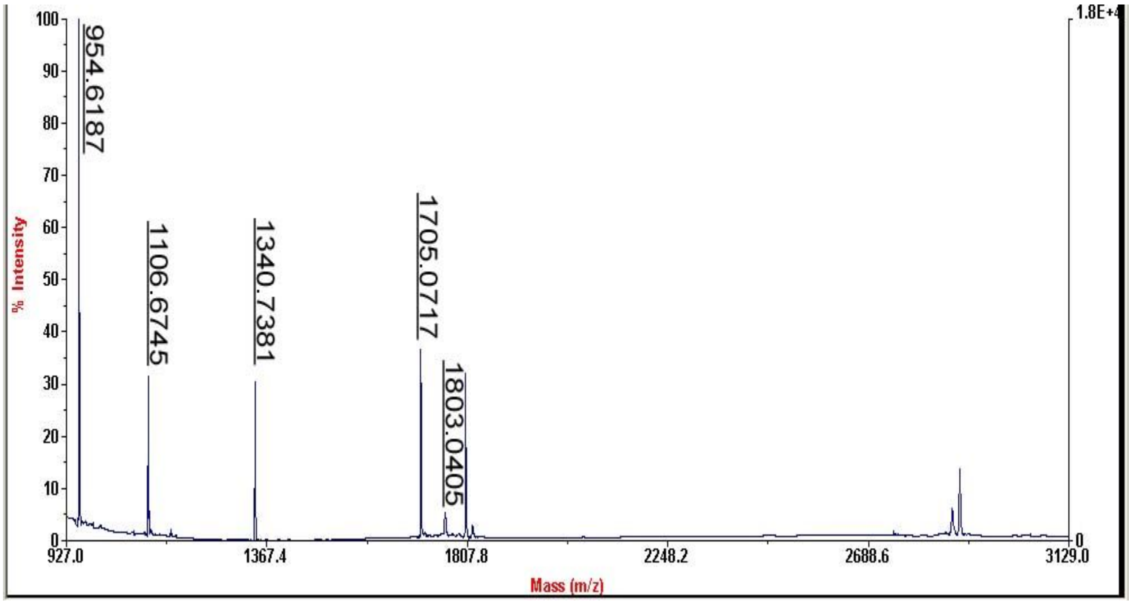
25） Transgelin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
21 - 29	1210.5955	1209.5882	1209.5513	0.0369	1	K.KYDEELEER.L	
22 - 29	1082.4734	1081.4661	1081.4563	0.0098	0	K.YDEELEER.L	
30 - 47	2109.1948	2108.1876	2108.0836	0.1039	0	R.LVEWIIVQCGPDVGRPDR.G	
65 - 78	1516.8427	1515.8354	1515.8296	0.0058	0	K.LVNSLYPDGSKPVK.V	
79 - 89	1244.6277	1243.6205	1243.6270	-0.0066	0	K.VPENPPSMVFK.Q	
79 - 89	1260.6080	1259.6007	1259.6220	-0.0213	0	K.VPENPPSMVFK.Q	Oxidation (M)
109 - 121	1530.7352	1529.7279	1529.7072	0.0208	0	K.TDMFQTVDLFEGK.D	
109 - 121	1546.7153	1545.7080	1545.7021	0.0059	0	K.TDMFQTVDLFEGK.D	Oxidation (M)
109 - 128	2318.1906	2317.1833	2317.0718	0.1115	1	K.TDMFQTVDLFEGKDMAAVQR.T	Oxidation (M)
129 - 140	1204.5896	1203.5824	1203.6897	-0.1073	0	R.TLMALGSLAVTK.N	
147 - 154	994.4437	993.4364	993.4378	-0.0014	0	R.GDPNWFMK.K	
147 - 154	1010.4283	1009.4211	1009.4327	-0.0117	0	R.GDPNWFMK.K	Oxidation (M)

No match to: 2092.0082, 2213.8794, 2259.2073, 2274.2071

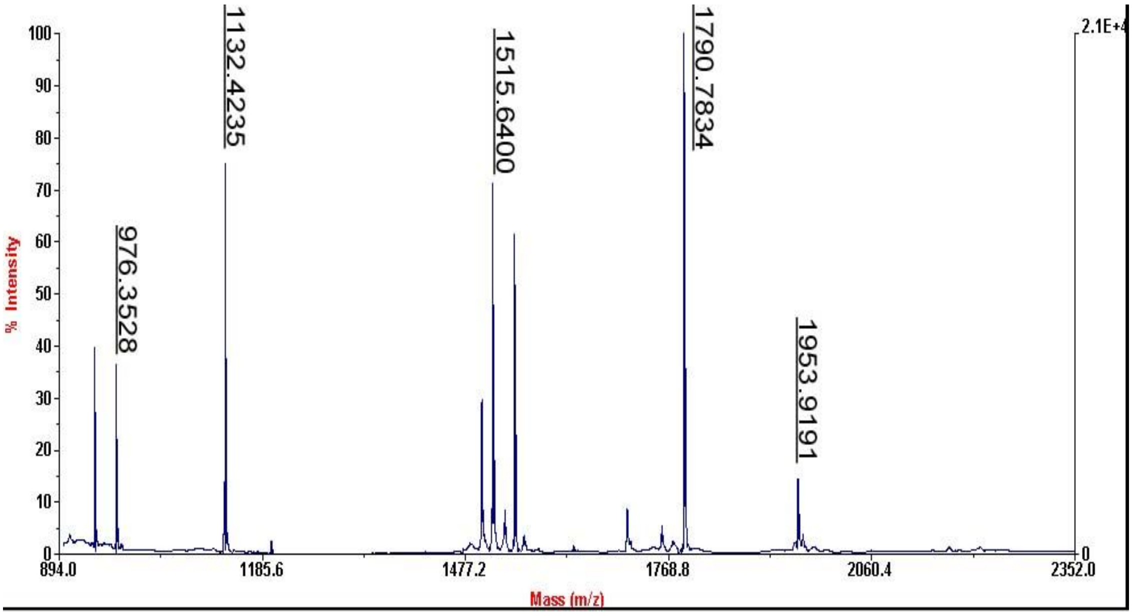
26） Annexin A5



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 18	1340.7381	1339.7308	1339.6044	0.1264	0	R.GTVTDFPGFDER.A
30 - 45	1705.0717	1704.0644	1703.8941	0.1703	0	K.GLGTDEESILTLLTSR.S
194 - 201	954.6187	953.6114	953.5334	0.0780	0	K.FITIFGTR.S
213 - 227	1803.0405	1802.0332	1801.8556	0.1776	0	K.YMTISGFQIEETIDR.E
277 - 285	1106.6745	1105.6672	1105.5767	0.0905	0	R.SEIDLFNIR.K

No match to: 2888.5858

27） Actin, cytoplasmic 1 (Beta-actin)

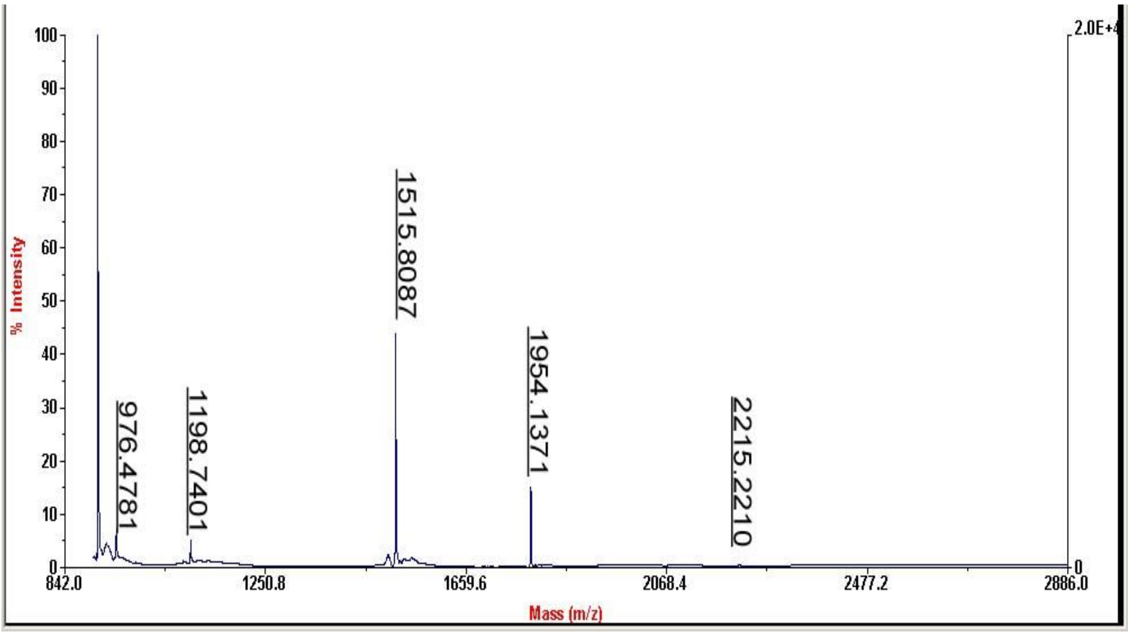


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

19 - 28	976.3528	975.3455	975.4410	-0.0954	0	K.AGFAGDDAPR.A
85 - 95	1515.6400	1514.6327	1514.7419	-0.1092	0	K.IWHHTFYNELR.V
96 - 113	1953.9191	1952.9118	1953.0571	-0.1453	0	R.VAPEEHPVLLTEAPLNPK.A
197 - 206	1132.4235	1131.4162	1131.5196	-0.1034	0	R.GYSFTTTAER.E
239 - 254	1790.7834	1789.7761	1789.8846	-0.1085	0	K.SYELPDGQVITIGNER.F
360 - 372	1516.5988	1515.5916	1515.6953	-0.1038	0	K.QEYDESGPSIVHR.K

No match to: 945.4407, 1130.4573, 1499.5489, 1533.6220, 1547.6311, 1708.7797, 1758.8002

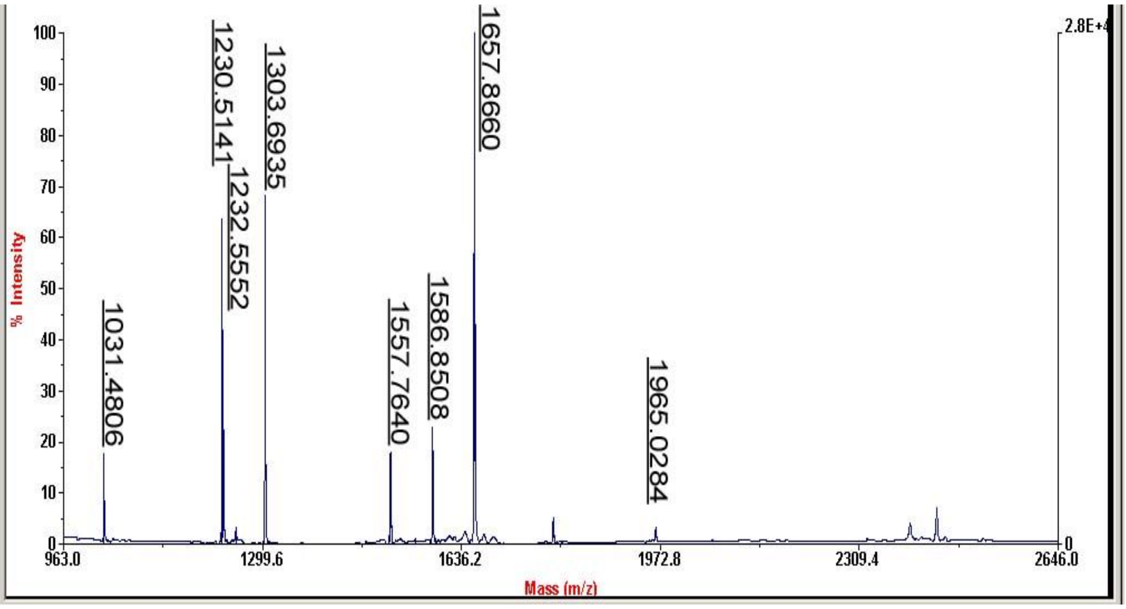
28） Actin, cytoplasmic 2 (Gamma-actin)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
19 - 28	976.4781	975.4709	975.4410	0.0299	0	K.AGFAGDDAPR.A
29 - 39	1198.7401	1197.7329	1197.6982	0.0347	0	R.AVFPSIVGRPR.H
85 - 95	1515.8087	1514.8014	1514.7419	0.0595	0	K.IWHHTFYNELR.V
96 - 113	1954.1371	1953.1298	1953.0571	0.0727	0	R.VAPEEHPVLLTEAPLNPK.A
197 - 206	1132.5671	1131.5599	1131.5196	0.0402	0	R.GYSFTTTAER.E
239 - 254	1790.9888	1789.9815	1789.8846	0.0969	0	K.SYELPDGQVITIGNER.F
292 - 312	2215.2210	2214.2137	2214.0626	0.1511	0	K.DLYANTVLSGGTTMYPGIADR.M
360 - 372	1516.7821	1515.7748	1515.6953	0.0795	0	K.QEYDESGPSIVHR.K

No match to: 945.5855, 1499.7350, 1547.7936, 4312.6452

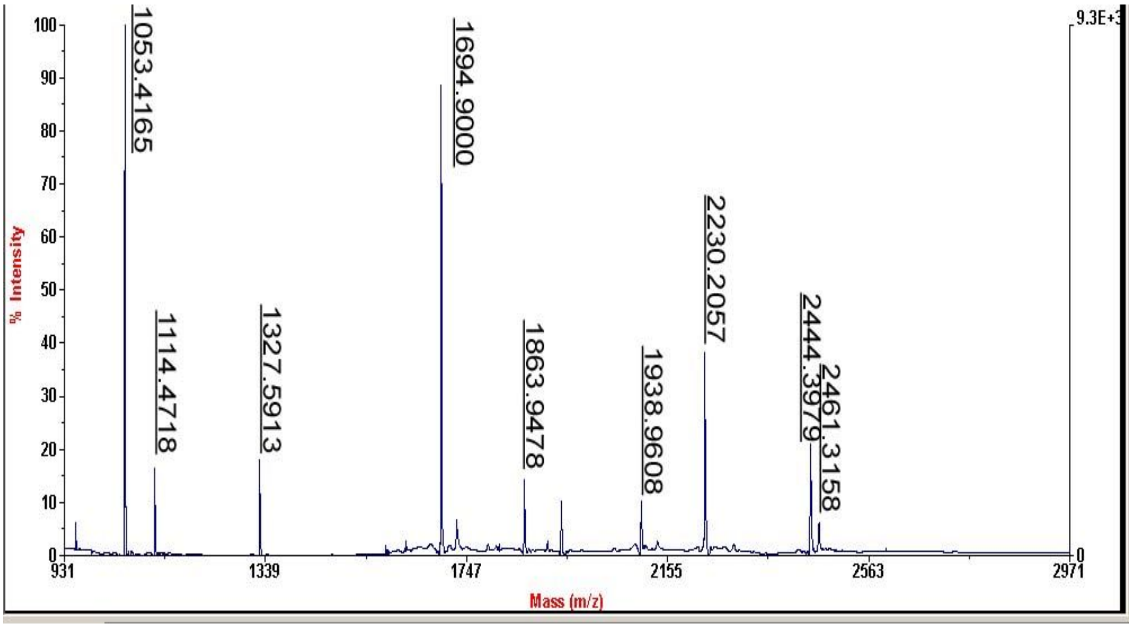
29） Creatine kinase B-type



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
33 - 43	1303.6935	1302.6863	1302.7183	-0.0321	0	K.VLTPELYAELR.A	
87 - 96	1232.5552	1231.5479	1231.6084	-0.0606	0	K.DLFDPIIEDR.H	
139 - 148	1230.5141	1229.5068	1229.5434	-0.0366	0	R.GFCLPPHCSR.G	2
157 - 172	1586.8508	1585.8435	1585.8311	0.0125	0	K.LAVEALSSLDGDLAGR.Y	
224 - 236	1657.8660	1656.8587	1656.8260	0.0328	0	K.TFLVWVNEEDHLR.V	
253 - 265	1557.7640	1556.7568	1556.7908	-0.0341	0	R.FCTGLTQIETLFK.S	
321 - 341	1965.0284	1964.0211	1963.9234	0.0976	0	R.GTGGVDTAAVGGVFDVSNADR.L	
359 - 366	1031.4806	1030.4734	1030.5481	-0.0747	0	K.LLIEMEQR.L	

No match to: 1790.9458, 2439.3994, 2518.4080

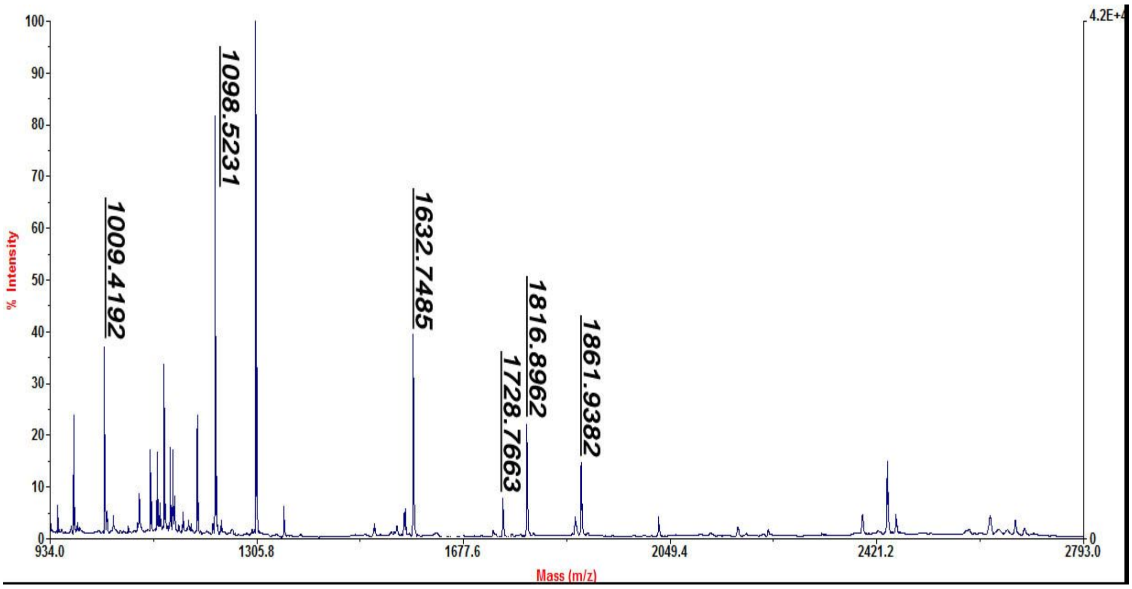
31）Inorganic pyrophosphatase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
10 - 18	1053.4165	1052.4093	1052.5291	-0.1198	0	R.AAPFSLEYR.V
26 - 41	1863.9478	1862.9405	1862.9203	0.0203	0	K.GQYISPFHDIPIYADK.D
42 - 52	1327.5913	1326.5840	1326.6754	-0.0914	0	K.DVFHMVVEVPR.W
80 - 88	1114.4718	1113.4645	1113.5858	-0.1213	0	R.YVANLFPYK.G
89 - 109	2461.3158	2460.3085	2460.1134	0.1951	0	K.GYIWNYGAIPQTWEDPGHNDK.H
156 - 177	2444.3979	2443.3907	2443.1979	0.1928	1	K.VIAINVDDPDAANYNDINDVKR.L
178 - 191	1694.9000	1693.8927	1693.8827	0.0100	0	R.LKPGYLEATVDWFR.R
193 - 211	2230.2057	2229.1984	2229.0741	0.1243	1	R.YKVPDGKPENEFAFNAEFK.D
195 - 211	1938.9608	1937.9535	1937.9158	0.0376	0	K.VPDGKPENEFAFNAEFK.D

No match to: 927.3504, 954.2963, 1726.8779, 2101.1307

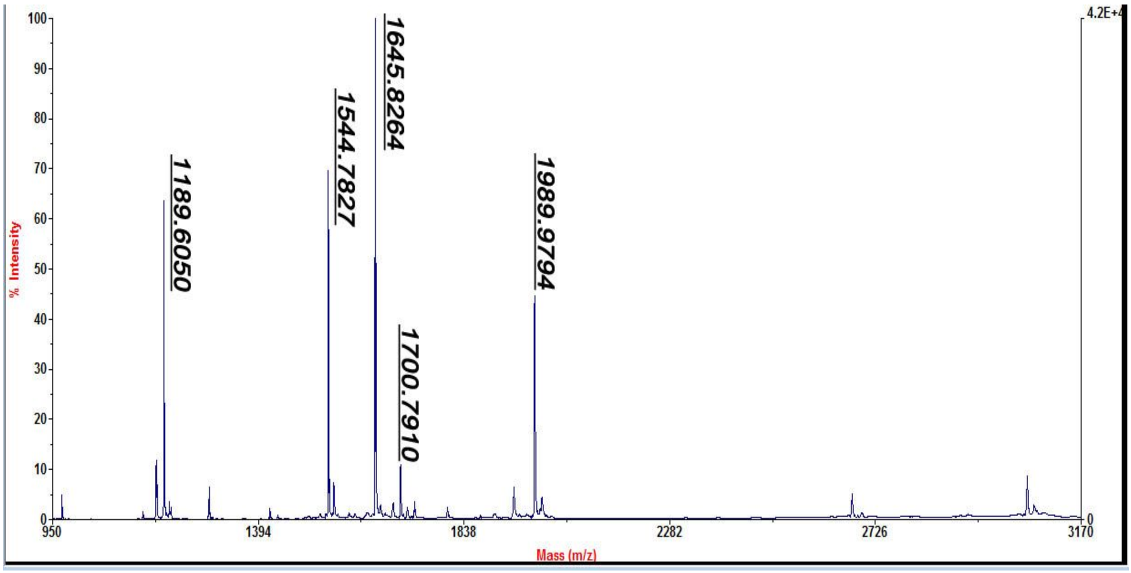
32) Betaine--homocysteine S-methyltransferase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
41 - 57	1816.8962	1815.8889	1815.8903	-0.0014	0	K.AGPWTPEAAVEHPEAVR.Q	
94 - 108	1632.7485	1631.7412	1631.7573	-0.0161	0	K.ISGQEVNEAACDIAR.Q	
259 - 274	1861.9382	1860.9310	1860.9410	-0.0100	0	K.QGFIDLPEFPFGLEPR.V	
295 - 308	1728.7663	1727.7590	1727.7548	0.0043	0	R.YIGGCCGFEPYHIR.A	2
309 - 318	1098.5231	1097.5158	1097.5716	-0.0558	0	R.AIAEELAPER.G	
350 - 356	1009.4192	1008.4119	1008.4665	-0.0545	0	K.EYWENLR.I	

No match to: 1180.5972, 1307.6235, 1471.7264, 1804.9472

33) Retinal dehydrogenase 1

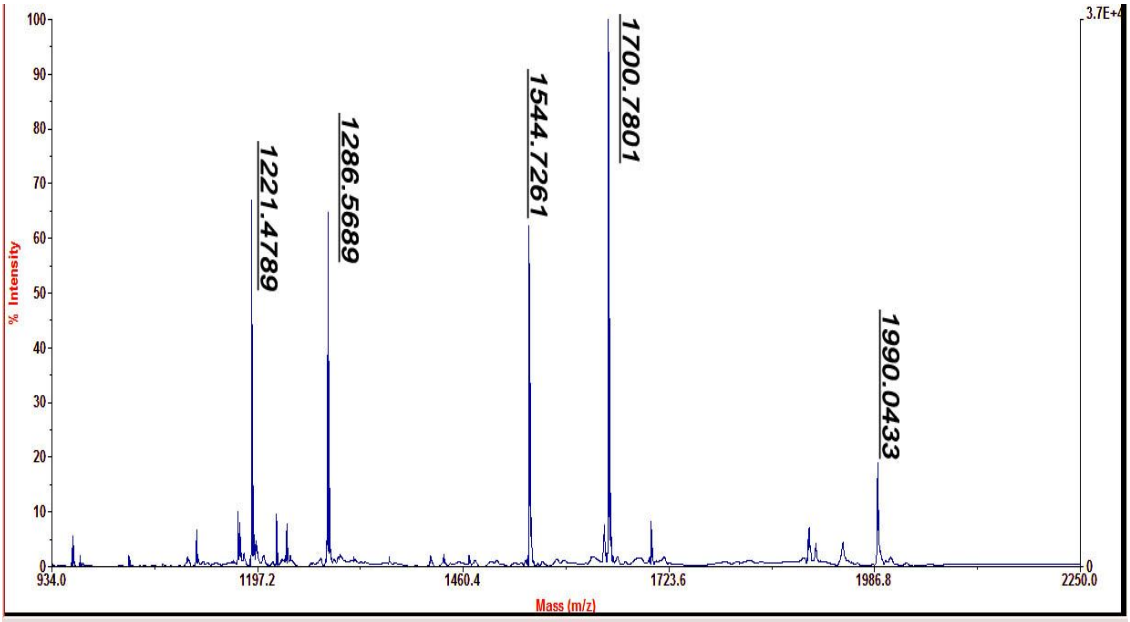


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

69 - 78	1189.6050	1188.5978	1188.6040	-0.0062	0	R.QAFQIGSPWR.T
144 - 156	1544.7827	1543.7755	1543.7671	0.0084	0	R.TIPIDGNFFTYTR.H
309 - 321	1645.8264	1644.8192	1644.8035	0.0157	0	R.IFVEESIYDEFVR.R
379 - 395	1989.9794	1988.9721	1988.9301	0.0420	0	K.GYFVQPTVFSNVTDEMR.I
477 - 490	1700.7910	1699.7837	1699.7729	0.0109	0	R.ELGEYGFHEYTEVK.T

No match to: 1172.5939, 1945.0640

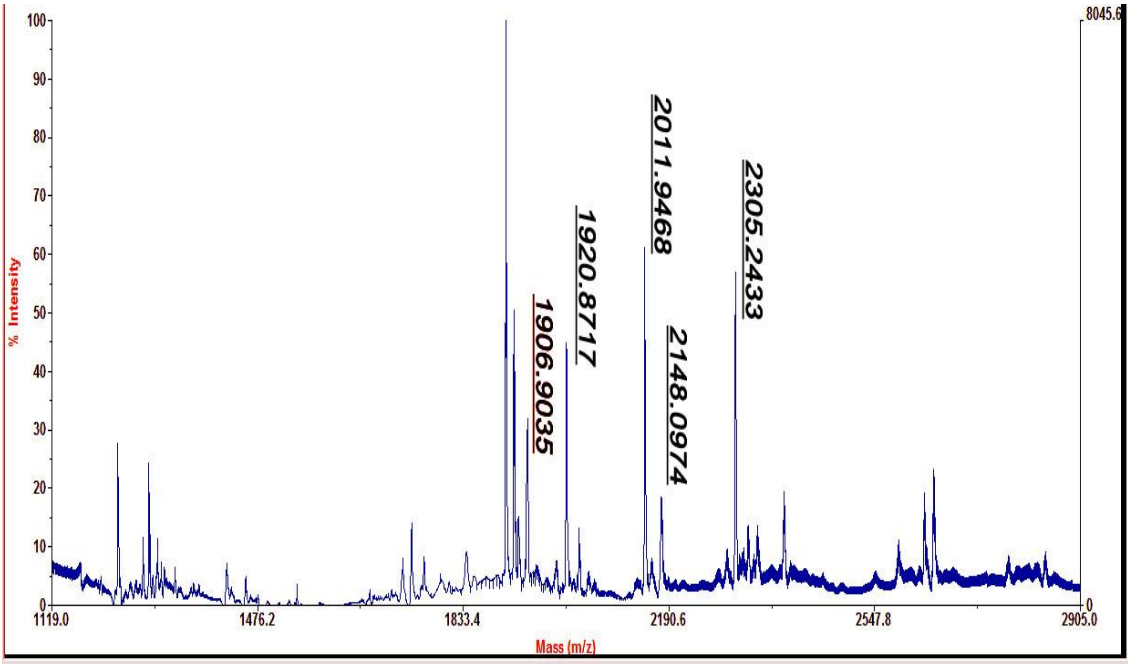
34) Golgi phosphoprotein 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
67 - 76	1221.4789	1220.4716	1220.6037	-0.1321	1	K.KNEFQGELEK.Q
104 - 115	1286.5689	1285.5617	1285.6990	-0.1373	0	K.AVLVNNITTGER.L
152 - 167	1990.0433	1989.0360	1988.9335	0.1025	1	K.FSYDLSQCINQMKEVK.E
233 - 247	1544.7261	1543.7188	1543.7729	-0.0541	0	K.SQTPAPSSEVVLDSK.R
233 - 248	1700.7801	1699.7728	1699.8740	-0.1012	1	K.SQTPAPSSEVVLDSKR.Q

No match to: 1172.4657, 1189.4799, 1645.7920

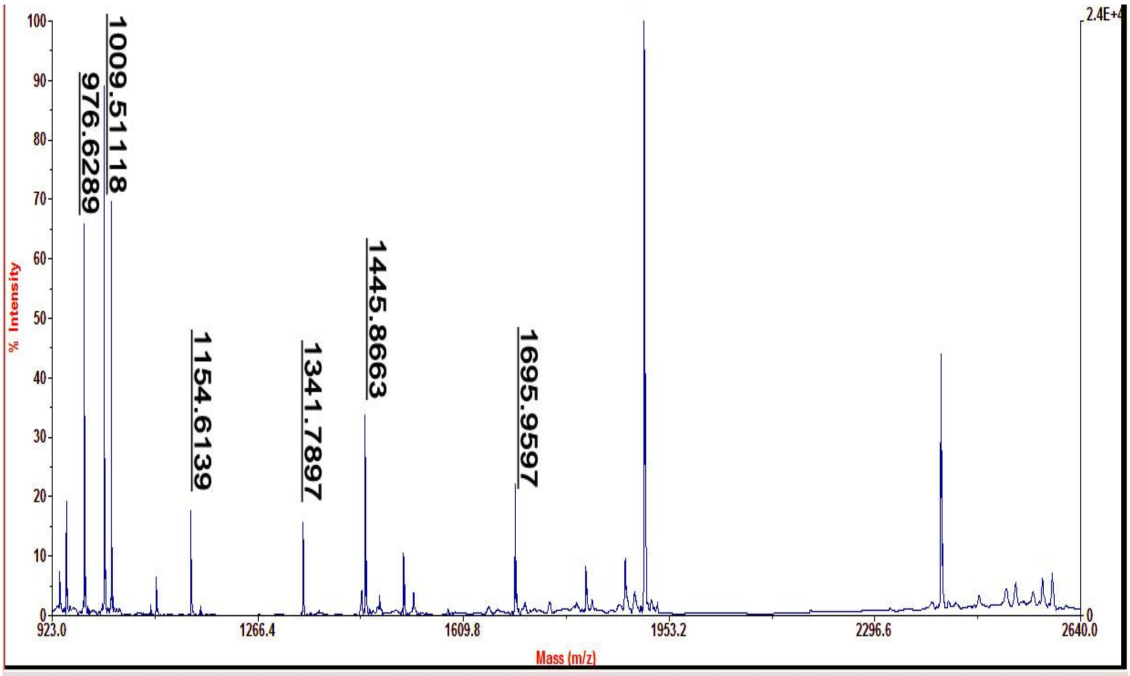
35) Alcohol dehydrogenase class 3 chi chain



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
10 - 31	2305.2433	2304.2360	2304.2364	-0.0004	0	K.AAVAWEAGKPLSIEEIEVAPPK.A	
85 - 101	1920.8717	1919.8644	1919.9121	-0.0477	0	K.AGDTVIPLYIPQCGECK.F	2
169 - 188	2011.9468	2010.9395	2010.9866	-0.0471	0	K.VCLLGCGISTGYGAAVNTAK.L	2
340 - 357	2148.0974	2147.0902	2147.0898	0.0004	1	K.IKVDEFVTHNLSFDEINK.A	
342 - 357	1906.9035	1905.8962	1905.9108	-0.0146	0	K.VDEFVTHNLSFDEINK.A	

No match to: 2188.0825

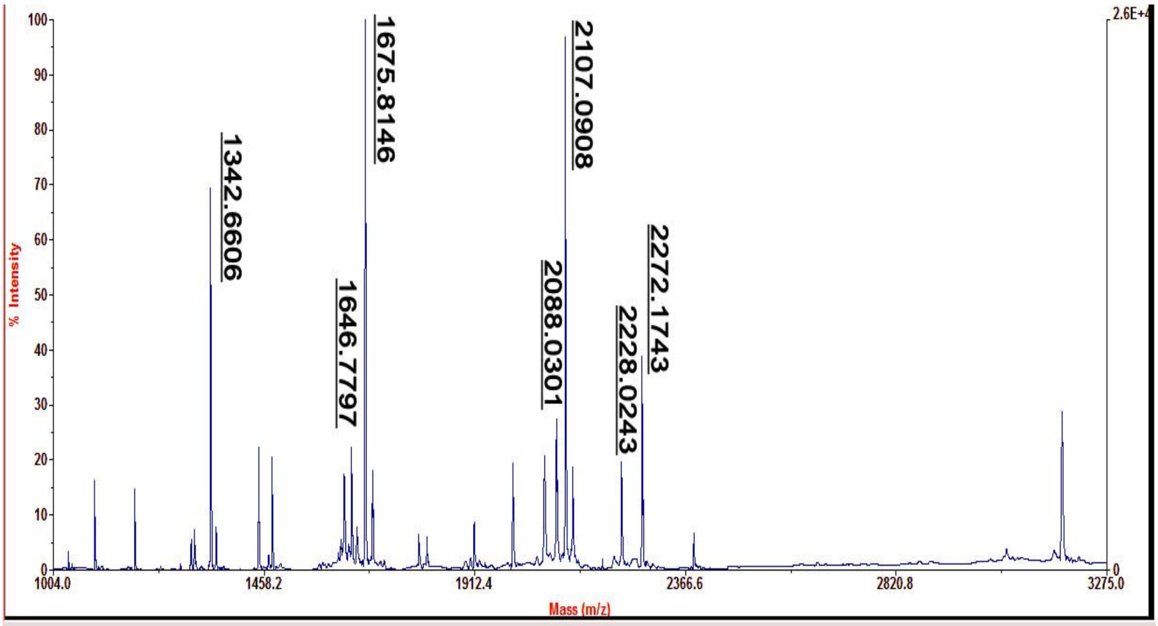
36) Isocitrate dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
5 - 20	1695.9597	1694.9524	1694.7603	0.1921	0	K.ISGGSVVEMQGDEMTR.I
101 - 109	976.6289	975.6216	975.5501	0.0715	0	R.NILGGTVFR.E
133 - 140	1009.5118	1008.5046	1008.4413	0.0633	0	R.HAYGDQYR.A
223 - 233	1445.8633	1444.8561	1444.7238	0.1323	1	R.FKDIFQEIYDK.Q
244 - 249	903.4992	902.4919	902.4399	0.0521	0	K.IWYEHR.L
261 - 270	1154.6139	1153.6066	1153.5226	0.0841	0	K.SEGGFIWACK.N
302 - 314	1341.7897	1340.7824	1340.6684	0.1140	0	K.TVEAEAAHGTVTR.H

No match to: 946.6210, 1021.5150, 1911.1206, 2406.5081

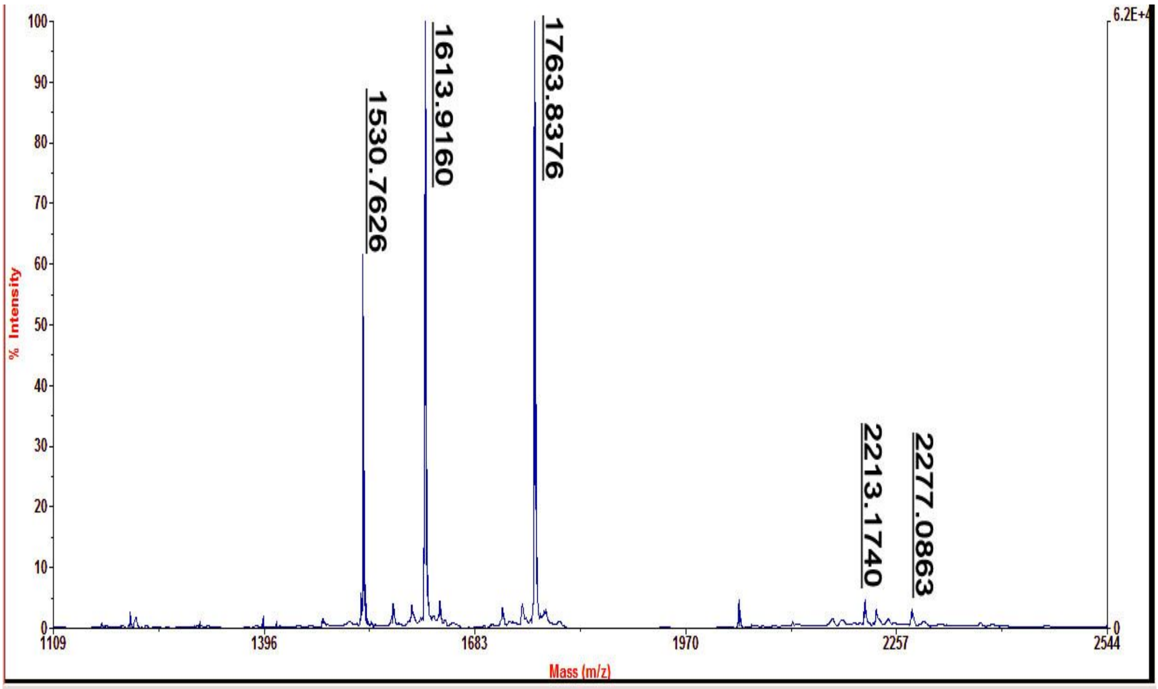
37) Fructose-bisphosphate aldolase A



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 57	1646.7797	1645.7724	1645.8019	-0.0295	1	R.LQSIGTENTEENRR.F
70 - 87	2088.0301	2087.0228	2087.0873	-0.0645	0	R.VNPCIGGVILFHETLYQK.A
88 - 99	1342.6606	1341.6533	1341.7041	-0.0507	0	K.ADDGRPFPQVIK.S
112 - 134	2272.1734	2271.1661	2271.1342	0.0319	0	K.GVVPLAGTNGETTTQGLDGLSER.C
154 - 173	2107.0908	2106.0836	2106.0891	-0.0055	0	K.IGEHTPSALAIMENANVLAR.Y
244 - 258	1675.8146	1674.8073	1674.8399	-0.0326	0	K.FSHEEIAMATVTALR.R
343 - 364	2228.0243	2227.0170	2227.0181	-0.0011	0	K.YTPSGQAGAAASESLFVSNHAY.-

No match to: 2062.1415, 3177.7975

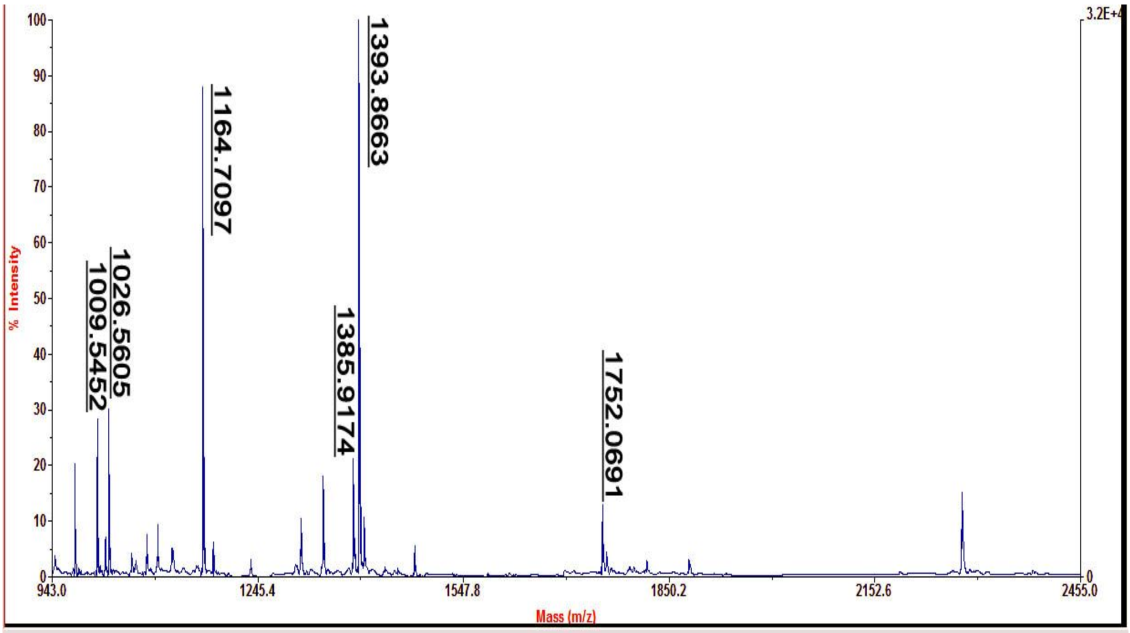
38) Glyceraldehyde-3-phosphate dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
67 - 80	1613.9160	1612.9087	1612.8936	0.0151	0	K.LVINGNPITIFQER.D
87 - 107	2277.0863	2276.0790	2276.0306	0.0484	0	K.WGDAGAEYVVESTGVFTTMEK.A
119 - 139	2213.1740	2212.1667	2212.1020	0.0648	0	R.VIISAPSADAPMFVMGVNHEK.Y
235 - 248	1530.7626	1529.7554	1529.7871	-0.0318	0	R.VPTANVSVVDLTCR.L
310 - 323	1763.8376	1762.8303	1762.7950	0.0353	0	K.LISWYDNEFGYSNR.V

No match to: 1634.7924, 2042.1574

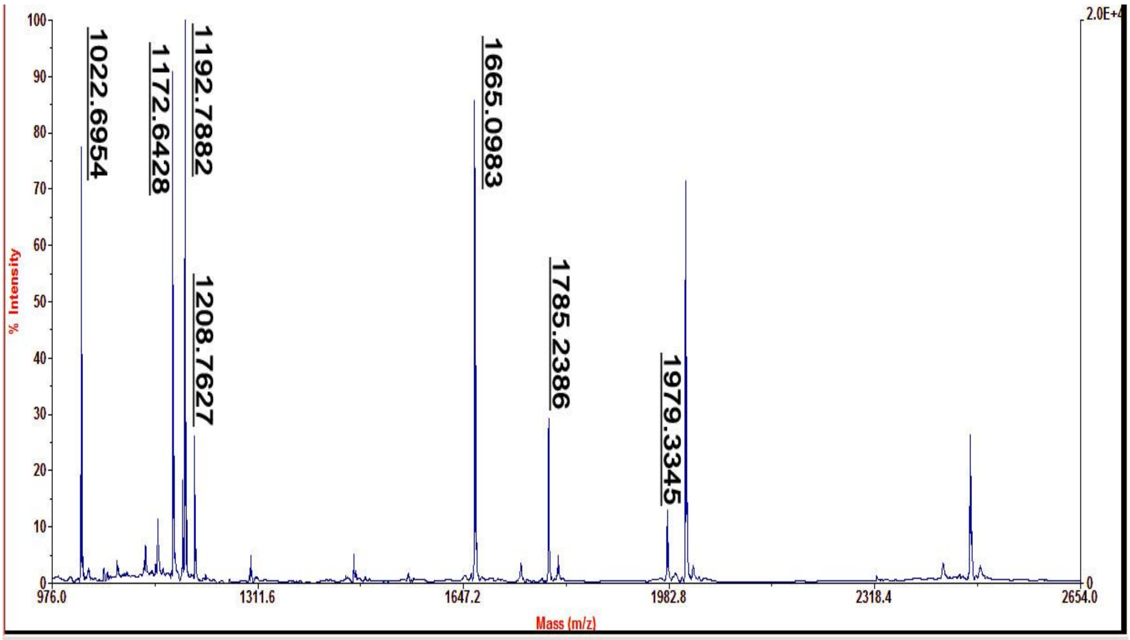
39) Malate dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
80 - 92	1385.9174	1384.9102	1384.7384	0.1718	0	K.DLDVAILVGSMPR.R	
150 - 157	1026.5605	1025.5532	1025.4600	0.0932	0	K.ENFSCLTR.L	
206 - 220	1752.0691	1751.0618	1750.8777	0.1841	1	K.EVGVYEALKDDSWLK.G	
221 - 230	1164.7097	1163.7025	1163.5934	0.1090	0	K.GEFVTTVQQR.G	
239 - 248	1009.5452	1008.5380	1008.5273	0.0106	1	R.KLSSAMSAAK.A	Oxidation (M)
299 - 310	1393.8663	1392.8591	1392.7037	0.1554	0	K.FVEGLPINDFSR.E	

No match to: 976.6465, 2280.3798

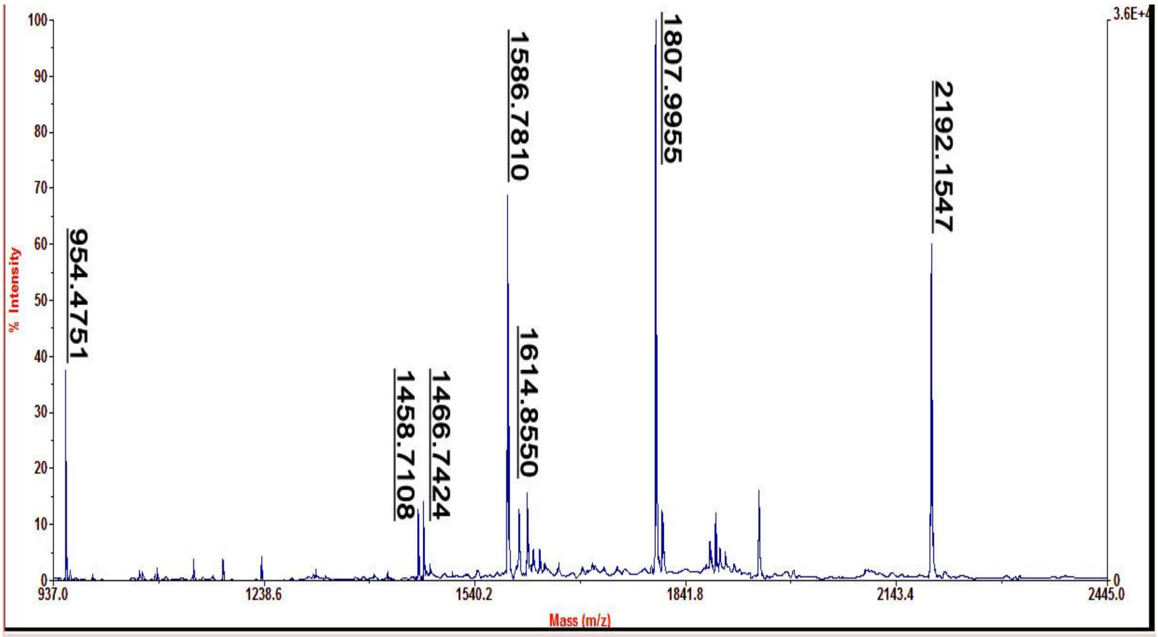
40) Purine nucleoside phosphorylase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
23 - 41	1979.3345	1978.3272	1978.0418	0.2855	0	K.HRPQVAIICGSGLGGLTDK.L	
68 - 76	1022.6954	1021.6881	1021.5708	0.1173	0	R.LVFGFLNGR.A	
124 - 133	1192.7908	1191.7835	1191.6321	0.1514	0	K.FEVGDIMLIR.D	
124 - 133	1208.7627	1207.7554	1207.6270	0.1283	0	K.FEVGDIMLIR.D	Oxidation (M)
159 - 168	1172.6428	1171.6355	1171.4968	0.1387	0	R.FPAMSDAYDR.T	
212 - 229	1785.2386	1784.2313	1783.9501	0.2811	0	K.LGADAVGMSTVPEVIVAR.H	
255 - 270	1665.0983	1664.0910	1663.8641	0.2269	1	K.ANHEEVLAAGKQAAQK.L	

No match to: 2009.3161, 2473.5816

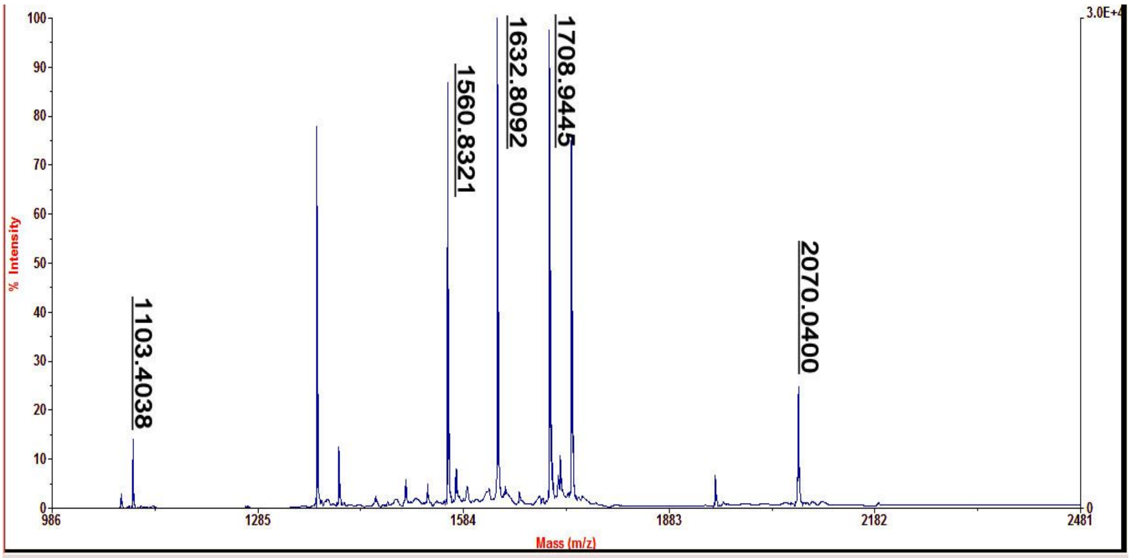
41) Triosephosphate isomerase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 14	954.4751	953.4679	953.4759	-0.0080	0	K.FFVGGNWK.M
34 - 53	2192.1547	2191.1474	2191.0619	0.0855	0	K.VPADTEVVCAPPTAYIDFAR.Q
86 - 99	1586.7810	1585.7737	1585.7307	0.0431	0	K.DCGATWVVLGHSER.R
100 - 113	1614.8550	1613.8477	1613.8161	0.0316	1	R.RHVFGESDELIGQK.V
101 - 113	1458.7108	1457.7035	1457.7150	-0.0115	0	R.HVFGESDELIGQK.V
114 - 131	1807.9955	1806.9882	1806.9661	0.0221	0	K.VAHALAEGLGVIACIGEK.L
176 - 188	1466.7424	1465.7351	1465.7161	0.0190	0	K.TATPQQAQEVHEK.L

No match to: 1797.9528, 1946.0694

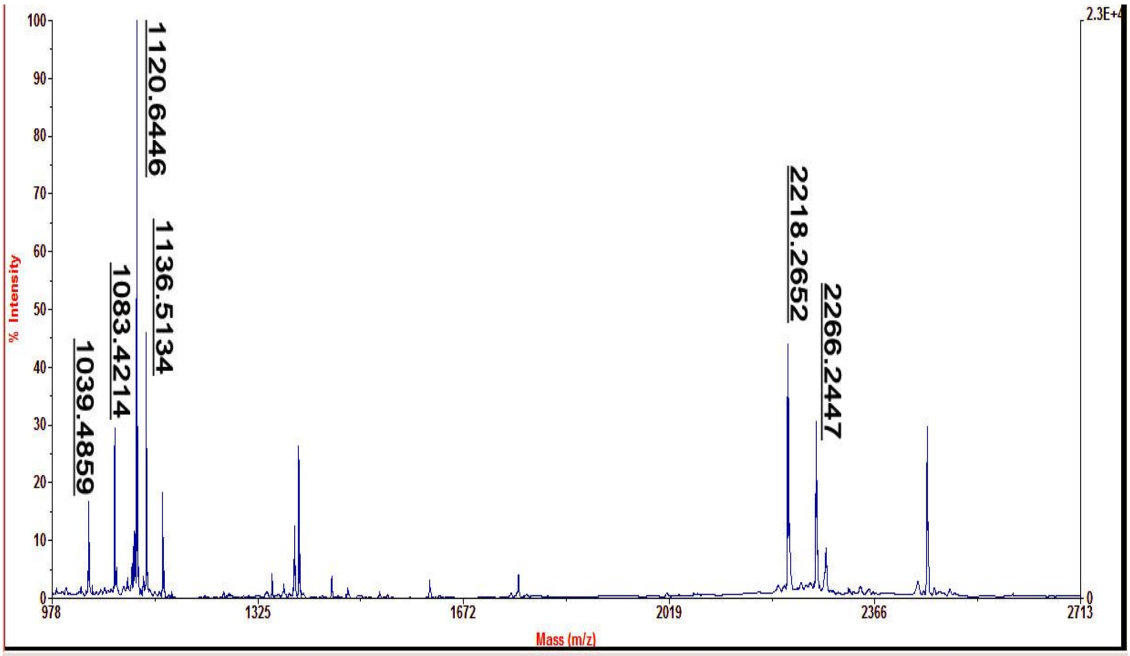
42) Phosphatidylethanolamine-binding protein 1 (PEBP-1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
48 - 62	1632.8092	1631.8019	1631.7903	0.0116	0	K.NRPTSISWDGLDSGK.L
63 - 76	1560.8321	1559.8249	1559.8195	0.0054	0	K.LYTLVLTDPDAPSR.K
120 - 132	1708.9445	1707.9372	1707.8984	0.0388	0	R.YVWLVYEQDRPLK.C
133 - 141	1103.4038	1102.3965	1102.5077	-0.1111	0	K.CDEPILSNR.S
162 - 179	2070.0400	2069.0327	2068.9200	0.1127	0	R.APVAGTCYQAEWDDYVPK.L

No match to: 1370.6300, 1402.6165, 1572.8070, 1740.8949

43) Aldose reductase

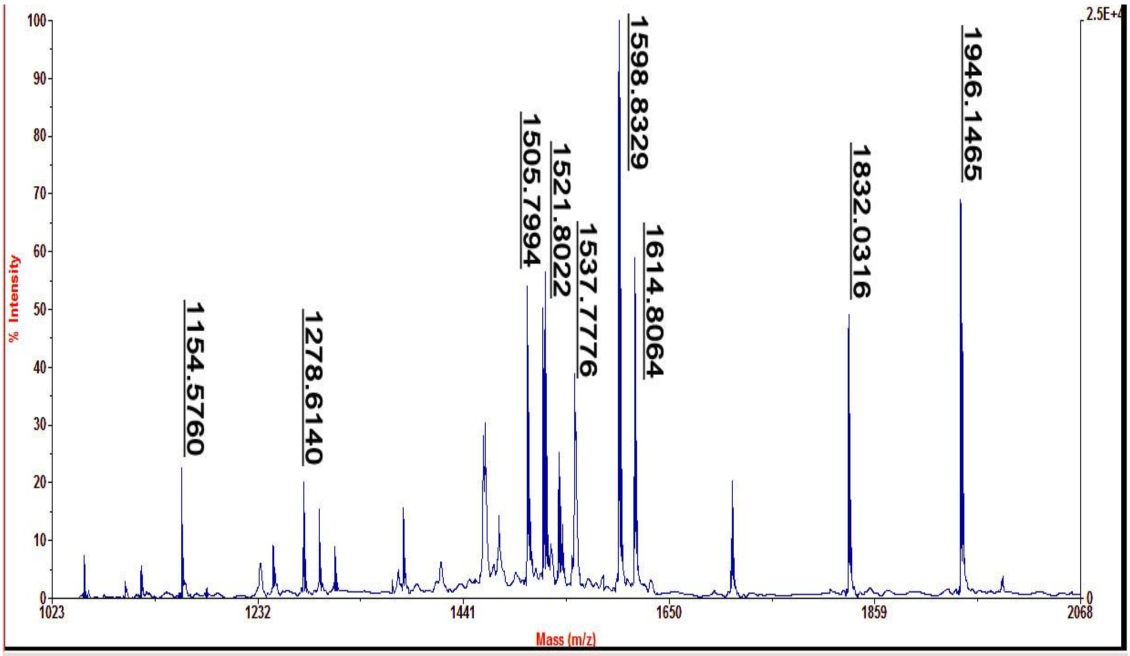


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
70 - 78	1120.6446	1119.6373	1119.6288	0.0085	1	K.REELFIVSK.L

79 - 86	1136.5134	1135.5061	1135.5121	-0.0059	0	K.LWCTYHEK.G
178 - 195	2218.2652	2217.2579	2217.0888	0.1691	0	K.YKPAVNQIECHPYLTQEK.L
196 - 203	1039.4859	1038.4786	1038.5168	-0.0382	0	K.LIQYCQSK.G
276 - 294	2266.2447	2265.2374	2265.0623	0.1751	0	K.VFDFELSSQDMTTLLSYNR.N
309 - 316	1083.4214	1082.4141	1082.4345	-0.0204	0	K.DYPFHEEF.-

No match to: 1164.6175, 1393.7638, 2453.3857

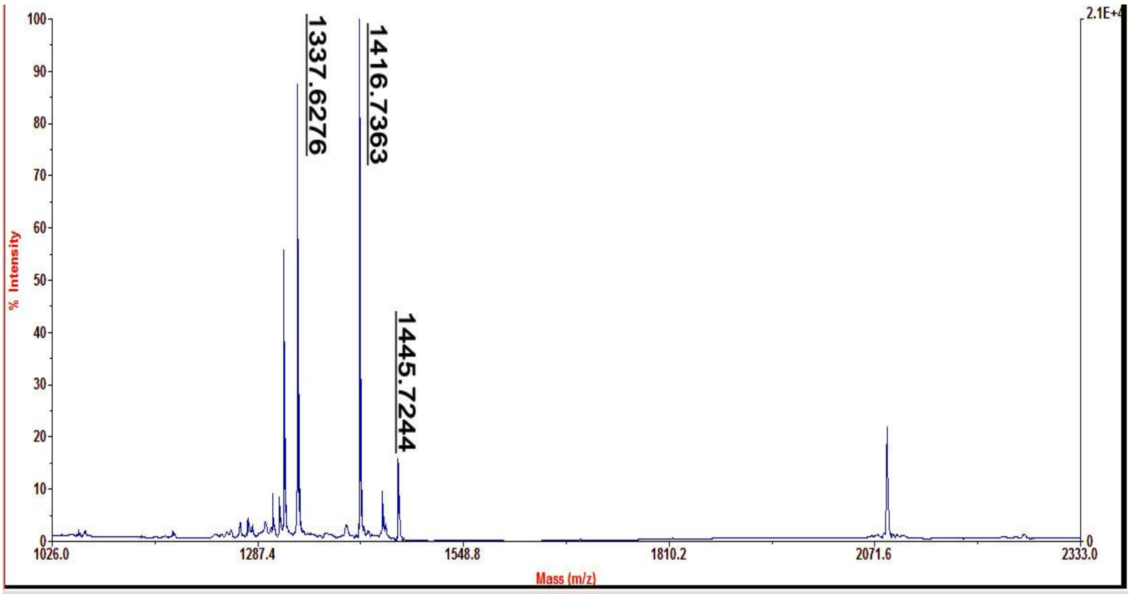
44) Peptidyl-prolyl cis-trans isomerase A



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
2 - 19	1946.1465	1945.1392	1944.9944	0.1447	0	M.VNPTVFFDIAVDGEPLGR.V	
56 - 69	1598.8329	1597.8256	1597.7381	0.0875	0	R.IIPGFMCQGGDFTR.H	
56 - 69	1614.8064	1613.7991	1613.7330	0.0661	0	R.IIPGFMCQGGDFTR.H	; Oxidation (M)
77 - 91	1832.0316	1831.0243	1830.9039	0.1204	1	K.SIYGEKFEDENFILK.H	
83 - 91	1154.5760	1153.5688	1153.5655	0.0033	0	K.FEDENFILK.H	
132 - 144	1505.7994	1504.7921	1504.7377	0.0544	1	K.VKEGMNIVEAMER.F	
132 - 144	1521.8022	1520.7949	1520.7326	0.0623	1	K.VKEGMNIVEAMER.F	Oxidation (M)
132 - 144	1537.7776	1536.7703	1536.7275	0.0428	1	K.VKEGMNIVEAMER.F	2 Oxidation (M)
134 - 144	1278.6140	1277.6067	1277.5743	0.0324	0	K.EGMNIVEAMER.F	

No match to: 1461.1423, 1523.7859

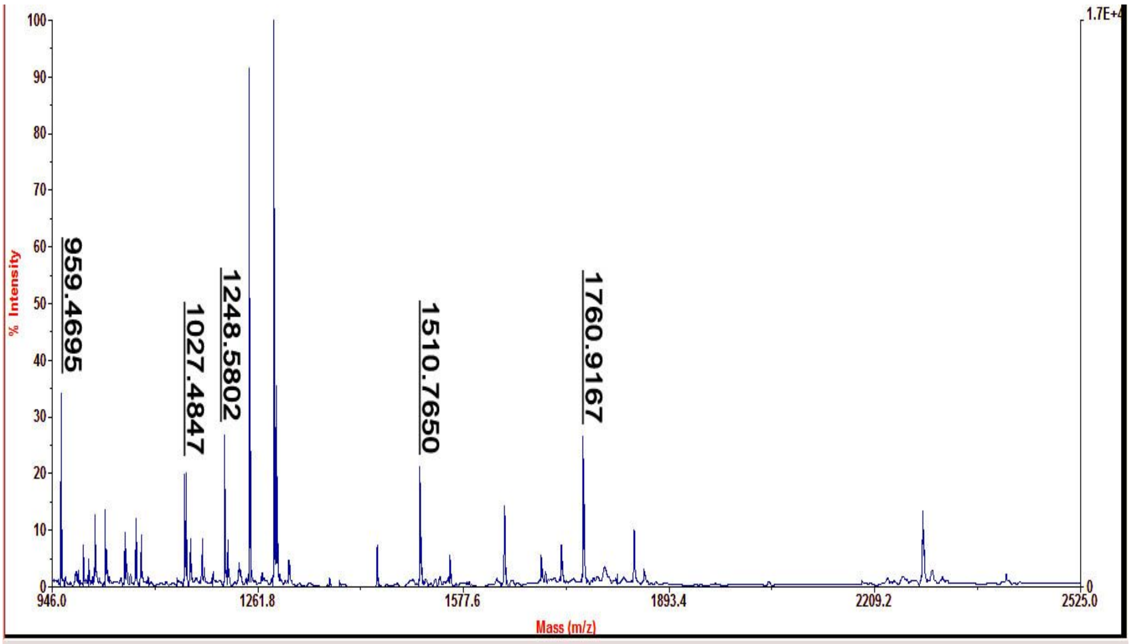
45) Histidine triad nucleotide-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 21	1416.7363	1415.7290	1415.7520	-0.0230	0	K.AQVARPGGDTIFGK.I
26 - 37	1445.7244	1444.7171	1444.7561	-0.0390	1	K.EIPAKIIFEDDR.C
31 - 37	907.3805	906.3733	906.4447	-0.0714	0	K.IIFEDDR.C
84 - 95	1337.6276	1336.6203	1336.6557	-0.0354	1	K.CAADLGLNKGYR.M

No match to: 1274.6894, 1314.6226, 1320.5821, 1465.7336, 2086.1098

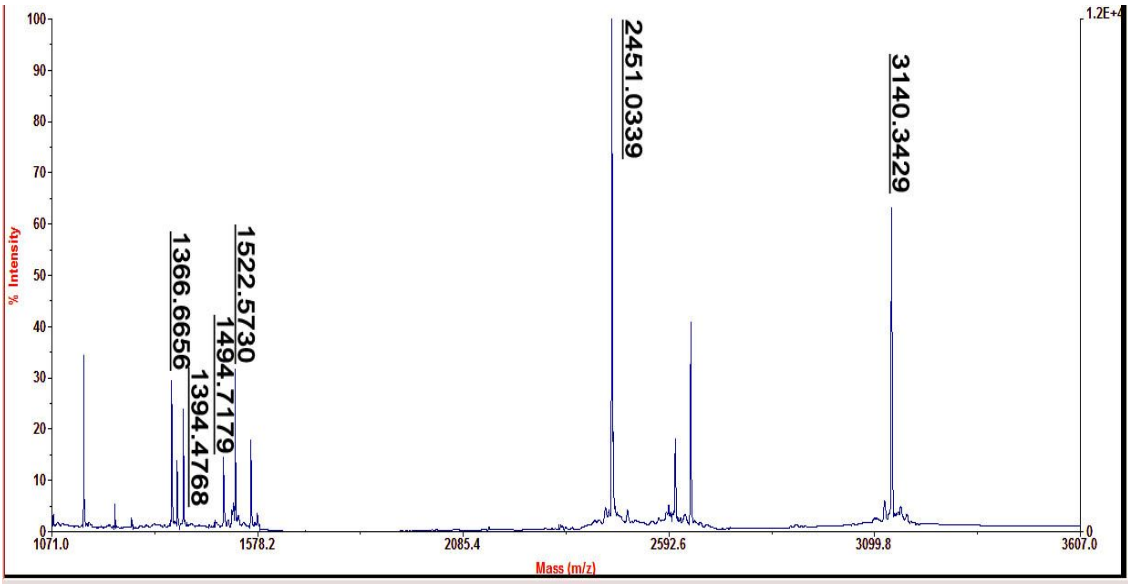
46) L-lactate dehydrogenase B chain



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
78 - 91	1510.7650	1509.7577	1509.7674	-0.0097	1	K.IVADKDYSVTANSK.I	
92 - 100	913.5142	912.5069	912.5756	-0.0687	0	K.IVVVTAGVR.Q	
159 - 170	1248.5802	1247.5729	1247.5928	-0.0199	0	R.VIGSGCNLDSAR.F	
230 - 244	1760.9167	1759.9094	1759.9178	-0.0084	1	K.EVHKMVVESAYEVIK.L	
271 - 279	1027.4847	1026.4775	1026.5532	-0.0757	0	R.IHPVSTMVK.G	Oxidation (M)
300 - 308	959.4695	958.4622	958.5447	-0.0825	0	R.GLTSVINQK.L	

No match to: 1149.5406, 1210.6269, 1286.6880, 1290.7086, 1639.9727

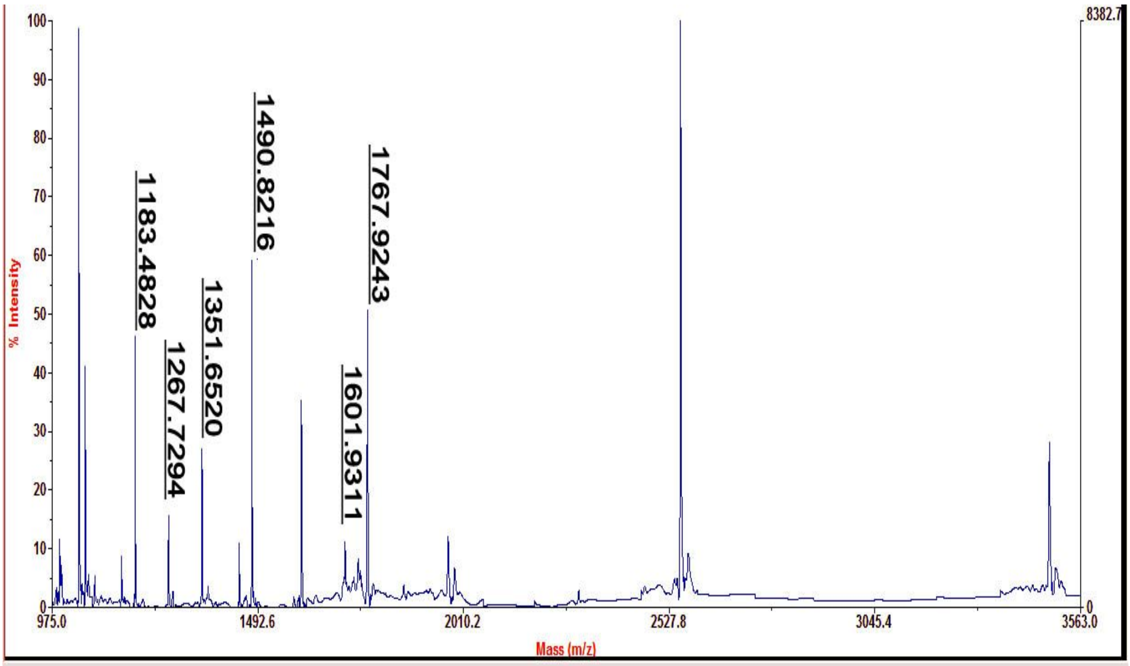
47) Transthyretin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
42 - 54	1366.6656	1365.6583	1365.7516	-0.0933	0	R.GSPAINVAVHVFR.K
42 - 55	1494.7179	1493.7106	1493.8466	-0.1360	1	R.GSPAINVAVHVFRK.A
55 - 68	1522.5730	1521.5657	1521.7099	-0.1443	1	R.KAADDTWEPFASGK.T
56 - 68	1394.4768	1393.4695	1393.6150	-0.1455	0	K.AADDTWEPFASGK.T
69 - 96	3140.3429	3139.3357	3139.5084	-0.1727	1	K.TSESGELHGLTTEEEFVEGIYKVEIDTK.S
101 - 123	2451.0339	2450.0266	2450.1978	-0.1712	0	K.ALGISPFHEHAEVVFTANDSGPR.R

No match to: 1149.4919, 2645.2055

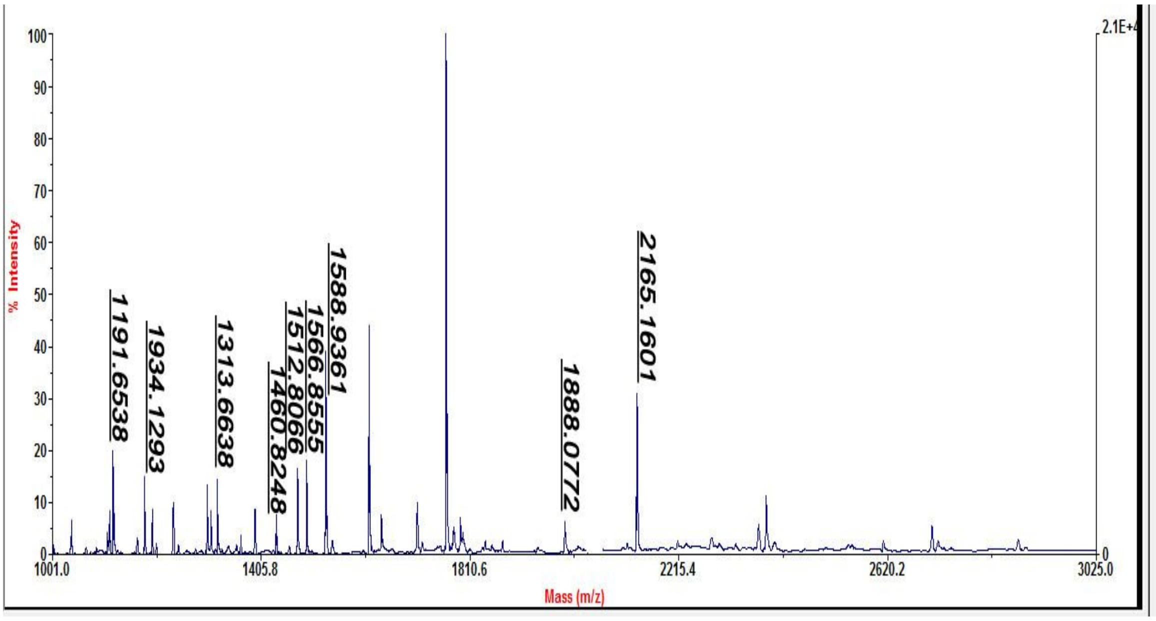
48) 6-phosphogluconolactonase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
57 - 72	1490.8216	1489.8143	1489.8252	-0.0109	0	R.ELPAAVAPAGPASLAR.W
73 - 81	1183.4828	1182.4755	1182.5128	-0.0373	0	R.WTLGFCDER.L
82 - 96	1767.9243	1766.9170	1766.8627	0.0543	0	R.LVPFDHAESTYGLYR.T
171 - 185	1601.9311	1600.9238	1600.8937	0.0302	0	K.IVAPISDSPKPPPQR.V
186 - 197	1267.7294	1266.7221	1266.7659	-0.0438	0	R.VTLTLPVLNAAR.T
236 - 246	1351.6520	1350.6447	1350.6390	0.0057	0	K.LCWFLDEAAAR.L

No match to: 913.4206, 998.2748, 1042.5545, 1058.5319, 1458.6937, 1971.0707, 2555.4199

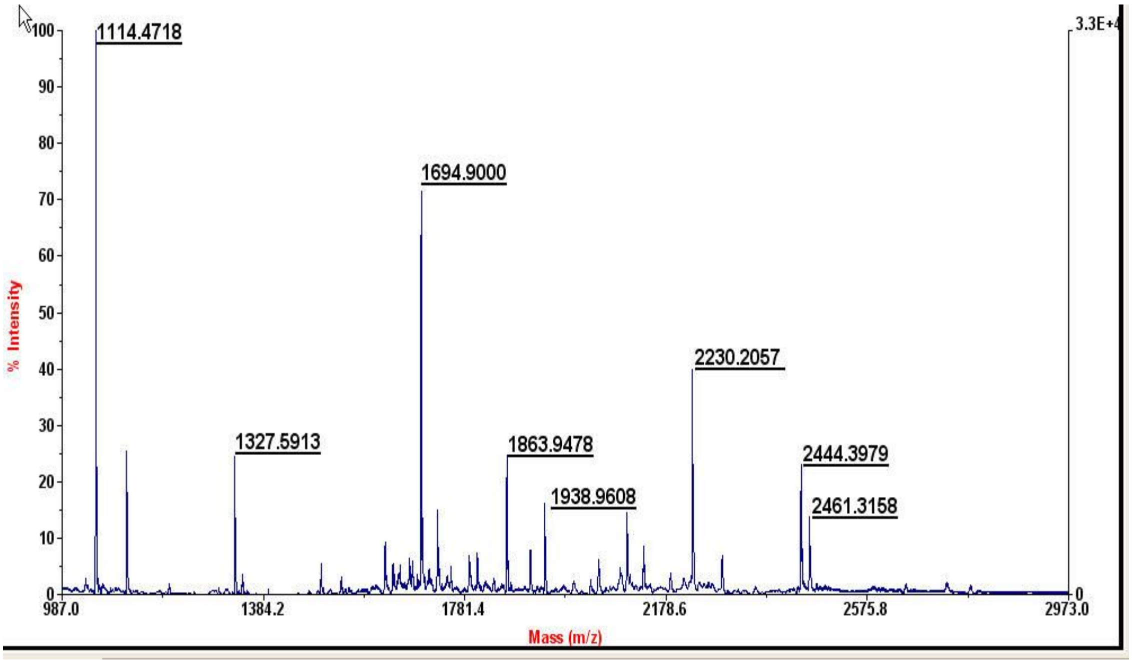
49） 78 kDa glucose-regulated protein



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
61 - 74	1566.8555	1565.8482	1565.7725	0.0757	0	R.ITPSYVAFTPEGER.L
165 - 181	1888.0772	1887.0700	1886.9638	0.1061	0	K.VTHAVVTVPAYFNDAQR.Q
298 - 306	997.5322	996.5250	996.5101	0.0149	0	R.ALSSQHQAR.I
307 - 324	2165.1601	2164.1528	2163.9847	0.1681	0	R.IEIESFYEGEDFSETLTR.A
325 - 336	1512.8066	1511.7993	1511.7442	0.0551	1	R.AKFEELNMDLFR.S
327 - 336	1313.6638	1312.6565	1312.6121	0.0444	0	K.FEELNMDLFR.S
353 - 367	1588.9361	1587.9289	1587.8467	0.0821	1	K.KSDIDEIVLVGGSTR.I
354 - 367	1460.8248	1459.8175	1459.7518	0.0657	0	K.SDIDEIVLVGGSTR.I
465 - 474	1191.6538	1190.6465	1190.6295	0.0170	0	K.VYEGERPLTK.D
475 - 492	1934.1293	1933.1221	1933.0057	0.1163	0	K.DNHLLGTFDLTGIPPAPR.G
602 - 617	1974.9910	1973.9837	1973.9007	0.0830	0	K.IEWLESHQDADIEDFK.A

No match to: 927.4941, 960.5595, 1211.5947, 1668.9296

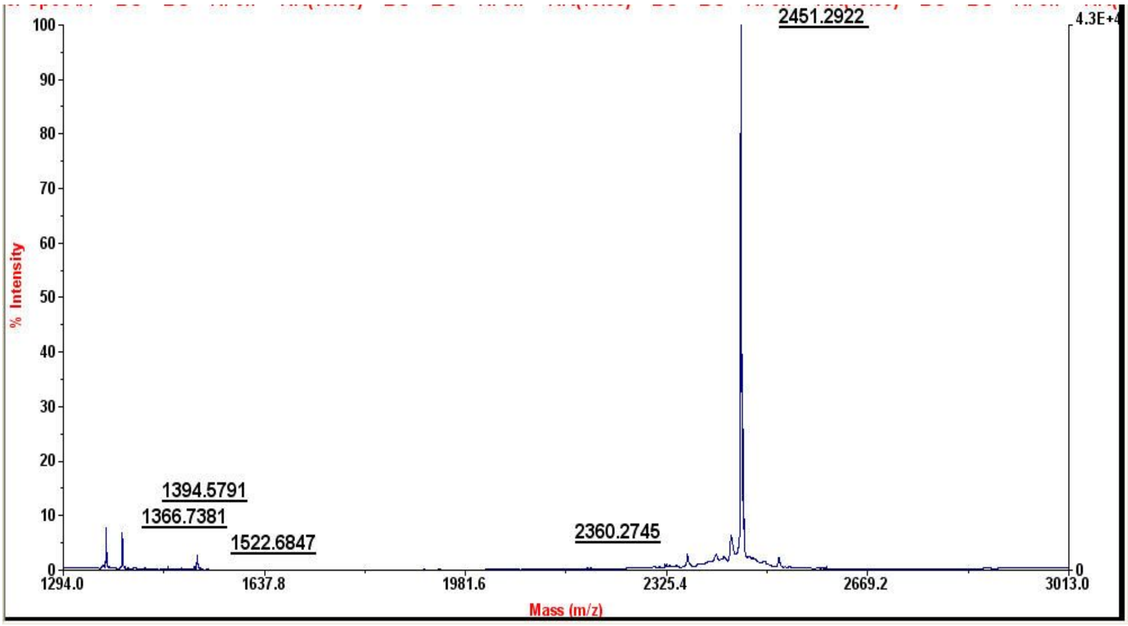
50）Inorganic pyrophosphatase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
10 - 18	1053.4165	1052.4093	1052.5291	-0.1198	0	R.AAPFSLEYR.V
26 - 41	1863.9478	1862.9405	1862.9203	0.0203	0	K.GQYISPFHDIPIYADK.D
42 - 52	1327.5913	1326.5840	1326.6754	-0.0914	0	K.DVFHMVVEVPR.W
80 - 88	1114.4718	1113.4645	1113.5858	-0.1213	0	R.YVANLFPYK.G
89 - 109	2461.3158	2460.3085	2460.1134	0.1951	0	K.GYIWNYGAIPQTWEDPGHNDK.H
156 - 177	2444.3979	2443.3907	2443.1979	0.1928	1	K.VIAINVDDPDAANYNDINDVKR.L
178 - 191	1694.9000	1693.8927	1693.8827	0.0100	0	R.LKPGYLEATVDWFR.R
193 - 211	2230.2057	2229.1984	2229.0741	0.1243	1	R.YKVPDGKPENEFAFNAEFK.D
195 - 211	1938.9608	1937.9535	1937.9158	0.0376	0	K.VPDGKPENEFAFNAEFK.D

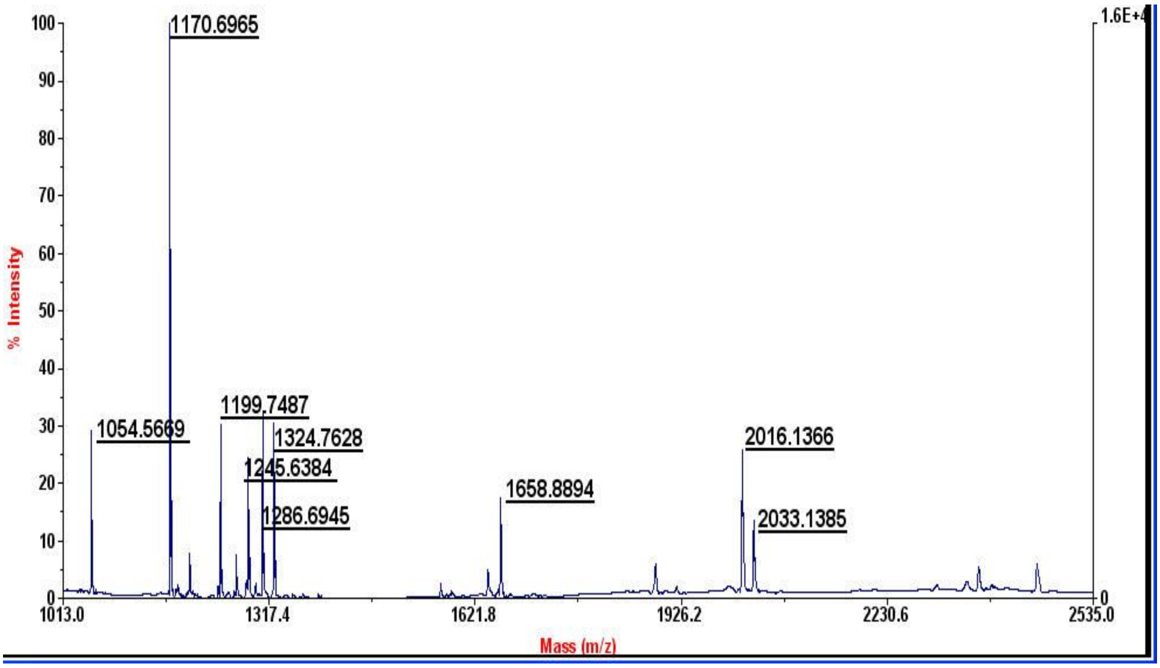
No match to: 927.3504, 954.2963, 1726.8779, 2101.1307

51 Transthyretin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
42 - 54	1366.7381	1365.7309	1365.7516	-0.0208	0	R.GSPAINVAVHVFR.K
55 - 68	1522.6847	1521.6774	1521.7099	-0.0325	1	R.KAADDTWEPFASGK.T
56 - 68	1394.5791	1393.5719	1393.6150	-0.0431	0	K.AADDTWEPFASGK.T
101 - 123	2451.2922	2450.2850	2450.1978	0.0872	0	K.ALGISPFHEHAEVVFTANDSGPR.R
125 - 146	2360.2745	2359.2672	2359.2311	0.0361	0	R.YTIAALLSPYSYSTTAVVTNPK.E

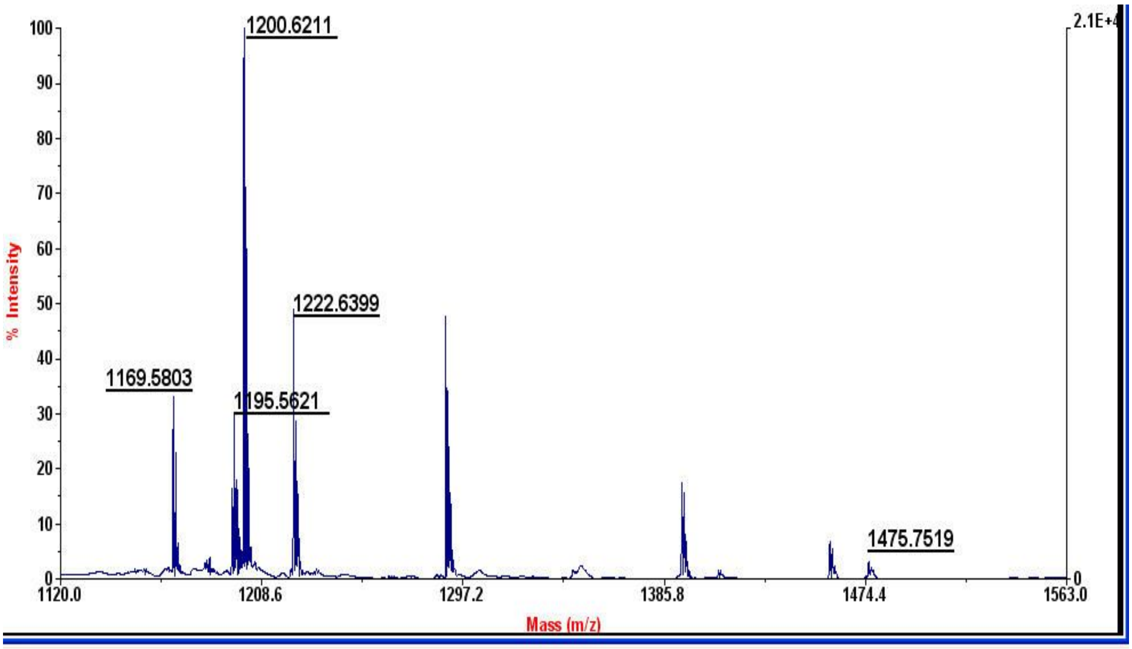
52） Galactokinase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
6 - 17	1324.7628	1323.7555	1323.7146	0.0409	0	R.QPQVAELLAEAR.R
19 - 37	2033.1385	2032.1313	2032.0013	0.1300	1	R.AFREEFGAEPELAVSAPGR.V
22 - 37	1658.8894	1657.8822	1657.7947	0.0875	0	R.EEFGAEPELAVSAPGR.V
69 - 87	2016.1366	2015.1293	2015.0171	0.1122	1	R.KDGLVSLLTTSEGADEPQR.L
88 - 97	1170.6965	1169.6892	1169.6557	0.0335	0	R.LQFPLPTAQR.S
196 - 204	1054.5669	1053.5596	1053.5389	0.0207	0	K.GHALLIDCR.S
218 - 228	1199.7487	1198.7415	1198.7033	0.0381	0	K.LAVLITNSNVR.H
229 - 239	1245.6384	1244.6311	1244.6149	0.0162	0	R.HSLASSEYPVR.R
257 - 267	1286.6945	1285.6872	1285.6513	0.0359	0	R.EVQLEELEAAR.D

No match to: 1307.7265, 1886.9577

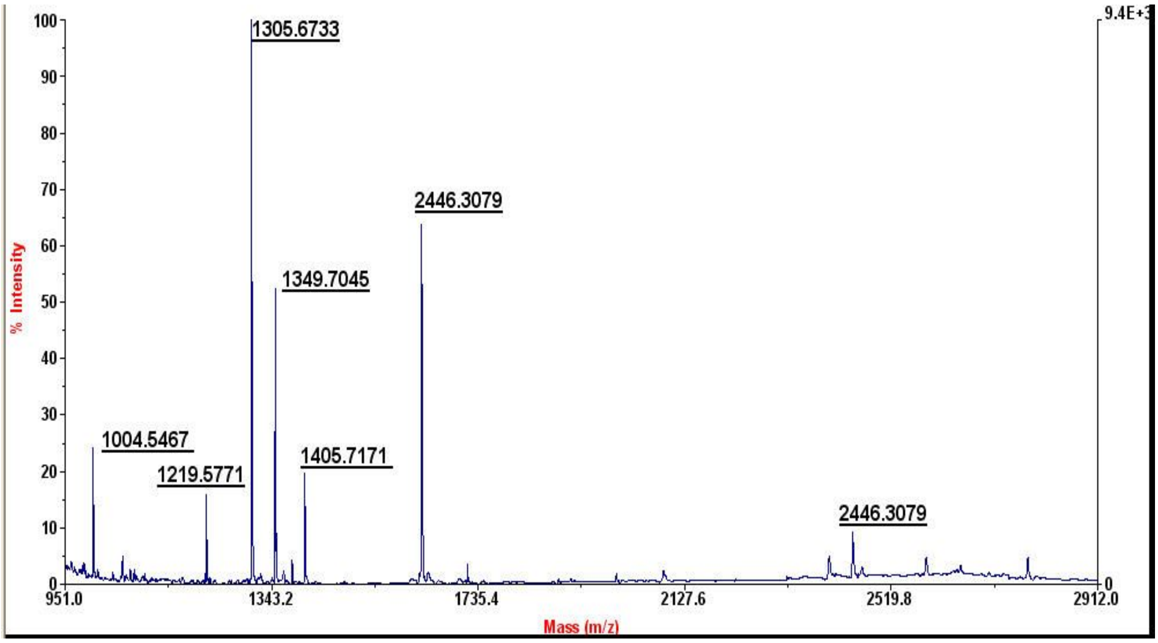
53) Nicotinate-nucleotide pyrophosphorylase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
92 - 102	1222.6399	1221.6327	1221.6288	0.0039	0	R.GPAHCLLLGER.V
111 - 126	1475.7519	1474.7446	1474.7198	0.0249	0	R.CSGIASAAAAAVEAAR.G
127 - 138	1169.5803	1168.5730	1168.5737	-0.0007	0	R.GAGWTGHVAGTR.K
150 - 161	1200.6211	1199.6139	1199.6410	-0.0272	0	K.YGLLVGGAASHR.Y
172 - 183	1195.5621	1194.5549	1194.5992	-0.0444	0	K.DNHVVAAGGVEK.A

No match to: 1289.5931, 1393.5964, 1458.7245, 1748.9066, 1855.9294, 1871.9182

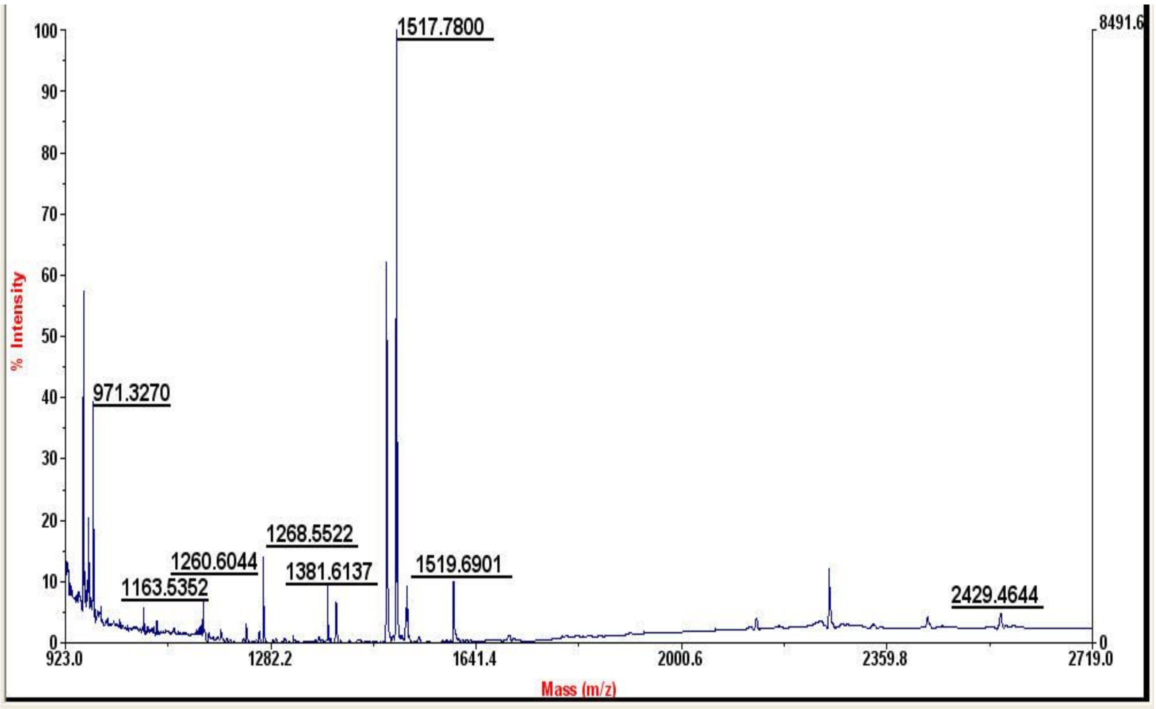
54) Lambda-crystallin homolog



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
34 - 43	1305.6733	1304.6660	1304.6724	-0.0064	0	K.LYDIEQQQIR.N
105 - 116	1405.7171	1404.7098	1404.7249	-0.0150	0	K.IFAQLDSIIDDR.V
189 - 197	1004.5467	1003.5394	1003.5450	-0.0056	0	K.EVAGFVLNR.L
198 - 208	1349.7045	1348.6972	1348.7139	-0.0167	0	R.LQYAIISEAWR.L
209 - 231	2446.3079	2445.3006	2445.2130	0.0876	0	R.LVEEGIVSPSDLDLVMSEGLGMR.Y
261 - 274	1627.8652	1626.8579	1626.8518	0.0061	0	K.HVLQTFGPIPEFSR.A
288 - 298	1219.5771	1218.5698	1218.5993	-0.0295	0	K.VPDDPEHLAAR.R
312 - 319	927.4600	926.4527	926.5185	-0.0658	1	K.LKSQVQPQ.-

No match to: 1381.7179, 1714.7737

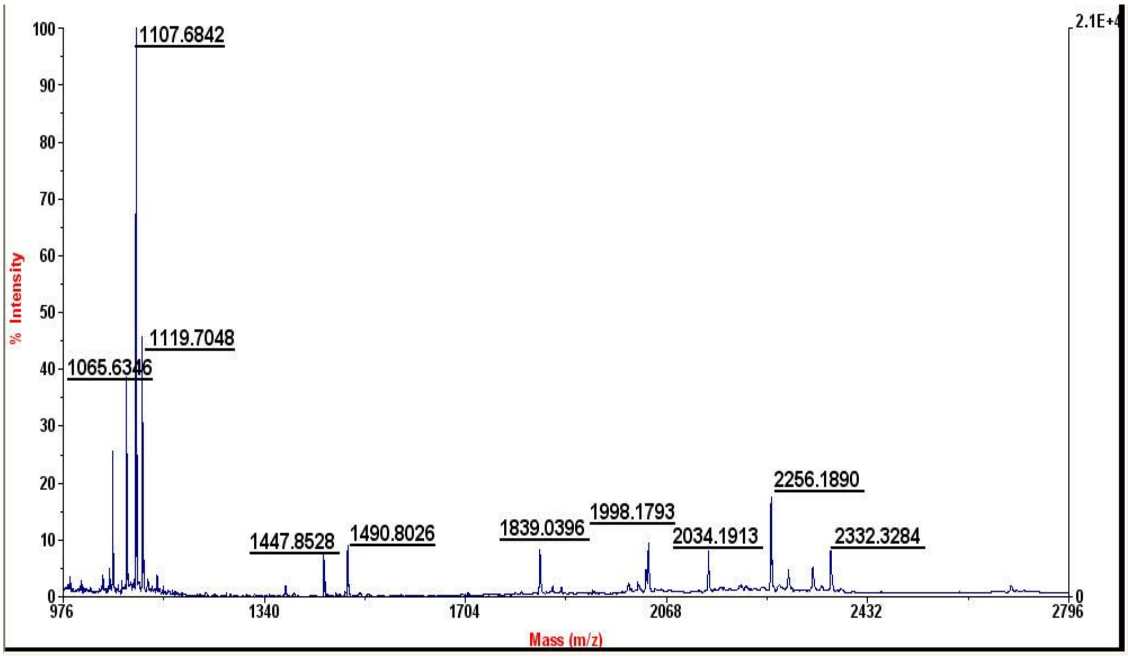
55) Proteasome activator complex subunit 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
14 - 24	1381.6137	1380.6064	1380.6707	-0.0643	1	K.VDVFREDLCTK.T	
25 - 35	1268.5522	1267.5450	1267.6448	-0.0998	0	K.TENLLGSYFPK.K	
36 - 45	1163.5352	1162.5279	1162.6597	-0.1318	1	K.KISELDAFLK.E	
37 - 58	2429.4644	2428.4571	2428.2849	0.1722	1	K.ISELDAFLKEPALNEANLSNLK.A	
59 - 70	1260.6044	1259.5971	1259.7125	-0.1154	0	K.APLDIPVPDPVK.E	
59 - 72	1517.7800	1516.7727	1516.8501	-0.0774	1	K.APLDIPVPDPVKEK.E	
142 - 155	1519.6901	1518.6829	1518.7314	-0.0485	0	R.IEDGNNFGVAVQEK.V	
167 - 176	1159.4649	1158.4576	1158.6033	-0.1457	0	K.LEGFHTQISK.Y	
191 - 198	971.3270	970.3197	970.4621	-0.1423	0	K.QPHVGDYR.Q	
199 - 210	1501.6923	1500.6850	1500.7208	-0.0358	0	R.QLVHELDEAEYR.D	
214 - 220	907.3074	906.3001	906.4667	-0.1665	0	R.LMVMEIR.N	Oxidation (M)
221 - 232	1395.6839	1394.6766	1394.7809	-0.1043	0	R.NAYAVLYDIILK.N	

No match to: 954.2988, 963.3323, 1239.5553, 1484.6568, 1601.8316, 2129.9870, 2258.1295, 2557.5716

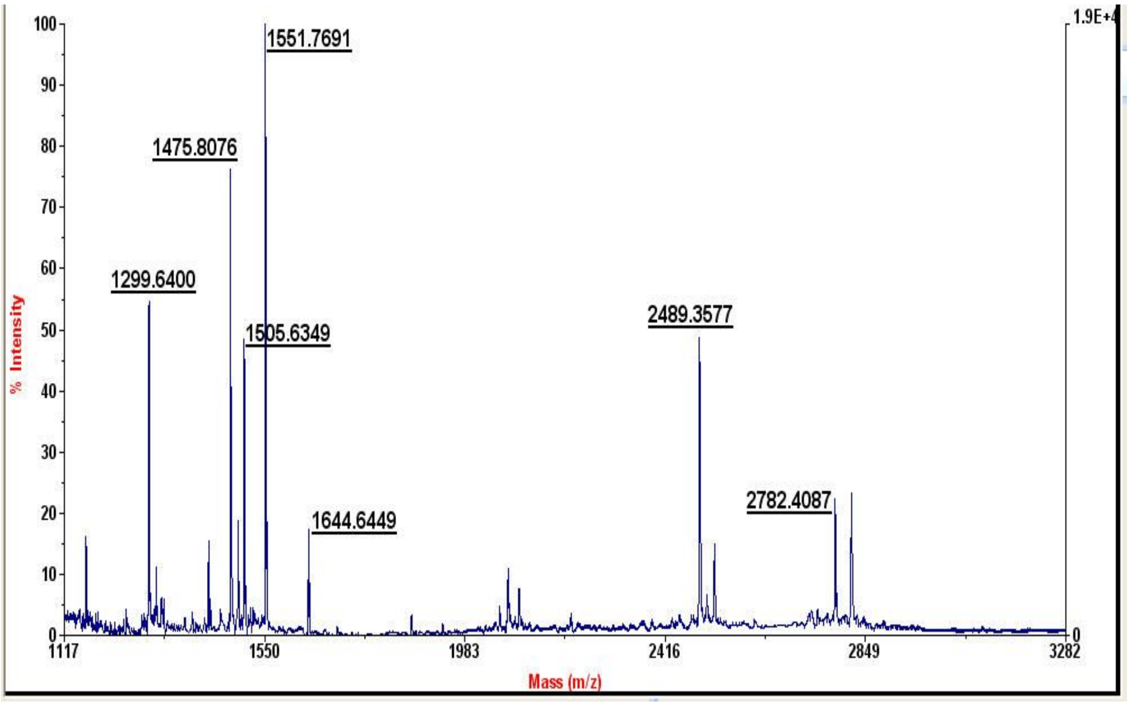
56) Aldose 1-epimerase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 21	1447.8528	1446.8456	1446.7354	0.1102	0	R.AVFGELPSGGGTVEK.F
22 - 30	1119.7048	1118.6975	1118.6084	0.0891	0	K.FQLQSDLLR.V
52 - 68	1839.0396	1838.0323	1837.9461	0.0862	0	R.ASDVVLGFAELEGYLQK.Q
69 - 78	1107.6842	1106.6770	1106.5872	0.0897	0	K.QPYFGAVIGR.V
94 - 111	2034.1913	2033.1841	2033.0442	0.1399	1	K.EYHLAINKEPNSLHGGVR.G
102 - 111	1065.6346	1064.6273	1064.5363	0.0910	0	K.EPNSLHGGVR.G
132 - 145	1490.8026	1489.7954	1489.6936	0.1018	0	R.ISPDGEEGYPGELK.V
146 - 162	1998.1793	1997.1720	1997.0258	0.1462	0	K.VWVTYTLDGGELIVNYR.A
301 - 319	2256.1890	2255.1817	2255.0178	0.1639	0	K.HSGFCLETQNWPDAVNQPR.F
320 - 338	2332.3284	2331.3211	2331.1687	0.1523	0	R.FPPVLLRPGEEYDHTTWFK.F

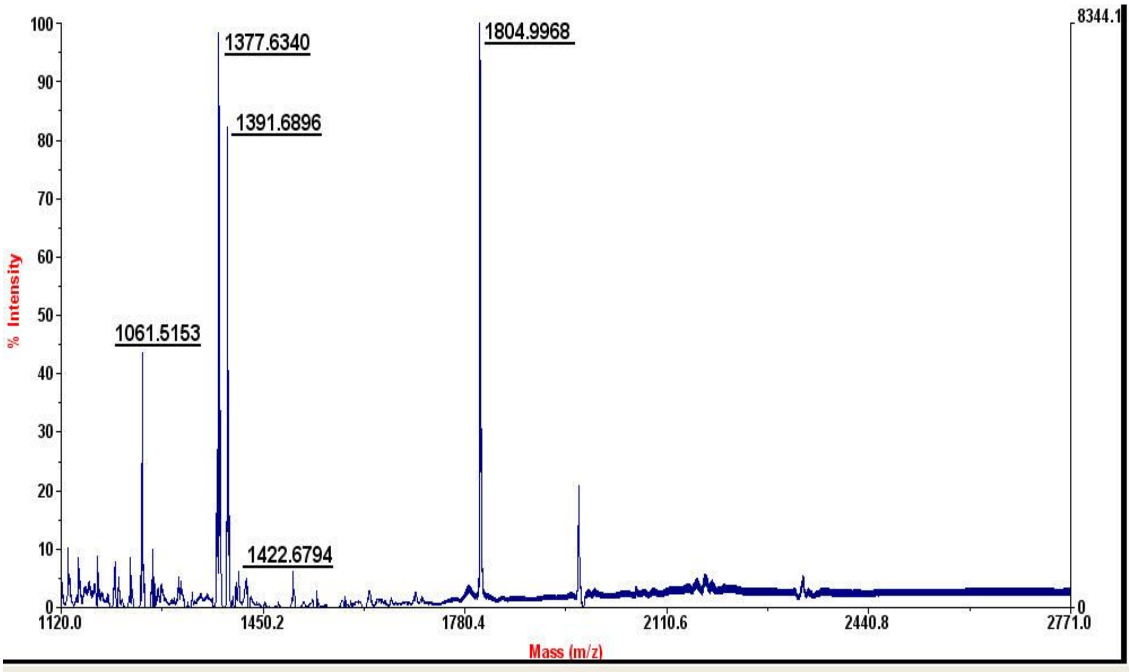
No match to: 1090.6630, 2288.1638, 2364.3200

57) Alcohol dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 42	928.4605	927.4532	927.4814	-0.0281	0	K.YALSVGYR.H
43 - 68	2782.4087	2781.4014	2781.3279	0.0735	1	R.HIDCAAIYGNEPEIGEALKEDVGPGK.A
86 - 96	1299.6400	1298.6327	1298.6367	-0.0040	0	K.HHPEDVEPALR.K
128 - 141	1644.6449	1643.6376	1643.6886	-0.0510	0	K.NADGTICYDSTHYK.E
154 - 167	1475.8076	1474.8003	1474.7892	0.0111	0	K.GLVQALGLSNFNSR.Q
204 - 218	1551.7691	1550.7618	1550.7576	0.0042	0	R.GLEVTAYSPLGSSDR.A
219 - 240	2489.3577	2488.3504	2488.3213	0.0291	1	R.AWRDPDEPVLLEEPVVLALAEK.Y
313 - 325	1505.6349	1504.6276	1504.6623	-0.0346	0	R.DAGHPLYPFNDPY.-

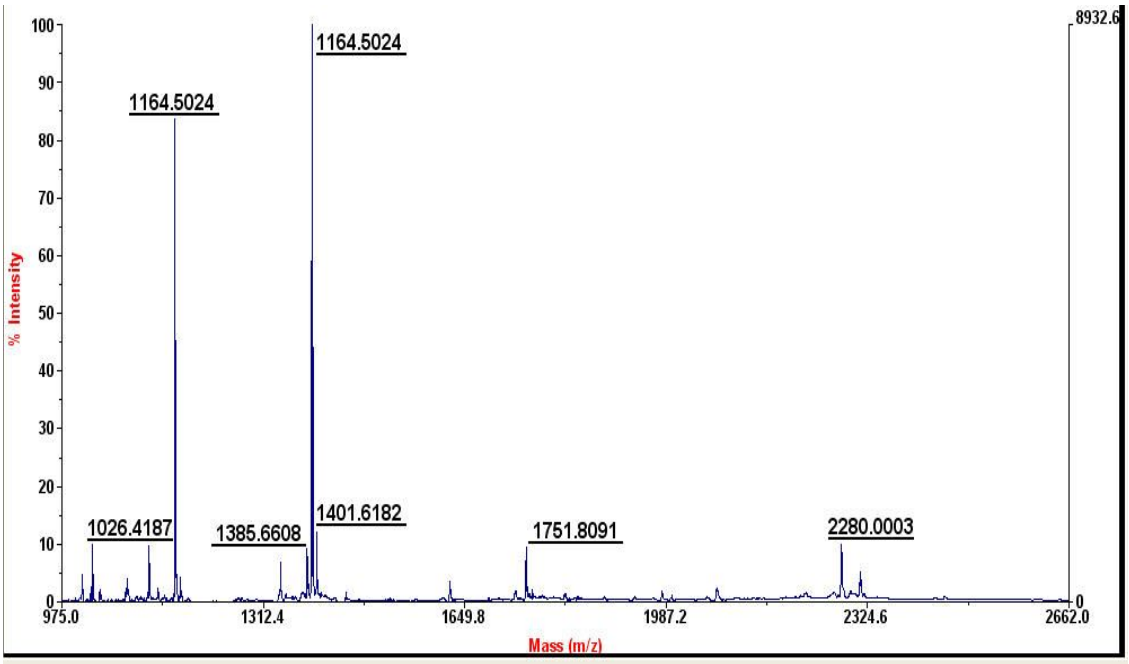
58) Aflatoxin B1 aldehyde reductase member 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
38 - 50	1422.6794	1421.6721	1421.7118	-0.0397	1	R.VASVLGTMEMGRR.M	Oxidation (M)
121 - 129	1061.5153	1060.5080	1060.5876	-0.0796	1	R.SQLETSLKR.L	
206 - 216	1391.6896	1390.6824	1390.6915	-0.0091	0	R.QVETELFPCLR.H	
251 - 261	1377.6340	1376.6267	1376.6149	0.0118	0	R.FFGNSWAETYR.N	
279 - 297	1804.9968	1803.9895	1803.9478	0.0416	0	K.ALQAAYGASAPSVTSAALR.W	

No match to: 1251.5709, 1276.6266, 1499.6726, 1966.0338

59) Malate dehydrogenase,

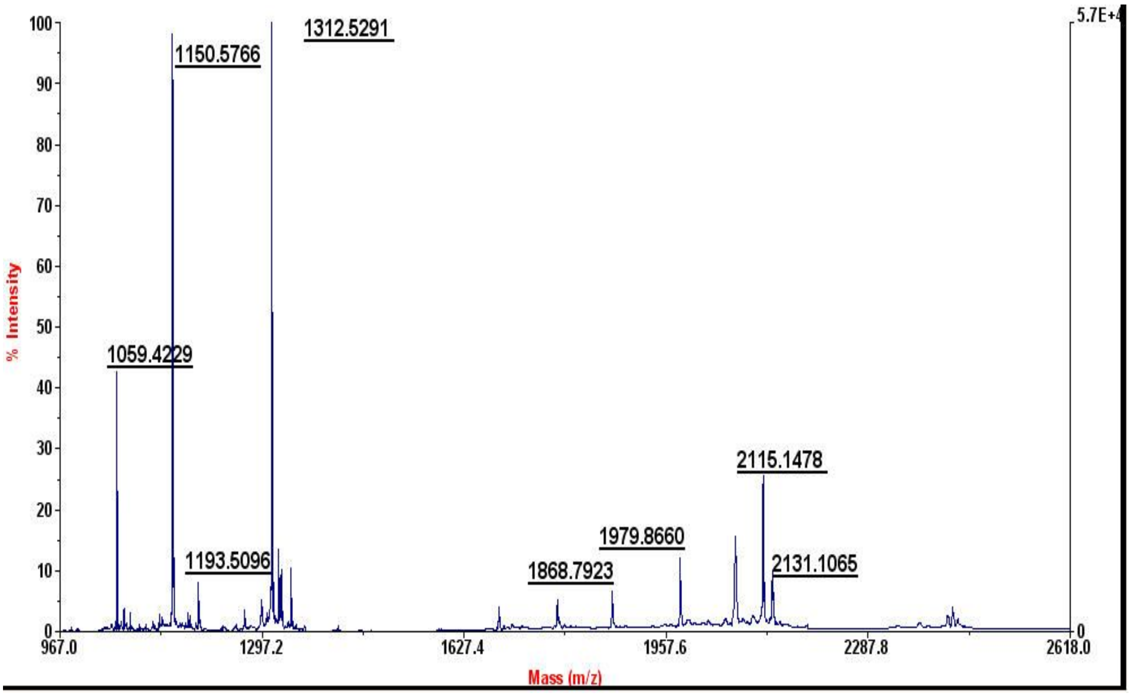


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

80 - 92	1385.6608	1384.6536	1384.7384	-0.0848	0	K.DLDVAILVGSMPR.R	
80 - 92	1401.6182	1400.6110	1400.7333	-0.1223	0	K.DLDVAILVGSMPR.R	Oxidation (M)
150 - 157	1026.4187	1025.4114	1025.4600	-0.0486	0	K.ENFSCLTR.L	
180 - 199	2280.0003	2278.9930	2279.1083	-0.1153	0	K.NVIIWGNHSSTQYPDVNHAK.V	
206 - 220	1751.8091	1750.8018	1750.8777	-0.0759	1	K.EVGVYEALKDDSWLK.G	
221 - 230	1164.5024	1163.4952	1163.5934	-0.0983	0	K.GEFVTTVQQR.G	
299 - 310	1393.6136	1392.6063	1392.7037	-0.0974	0	K.FVEGLPINDFSR.E	

No match to: 1120.5504, 1173.5001, 1340.8753, 1376.5317, 2311.9881

60) Phosphoglycerate mutase 1

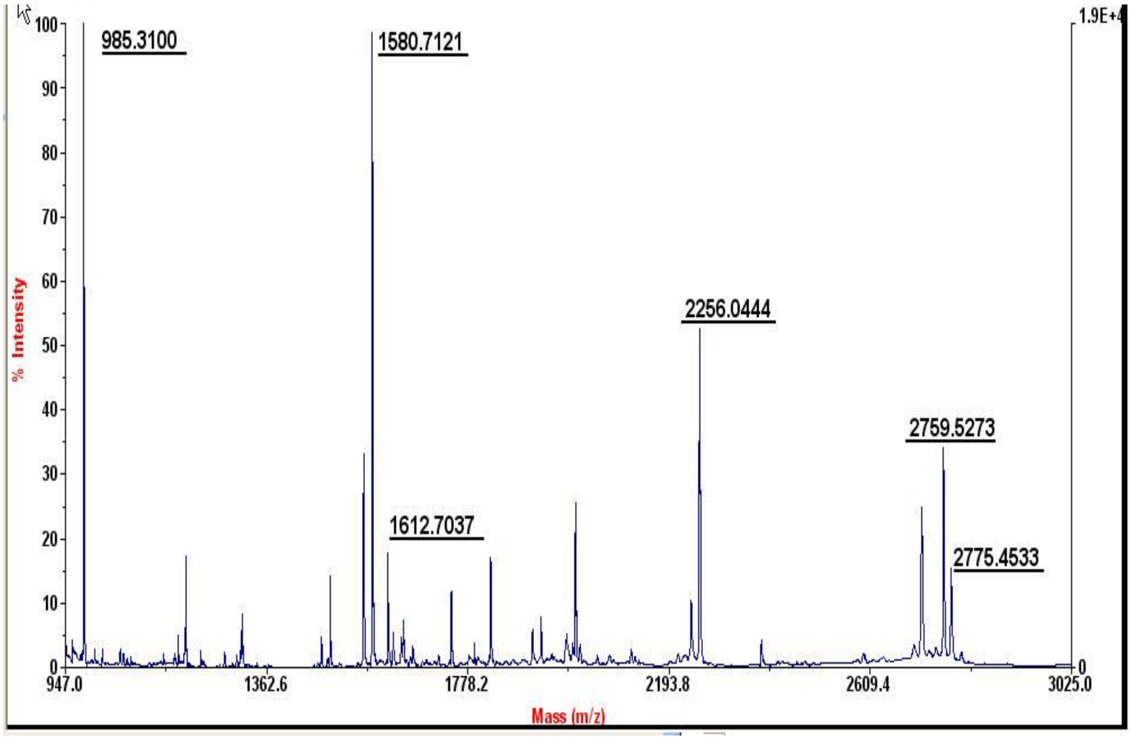


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 10	1193.5096	1192.5024	1192.7001	-0.1978	1	-.MAAYKLVLIR.H	Oxidation (M)
11 - 21	1312.5291	1311.5218	1311.5956	-0.0738	0	R.HGESAWNLENR.F	
22 - 39	1979.8660	1978.8587	1978.8697	-0.0109	0	R.FSGWYDADLSPAGHEEAK.R	
91 - 100	1059.4229	1058.4157	1058.5508	-0.1352	0	R.HYGGLTGLNK.A	
142 - 157	1868.7923	1867.7850	1867.8509	-0.0659	0	R.YADLTEDQLPSCESLK.D	
181 - 191	1150.5766	1149.5694	1149.6618	-0.0924	0	R.VLIAAHGNSLR.G	

223 - 240	2115.1478	2114.1405	2114.1193	0.0211	0	K.NLKPIKPMQFLGDEETVR.K
223 - 240	2131.1065	2130.0992	2130.1143	-0.0151	0	K.NLKPIKPMQFLGDEETVR.K Oxidation (M)

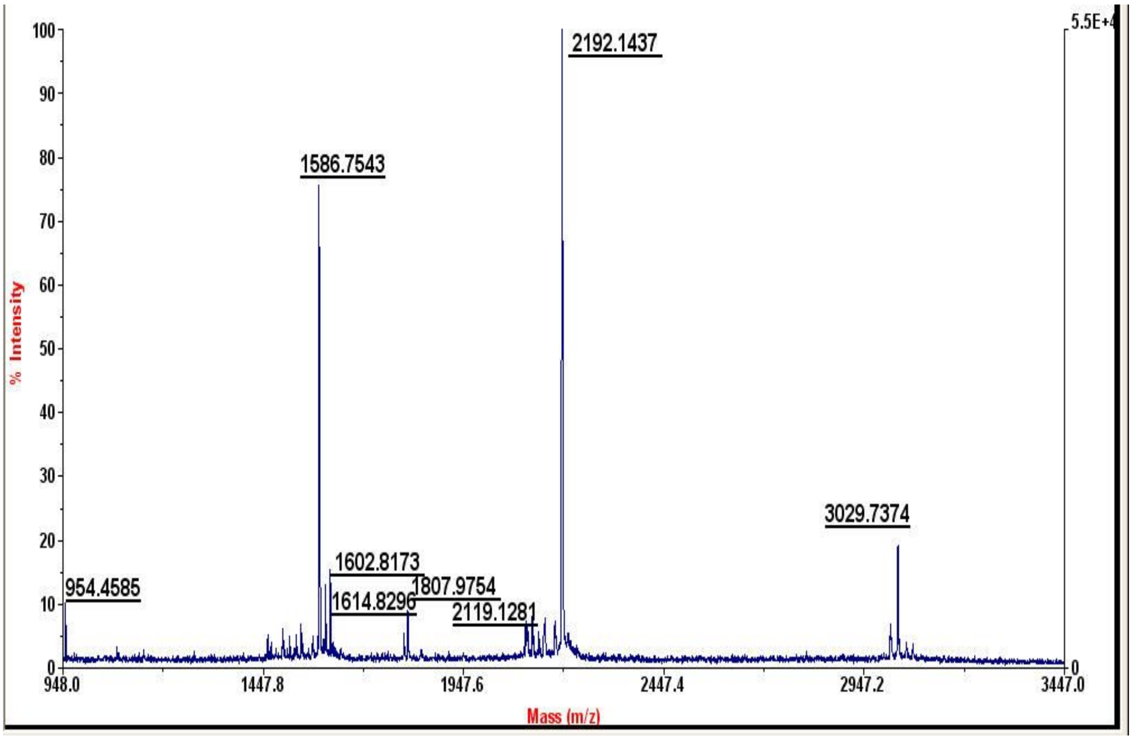
No match to: 1324.5223, 1344.4945, 2070.2202

61) Carbonic anhydrase 1



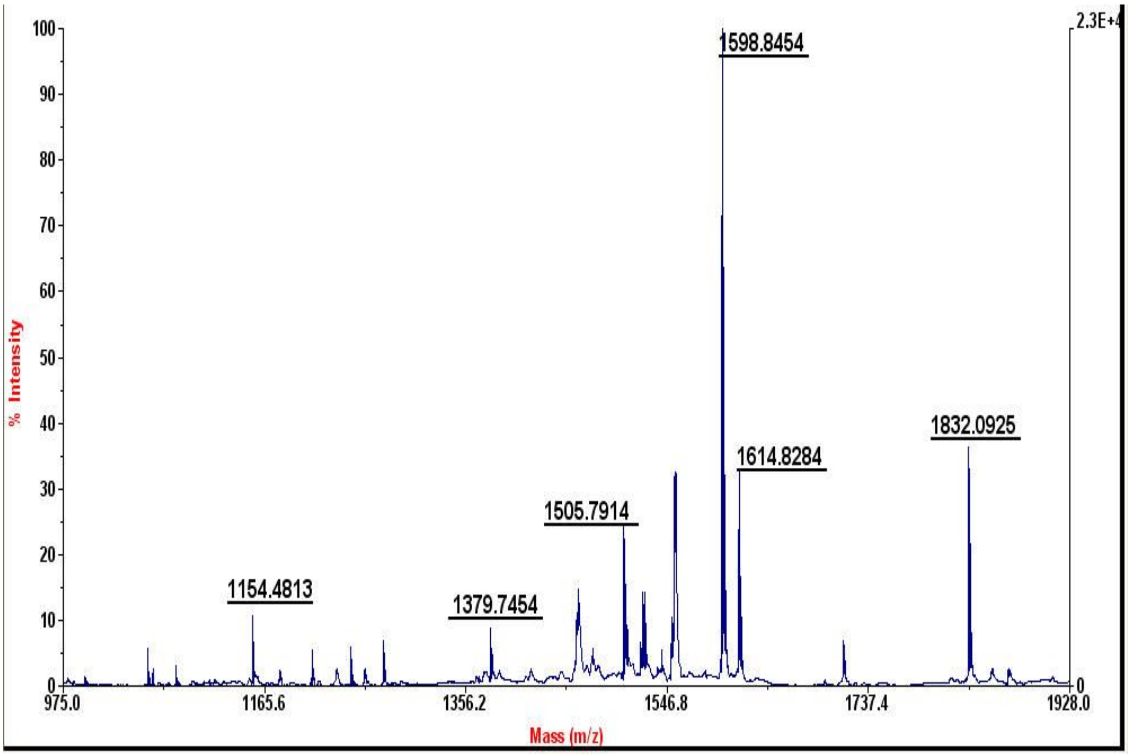
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
59 - 77	2256.0444	2255.0371	2255.0355	0.0016	0	K.EIINVGHSFHVNFEDNDNR.S
82 - 90	985.3100	984.3027	984.4301	-0.1274	0	K.GGPFSDSYR.L
115 - 128	1612.7037	1611.6964	1611.7793	-0.0829	0	K.YSAELHVAHWNSAK.Y
215 - 228	1580.7121	1579.7049	1579.7841	-0.0793	0	K.ESISVSSEQLAQFR.S
229 - 253	2759.5273	2758.5200	2758.3820	0.1380	0	R.SLLSNVEGDNAVPMQHNNRPTQPLK.G
229 - 253	2775.4533	2774.4461	2774.3769	0.0692	0	R.SLLSNVEGDNAVPMQHNNRPTQPLK.G Oxidation (M)

62) Triosephosphate isomerase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 14	954.4585	953.4513	953.4759	-0.0246	0	K.FFVGGNWK.M
34 - 53	2192.1437	2191.1364	2191.0619	0.0745	0	K.VPADTEVVCAPPTAYIDFAR.Q
86 - 99	1586.7543	1585.7470	1585.7307	0.0164	0	K.DCGATWVVLGHSER.R
100 - 113	1614.8296	1613.8223	1613.8161	0.0062	1	R.RHVFGESDELIGQK.V
114 - 131	1807.9754	1806.9681	1806.9661	0.0020	0	K.VAHALAEGLGVIACIGEK.L
157 - 175	2119.1281	2118.1208	2118.1149	0.0059	1	K.DWSKVVLAYEPVWAIGTGK.T
161 - 175	1602.8173	1601.8100	1601.8817	-0.0716	0	K.VVLAYEPVWAIGTGK.T
220 - 248	3029.7374	3028.7301	3028.5756	0.1545	0	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q

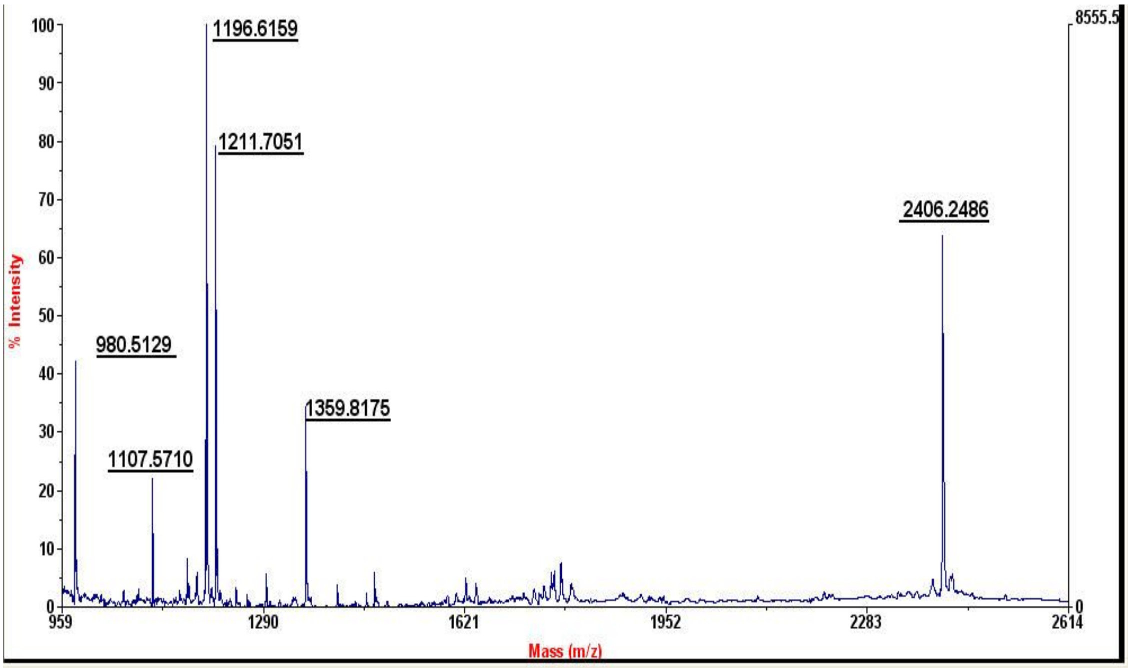
63） Peptidyl-prolyl cis-trans isomerase A



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 31	1379.7454	1378.7381	1378.7496	-0.0115	1	R.VSFELFADKVPK.T
56 - 69	1598.8454	1597.8381	1597.7381	0.1000	0	R.IIPGFMCQGGDFTR.H
56 - 69	1614.8284	1613.8212	1613.7330	0.0882	0	R.IIPGFMCQGGDFTR.H ; Oxidation (M)
77 - 91	1832.0925	1831.0853	1830.9039	0.1814	1	K.SIYGEKFEDENFILK.H
83 - 91	1154.4813	1153.4740	1153.5655	-0.0915	0	K.FEDENFILK.H
132 - 144	1505.7914	1504.7841	1504.7377	0.0464	1	K.VKEGMNIVEAMER.F

No match to: 1523.7634, 1554.0185, 1713.9247, 1946.2642, 1988.2967

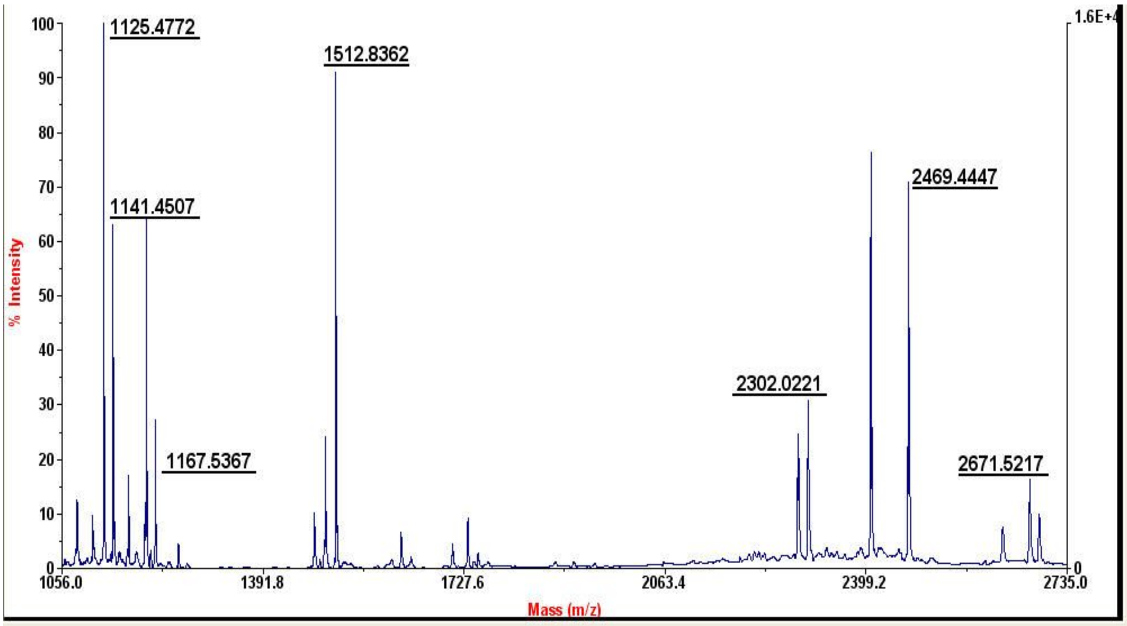
64） Peroxiredoxin-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 16	980.5129	979.5056	979.5239	-0.0183	0	K.IGHPAPNFK.A
111 - 120	1107.5710	1106.5637	1106.5971	-0.0334	0	R.TIAQDYGVLK.A
129 - 140	1359.8175	1358.8102	1358.7921	0.0181	1	R.GLFIIDDKGILR.Q
141 - 151	1211.7051	1210.6978	1210.6669	0.0309	0	R.QITVNDLPVGR.S
159 - 168	1196.6159	1195.6086	1195.6237	-0.0151	0	R.LVQAFQFTDK.H
169 - 190	2406.2486	2405.2414	2405.1797	0.0616	0	K.HGEVCPAGWKPGSDTIKPDVQK.S

No match to: 922.4665, 1194.6617

65） Flavin reductase

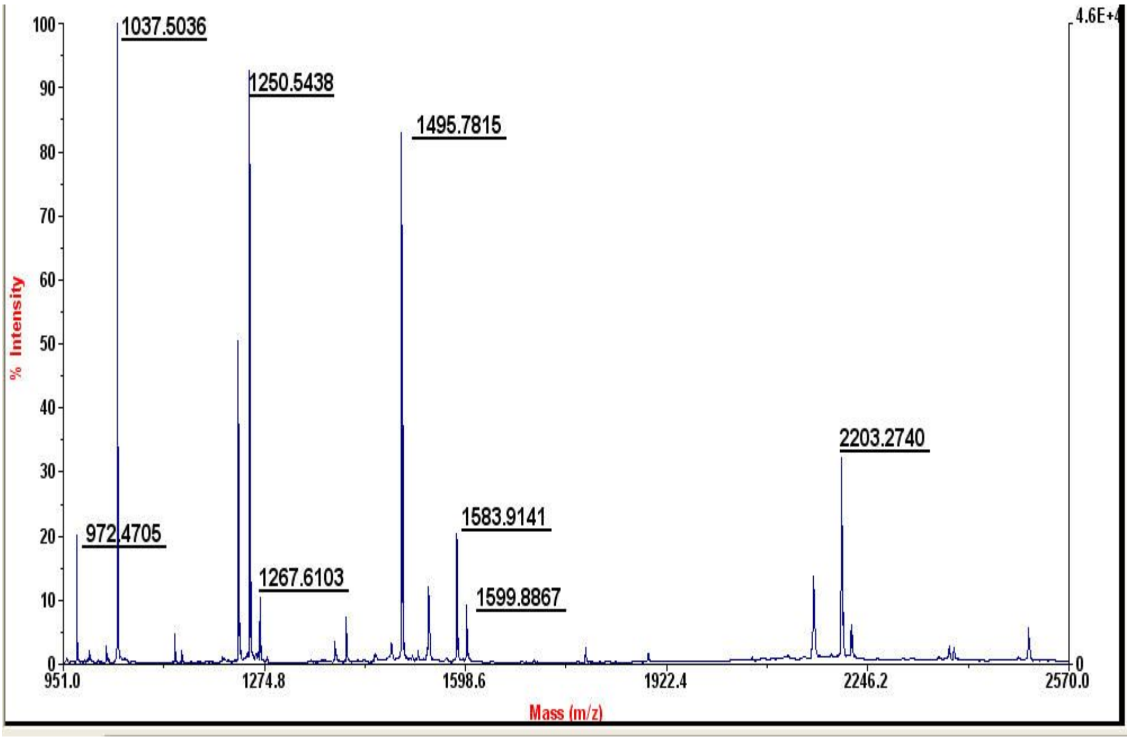


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

40 - 63	2469.4447	2468.4375	2468.3022	0.1352	0	R.LPSEGPRPAHVVVGDVLQAADVDK.T	
64 - 78	1512.8362	1511.8289	1511.8671	-0.0382	0	K.TVAGQDAVIVLLGTR.N	
125 - 134	1167.5367	1166.5294	1166.6044	-0.0750	0	R.LQAVTDDHIR.M	
146 - 170	2671.5217	2670.5144	2670.3475	0.1669	0	K.YVAVMPPHIGDQPLTGAYTVTLDGR.G	
179 - 187	1125.4772	1124.4699	1124.5549	-0.0850	0	K.HDLGHFMLR.C	
179 - 187	1141.4507	1140.4434	1140.5498	-0.1064	0	K.HDLGHFMLR.C	Oxidation (M)
188 - 206	2302.0221	2301.0148	2300.9280	0.0868	0	R.CLTTDEYDGHSTYPSHQYQ.-	

No match to: 980.4153, 1037.4595, 1196.5386, 1211.6023, 1495.7211, 2284.9594, 2406.2787

66） Adenylate kinase isoenzyme 1

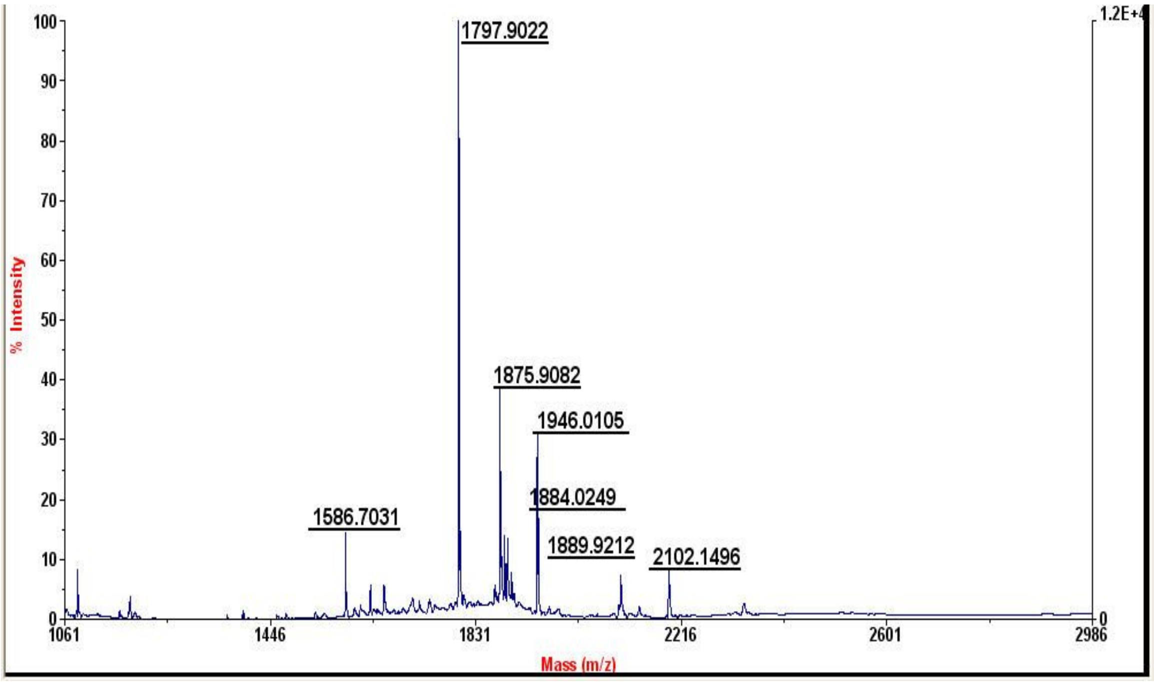


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
32 - 44	1495.7815	1494.7742	1494.7467	0.0275	0	K.YGYTHLSTGDLLR.S	
64 - 77	1583.9141	1582.9068	1582.8752	0.0316	0	K.GQLVPLETVLDMLR.D	
64 - 77	1599.8867	1598.8794	1598.8701	0.0093	0	K.GQLVPLETVLDMLR.D	Oxidation (M)

89 - 97	1037.5036	1036.4963	1036.5341	-0.0379	0	K.GFLIDGYPR.E
98 - 107	1250.5438	1249.5366	1249.5574	-0.0209	0	R.EVQQGEEFER.R
109 - 128	2203.2740	2202.2667	2202.1354	0.1313	0	R.IGQPTLLLYVDAGPETMTQR.L
149 - 155	972.4705	971.4632	971.5076	-0.0444	1	K.RLETYYK.A
156 - 166	1267.6103	1266.6030	1266.6496	-0.0465	0	K.ATEPVIAFYEK.R

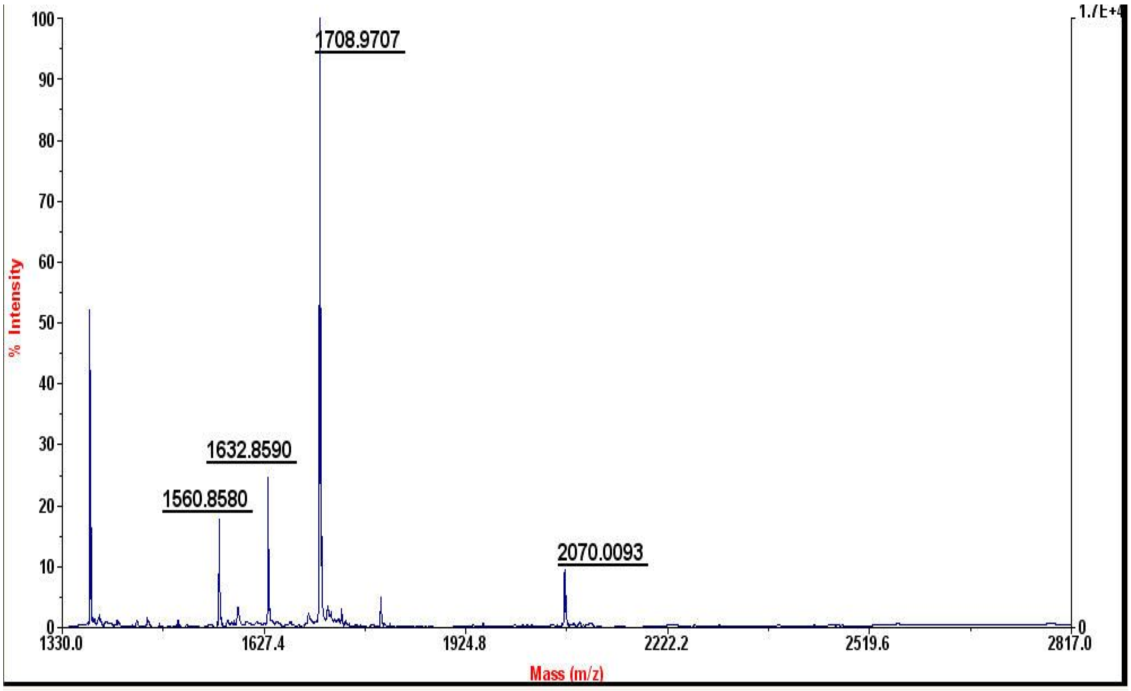
No match to: 1232.5433, 1539.0805, 2158.2752

67）Spectrin beta chain, brain 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
128 - 144	1946.0105	1945.0032	1944.8860	0.1172	0	R.VHLENMGSHDIVDGNHR.L
Oxidation (M)						
265 - 279	1884.0249	1883.0177	1882.9505	0.0672	0	K.SIITYVVTYYHYFSK.M
1355 - 1372	2102.1496	2101.1423	2101.0877	0.0546	1	K.LTGLHKMWEVLESTTQTK.A
1395 - 1410	1875.9082	1874.9010	1874.8799	0.0211	0	K.WLHGLESQIQSDDYGK.D
1657 - 1672	1797.9022	1796.8950	1796.8839	0.0111	1	R.ALVADSHPESERISMR.Q
2044 - 2057	1586.7031	1585.6958	1585.8562	-0.1604	1	R.EIGQSVDEVEKLIK.R
2073 - 2088	1889.9212	1888.9139	1889.0621	-0.1483	1	R.FSALERLTTLELLEVR.R

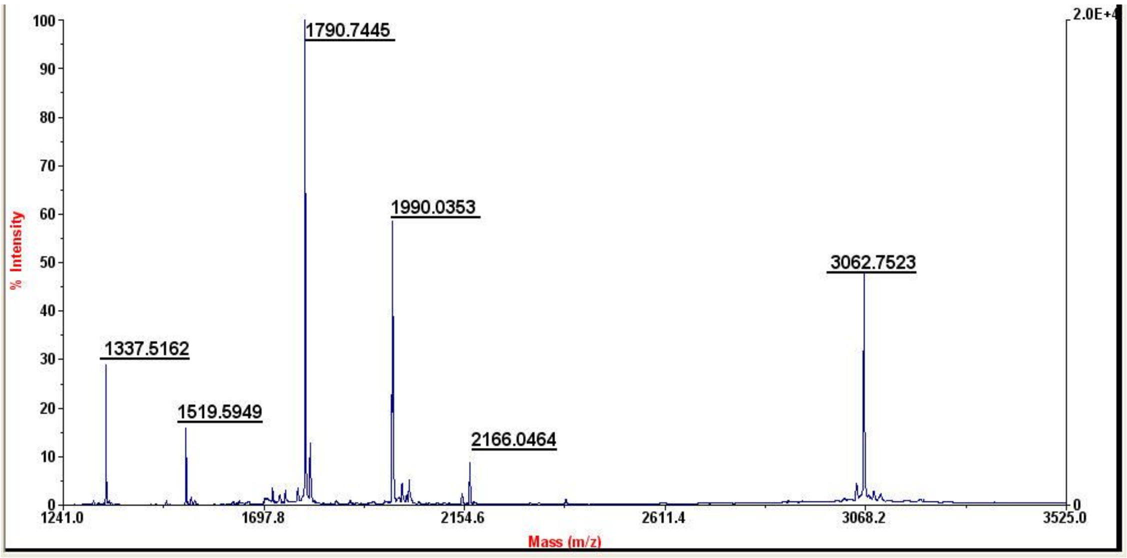
68） Phosphatidylethanolamine-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
48 - 62	1632.8590	1631.8517	1631.7903	0.0614	0	K.NRPTSISWDGLDSGK.L
63 - 76	1560.8580	1559.8507	1559.8195	0.0312	0	K.LYTLVLTDPDAPSR.K
120 - 132	1708.9707	1707.9634	1707.8984	0.0650	0	R.YVWLVYEQDRPLK.C
162 - 179	2070.0093	2069.0021	2068.9200	0.0821	0	R.APVAGTCYQAEWDDYVPK.L

No match to: 1370.7044, 3473.0676

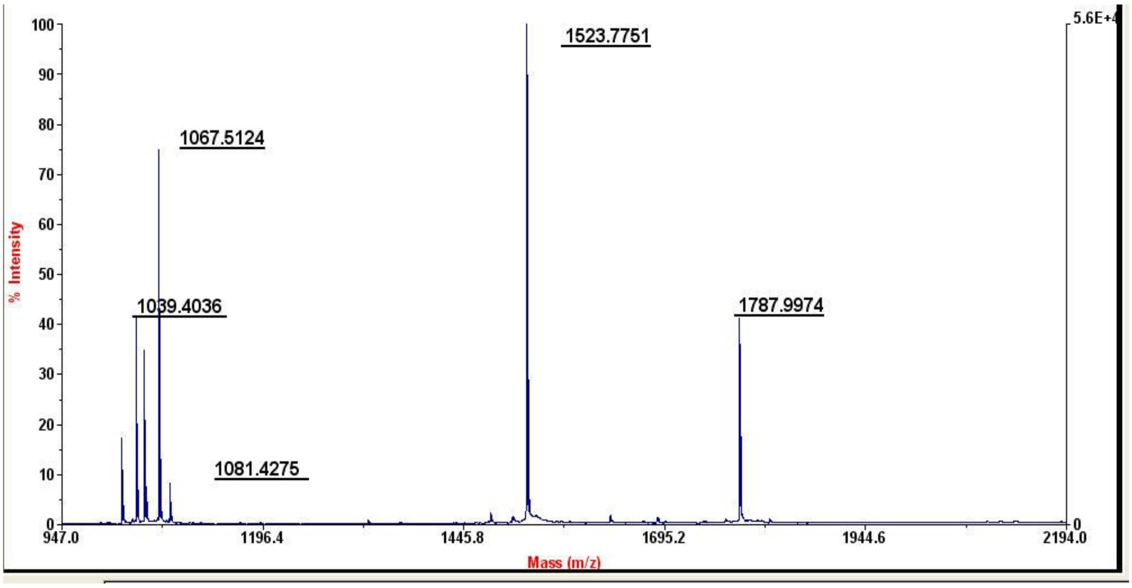
69） Cofilin-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
46 - 73	3062.7523	3061.7450	3061.5858	0.1592	1	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M
54 - 73	2166.0464	2165.0391	2165.0891	-0.0501	0	K.EILVGDVGQTVDDPYATFVK.M
82 - 92	1337.5162	1336.5089	1336.6187	-0.1098	0	R.YALYDATYETK.E
96 - 112	1990.0353	1989.0281	1989.0611	-0.0330	1	K.KEDLVFIFWAPESAPLK.S
133 - 144	1519.5949	1518.5877	1518.6772	-0.0896	0	K.HELQANCYEEVK.D
133 - 146	1790.7445	1789.7373	1789.8053	-0.0680	1	K.HELQANCYEEVKDR.C

No match to: 1789.7752, 1802.7323

70）Ubiquitin

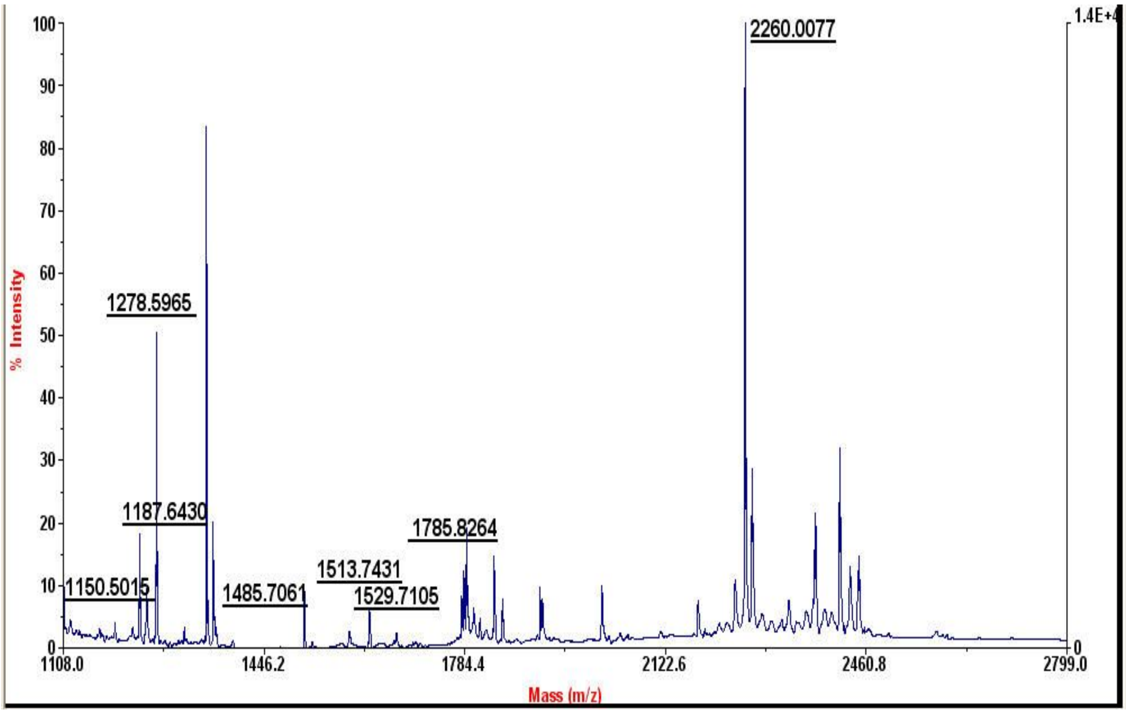


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
12 - 27	1787.9974	1786.9901	1786.9200	0.0702	0	K.TITLEVEPSDTIENVK.A

30 - 42	1523.7751	1522.7678	1522.7739	-0.0061	1	K.IQDKEGIPPDQQR.L
34 - 42	1039.4036	1038.3963	1038.5094	-0.1131	0	K.EGIPPDQQR.L
55 - 63	1081.4275	1080.4202	1080.5451	-0.1249	0	R.TLSDYNIQK.E
64 - 72	1067.5124	1066.5051	1066.6135	-0.1084	0	K.ESTLHLVLR.L

No match to: 1021.3893, 1049.4933

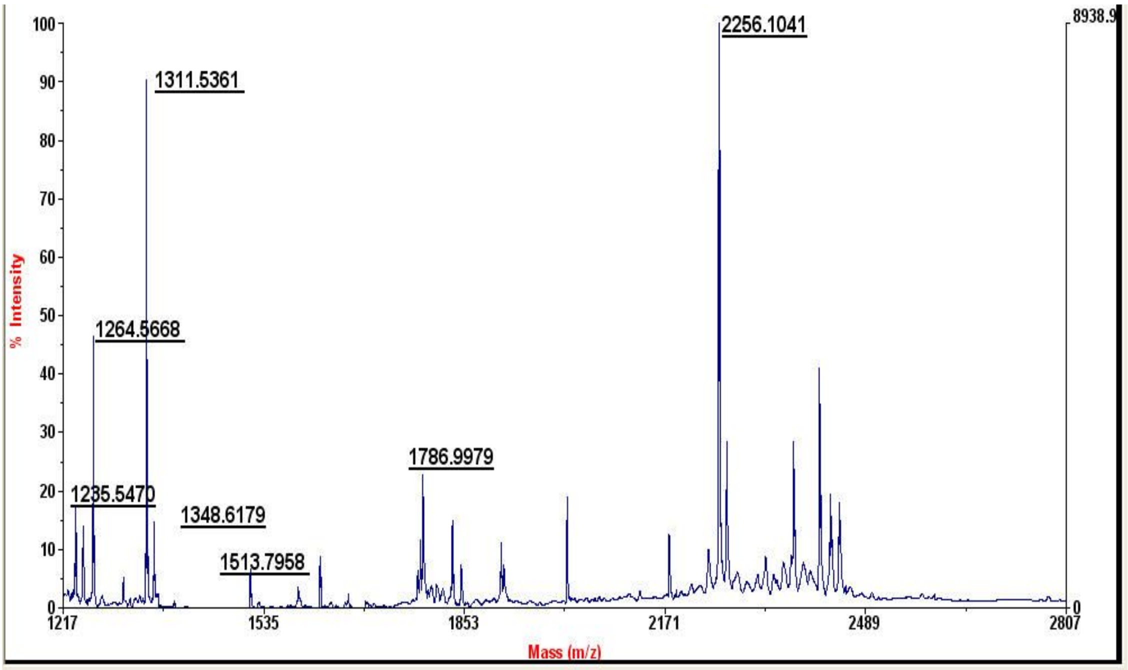
71） Endoplasmin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
52 - 67	1785.8264	1784.8191	1784.8904	-0.0713	0	R.EEEAIQLDGLNASQIR.E	
76 - 84	1081.5124	1080.5051	1080.5352	-0.0301	0	K.FAFQAEVNR.M	
143 - 156	1513.7431	1512.7359	1512.7718	-0.0359	0	K.NLLHVTDTGVGMTR.E	
143 - 156	1529.7105	1528.7032	1528.7667	-0.0635	0	K.NLLHVTDTGVGMTR.E	Oxidation (M)
385 - 395	1187.6430	1186.6358	1186.6710	-0.0352	0	K.SILFVPTSAPR.G	
396 - 404	1015.4297	1014.4225	1014.4658	-0.0433	0	R.GLFDEYGSK.K	
435 - 448	1485.7061	1484.6989	1484.7470	-0.0482	0	K.GVVDSDDLPLNVSR.E	
494 - 503	1139.5575	1138.5502	1138.5730	-0.0228	0	K.LGVIEDHSNR.T	
512 - 530	2260.0077	2259.0004	2259.0556	-0.0552	0	R.FQSSHHPTDITSLDQYVER.M	
547 - 557	1278.5965	1277.5892	1277.6251	-0.0359	1	R.KEAESSPFVER.L	

548 - 557	1150.5015	1149.4943	1149.5302	-0.0359	0	K.EAESSPFVER.L

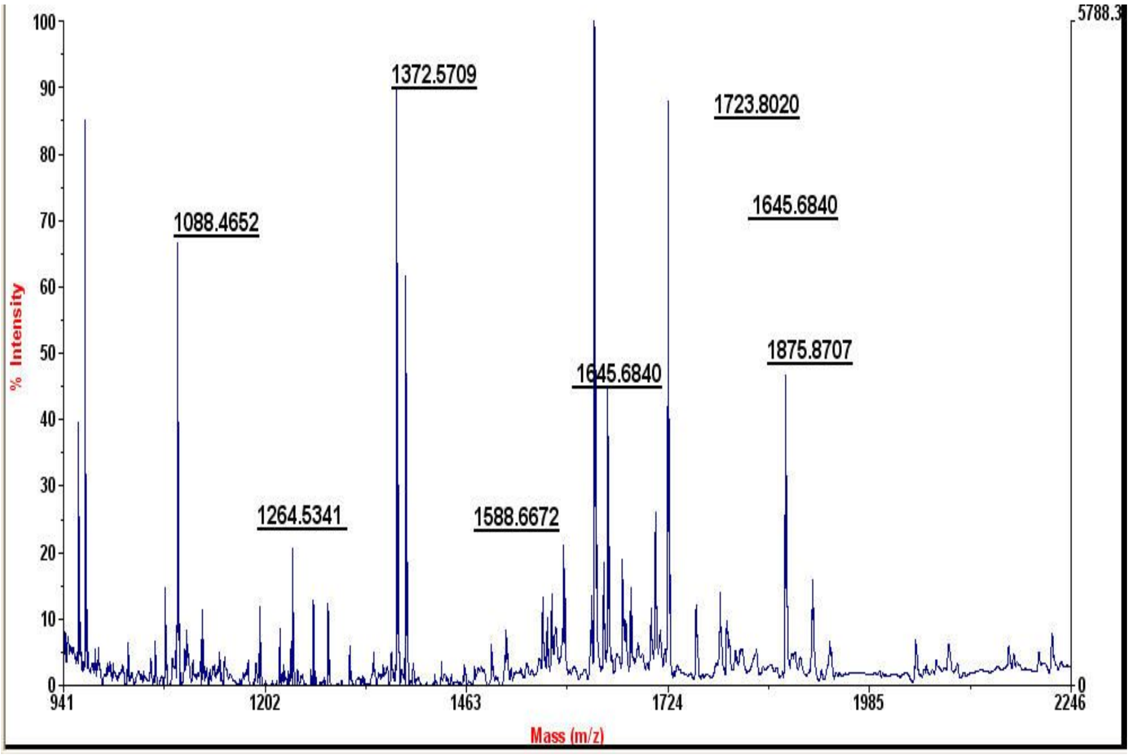
72） Heat shock protein HSP 90-alpha



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
154 - 173	2256.1041	2255.0968	2254.9515	0.1453	0	K.HNDDEQYAWESSAGGSFTVR.T
192 - 201	1311.5361	1310.5289	1310.5626	-0.0338	0	K.EDQTEYLEER.R
346 - 355	1264.5668	1263.5595	1263.6360	-0.0765	1	R.RAPFDLFENR.K
347 - 355	1108.4895	1107.4822	1107.5349	-0.0527	0	R.APFDLFENR.K
387 - 400	1513.7958	1512.7885	1512.7783	0.0102	0	R.GVVDSEDLPLNISR.E
447 - 456	1168.4961	1167.4888	1167.5632	-0.0744	0	K.LGIHEDSQNR.K
500 - 510	1235.5470	1234.5397	1234.5942	-0.0544	0	K.DQVANSAFVER.L
621 - 632	1348.6179	1347.6106	1347.5798	0.0308	1	R.DNSTMGYMAAKK.H 2 Oxidation (M)
633 - 647	1786.9979	1785.9907	1785.9373	0.0534	0	K.HLEINPDHSIIETLR.Q

No match to: 1782.9945, 1911.0963, 2177.1023

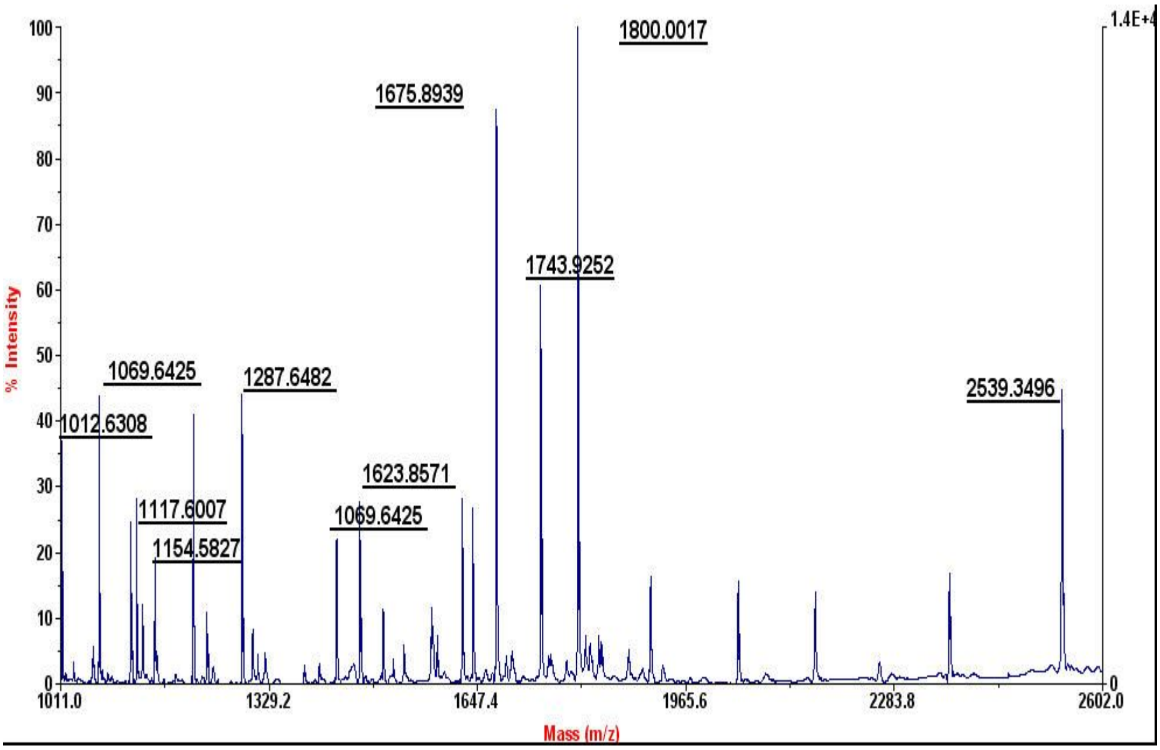
73） Alpha-1B-glycoprotein precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
79 - 90	1372.5709	1371.5636	1371.6895	-0.1259	0	K.HQFLLTGDTQGR.Y
95 - 106	1264.5341	1263.5268	1263.6459	-0.1191	0	R.SGLSTGWTQLSK.L
228 - 244	1875.8707	1874.8634	1874.9924	-0.1289	0	K.VTLTCVAPLSGVDFQLR.R
392 - 406	1723.8020	1722.7948	1722.9529	-0.1581	0	R.LELHVDGPPPRPQLR.A
407 - 417	1088.4652	1087.4579	1087.5774	-0.1194	0	R.ATWSGAVLAGR.D
423 - 436	1588.6672	1587.6599	1587.7966	-0.1367	0	R.CEGPIPDVTFELLR.E
423 - 436	1645.6840	1644.6767	1644.8181	-0.1414	0	R.CEGPIPDVTFELLR.E

No match to: 1384.5600, 1628.6499, 1664.6698, 1707.5721

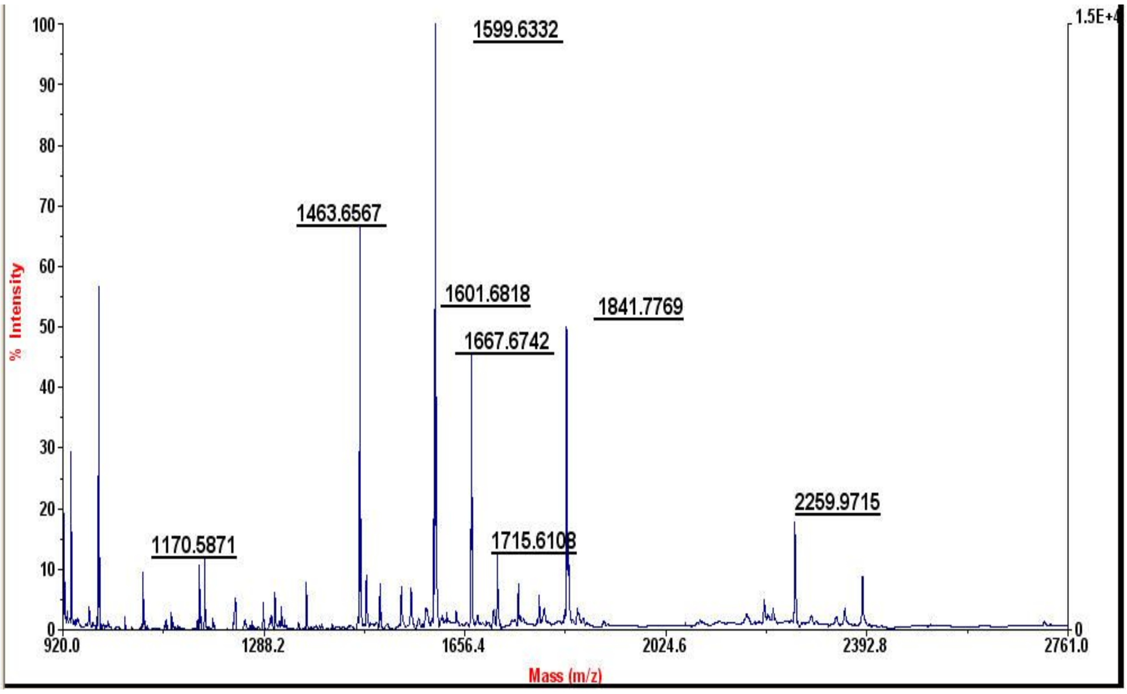
74） Plastin-2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
40 - 49	1117.6007	1116.5935	1116.5750	0.0185	0	K.AACLPLPGYR.V	
124 - 132	1154.5827	1153.5754	1153.5920	-0.0166	0	K.YAFVNWINK.A	
245 - 253	1012.6308	1011.6235	1011.6076	0.0159	0	R.NEALIALLR.E	
264 - 272	1069.6425	1068.6353	1068.6179	0.0174	0	K.LSPEELLLR.W	
298 - 309	1431.7436	1430.7363	1430.7558	-0.0194	0	K.AYYHLLEQVAPK.G	
310 - 326	1743.9252	1742.9179	1742.8508	0.0671	0	K.GDEEGVPAVVIDMSGLR.E	
334 - 347	1623.8571	1622.8499	1622.7327	0.1172	1	R.AECMLQQAERLGCR.Q	Oxidation (M)
374 - 395	2539.3496	2538.3423	2538.2139	0.1284	0	R.YPALHKPENQDIDWGALEGETR.E	
402 - 412	1287.6482	1286.6409	1286.6189	0.0220	0	R.NWMNSLGVNPR.V	
433 - 441	1126.6520	1125.6447	1125.6294	0.0152	1	K.IKVPVDWNR.V	
473 - 488	1675.8939	1674.8866	1674.8325	0.0542	0	K.FSLVGIGGQDLNEGNR.T	
516 - 530	1800.0017	1798.9945	1798.9213	0.0732	0	K.VNDDIIVNWVNETLR.E	

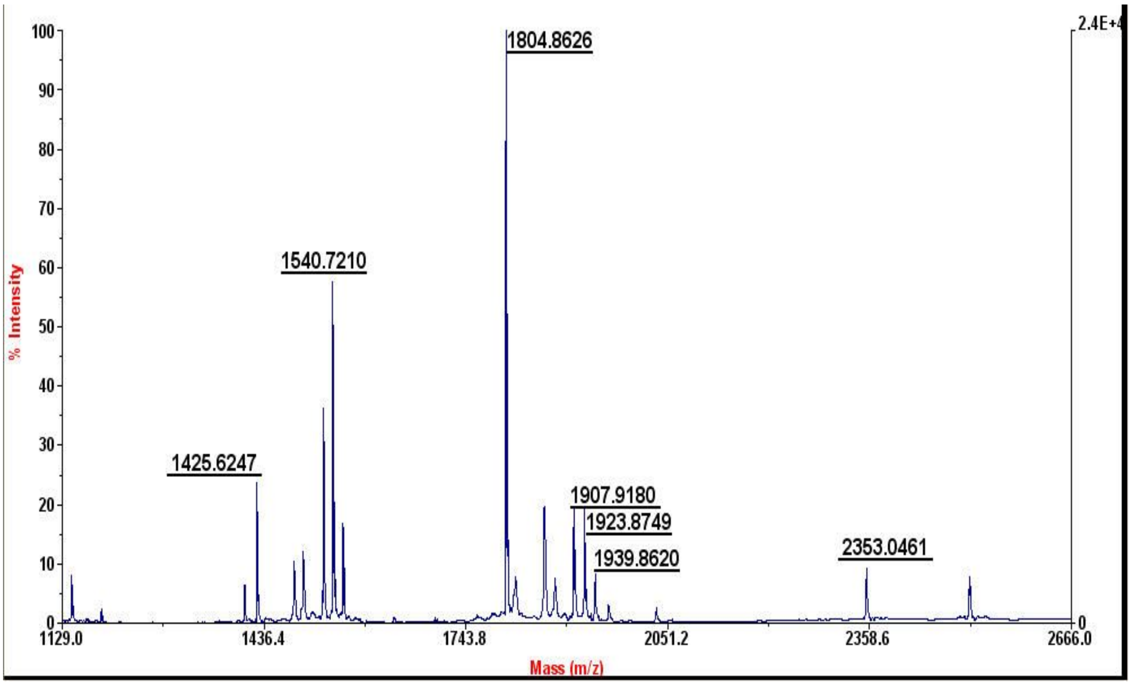
No match to: 960.5659, 1213.6339, 1467.8611, 1639.9042

75）Aconitate hydratase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
59 - 68	1170.5871	1169.5798	1169.6768	-0.0970	0	R.LNRPLTLSEK.I
69 - 84	1841.7769	1840.7697	1840.8955	-0.1258	0	K.IVYGHLDDPASQEIER.G
118 - 138	2259.9715	2258.9642	2259.1317	-0.1675	0	K.VAVPSTIHCDHLIEAQVGGEK.D
371 - 378	985.4262	984.4190	984.5029	-0.0839	0	K.EGWPLDIR.V
412 - 424	1463.6567	1462.6494	1462.7416	-0.0922	0	K.SQFTITPGSEQIR.A
430 - 437	935.4036	934.3963	934.4872	-0.0909	0	R.DGYAQILR.D
522 - 534	1500.6336	1499.6264	1499.7620	-0.1356	1	K.FRLEAPDADELPK.G
535 - 549	1715.6108	1714.6035	1714.7587	-0.1551	0	K.GEFDPGQDTYQHPPK.D
550 - 564	1599.6332	1598.6260	1598.7285	-0.1025	0	K.DSSGQHVDVSPTSQR.L
634 - 648	1601.6818	1600.6745	1600.7845	-0.1100	0	R.NAVTQEFGPVPDTAR.Y
657 - 671	1667.6742	1666.6670	1666.7586	-0.0917	0	R.WVVIGDENYGEGSSR.E
672 - 679	922.3976	921.3903	921.4668	-0.0764	0	R.EHAALEPR.H

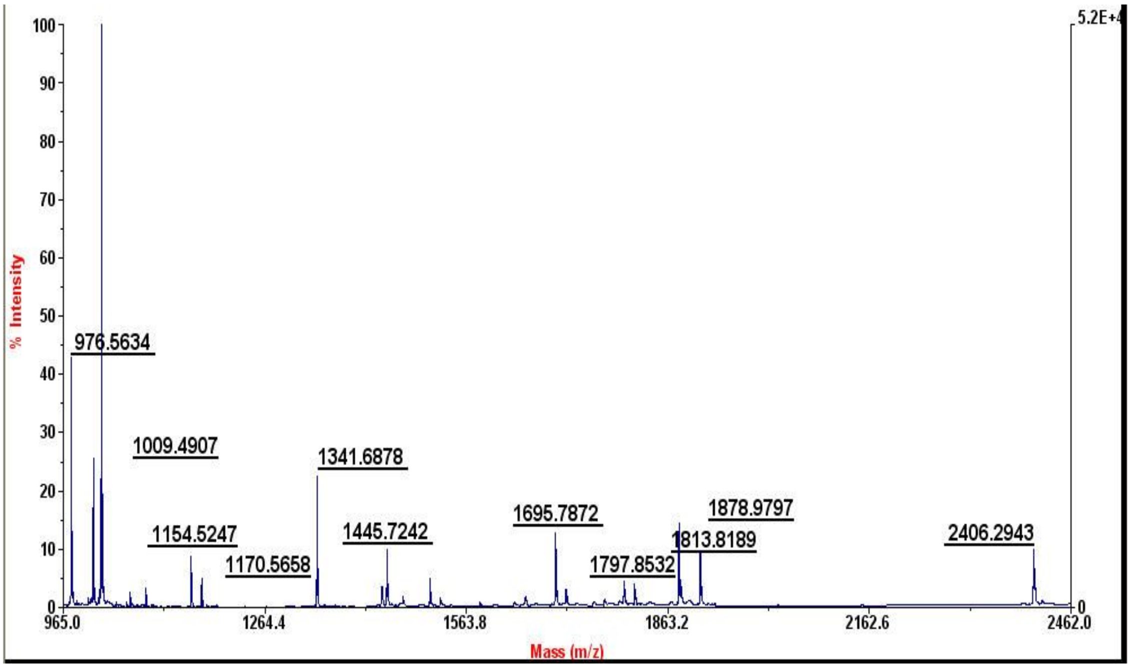
76） Alpha-enolase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
33 - 50	1804.8626	1803.8553	1803.9366	-0.0813	0	R.AAVPSGASTGIYEALELR.D	
163 - 179	1907.9180	1906.9107	1906.9797	-0.0689	0	K.LAMQEFMILPVGAANFR.E	
163 - 179	1923.8749	1922.8676	1922.9746	-0.1070	0	K.LAMQEFMILPVGAANFR.E	Oxidation (M)
163 - 179	1939.8620	1938.8548	1938.9695	-0.1147	0	K.LAMQEFMILPVGAANFR.E	2 Oxidation (M)
240 - 253	1540.7210	1539.7138	1539.7755	-0.0617	0	K.VVIGMDVAASEFFR.S	
240 - 253	1556.6522	1555.6449	1555.7704	-0.1254	0	K.VVIGMDVAASEFFR.S	Oxidation (M)
270 - 281	1425.6247	1424.6174	1424.7187	-0.1013	0	R.YISPDQLADLYK.S	
373 - 394	2353.0461	2352.0388	2352.1518	-0.1130	0	R.SGETEDTFIADLVVGLCTGQIK.T	

No match to: 1526.6699

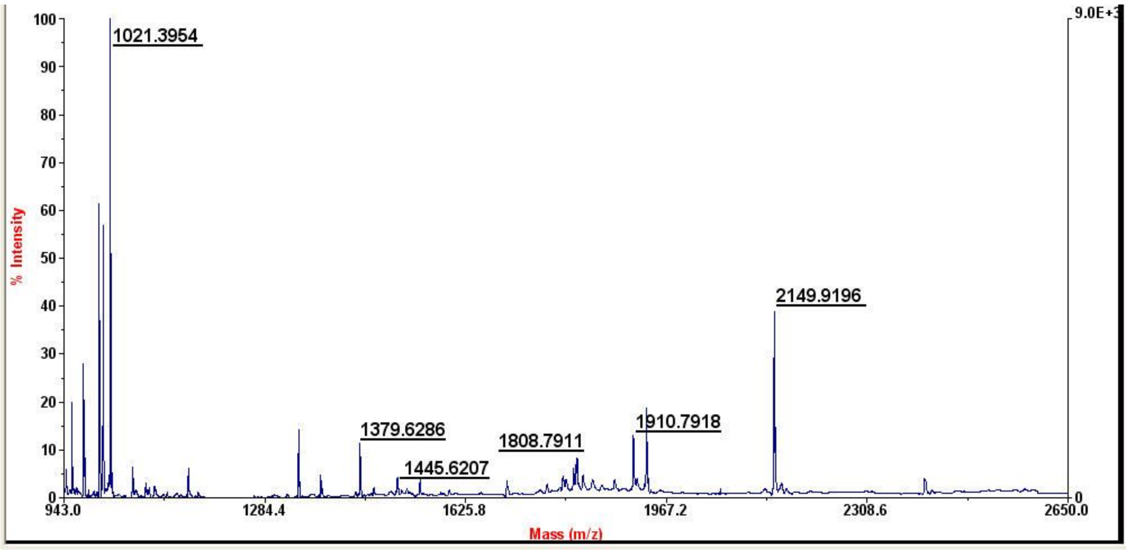
77）Isocitrate dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
5 - 20	1695.7872	1694.7799	1694.7603	0.0196	0	K.ISGGSVVEMQGDEMTR.I	
30 - 49	2406.2943	2405.2870	2405.2266	0.0604	0	K.LIFPYVELDLHSYDLGIENR.D	
101 - 109	976.5634	975.5561	975.5501	0.0060	0	R.NILGGTVFR.E	
133 - 140	1009.4907	1008.4834	1008.4413	0.0421	0	R.HAYGDQYR.A	
188 - 203	1797.8532	1796.8460	1796.8403	0.0057	0	K.SIEDFAHSSFQMALSK.G	
188 - 203	1813.8189	1812.8117	1812.8352	-0.0235	0	K.SIEDFAHSSFQMALSK.G	Oxidation (M)
223 - 233	1445.7242	1444.7169	1444.7238	-0.0069	1	R.FKDIFQEIYDK.Q	
225 - 233	1170.5658	1169.5586	1169.5604	-0.0019	0	K.DIFQEIYDK.Q	
261 - 270	1154.5247	1153.5174	1153.5226	-0.0051	0	K.SEGGFIWACK.N	
302 - 314	1341.6878	1340.6805	1340.6684	0.0121	0	K.TVEAEAAHGTVTR.H	
322 - 338	1878.9797	1877.9724	1877.9271	0.0452	0	K.GQETSTNPIASIFAWTR.G	
389 - 400	1509.6656	1508.6583	1508.6493	0.0090	0	R.SDYLNTFEFMDK.L	

No match to: 1021.4793, 1910.9660

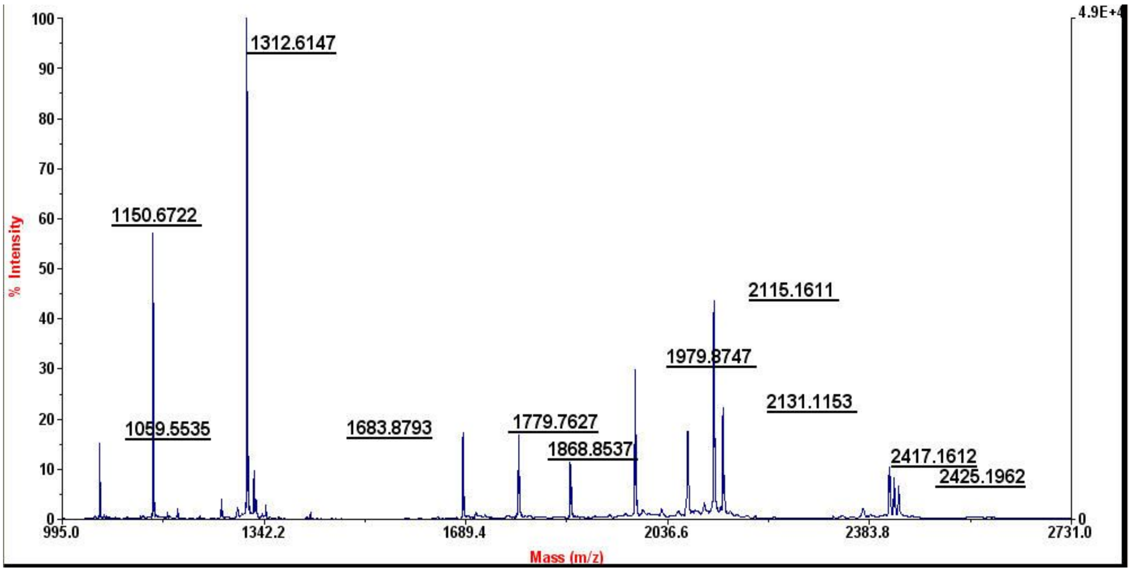
78） Tigger transposable element-derived protein 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 43	1379.6286	1378.6214	1378.7456	-0.1242	0	K.LSVVYGIGESTVR.D
52 - 68	1808.7911	1807.7838	1807.9064	-0.1226	1	R.IINYANSSDPTSGVSKR.K
70 - 81	1445.6207	1444.6134	1444.6504	-0.0369	1	K.SMKSSTYEELDR.V
147 - 165	2149.9196	2148.9123	2148.9421	-0.0298	1	K.GDETAAREFCGSFQEFVEK.E
254 - 268	1910.7918	1909.7845	1909.9474	-0.1629	1	K.GAWIEQSVFRQWFEK.Y
378 - 386	1021.3954	1020.3881	1020.5604	-0.1722	1	K.SSTITKAWK.K

No match to: 1002.4287, 1009.4070, 1341.5977, 1932.8442

79）Phosphoglycerate mutase 1



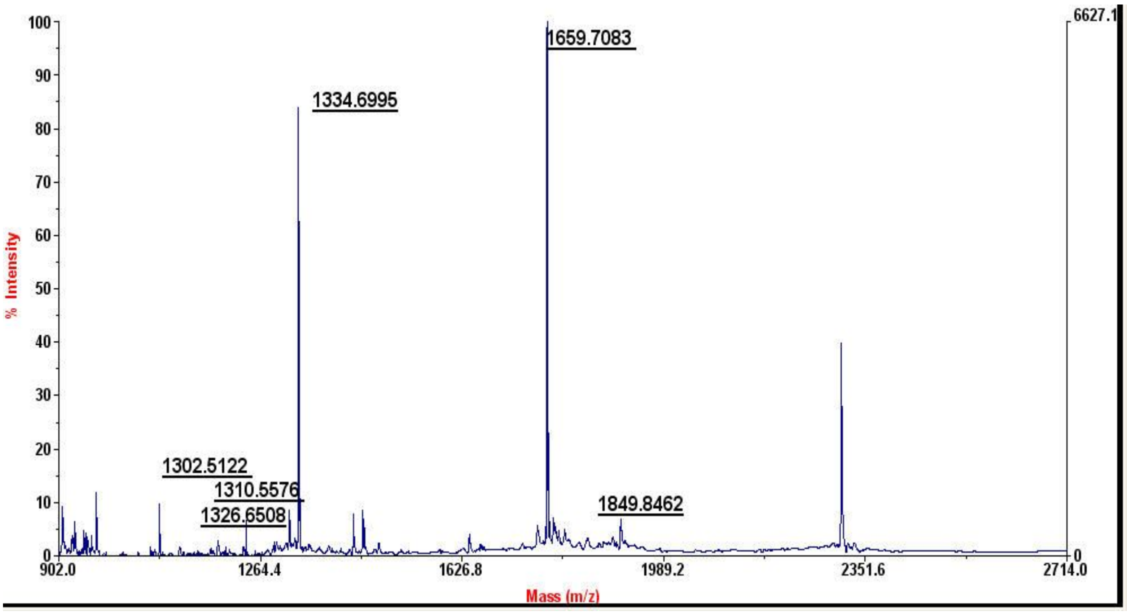
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

11 - 21	1312.6147	1311.6074	1311.5956	0.0119	0	R.HGESAWNLENR.F
22 - 39	1979.8747	1978.8675	1978.8697	-0.0022	0	R.FSGWYDADLSPAGHEEAK.R
47 - 61	1779.7627	1778.7554	1778.7821	-0.0267	0	R.DAGYEFDICFTSVQK.R
91 - 100	1059.5535	1058.5462	1058.5508	-0.0046	0	R.HYGGLTGLNK.A
118 - 138	2417.1612	2416.1539	2416.1045	0.0494	0	R.SYDVPPPPMEPDHPFYSNISK.D
142 - 157	1868.8537	1867.8464	1867.8509	-0.0045	0	R.YADLTEDQLPSCESLK.D
142 - 162	2425.1962	2424.1889	2424.1478	0.0411	1	R.YADLTEDQLPSCESLKDTIAR.A
163 - 176	1683.8793	1682.8720	1682.9031	-0.0312	0	R.ALPFWNEEIVPQIK.E
181 - 191	1150.6722	1149.6649	1149.6618	0.0032	0	R.VLIAAHGNSLR.G
223 - 240	2115.1611	2114.1538	2114.1193	0.0345	0	K.NLKPIKPMQFLGDEETVR.K
223 - 240	2131.1153	2130.1080	2130.1143	-0.0062	0	K.NLKPIKPMQFLGDEETVR.K

Oxidation (M)

No match to: 2070.2442

80） Probable isomerase MAWBP

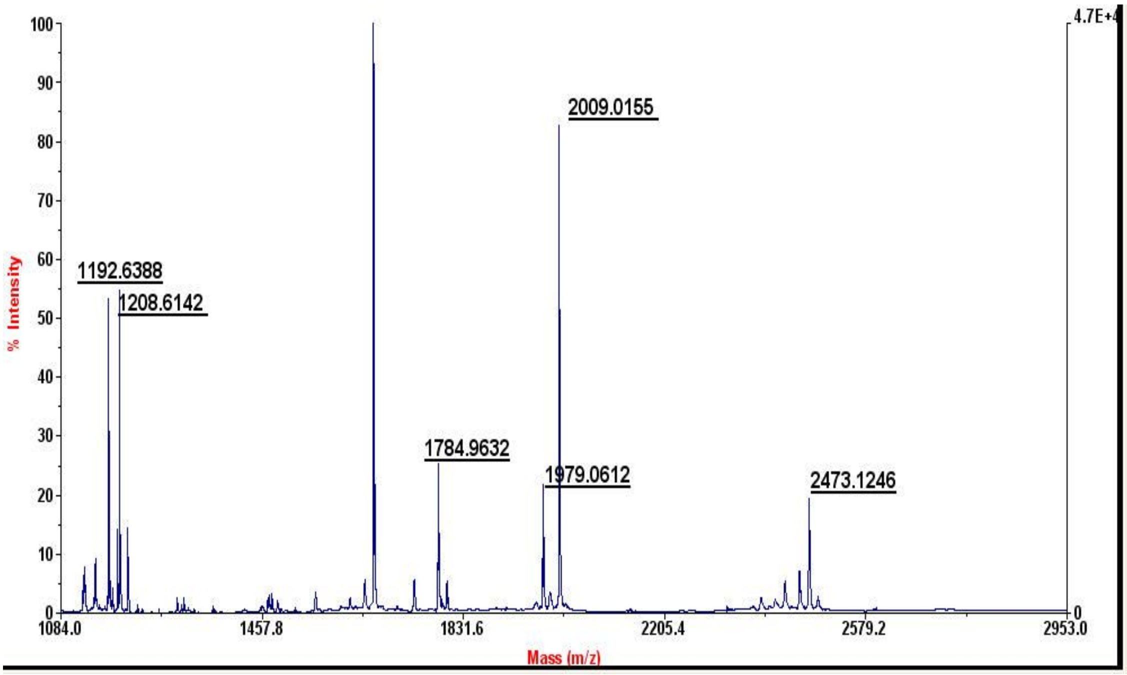


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
3 - 14	1334.6995	1333.6922	1333.7394	-0.0471	0	K.LPIFIADAFTAR.A
41 - 51	1310.5576	1309.5503	1309.6336	-0.0833	0	R.EMNLSETAFIR.K
41 - 51	1326.6508	1325.6435	1325.6285	0.0150	0	R.EMNLSETAFIR.K Oxidation (M)
53 - 68	1849.8462	1848.8389	1848.8577	-0.0188	0	K.LHPTDNFAQSSCFGLR.W

202 - 216	1659.7083	1658.7010	1658.7324	-0.0314	0	K.GEPGGQTQAFDFYSR.Y
249 - 258	1302.5122	1301.5049	1301.5393	-0.0345	0	K.EMHAFQCSHR.G

No match to: 1284.4988, 1292.6261, 1332.6794, 1778.7753

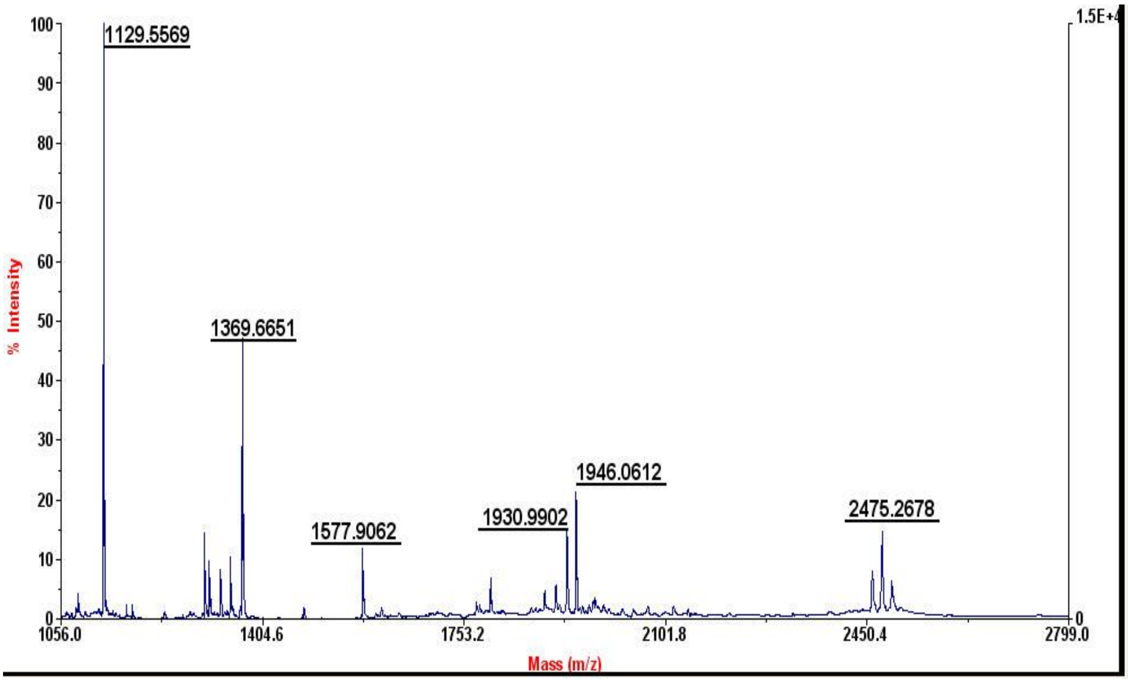
81) XTP3-transactivated gene B protein



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
45 - 62	2009.0155	2008.0082	2008.0305	-0.0223	0	R.VNWPGTEFSLPTTGVLYK.E
180 - 202	2473.1246	2472.1173	2472.1123	0.0051	0	K.NIEGQMTPYYPVGMGNGTPCSLK.Q
Oxidation (M)						
276 - 289	1784.9632	1783.9559	1783.9580	-0.0021	1	R.QLEQQEEILRVPFR.R
337 - 346	1208.6142	1207.6069	1207.5331	0.0738	0	K.EFLSGSYCFR.G
337 - 353	1979.0612	1978.0540	1977.9195	0.1345	1	K.EFLSGSYCFRGGVGWWK.Y
361 - 369	1192.6388	1191.6315	1191.5421	0.0894	0	K.HVHQYHEDK.D

No match to: 1022.5853, 1172.5006, 1188.4765, 1664.8513

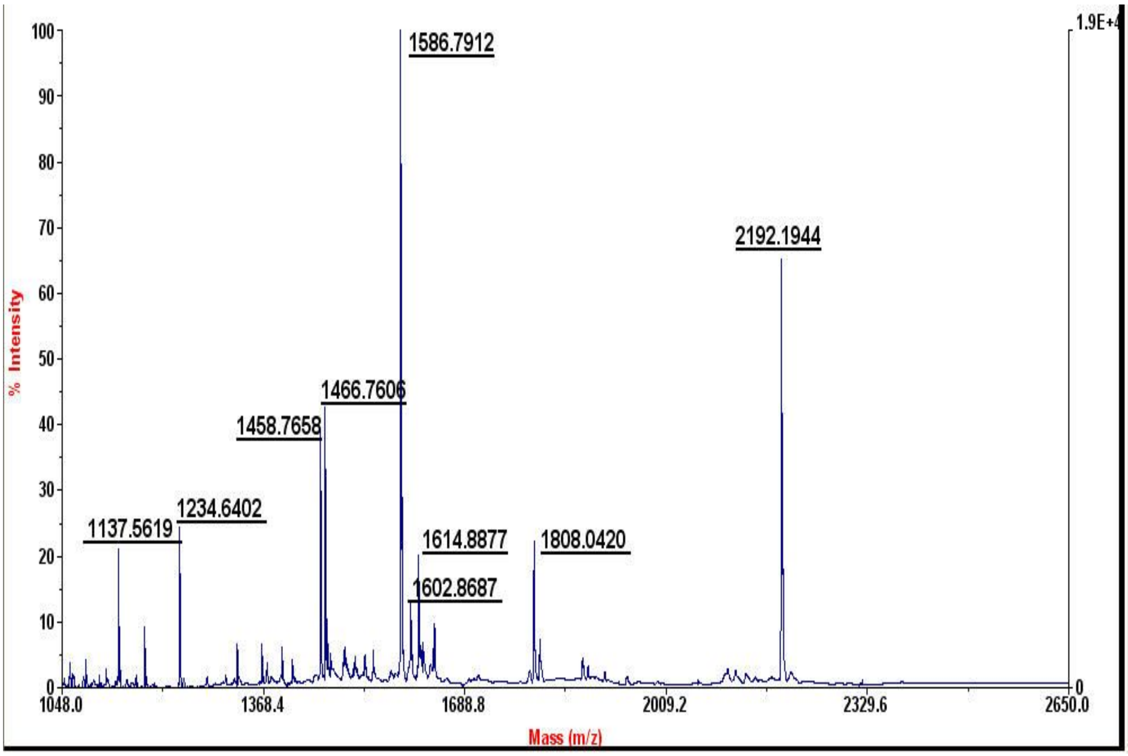
82) Carbonic anhydrase 3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
40 - 57	1930.9902	1929.9829	1929.8857	0.0972	0	R.HDPSLQPWSVSYDGGSAK.T	
68 - 76	1129.5569	1128.5496	1128.5087	0.0409	0	R.VVFDDTYDR.S	
81 - 89	913.5213	912.5140	912.4817	0.0323	0	R.GGPLPGPYR.L	
92 - 113	2475.2678	2474.2606	2474.0999	0.1607	0	R.QFHLHWGSSDDHGSEHTVDGVK.Y	
114 - 126	1577.9062	1576.8989	1576.8150	0.0839	0	K.YAAELHLVHWNPK.Y	
149 - 165	1946.0612	1945.0539	1944.9581	0.0959	0	K.IGHENGEFQIFLDALDK.I	
178 - 188	1369.6651	1368.6578	1368.5955	0.0624	0	K.FDPSCLFPACR.D	2

No match to: 1304.7676, 1348.7194

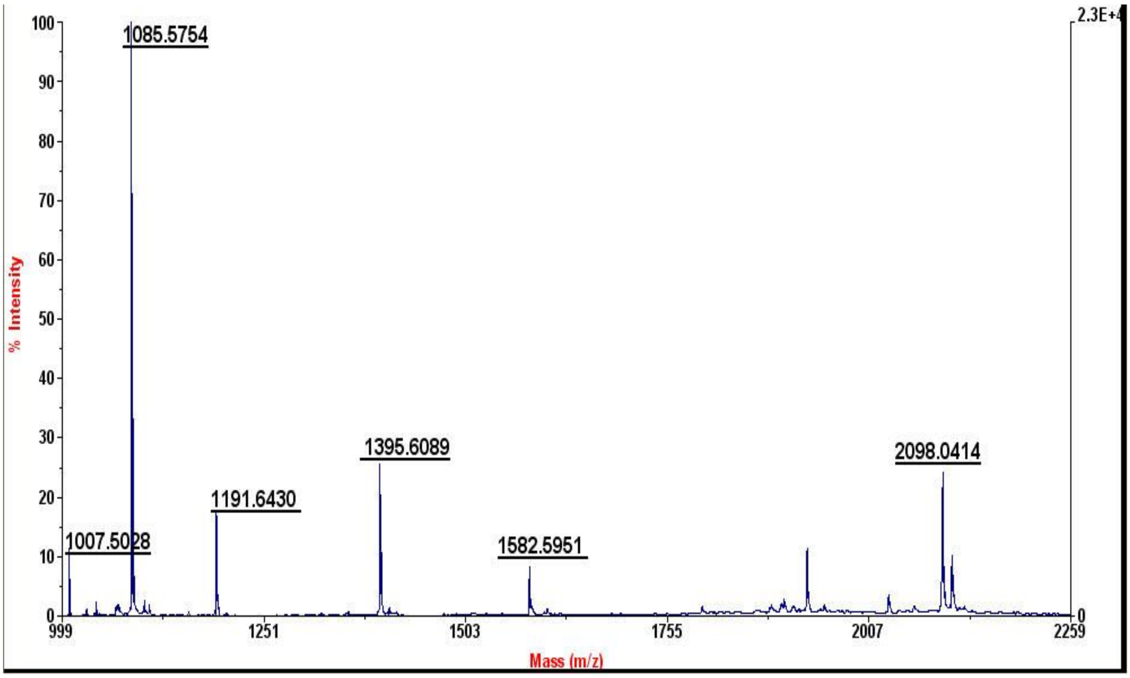
83) Triosephosphate isomerase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
34 - 53	2192.1944	2191.1871	2191.0619	0.1252	0	K.VPADTEVVCAPPTAYIDFAR.Q
60 - 69	1137.5619	1136.5547	1136.5648	-0.0101	0	K.IAVAAQNCYK.V
86 - 99	1586.7912	1585.7839	1585.7307	0.0532	0	K.DCGATWVVLGHSER.R
100 - 113	1614.8877	1613.8804	1613.8161	0.0643	1	R.RHVFGESDELIGQK.V
101 - 113	1458.7658	1457.7586	1457.7150	0.0436	0	R.HVFGESDELIGQK.V
114 - 131	1808.0420	1807.0347	1806.9661	0.0686	0	K.VAHALAEGLGVIACIGEK.L
161 - 175	1602.8687	1601.8614	1601.8817	-0.0202	0	K.VVLAYEPVWAIGTGK.T
176 - 188	1466.7606	1465.7534	1465.7161	0.0373	0	K.TATPQQAQEVHEK.L
195 - 206	1234.6402	1233.6329	1233.5949	0.0380	0	K.SNVSDAVAQSTR.I

No match to: 1179.6307, 1365.6903, 1797.9882

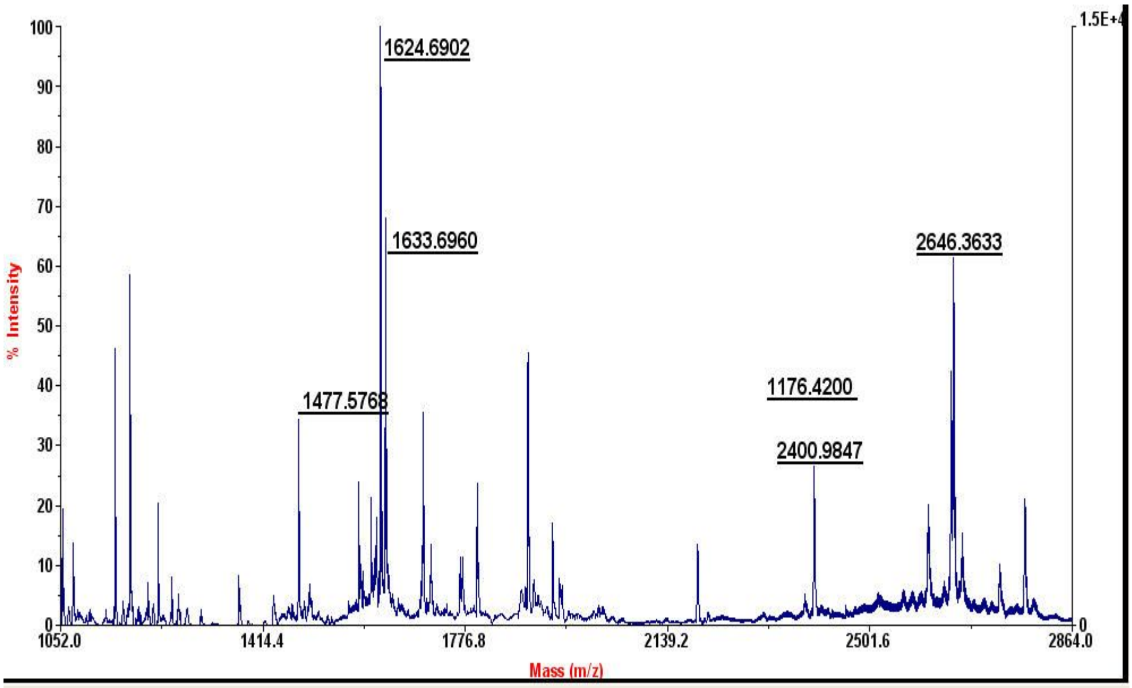
84) Peroxiredoxin-6



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 22	2098.0414	2097.0341	2097.0854	-0.0512	0	M.PGGLLLGDVAPNFEANTTVGR.I
42 - 53	1395.6089	1394.6016	1394.6500	-0.0484	0	R.DFTPVCTTELGR.A
85 - 97	1582.5951	1581.5878	1581.6617	-0.0739	0	K.DINAYNCEEPTEK.L
98 - 106	1085.5754	1084.5681	1084.5917	-0.0236	0	K.LPFPIIDDR.N
133 - 141	1007.5028	1006.4955	1006.5487	-0.0532	0	R.VVFVFGPDK.K
145 - 155	1191.6430	1190.6357	1190.6659	-0.0302	0	K.LSILYPATTGR.N
156 - 162	906.4486	905.4413	905.4606	-0.0193	0	R.NFDEILR.V

No match to: 1928.9092, 2110.0370

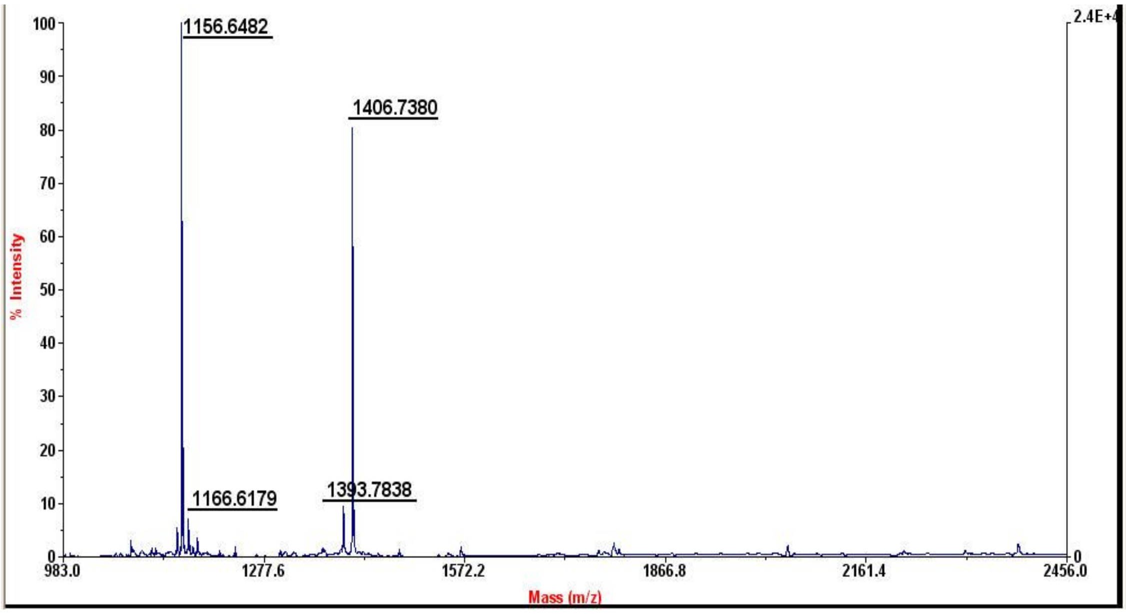
85) 5'(3')-deoxyribonucleotidase, cytosolic type



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
30 - 41	1477.5768	1476.5696	1476.7361	-0.1665	0	R.FPEEPHVPLEQR.R	
30 - 42	1633.6960	1632.6887	1632.8372	-0.1485	1	R.FPEEPHVPLEQRR.G	
61 - 85	2646.3633	2645.3560	2645.3740	-0.0179	0	K.VASVYEAPGFFLDLEPIPGALDAVR.E	
115 - 127	1624.6902	1623.6830	1623.8157	-0.1327	0	R.WVEQHLGPQFVER.I	
151 - 169	2400.9847	2399.9774	2400.0375	-0.0601	0	R.GQEETPSWEHILFTCCHNR.H	2
170 - 177	932.3828	931.3755	931.5603	-0.1848	0	R.HLVLPPTR.R	
180 - 188	1176.4200	1175.4127	1175.5723	-0.1596	0	R.LLSWSDNWR.E	

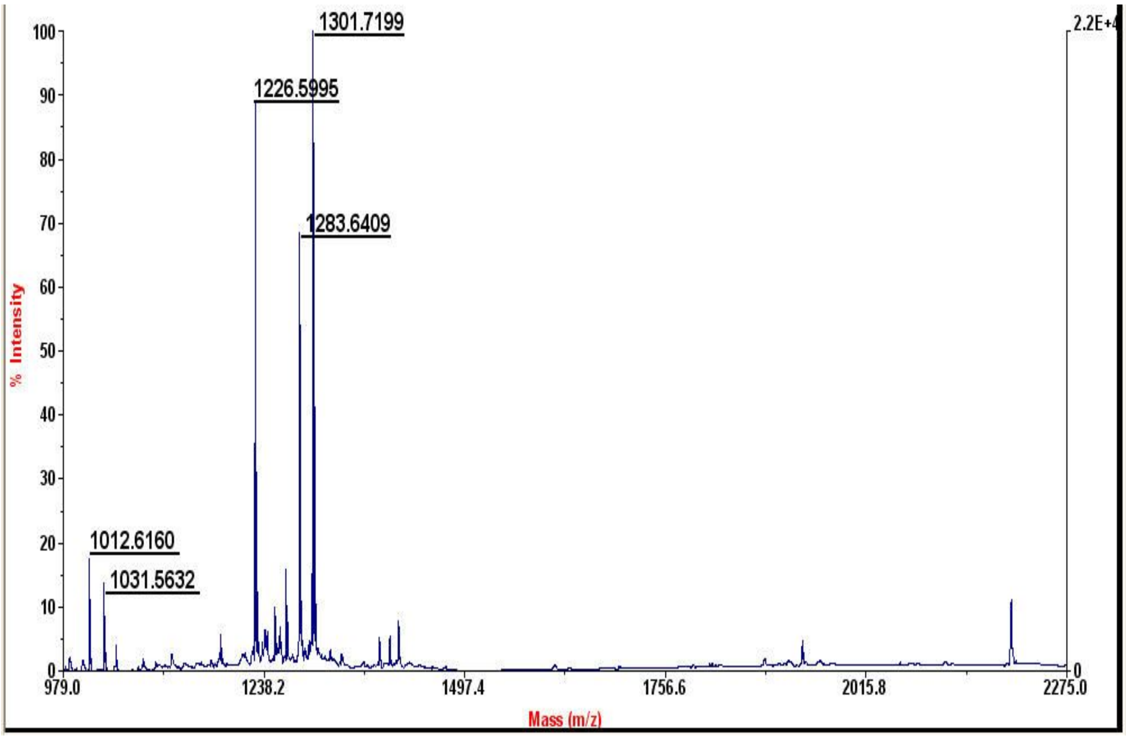
No match to: 1148.4339, 1226.4280, 1586.5995, 1797.7778, 1888.9567, 2795.6382

86） Serum amyloid P-component precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
65 - 76	1406.7380	1405.7308	1405.6626	0.0682	0	R.AYSLFSYNTQGR.D
87 - 96	1156.6482	1155.6409	1155.5924	0.0485	0	R.VGEYSLYIGR.H
140 - 149	1166.6179	1165.6106	1165.5767	0.0339	0	R.QGYFVEAQPK.I
150 - 162	1393.7838	1392.7765	1392.6884	0.0881	0	K.IVLGQEQDSYGGK.F

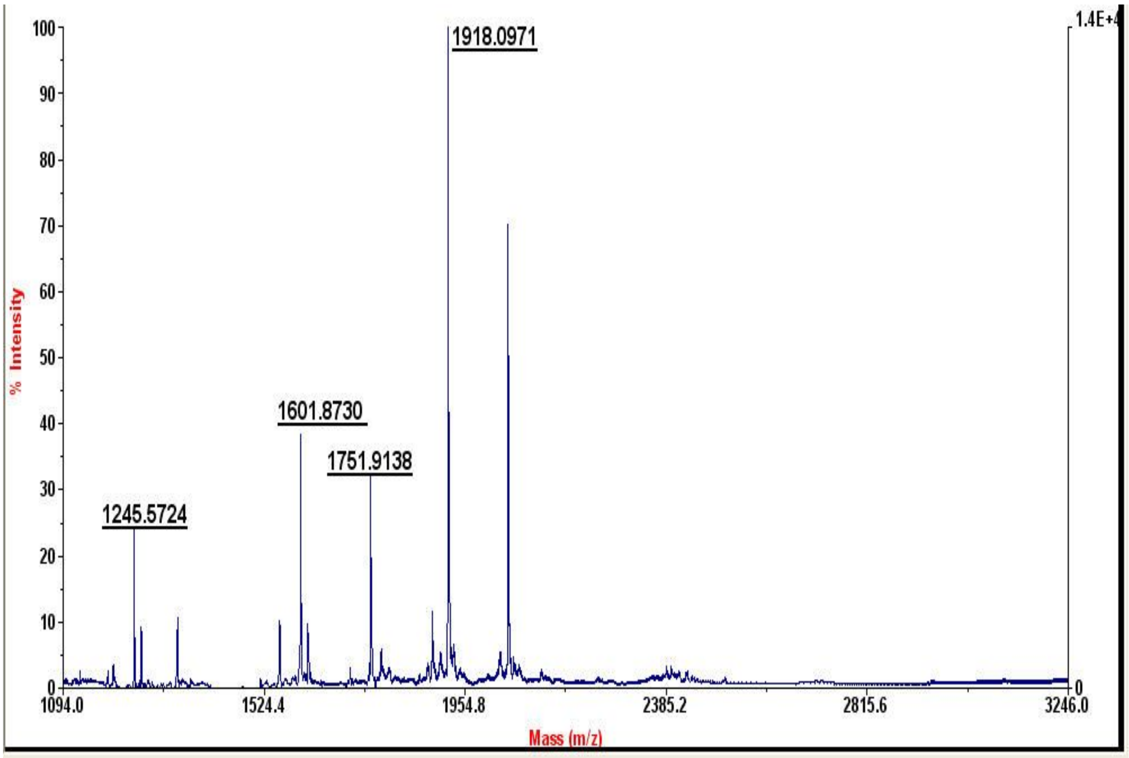
87） Kelch-like protein 15



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
58 - 67	1301.7199	1300.7126	1300.5904	0.1222	1	R.IMFTADMRER.D	2 Oxidation (M)
119 - 127	1031.5632	1030.5559	1030.4980	0.0579	0	K.FCCSFLLAK.I	
474 - 482	1226.5995	1225.5922	1225.5484	0.0438	1	K.MNYARCFHK.M	
533 - 542	1012.6160	1011.6087	1011.5349	0.0739	0	R.SGHGVTVLDK.Q	
572 - 581	1283.6409	1282.6336	1282.5322	0.1014	1	K.EDEYPRMPCK.L	Oxidation (M)

No match to: 909.0651

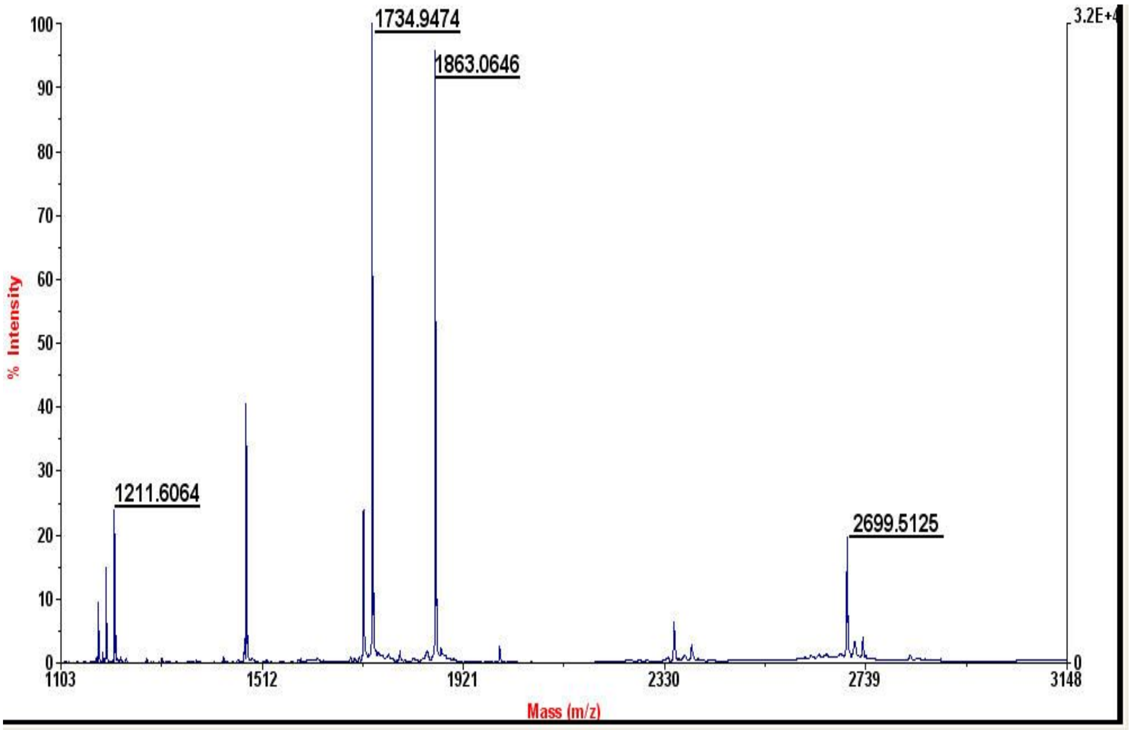
88） Rho GDP-dissociation inhibitor 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
34 - 49	1918.0971	1917.0898	1916.9327	0.1572	1	K.SIQEIQELDKDDESLR.K
128 - 134	980.4574	979.4501	979.4875	-0.0375	0	K.YIQHTYR.K
139 - 152	1601.8730	1600.8657	1600.7555	0.1102	1	K.IDKTDYMVGSYGPR.A
142 - 152	1245.5724	1244.5652	1244.5495	0.0156	0	K.TDYMVGSYGPR.A
153 - 167	1751.9138	1750.9065	1750.8301	0.0765	0	R.AEEYEFLTPVEEAPK.G

No match to: 2046.1784

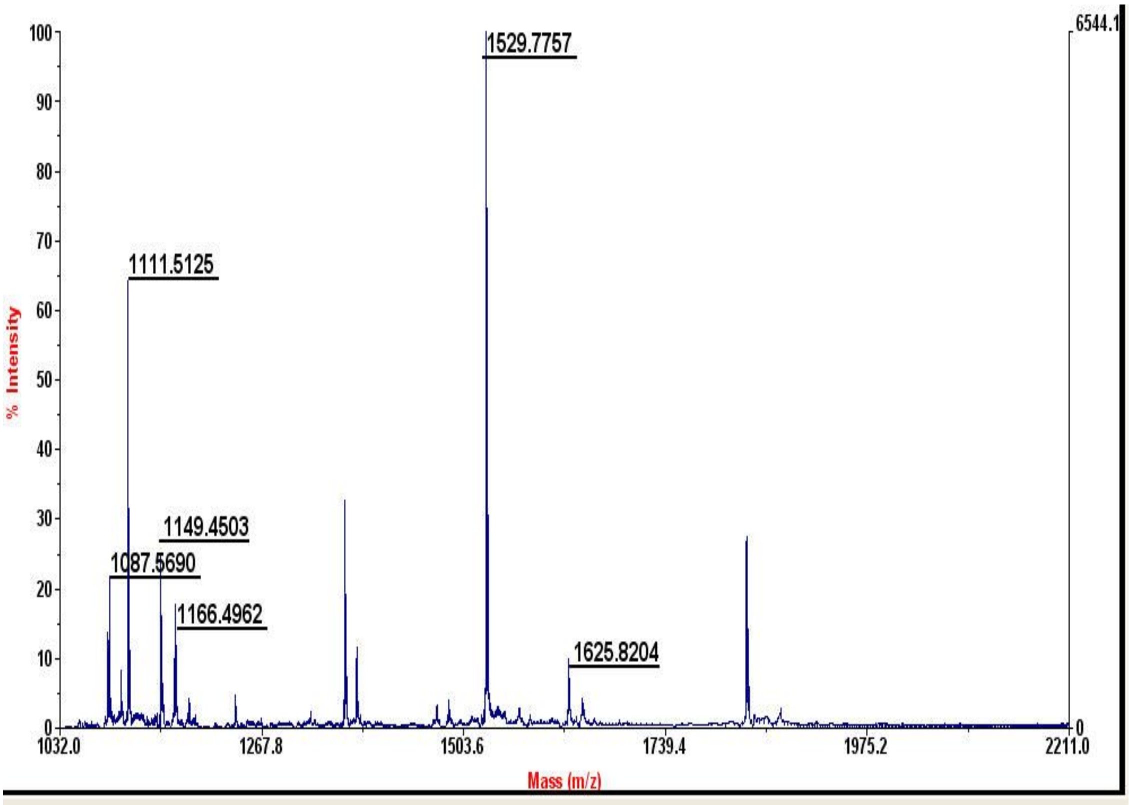
89） Peroxiredoxin-2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
68 - 91	2699.5125	2698.5052	2698.3537	0.1516	0	K.LGCEVLGVSVDSQFTHLAWINTPR.K
92 - 109	1863.0646	1862.0573	1862.0625	-0.0052	1	R.KEGGLGPLNIPLLADVTR.R
93 - 109	1734.9474	1733.9401	1733.9675	-0.0274	0	K.EGGLGPLNIPLLADVTR.R
140 - 150	1211.6064	1210.5991	1210.6669	-0.0678	0	R.QITVNDLPVGR.S

No match to: 1194.5728, 1479.6989, 1716.9480

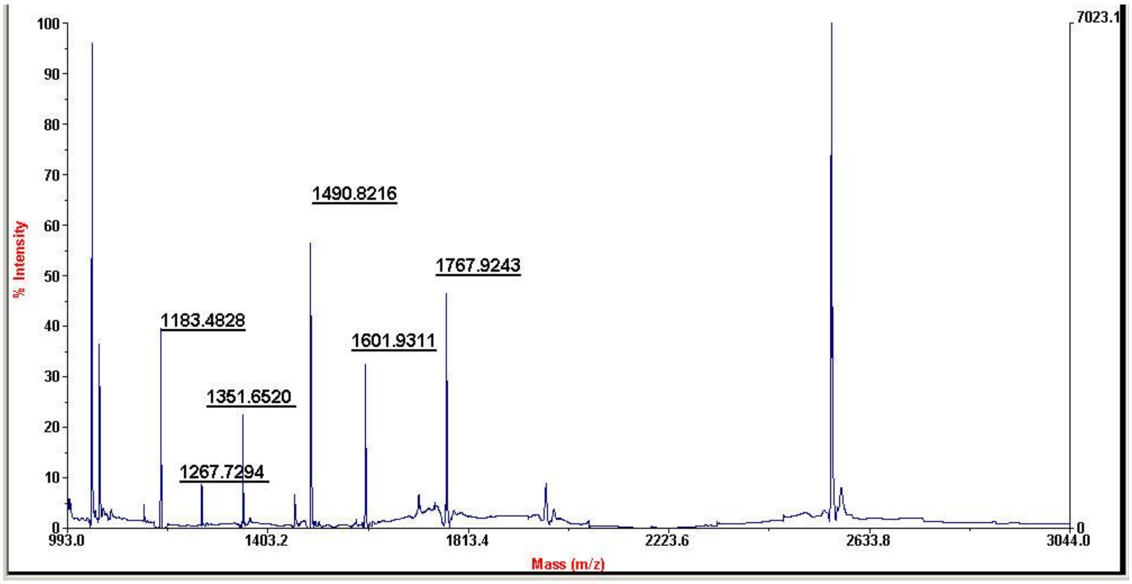
90） Cartilage homeoprotein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
49 - 58	1087.5690	1086.5618	1086.5644	-0.0026	0	K.CVQAFGPLPR.A	
104 - 113	1166.4962	1165.4889	1165.5471	-0.0582	1	R.MSPVKGMQEK.G	2 Oxidation (M)
123 - 132	1111.5125	1110.5052	1110.4975	0.0077	1	K.CDSNVSSSKK.R	
154 - 162	1149.4503	1148.4430	1148.5614	-0.1184	0	K.THYPDVYVR.E	
163 - 175	1529.7757	1528.7684	1528.8209	-0.0525	1	R.EQLALRTELTEAR.V	
244 - 257	1625.8204	1624.8131	1624.6610	0.1521	0	R.DTSSCMTPYSHSPR.T	

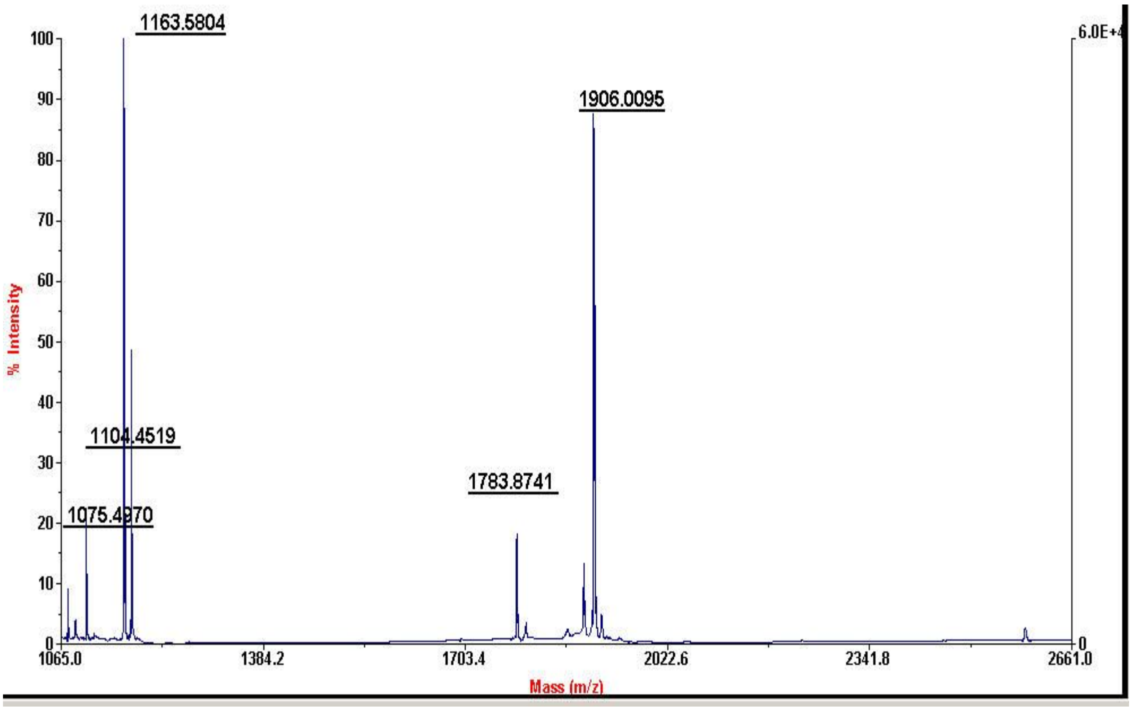
No match to: 1165.4588, 1363.6738, 1378.6817, 1833.9952

91） 6-phosphogluconolactonase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
57 - 72	1490.8216	1489.8143	1489.8252	-0.0109	0	R.ELPAAVAPAGPASLAR.W
73 - 81	1183.4828	1182.4755	1182.5128	-0.0373	0	R.WTLGFCDER.L
82 - 96	1767.9243	1766.9170	1766.8627	0.0543	0	R.LVPFDHAESTYGLYR.T
171 - 185	1601.9311	1600.9238	1600.8937	0.0302	0	K.IVAPISDSPKPPPQR.V
186 - 197	1267.7294	1266.7221	1266.7659	-0.0438	0	R.VTLTLPVLNAAR.T
236 - 246	1351.6520	1350.6447	1350.6390	0.0057	0	K.LCWFLDEAAAR.L

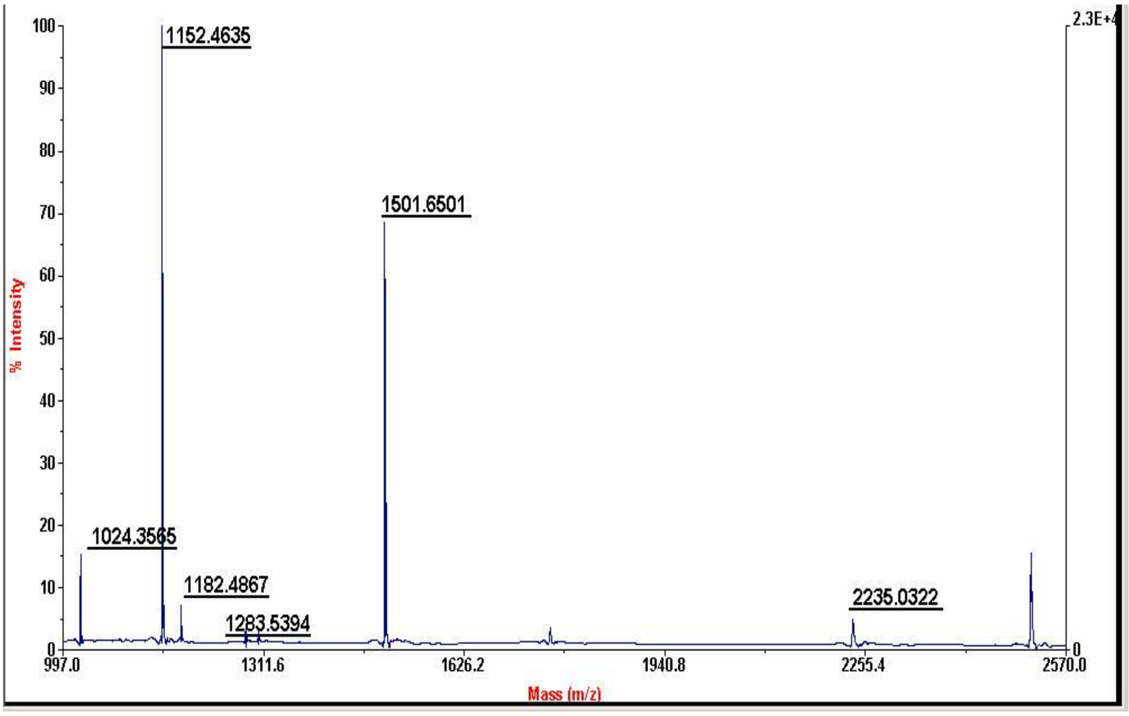
92） Heat-shock protein beta-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
13 - 20	961.3769	960.3696	960.4453	-0.0757	0	R.GPSWDPFR.D
21 - 27	960.3644	959.3572	959.4250	-0.0678	0	R.DWYPHSR.L
28 - 37	1163.5804	1162.5731	1162.6134	-0.0403	0	R.LFDQAFGLPR.L
80 - 89	1075.4970	1074.4897	1074.5669	-0.0772	0	R.QLSSGVSEIR.H
97 - 112	1783.8741	1782.8668	1782.9152	-0.0483	0	R.VSLDVNHFAPDELTVK.T
128 - 136	1104.4519	1103.4446	1103.4996	-0.0550	0	R.QDEHGYISR.C
172 - 188	1906.0095	1905.0022	1904.9843	0.0179	0	K.LATQSNEITIPVTFESR.A

No match to: 1175.5698, 1890.0156

93） Mitogen-activated protein kinase kinase kinase kinase 4



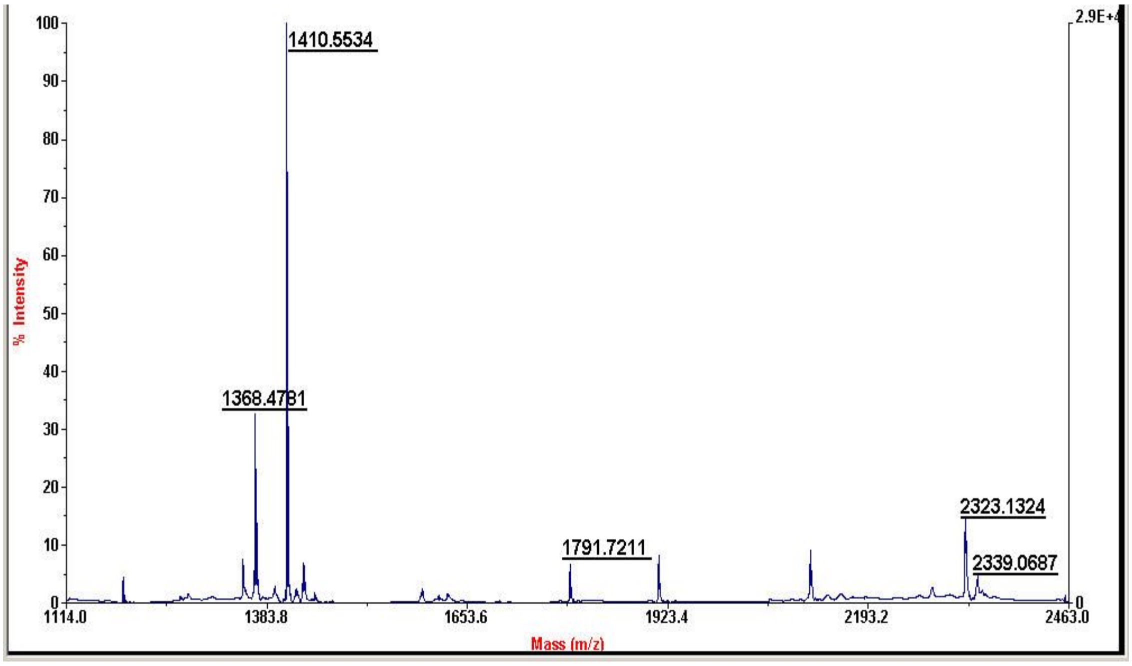
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
127 - 135	1152.4635	1151.4562	1151.5611	-0.1049	0	K.EDWIAYISR.E
373 - 382	1283.5394	1282.5321	1282.6993	-0.1672	0	R.QQLLQEQQLR.E
712 - 725	1501.6501	1500.6428	1500.7532	-0.1104	1	K.SEGSPSQRLENAVK.K
967 - 986	2235.0322	2234.0250	2234.1980	-0.1730	1	R.FQQMDVLEGLNVLVTISGKK.D

Oxidation (M)

1205 - 1212	1024.3565	1023.3493	1023.4807	-0.1315	1	K.FLCERNDK.V
1210 - 1219	1182.4867	1181.4795	1181.6192	-0.1398	1	R.NDKVFFASVR.S

No match to: 2514.3436

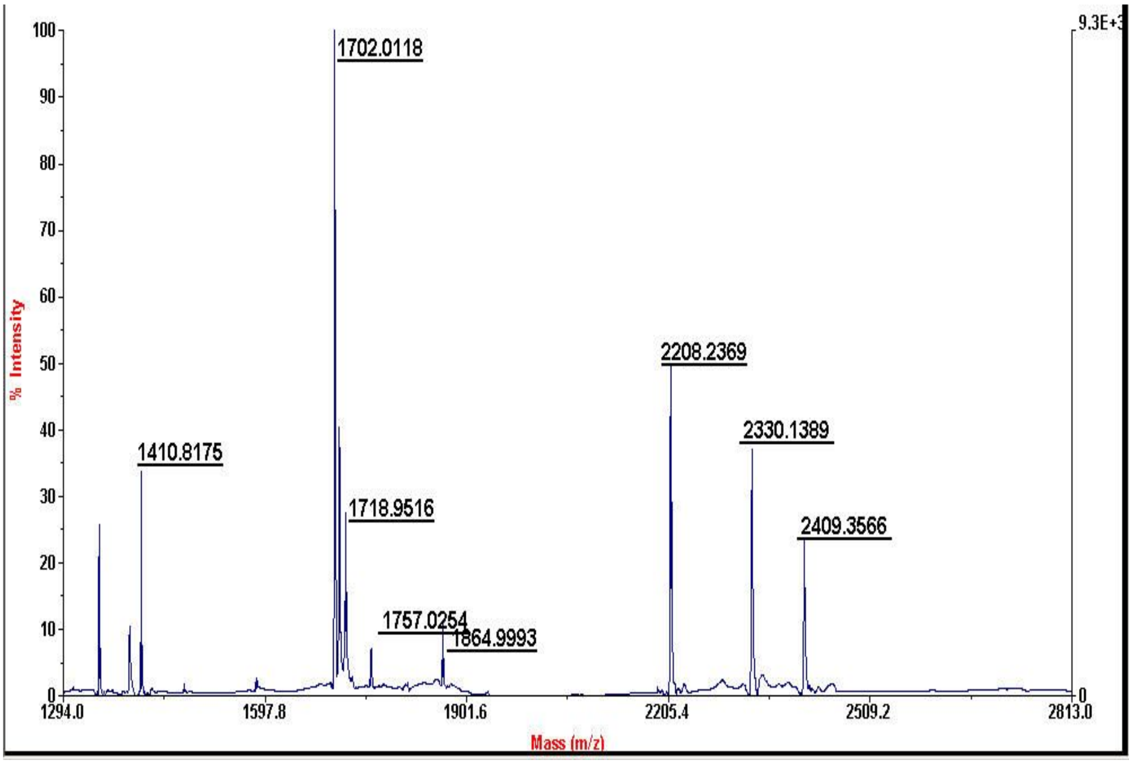
94） 14 kDa phosphohistidine phosphatase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
49 - 59	1410.5534	1409.5461	1409.6252	-0.0790	0	K.WAEYHADIYDK.V	
67 - 78	1368.4781	1367.4708	1367.5016	-0.0308	0	K.QGCDCECLGGGR.I	3
88 - 108	2323.1324	2322.1251	2322.1102	0.0149	0	K.IHVYGYSMAYGPAQHAISTEK.I	
88 - 108	2339.0687	2338.0614	2338.1051	-0.0438	0	K.IHVYGYSMAYGPAQHAISTEK.I	
Oxidation (M)							
111 - 125	1791.7211	1790.7139	1790.7787	-0.0649	1	K.AKYPDYEVTWANDGY.-	

No match to: 1190.4344, 1351.4492, 1432.5530, 1910.9165, 2115.0565

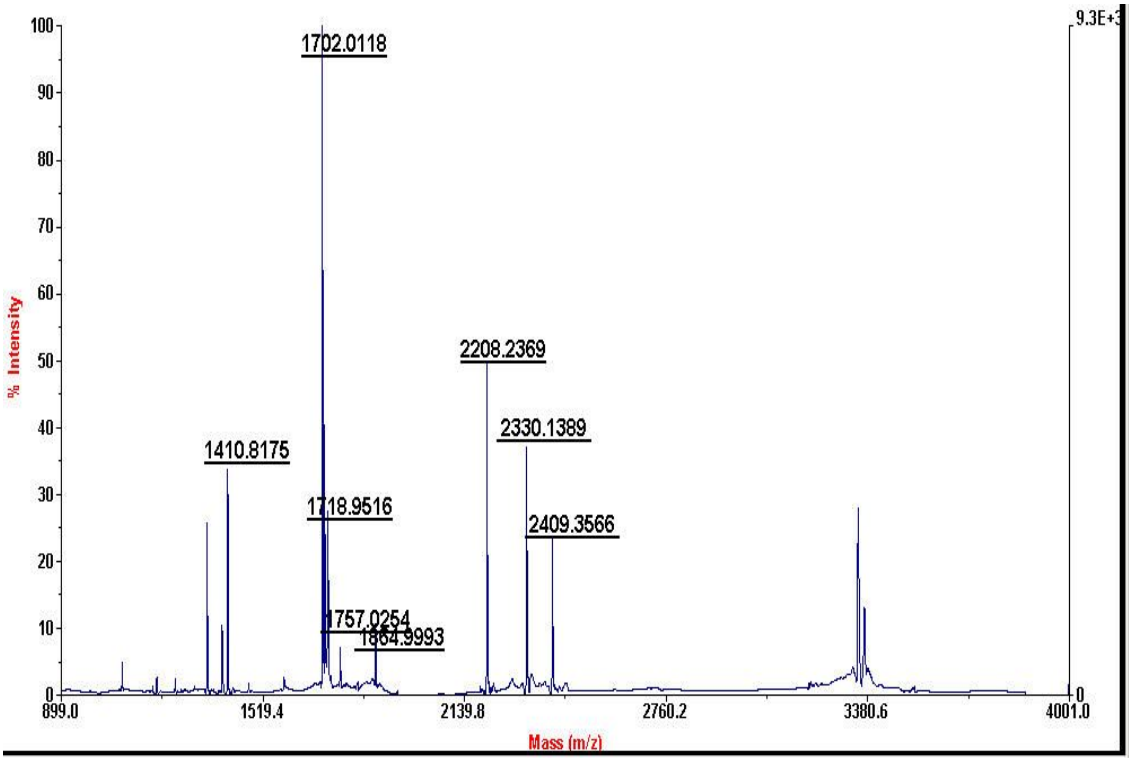
95）TBA3_HUMAN



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
65 - 79	1702.0118	1701.0045	1700.8984	0.1061	0	R.AVFVDLEPTVIDEVR.T
85 - 96	1410.8175	1409.8102	1409.7667	0.0435	0	R.QLFHPEQLITGK.E
216 - 229	1718.9516	1717.9443	1717.8747	0.0696	0	R.NLDIERPTYTNLNR.L
244 - 264	2409.3566	2408.3493	2408.2012	0.1482	0	R.FDGALNVDLTEFQTNLVPYPR.I
265 - 280	1757.0254	1756.0181	1755.9559	0.0622	0	R.IHFPLATYAPVISAEK.A
353 - 373	2208.2369	2207.2296	2207.2062	0.0234	1	K.VGINYQPPTVVPGGDLAKVQR.A
374 - 390	1864.9993	1863.9920	1863.8971	0.0949	0	R.AVCMLSNTTAIAEAWAR.L
403 - 422	2330.1389	2329.1316	2329.0109	0.1208	0	R.AFVHWYVGEGMEEGEFSEAR.E

No match to: 1347.7789, 1393.7947, 1708.9361, 3350.8559

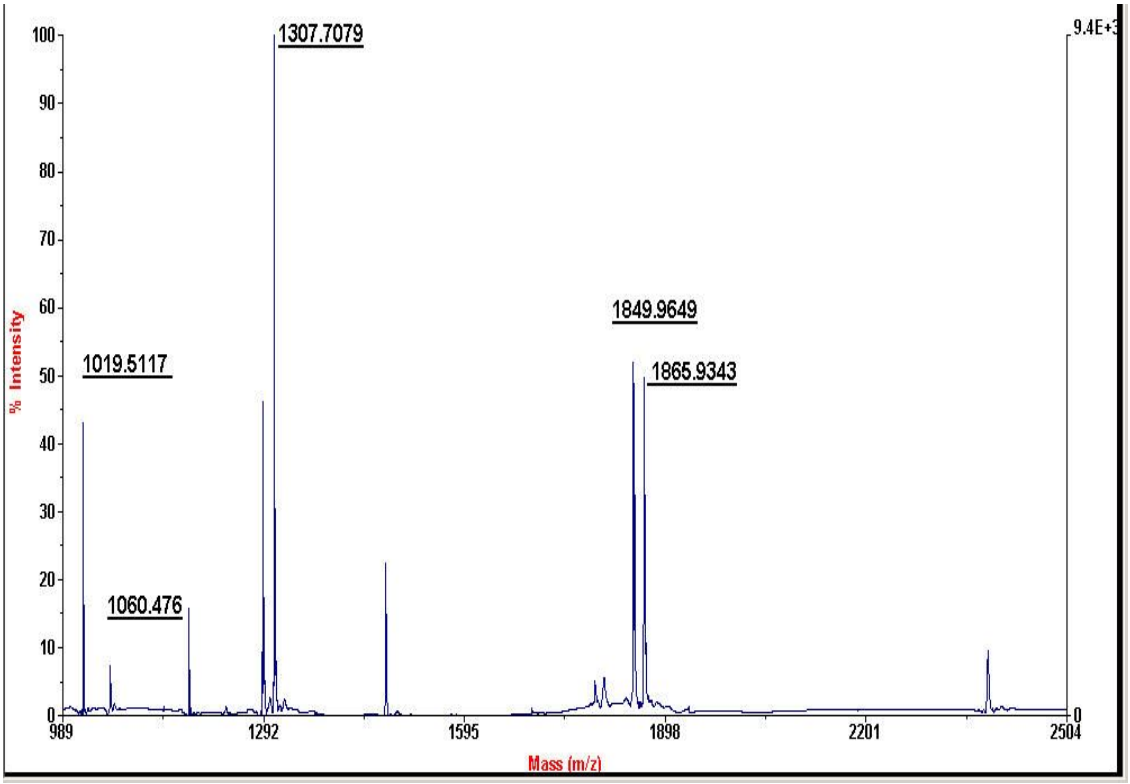
96） Tubulin alpha-ubiquitous chain



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
65 - 79	1702.0118	1701.0045	1700.8984	0.1061	0	R.AVFVDLEPTVIDEVR.T
85 - 96	1410.8175	1409.8102	1409.7667	0.0435	0	R.QLFHPEQLITGK.E
216 - 229	1718.9516	1717.9443	1717.8747	0.0696	0	R.NLDIERPTYTNLNR.L
244 - 264	2409.3566	2408.3493	2408.2012	0.1482	0	R.FDGALNVDLTEFQTNLVPYPR.I
265 - 280	1757.0254	1756.0181	1755.9559	0.0622	0	R.IHFPLATYAPVISAEK.A
353 - 373	2208.2369	2207.2296	2207.2062	0.0234	1	K.VGINYQPPTVVPGGDLAKVQR.A
374 - 390	1864.9993	1863.9920	1863.8971	0.0949	0	R.AVCMLSNTTAIAEAWAR.L
403 - 422	2330.1389	2329.1316	2329.0109	0.1208	0	R.AFVHWYVGEGMEEGEFSEAR.E

No match to: 1347.7789, 1393.7947, 1708.9361, 3350.8559

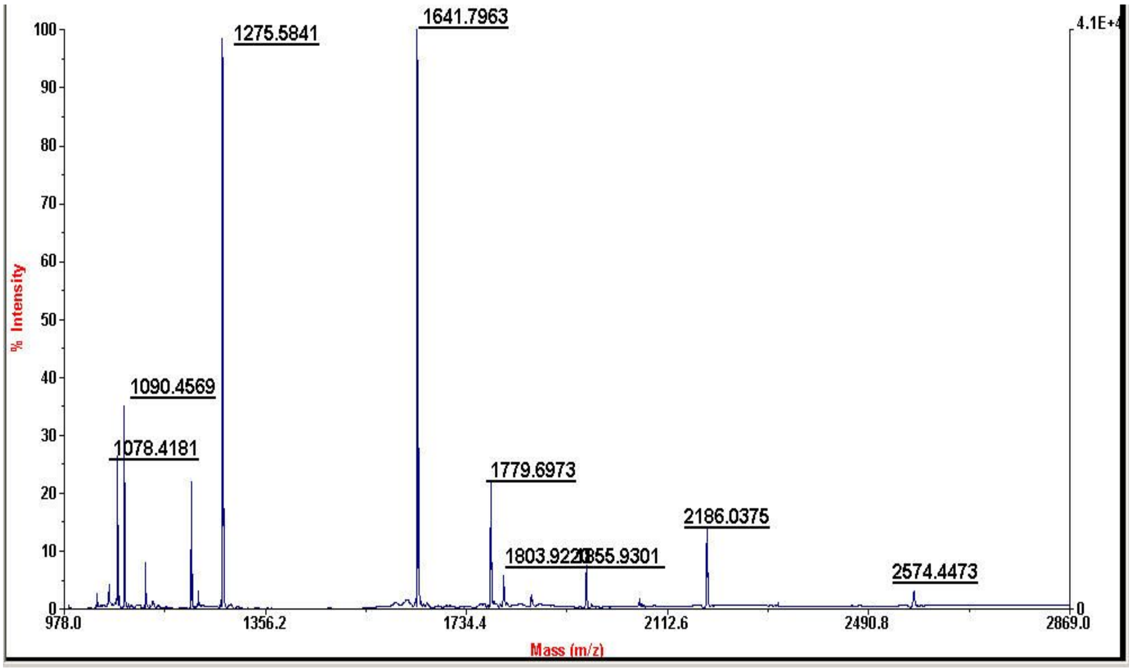
97） Protein S100-A11



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
4 - 12	1019.5117	1018.5044	1018.4931	0.0113	0	K.ISSPTETER.C	
13 - 23	1307.7079	1306.7007	1306.6955	0.0052	0	R.CIESLIAVFQK.Y	
28 - 36	1060.4760	1059.4687	1059.4873	-0.0185	0	K.DGYNYTLSK.T	
37 - 52	1849.9649	1848.9576	1848.8967	0.0609	0	K.TEFLSFMNTELAAFTK.N	
37 - 52	1865.9343	1864.9270	1864.8916	0.0353	0	K.TEFLSFMNTELAAFTK.N	Oxidation (M)

No match to: 1179.6106, 1290.6898, 1475.7855, 2384.0918

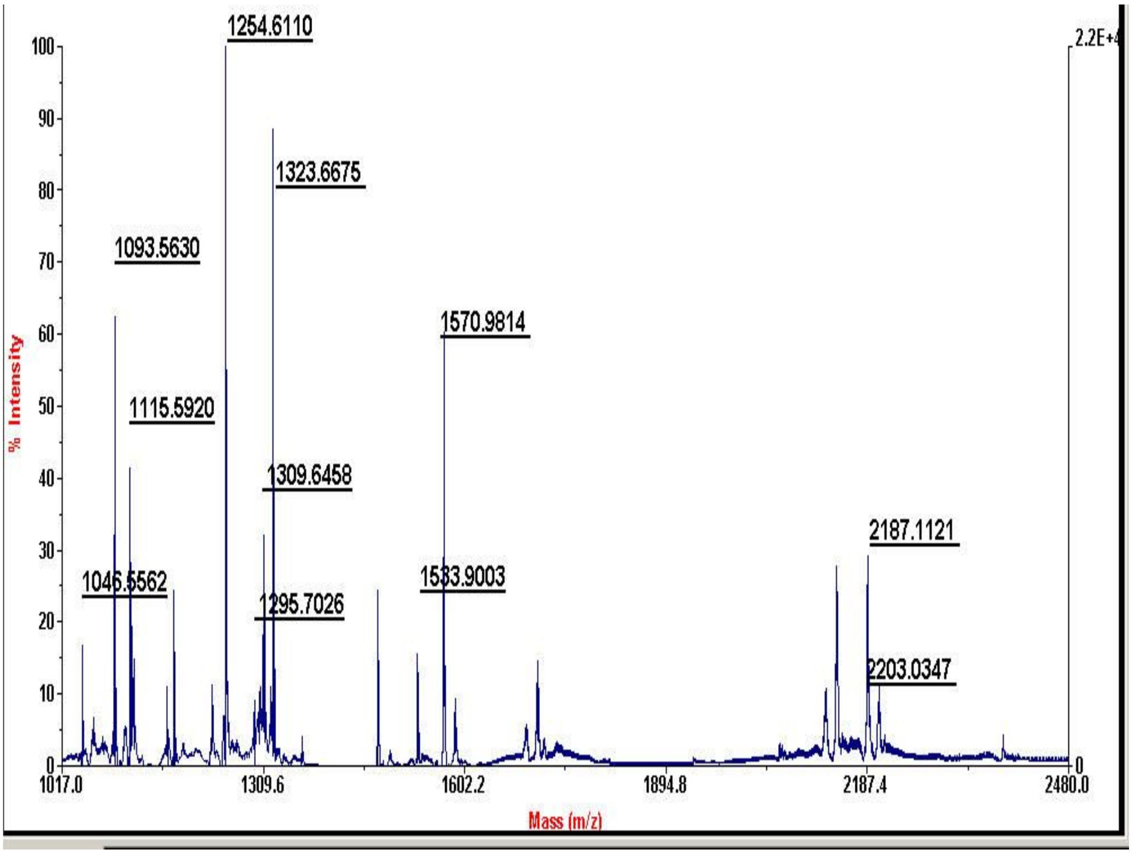
98） Alpha-1-antiproteinase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 49	1779.6973	1778.6900	1778.7608	-0.0708	0	K.TDTSHHDQDHPTFNK.I
50 - 63	1641.7963	1640.7890	1640.8562	-0.0671	0	K.ITPNLAEFAFSLYR.Q
126 - 149	2574.4473	2573.4400	2573.3336	0.1063	0	R.TLNQPDSQLQLTTGNGLFLSEGLK.L
161 - 179	2186.0375	2185.0302	2185.0327	-0.0024	1	K.LYHSEAFTVNFGDTEEAKK.Q
216 - 225	1275.5841	1274.5768	1274.6771	-0.1003	1	K.GKWERPFEVK.D
218 - 225	1090.4569	1089.4496	1089.5607	-0.1111	0	K.WERPFEVK.D
284 - 298	1803.9220	1802.9147	1802.9526	-0.0379	0	K.LQHLENELTHDIITK.F
299 - 305	922.3266	921.3193	921.4192	-0.0999	0	K.FLENEDR.R
299 - 306	1078.4181	1077.4108	1077.5203	-0.1095	1	K.FLENEDRR.S
390 - 404	1855.9301	1854.9228	1854.9702	-0.0473	0	K.FNKPFVFLMIEQNTK.S

No match to: 1130.4992, 1143.5468, 1216.5306, 1229.5192, 1958.9340

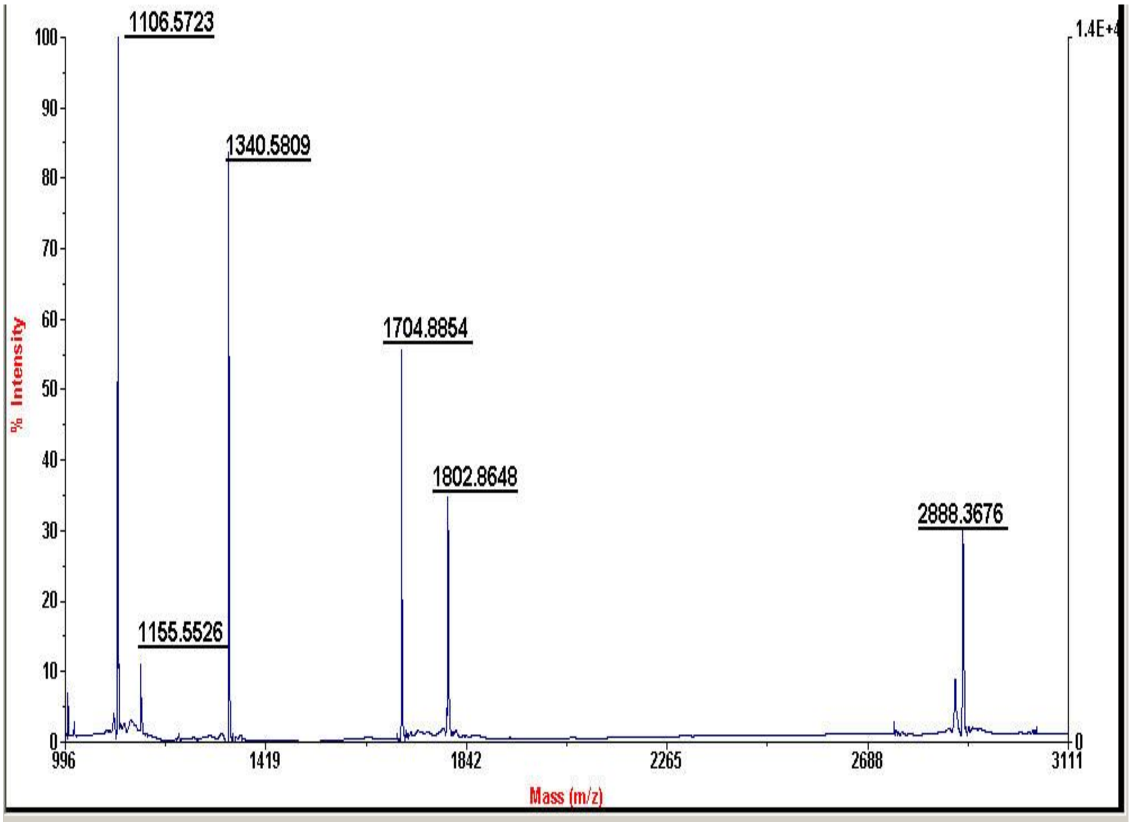
99）Vimentin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
105 - 113	1115.5920	1114.5848	1114.5618	0.0229	0	K.VELQELNDR.F
146 - 155	1254.6110	1253.6037	1253.5598	0.0439	0	R.LGDLYEEEMR.E
189 - 196	1046.5562	1045.5489	1045.5226	0.0263	0	K.LQEEMLQR.E
197 - 207	1323.6675	1322.6602	1322.6102	0.0500	0	R.EEAENTLQSFR.Q
224 - 236	1533.9003	1532.8930	1532.8449	0.0480	1	K.VESLQEEIAFLKK.L
283 - 292	1309.6458	1308.6385	1308.5986	0.0399	0	K.NLQEAEEWYK.S
295 - 304	1093.5630	1092.5557	1092.5199	0.0358	0	K.FADLSEAANR.N
346 - 364	2187.1121	2186.1048	2185.9585	0.1463	0	R.EMEENFAVEAANYQDTIGR.L
346 - 364	2203.0347	2202.0274	2201.9534	0.0740	0	R.EMEENFAVEAANYQDTIGR.L
Oxidation (M)						
391 - 401	1295.7026	1294.6953	1294.6591	0.0362	0	K.MALDIEIATYR.K
411 - 424	1570.9814	1569.9741	1569.8878	0.0863	0	R.ISLPLPNFSSLNLR.E

No match to: 1179.6232, 1475.8160, 1707.8506

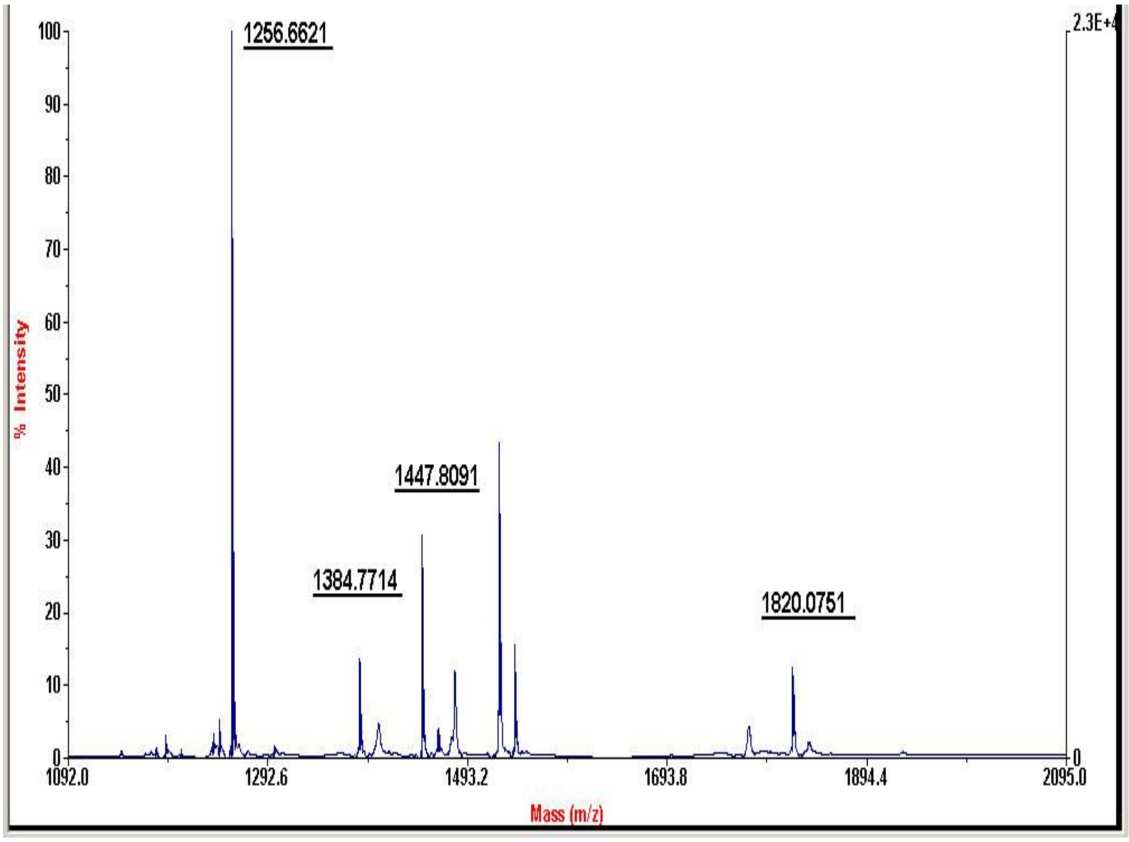
101 ） Annexin A5



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 18	1340.5809	1339.5737	1339.6044	-0.0307	0	R.GTVTDFPGFDER.A
30 - 45	1704.8854	1703.8782	1703.8941	-0.0159	0	K.GLGTDEESILTLLTSR.S
127 - 151	2888.3676	2887.3603	2887.2307	0.1296	0	K.QVYEEEYGSSLEDDVVGDTSGYYQR.M
194 - 201	954.5269	953.5196	953.5334	-0.0138	0	K.FITIFGTR.S
213 - 227	1802.8648	1801.8575	1801.8556	0.0019	0	K.YMTISGFQIEETIDR.E
261 - 271	1155.5526	1154.5454	1154.5680	-0.0226	0	K.GAGTDDHTLIR.V
277 - 285	1106.5723	1105.5651	1105.5767	-0.0117	0	R.SEIDLFNIR.K

No match to: 909.0362, 911.0325, 946.9072

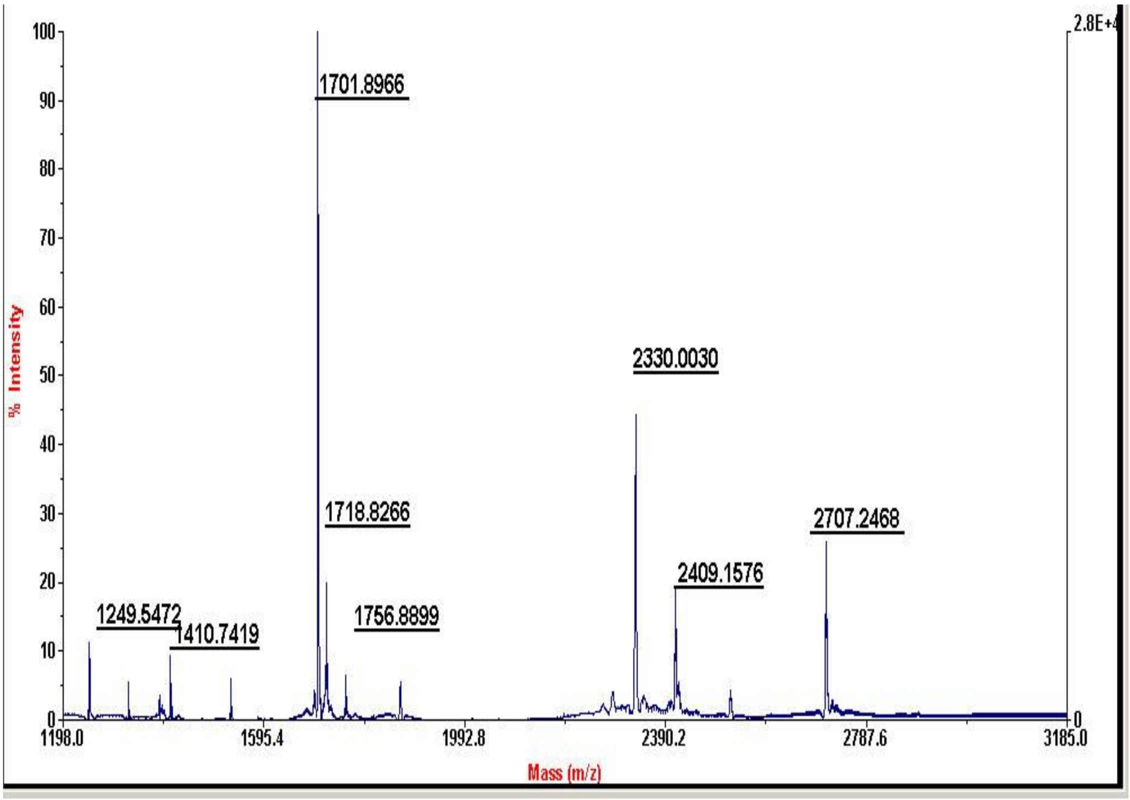
102 ） 14-3-3 protein epsilon



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
30 - 42	1447.8091	1446.8018	1446.7024	0.0994	0	K.VAGMDVELTVEER.N
124 - 130	906.4573	905.4501	905.4177	0.0323	1	K.MKGDYHR.Y
124 - 130	922.4443	921.4370	921.4127	0.0243	1	K.MKGDYHR.Y Oxidation (M)
131 - 141	1256.6621	1255.6548	1255.5833	0.0715	0	R.YLAEFATGNDR.K
131 - 142	1384.7714	1383.7642	1383.6782	0.0859	1	R.YLAEFATGNDRK.E
154 - 170	1820.0751	1819.0679	1818.9298	0.1381	0	K.AASDIAMTELPPTHPIR.L

No match to: 1524.8188, 1540.7845

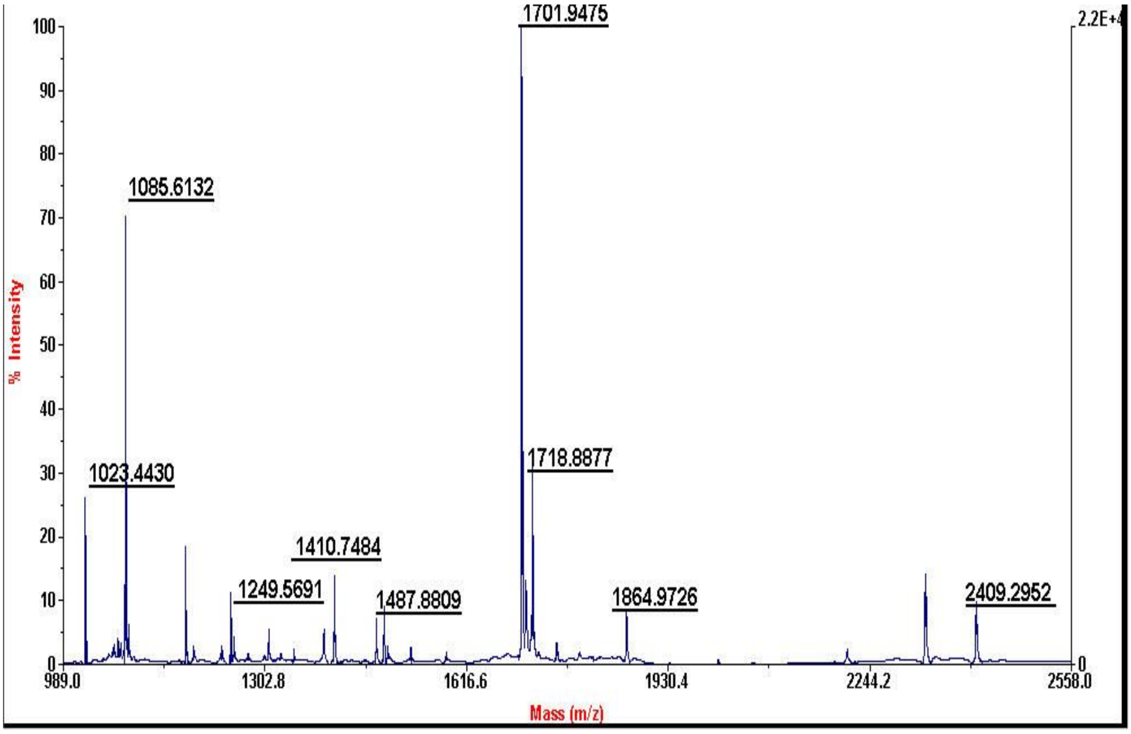
103 ） Tubulin alpha-6 chain



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
65 - 79	1701.8966	1700.8893	1700.8984	-0.0091	0	R.AVFVDLEPTVIDEVR.T	
85 - 96	1410.7419	1409.7346	1409.7667	-0.0321	0	R.QLFHPEQLITGK.E	
216 - 229	1718.8266	1717.8193	1717.8747	-0.0554	0	R.NLDIERPTYTNLNR.L	
244 - 264	2409.1576	2408.1503	2408.2012	-0.0509	0	R.FDGALNVDLTEFQTNLVPYPR.I	
265 - 280	1756.8899	1755.8826	1755.9559	-0.0733	0	R.IHFPLATYAPVISAEK.A	
281 - 304	2707.2468	2706.2395	2706.2781	-0.0386	0	K.AYHEQLTVAEITNACFEPANQMVK.C	
312 - 320	1249.5472	1248.5399	1248.5453	-0.0054	0	K.YMACCLLYR.G	2
403 - 422	2330.0030	2328.9957	2329.0109	-0.0151	0	R.AFVHWYVGEGMEEGEFSEAR.E	

No match to: 915.4490, 1326.7436, 1388.6606, 1529.7669, 1864.8819, 2286.1939

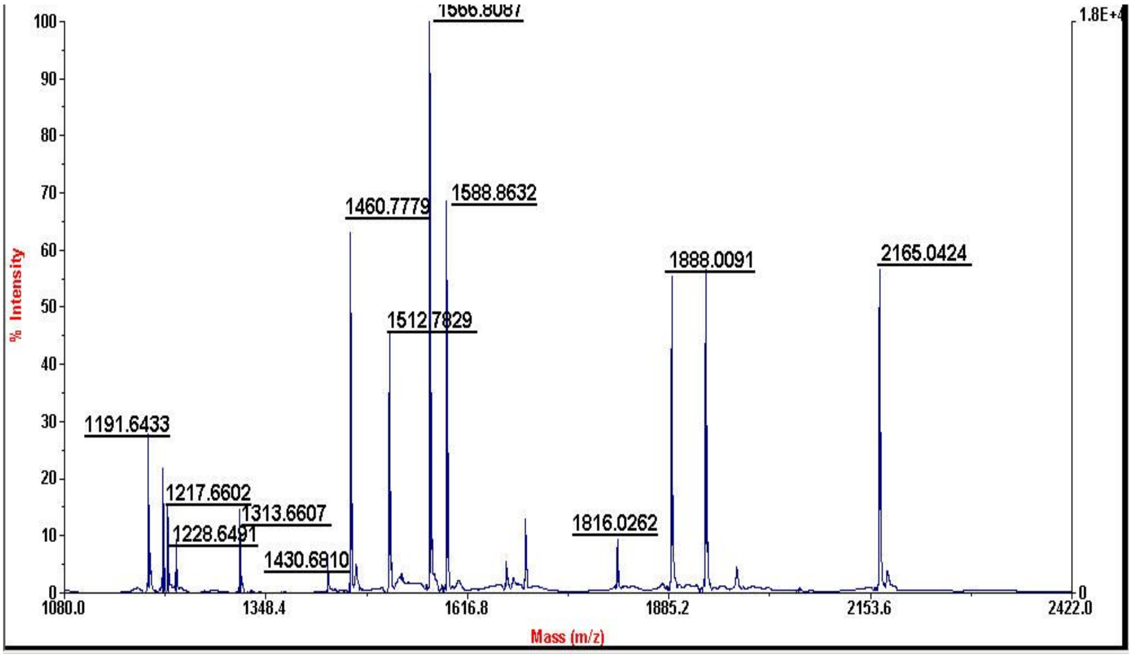
104 ） Tubulin alpha-ubiquitous chain



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
65 - 79	1701.9475	1700.9402	1700.8984	0.0418	0	R.AVFVDLEPTVIDEVR.T
85 - 96	1410.7484	1409.7411	1409.7667	-0.0255	0	R.QLFHPEQLITGK.E
97 - 105	1023.4430	1022.4357	1022.4417	-0.0060	0	K.EDAANNYAR.G
113 - 121	1085.6132	1084.6060	1084.6128	-0.0068	0	K.EIIDLVLDR.I
216 - 229	1718.8877	1717.8804	1717.8747	0.0057	0	R.NLDIERPTYTNLNR.L
230 - 243	1487.8809	1486.8736	1486.8719	0.0018	0	R.LISQIVSSITASLR.F
244 - 264	2409.2952	2408.2879	2408.2012	0.0868	0	R.FDGALNVDLTEFQTNLVPYPR.I
265 - 280	1756.9540	1755.9467	1755.9559	-0.0092	0	R.IHFPLATYAPVISAEK.A
312 - 320	1249.5691	1248.5619	1248.5453	0.0165	0	K.YMACCLLYR.G 2
374 - 390	1864.9726	1863.9654	1863.8971	0.0683	0	R.AVCMLSNTTAIAEAWAR.L
403 - 422	2330.1230	2329.1157	2329.0109	0.1049	0	R.AFVHWYVGEGMEEGEFSEAR.E

No match to: 915.4555, 1179.6035, 1307.6867, 1475.7585, 1708.8631

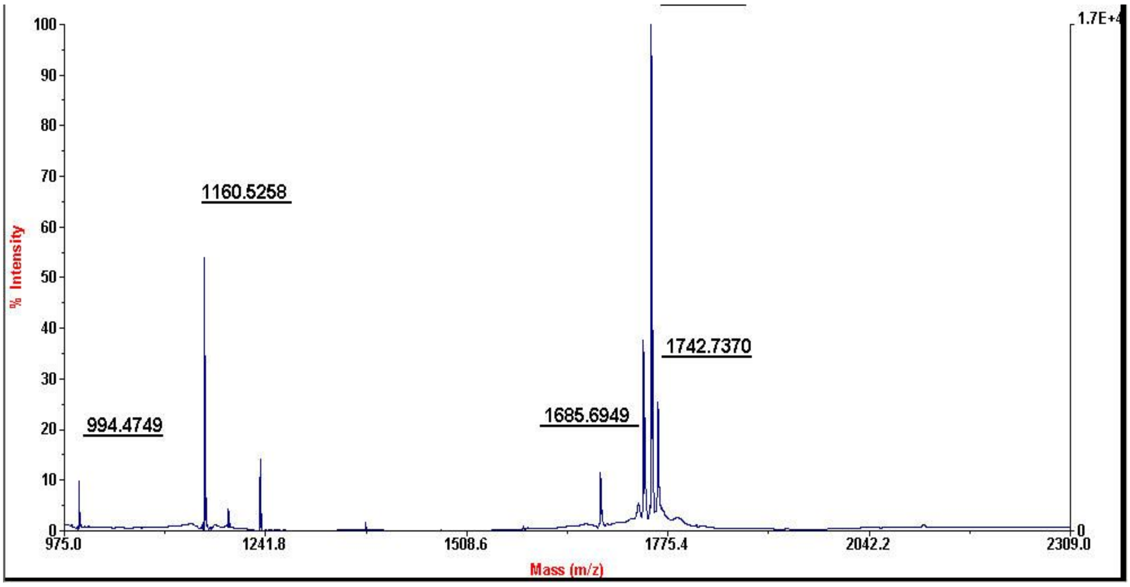
105 ） 78 kDa glucose-regulated protein precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
50 - 60	1228.6491	1227.6418	1227.6207	0.0211	0	R.VEIIANDQGNR.I
61 - 74	1566.8087	1565.8015	1565.7725	0.0289	0	R.ITPSYVAFTPEGER.L
102 - 113	1430.6810	1429.6737	1429.6837	-0.0100	0	R.TWNDPSVQQDIK.F
165 - 181	1888.0091	1887.0018	1886.9638	0.0380	0	K.VTHAVVTVPAYFNDAQR.Q
186 - 197	1217.6602	1216.6529	1216.6234	0.0296	0	K.DAGTIAGLNVMR.I
198 - 214	1816.0262	1815.0189	1814.9890	0.0299	1	R.IINEPTAAAIAYGLDKR.E
298 - 306	997.5420	996.5347	996.5101	0.0246	0	R.ALSSQHQAR.I
307 - 324	2165.0424	2164.0351	2163.9847	0.0503	0	R.IEIESFYEGEDFSETLTR.A
325 - 336	1512.7829	1511.7756	1511.7442	0.0314	1	R.AKFEELNMDLFR.S
327 - 336	1313.6607	1312.6534	1312.6121	0.0413	0	K.FEELNMDLFR.S
353 - 367	1588.8632	1587.8559	1587.8467	0.0091	1	K.KSDIDEIVLVGGSTR.I
354 - 367	1460.7779	1459.7706	1459.7518	0.0188	0	K.SDIDEIVLVGGSTR.I
465 - 474	1191.6433	1190.6360	1190.6295	0.0065	0	K.VYEGERPLTK.D
475 - 492	1934.0573	1933.0501	1933.0057	0.0443	0	K.DNHLLGTFDLTGIPPAPR.G
524 - 532	1074.5835	1073.5762	1073.5465	0.0297	0	K.ITITNDQNR.L
533 - 540	986.5365	985.5293	985.5080	0.0213	0	R.LTPEEIER.M

No match to: 1024.5785, 1211.6066, 1693.8921

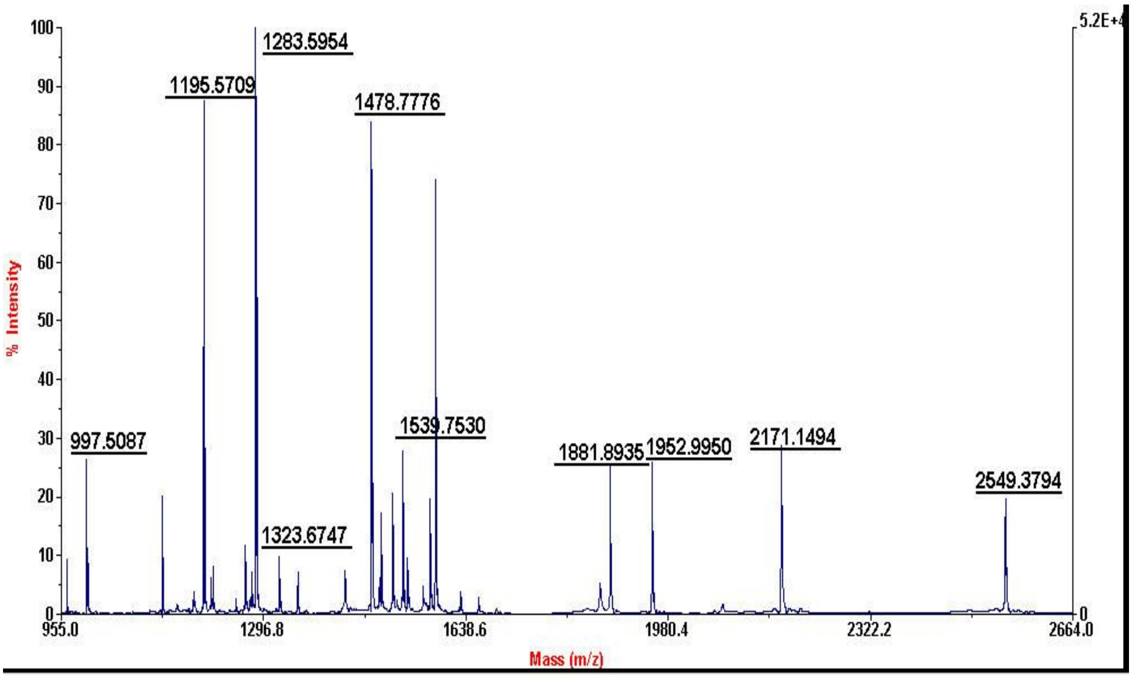
106 ） Alpha-1-acid glycoprotein 1 precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
43 - 51	1160.5258	1159.5186	1159.5814	-0.0628	0	K.WFYIASAFR.N
74 - 81	994.4749	993.4677	993.5131	-0.0454	0	K.TEDTIFLR.E
109 - 123	1752.8589	1751.8516	1751.9471	-0.0954	0	R.YVGGQEHFAHLLILR.D
154 - 167	1685.6949	1684.6877	1684.7766	-0.0890	0	K.EQLGEFYEALDCLR.I
154 - 167	1742.7370	1741.7297	1741.7981	-0.0684	0	K.EQLGEFYEALDCLR.I

No match to: 1192.5193, 1234.6381, 1374.5800, 1761.6782

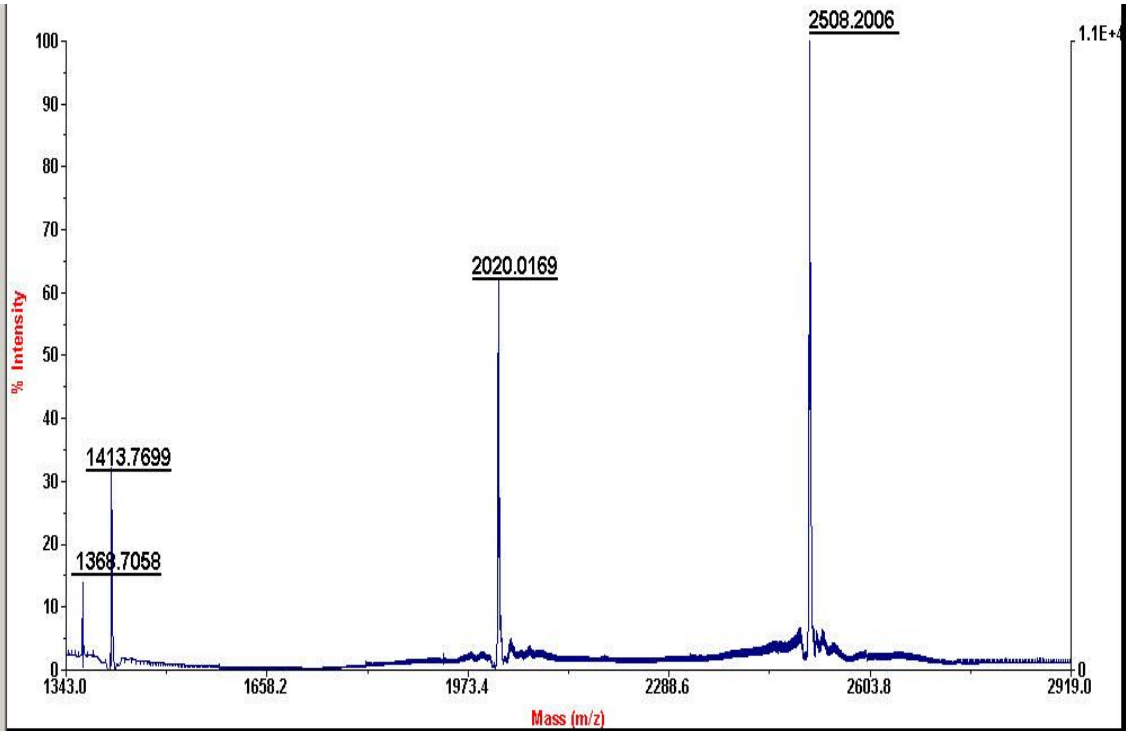
107 ） Serotransferrin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
62 - 69	997.5087	996.5014	996.4698	0.0315	0	K.ASYLDCIR.A	
122 - 132	1323.6747	1322.6674	1322.6401	0.0273	1	K.KDSGFQMNQLR.G	
123 - 132	1195.5709	1194.5636	1194.5451	0.0185	0	K.DSGFQMNQLR.G	
144 - 162	2171.1494	2170.1421	2170.0881	0.0540	0	R.SAGWNIPIGLLYCDLPEPR.K	
237 - 251	1881.8935	1880.8862	1880.8687	0.0176	1	K.ADRDQYELLCLDNTR.K	
240 - 251	1539.7530	1538.7457	1538.7035	0.0422	0	R.DQYELLCLDNTR.K	
252 - 273	2549.3794	2548.3721	2548.2856	0.0866	1	R.KPVDEYKDCHLAQVPSHTVVAR.S	
332 - 343	1478.7776	1477.7704	1477.7275	0.0429	0	K.MYLGYEYVTAIR.N	
332 - 343	1494.7339	1493.7266	1493.7224	0.0042	0	K.MYLGYEYVTAIR.N	Oxidation (M)
454 - 466	1434.8600	1433.8527	1433.7150	0.1377	1	K.SASDLTWDNLKGK.K	
495 - 508	1577.7146	1576.7073	1576.6503	0.0569	0	R.FDEFFSEGCAPGSK.K	
531 - 541	1283.5954	1282.5882	1282.5618	0.0264	0	K.EGYYGYTGAFR.C	
572 - 587	1952.9950	1951.9877	1951.9309	0.0568	1	K.NLNEKDYELLCLDGTR.K	
577 - 587	1354.6696	1353.6623	1353.6234	0.0389	0	K.DYELLCLDGTR.K	
588 - 600	1586.8035	1585.7962	1585.7671	0.0292	0	R.KPVEEYANCHLAR.A	
601 - 609	964.5322	963.5249	963.5250	-0.0000	0	R.APNHAVVTR.K	
613 - 621	1125.6014	1124.5941	1124.6124	-0.0183	1	K.EACVHKILR.Q	
684 - 696	1531.7133	1530.7060	1530.6806	0.0254	0	K.CSTSSLLEACTFR.R	2

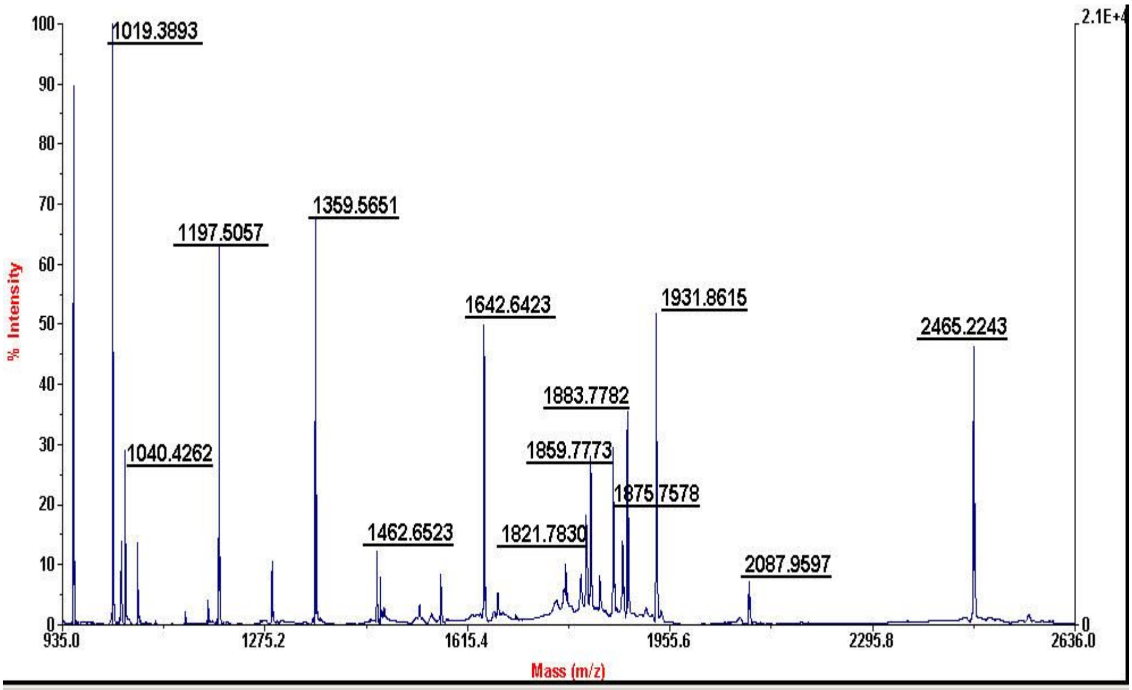
No match to: 1265.5937, 1514.7012

108 ） Transketolase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
175 - 186	1368.7058	1367.6985	1367.7772	-0.0787	0	K.LDNLVAILDINR.L
284 - 302	2020.0169	2019.0097	2019.0636	-0.0540	0	K.ILATPPQEDAPSVDIANIR.M
472 - 493	2508.2006	2507.1933	2507.2040	-0.0107	0	R.TSRPENAIIYNNNEDFQVGQAK.V
531 - 542	1413.7699	1412.7626	1412.8027	-0.0401	0	R.VLDPFTIKPLDR.K

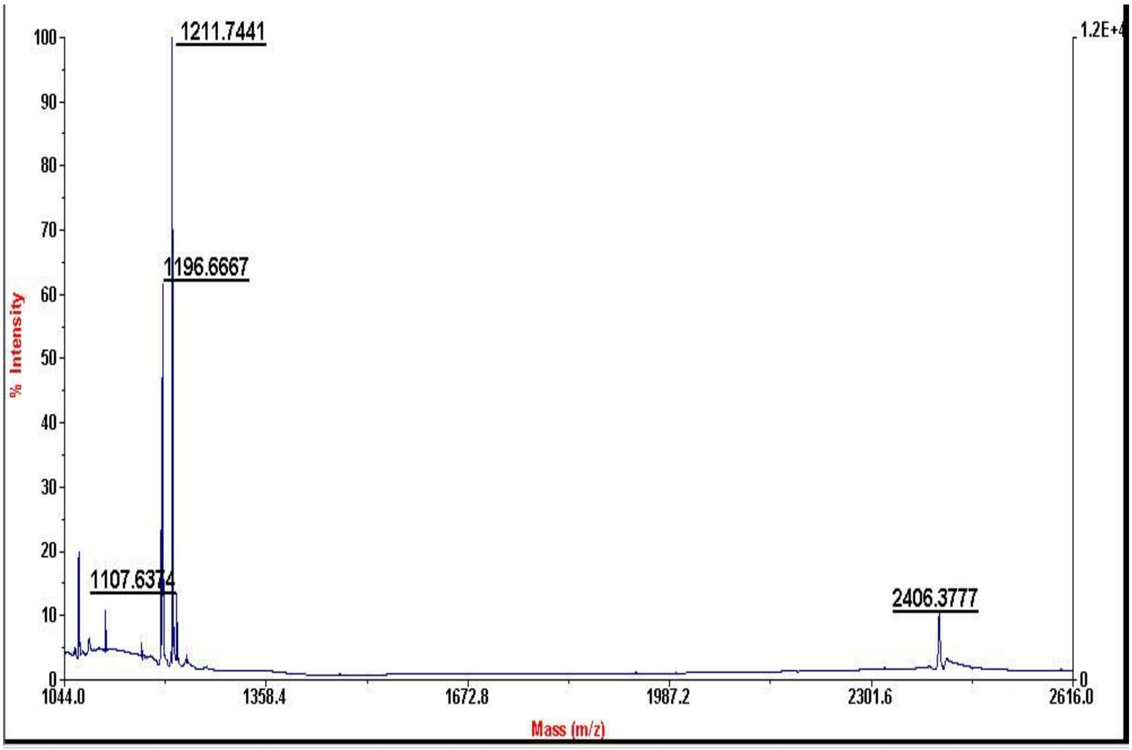
109 ） Pyruvate kinase isozymes M1/M2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 56	1359.5651	1358.5579	1358.6976	-0.1397	0	R.NTGIICTIGPASR.S
74 - 89	1883.7782	1882.7709	1882.8962	-0.1252	0	R.LNFSHGTHEYHAETIK.N
93 - 115	2465.2243	2464.2170	2464.2849	-0.0679	0	R.TATESFASDPILYRPVAVALDTK.G
142 - 151	1197.5057	1196.4984	1196.5747	-0.0762	0	K.ITLDNAYMEK.C
174 - 186	1462.6523	1461.6451	1461.8078	-0.1628	0	K.IYVDDGLISLQVK.Q
231 - 246	1859.7773	1858.7701	1858.8923	-0.1222	0	K.FGVEQDVDMVFASFIR.K
231 - 246	1875.7578	1874.7505	1874.8872	-0.1367	0	K.FGVEQDVDMVFASFIR.K Oxidation (M)
248 - 256	1040.4262	1039.4189	1039.5410	-0.1221	1	K.ASDVHEVRK.V
271 - 278	953.3509	952.3436	952.4726	-0.1290	0	K.IENHEGVR.R
279 - 294	1821.7830	1820.7757	1820.9090	-0.1333	1	R.RFDEILEASDGIMVAR.G
368 - 376	1019.3893	1018.3820	1018.5083	-0.1263	0	K.GDYPLEAVR.M
384 - 399	1931.8615	1930.8542	1930.9788	-0.1246	0	R.EAEAAIYHLQLFEELR.R
384 - 400	2087.9597	2086.9524	2087.0799	-0.1275	1	R.EAEAAIYHLQLFEELRR.L
476 - 489	1642.6423	1641.6350	1641.7634	-0.1284	0	K.DPVQEAWAEDVDLR.V

No match to: 1033.4619, 1061.3772, 1286.5581, 1814.9551

110 ） Peroxiredoxin-1

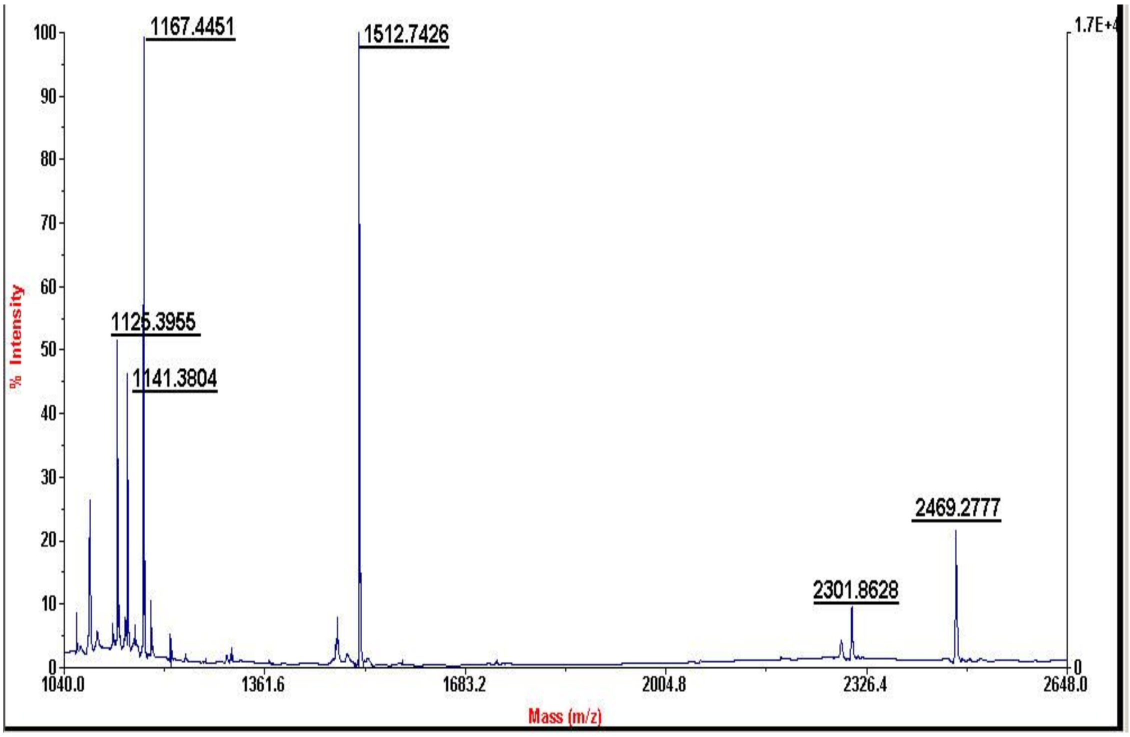


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

8 - 16	980.5554	979.5481	979.5239	0.0242	0	K.IGHPAPNFK.A
111 - 120	1107.6374	1106.6301	1106.5971	0.0330	0	R.TIAQDYGVLK.A
141 - 151	1211.7441	1210.7368	1210.6669	0.0699	0	R.QITVNDLPVGR.S
159 - 168	1196.6667	1195.6594	1195.6237	0.0358	0	R.LVQAFQFTDK.H
169 - 190	2406.3777	2405.3705	2405.1797	0.1907	0	K.HGEVCPAGWKPGSDTIKPDVQK.S

No match to: 909.2417, 1002.5432, 1066.1162, 1194.6845, 1218.6968

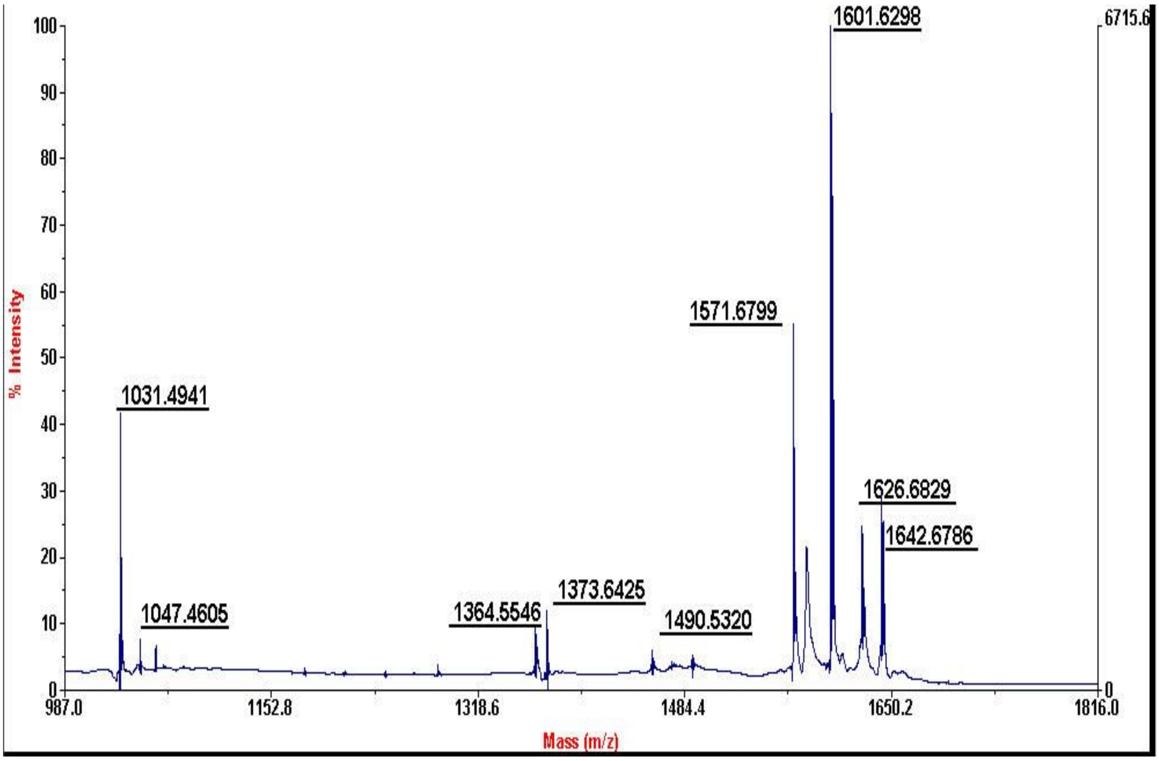
111 ） Flavin reductase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
40 - 63	2469.2777	2468.2704	2468.3022	-0.0318	0	R.LPSEGPRPAHVVVGDVLQAADVDK.T
64 - 78	1512.7426	1511.7353	1511.8671	-0.1318	0	K.TVAGQDAVIVLLGTR.N
125 - 134	1167.4451	1166.4378	1166.6044	-0.1666	0	R.LQAVTDDHIR.M
179 - 187	1125.3955	1124.3883	1124.5549	-0.1666	0	K.HDLGHFMLR.C
179 - 187	1141.3804	1140.3732	1140.5498	-0.1767	0	K.HDLGHFMLR.C Oxidation (M)
188 - 206	2301.8628	2300.8556	2300.9280	-0.0725	0	R.CLTTDEYDGHSTYPSHQYQ.-

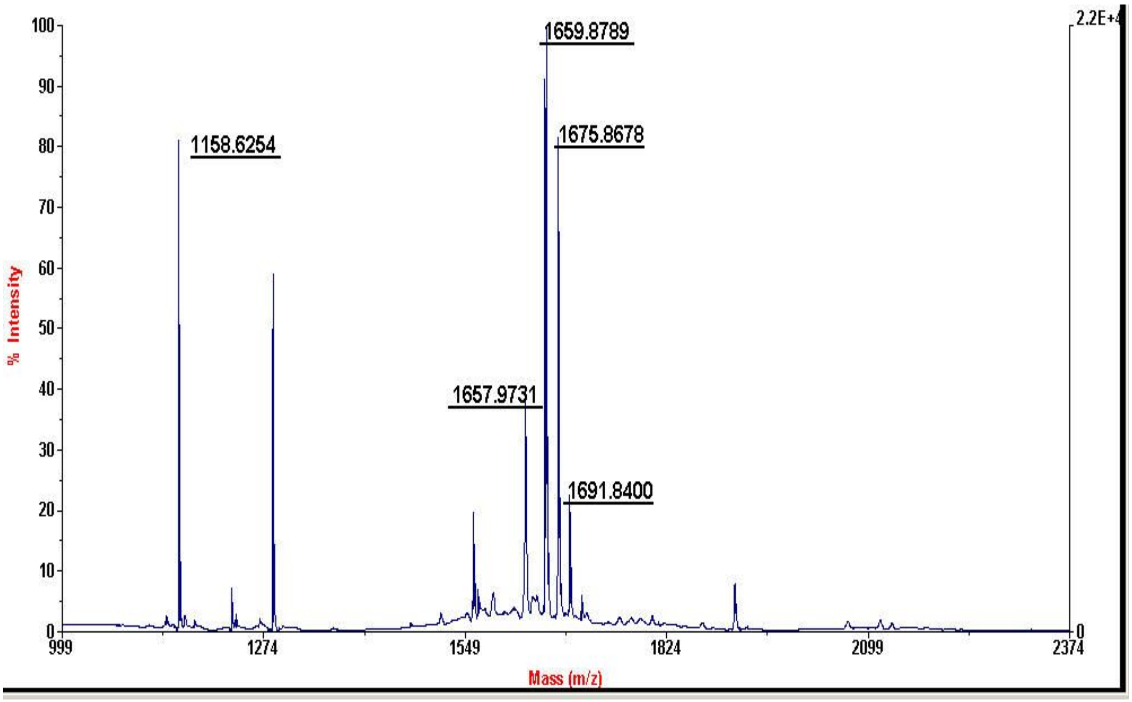
No match to: 1080.8350, 1179.4333, 1475.6493

112 ）Peptidyl-prolyl cis-trans isomerase B precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
64 - 76	1364.5546	1363.5473	1363.6983	-0.1510	0	K.TVDNFVALATGEK.G	
88 - 101	1626.6829	1625.6756	1625.8235	-0.1479	1	R.VIKDFMIQGGDFTR.G	
88 - 101	1642.6786	1641.6713	1641.8184	-0.1471	1	R.VIKDFMIQGGDFTR.G	Oxidation (M)
109 - 121	1601.6298	1600.6225	1600.7521	-0.1296	1	K.SIYGERFPDENFK.L	
124 - 137	1490.5320	1489.5247	1489.6772	-0.1524	0	K.HYGPGWVSMANAGK.D	Oxidation (M)
164 - 172	1031.4941	1030.4868	1030.5481	-0.0612	0	K.VLEGMEVVR.K	
164 - 172	1047.4605	1046.4532	1046.5430	-0.0898	0	K.VLEGMEVVR.K	Oxidation (M)
183 - 196	1571.6799	1570.6726	1570.8388	-0.1662	1	R.DKPLKDVIIADCGK.I	
197 - 208	1373.6425	1372.6352	1372.7601	-0.1249	1	K.IEVEKPFAIAKE.-	

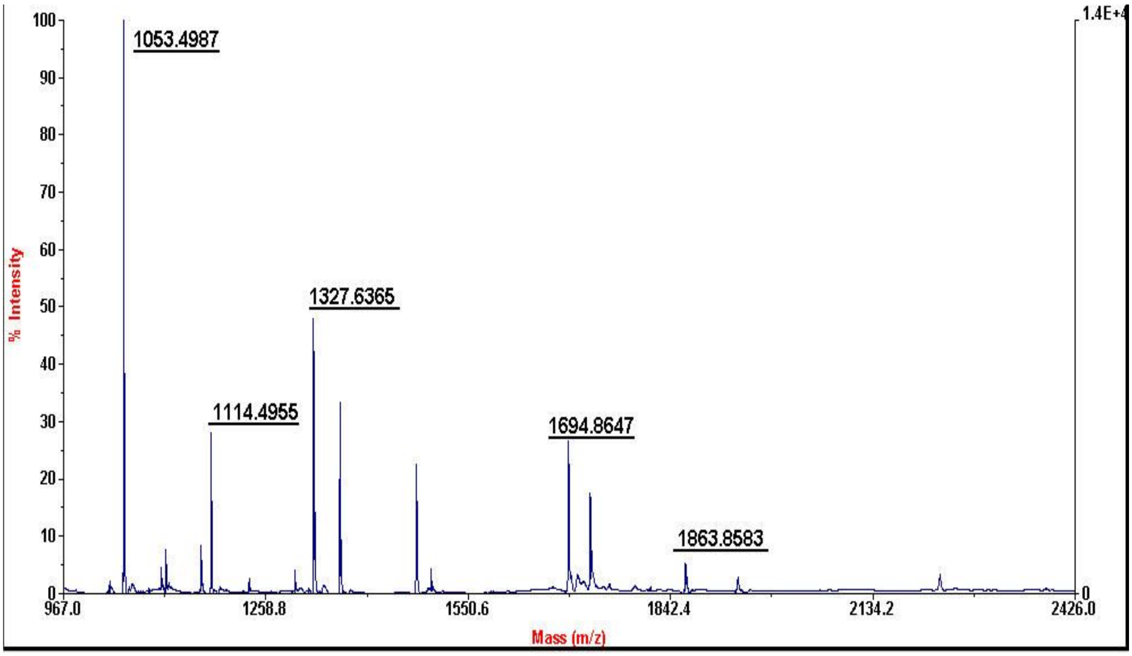
113 ） Protein DJ-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
13 - 27	1675.8678	1674.8605	1674.7956	0.0649	0	K.GAEEMETVIPVDVMR.R
13 - 27	1691.8400	1690.8328	1690.7905	0.0422	0	K.GAEEMETVIPVDVMR.R Oxidation (M)
33 - 48	1657.9731	1656.9658	1656.8617	0.1041	1	K.VTVAGLAGKDPVQCSR.D
49 - 63	1659.8789	1658.8716	1658.8185	0.0531	1	R.DVVICPDASLEDAKK.E
90 - 98	1158.6254	1157.6181	1157.6040	0.0141	1	K.EILKEQENR.K

No match to: 1286.7447, 1560.6667, 2584.5953

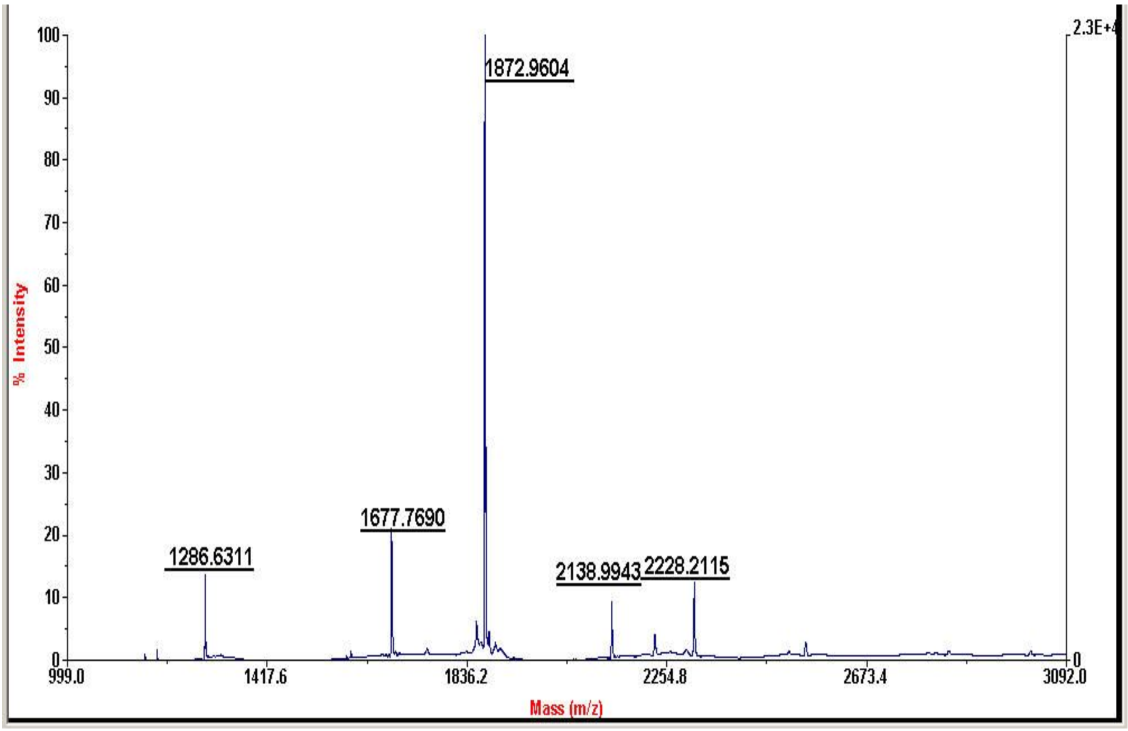
114 ） Inorganic pyrophosphatase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
10 - 18	1053.4987	1052.4914	1052.5291	-0.0377	0	R.AAPFSLEYR.V
26 - 41	1863.8583	1862.8510	1862.9203	-0.0693	0	K.GQYISPFHDIPIYADK.D
42 - 52	1327.6365	1326.6292	1326.6754	-0.0462	0	K.DVFHMVVEVPR.W
80 - 88	1114.4955	1113.4882	1113.5858	-0.0976	0	R.YVANLFPYK.G
178 - 191	1694.8647	1693.8574	1693.8827	-0.0253	0	R.LKPGYLEATVDWFR.R

No match to: 1165.5504, 1365.5973, 1726.8564

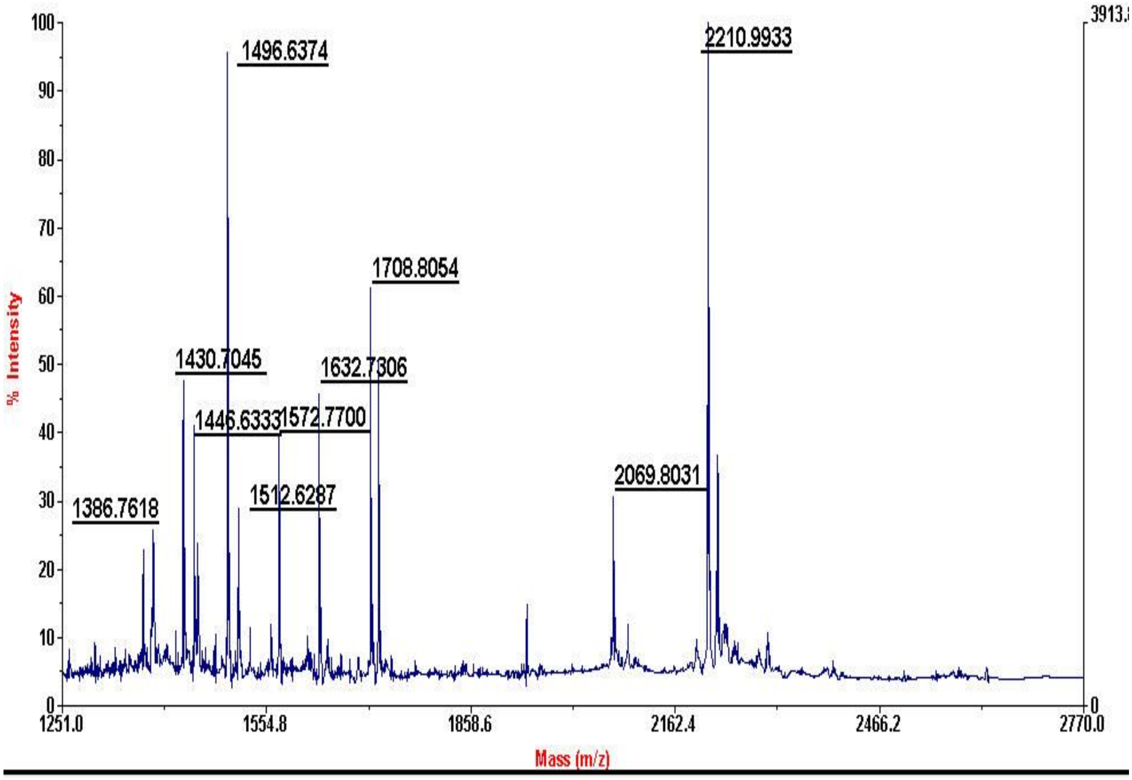
115 ）Ig gamma-1 chain C region



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
139 - 157	2138.9943	2137.9870	2138.0201	-0.0331	0	R.TPEVTCVVVDVSHEDPEVK.F
158 - 171	1677.7690	1676.7618	1676.7946	-0.0329	0	K.FNWYVDGVEVHNAK.T
185 - 203	2228.2115	2227.2043	2227.2000	0.0042	1	R.VVSVLTVLHQDWLNGKEYK.C
228 - 238	1286.6311	1285.6238	1285.6666	-0.0428	0	R.EPQVYTLPPSR.D
228 - 243	1872.9604	1871.9531	1871.9629	-0.0097	1	R.EPQVYTLPPSRDELTK.N

No match to: 970.5473, 1287.6306, 1854.9541, 2311.1819, 2545.1070

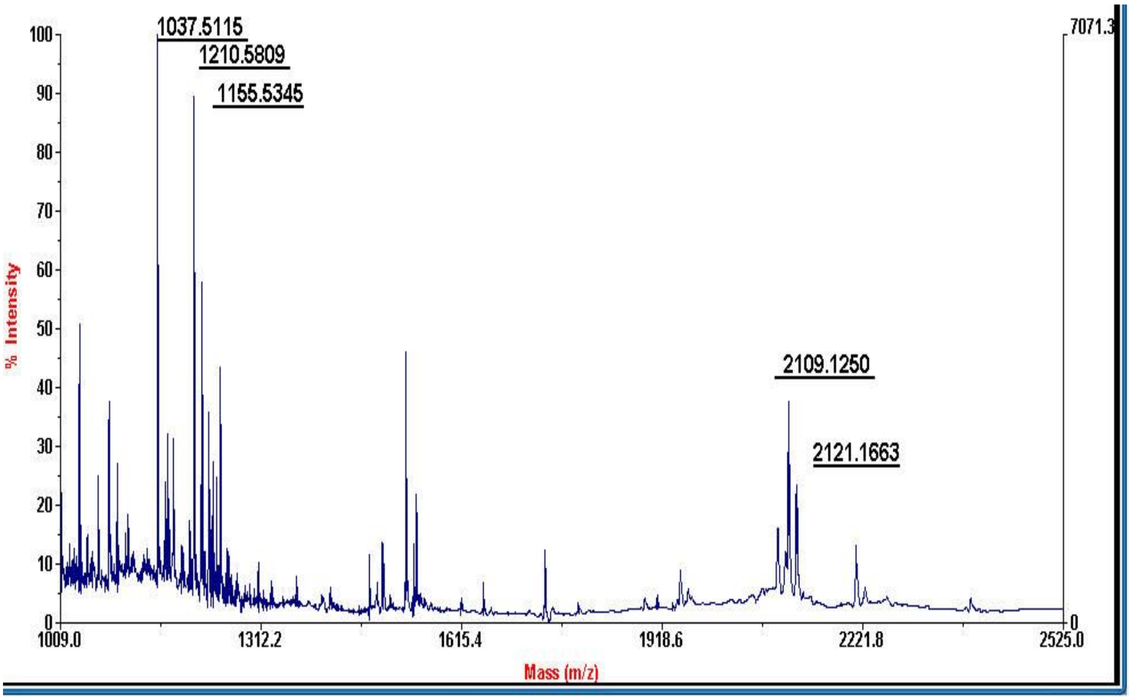
116) Fibrillin-1 precursor - Homo sapiens (Human)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
526 - 539	1708.8054	1707.7981	1707.7305	0.0677	1	R.TECRDIDECLQNGR.I
935 - 948	1512.6287	1511.6214	1511.6167	0.0047	0	K.CQCPSGMTLDATGR.I ; Oxidation (M)
1301 - 1315	1632.7306	1631.7233	1631.6895	0.0338	1	K.GSFICHCDMGYSGKK.G
1429 - 1442	1572.7700	1571.7627	1571.6055	0.1573	0	R.CECDMGFVPSADGK.A 2

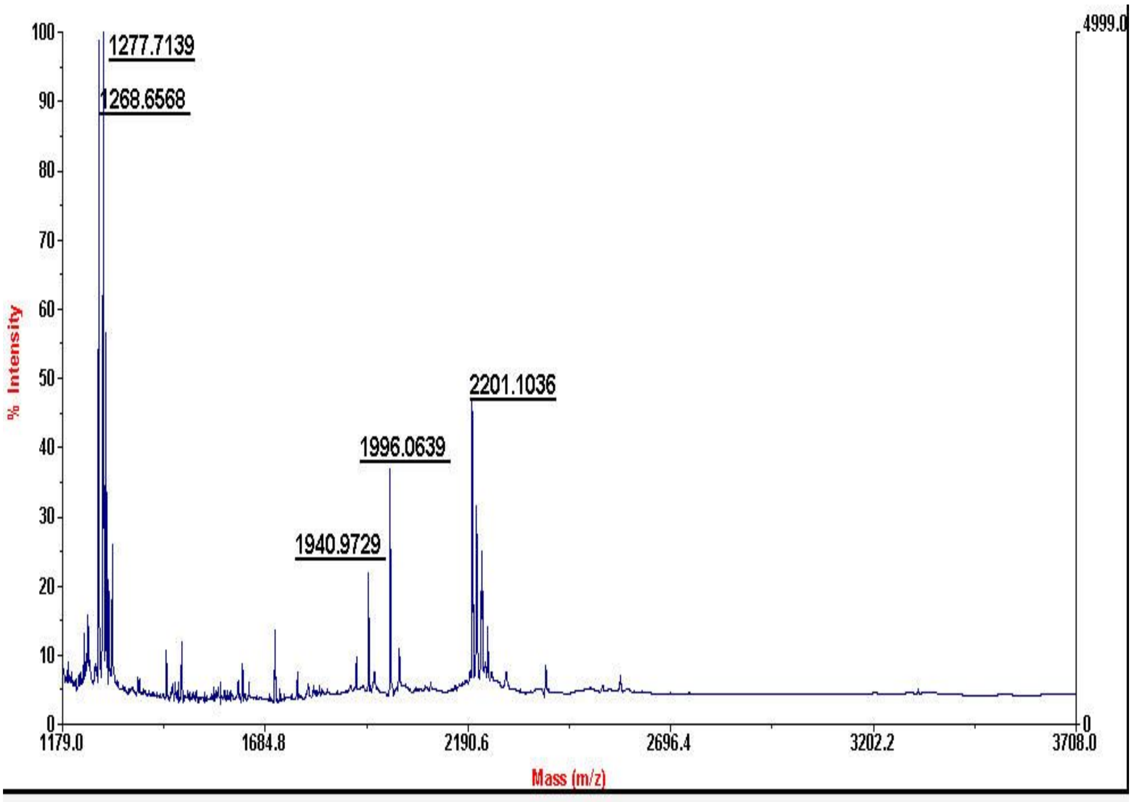
1470 - 1480	1386.7618	1385.7545	1385.5591	0.1954	0	R.CECEIGYELDR.S	
2053 - 2064	1496.6374	1495.6302	1495.6258	0.0044	1	R.CQDLRMSYCYAK.F	Oxidation (M)
2221 - 2239	2210.9933	2209.9860	2209.9959	-0.0098	1	R.CVNTYGSYECKCPVGYVLR.E	
2461 - 2472	1430.7045	1429.6972	1429.5602	0.1370	0	K.NTEGSYQCSCPK.G	2
2493 - 2510	2069.8031	2068.7958	2068.9281	-0.1323	0	K.QHNCQFLCVNTIGGFTCK.C	
2681 - 2694	1446.6333	1445.6260	1445.6326	-0.0066	0	R.IGQGHCVSGMGMGR.G	

117) BTB/POZ domain-containing protein 6



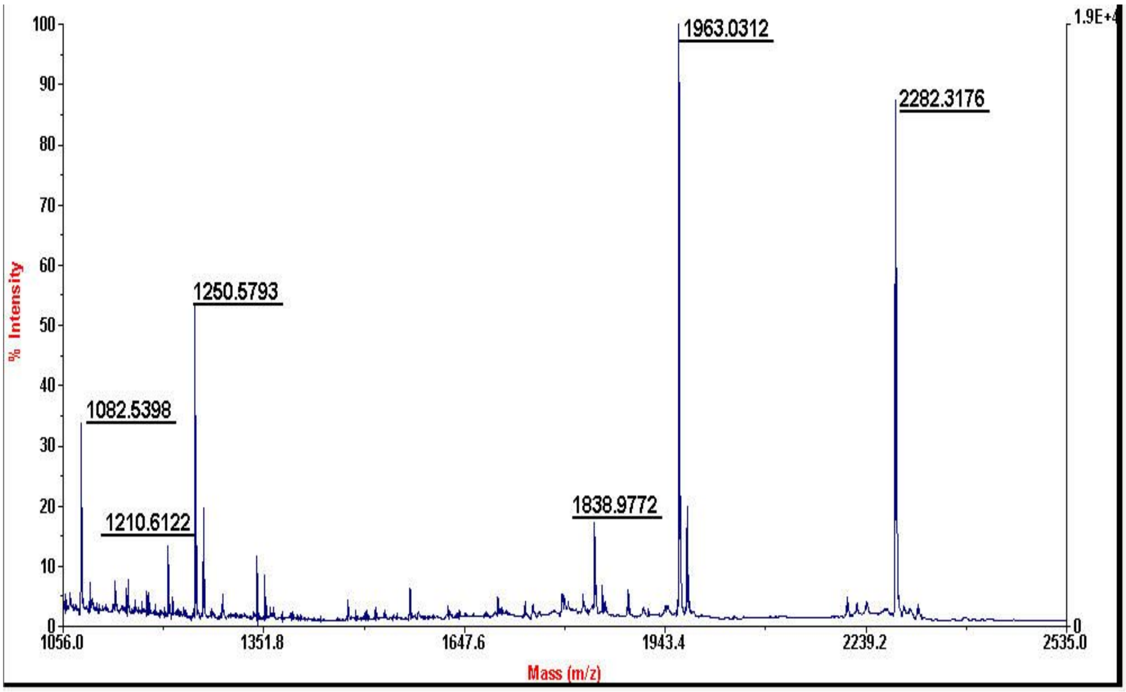
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
146 - 163	2109.1250	2108.1177	2108.0572	0.0605	1	R.SEGFCEIDRQTLEIIVTR.E
170 - 187	2121.1663	2120.1590	2120.0360	0.1230	1	K.EAVVFEAVLNWAEAECKR.Q
257 - 265	1037.5115	1036.5042	1036.5349	-0.0306	1	K.GLAPQRCHR.F
282 - 291	1210.5809	1209.5736	1209.5448	0.0288	0	R.CDSIQFAVDR.R
319 - 329	1155.5345	1154.5272	1154.7023	-0.1751	0	R.LGVVLAQNLTK.F

118) Anterior gradient protein 2



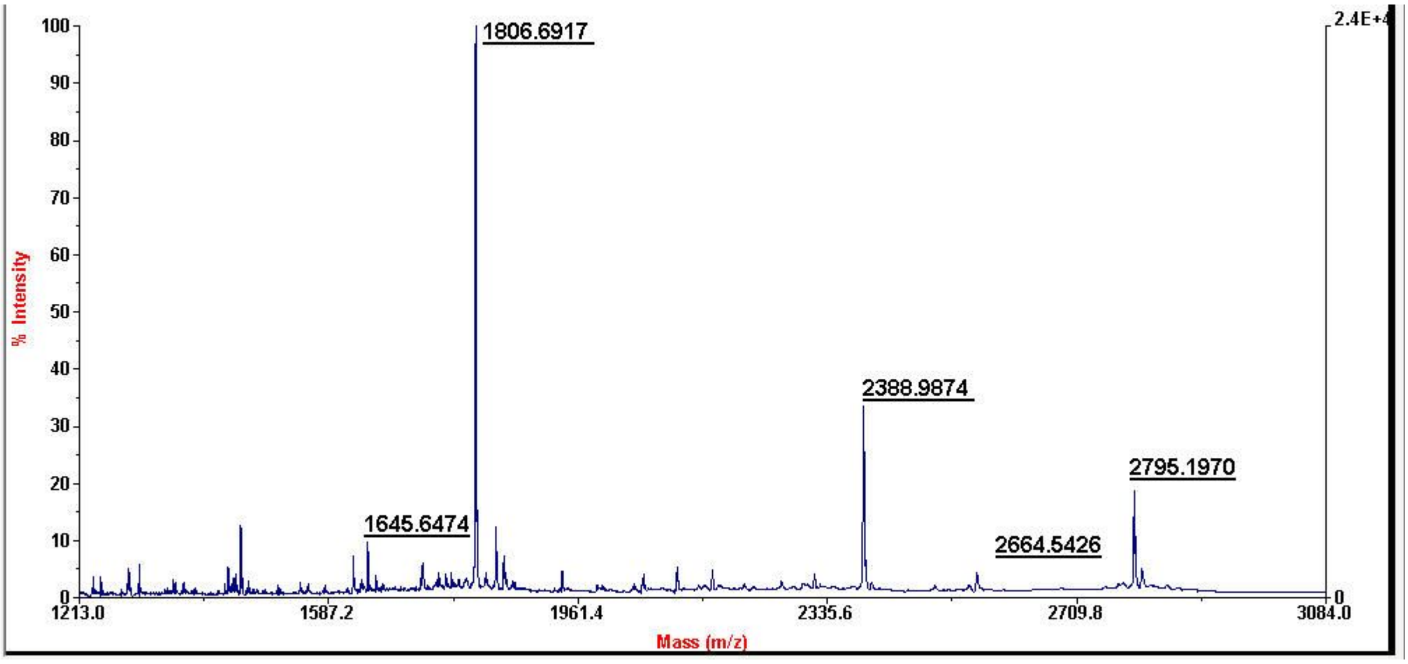
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
47 - 64	2201.1036	2200.0963	2200.0477	0.0487	0	R.GWGDQLIWTQTYEEALYK.S
100 - 116	1996.0639	1995.0566	1995.0564	0.0001	0	K.LAEQFVLLNLVYETTDK.H
117 - 127	1268.6568	1267.6495	1267.6309	0.0186	0	K.HLSPDGQYVPR.I
128 - 138	1277.7139	1276.7067	1276.6850	0.0217	0	R.IMFVDPSLTVR.A
149 - 165	1940.9729	1939.9656	1939.9601	0.0056	0	R.LYAYEPADTALLLDNMK.K

119) Pyridoxal kinase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
54 - 70	1963.0312	1962.0240	1961.9694	0.0546	0	K.GQVLNSDELQELYEGLR.L
77 - 86	1250.5793	1249.5721	1249.5979	-0.0258	0	K.YDYVLTGYTR.D
140 - 160	2282.3176	2281.3103	2281.2318	0.0785	0	K.VVPLADIITPNQFEAELLSGR.K
161 - 170	1210.6122	1209.6050	1209.6465	-0.0416	1	R.KIHSQEEALR.V
162 - 170	1082.5398	1081.5325	1081.5516	-0.0191	0	K.IHSQEEALR.V
276 - 292	1838.9772	1837.9699	1837.9468	0.0231	0	K.AQAGEGVRPSPMQLELR.M

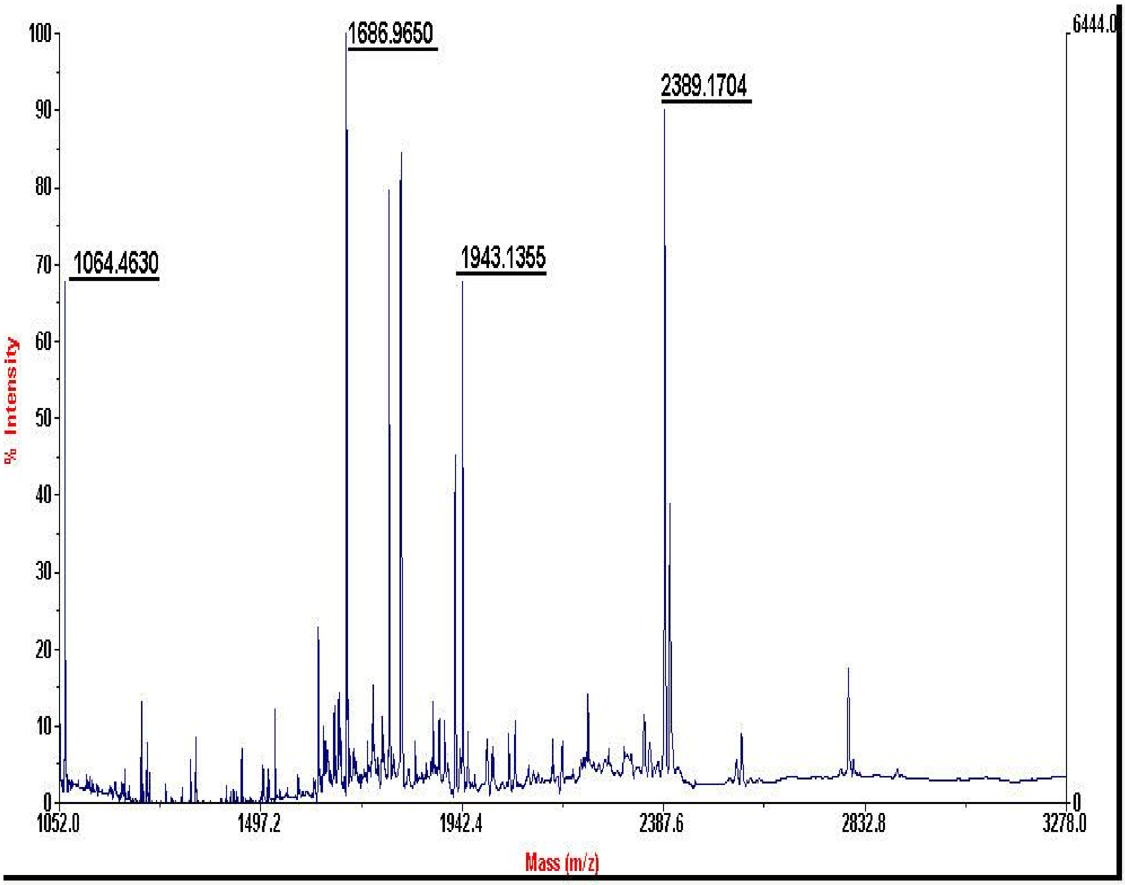
120) RhoGEF and PH domain-containing protein 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
206 - 226	2388.9874	2387.9801	2388.2689	-0.2888	1	R.AAELLATWTDKSPLFQEVLTR.I
334 - 354	2664.5426	2663.5353	2663.2698	0.2655	1	R.NDPMERYLFLFNNMLLYCVPR.V
Oxidation (M)						
377 - 392	1806.6917	1805.6844	1805.8658	-0.1814	0	R.ELMDAEFPHSFLVSGK.Q
479 - 491	1645.6474	1644.6401	1644.7184	-0.0783	1	R.HHCRACGYVVCAR.C 3
532 - 557	2795.1970	2794.1898	2794.3881	-0.1983	1	R.GILEKGSSATPDQSLMCSFLQLIGDK.W

No match to: 1454.5853

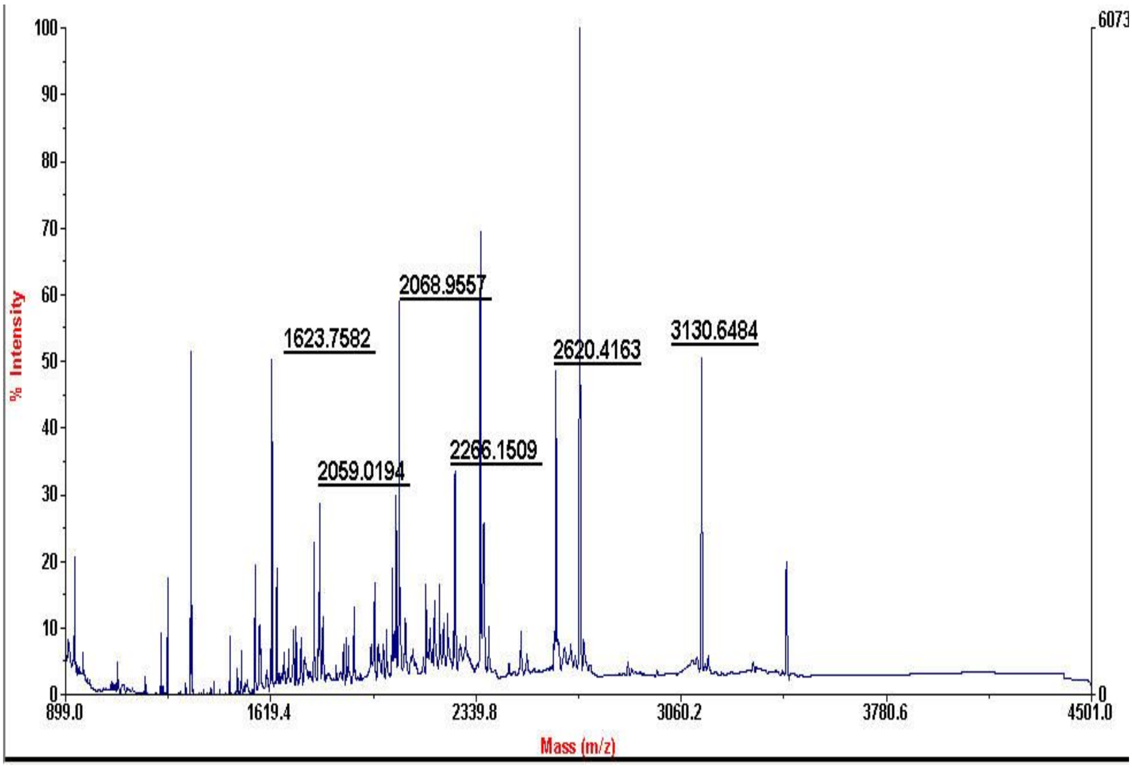
121) Cytosolic nonspecific dipeptidase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 53	1064.4630	1063.4557	1063.5042	-0.0485	0	R.MMEVAAADVK.Q

67 - 84	1943.1355	1942.1282	1942.1251	0.0031	1	K.QKLPDGSEIPLPPILLGR.L
69 - 84	1686.9650	1685.9577	1685.9716	-0.0138	0	K.LPDGSEIPLPPILLGR.L
160 - 180	2389.1704	2388.1631	2388.0613	0.1017	0	R.FCLEGMEESGSEGLDELIFAR.K

122) Plexin-A4 precursor

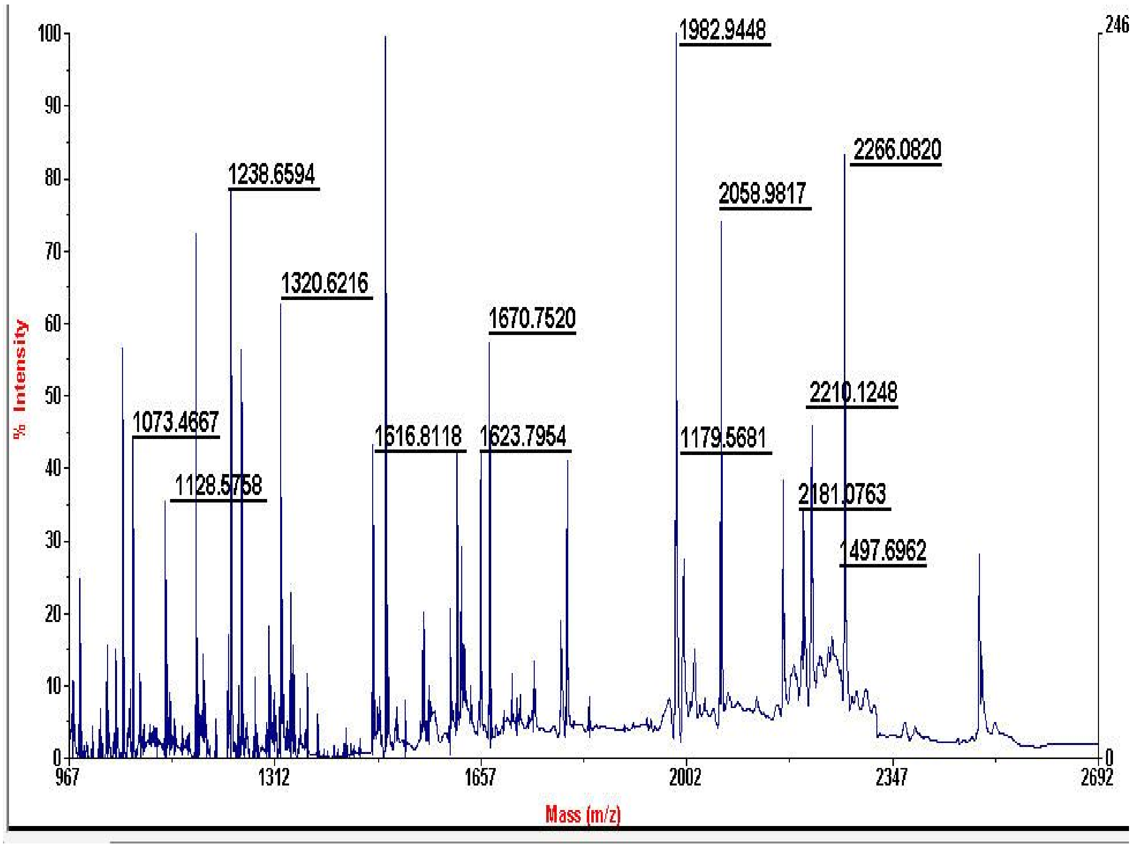


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
286 - 308	2620.4163	2619.4090	2619.1911	0.2179	1	K.EDTAFNSYVEVPIGCERSGVEYR.L
623 - 640	2059.0194	2058.0122	2058.1222	-0.1100	1	R.IITENGDHHVVQLQLKSK.E
945 - 963	2266.1509	2265.1436	2265.1351	0.0085	0	R.SSQLYYFMTLTLSDLKPSR.G

Oxidation (M)

1499 - 1518	2068.9557	2067.9484	2068.0511	-0.1026	0	K.TLVLSCVSPDNANSPEVPVK.I
1601 - 1615	1623.7582	1622.7509	1622.8012	-0.0503	0	K.QVTAYNAVNNSTVSR.T
1764 - 1788	2702.3293	2701.3220	2701.1782	0.1438	0	K.NSITDACLSVVAQTFMDSCSTSEHR.L
1764 - 1791	3130.6484	3129.6411	3129.4165	0.2246	1	K.NSITDACLSVVAQTFMDSCSTSEHRLGK.D

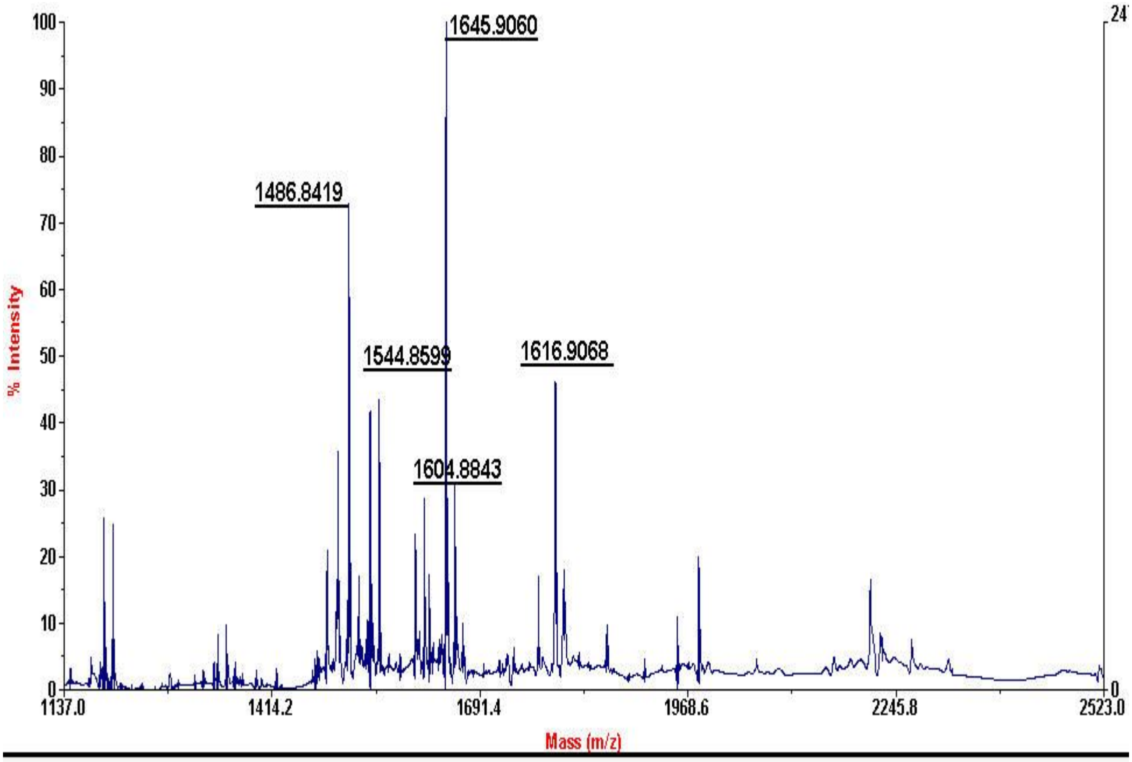
123) NA-dependent protein kinase catalytic subunit



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
109 - 117	1073.4667	1072.4594	1072.4859	-0.0265	0	K.NTCTSVYTK.D	
140 - 148	1128.5758	1127.5685	1127.5281	0.0404	1	R.SSRLMDEFK.I	Oxidation (M)
237 - 246	1179.5681	1178.5609	1178.4874	0.0735	0	K.SMEEDPQTSR.E	
747 - 757	1238.6594	1237.6522	1237.6529	-0.0007	0	R.AYVPALQMAFK.L	
1153 - 1170	1982.9448	1981.9375	1982.1023	-0.1647	1	R.LPRGFPPSASLCLLDLVK.W	
1156 - 1170	1616.8118	1615.8045	1615.8644	-0.0599	0	R.GFPPSASLCLLDLVK.W	
1490 - 1508	2058.9817	2057.9744	2057.9874	-0.0130	1	K.GIAPGDERQCLPSLDLSCK.Q	
1498 - 1508	1320.6216	1319.6143	1319.6214	-0.0071	0	R.QCLPSLDLSCK.Q	2
1871 - 1883	1670.7520	1669.7447	1669.7844	-0.0397	1	K.MGYYKILDVMYSR.L	2 Oxidation (M)
2215 - 2227	1623.7954	1622.7881	1622.9119	-0.1238	1	R.LLNFLMKHVFHPK.R	
2314 - 2333	2266.0820	2265.0747	2265.2191	-0.1443	1	K.EVYAAAAEVLGLILRYVMER.K	
2370 - 2388	2210.1248	2209.1175	2209.1758	-0.0583	1	K.SFPPLADRFMNAVFFLLPK.F	
2765 - 2776	1497.6962	1496.6890	1496.7736	-0.0846	1	K.QDAQVVLYRSYR.H	
3218 - 3235	2181.0763	2180.0690	2180.0089	0.0602	1	R.MEVQEQEEDISSLIRSCK.F	

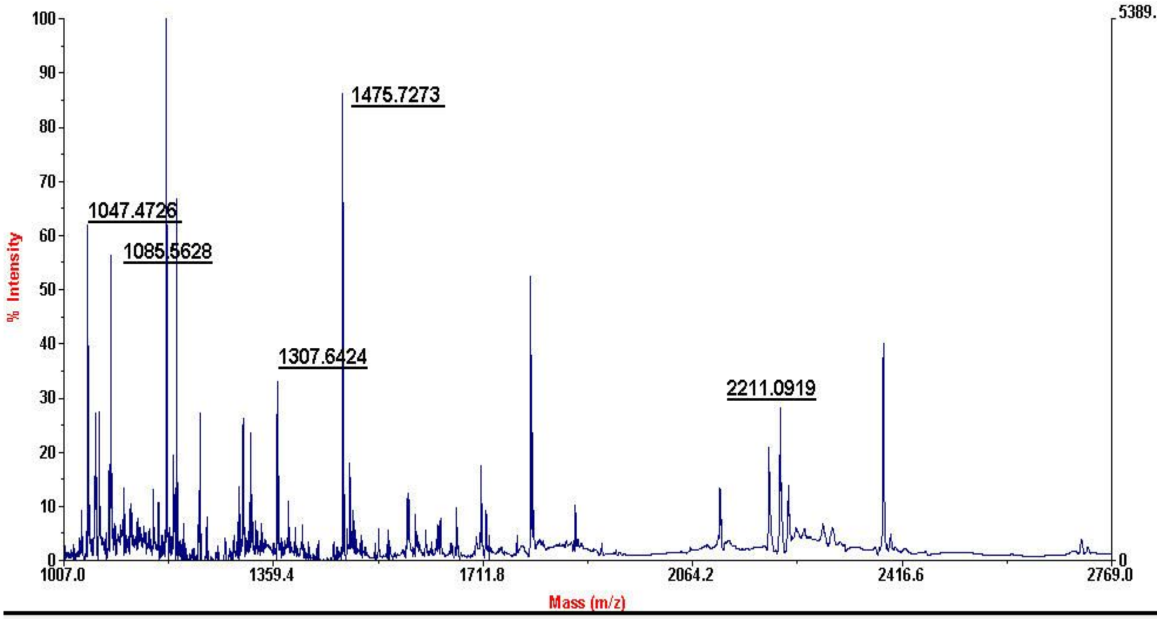
No match to: 1655.7507, 2015.2068

124) Uncharacterized protein C6orf152



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
53 - 66	1616.9068	1615.8995	1615.7928	0.1068	1	K.RQTSDGQVHHQAPR.K	
264 - 276	1544.8599	1543.8526	1543.7630	0.0895	1	R.AYEAHDENKVLQK.E	
318 - 331	1486.8419	1485.8347	1485.6228	0.2119	0	K.NAACQSDFADLCTK.G	
574 - 586	1604.8843	1603.8770	1603.7300	0.1470	1	K.SSFLDFQRNSMEK.L	Oxidation (M)
683 - 697	1645.9060	1644.8987	1644.7842	0.1145	0	K.AADSVEDEIEEVALR.-	

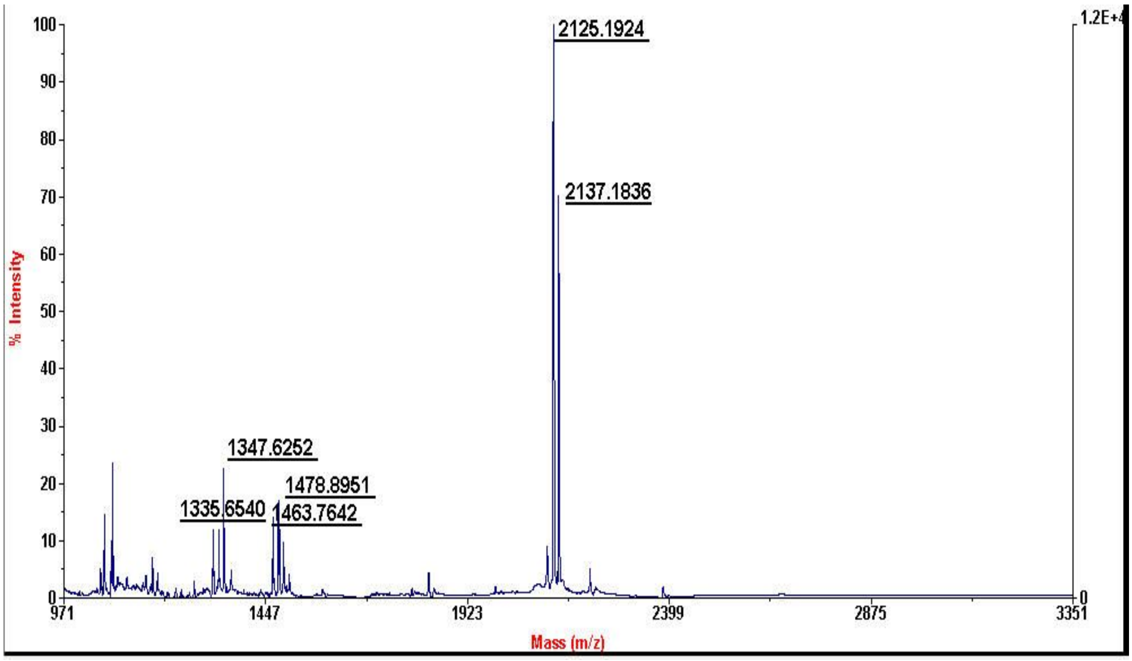
125) SH3 domain-binding protein 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
36 - 45	1085.5628	1084.5556	1084.6604	-0.1049	1	K.KGGTQLQLLK.W
107 - 118	1475.7273	1474.7201	1474.6365	0.0836	0	R.TWFFSASSEEER.K
194 - 213	2211.0919	2210.0846	2210.1194	-0.0348	0	R.LEDALMHPPAYPPPPVPTPR.K
Oxidation (M)						
478 - 488	1307.6424	1306.6351	1306.5976	0.0375	0	R.GEPQDGLYCIR.N
553 - 561	1047.4726	1046.4654	1046.4934	-0.0280	0	R.HPYGYTGPR.-

No match to: 1196.5100, 1365.6444

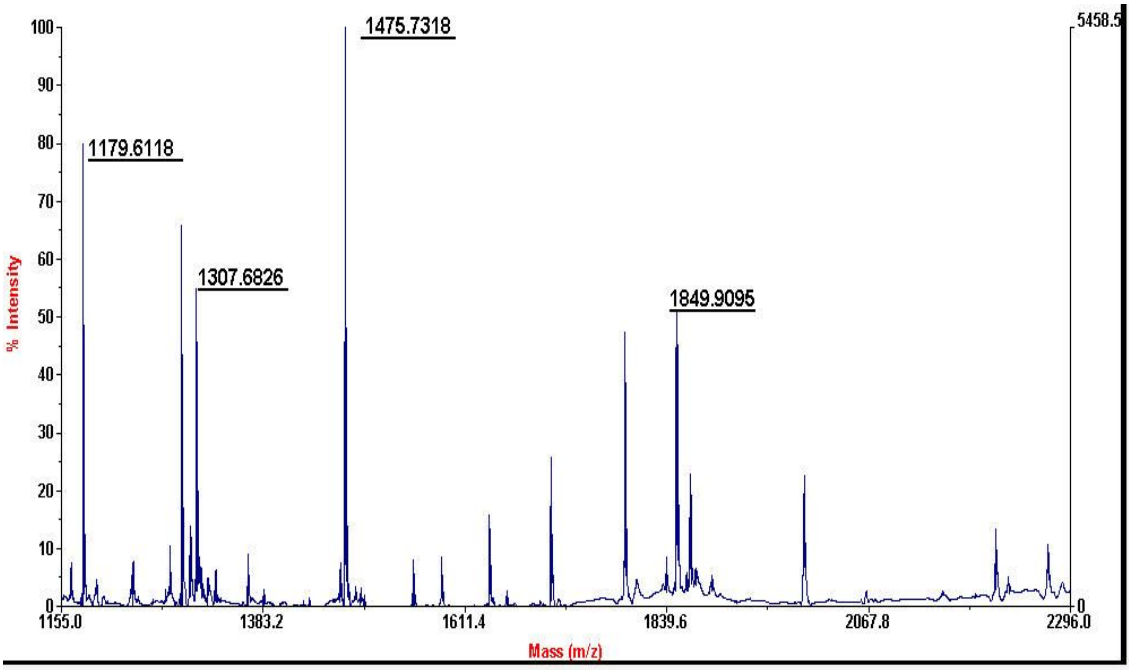
126 IQ motif and Sec7 domain-containing protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 10	1335.6540	1334.6467	1334.5318	0.1149	0	-.MWCLHCNSER.T
249 - 261	1463.7642	1462.7569	1462.6722	0.0847	0	K.SLAESIDDALNCR.S
624 - 634	1347.6252	1346.6179	1346.7306	-0.1127	1	K.VERLIEAFSQR.Y
627 - 644	2125.1924	2124.1851	2124.0608	0.1242	1	R.LIEAFSQRYCICNPGVVR.Q
733 - 752	2137.1836	2136.1763	2136.2102	-0.0339	1	K.KPIGSLHPGLGCVLSLPHRR.L
881 - 894	1478.8951	1477.8878	1477.7381	0.1497	0	K.GVVRPSMSQCSSLK.K

No match to: 1085.6798, 1487.7754, 2086.9407

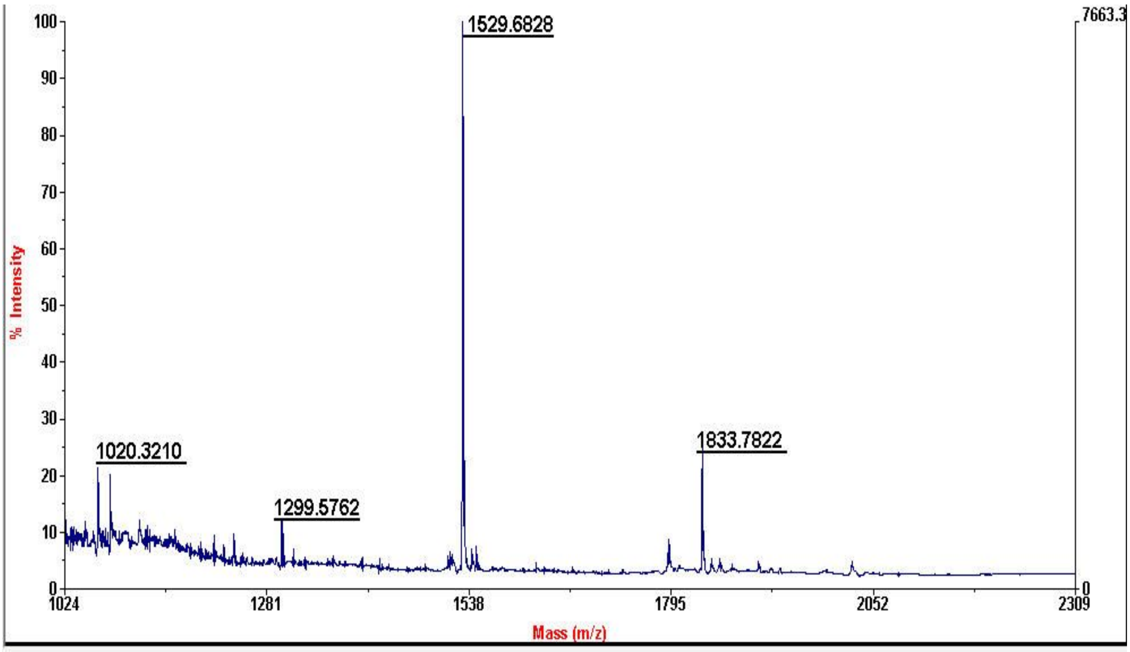
127) Chorionic somatomammotropin hormone-like 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
79 - 94	1849.9095	1848.9022	1849.0672	-0.1651	0	K.SNLELLHISLLLIESR.L
167 - 175	1179.6118	1178.6045	1178.5655	0.0390	0	K.NYGLLHCFR.K
167 - 176	1307.6826	1306.6753	1306.6604	0.0148	1	K.NYGLLHCFRK.D
187 - 199	1475.7318	1474.7246	1474.6003	0.1242	1	R.MVQCRSVEGSCGF.- ; Oxidation (M)

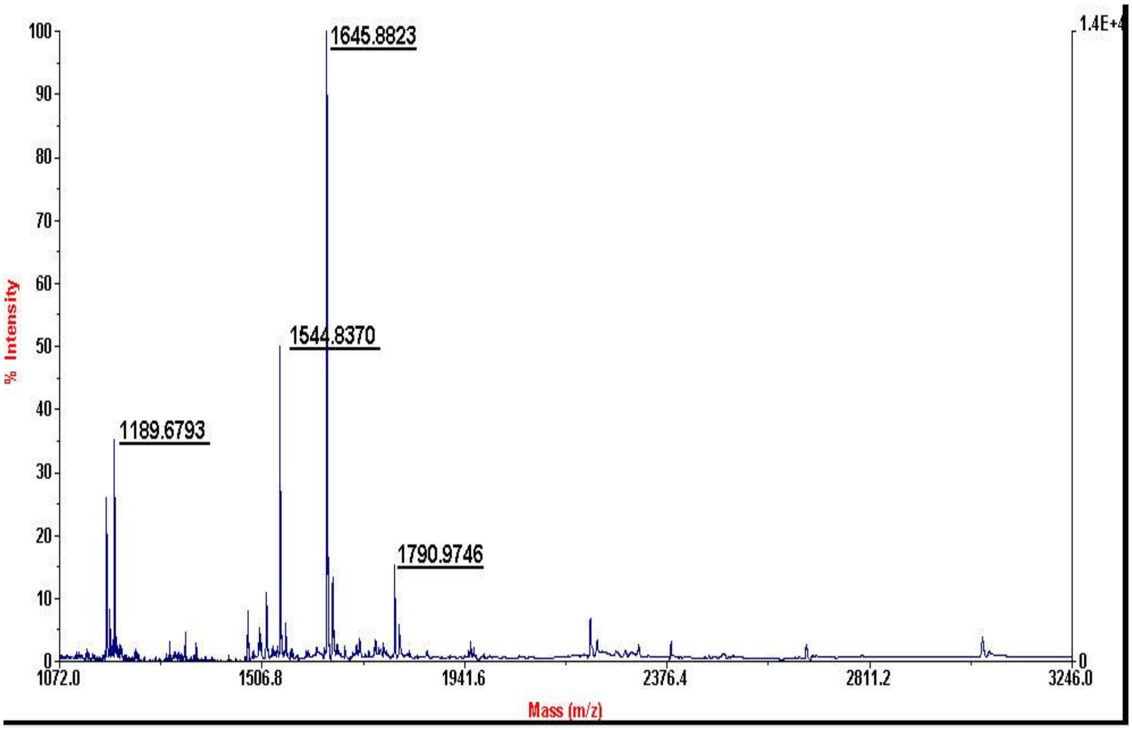
No match to: 1290.6699

128 Tektin-4



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
150 - 157	1020.3210	1019.3137	1019.5624	-0.2487	1	R.REHPNLVR.D	
181 - 193	1529.6828	1528.6755	1528.8508	-0.1752	1	R.TIMQAVSQIRLNR.E	
349 - 358	1299.5762	1298.5690	1298.5972	-0.0282	0	R.SHRPNMELCR.D	
365 - 380	1833.7822	1832.7749	1832.9553	-0.1804	0	R.LLSEVEELNMSLTALR.E	Oxidation

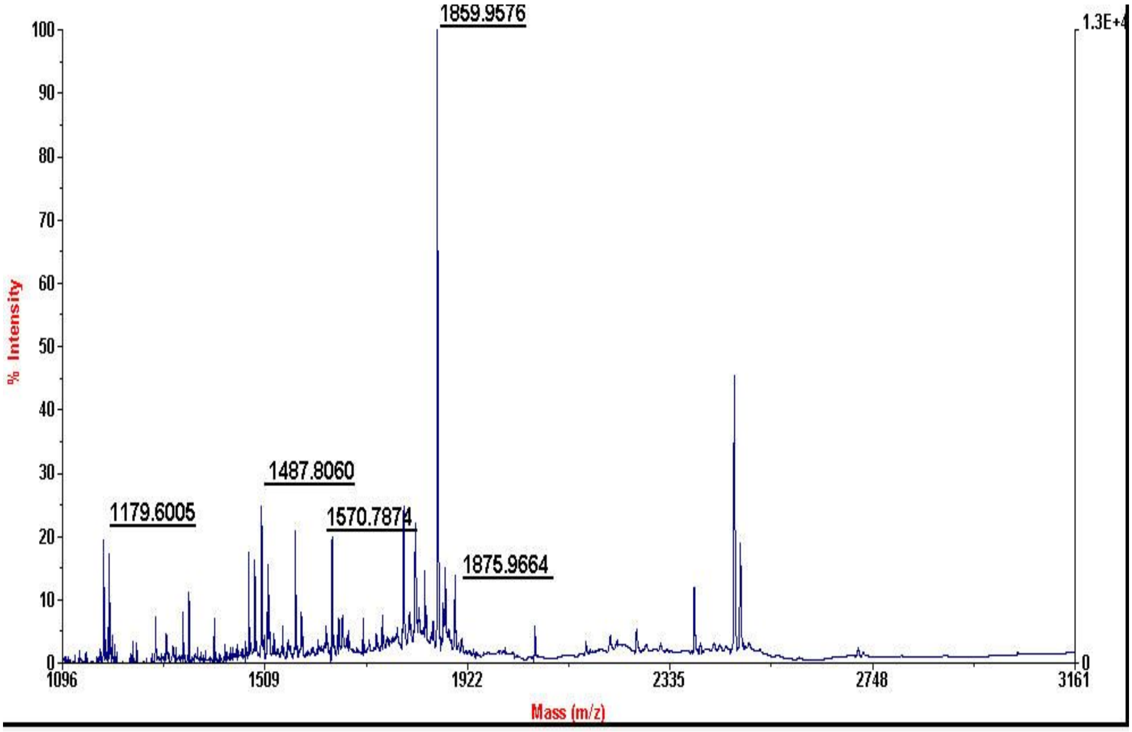
128) Krueppel-like factor 5



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
42 - 52	1189.6793	1188.6720	1188.6026	0.0694	0	R.DAALFPGEELK.H	
372 - 386	1790.9746	1789.9673	1789.8168	0.1506	1	R.IHYCDYPGCTKVYTK.S	
426 - 440	1645.8823	1644.8750	1644.7977	0.0773	1	R.KHTGAKPFQCGVCNR.S	
441 - 453	1544.8370	1543.8297	1543.7565	0.0732	1	R.SFSRSDHLALHMK.R	Oxidation (M)

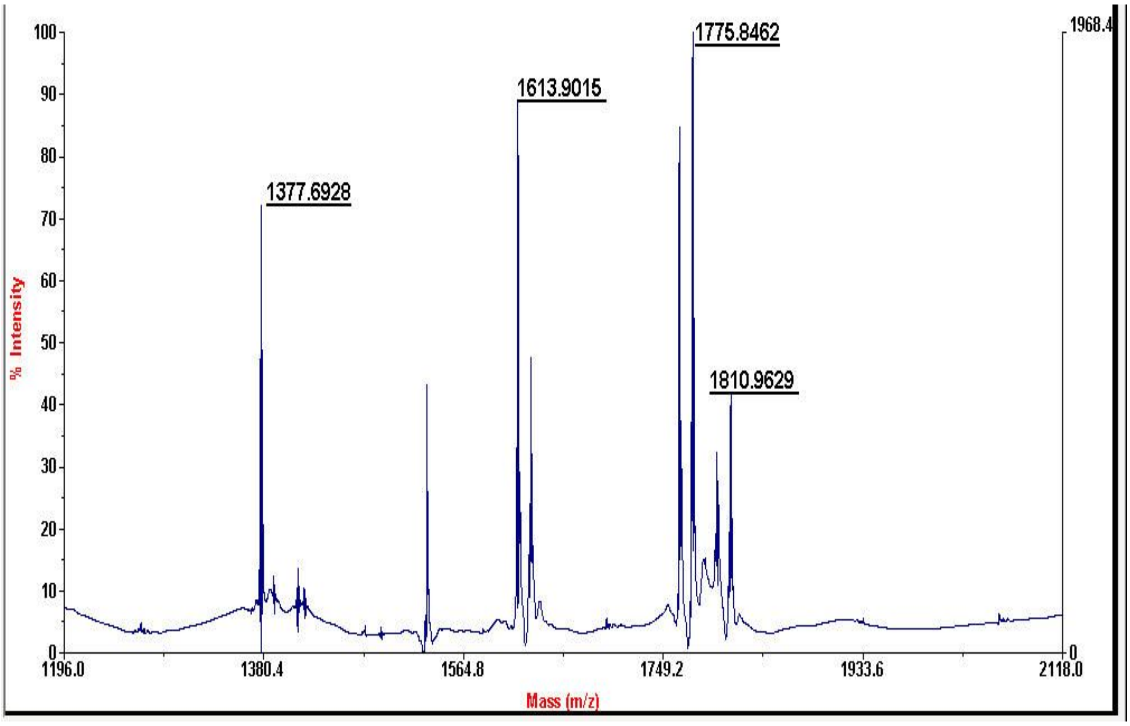
No match to: 1172.6429

129) Coiled-coil domain-containing protein 74A



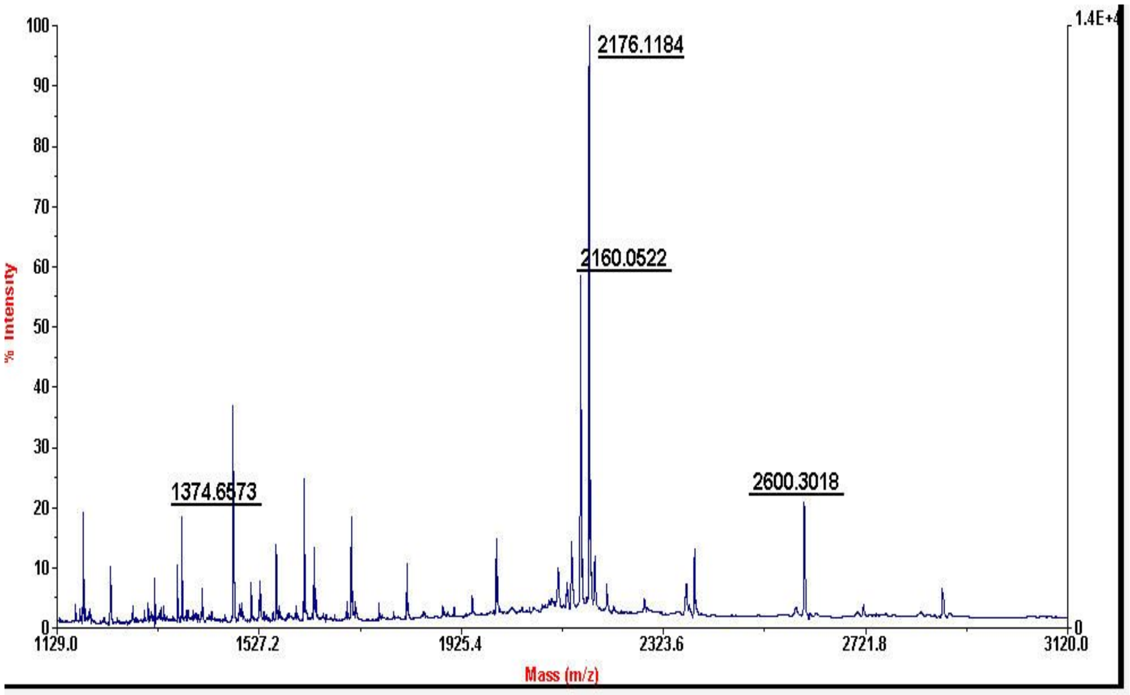
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
162 - 176	1570.7874	1569.7801	1569.7345	0.0456	0	R.SPADSLSMSSFQSVK.S
232 - 250	1859.9576	1858.9504	1858.7798	0.1705	0	K.AEASNAGAACMGNSQHQGR.Q
232 - 250	1875.9664	1874.9591	1874.7748	0.1843	0	K.AEASNAGAACMGNSQHQGR.Q Oxidation (M)
318 - 330	1487.8060	1486.7987	1486.7416	0.0571	1	R.DQEATHFPKVSTK.S
345 - 355	1179.6005	1178.5932	1178.7387	-0.1454	1	R.AILPALKQTPK.N

131 THUMP domain-containing protein 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
190 - 206	1775.8462	1774.8389	1775.0015	-0.1626	1	K.AFTAQEVGKVIGIAIMK.H
356 - 366	1377.6928	1376.6855	1376.6969	-0.0114	1	K.DIKSILQEMER.V Oxidation (M)
423 - 438	1810.9629	1809.9556	1809.8646	0.0910	1	K.TASTSFEASNHKFLDR.M
439 - 452	1613.9015	1612.8943	1612.7629	0.1313	0	R.MSPFGSLVPVECYK.V

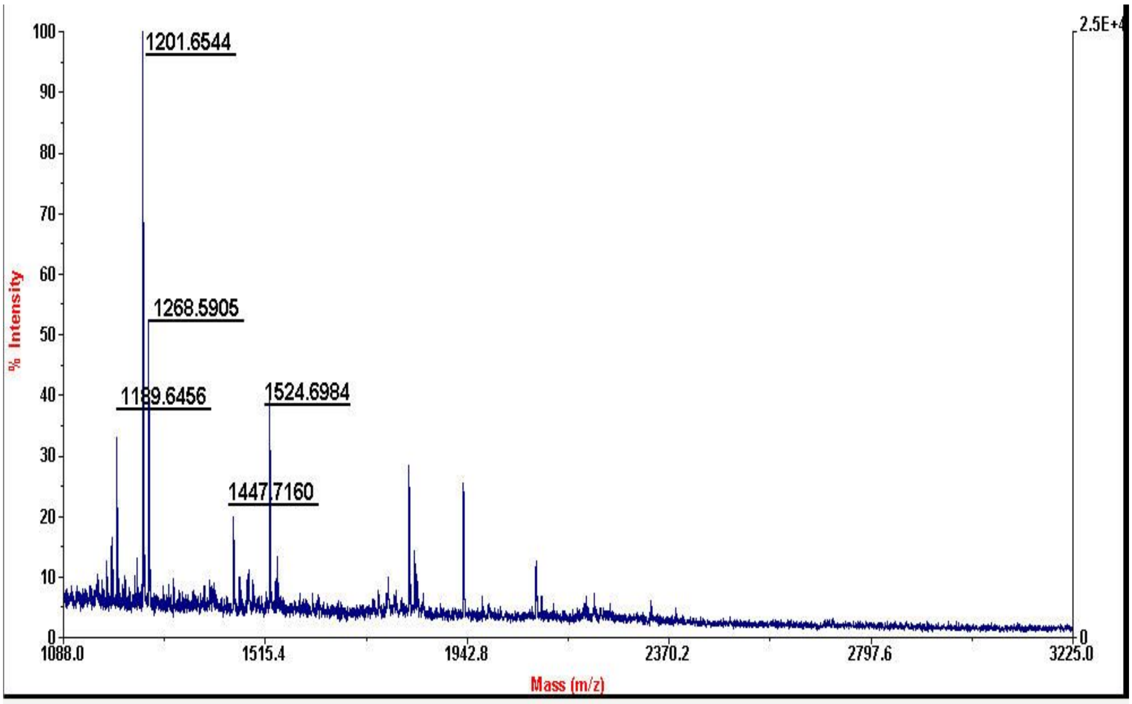
132 Voltage-dependent anion-selective channel protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
64 - 74	1374.6573	1373.6501	1373.6503	-0.0003	0	R.WTEYGLTFTEK.W
75 - 93	2176.1184	2175.1111	2175.0444	0.0667	0	K.WNTDNTLGTEITVEDQLAR.G
121 - 139	2160.0522	2159.0450	2158.9776	0.0674	0	R.EHINLGCDMDFDIAGPSIR.G
175 - 197	2600.3018	2599.2945	2599.1827	0.1118	0	K.TDEFQLHTNVNDGTEFGGSIYQK.V

No match to: 1560.8427, 1614.8994

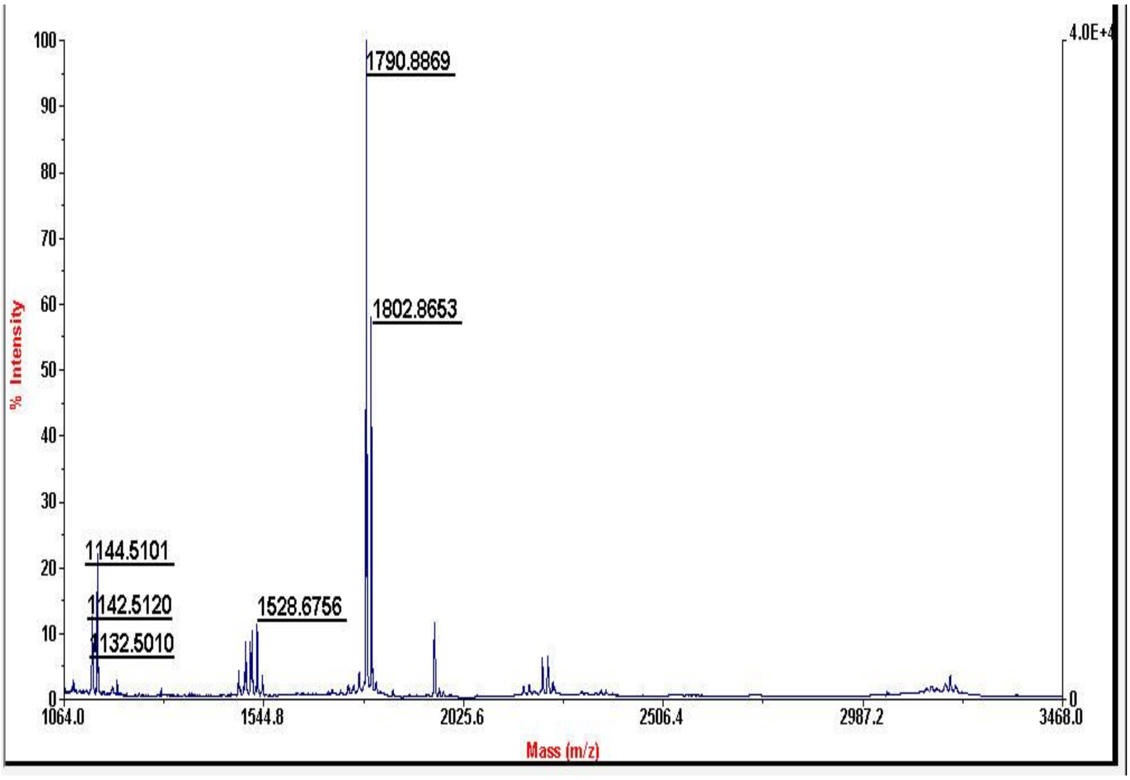
133) Kelch repeat and BTB domain-containing protein 3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
43 - 51	1189.6456	1188.6383	1188.5451	0.0932	0	R.EQNVFYDFK.I
52 - 63	1524.6984	1523.6911	1523.7952	-0.1041	1	K.IIMKDEIIPCHR.C
227 - 236	1268.5905	1267.5832	1267.7288	-0.1456	1	R.QKYLPHLIEK.V
377 - 386	1201.6544	1200.6471	1200.5849	0.0622	0	K.NDFFLVSTMK.T
517 - 528	1447.7160	1446.7087	1446.6312	0.0775	0	K.VYSFCPDTCVWK.G

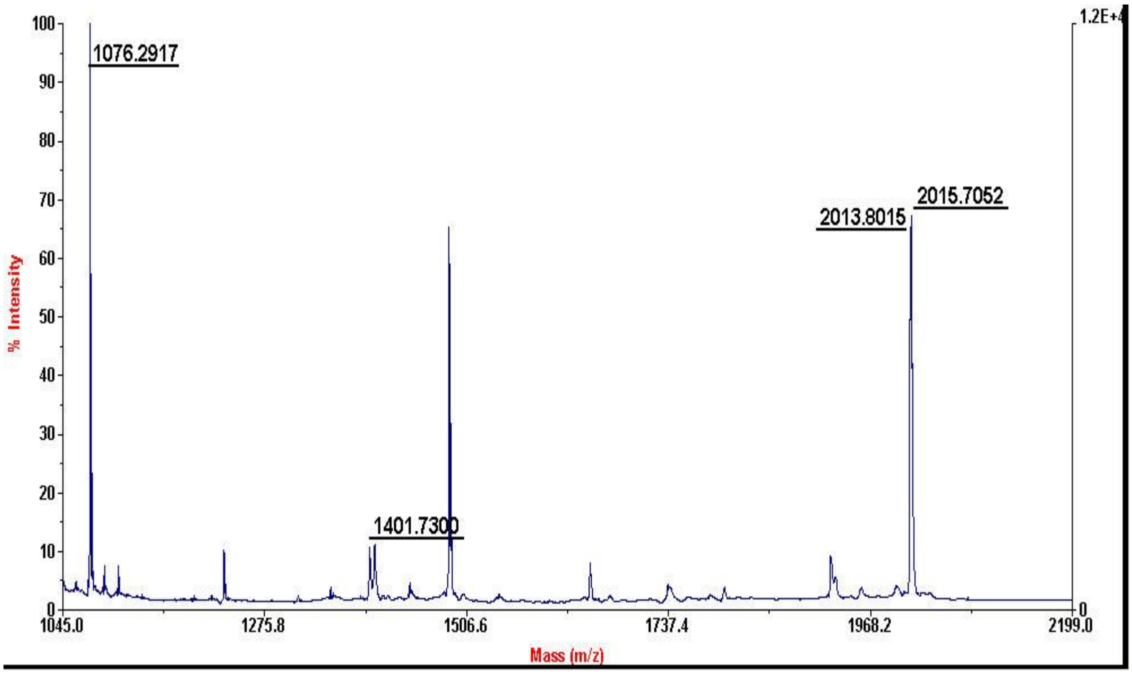
No match to: 1819.9681

134 Zinc finger protein 484



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
278 - 291	1802.8653	1801.8580	1801.7512	0.1068	0	K.QHECHECEAVFTQK.S	2
383 - 395	1528.6756	1527.6684	1527.6599	0.0085	1	K.HFECTECGKAFTR.K	
452 - 460	1132.5010	1131.4937	1131.6261	-0.1324	1	K.KSQLHVHQR.I	
489 - 503	1790.8869	1789.8796	1789.8604	0.0193	0	K.IHTGERPYICTVCGK.A	2
666 - 675	1144.5101	1143.5028	1143.4801	0.0227	1	K.CSDCGKAFTR.K	
797 - 805	1142.5120	1141.5047	1141.6608	-0.1561	1	K.IHTKQKPYK.C	

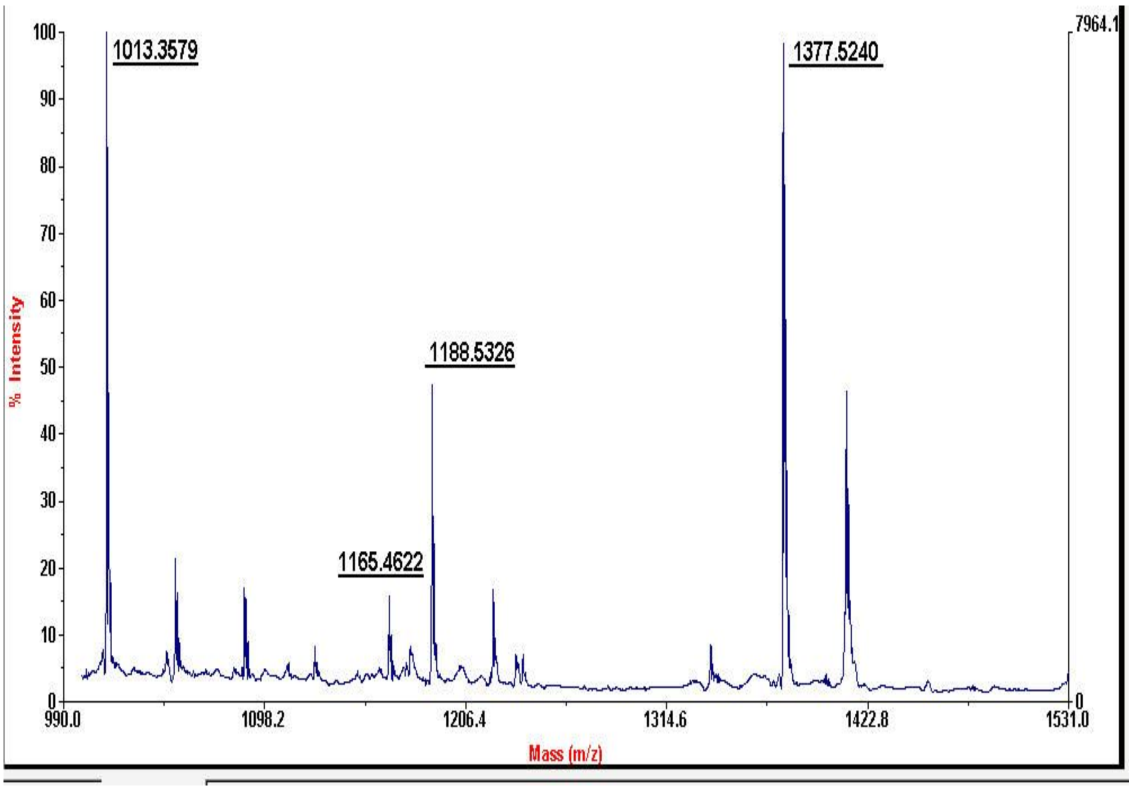
135 WNT1-inducible-signaling pathway protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
98 - 109	1401.7300	1400.7227	1400.6143	0.1084	0	R.GLYCDYSGDRPR.Y	
142 - 159	2015.7052	2014.6979	2014.8733	-0.1754	0	K.YNCTCIDGAVGCTPLCLR.V	2
300 - 308	1076.2917	1075.2844	1075.3885	-0.1041	0	K.YCGVCMDNR.C	Oxidation (M)
315 - 332	2013.8015	2012.7942	2012.9626	-0.1684	1	K.SKTIDVSFQCPDGLGFSR.Q	

No match to: 1486.4408

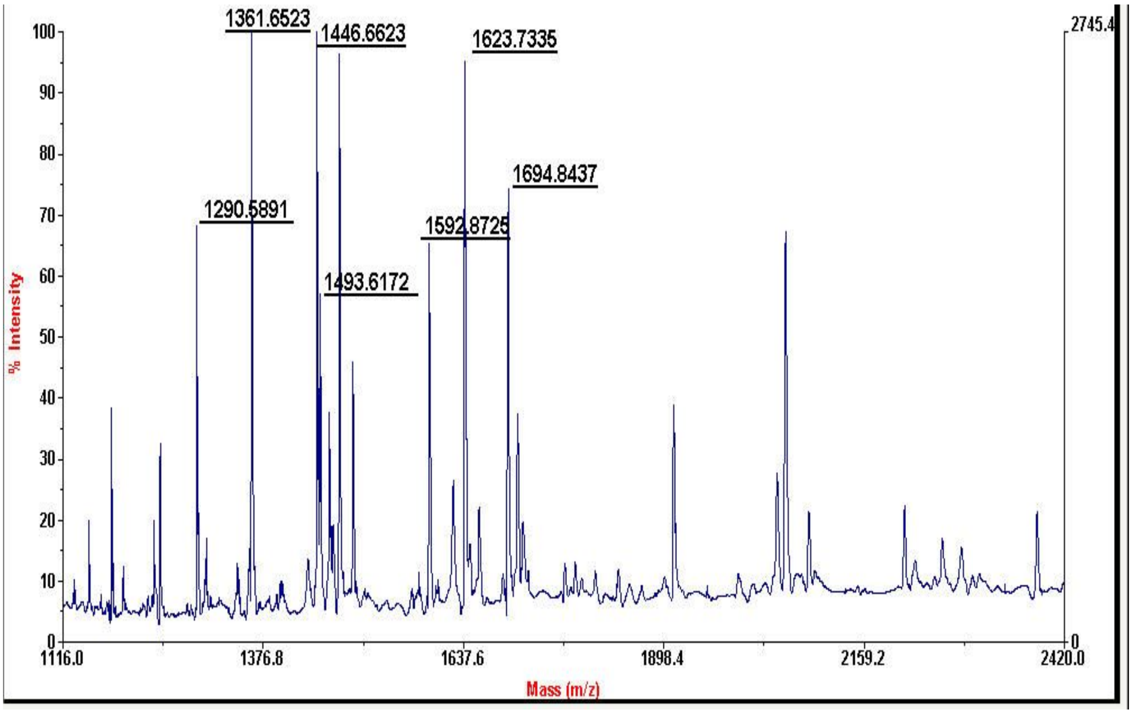
136 Heterogeneous nuclear ribonucleoproteins A2/B1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
121 - 129	1165.4622	1164.4549	1164.5159	-0.0610	0	K.EDTEEHHLR.D
138 - 147	1188.5326	1187.5253	1187.6398	-0.1144	0	K.IDTIEIITDR.Q
204 - 213	1013.3579	1012.3507	1012.4363	-0.0856	0	R.GGNFGFGDSR.G
214 - 228	1377.5240	1376.5167	1376.6222	-0.1055	0	R.GGGGNFGPGPGSNFR.G

No match to: 1995.0497

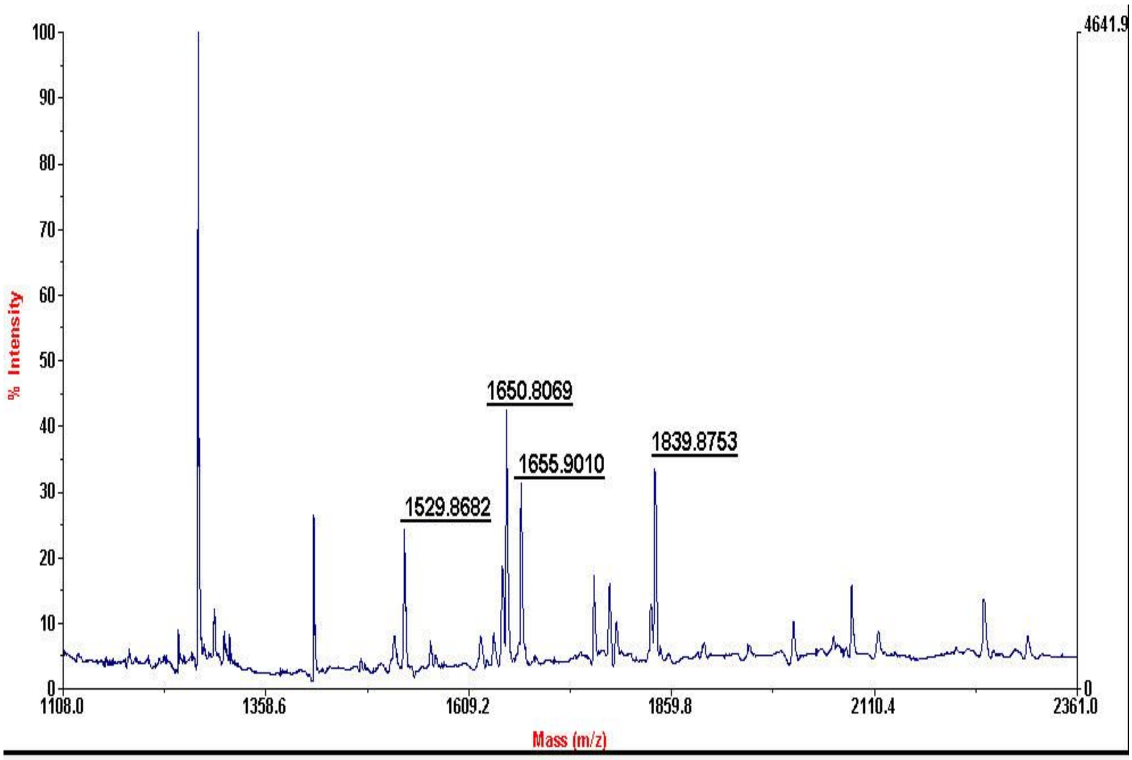
137 Stress-70 protein



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
188 - 202	1694.8437	1693.8365	1693.8424	-0.0059	0	K.NAVITVPAYFNDSQR.Q
349 - 360	1361.6523	1360.6450	1360.7351	-0.0901	0	R.AQFEGIVTDLIR.R
378 - 391	1446.6623	1445.6550	1445.7548	-0.0998	0	K.SDIGEVILVGGMTR.M
395 - 405	1290.5891	1289.5818	1289.6728	-0.0910	0	K.VQQTVQDLFGR.A
486 - 498	1493.6172	1492.6099	1492.6398	-0.0300	1	K.VCQGEREMAGDNK.L
499 - 513	1592.8725	1591.8652	1591.9450	-0.0797	0	K.LLGQFTLIGIPPAPR.G
660 - 675	1623.7335	1622.7262	1622.7020	0.0243	1	R.EGSGSSGTGEQKEDQK.E

No match to: 1475.6811, 1638.8288, 1708.3663

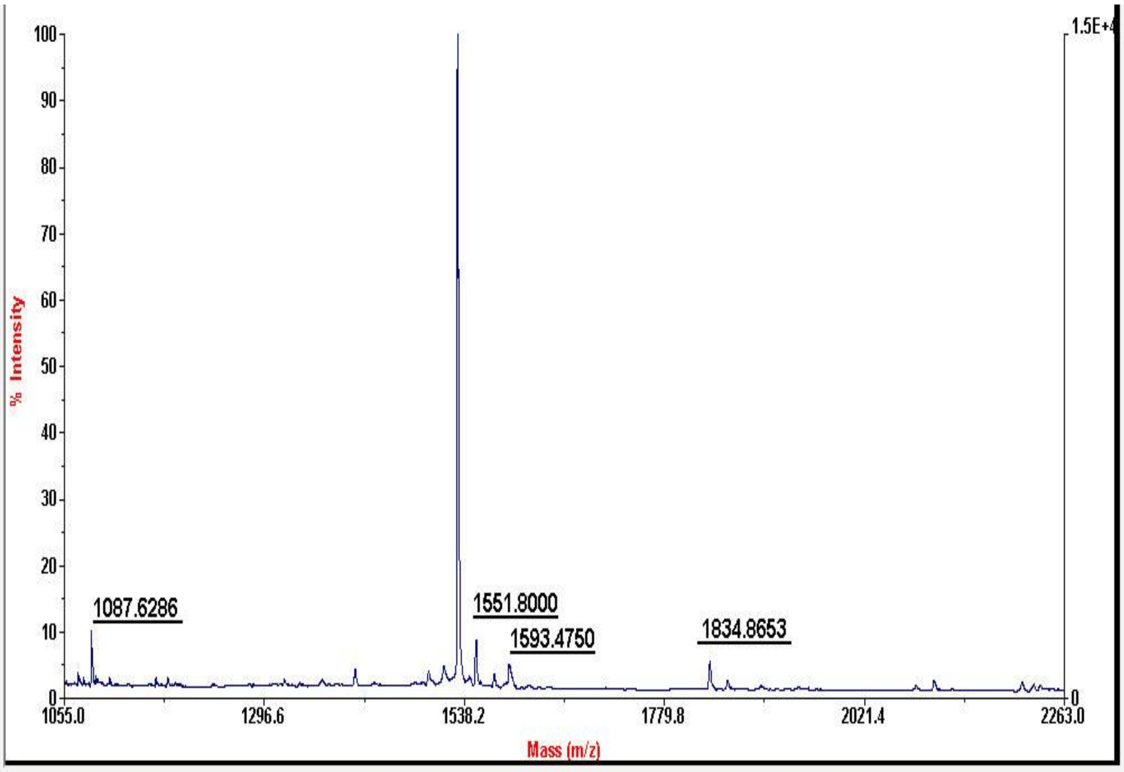
138 Pantothenate kinase 3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
65 - 78	1655.9010	1654.8937	1654.9043	-0.0105	1	R.DVHLELKDLTLFGR.R	
87 - 100	1650.8069	1649.7996	1649.8236	-0.0240	0	R.FPTQDLPTFIQMGR.D	
292 - 306	1529.8682	1528.8610	1528.8573	0.0037	0	R.ATLVTITNNIGSVAR.M	
317 - 332	1839.8753	1838.8680	1839.0077	-0.1397	1	R.VVFVGNFLRVNTLSMK.L	Oxidation (M)

No match to: 1274.7094, 1783.4429

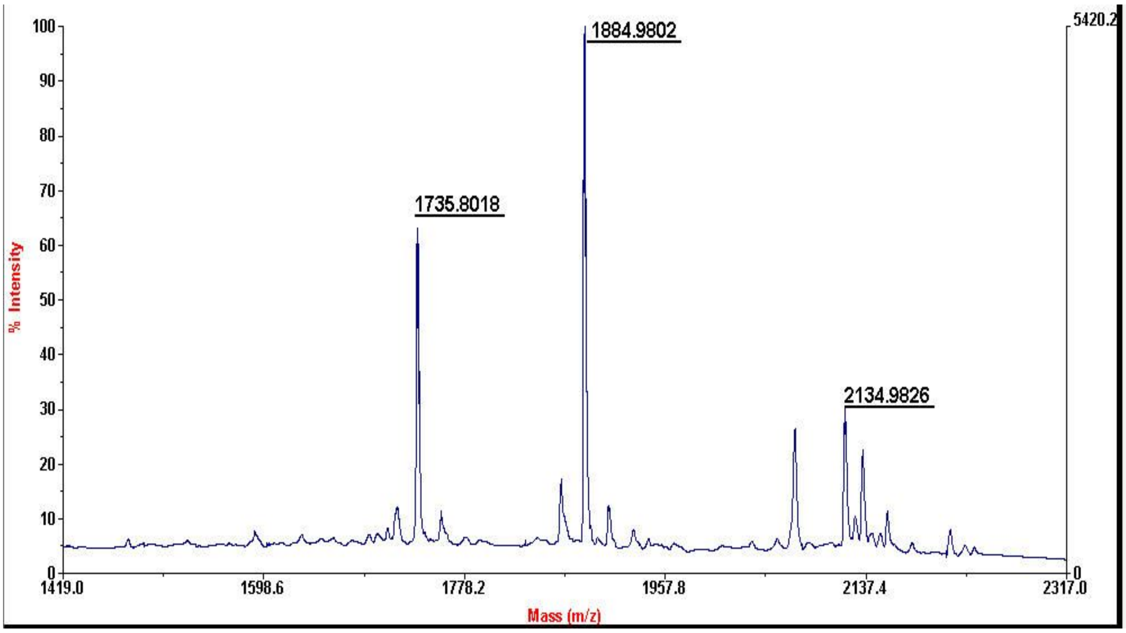
139 L-lactate dehydrogenase A-like 6A



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
133 - 140	1009.3673	1008.3600	1008.4413	-0.0813	0	R.HAYGDQYR.A
223 - 233	1445.6523	1444.6450	1444.7238	-0.0788	1	R.FKDIFQEIYDK.Q
225 - 233	1170.5532	1169.5459	1169.5604	-0.0145	0	K.DIFQEIYDK.Q
261 - 270	1154.4510	1153.4437	1153.5226	-0.0789	0	K.SEGGFIWACK.N
302 - 314	1341.6046	1340.5973	1340.6684	-0.0711	0	K.TVEAEAAHGTVTR.H
322 - 338	1879.0925	1878.0853	1877.9272	0.1581	0	K.GQETSTNPIASIFAWTR.G

No match to: 1021.3626, 1138.6243, 1910.9845

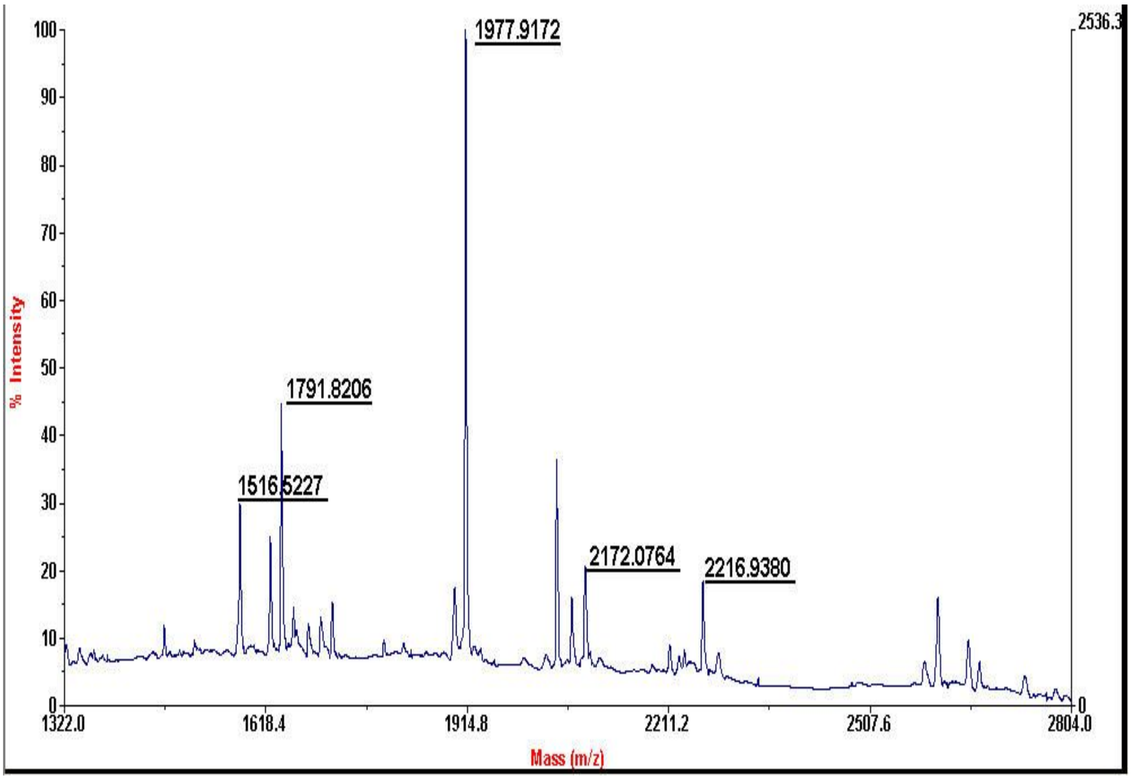
140 Spermatogenesis- and oogenesis-specific basic helix-loop-helix-containing protein 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
39 - 54	1735.8018	1734.7945	1734.9404	-0.1458	0	K.LFANIAEVTITISDTK.E	
109 - 128	2134.9826	2133.9754	2133.9745	0.0009	0	K.GCISGHGMDIALTEPLTMEK.M	2 Oxidation (M)
278 - 294	1884.9802	1883.9729	1883.9775	-0.0046	0	K.QQTPIELSLPGTVMAQR.E	Oxidation (M)

No match to: 1338.4548

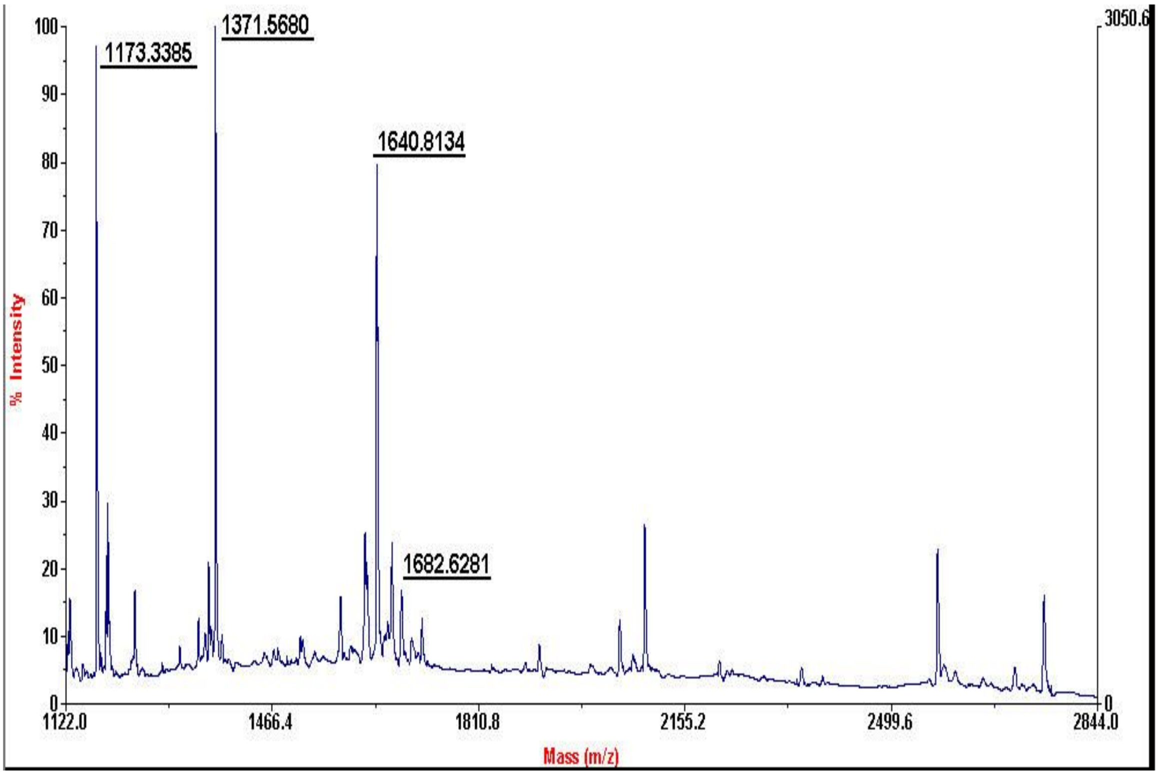
141 spermatogenesis associated 6



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
6 - 26	2172.0764	2171.0691	2171.1694	-0.1002	0	K.ALQCALALEISSVTCPGVVLK.D
27 - 42	1977.9172	1976.9099	1976.9554	-0.0455	1	K.DKEDIYLSICVFGQYK.K
43 - 58	1791.8206	1790.8133	1790.9502	-0.1368	1	K.KTQCVPATFPLVFNAR.M
307 - 319	1516.5227	1515.5155	1515.6954	-0.1799	1	R.TPHGRDFDDSLEK.C
420 - 438	2216.9380	2215.9308	2215.9923	-0.0615	1	R.GTFHLDDGEYWSNRAASYK.G

No match to: 1500.4144

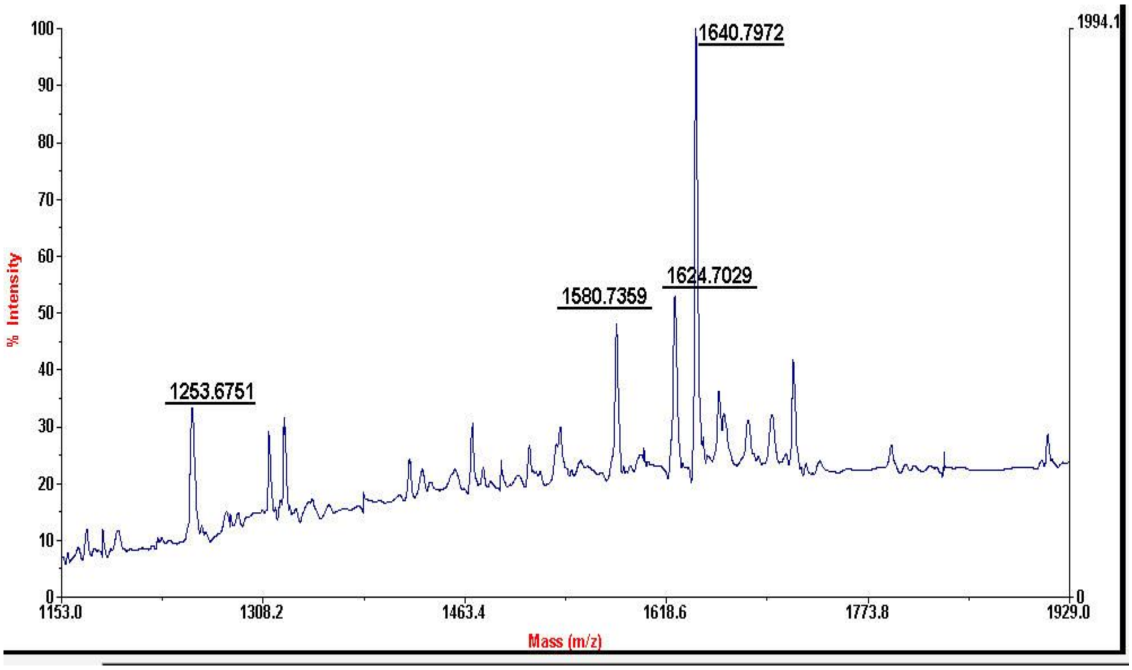
142 60S ribosomal protein L13a



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
21 - 32	1371.5680	1370.5607	1370.7493	-0.1885	1	R.KHGVVPLATYMR.I	
51 - 60	1173.3385	1172.3312	1172.5219	-0.1907	1	K.GMPHKCYHGK.T	Oxidation (M)
64 - 78	1640.8134	1639.8061	1639.9046	-0.0985	0	R.VYNVTQHAVGIVVNK.Q	
147 - 160	1682.6281	1681.6208	1681.7909	-0.1701	0	K.QPELLEPISYEFMA.-	Oxidation (M)

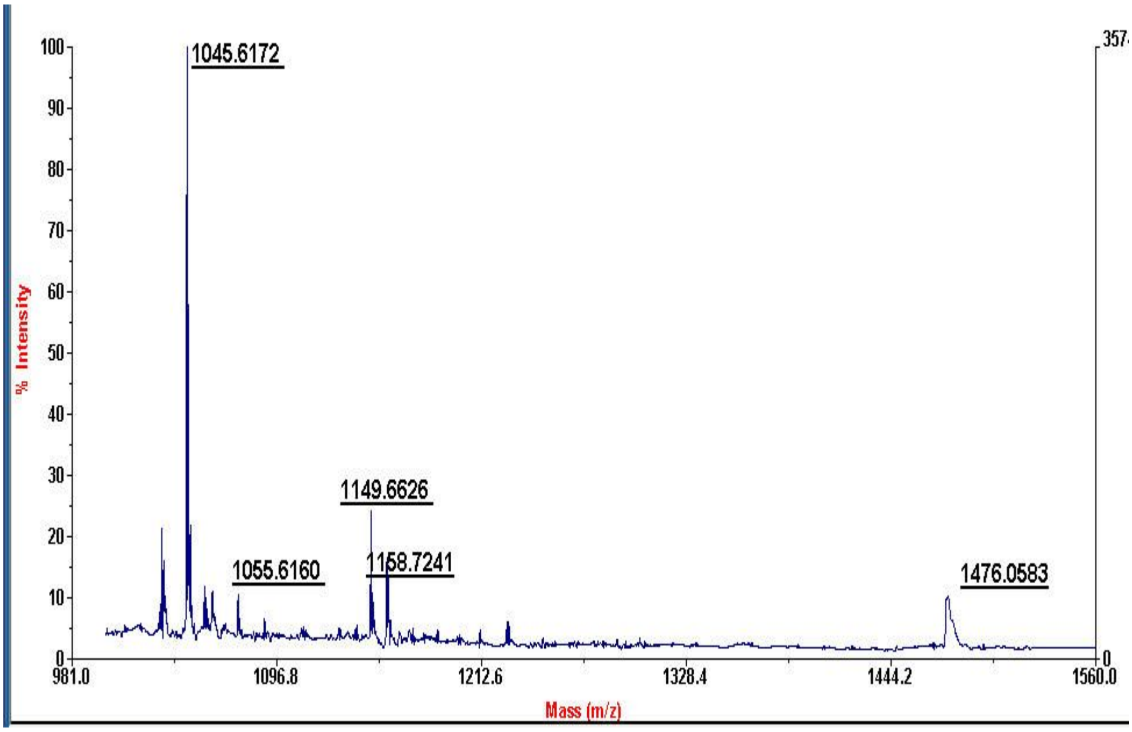
No match to: 2088.8146

143 SALL1 protein



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 15	1624.7029	1623.6956	1623.7399	-0.0443	0	M.VHMGTHMWNSTPAR.R
2 - 15	1640.7972	1639.7899	1639.7348	0.0552	0	M.VHMGTHMWNSTPAR.R Oxidation (M)
108 - 122	1580.7359	1579.7286	1579.8205	-0.0919	0	R.LQNSEPNAPLAGLEK.M
137 - 147	1253.6751	1252.6678	1252.6187	0.0492	1	R.FVEDSKEIVTS.-

144 Adenylate kinase isoenzyme 4

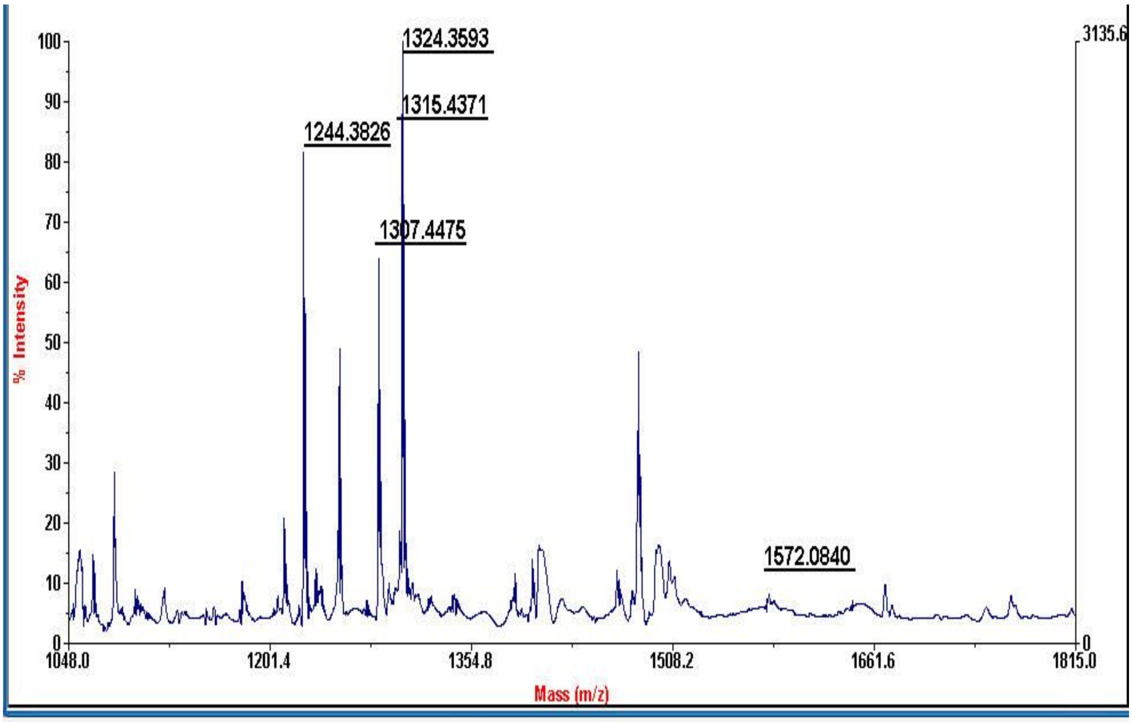


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

1 - 9	1055.6160	1054.6087	1054.4576	0.1511	0	-.MGGFMEDLR.K
13 - 24	1158.7241	1157.7168	1157.6808	0.0360	0	K.IIFIIGGPGSGK.G
59 - 66	1045.6172	1044.6099	1044.5750	0.0350	1	K.LIRDIMER.G
81 - 91	1149.6626	1148.6553	1148.5496	0.1058	0	K.EAMVASLGDTR.G
138 - 151	1476.0583	1475.0510	1474.7879	0.2631	1	R.SSLPVDDTTKTIAK.R

No match to: 1031.5269, 1607.0269

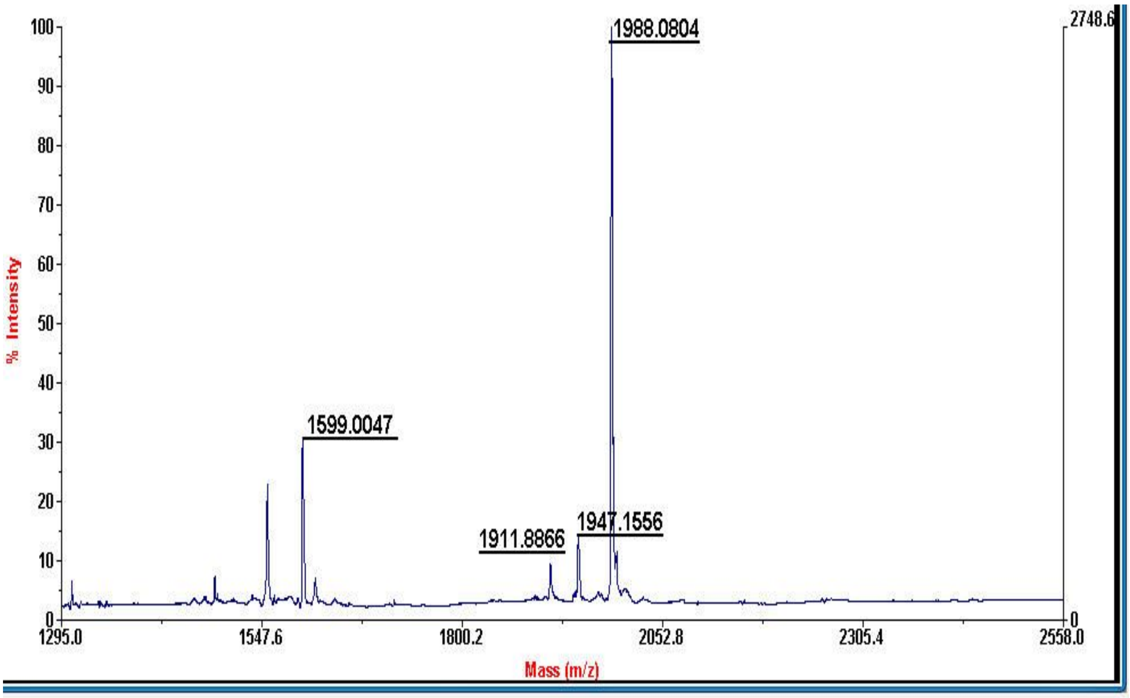
145 WAP four-disulfide core domain 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
5 - 17	1324.3593	1323.3520	1323.7510	-0.3990	0	R.NTIKPGSAQLPAK.H	
82 - 91	1315.4371	1314.4298	1314.5672	-0.1373	1	R.KCCYLHCGFK.C	2
83 - 91	1244.3826	1243.3754	1243.4937	-0.1183	0	K.CCYLHCGFK.C	3
92 - 105	1572.0840	1571.0768	1570.8025	0.2743	1	K.CVIPVKELEEGGNK.D	
122 - 133	1307.4475	1306.4403	1306.5758	-0.1356	1	K.CPGSSSTRCPQK.-	

No match to: 2143.8098

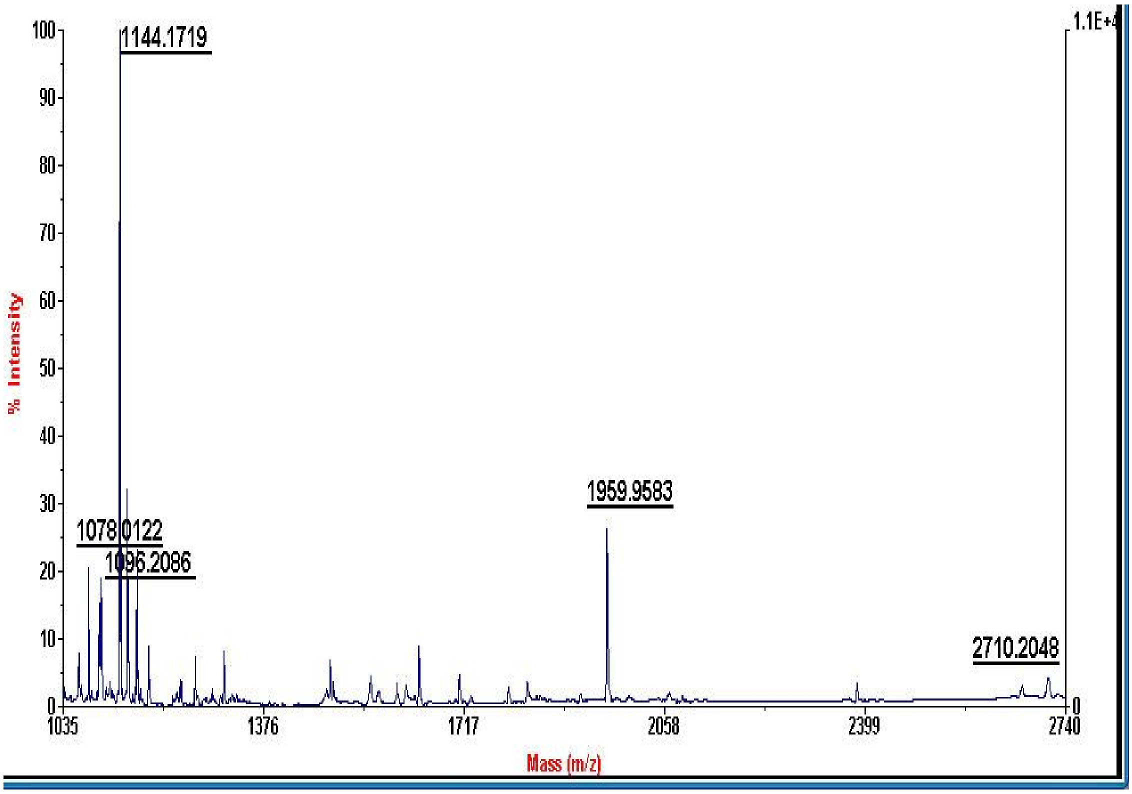
146 Calpain small subunit 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
229 - 246	1988.0804	1987.0732	1987.0275	0.0456	1	R.AGARELGEFHAFIVSDLR.E
247 - 260	1599.0047	1597.9975	1597.8610	0.1365	0	R.ELQGQAGQCILLLR.I
416 - 432	1947.1556	1946.1484	1946.0275	0.1209	1	K.HYQAVGLHLWKVPEGGR.S
453 - 469	1911.8866	1910.8793	1910.9924	-0.1131	1	R.YAQEVSRLCLLPAGTYK.V

No match to: 1554.4414

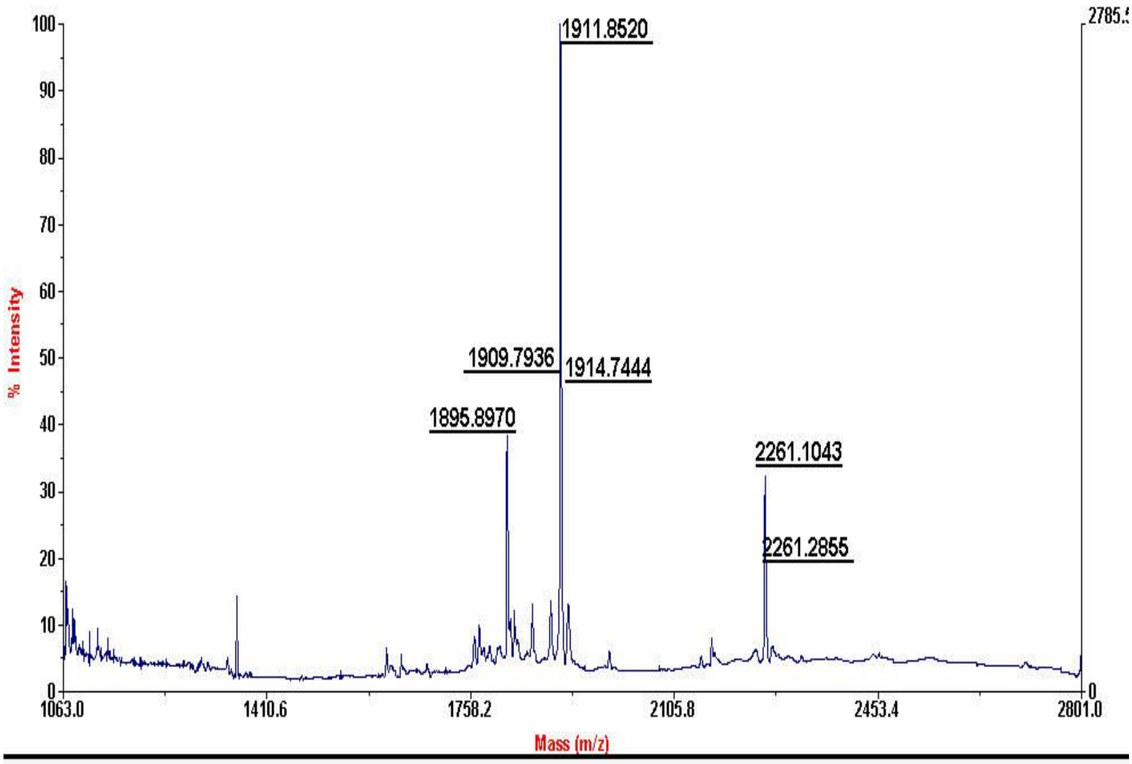
147 Glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
50 - 73	2710.2048	2709.1975	2709.1222	0.0753	0	R.HSDDNGQNHLEGQMNFNADSSQHK.D
87 - 102	1959.9583	1958.9511	1959.0070	-0.0560	1	K.VRILCWVMTGPQNLEK.K ; Oxidation (M)
106 - 114	1096.2086	1095.2013	1095.5938	-0.3924	1	K.HVKATWAQR.C
109 - 117	1078.0122	1077.0049	1076.5185	0.4864	1	K.ATWAQRCNK.V
343 - 352	1144.1719	1143.1646	1142.6659	0.4987	1	R.ILKEISQANK.N

No match to: 1099.9361, 1160.1693

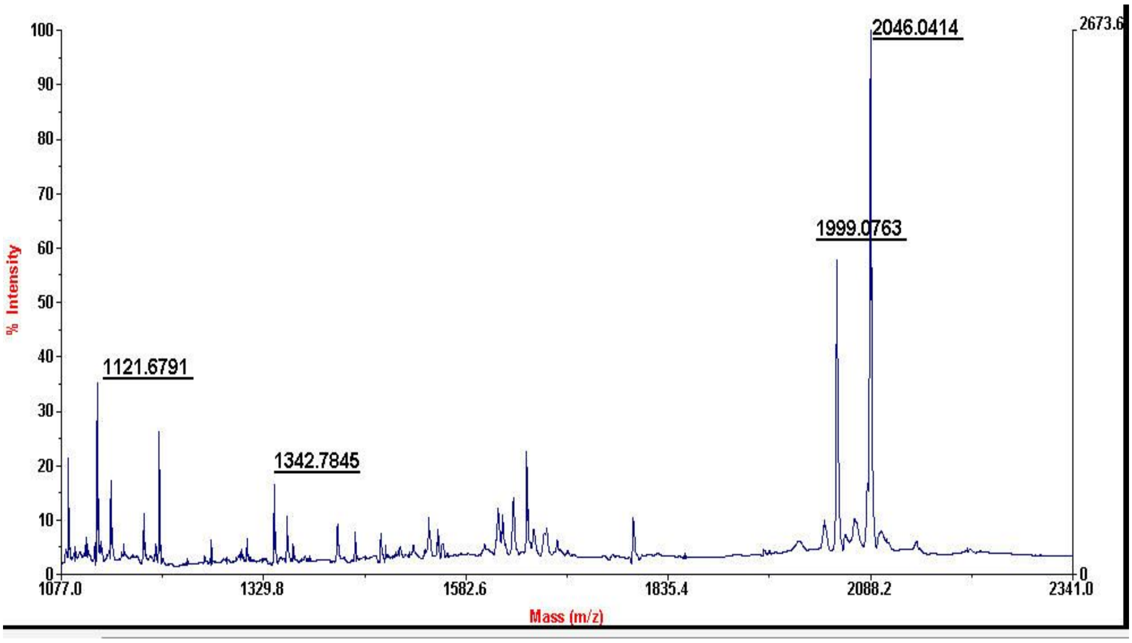
148 RNA (guanine-9-) methyltransferase domain containing 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 18	1895.8970	1894.8897	1894.9346	-0.0449	1	M.SSEMLPAFIETSNVDKK.Q
2 - 18	1911.8520	1910.8448	1910.9295	-0.0848	1	M.SSEMLPAFIETSNVDKK.Q
Oxidation (M)						
74 - 89	1914.7444	1913.7372	1913.8108	-0.0736	1	K.LERQCQMEPNSDGHDR.K
196 - 215	2261.1043	2260.0971	2260.1236	-0.0266	1	K.ELDESKAYVIGGLVDHNHHK.G
196 - 215	2261.2855	2260.2783	2260.1236	0.1546	1	K.ELDESKAYVIGGLVDHNHHK.G
297 - 313	1909.7936	1908.7864	1908.6803	0.1061	0	R.MEEGGSDSDSSEEEYSR.N
Oxidation (M)						

No match to: 1820.7724

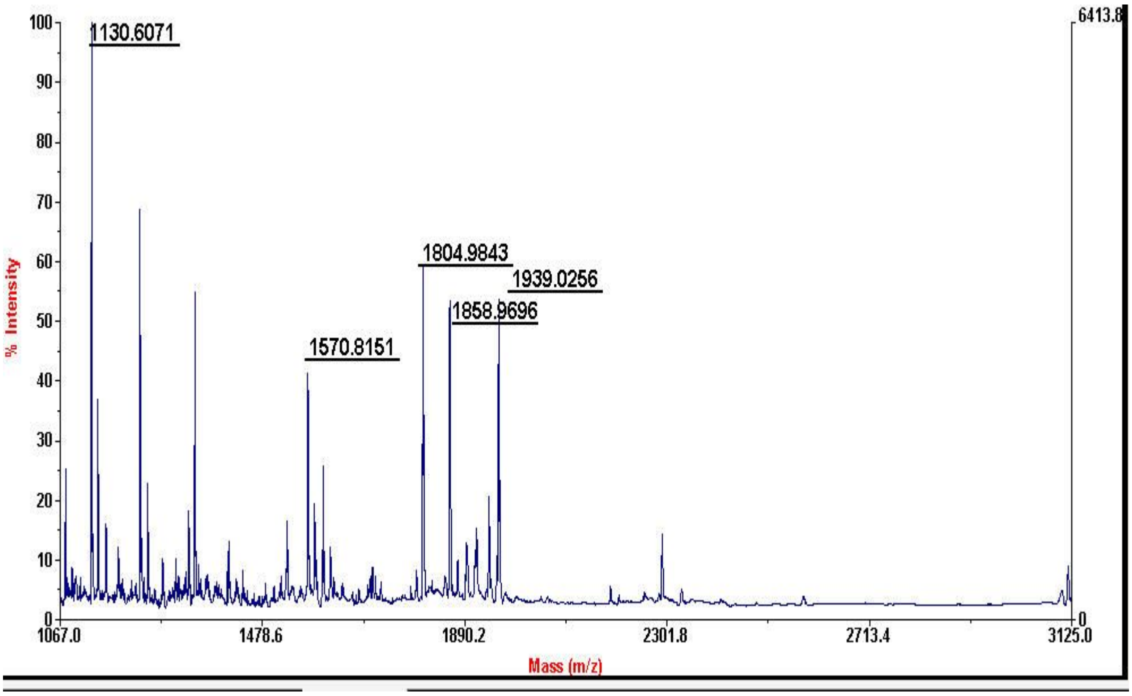
149 Sperm-associated antigen 4-like protein



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
37 - 54	2046.0414	2045.0341	2044.9558	0.0784	0	R.MAEDTSPNMNDNILLPVR.N	Oxidation (M)
96 - 104	1121.6791	1120.6718	1120.5984	0.0734	1	K.LLCQKLMEK.T	Oxidation (M)
295 - 306	1342.7845	1341.7772	1341.6275	0.1497	0	K.DFVIYGMEGSPK.E	
340 - 356	1999.0763	1998.0690	1997.9782	0.0909	1	K.VKISSNWGNPGFTCLYR.V	

No match to: 1641.9232

150Gamma-enolase

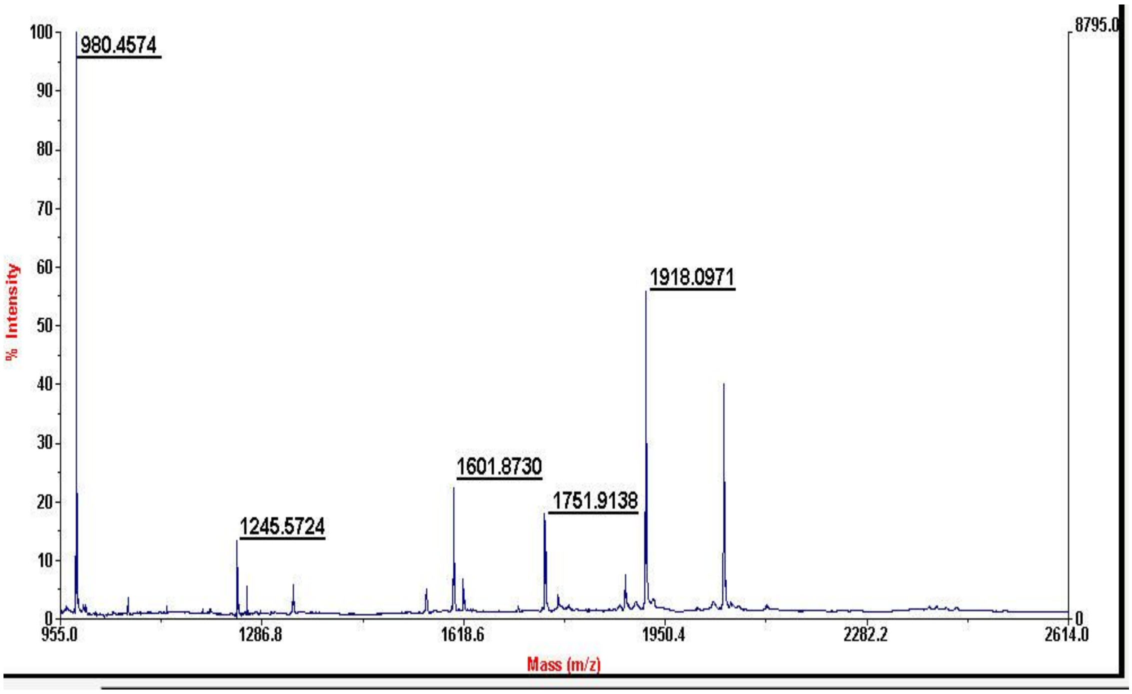


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

33 - 50	1804.9843	1803.9771	1803.9366	0.0405	0	R.AAVPSGASTGIYEALELR.D
163 - 179	1939.0256	1938.0183	1937.9742	0.0441	0	K.LAMQEFMILPVGAESFR.D
184 - 193	1130.6071	1129.5998	1129.6131	-0.0133	0	R.LGAEVYHTLK.G
240 - 253	1570.8151	1569.8078	1569.7860	0.0218	0	K.IVIGMDVAASEFYR.D
270 - 285	1858.9696	1857.9623	1857.9261	0.0363	0	R.YITGDQLGALYQDFVR.D

No match to: 1143.6408, 1229.6032, 1340.6368, 1959.0208

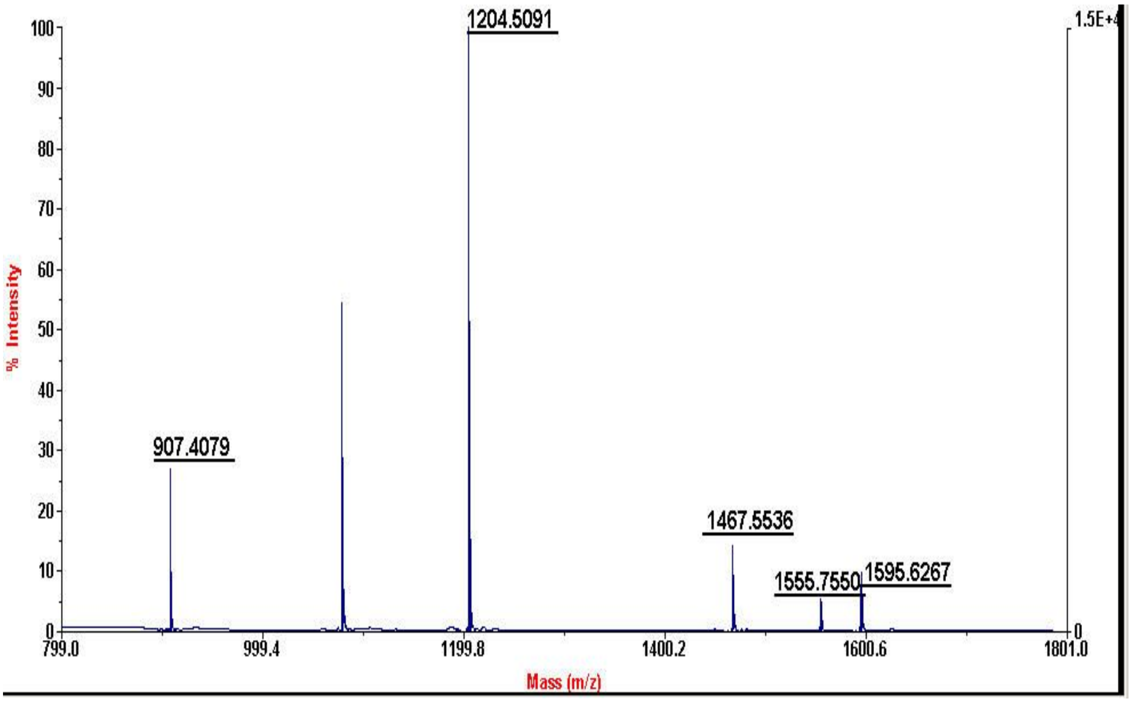
151 Rho GDP-dissociation inhibitor 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
34 - 49	1918.0971	1917.0898	1916.9327	0.1572	1	K.SIQEIQELDKDDESLR.K
128 - 134	980.4574	979.4501	979.4875	-0.0375	0	K.YIQHTYR.K
139 - 152	1601.8730	1600.8657	1600.7555	0.1102	1	K.IDKTDYMVGSYGPR.A
142 - 152	1245.5724	1244.5652	1244.5495	0.0156	0	K.TDYMVGSYGPR.A
153 - 167	1751.9138	1750.9065	1750.8301	0.0765	0	R.AEEYEFLTPVEEAPK.G

No match to: 2046.1784

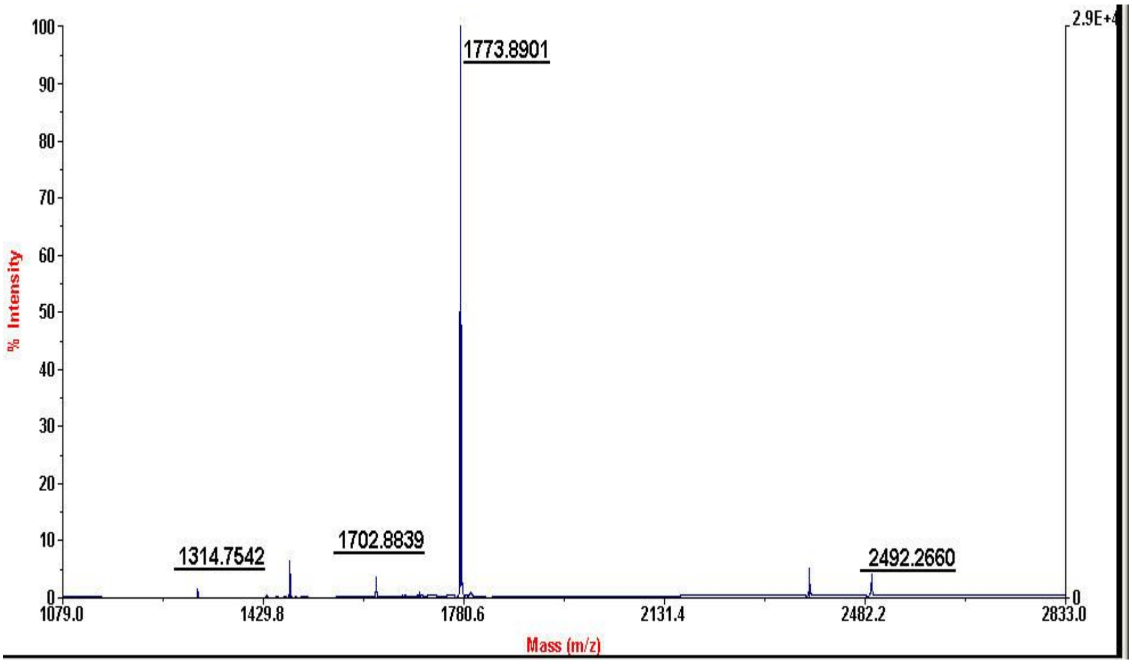
152 ） Fatty acid-binding protein



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 31	907.4079	906.4007	906.4923	-0.0917	0	K.SLGVGFATR.Q
67 - 79	1467.5536	1466.5463	1466.6525	-0.1062	0	K.LGVEFDETTADDR.K
67 - 80	1595.6267	1594.6194	1594.7475	-0.1281	1	K.LGVEFDETTADDRK.V
98 - 107	1204.5091	1203.5018	1203.5884	-0.0866	0	K.WDGQETTLVR.E
114 - 127	1555.7550	1554.7477	1554.8552	-0.1075	0	K.LILTLTHGTAVCTR.T

No match to: 1078.4533, 1186.5096

153 ） Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthetase 2

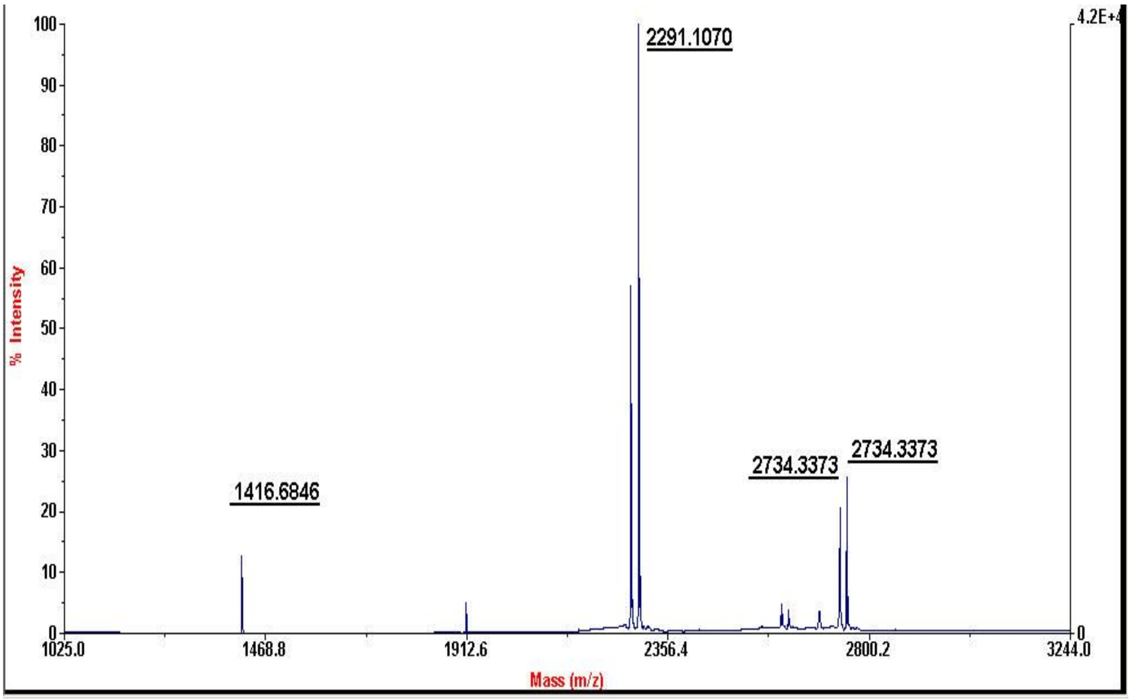


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

412 - 426	1702.8839	1701.8767	1701.8369	0.0398	0	R.NPVHNGHALLMQDTR.R	
535 - 557	2492.2660	2491.2587	2491.3508	-0.0921	1	K.VLSMAPGLTSVEIIPFRVAAYNK.A	Oxidation (M)
570 - 582	2492.2660	1624.8918	1624.7416	0.1502	1	R.HNEFDFISGTRMR.K	Oxidation (M)
587 - 602	1773.8901	1772.8828	1772.8192	0.0636	1	R.EGENPPDGFMAPKAWK.V	
600 - 609	1314.7542	1313.7469	1313.6768	0.0701	1	K.AWKVLTDYYR.S	

No match to: 1434.7780

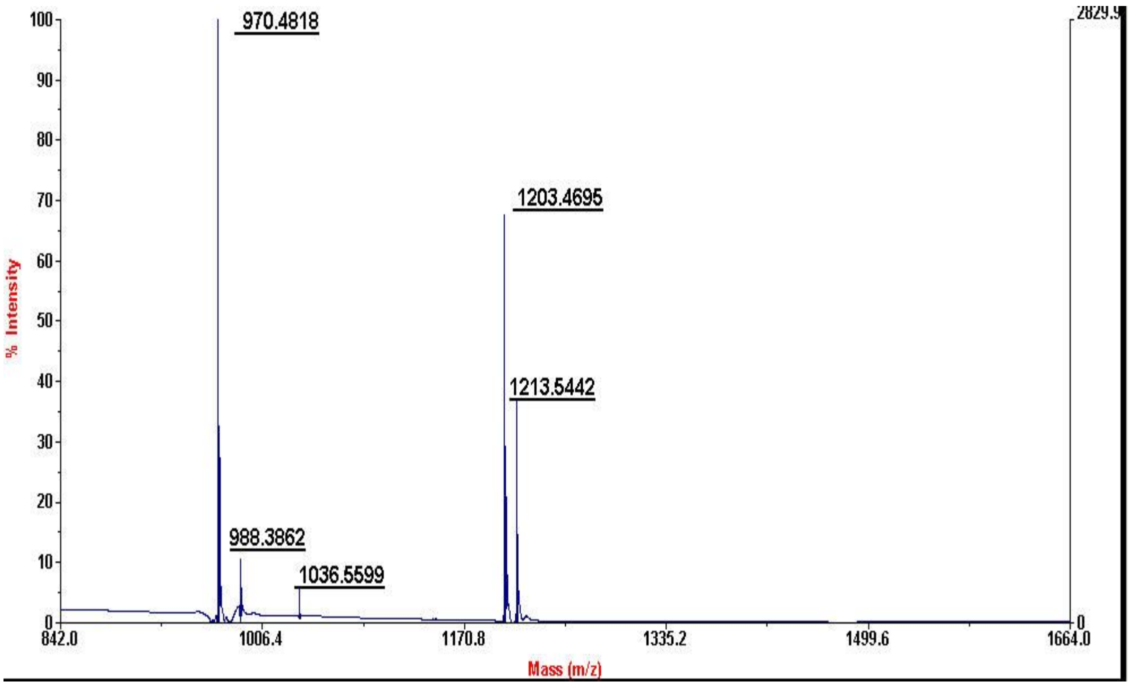
154 ） Histidine triad nucleotide-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
8 - 21	1416.6846	1415.6773	1415.7521	-0.0748	0	K.AQVARPGGDTIFGK.I	
31 - 37	907.4288	906.4215	906.4447	-0.0232	0	K.IIFEDDR.C	
38 - 57	2291.1070	2290.0998	2290.1933	-0.0935	0	R.CLAFHDISPQAPTHFLVIPK.K	
59 - 83	2734.3373	2733.3300	2733.4007	-0.0707	1	K.HISQISVAEDDDESLLGHLMIVGKK.C	
59 - 83	2750.3017	2749.2944	2749.3956	-0.1012	1	K.HISQISVAEDDDESLLGHLMIVGKK.C	Oxidation (M)

No match to: 1910.8632, 2274.0976, 2313.0702, 2329.0537, 2621.1316

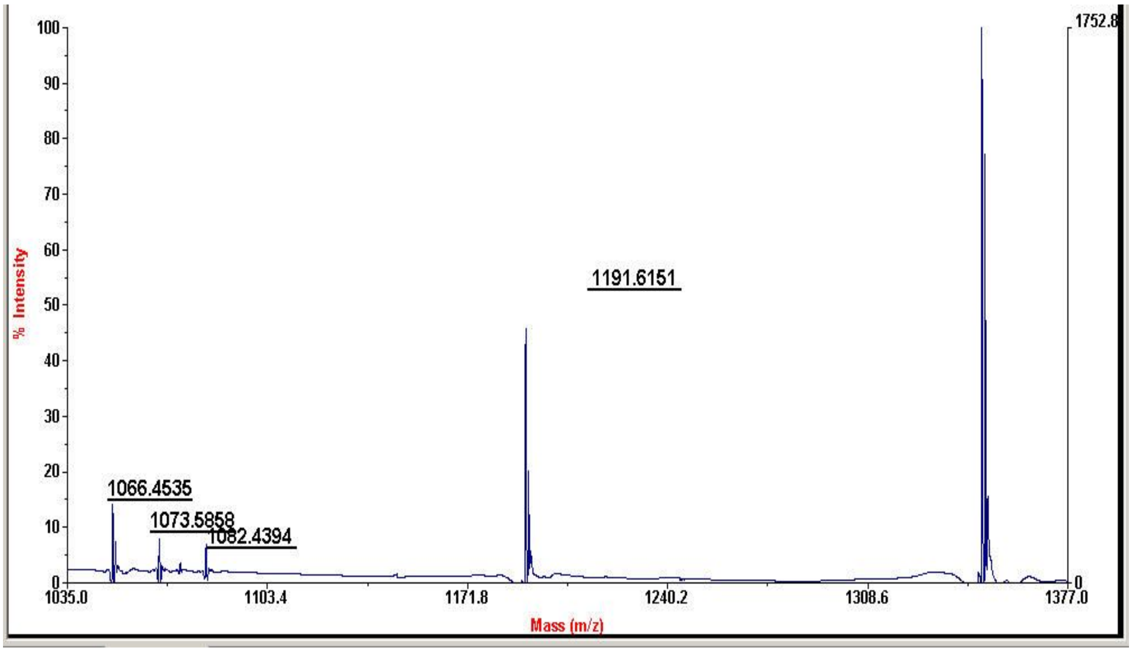
155 ） Ubiquitin-conjugating enzyme E2 N



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
15 - 24	1036.5599	1035.5527	1035.6328	-0.0801	0	R.LLAEPVPGIK.A
25 - 33	988.3862	987.3789	987.4257	-0.0468	0	K.AEPDESNAR.Y
93 - 102	1213.5442	1212.5369	1212.6615	-0.1246	1	K.DKWSPALQIR.T
95 - 102	970.4818	969.4745	969.5396	-0.0651	0	K.WSPALQIR.T
131 - 141	1203.4695	1202.4622	1202.5891	-0.1269	0	K.TNEAQAIETAR.A

No match to: 984.3671, 1747.6849, 1763.6197, 2195.7463, 2209.8172

156 ） Tubulin-specific chaperone A

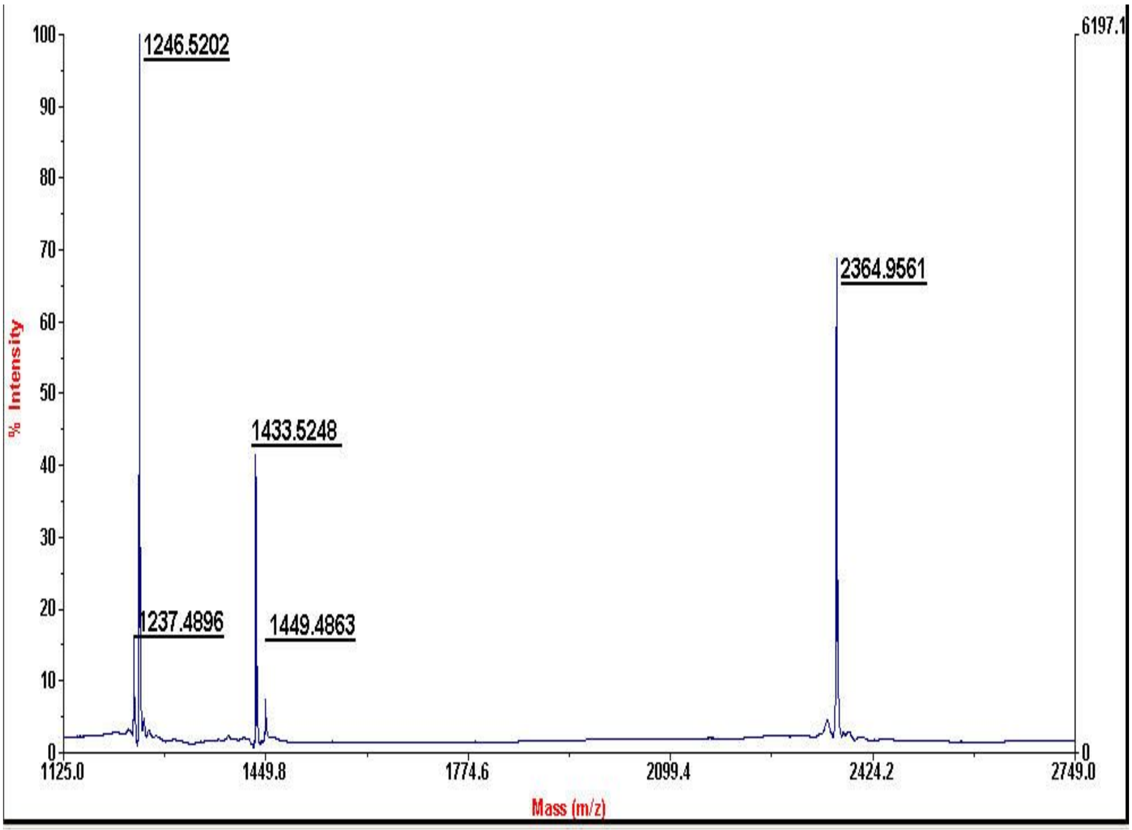


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

53 - 61	1073.5858	1072.5785	1072.5513	0.0273	0	K.QAEILQESR.M	
62 - 69	1050.4906	1049.4833	1049.4456	0.0377	0	R.MMIPDCQR.R	
62 - 69	1066.4535	1065.4462	1065.4406	0.0057	0	R.MMIPDCQR.R	; Oxidation (M)
62 - 69	1082.4394	1081.4321	1081.4355	-0.0034	0	R.MMIPDCQR.R	; 2 Oxidation (M)
70 - 80	1347.7146	1346.7073	1346.7306	-0.0233	1	R.RLEAAYLDLQR.I	
71 - 80	1191.6151	1190.6079	1190.6295	-0.0216	0	R.LEAAYLDLQR.I	

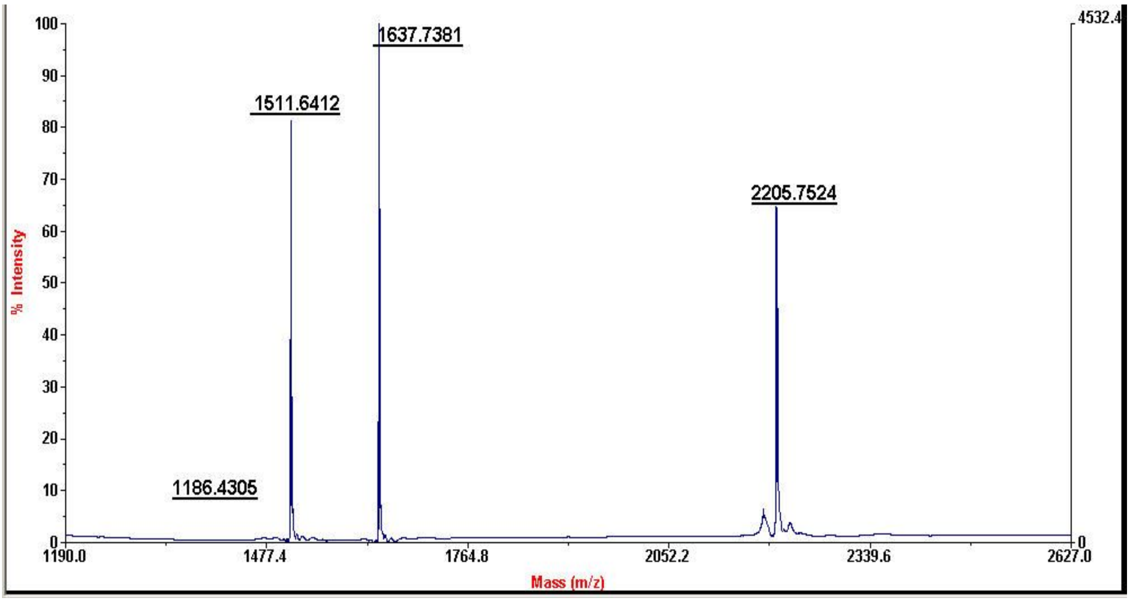
No match to: 2207.9777

157 ） Myosin regulatory light chain 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
36 - 45	1237.4896	1236.4823	1236.5557	-0.0734	0	K.EAFNMIDQNR.D	
105 - 124	2364.9561	2363.9488	2364.0229	-0.0741	0	R.NAFACFDEEASGFIHEDHLR.E	
134 - 144	1433.5248	1432.5175	1432.5817	-0.0641	0	R.FTDEEVDEMYR.E	
134 - 144	1449.4863	1448.4790	1448.5766	-0.0976	0	R.FTDEEVDEMYR.E	Oxidation (M)
152 - 161	1246.5202	1245.5129	1245.5778	-0.0649	0	K.GNFNYVEFTR.I	

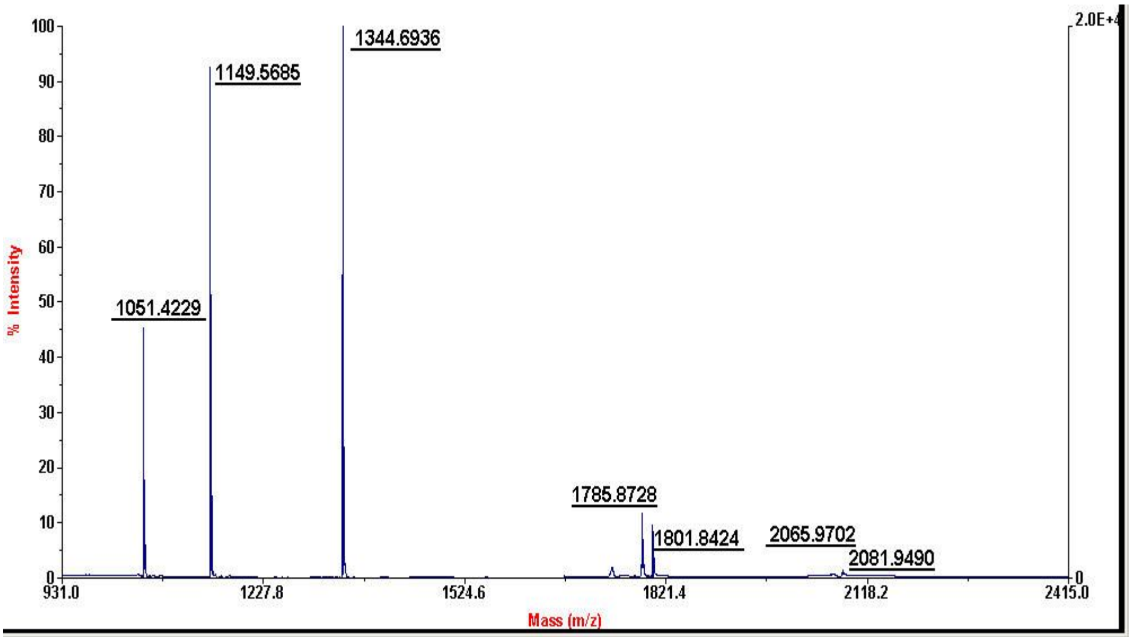
158 ） Cytochrome b5



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
11 - 19	1186.4305	1185.4232	1185.5917	-0.1685	0	K.YYTLEEIQK.H
40 - 52	1511.6412	1510.6339	1510.7416	-0.1077	0	K.FLEEHPGGEEVLR.E
53 - 73	2205.7524	2204.7451	2204.9207	-0.1755	0	R.EQAGGDATENFEDVGHSTDAR.E
78 - 91	1637.7381	1636.7308	1636.8573	-0.1265	0	K.TFIIGELHPDDRPK.L

No match to: 2185.8781, 2189.7801, 2223.8476

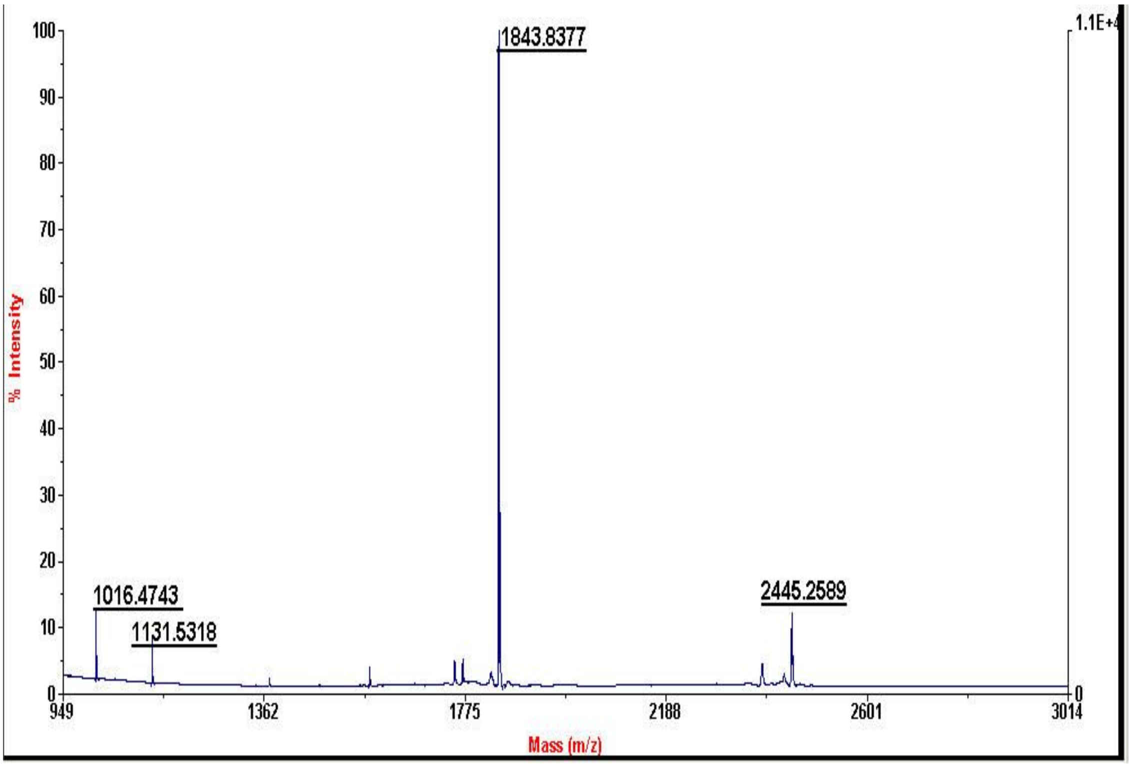
159 ） Nucleoside diphosphate kinase A



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 18	1344.6936	1343.6864	1343.7561	-0.0698	0	R.TFIAIKPDGVQR.G
40 - 56	2065.9702	2064.9629	2065.0190	-0.0561	1	K.FMQASEDLLKEHYVDLK.D

40 - 56	2081.9490	2080.9417	2081.0139	-0.0722	1	K.FMQASEDLLKEHYVDLK.D
Oxidation (M)						
57 - 66	1149.5685	1148.5612	1148.6342	-0.0731	0	K.DRPFFAGLVK.Y
89 - 105	1785.8728	1784.8655	1784.9091	-0.0436	0	R.VMLGETNPADSKPGTIR.G
89 - 105	1801.8424	1800.8352	1800.9040	-0.0688	0	R.VMLGETNPADSKPGTIR.G
Oxidation (M)						
106 - 114	1051.4229	1050.4156	1050.4917	-0.0761	0	R.GDFCIQVGR.N

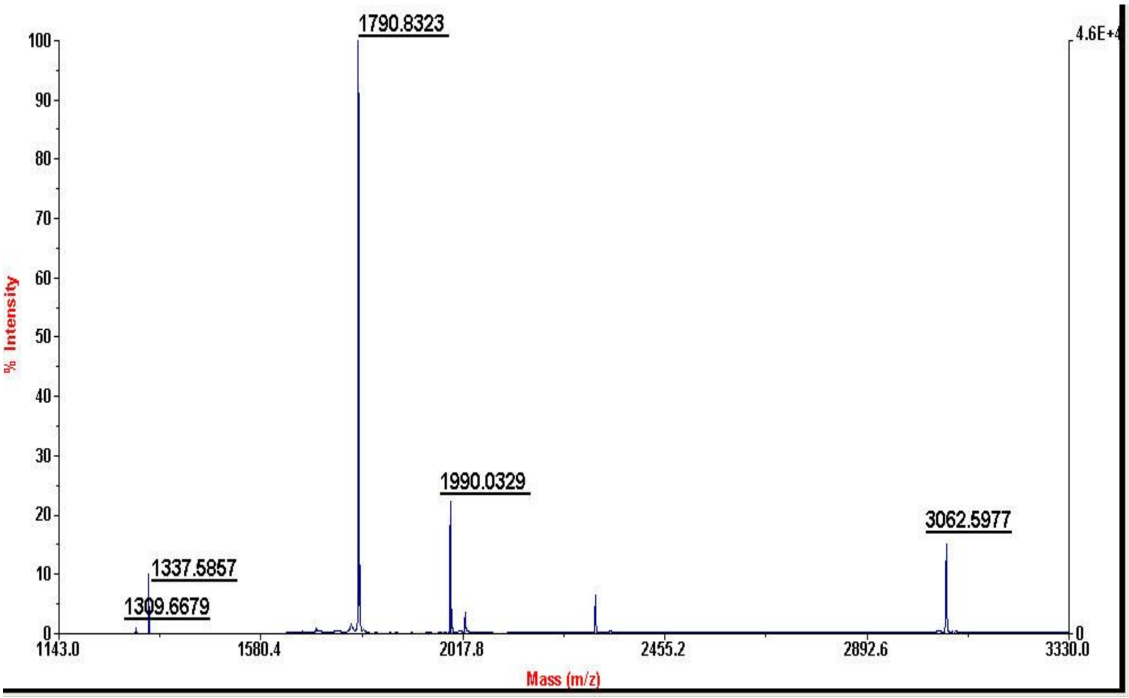
160 ） Epididymal secretory protein E1 precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
36 - 51	1843.8377	1842.8304	1842.8604	-0.0300	0	K.EVNVSPCPTQPCQLSK.G 2
72 - 94	2445.2589	2444.2516	2444.2596	-0.0081	0	K.AVVHGILMGVPVPFPIPEPDGCK.S ;
Oxidation (M)						
95 - 103	1016.4743	1015.4671	1015.5121	-0.0450	0	K.SGINCPIQK.D
104 - 112	1131.5318	1130.5245	1130.5608	-0.0363	1	K.DKTYSYLNK.L

No match to: 1578.7361, 1752.8107, 1826.7324

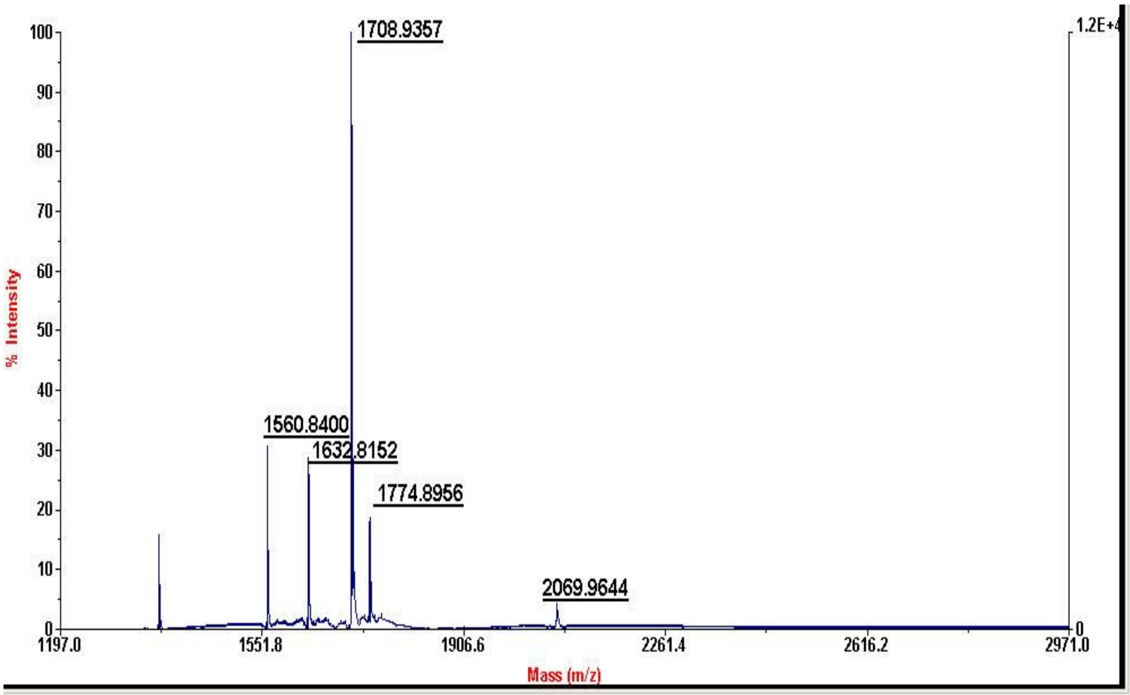
161 ） Cofilin-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 45	1309.6679	1308.6606	1308.6748	-0.0142	1	K.AVLFCLSEDKK.N
46 - 73	3062.5977	3061.5905	3061.5860	0.0045	1	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M
82 - 92	1337.5857	1336.5784	1336.6187	-0.0403	0	R.YALYDATYETK.E
96 - 112	1990.0329	1989.0256	1989.0611	-0.0355	1	K.KEDLVFIFWAPESAPLK.S
133 - 146	1790.8323	1789.8250	1789.8053	0.0197	1	K.HELQANCYEEVKDR.C

No match to: 1026.5439, 1774.6063, 2022.0340, 2303.1671

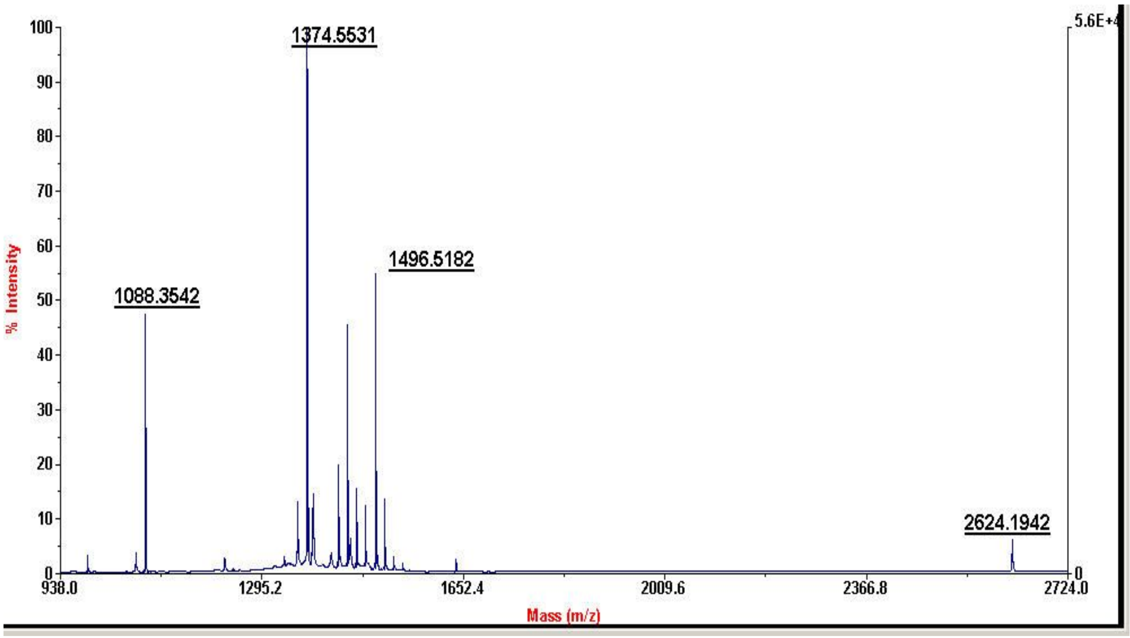
162 ） Phosphatidylethanolamine-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 39	3471.8596	3470.8523	3470.7106	0.1417	0	K.WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK.V
48 - 62	1632.8152	1631.8080	1631.7903	0.0176	0	K.NRPTSISWDGLDSGK.L
63 - 76	1560.8400	1559.8327	1559.8195	0.0132	0	K.LYTLVLTDPDAPSR.K
81 - 93	1774.8956	1773.8883	1773.8773	0.0110	1	K.YREWHHFLVVNMK.G Oxidation (M)
120 - 132	1708.9357	1707.9284	1707.8984	0.0300	0	R.YVWLVYEQDRPLK.C
162 - 179	2069.9644	2068.9571	2068.9200	0.0371	0	R.APVAGTCYQAEWDDYVPK.L

No match to: 1370.6873, 1740.9123

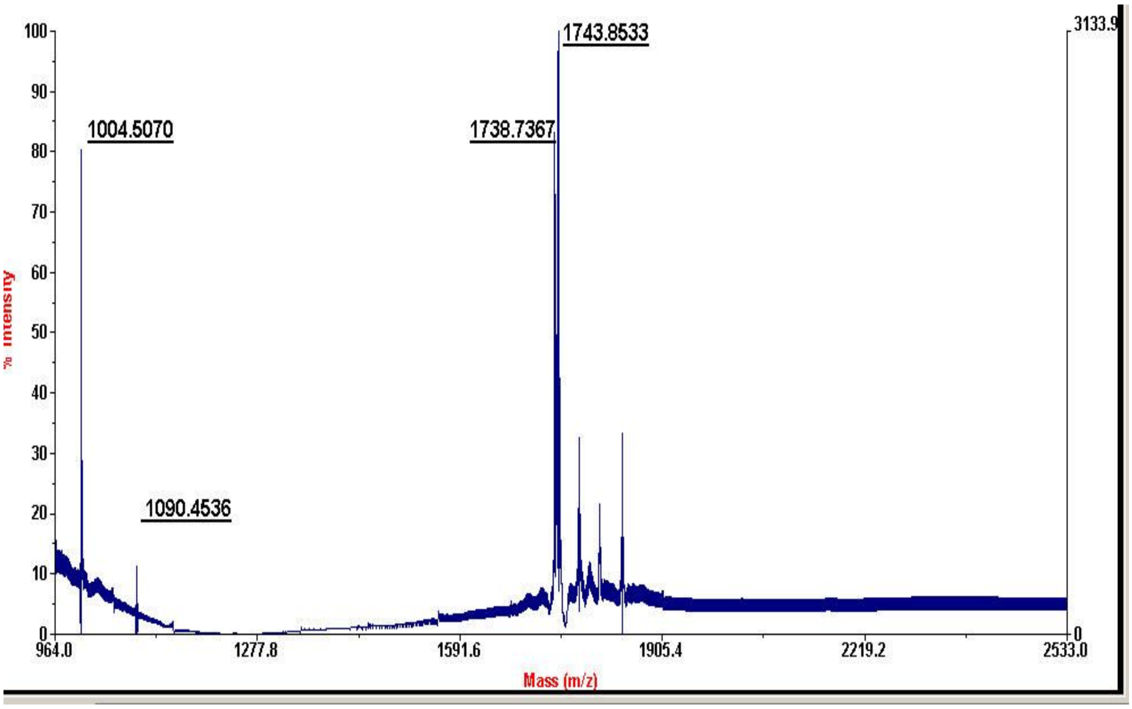
163 ） Alpha crystallin B chain



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
12 - 22	1374.5531	1373.5459	1373.6993	-0.1534	0	R.RPFFPFHSPSR.L
57 - 69	1496.5182	1495.5109	1495.6766	-0.1656	0	R.APSWFDTGLSEMR.L
108 - 116	1088.3542	1087.3470	1087.5047	-0.1577	0	R.QDEHGFISR.E
124 - 149	2624.1942	2623.1869	2623.3705	-0.1836	0	R.IPADVDPLTITSSLSSDGVLTVNGPR.K

No match to: 1386.7695, 1430.5848, 1446.5445, 1462.5765, 1478.5436, 1512.4561

164 ） Superoxide dismutase [Mn]

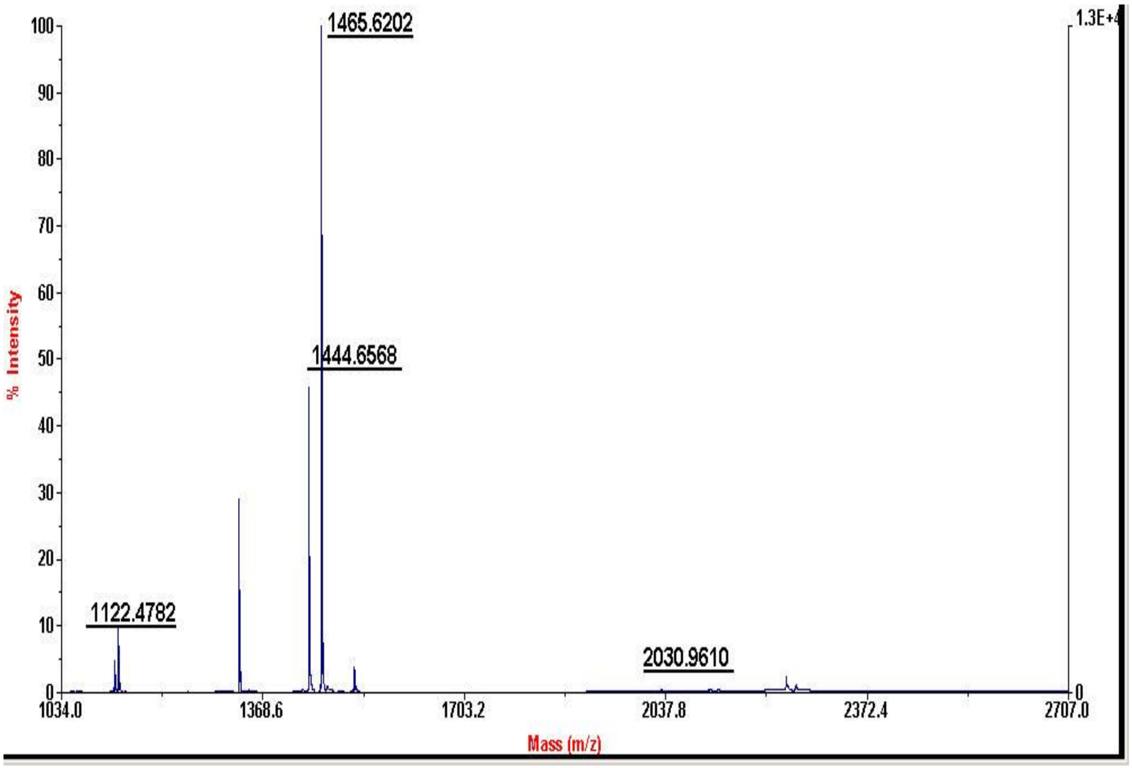


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

54 - 68	1738.7367	1737.7295	1737.8434	-0.1140	0	K.HHAAYVNNLNVTEEK.Y
124 - 132	1090.4536	1089.4463	1089.5131	-0.0668	1	R.DFGSFDKFK.E
195 - 202	1004.5070	1003.4998	1003.5451	-0.0453	0	K.NVRPDYLK.A
203 - 216	1743.8533	1742.8460	1742.8740	-0.0280	0	K.AIWNVINWENVTER.Y

No match to: 1775.8370, 1807.8601, 1842.7914

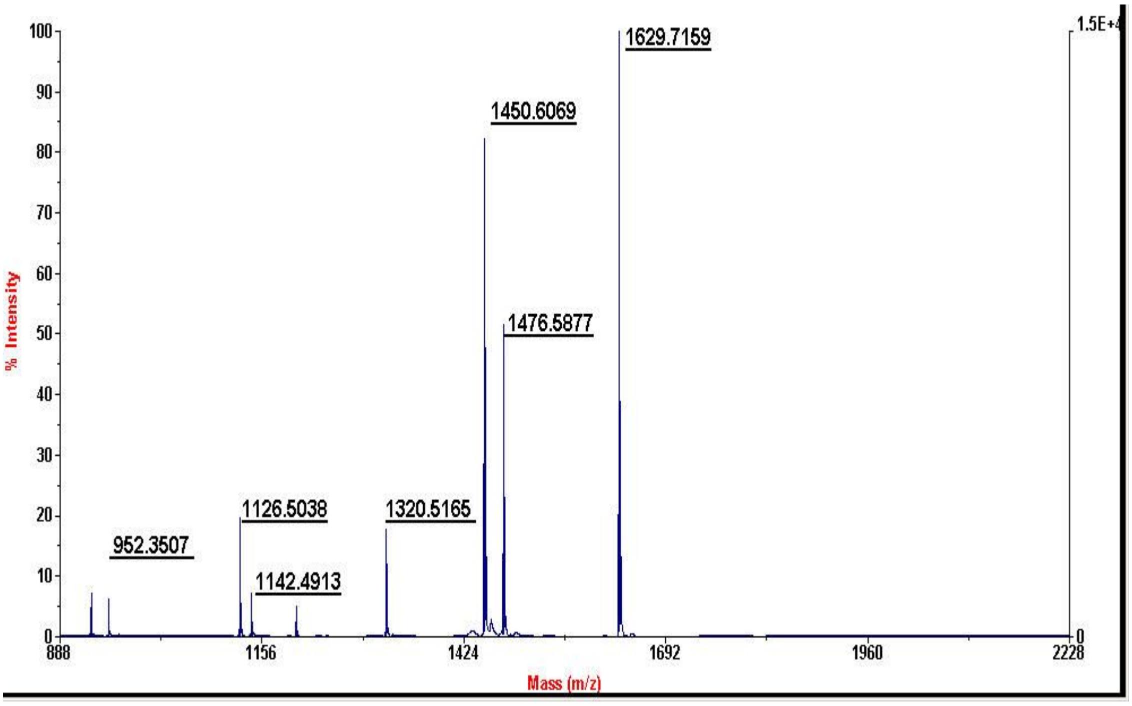
165 ） Adenine phosphoribosyltransferase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
15 - 27	1465.6202	1464.6129	1464.7402	-0.1272	0	R.SFPDFPTPGVVFR.D
28 - 40	1444.6568	1443.6496	1443.7722	-0.1226	1	R.DISPVLKDPASFR.A
58 - 67	1122.4782	1121.4709	1121.5717	-0.1008	0	R.IDYIAGLDSR.G
146 - 163	2030.9610	2029.9537	2030.0969	-0.1432	0	R.LQAEVLECVSLVELTSLK.G

No match to: 1329.5559, 2237.9236, 2389.9583

166 ）Calcyphosin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 10	1126.5038	1125.4965	1125.4682	0.0283	0	-.MDAVDATMEK.L	Oxidation (M)
1 - 10	1142.4913	1141.4840	1141.4631	0.0209	0	-.MDAVDATMEK.L	2 Oxidation (M)
40 - 47	952.3507	951.3434	951.4298	-0.0863	0	R.SLDADEFR.Q	
53 - 67	1629.7159	1628.7086	1628.8192	-0.1106	0	K.LGLVLDQAEAEGVCR.K	
72 - 84	1450.6069	1449.5996	1449.7100	-0.1103	0	R.NGSGTLDLEEFLR.A	
132 - 142	1320.5165	1319.5092	1319.5993	-0.0901	0	R.SGEWTEDEVLR.R	
132 - 143	1476.5877	1475.5804	1475.7005	-0.1200	1	R.SGEWTEDEVLRR.F	

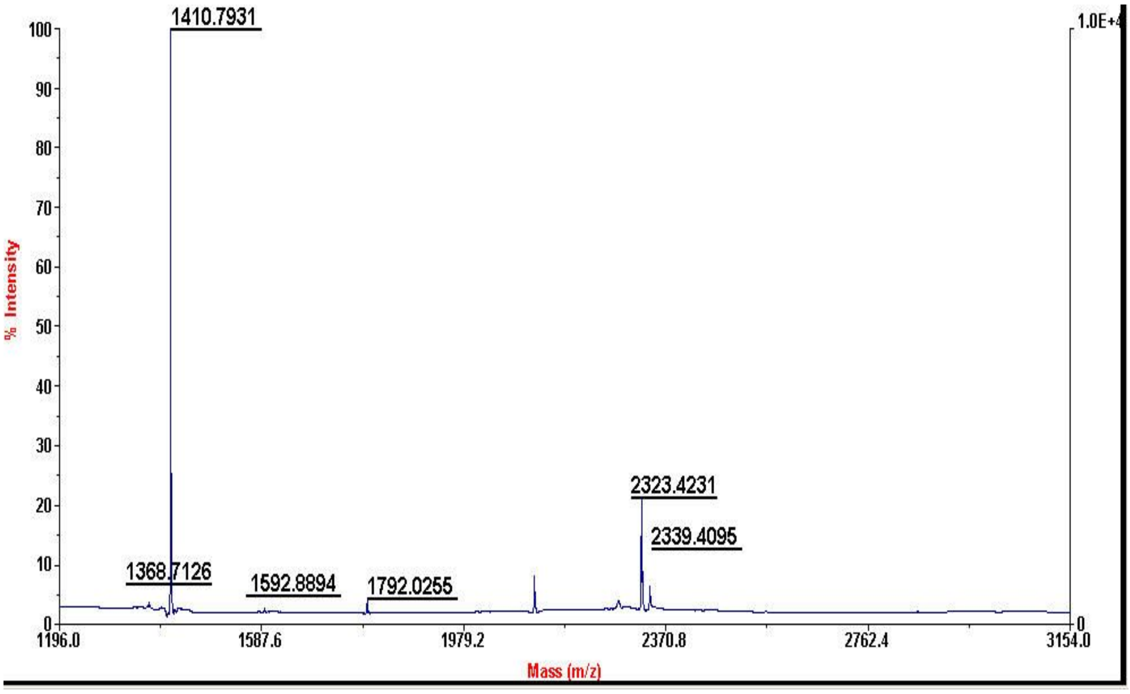
No match to: 1459.4444

168 ） ARF-related protein 1

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 40	1210.1685	1209.1612	1209.6353	-0.4741	1	K.TTFLEQSKTR.F
53 - 68	1588.3186	1587.3114	1586.8880	0.4234	0	K.ITTTVGLNIGTVDVGK.A
53 - 70	1815.4120	1814.4048	1814.0262	0.3786	1	K.ITTTVGLNIGTVDVGKAR.L
136 - 148	1460.2712	1459.2639	1459.7228	-0.4590	0	K.QDVETCLSIPDIK.T

No match to: 1887.3421

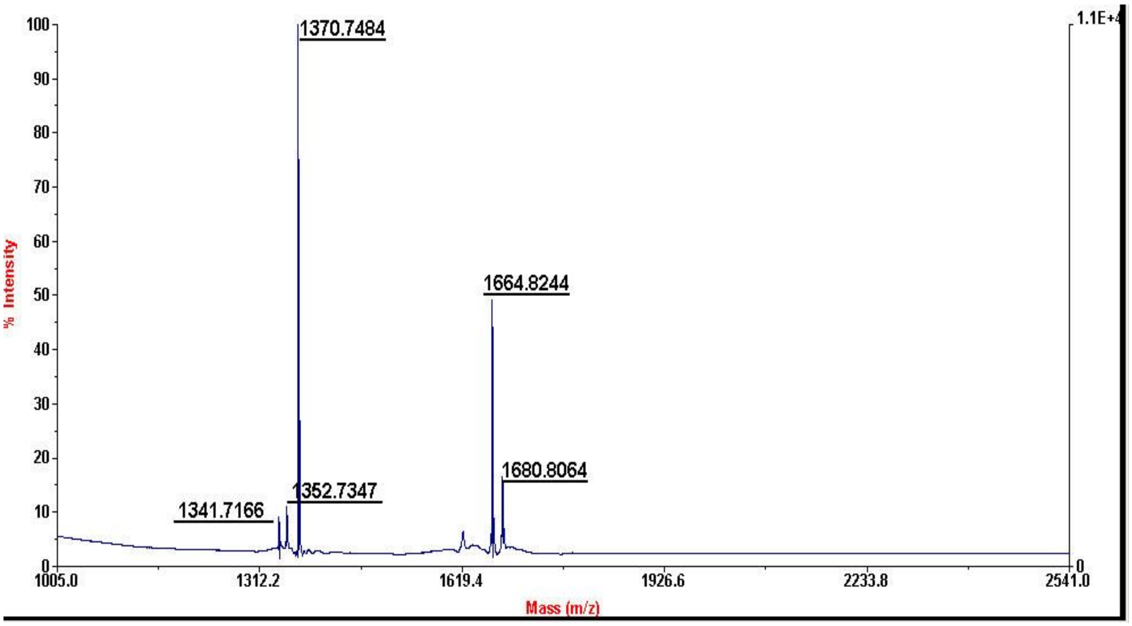
169 ） 14 kDa phosphohistidine phosphatase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
49 - 59	1410.7931	1409.7858	1409.6252	0.1607	0	K.WAEYHADIYDK.V
67 - 78	1368.7126	1367.7053	1367.5017	0.2036	0	K.QGCDCECLGGGR.I 3
88 - 108	2323.4231	2322.4158	2322.1103	0.3056	0	K.IHVYGYSMAYGPAQHAISTEK.I
88 - 108	2339.4095	2338.4022	2338.1052	0.2970	0	K.IHVYGYSMAYGPAQHAISTEK.I Oxidation (M)
111 - 125	1792.0255	1791.0183	1790.7788	0.2395	1	K.AKYPDYEVTWANDGY.-
113 - 125	1592.8894	1591.8821	1591.6467	0.2354	0	K.YPDYEVTWANDGY.-

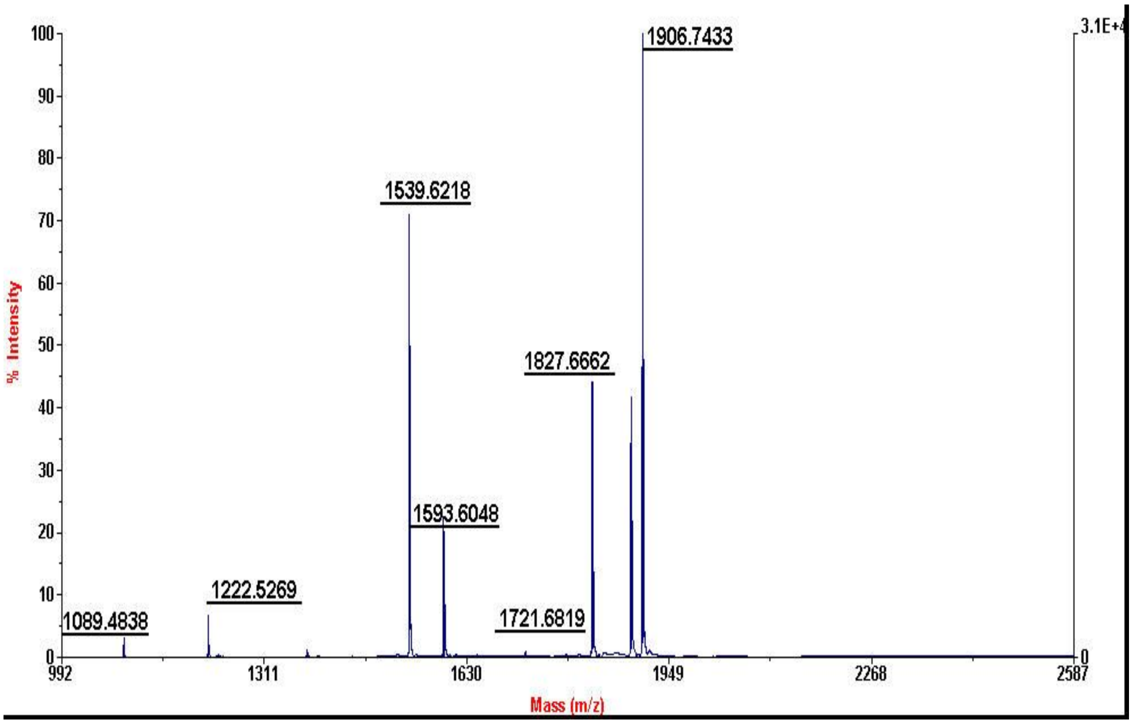
No match to: 1351.7058, 2115.3518

170 ） Protein Wnt-5a



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
213 - 224	1352.7347	1351.7274	1351.6918	0.0356	1	R.RTVYNLADVACK.C	
255 - 266	1370.7484	1369.7412	1369.6408	0.1004	1	K.YDSAAAMRLNSR.G	Oxidation (M)
297 - 312	1664.8244	1663.8171	1663.7948	0.0223	1	R.NESTGSLGTQGRLCNK.T	
313 - 327	1680.8064	1679.7992	1679.5718	0.2274	0	K.TSEGMDGCELMCCGR.G	; 2 Oxidation (M)
355 - 365	1341.7166	1340.7093	1340.6105	0.0988	0	K.CTEIVDQFVCK.-	

171 ） Peroxiredoxin-5, mitochondrial precursor

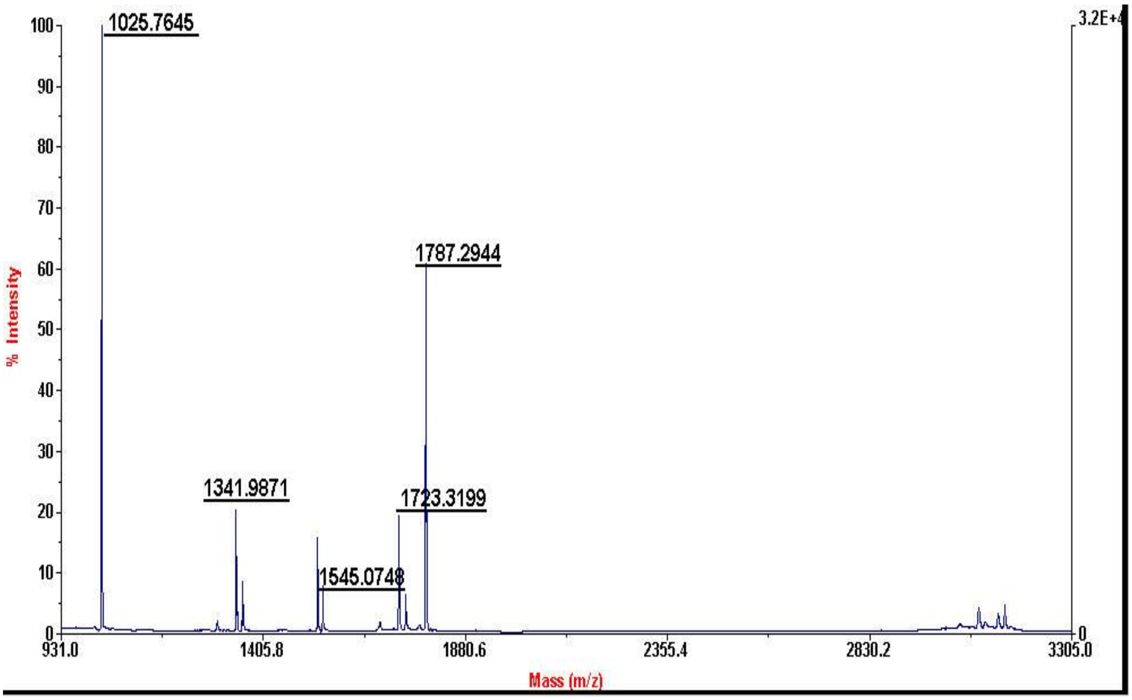


Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

58 - 75	1827.6662	1826.6589	1826.9050	-0.2461	0	K.VGDAIPAVEVFEGEPGNK.V
86 - 102	1721.6819	1720.6746	1720.8971	-0.2224	1	K.KGVLFGVPGAFTPGCSK.T
87 - 102	1593.6048	1592.5975	1592.8021	-0.2047	0	K.GVLFGVPGAFTPGCSK.T
103 - 116	1539.6218	1538.6145	1538.8093	-0.1948	0	K.THLPGFVEQAEALK.A
149 - 159	1089.4838	1088.4766	1088.5866	-0.1101	0	R.LLADPTGAFGK.E
160 - 176	1906.7433	1905.7360	1905.9684	-0.2323	0	K.ETDLLLDDSLVSIFGNR.R
181 - 191	1222.5269	1221.5197	1221.6428	-0.1231	0	R.FSMVVQDGIVK.A

No match to: 1888.7512

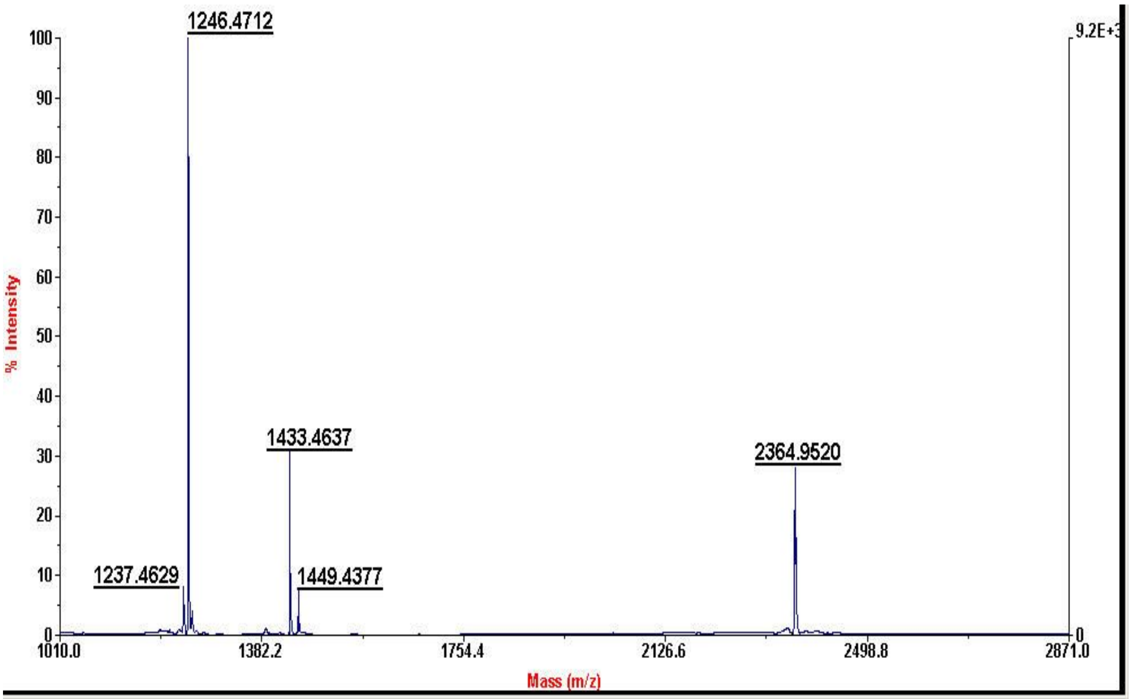
172 ） Myosin light polypeptide 6



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
14 - 21	1025.7645	1024.7572	1024.4978	0.2594	0	K.EAFQLFDR.T
27 - 37	1341.9871	1340.9799	1340.6217	0.3582	0	K.ILYSQCGDVMR.A
80 - 94	1787.2944	1786.2872	1785.8169	0.4702	1	K.NKDQGTYEDYVEGLR.V
82 - 94	1545.0748	1544.0675	1543.6791	0.3885	0	K.DQGTYEDYVEGLR.V
95 - 110	1723.3199	1722.3126	1721.8407	0.4720	1	R.VFDKEGNGTVMGAEIR.H

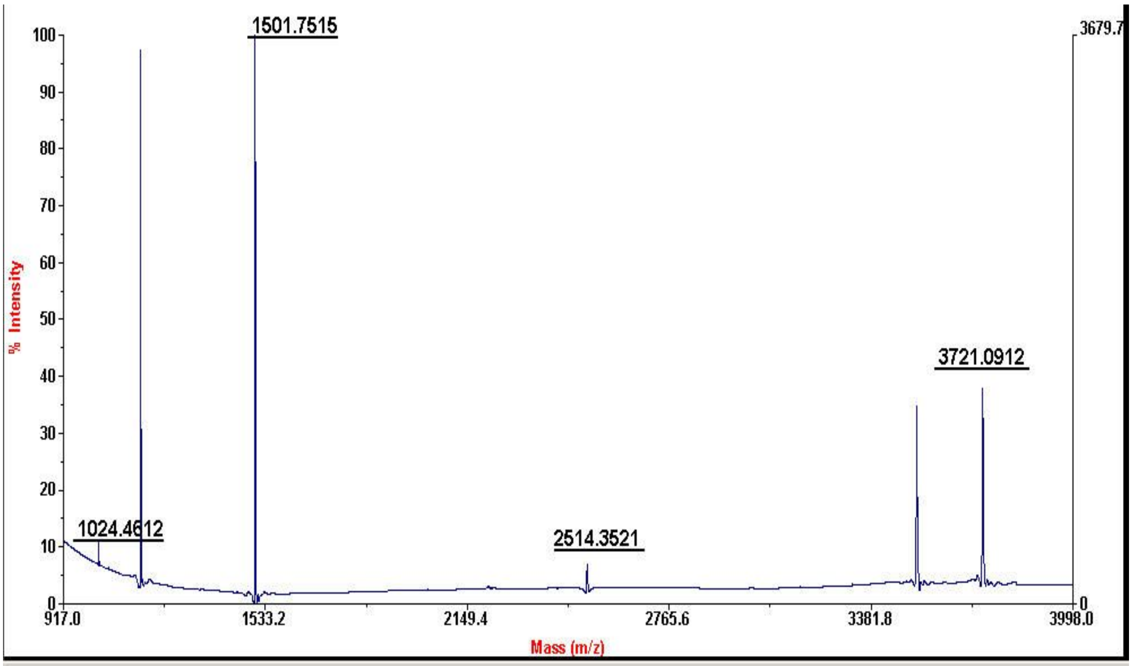
No match to: 1533.0106, 1724.2939

173 ） Myosin regulatory light chain 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
36 - 45	1237.4629	1236.4556	1236.5557	-0.1001	0	K.EAFNMIDQNR.D	
105 - 124	2364.9520	2363.9447	2364.0229	-0.0782	0	R.NAFACFDEEASGFIHEDHLR.E	
134 - 144	1433.4637	1432.4564	1432.5817	-0.1253	0	R.FTDEEVDEMYR.E	
134 - 144	1449.4377	1448.4305	1448.5766	-0.1461	0	R.FTDEEVDEMYR.E	Oxidation (M)
152 - 161	1246.4712	1245.4639	1245.5778	-0.1140	0	K.GNFNYVEFTR.I	

174) Superoxide dismutase [Cu-Zn]

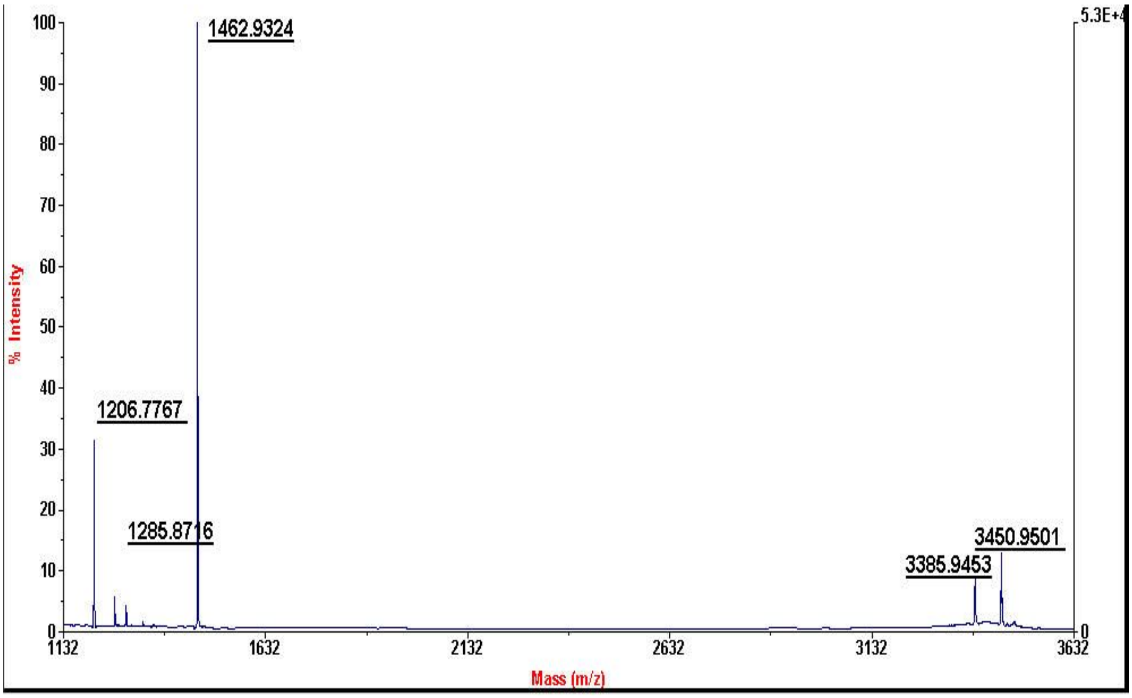


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

11 - 24	1501.7515	1500.7442	1500.7573	-0.0130	0	K.GDGPVQGIINFEQK.E
72 - 80	1024.4612	1023.4539	1023.4734	-0.0194	1	K.HGGPKDEER.H
81 - 116	3721.0912	3720.0839	3719.8061	0.2778	1	R.HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR.T
93 - 116	2514.3521	2513.3449	2513.2068	0.1381	0	K.DGVADVSIEDSVISLSGDHCIIGR.T

No match to: 1152.5752, 3518.8614, 3720.0078

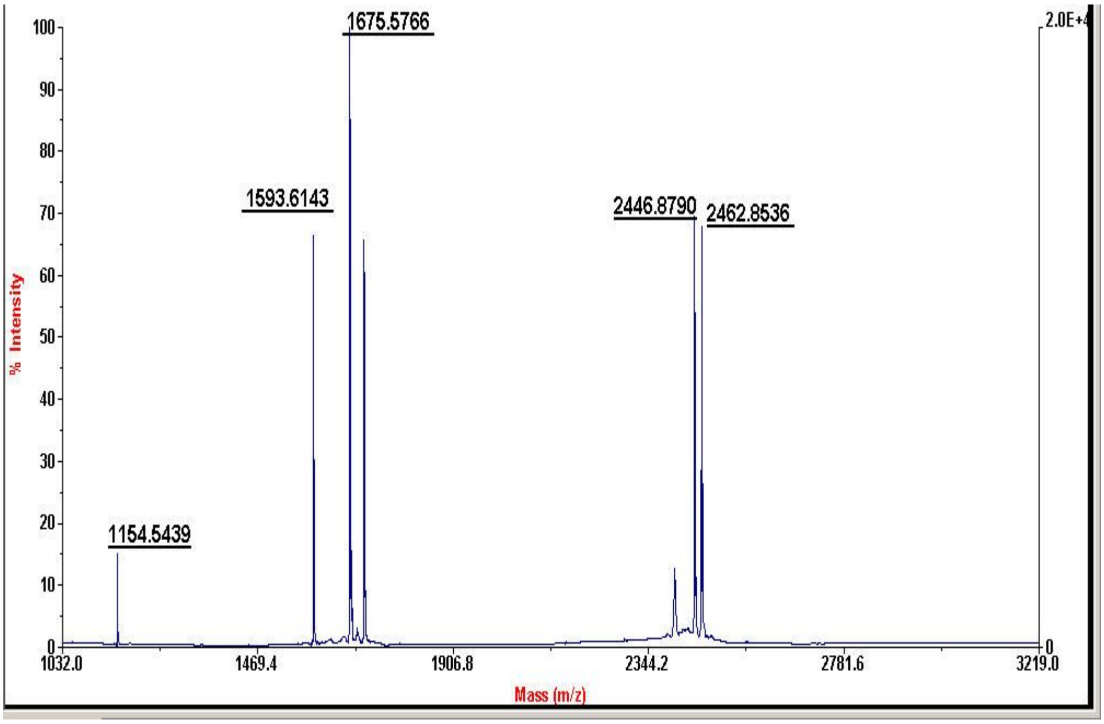
175) Thioredoxin-dependent peroxide reductase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
119 - 148	3450.9501	3449.9428	3449.6211	0.3217	0	K.ANEFHDVNCEVVAVSVDSHFSHLAWINTPR.K
171 - 184	1462.9324	1461.9251	1461.7827	0.1424	0	R.DYGVLLEGSGLALR.G
185 - 196	1285.8716	1284.8644	1284.7442	0.1202	0	R.GLFIIDPNGVIK.H
197 - 207	1206.7767	1205.7694	1205.6517	0.1177	0	K.HLSVNDLPVGR.S
218 - 248	3385.9453	3384.9380	3384.6085	0.3295	0	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E

No match to: 1258.7503, 1329.8171

176) Abhydrolase domain-containing protein 14B

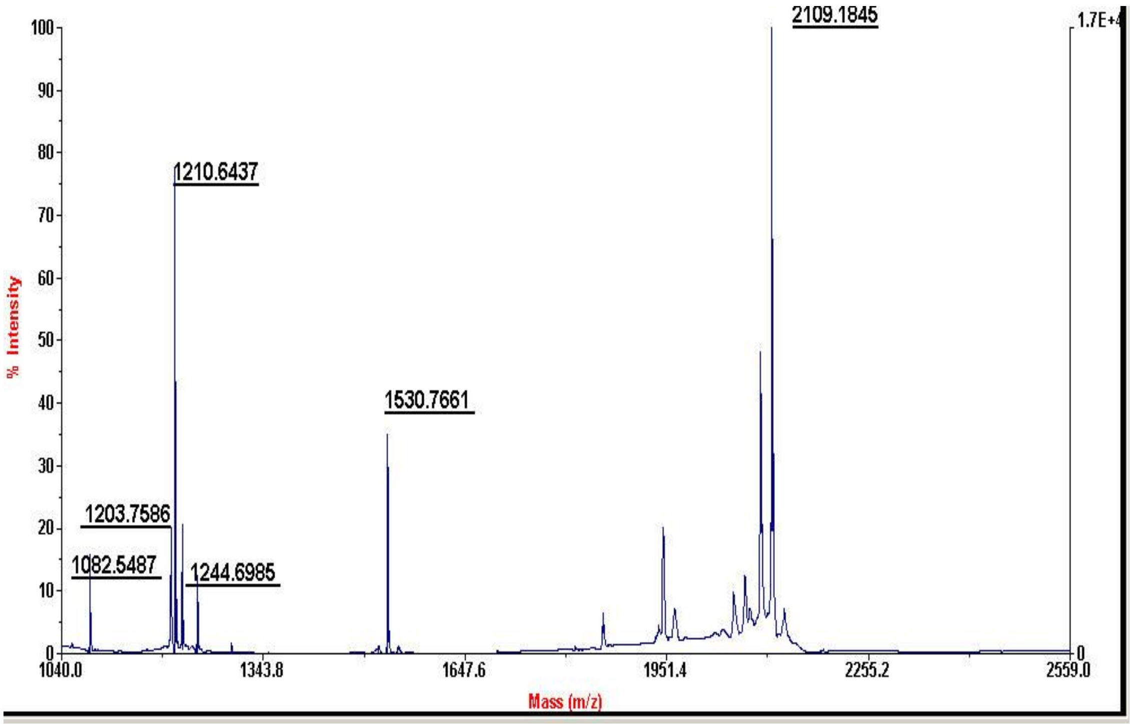


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
9 - 22	1593.6143	1592.6070	1592.8311	-0.2241	0	R.EGTIQVQGQALFFR.E
33 - 42	1154.5439	1153.5367	1153.6972	-0.1605	0	R.FSVLLLHGIR.F
43 - 56	1675.5766	1674.5694	1674.8114	-0.2421	0	R.FSSETWQNLGTLHR.L
152 - 173	2446.8790	2445.8717	2446.1839	-0.3121	0	K.TPALIVYGDQDPMGQTSFEHLK.Q
152 - 173	2462.8536	2461.8463	2462.1788	-0.3324	0	K.TPALIVYGDQDPMGQTSFEHLK.Q

Oxidation (M)

No match to: 1707.5649, 2386.9207

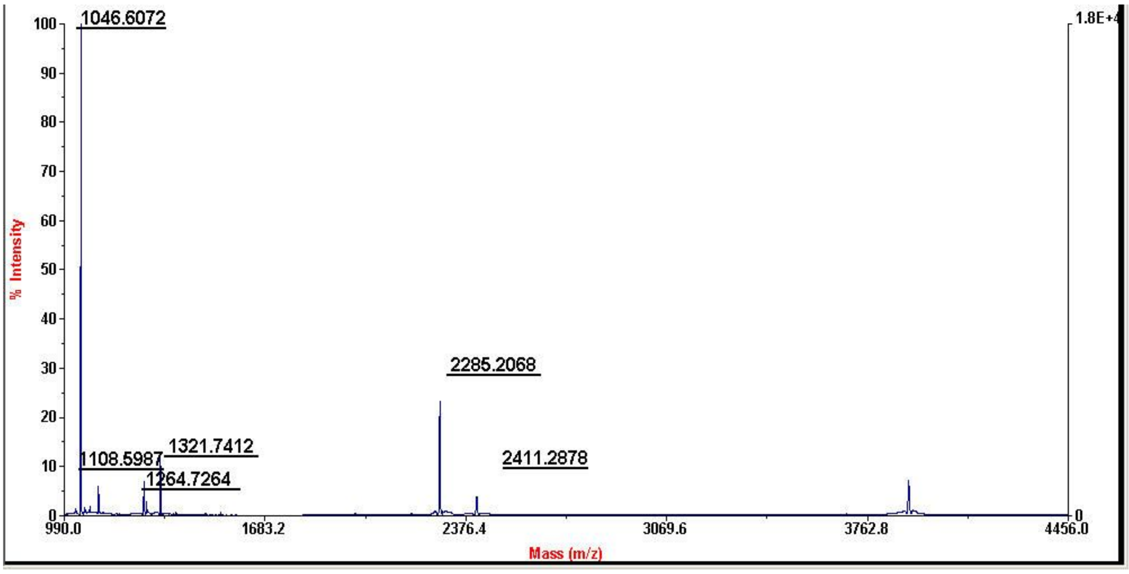
177 ） Transgelin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 28	1210.6437	1209.6364	1209.5513	0.0851	1	K.KYDEELEER.L
21 - 28	1082.5487	1081.5414	1081.4563	0.0851	0	K.YDEELEER.L
29 - 46	2109.1845	2108.1772	2108.0836	0.0936	0	R.LVEWIIVQCGPDVGRPDR.G
47 - 56	1203.7586	1202.7513	1202.6924	0.0590	1	R.GRLGFQVWLK.N
49 - 56	990.6340	989.6267	989.5698	0.0569	0	R.LGFQVWLK.N
78 - 88	1244.6985	1243.6912	1243.6270	0.0642	0	K.VPENPPSMVFK.Q
89 - 98	1221.6944	1220.6872	1220.6223	0.0649	0	K.QMEQVAQFLK.A
108 - 120	1530.7661	1529.7588	1529.7072	0.0516	0	K.TDMFQTVDLFEGK.D
146 - 153	994.5094	993.5021	993.4378	0.0643	0	R.GDPNWFMK.K

No match to: 1855.0070, 2092.0008

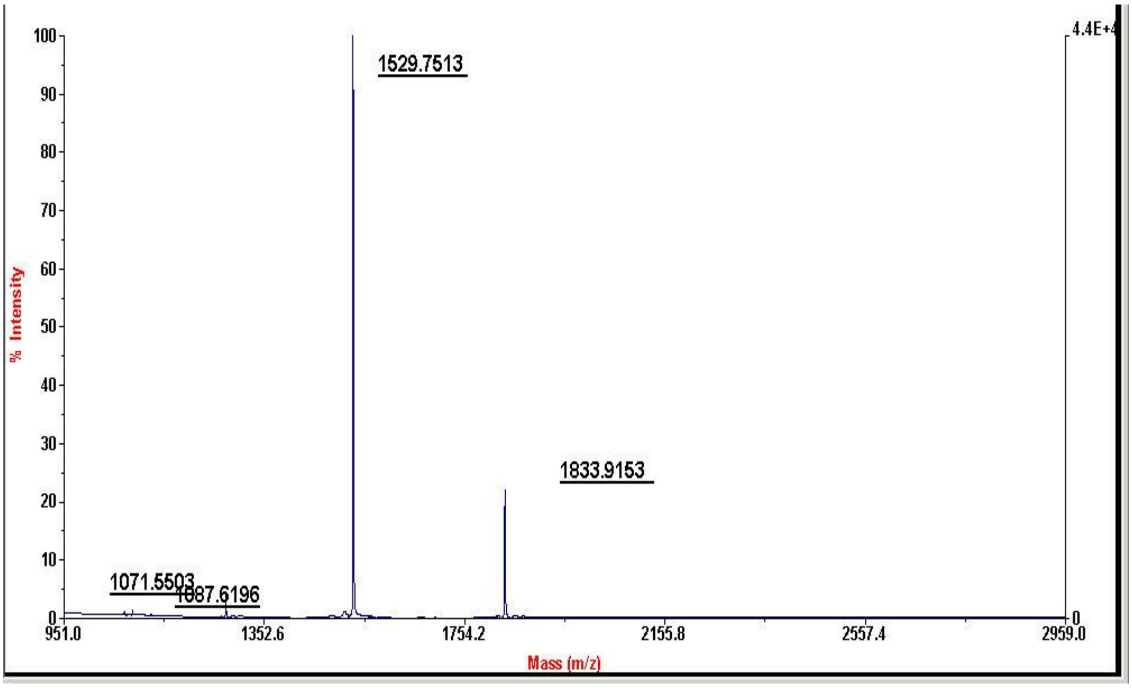
178) Calponin-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
36 - 44	1046.6072	1045.5999	1045.5192	0.0807	0	R.EWIEGVTGR.R
46 - 55	1108.5987	1107.5914	1107.5382	0.0532	0	R.IGNNFMDGLK.D
46 - 66	2411.2878	2410.2805	2410.2024	0.0781	1	R.IGNNFMDGLKDGIILCEFINK.L
56 - 66	1264.7264	1263.7191	1263.6533	0.0659	0	K.DGIILCEFINK.L
56 - 66	1321.7412	1320.7339	1320.6747	0.0592	0	K.DGIILCEFINK.L
75 - 93	2285.2068	2284.1996	2284.1236	0.0760	0	K.INESTQNWHQLENIGNFIK.A

No match to: 1078.6171, 1274.8056

179) Hemoglobin subunit alpha

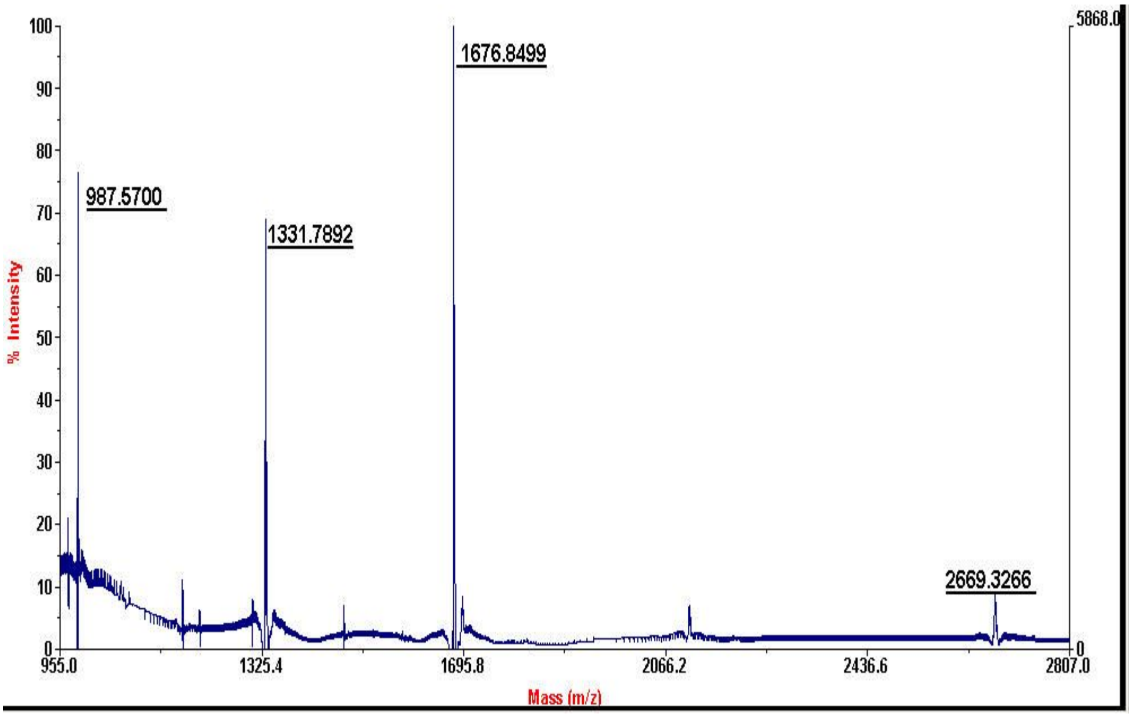


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

17 - 31	1529.7513	1528.7440	1528.7269	0.0171	0	K.VGAHAGEYGAEALER.M
32 - 40	1071.5503	1070.5430	1070.5470	-0.0040	0	R.MFLSFPTTK.T
41 - 56	1833.9153	1832.9081	1832.8845	0.0235	0	K.TYFPHFDLSHGSAQVK.G
91 - 99	1087.6196	1086.6123	1086.6185	-0.0062	1	K.LRVDPVNFK.L

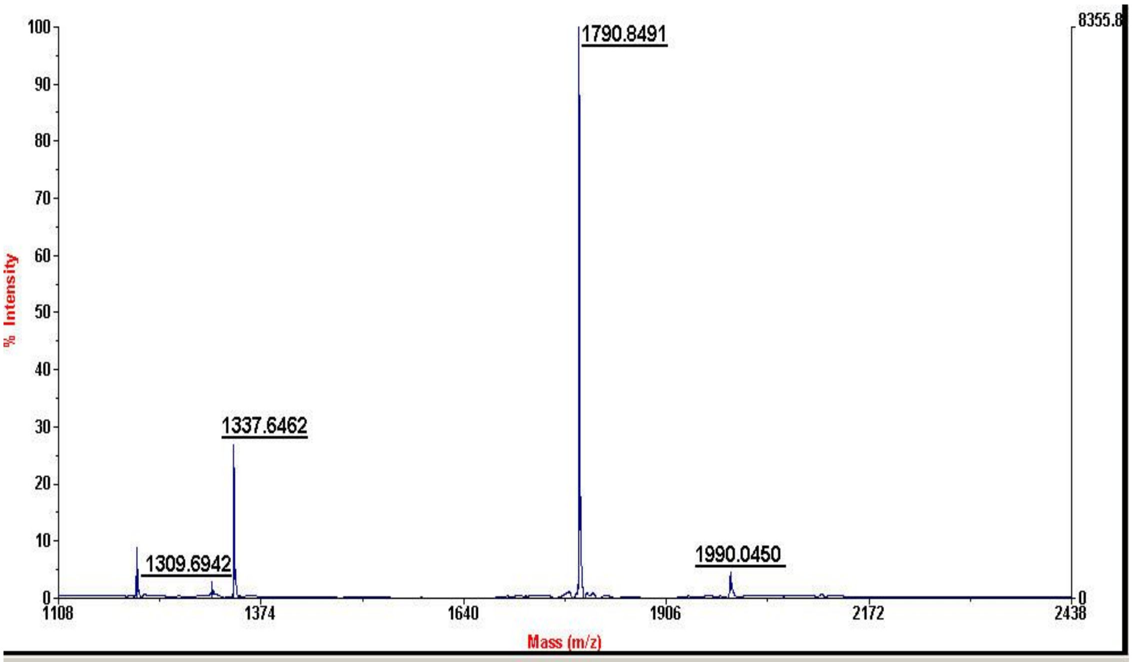
No match to: 1274.7467, 2997.5755

180) Epididymal secretory protein E3 beta precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
36 - 43	987.5700	986.5627	986.4934	0.0693	0	K.QHYLSPSR.E
76 - 88	1676.8499	1675.8426	1675.7083	0.1344	0	K.IEHICTSDNWMDR.F
91 - 101	1331.7892	1330.7819	1330.7033	0.0786	0	R.NAYVWVQNPLK.V
119 - 140	2669.3266	2668.3193	2668.1461	0.1733	0	R.SFNYIEFHCSMDGYVDSIEDLK.M

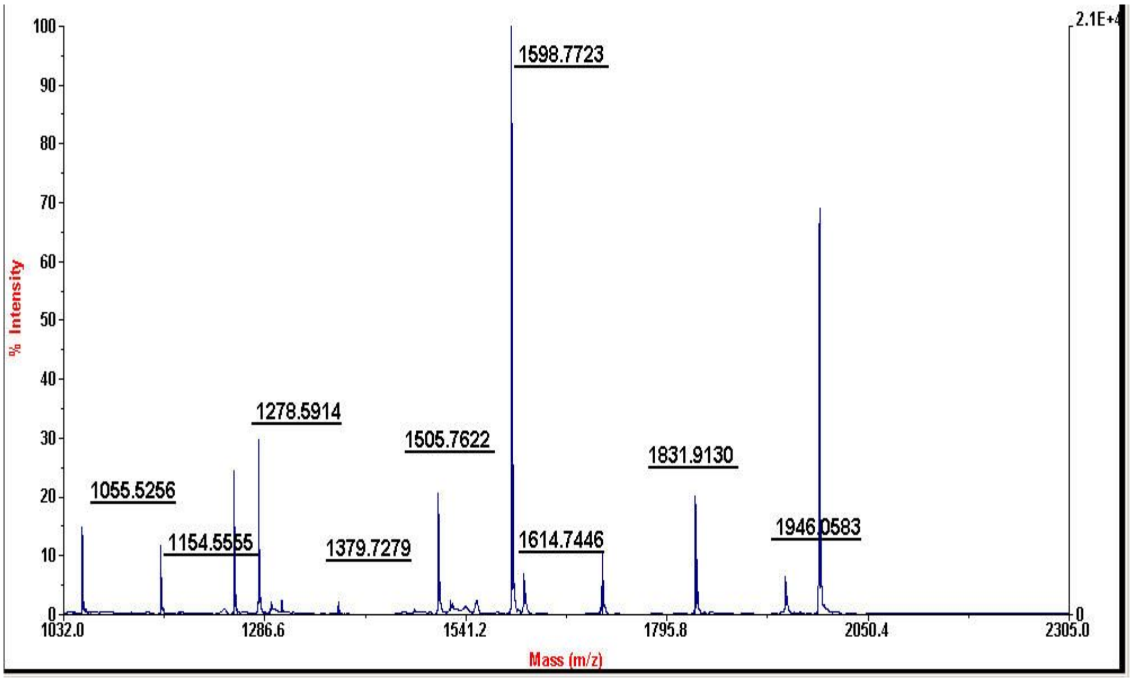
181) Cofilin-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
34 - 44	1309.6942	1308.6869	1308.6747	0.0122	1	K.AVLFCLSEDKK.N
81 - 91	1337.6462	1336.6390	1336.6187	0.0203	0	R.YALYDATYETK.E
95 - 111	1990.0450	1989.0377	1989.0611	-0.0234	1	K.KEDLVFIFWAPESAPLK.S
132 - 145	1790.8491	1789.8419	1789.8053	0.0366	1	K.HELQANCYEEVKDR.C

No match to: 1210.5613, 2109.0728

182) Peptidyl-prolyl cis-trans isomerase A

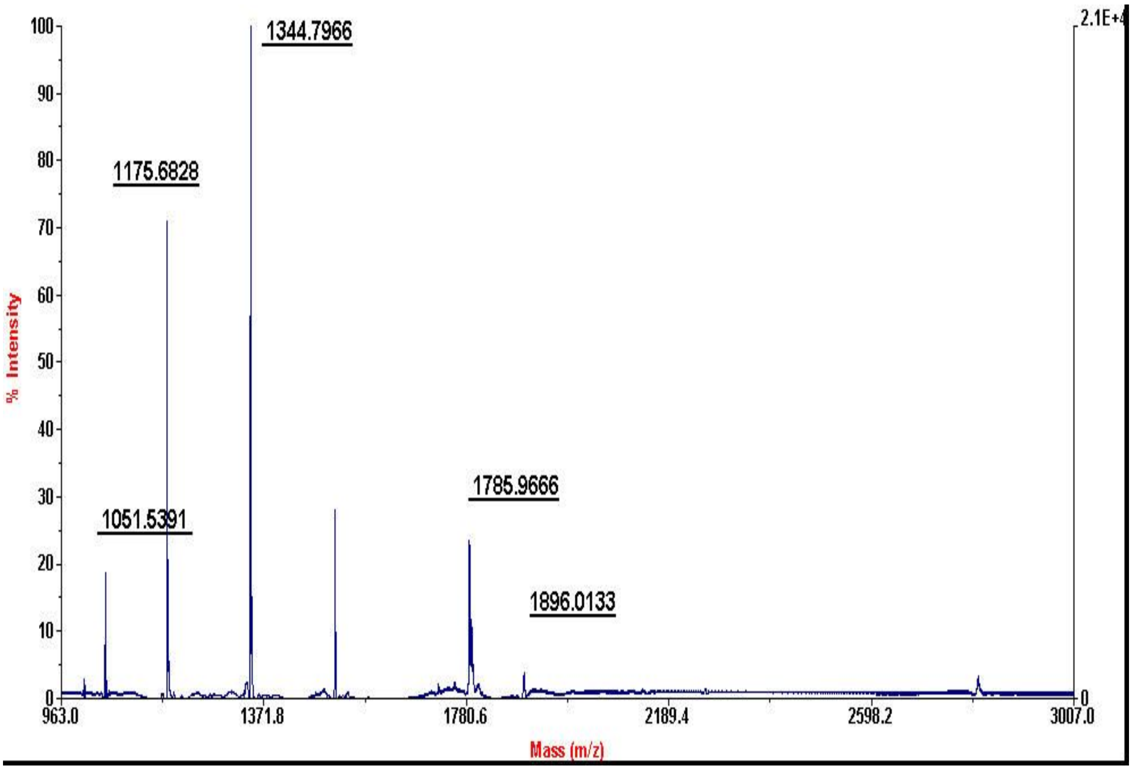


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 18	1946.0583	1945.0511	1944.9944	0.0566	0	-.VNPTVFFDIAVDGEPLGR.V

19 - 27	1055.5256	1054.5184	1054.5335	-0.0151	0	R.VSFELFADK.V	
19 - 30	1379.7279	1378.7206	1378.7496	-0.0290	1	R.VSFELFADKVPK.T	
55 - 68	1598.7723	1597.7650	1597.7381	0.0270	0	R.IIPGFMCQGGDFTR.H	
55 - 68	1614.7446	1613.7373	1613.7330	0.0044	0	R.IIPGFMCQGGDFTR.H	; Oxidation (M)
76 - 90	1831.9130	1830.9057	1830.9039	0.0018	1	K.SIYGEKFEDENFILK.H	
82 - 90	1154.5555	1153.5483	1153.5655	-0.0172	0	K.FEDENFILK.H	
131 - 143	1505.7622	1504.7549	1504.7377	0.0172	1	K.VKEGMNIVEAMER.F	
133 - 143	1278.5914	1277.5841	1277.5743	0.0097	0	K.EGMNIVEAMER.F	
154 - 164	1247.5788	1246.5715	1246.6227	-0.0512	1	K.KITIADCGQLE.-	

No match to: 1307.5892, 1713.7989, 1988.0615

183) Nucleoside diphosphate kinase B

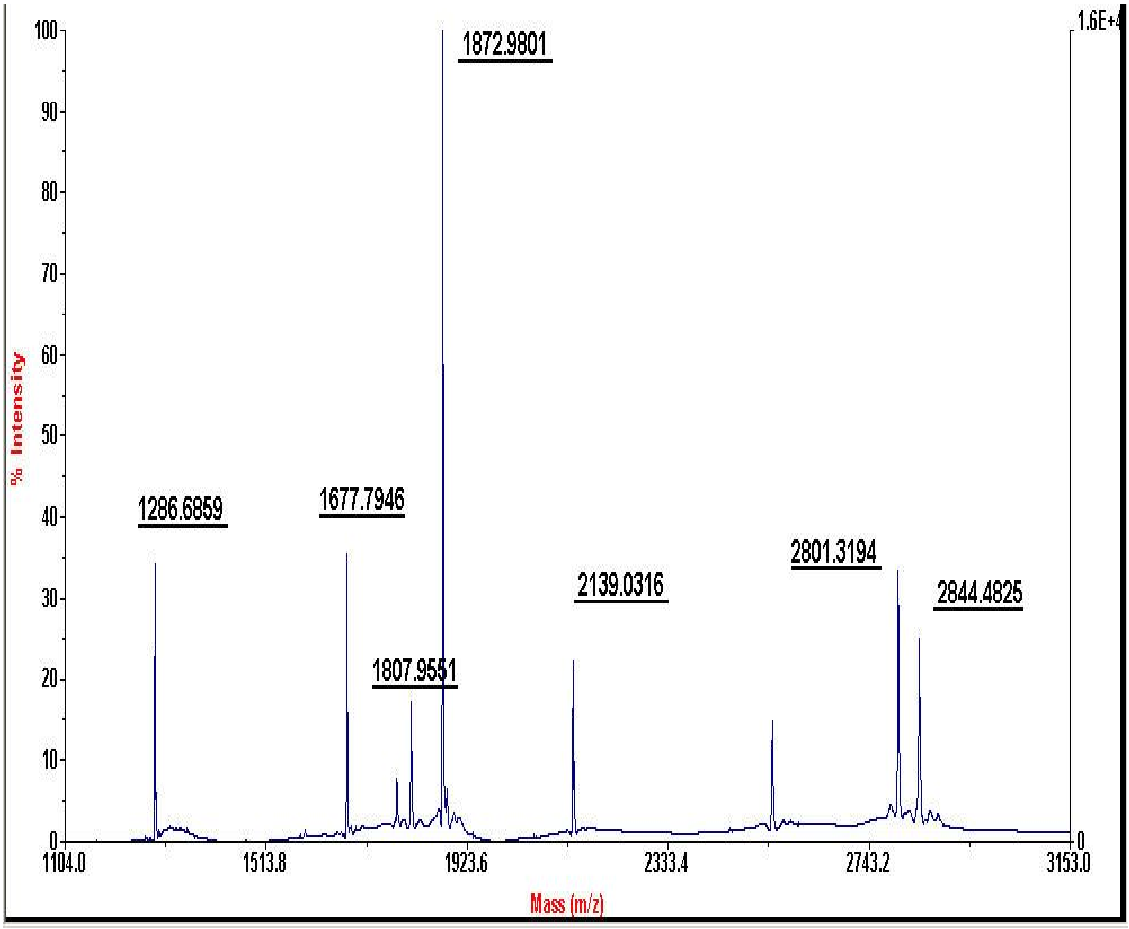


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 18	1344.7966	1343.7893	1343.7561	0.0332	0	R.TFIAIKPDGVQR.G
57 - 66	1175.6828	1174.6755	1174.6498	0.0257	0	K.DRPFFPGLVK.Y
89 - 105	1785.9666	1784.9593	1784.9090	0.0503	0	R.VMLGETNPADSKPGTIR.G

106 - 114	1051.5391	1050.5318	1050.4916	0.0402	0	R.GDFCIQVGR.N
129 - 143	1896.0133	1895.0060	1894.9716	0.0344	0	K.EISLWFKPEELVDYK.S

No match to: 1009.5716, 1514.8594, 1790.8626

185) WD repeat protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 17	1273.6504	1272.6432	1272.7190	-0.0758	1	K.KVFASLPQVER.G
8 - 17	1145.5627	1144.5555	1144.6240	-0.0685	0	K.VFASLPQVER.G
44 - 65	2418.0699	2417.0626	2417.2339	-0.1712	0	R.NIDNPALADIYTEHAHQVVVAK.Y
66 - 81	1618.6241	1617.6168	1617.7674	-0.1506	0	K.YAPSGFYIASGDVSGK.L
127 - 147	2207.8932	2206.8860	2207.0646	-0.1787	0	K.FGAVFLWDSGSSVGEITGHNK.V
162 - 180	2043.7354	2042.7281	2042.9043	-0.1762	0	R.LATGSDDNCAAFFEGPPFK.F
371 - 389	2143.7457	2142.7384	2142.9231	-0.1847	0	R.MTVDESGQLISCSMDDTVR.Y
490 - 511	2279.8700	2278.8627	2279.0528	-0.1900	0	K.GPVTDVAYSHDGAFLAVCDASK.V

No match to: 1193.5267, 1461.6590, 2540.0058, 2584.9694

185) Ig gamma-1 chain C region

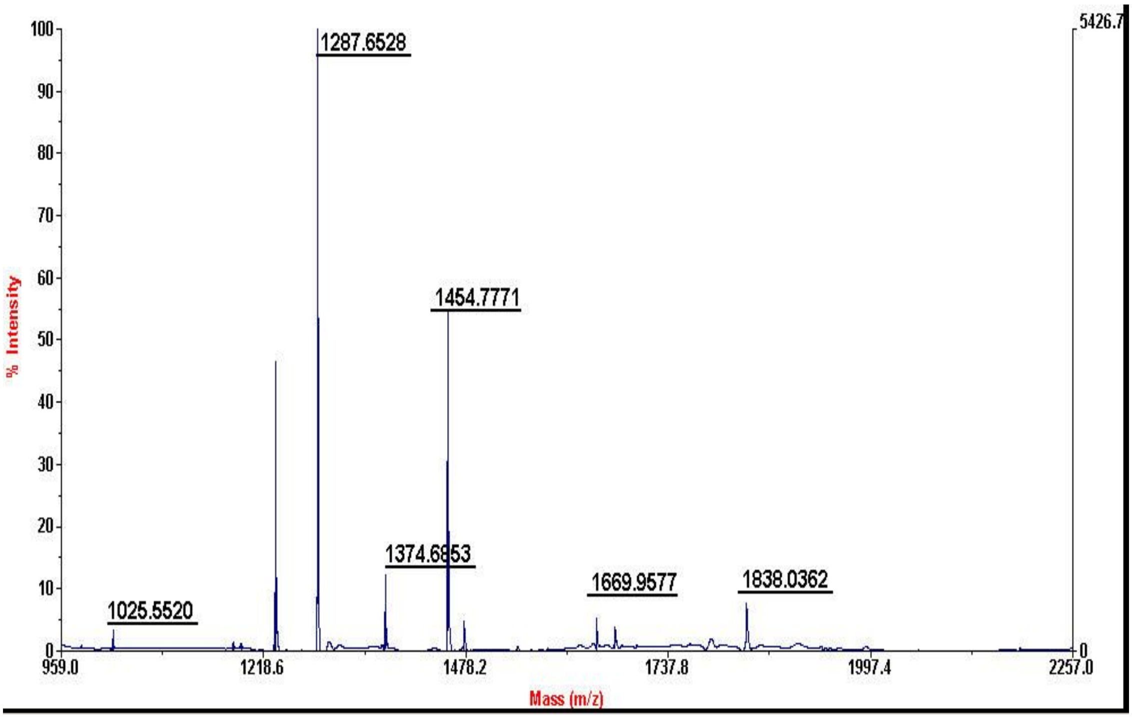
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
106 - 131	2844.4825	2843.4752	2843.4502	0.0250	0	K.THTCPPCPAPELLGGPSVFLFPPKPK.D 2
139 - 157	2139.0316	2138.0243	2138.0201	0.0042	0	R.TPEVTCVVVDVSHEDPEVK.F
158 - 171	1677.7946	1676.7873	1676.7946	-0.0073	0	K.FNWYVDGVEVHNAK.T
185 - 200	1807.9551	1806.9479	1806.9992	-0.0513	0	R.VVSVLTVLHQDWLNGK.E
228 - 238	1286.6859	1285.6786	1285.6666	0.0120	0	R.EPQVYTLPPSR.D
228 - 243	1872.9801	1871.9729	1871.9629	0.0100	1	R.EPQVYTLPPSRDELTK.N
300 - 322	2801.3194	2800.3121	2800.2598	0.0523	0	R.WQQGNVFSCSVMHEALHNHYTQK.S

186) Rab GDP dissociation inhibitor beta

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
56 - 68	1402.6491	1401.6419	1401.7074	-0.0655	1	R.FKIPGSPPESMGR.G
69 - 79	1312.6361	1311.6288	1311.6935	-0.0647	1	R.GRDWNVDLIPK.F
90 - 98	1125.5238	1124.5165	1124.5900	-0.0734	0	K.MLLYTEVTR.Y
143 - 156	1712.8179	1711.8107	1711.8569	-0.0463	1	K.FLVYVANFDEKDPR.T
194 - 208	1902.7915	1901.7842	1901.8102	-0.0259	0	R.TDDYLDQPCYETINR.I
209 - 218	1179.6210	1178.6137	1178.6659	-0.0521	1	R.IKLYSESLAR.Y
222 - 240	2141.0916	2140.0843	2140.0992	-0.0150	0	K.SPYLYPLYGLGELPQGFAR.L
391 - 402	1365.6473	1364.6400	1364.6936	-0.0536	0	K.DLGTESQIFISR.T
424 - 436	1606.6357	1605.6285	1605.6803	-0.0518	1	R.MTGSEFDFEEMKR.K

No match to: 2592.2402

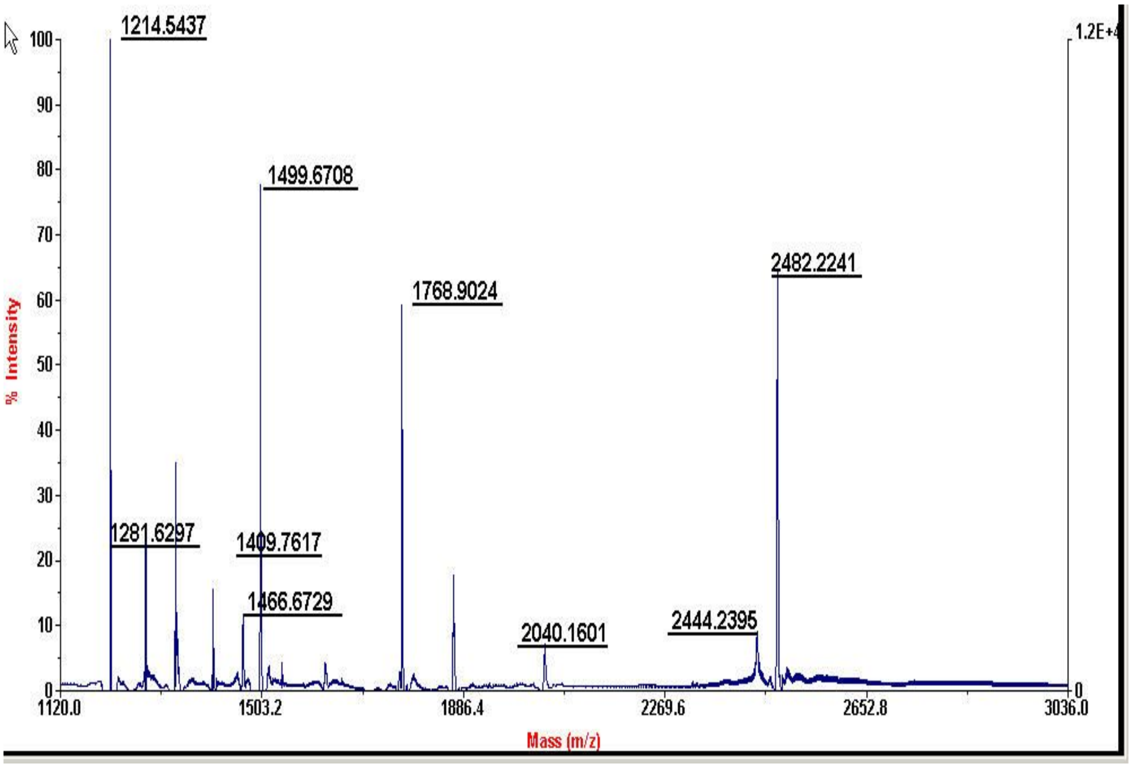
187) Selenium-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
24 - 34	1454.7771	1453.7698	1453.7275	0.0423	0	R.EEIVYLPCIYR.N
53 - 62	1287.6528	1286.6455	1286.6190	0.0265	0	K.SPQYCQVIHR.L
196 - 211	1838.0362	1837.0289	1836.9304	0.0985	0	R.HNVMISTEWAAPNVLR.D
246 - 254	1025.5520	1024.5447	1024.5917	-0.0470	0	K.DGLIPLEIR.F
334 - 344	1374.6853	1373.6781	1373.6688	0.0093	0	R.QYDISDPQRPR.L
383 - 398	1669.9577	1668.9504	1668.8981	0.0523	1	R.VAGGPQMIQLSLDGKR.L

No match to: 1233.6546, 1544.8122, 1645.8913, 2389.3592, 2547.5428

188) Actin-like protein 3

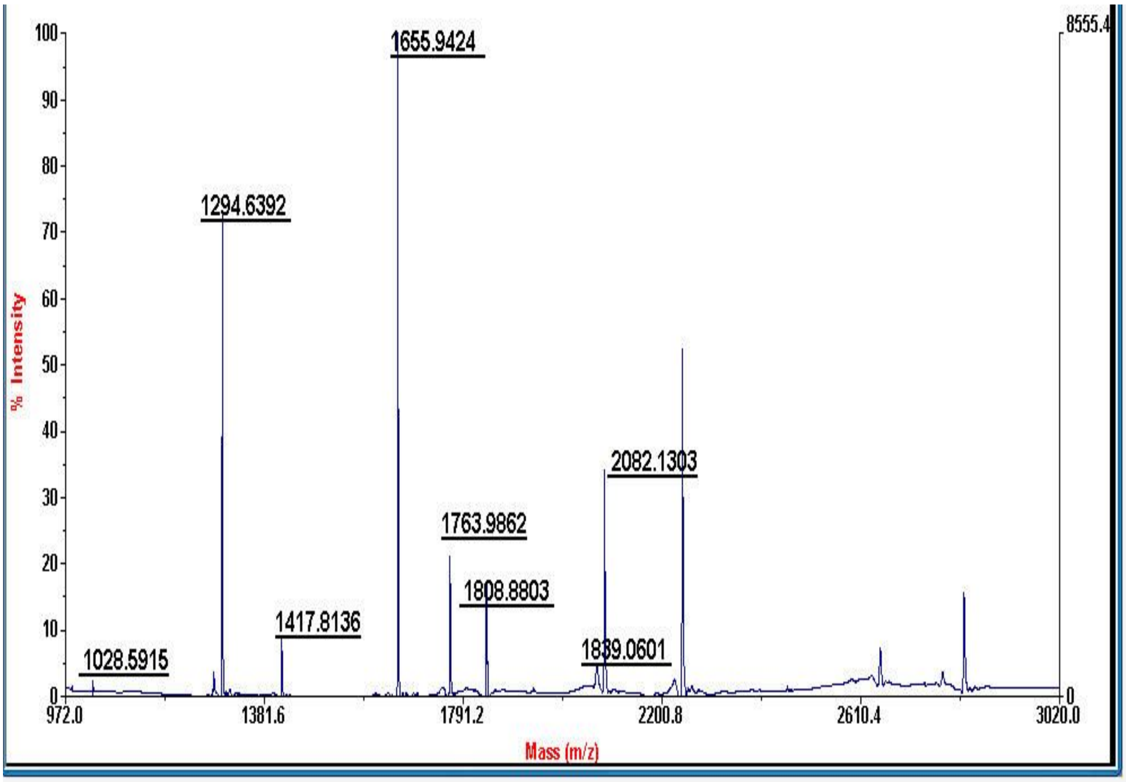


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
54 - 75	2444.2395	2443.2322	2443.1794	0.0528	0	K.GVDDLDFFIGDEAIEKPTYATK.W
80 - 91	1499.6708	1498.6635	1498.6874	-0.0239	0	R.HGIVEDWDLMER.F
103 - 123	2482.2241	2481.2168	2481.1812	0.0356	0	R.AEPEDHYFLLTEPPLNTPENR.E
199 - 209	1409.7617	1408.7544	1408.7714	-0.0170	0	R.DITYFIQQLLR.D
210 - 225	1768.9024	1767.8951	1767.9002	-0.0051	1	R.DREVGIPPEQSLETAK.A
266 - 275	1214.5437	1213.5364	1213.5615	-0.0251	0	K.EFSIDVGYER.F
318 - 329	1281.6297	1280.6225	1280.6546	-0.0322	0	K.NIVLSGGSTMFR.D
358 - 374	2040.1601	2039.1528	2039.1462	0.0066	0	R.LKPKPIDVQVITHHMQR.Y
398 - 409	1466.6729	1465.6656	1465.6871	-0.0215	1	K.KDYEEIGPSICR.H
399 - 409	1338.5784	1337.5711	1337.5921	-0.0210	0	K.DYEEIGPSICR.H

No match to: 1866.8906

189)

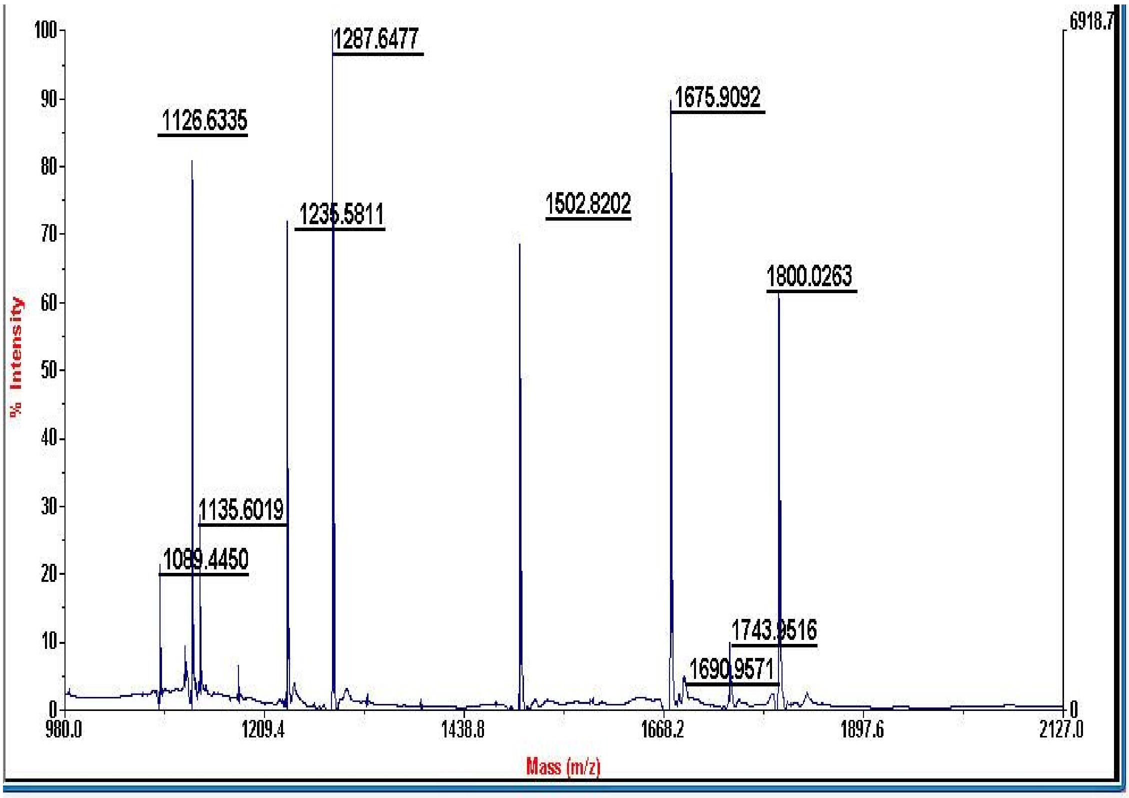
Glutathione synthetase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
113 - 125	1417.8136	1416.8063	1416.7724	0.0338	0	K.EGIAQTVFLGLNR.S
126 - 132	946.4164	945.4091	945.4014	0.0077	0	R.SDYMFQR.S
142 - 158	1763.9862	1762.9790	1762.9213	0.0577	0	K.QIEINTISASFGGLASR.T
222 - 230	1028.5915	1027.5842	1027.5662	0.0180	0	R.AIENELLAR.N
254 - 267	1655.9424	1654.9351	1654.8718	0.0633	0	R.LFVDGQEIAVVYFR.D
274 - 283	1294.6392	1293.6320	1293.6102	0.0218	0	R.QYSLQNWEAR.L
368 - 384	1808.8803	1807.8731	1807.8410	0.0321	0	R.EGGGNNLYGEEMVQALK.Q
401 - 418	2082.1303	2081.1230	2081.0363	0.0867	0	K.IEPEPFENCLLRPGSPAR.V
419 - 434	1839.0601	1838.0528	1837.9760	0.0769	0	R.VVQCISELGIFGVYVR.Q

No match to: 1277.6068, 2242.2811, 2822.6126

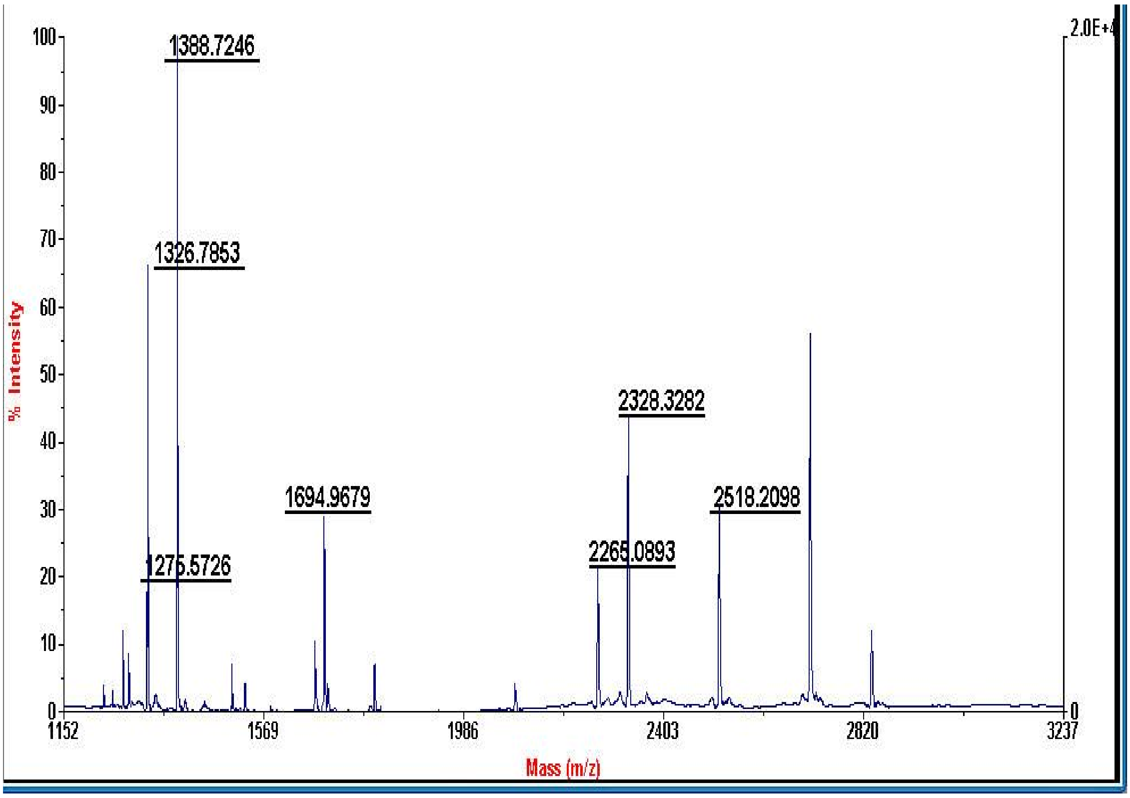
190) Plastin-2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
133 - 141	1089.4450	1088.4377	1088.4557	-0.0180	0	K.ALENDPDCR.H
166 - 178	1502.8202	1501.8129	1501.7446	0.0683	0	K.MINLSVPDTIDER.T
310 - 326	1743.9516	1742.9443	1742.8508	0.0935	0	K.GDEEGVPAVVIDMSGLR.E
334 - 343	1235.5811	1234.5738	1234.5434	0.0304	0	R.AECMLQQAER.L
348 - 357	1135.6019	1134.5946	1134.6033	-0.0086	0	R.QFVTATDVVR.G
402 - 412	1287.6477	1286.6404	1286.6189	0.0214	0	R.NWMNSLGVNPR.V
433 - 441	1126.6335	1125.6263	1125.6294	-0.0032	1	K.IKVPVDWNR.V
473 - 488	1675.9092	1674.9019	1674.8325	0.0694	0	K.FSLVGIGGQDLNEGNR.T
501 - 515	1690.9571	1689.9498	1689.9049	0.0449	1	R.RYTLNILEEIGGGQK.V
516 - 530	1800.0263	1799.0190	1798.9213	0.0977	0	K.VNDDIIVNWVNETLR.E

No match to: 1118.5834, 1326.7191, 1388.7556

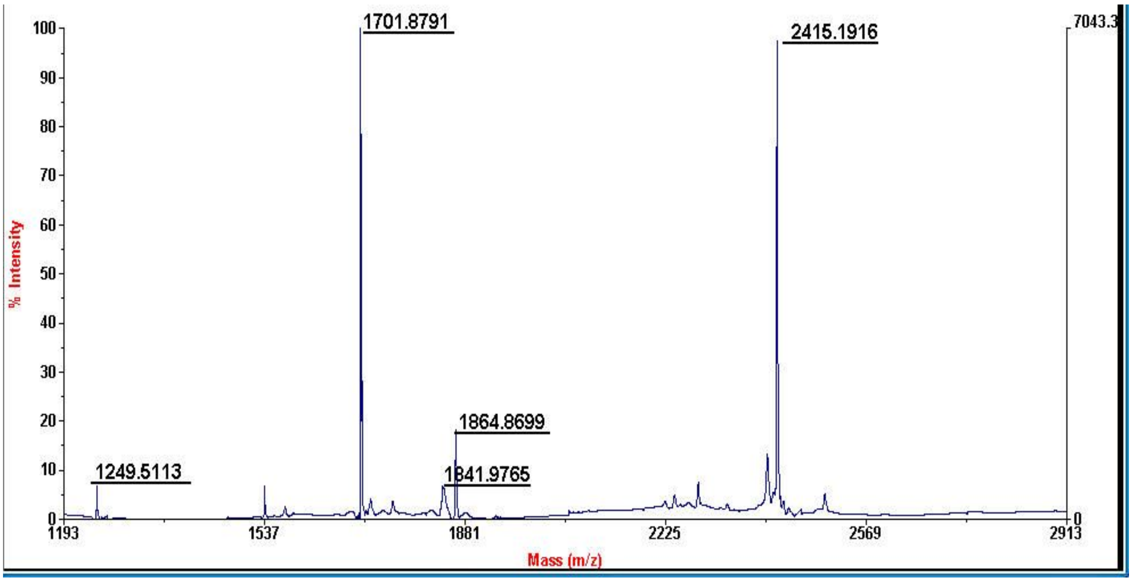
191 ） Vitamin D-binding protein precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 50	2328.3282	2327.3209	2327.1797	0.1412	1	K.EFSHLGKEDFTSLSLVLYSR.K
51 - 65	1694.9679	1693.9606	1693.9039	0.0567	1	R.KFPSGTFEQVSQLVK.E
66 - 87	2518.2098	2517.2025	2517.0094	0.1931	0	K.EVVSLTEACCAEGADPDCYDTR.T 3
95 - 114	2265.0893	2264.0821	2263.9296	0.1525	0	K.SCESNSPFPVHPGTAECCTK.E 3
219 - 229	1275.5726	1274.5653	1274.5601	0.0052	0	R.VCSQYAAYGEK.K
342 - 352	1388.7246	1387.7173	1387.6805	0.0368	1	K.VMDKYTFELSR.R
353 - 363	1326.7853	1325.7780	1325.7455	0.0325	1	R.RTHLPEVFLSK.V

No match to: 1675.9278, 2312.3079, 2707.4172, 2835.6021

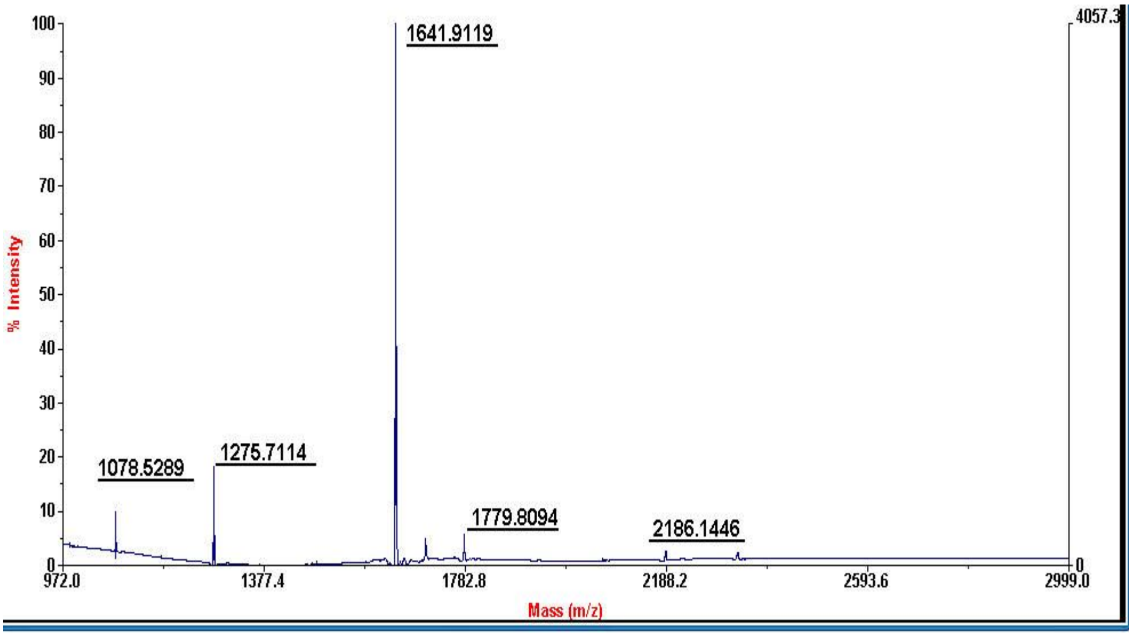
192 ） Tubulin alpha-3 chain



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
65 - 79	1701.8791	1700.8718	1700.8984	-0.0266	0	R.AVFVDLEPTVIDEVR.T
85 - 105	2415.1916	2414.1843	2414.1978	-0.0135	1	R.QLFHPEQLITGKEDAANNYAR.G
106 - 121	1841.9765	1840.9692	1841.0046	-0.0354	1	R.GHYTIGKEIIDLVLDR.I
312 - 320	1249.5113	1248.5040	1248.5453	-0.0413	0	K.YMACCLLYR.G 2
374 - 390	1864.8699	1863.8626	1863.8971	-0.0345	0	R.AVCMLSNTTAIAEAWAR.L

No match to: 1536.7079

193 ） Alpha-1-antitrypsin precursor

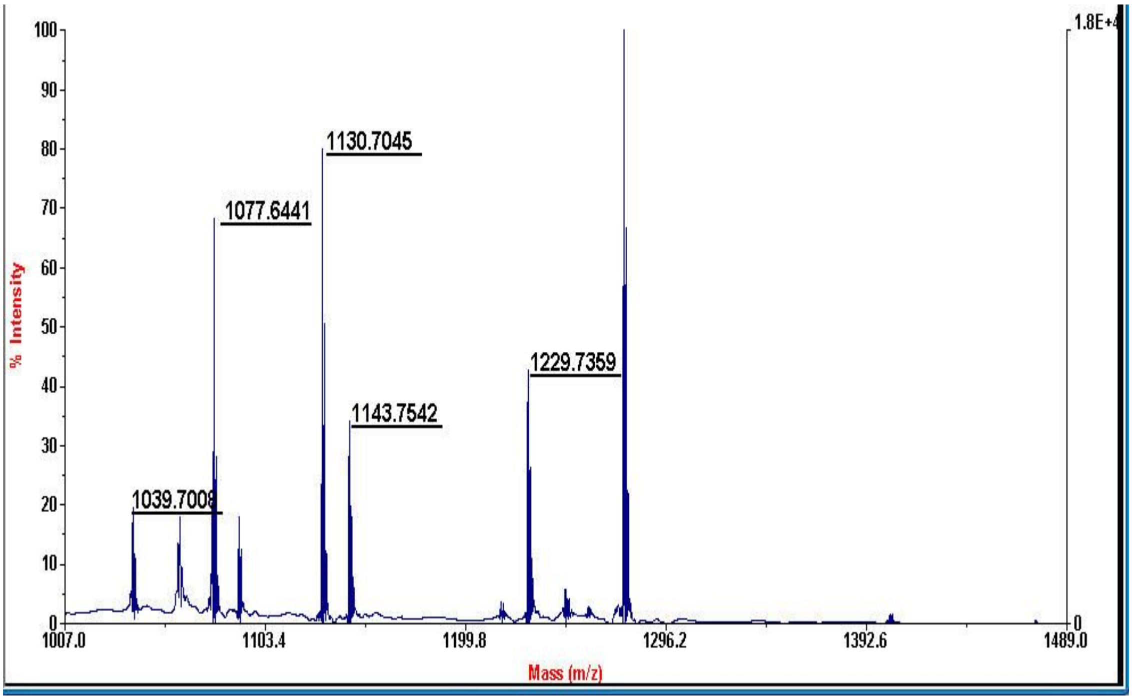


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 49	1779.8094	1778.8021	1778.7608	0.0413	0	K.TDTSHHDQDHPTFNK.I
50 - 63	1641.9119	1640.9046	1640.8562	0.0484	0	K.ITPNLAEFAFSLYR.Q

161 - 179	2186.1446	2185.1374	2185.0327	0.1047	1	K.LYHSEAFTVNFGDTEEAKK.Q
216 - 225	1275.7114	1274.7042	1274.6771	0.0271	1	K.GKWERPFEVK.D
299 - 306	1078.5289	1077.5216	1077.5203	0.0013	1	K.FLENEDRR.S

No match to: 1483.7550, 1701.9693, 2330.1319

194 ） Tubulin beta chain (Tubulin beta-5 chain)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
155 - 162	1077.6441	1076.6368	1076.5250	0.1118	1	K.IREEYPDR.I
242 - 251	1130.7045	1129.6972	1129.5880	0.1092	0	R.FPGQLNADLR.K
253 - 262	1143.7542	1142.7469	1142.6270	0.1199	0	K.LAVNMVPFPR.L
310 - 318	1039.7008	1038.6935	1038.5862	0.1074	0	R.YLTVAAVFR.G
381 - 390	1229.7359	1228.7287	1228.5910	0.1377	0	R.ISEQFTAMFR.R

No match to: 1275.8303, 1642.0975, 1959.2850

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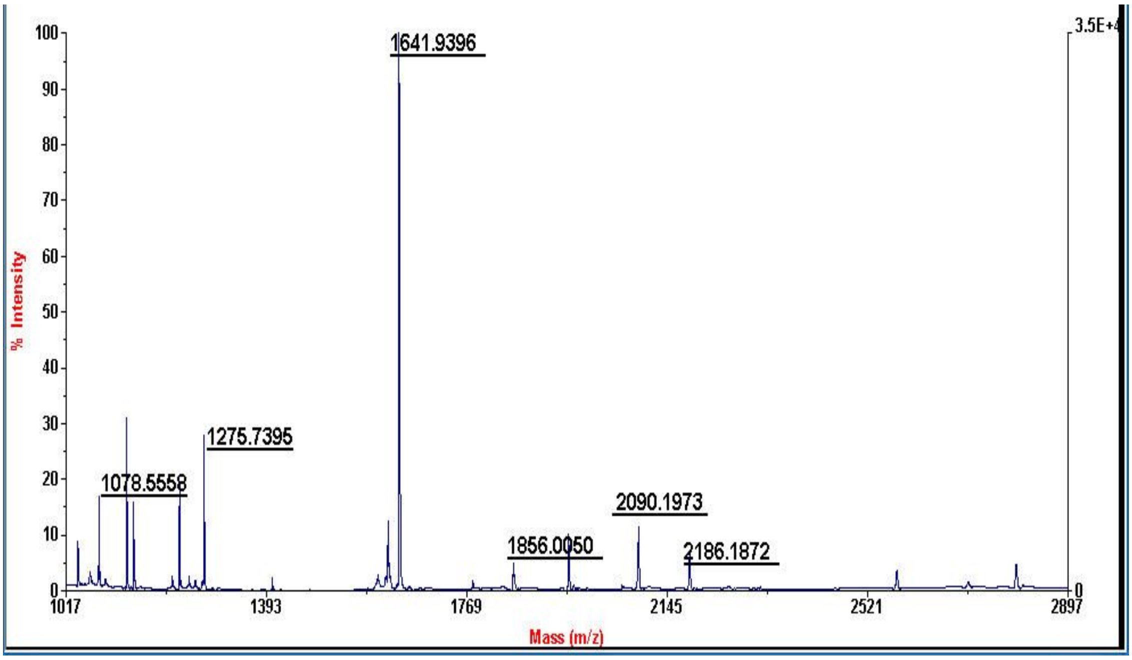
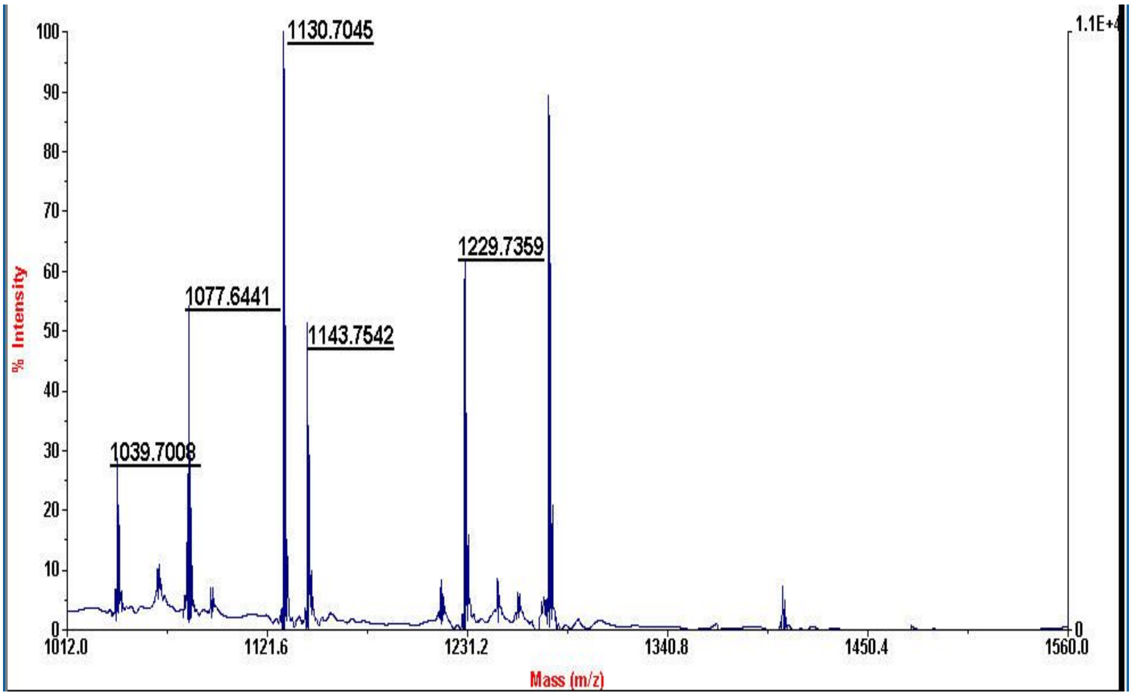
195 ） Alpha-1-antitrypsin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
50 - 63	1641.9396	1640.9323	1640.8562	0.0761	0	K.ITPNLAEFAFSLYR.Q
161 - 179	2186.1872	2185.1799	2185.0327	0.1472	1	K.LYHSEAFTVNFGDTEEAKK.Q
199 - 215	2090.1973	2089.1900	2089.0883	0.1016	1	K.ELDRDTVFALVNYIFFK.G
216 - 225	1275.7395	1274.7322	1274.6771	0.0551	1	K.GKWERPFEVK.D
299 - 306	1078.5558	1077.5485	1077.5203	0.0283	1	K.FLENEDRR.S
390 - 404	1856.0050	1854.9977	1854.9702	0.0276	0	K.FNKPFVFLMIEQNTK.S

No match to: 1039.6252, 1130.6368, 1143.6830, 1229.6539, 1620.9178, 1959.0886, 2799.5186

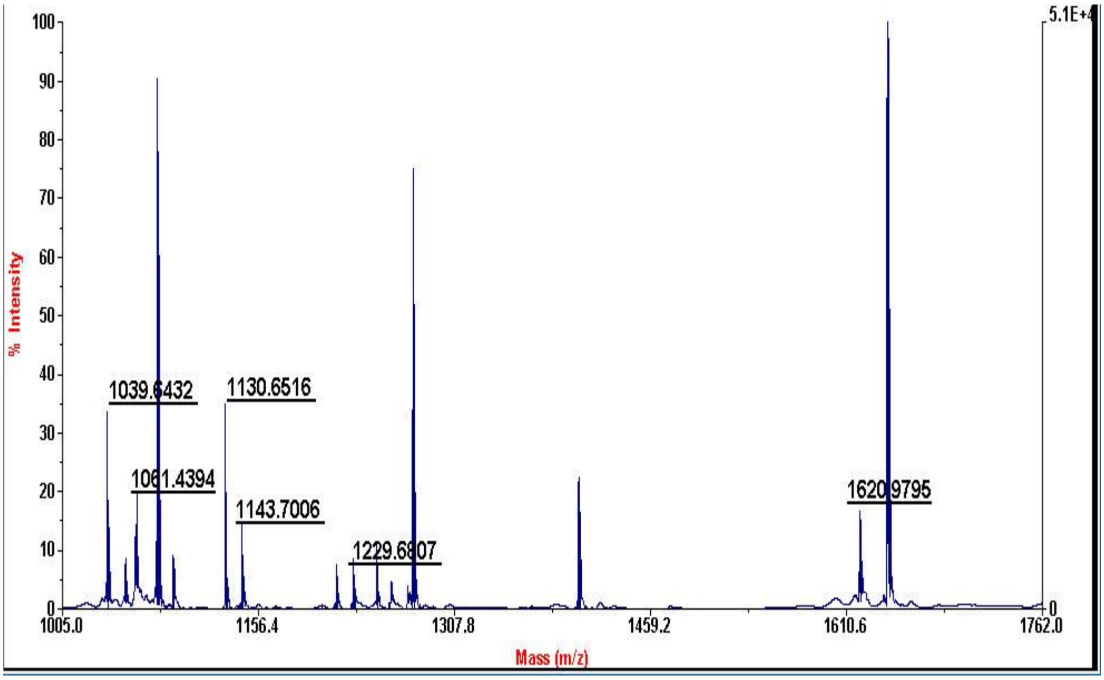
196 ） Tubulin beta-2C chain (Tubulin beta-2 chain)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
155 - 162	1077.6441	1076.6368	1076.5250	0.1118	1	K.IREEYPDR.I
242 - 251	1130.7045	1129.6972	1129.5880	0.1092	0	R.FPGQLNADLR.K
253 - 262	1143.7542	1142.7469	1142.6270	0.1199	0	K.LAVNMVPFPR.L
310 - 318	1039.7008	1038.6935	1038.5862	0.1074	0	R.YLTVAAVFR.G
381 - 390	1229.7359	1228.7287	1228.5910	0.1377	0	R.ISEQFTAMFR.R

No match to: 1275.8303, 1642.0975, 1959.2850

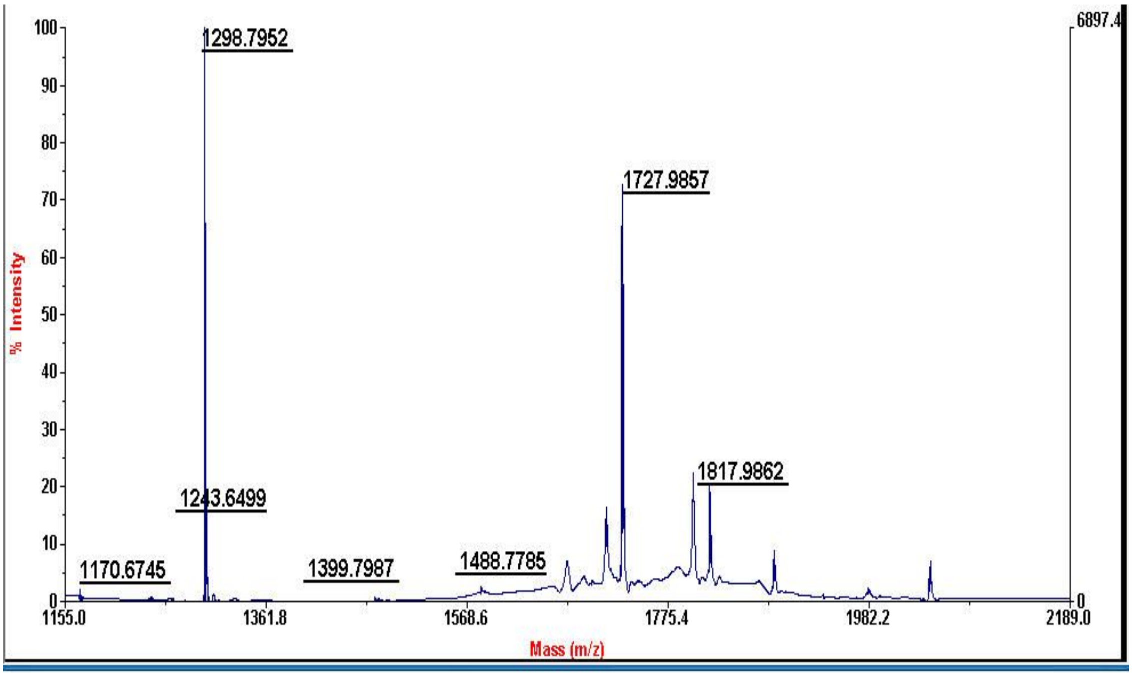
197 ） Tubulin beta-4 chain (Tubulin 5 beta)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
155 - 162	1061.4394	1060.4321	1060.5301	-0.0980	1	K.IREEFPDR.I
242 - 251	1130.6516	1129.6443	1129.5880	0.0564	0	R.FPGQLNADLR.K
253 - 262	1143.7006	1142.6933	1142.6270	0.0663	0	K.LAVNMVPFPR.L
263 - 276	1620.9795	1619.9722	1619.8282	0.1440	0	R.LHFFMPGFAPLTSR.G
310 - 318	1039.6432	1038.6359	1038.5862	0.0497	0	R.YLTVAAVFR.G
381 - 390	1229.6807	1228.6734	1228.5910	0.0824	0	R.ISEQFTAMFR.R

No match to: 1078.5613, 1090.6066, 1247.6591, 1275.7576, 1403.7960, 1641.9997, 1779.9016, 1856.1159, 1959.1804, 2090.3126, 2186.2275

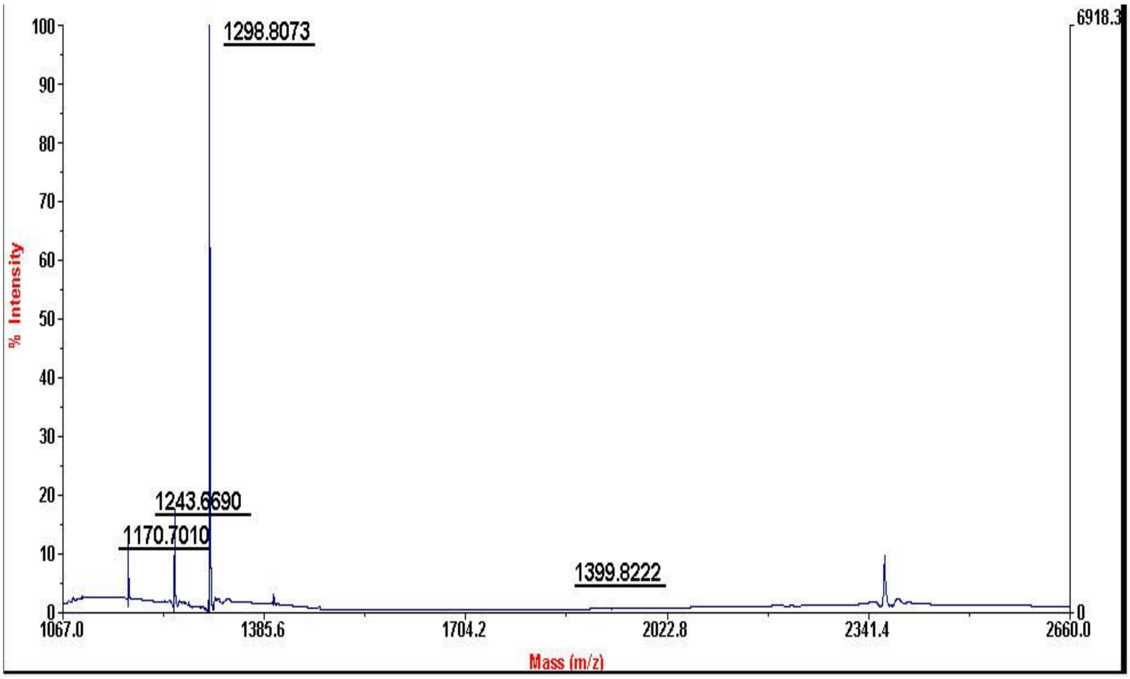
198 ）Tropomyosin beta chain (Tropomyosin 2) (Beta-tropomyosin)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
78 - 91	1488.7785	1487.7712	1487.7328	0.0384	1	K.ATDAEADVASLNRR.I
91 - 101	1399.7987	1398.7915	1398.7466	0.0448	1	R.RIQLVEEELDR.A
92 - 101	1243.6499	1242.6426	1242.6455	-0.0029	0	R.IQLVEEELDR.A
92 - 105	1727.9857	1726.9785	1726.8849	0.0935	1	R.IQLVEEELDRAQER.L
168 - 178	1298.7952	1297.7879	1297.7605	0.0274	1	R.KLVILEGELER.S
169 - 178	1170.6745	1169.6672	1169.6655	0.0017	0	K.LVILEGELER.S
190 - 205	1817.9862	1816.9789	1816.9240	0.0549	1	K.CGDLEEELKIVTNNLK.S

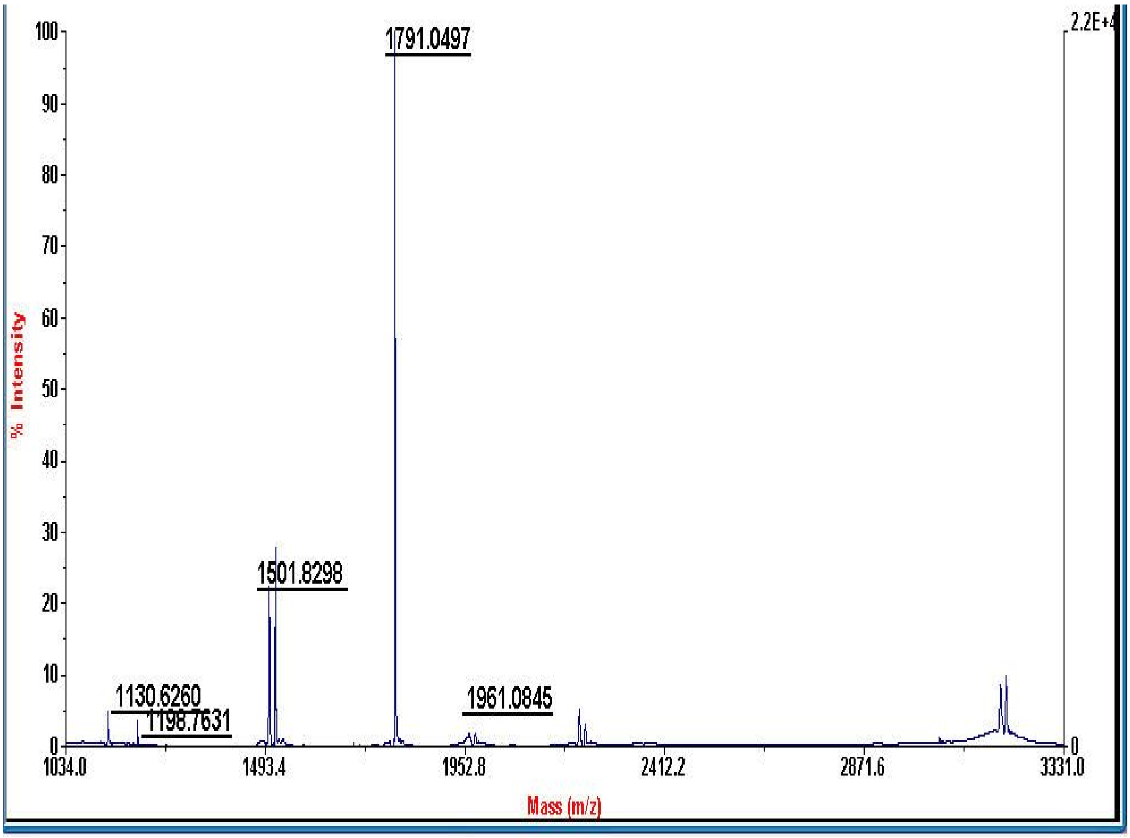
No match to: 1710.7837, 1800.0945, 1884.1100, 1981.1106, 1996.1232, 2044.2065, 2202.3341, 2538.4336

201 ） Tropomyosin alpha-4 chain (Tropomyosin-4) (TM30p1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
55 - 65	1399.8222	1398.8149	1398.7466	0.0683	1	R.RIQLVEEELDR.A
56 - 65	1243.6690	1242.6617	1242.6455	0.0162	0	R.IQLVEEELDR.A
132 - 142	1298.8073	1297.8000	1297.7605	0.0396	1	R.KLVILEGELER.A
133 - 142	1170.7010	1169.6937	1169.6655	0.0282	0	K.LVILEGELER.A

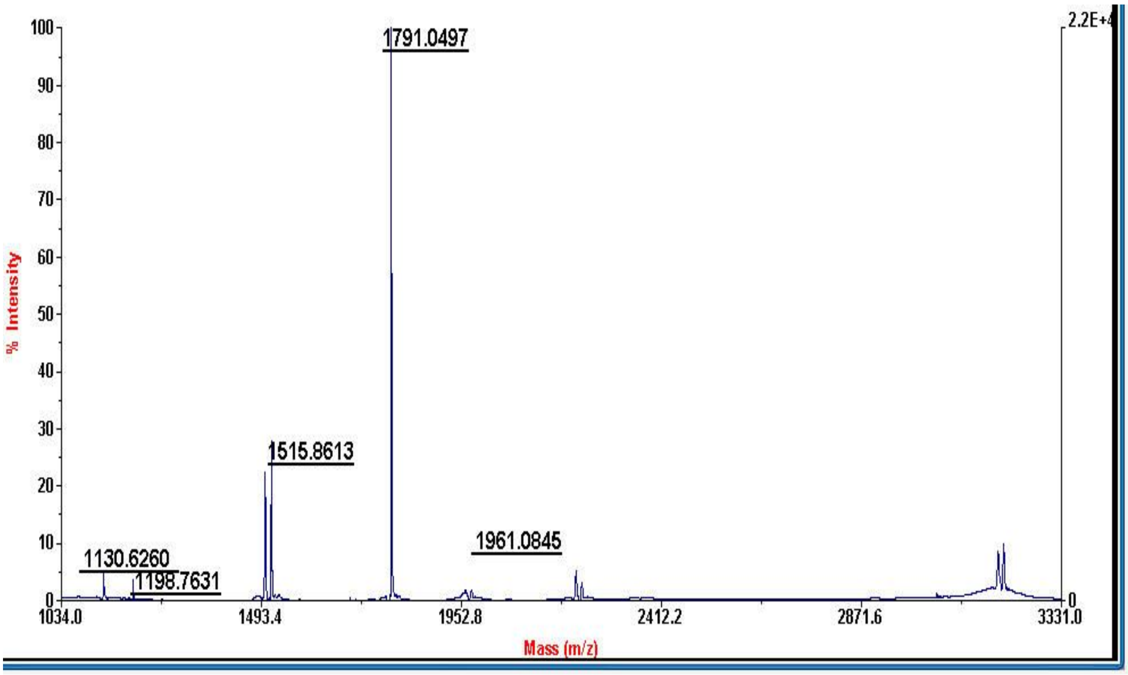
202 ） Actin, gamma-enteric smooth muscle (Smooth muscle gamma actin) (Gamma-2-actin) (Alpha-actin-3)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
30 - 40	1198.7631	1197.7558	1197.6982	0.0577	0	R.AVFPSIVGRPR.H
70 - 85	1961.0845	1960.0772	1959.9036	0.1736	0	K.YPIEHGIITNWDDMEK.I
86 - 96	1501.8298	1500.8225	1500.7262	0.0963	0	K.IWHHSFYNELR.V
198 - 207	1130.6260	1129.6188	1129.5403	0.0784	0	R.GYSFVTTAER.E
240 - 255	1791.0497	1790.0424	1789.8846	0.1579	0	K.SYELPDGQVITIGNER.F

No match to: 1499.7788, 1515.8613, 1975.0948, 2215.2821, 2228.2983

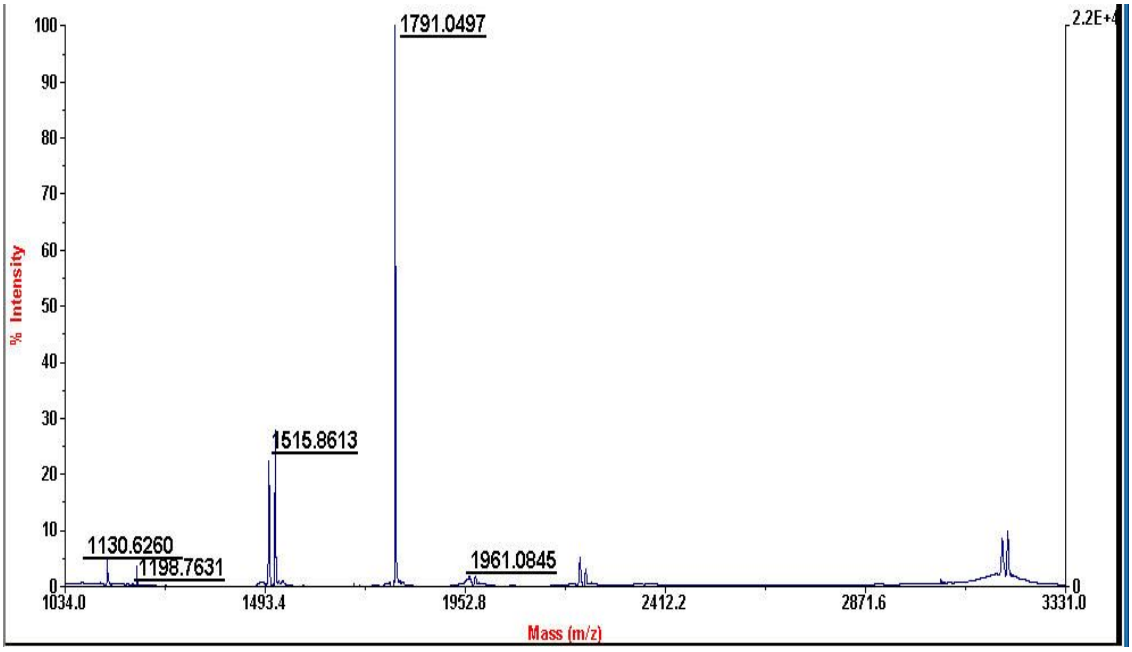
203 ） Actin, alpha cardiac muscle 1 (Alpha-cardiac actin)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 41	1198.7631	1197.7558	1197.6982	0.0577	0	R.AVFPSIVGRPR.H
71 - 86	1961.0845	1960.0772	1959.9036	0.1736	0	K.YPIEHGIITNWDDMEK.I
87 - 97	1515.8613	1514.8540	1514.7419	0.1121	0	K.IWHHTFYNELR.V
199 - 208	1130.6260	1129.6188	1129.5403	0.0784	0	R.GYSFVTTAER.E
241 - 256	1791.0497	1790.0424	1789.8846	0.1579	0	K.SYELPDGQVITIGNER.F

No match to: 1499.7788, 1501.8298, 1975.0948, 2215.2821, 2228.2983

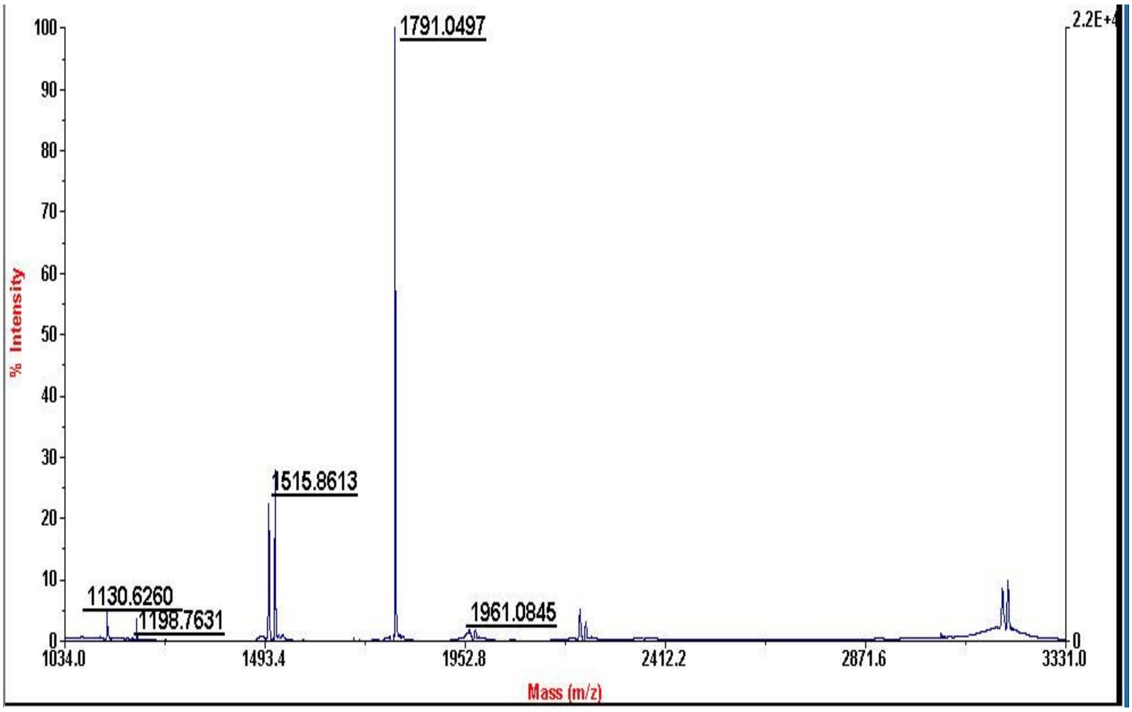
204 ） Actin, alpha skeletal muscle (Alpha-actin-1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 41	1198.7631	1197.7558	1197.6982	0.0577	0	R.AVFPSIVGRPR.H
71 - 86	1961.0845	1960.0772	1959.9036	0.1736	0	K.YPIEHGIITNWDDMEK.I
87 - 97	1515.8613	1514.8540	1514.7419	0.1121	0	K.IWHHTFYNELR.V
199 - 208	1130.6260	1129.6188	1129.5403	0.0784	0	R.GYSFVTTAER.E
241 - 256	1791.0497	1790.0424	1789.8846	0.1579	0	K.SYELPDGQVITIGNER.F

No match to: 1499.7788, 1501.8298, 1975.0948, 2215.2821, 2228.2983

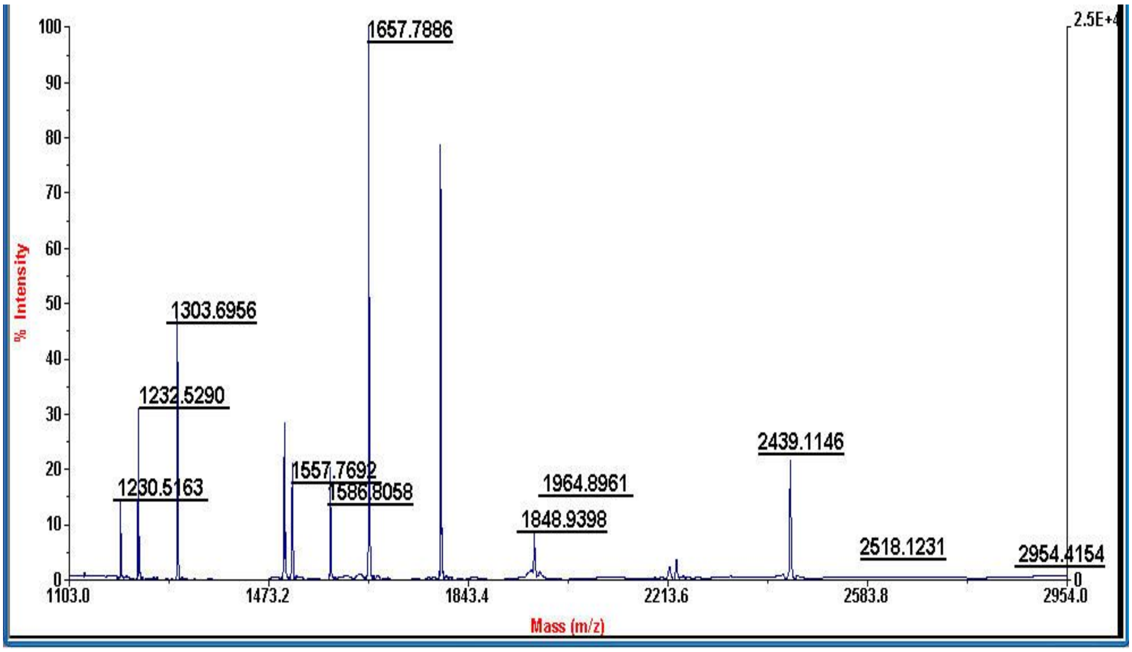
205 ） Actin, aortic smooth muscle (Alpha-actin-2)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 41	1198.7631	1197.7558	1197.6982	0.0577	0	R.AVFPSIVGRPR.H
71 - 86	1961.0845	1960.0772	1959.9036	0.1736	0	K.YPIEHGIITNWDDMEK.I
87 - 97	1501.8298	1500.8225	1500.7262	0.0963	0	K.IWHHSFYNELR.V
199 - 208	1130.6260	1129.6188	1129.5403	0.0784	0	R.GYSFVTTAER.E
241 - 256	1791.0497	1790.0424	1789.8846	0.1579	0	K.SYELPDGQVITIGNER.F

No match to: 1499.7788, 1515.8613, 1975.0948, 2215.2821, 2228.2983

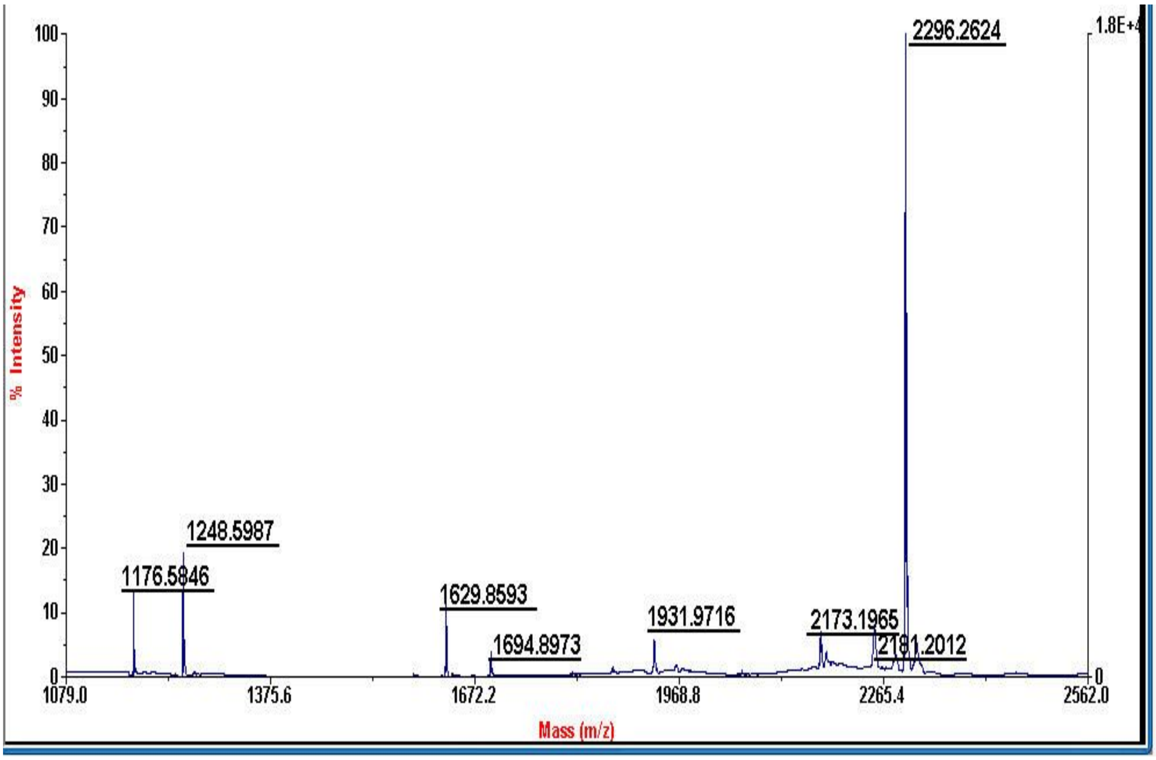
206 ） Creatine kinase B-type (EC 2.7.3.2) (Creatine kinase B chain) (B-CK)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
12 - 32	2439.1146	2438.1073	2438.1437	-0.0363	1	K.LRFPAEDEFPDLSAHNNHMAK.V
33 - 43	1303.6956	1302.6883	1302.7183	-0.0300	0	K.VLTPELYAELR.A
87 - 96	1232.5290	1231.5218	1231.6084	-0.0867	0	K.DLFDPIIEDR.H
108 - 130	2518.1231	2517.1158	2517.1619	-0.0461	0	K.TDLNPDNLQGGDDLDPNYVLSSR.V
139 - 148	1230.5163	1229.5090	1229.5434	-0.0344	0	R.GFCLPPHCSR.G 2
157 - 172	1586.8058	1585.7986	1585.8311	-0.0325	0	K.LAVEALSSLDGDLAGR.Y
224 - 236	1657.7886	1656.7813	1656.8260	-0.0447	0	K.TFLVWVNEEDHLR.V
253 - 265	1557.7692	1556.7619	1556.7908	-0.0289	0	R.FCTGLTQIETLFK.S

268 - 292	2954.4154	2953.4081	2953.3891	0.0191	0	K.DYEFMWNPHLGYILTCPSNLGTGLR.A
321 - 341	1964.8961	1963.8889	1963.9234	-0.0346	0	R.GTGGVDTAAVGGVFDVSNADR.L
342 - 358	1848.9398	1847.9325	1847.9702	-0.0377	0	R.LGFSEVELVQMVVDGVK.L
359 - 366	1031.5316	1030.5243	1030.5481	-0.0238	0	K.LLIEMEQR.L
367 - 381	1656.7952	1655.7880	1655.8188	-0.0309	0	R.LEQGQAIDDLMPAQK.-

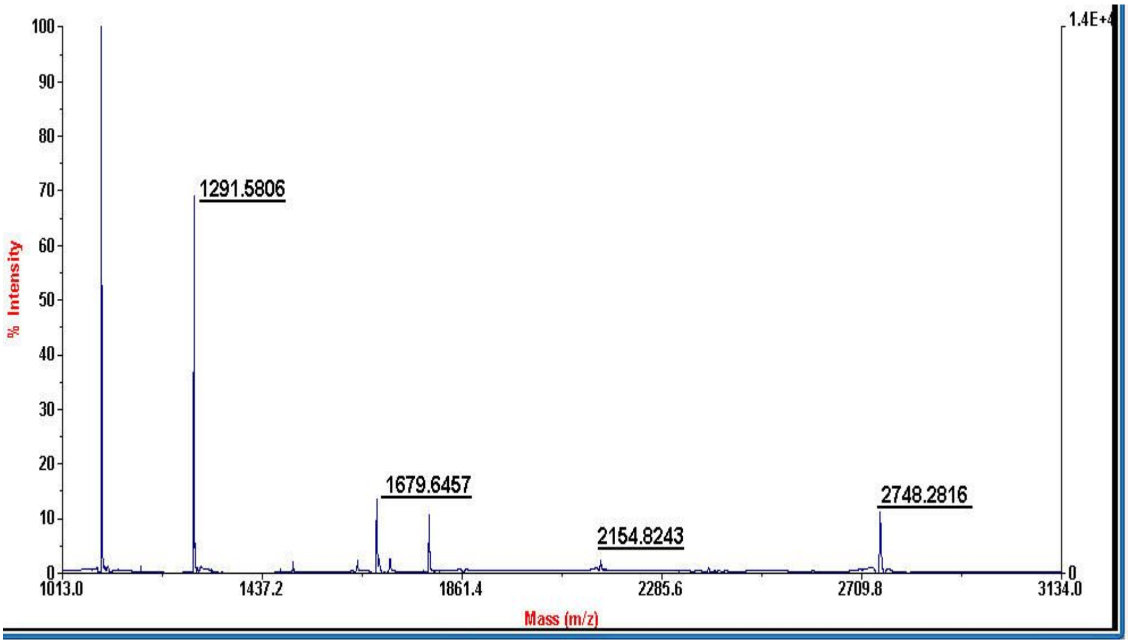
207 ） L-lactate dehydrogenase B chain



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 23	1694.8973	1693.8900	1693.8886	0.0014	0	K.LIAPVAEEEATVPNNK.I
44 - 58	1629.8593	1628.8520	1628.8508	0.0012	0	K.SLADELALVDVLEDK.L
59 - 77	2173.1965	2172.1892	2172.1071	0.0821	1	K.LKGEMMDLQHGSLFLQTPK.I
61 - 77	1931.9716	1930.9644	1930.9281	0.0363	0	K.GEMMDLQHGSLFLQTPK.I
159 - 170	1248.5987	1247.5914	1247.5928	-0.0014	0	R.VIGSGCNLDSAR.F
247 - 266	2181.2012	2180.1939	2180.1187	0.0753	0	K.GYTNWAIGLSVADLIESMLK.N
280 - 299	2296.2624	2295.2551	2295.1391	0.1161	0	K.GMYGIENEVFLSLPCILNAR.G
320 - 329	1176.5846	1175.5773	1175.5822	-0.0049	0	K.SADTLWDIQK.D

No match to: 2251.3627, 2253.1991

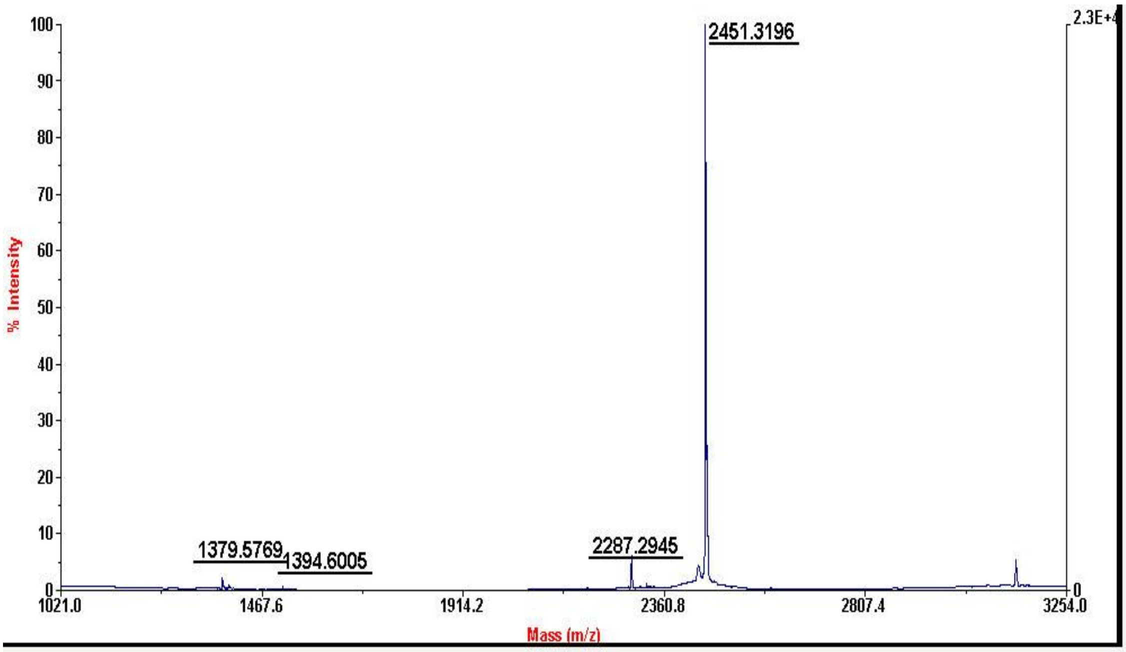
208) NG,NG-dimethylarginine dimethylaminohydrolase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 31	1291.5806	1290.5733	1290.7044	-0.1311	0	R.ALPESLGQHALR.S
112 - 136	2748.2816	2747.2743	2747.3799	-0.1056	1	K.LQLNIVEMKDENATLDGGDVLFTGR.E
121 - 136	1679.6457	1678.6385	1678.7798	-0.1413	0	K.DENATLDGGDVLFTGR.E
176 - 196	2154.8243	2153.8170	2154.0085	-0.1915	0	K.SFCSMAGPNLIAIGSSESAQK.A

No match to: 1095.4432, 1790.7375

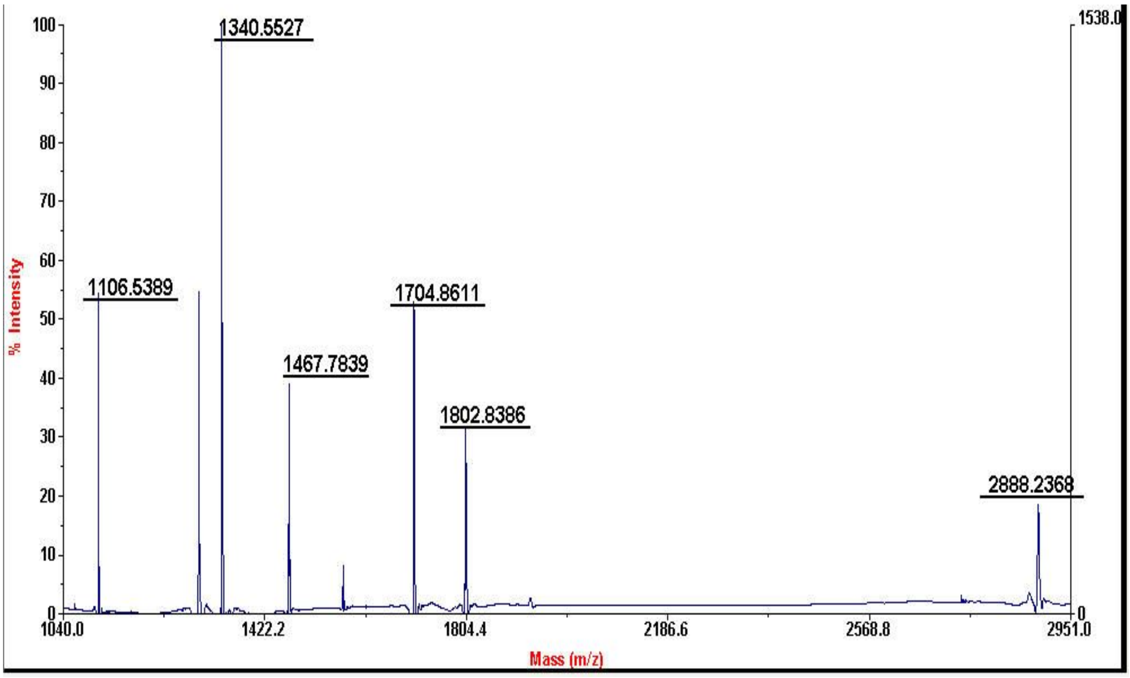
209) 3'(2'),5'-bisphosphate nucleotidase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
41 - 52	1379.5769	1378.5696	1378.6511	-0.0815	1	K.TCATDLQTKADR.L
145 - 167	2451.3196	2450.3123	2450.2229	0.0894	0	K.AIAGVINQPYYNYEAGPDAVLGR.T
190 - 201	1394.6005	1393.5932	1393.7426	-0.1494	1	K.HIITTTRSHSNK.L
202 - 224	2287.2945	2286.2873	2286.1459	0.1413	1	K.LVTDCVAAMNPDAVLRVGGAGNK.I Oxidation (M)

No match to: 1514.5755, 3140.7915

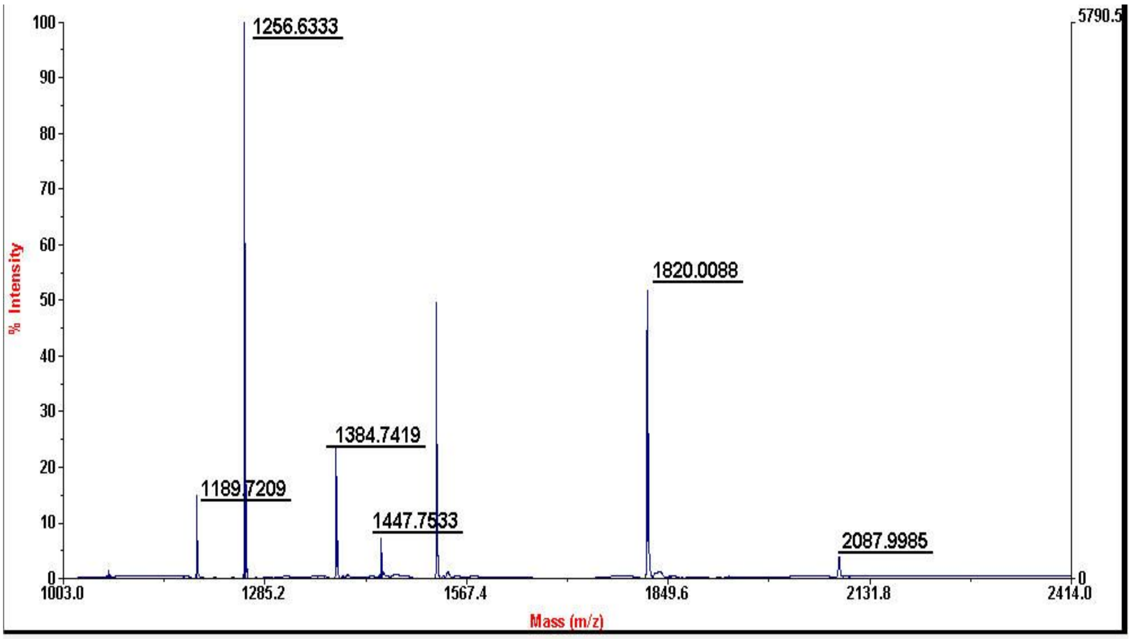
210) Annexin A5



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 18	1340.5527	1339.5455	1339.6044	-0.0589	0	R.GTVTDFPGFDER.A
30 - 45	1704.8611	1703.8538	1703.8941	-0.0403	0	K.GLGTDEESILTLLTSR.S
51 - 63	1467.7839	1466.7766	1466.7881	-0.0115	1	R.QEISAAFKTLFGR.D
127 - 151	2888.2368	2887.2295	2887.2307	-0.0012	0	K.QVYEEEYGSSLEDDVVGDTSGYYQR.M
194 - 201	954.5215	953.5142	953.5334	-0.0192	0	K.FITIFGTR.S
213 - 227	1802.8386	1801.8313	1801.8556	-0.0243	0	K.YMTISGFQIEETIDR.E
277 - 285	1106.5389	1105.5317	1105.5767	-0.0451	0	R.SEIDLFNIR.K

No match to: 1062.5389, 1296.6490

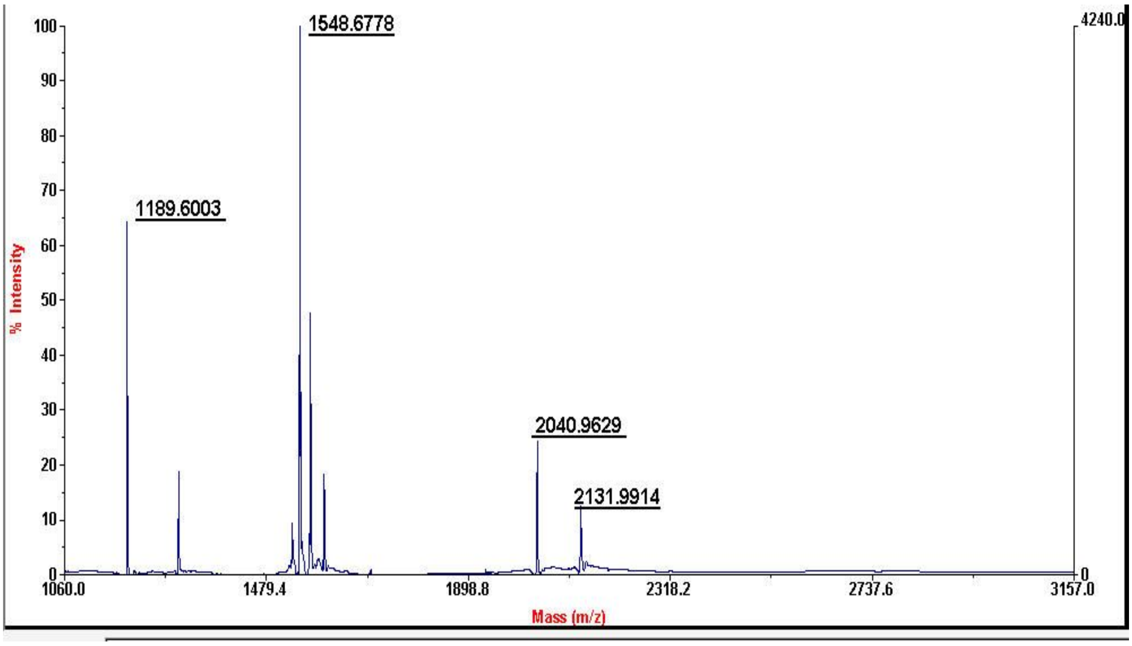
211) 14-3-3 protein epsilon (14-3-3E)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
30 - 42	1447.7533	1446.7460	1446.7024	0.0437	0	K.VAGMDVELTVEER.N
131 - 141	1256.6333	1255.6260	1255.5833	0.0428	0	R.YLAEFATGNDR.K
131 - 142	1384.7419	1383.7346	1383.6782	0.0564	1	R.YLAEFATGNDRK.E
154 - 170	1820.0088	1819.0015	1818.9298	0.0717	0	K.AASDIAMTELPPTHPIR.L
197 - 215	2087.9985	2086.9912	2086.9582	0.0330	0	K.AAFDDAIAELDTLSEESYK.D
216 - 225	1189.7209	1188.7136	1188.6536	0.0600	0	K.DSTLIMQLLR.D

No match to: 1066.1015, 1175.9428, 1524.7420

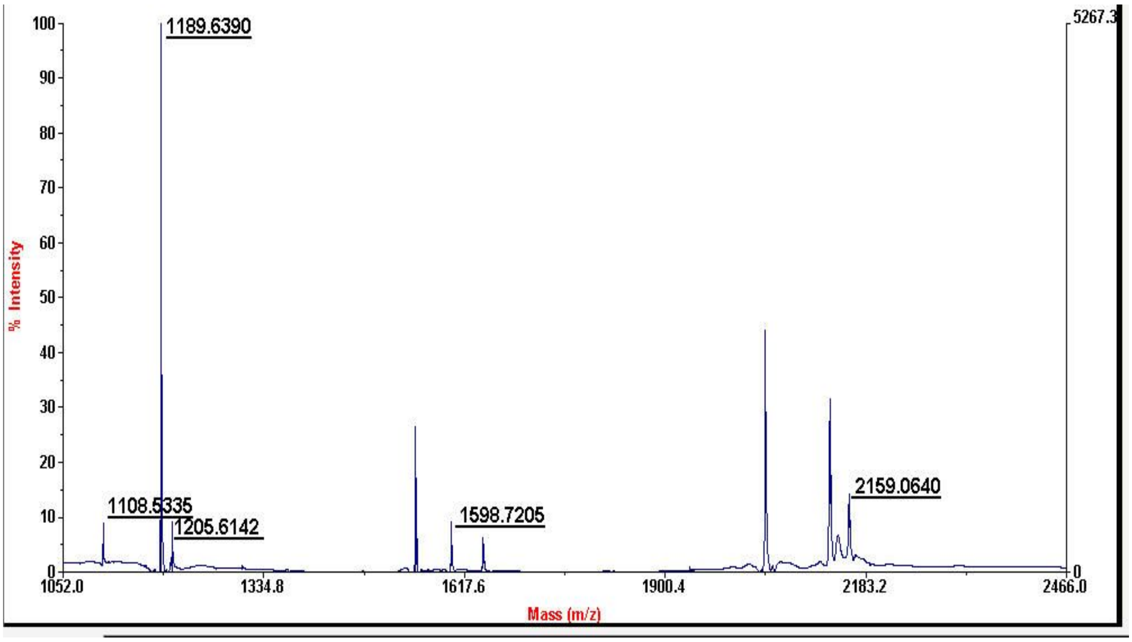
212) 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
28 - 41	1548.6778	1547.6705	1547.7063	-0.0357	0	K.SVTEQGAELSNEER.N
140 - 157	2040.9629	2039.9556	2039.9799	-0.0243	0	K.GIVDQSQQAYQEAFEISK.K
194 - 212	2131.9914	2130.9841	2130.9844	-0.0003	0	K.TAFDEAIAELDTLSEESYK.D
213 - 222	1189.6003	1188.5930	1188.6536	-0.0606	0	K.DSTLIMQLLR.D

No match to: 1296.6143, 1570.6365, 1598.7233

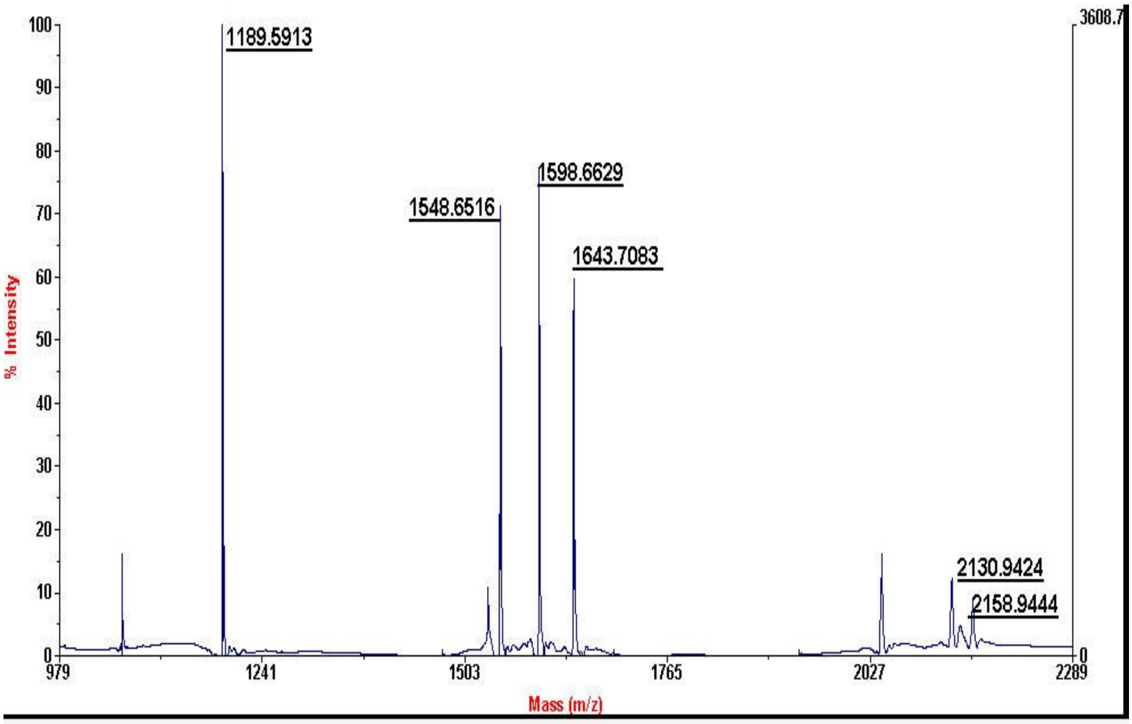
213) 14-3-3 protein beta/alpha (Protein kinase C inhibitor protein 1) (KCIP-1) (Protein 1054)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
30 - 43	1598.7205	1597.7133	1597.7332	-0.0199	0	K.AVTEQGHELSNEER.N	
141 - 159	2159.0640	2158.0568	2158.0178	0.0390	0	K.QTTVSNSQQAYQEAFEISK.K	
161 - 169	1108.5335	1107.5262	1107.5495	-0.0233	0	K.EMQPTHPIR.L	
215 - 224	1189.6390	1188.6317	1188.6536	-0.0219	0	K.DSTLIMQLLR.D	
215 - 224	1205.6142	1204.6070	1204.6485	-0.0416	0	K.DSTLIMQLLR.D	Oxidation (M)

No match to: 1548.7029, 2041.0341

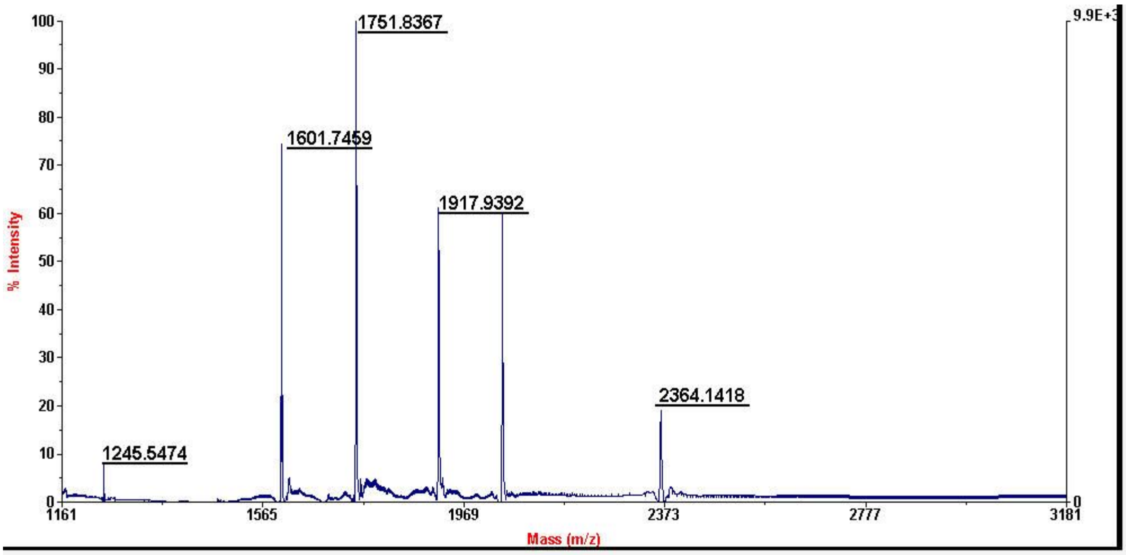
214) Nuclear pore complex protein Nup160 (Nucleoporin Nup160) (160 kDa nucleoporin)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
45 - 59	1643.7083	1642.7010	1642.7150	-0.0140	0	K.YSESAGGFYYVESGK.L	
281 - 298	2158.9444	2157.9371	2158.0182	-0.0811	1	K.EQMCLMVADMLEYVPVKK.D	2 Oxidation (M)
644 - 655	1548.6516	1547.6443	1547.6007	0.0436	0	R.EMDYETEVEMEK.G	Oxidation (M)
915 - 925	1189.5913	1188.5840	1188.5622	0.0218	0	R.SEDGEIVSTPR.L	
1126 - 1139	1598.6629	1597.6556	1597.7015	-0.0459	1	K.RNHDGECTAAPTNR.Q	
1140 - 1157	2130.9424	2129.9352	2130.0878	-0.1526	1	R.QIEILELEDLEKECSLAR.I	

No match to: 2040.9201

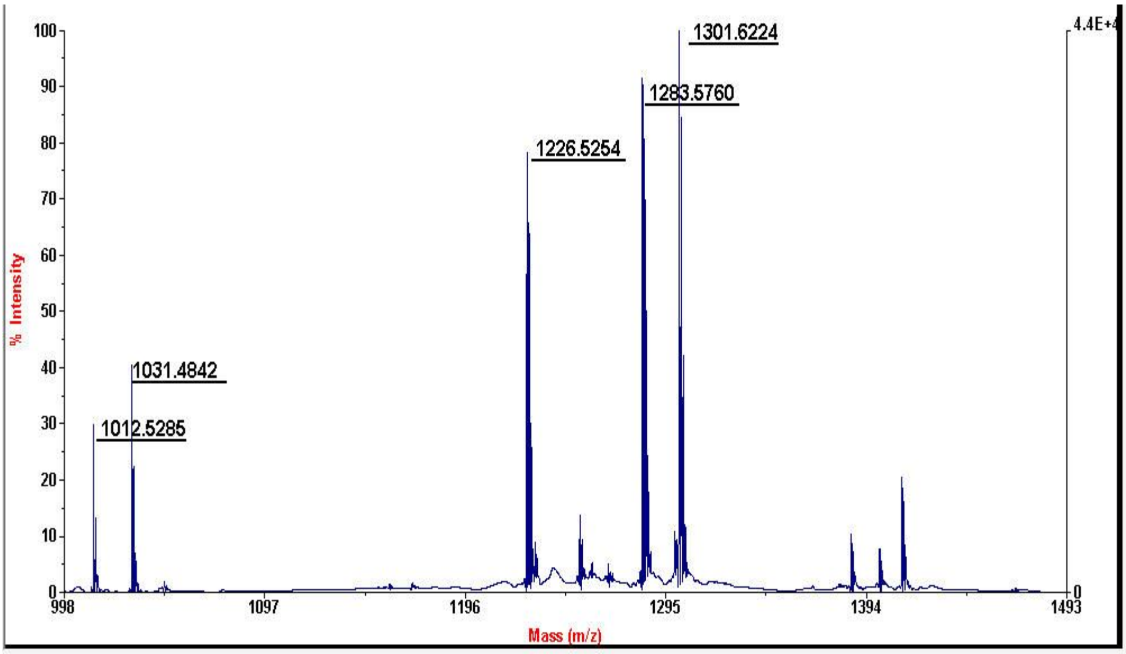
215) Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
34 - 49	1917.9392	1916.9319	1916.9327	-0.0008	1	K.SIQEIQELDKDDESLR.K
128 - 134	980.4556	979.4483	979.4875	-0.0393	0	K.YIQHTYR.K
139 - 152	1601.7459	1600.7386	1600.7555	-0.0169	1	K.IDKTDYMVGSYGPR.A
142 - 152	1245.5474	1244.5401	1244.5495	-0.0094	0	K.TDYMVGSYGPR.A
153 - 167	1751.8367	1750.8294	1750.8301	-0.0007	0	R.AEEYEFLTPVEEAPK.G
181 - 199	2364.1418	2363.1345	2363.1070	0.0276	1	R.FTDDDKTDHLSWEWNLTIK.K

No match to: 2046.0320

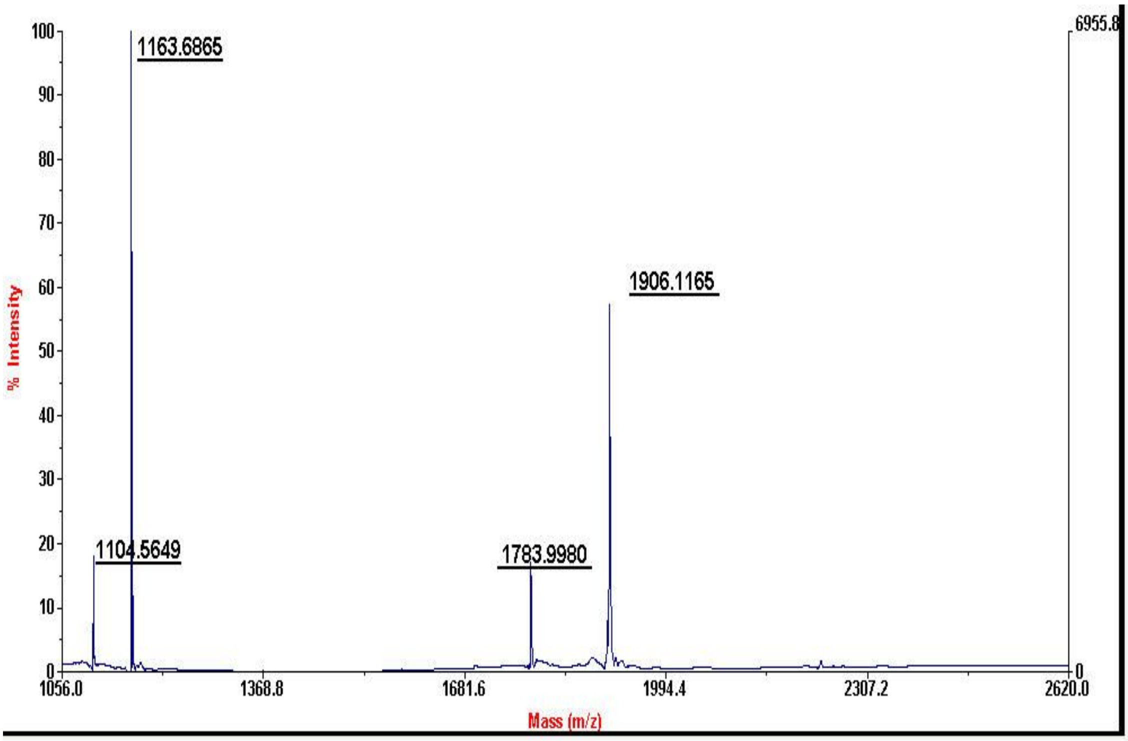
216) Kelch-like protein 15



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
58 - 67	1301.6224	1300.6151	1300.5904	0.0247	1	R.IMFTADMRER.D	2 Oxidation (M)
119 - 127	1031.4842	1030.4769	1030.4980	-0.0210	0	K.FCCSFLLAK.I	
474 - 482	1226.5254	1225.5181	1225.5484	-0.0303	1	K.MNYARCFHK.M	
533 - 542	1012.5285	1011.5212	1011.5349	-0.0137	0	R.SGHGVTVLDK.Q	
572 - 581	1283.5760	1282.5688	1282.5322	0.0366	1	K.EDEYPRMPCK.L	Oxidation (M)

No match to: 1411.6764, 2202.1581

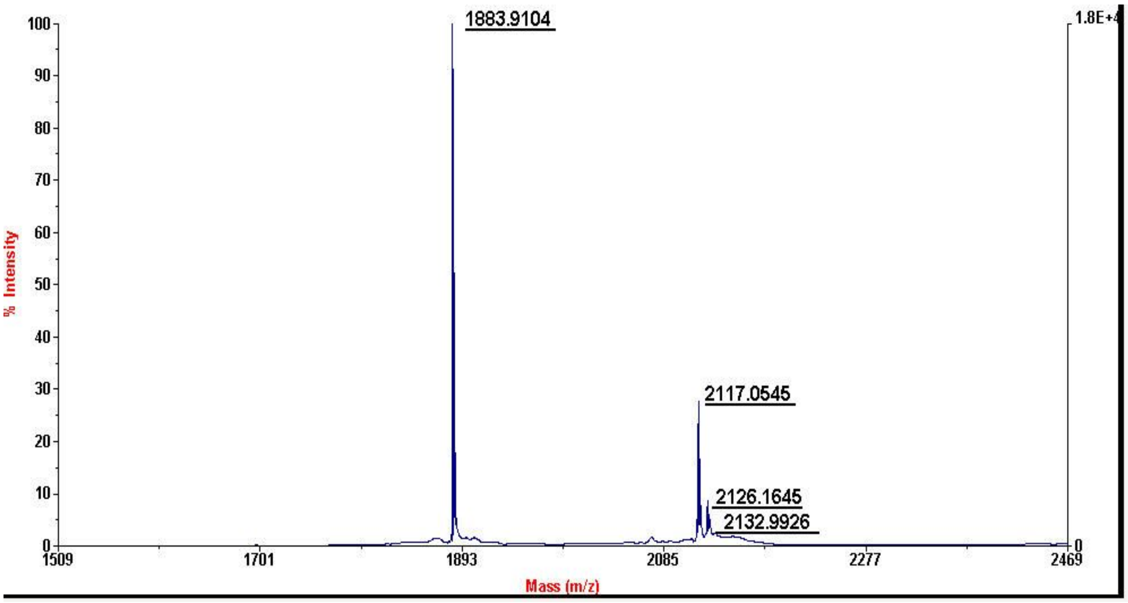
217) Heat-shock protein beta-1 (HspB1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
28 - 37	1163.6865	1162.6792	1162.6134	0.0658	0	R.LFDQAFGLPR.L
97 - 112	1783.9980	1782.9907	1782.9152	0.0756	0	R.VSLDVNHFAPDELTVK.T
128 - 136	1104.5649	1103.5576	1103.4996	0.0581	0	R.QDEHGYISR.C
172 - 188	1906.1165	1905.1092	1904.9843	0.1249	0	K.LATQSNEITIPVTFESR.A

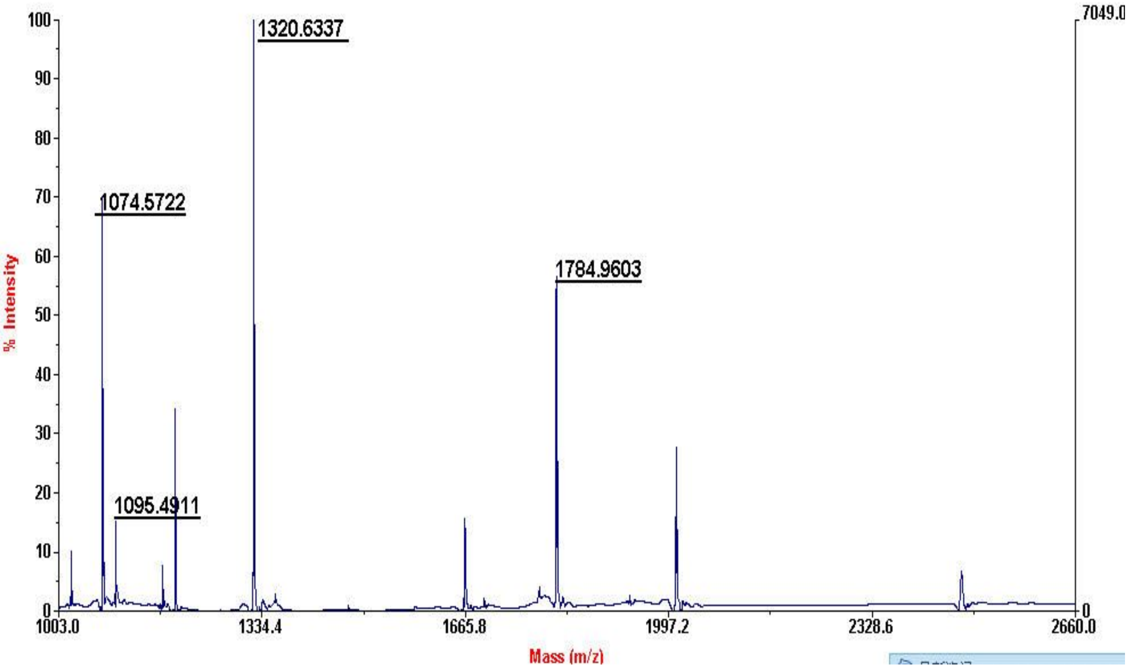
No match to: 1540.8895, 1805.0752

218 ） Glutathione S-transferase P



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
56 - 71	1883.9104	1882.9031	1882.9425	-0.0393	0	K.FQDGDLTLYQSNTILR.H
83 - 101	2117.0545	2116.0473	2115.9742	0.0731	0	K.DQQEAALVDMVNDGVEDLR.C
83 - 101	2132.9926	2131.9853	2131.9691	0.0162	0	K.DQQEAALVDMVNDGVEDLR.C
Oxidation (M)						
122 - 141	2126.1645	2125.1573	2125.1531	0.0042	0	K.ALPGQLKPFETLLSQNQGGK.T

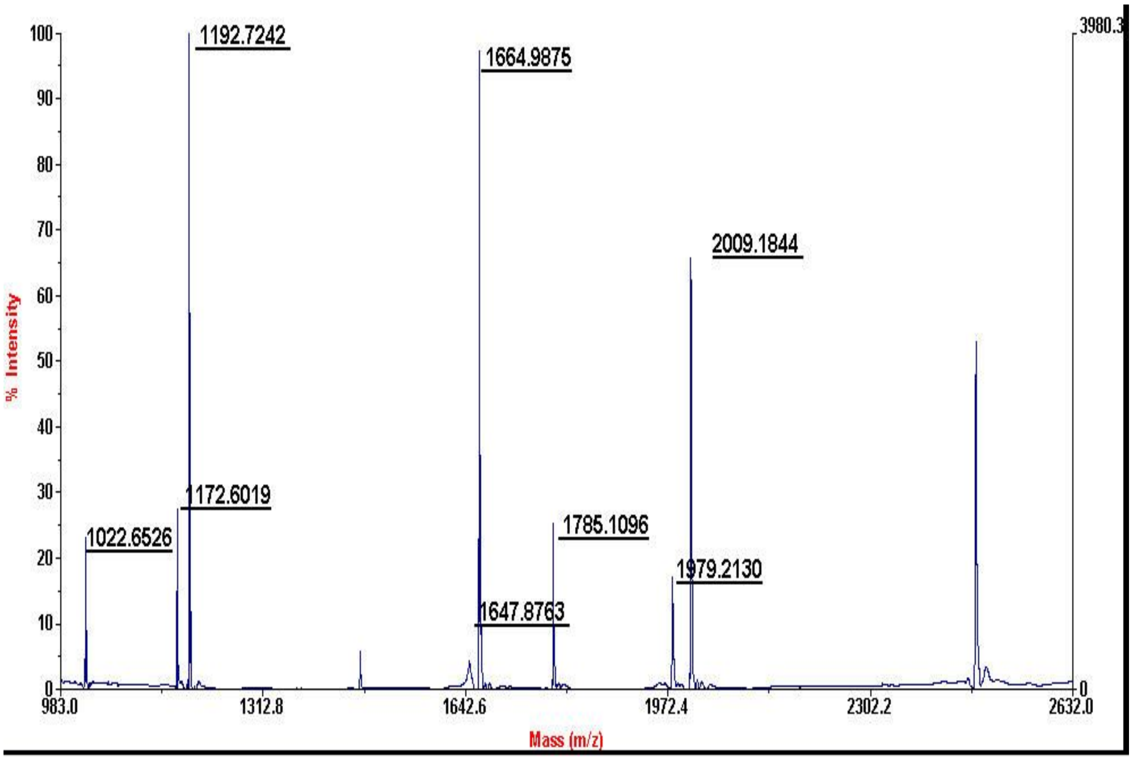
219 ）Glutathione transferase omega-1 (EC 2.5.1.18) (GSTO 1-1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
12 - 25	1320.6337	1319.6265	1319.6833	-0.0568	0	K.GSAPPGPVPEGSIR.I
31 - 37	926.3547	925.3474	925.4116	-0.0641	0	R.FCPFAER.T
58 - 65	1095.4911	1094.4839	1094.5549	-0.0710	0	K.NKPEWFFK.K
123 - 132	1074.5722	1073.5649	1073.6233	-0.0583	0	K.VPSLVGSFIR.S
184 - 198	1784.9603	1783.9530	1783.8597	0.0934	1	R.LEAMKLNECVDHTPK.L

No match to: 1172.4600, 1192.5948, 1664.8363, 1813.8745, 2009.0417, 2473.2334

220) Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine phosphorylase) (PNP)

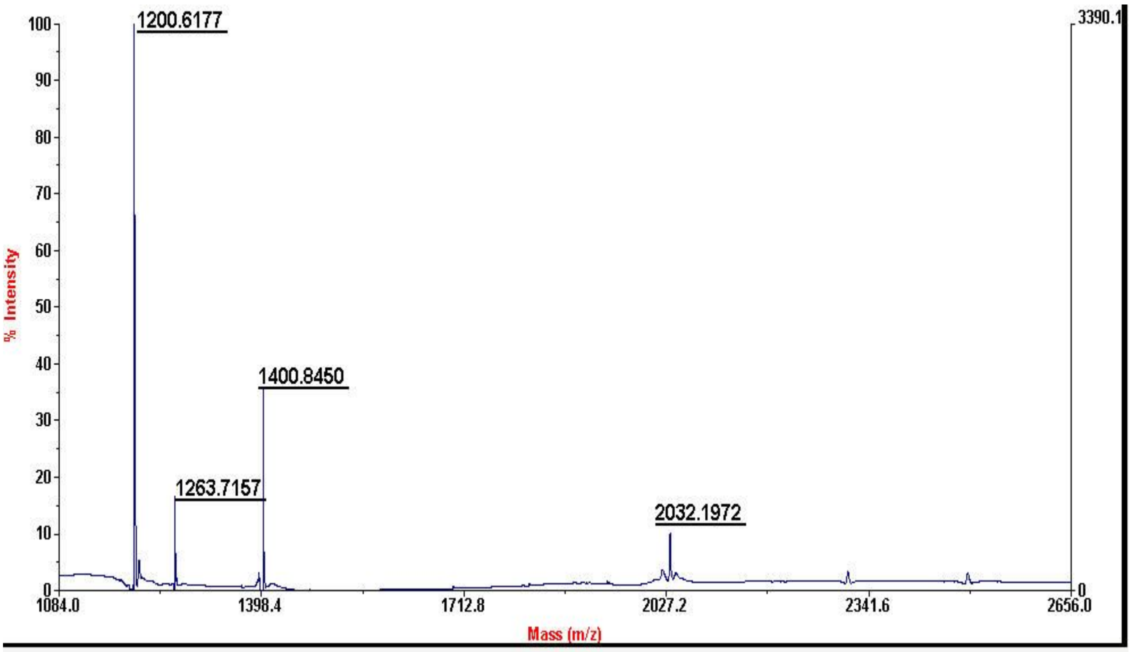


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 41	1979.2130	1978.2058	1978.0418	0.1640	0	K.HRPQVAIICGSGLGGLTDK.L
42 - 58	2009.1844	2008.1771	2008.0054	0.1718	0	K.LTQAQIFDYGEIPNFPR.S
68 - 76	1022.6526	1021.6454	1021.5708	0.0745	0	R.LVFGFLNGR.A
124 - 133	1192.7242	1191.7169	1191.6321	0.0848	0	K.FEVGDIMLIR.D
155 - 168	1647.8763	1646.8691	1646.7147	0.1544	1	R.FGDRFPAMSDAYDR.T
159 - 168	1172.6019	1171.5946	1171.4968	0.0978	0	R.FPAMSDAYDR.T
212 - 229	1785.1096	1784.1023	1783.9501	0.1522	0	K.LGADAVGMSTVPEVIVAR.H

255 - 270	1664.9875	1663.9802	1663.8641	0.1161	1	K.ANHEEVLAAGKQAAQK.L

No match to: 2473.3726

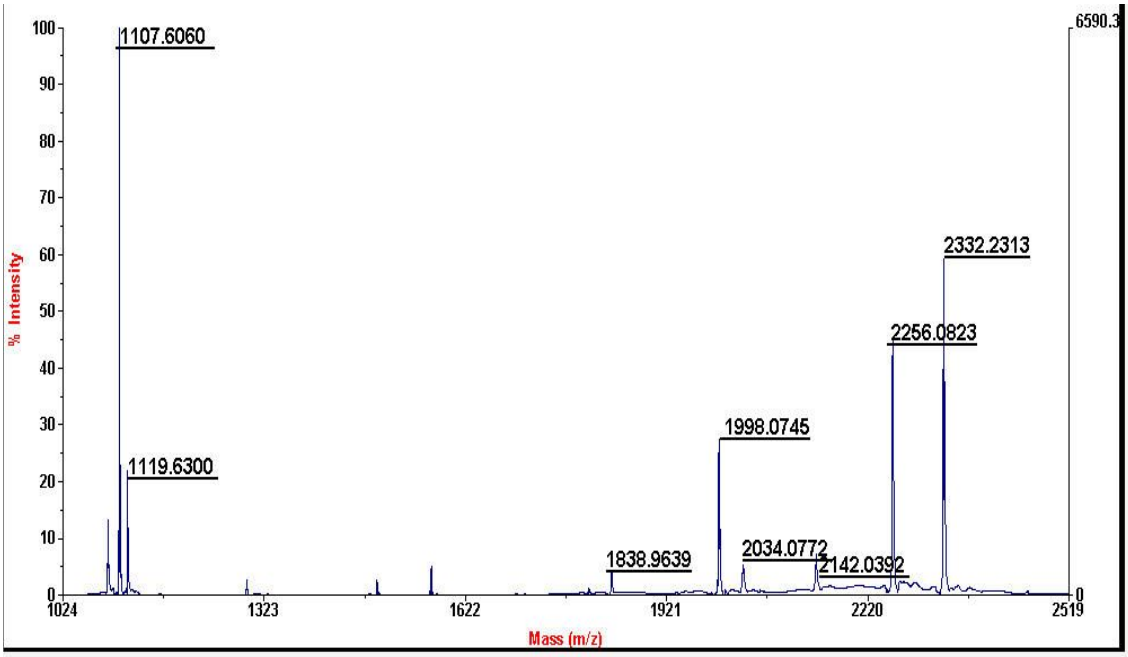
221) Phosphatidylinositol transfer protein alpha isoform (PtdIns transfer protein alpha) (PtdInsTP) (PI-TP-alpha)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
87 - 95	1200.6177	1199.6105	1199.5182	0.0923	0	K.AWNAYPYCR.T
111 - 127	2032.1972	2031.1900	2031.0173	0.1726	0	K.IETWHKPDLGTQENVHK.L
135 - 146	1400.8450	1399.8378	1399.7095	0.1282	0	K.HVEAVYIDIADR.S
220 - 226	934.5691	933.5618	933.4821	0.0798	0	R.LFTNFHR.Q
235 - 244	1263.7157	1262.7084	1262.5965	0.1119	0	K.WVDLTMDDIR.R

No match to: 2020.1867, 2494.5846

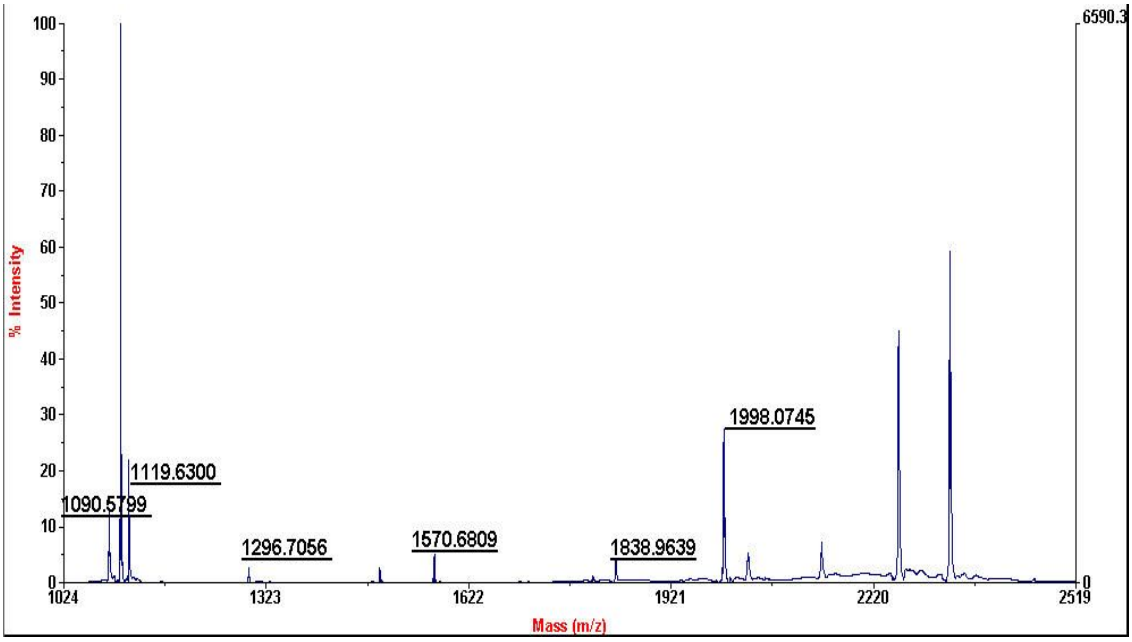
222) Aldose 1-epimerase (EC 5.1.3.3) (Galactose mutarotase) (BLOCK25 protein)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
22 - 30	1119.6300	1118.6227	1118.6084	0.0143	0	K.FQLQSDLLR.V
52 - 68	1838.9639	1837.9567	1837.9461	0.0106	0	R.ASDVVLGFAELEGYLQK.Q
69 - 78	1107.6060	1106.5988	1106.5872	0.0115	0	K.QPYFGAVIGR.V
94 - 111	2034.0772	2033.0699	2033.0442	0.0257	1	K.EYHLAINKEPNSLHGGVR.G
146 - 162	1998.0745	1997.0672	1997.0258	0.0415	0	K.VWVTYTLDGGELIVNYR.A
233 - 249	2142.0392	2141.0319	2140.9901	0.0418	0	K.HLQDFHLNGFDHNFCLK.G
301 - 319	2256.0823	2255.0750	2255.0178	0.0573	0	K.HSGFCLETQNWPDAVNQPR.F
320 - 338	2332.2313	2331.2241	2331.1687	0.0553	0	R.FPPVLLRPGEEYDHTTWFK.F

No match to: 1090.5799, 1296.7056, 1570.6809, 2691.3954

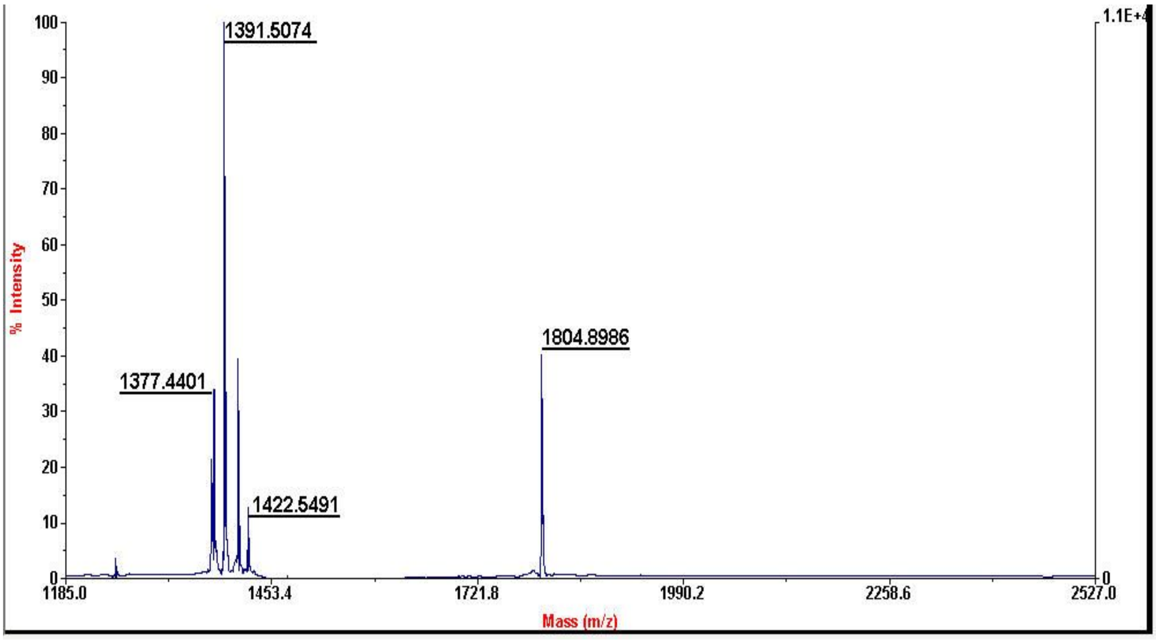
223) F-box only protein 25



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 34	1296.7056	1295.6983	1295.5598	0.1385	1	R.CESCSQKLER.E 2
128 - 146	1998.0745	1997.0672	1997.1884	-0.1212	1	K.LLQLIAKSQLTSLSGVAQK.N
155 - 167	1570.6809	1569.6736	1569.8375	-0.1640	1	K.IVQKVLDDHHNPR.L
322 - 329	1090.5799	1089.5726	1089.5430	0.0297	0	R.HCSILFWK.D
330 - 338	1119.6300	1118.6227	1118.6124	0.0103	0	K.DYHLALLFK.D

No match to: 1107.6060, 1838.9639, 2034.0772, 2142.0392, 2256.0823, 2332.2313, 2691.3954

224) Aflatoxin B1 aldehyde reductase member 2 (EC 1.-.-.-) (AFB1-AR 1) (Aldoketoreductase 7)

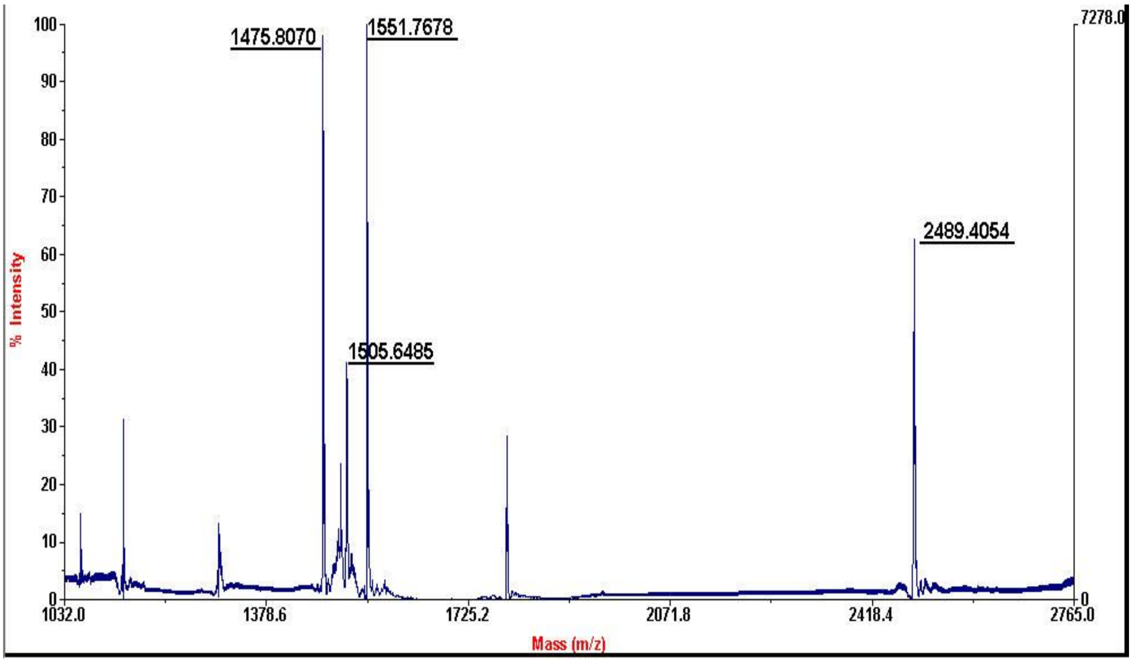


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

38 - 50	1422.5491	1421.5418	1421.7118	-0.1701	1	R.VASVLGTMEMGRR.M	Oxidation (M)
206 - 216	1391.5074	1390.5001	1390.6915	-0.1913	0	R.QVETELFPCLR.H	
251 - 261	1377.4401	1376.4329	1376.6149	-0.1820	0	R.FFGNSWAETYR.N	
279 - 297	1804.8986	1803.8913	1803.9478	-0.0565	0	K.ALQAAYGASAPSVTSAALR.W	

No match to: 1409.4225

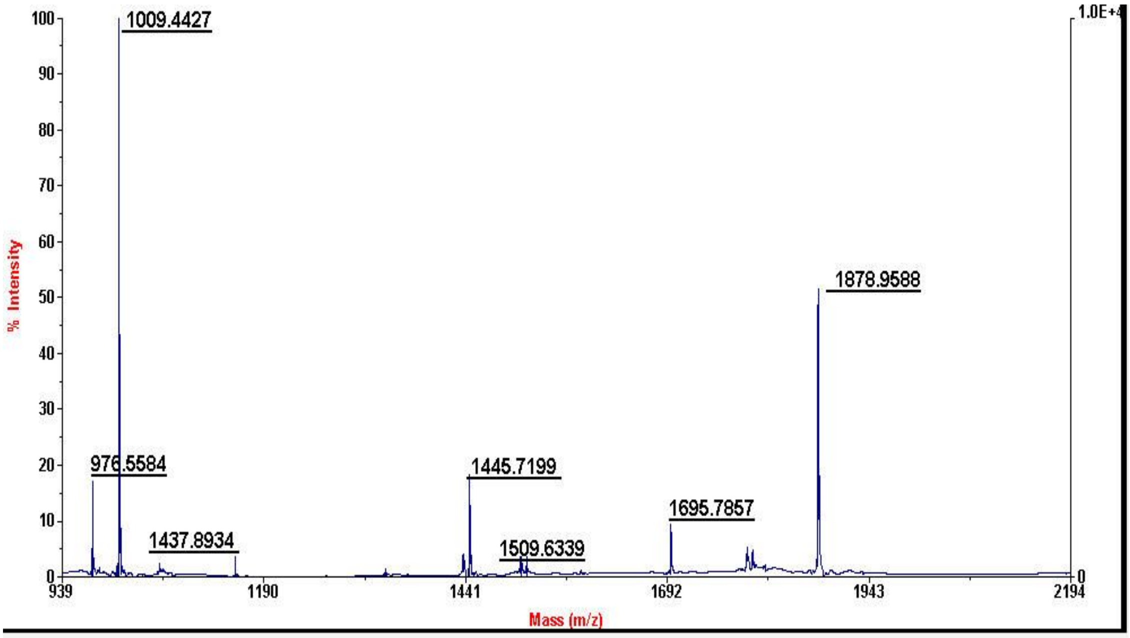
225) Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (Aldehyde reductase) (Aldo-keto reductase family 1 member A1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
154 - 167	1475.8070	1474.7997	1474.7892	0.0106	0	K.GLVQALGLSNFNSR.Q
204 - 218	1551.7678	1550.7605	1550.7576	0.0029	0	R.GLEVTAYSPLGSSDR.A
219 - 240	2489.4054	2488.3981	2488.3213	0.0768	1	R.AWRDPDEPVLLEEPVVLALAEK.Y
313 - 325	1505.6485	1504.6412	1504.6623	-0.0211	0	R.DAGHPLYPFNDPY.-

No match to: 1296.6669

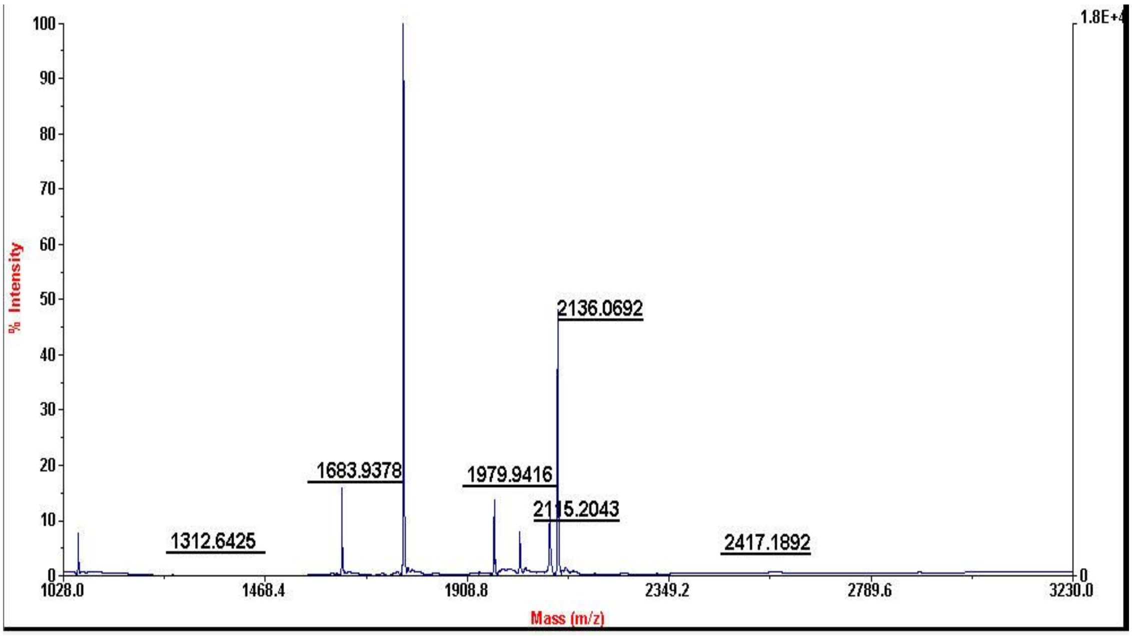
226) Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42) (Cytosolic NADP-isocitrate dehydrogenase) (Oxalosuccinate decarboxylase)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
5 - 20	1695.7857	1694.7784	1694.7603	0.0181	0	K.ISGGSVVEMQGDEMTR.I
30 - 49	2406.2798	2405.2725	2405.2266	0.0459	0	K.LIFPYVELDLHSYDLGIENR.D
101 - 109	976.5584	975.5511	975.5501	0.0010	0	R.NILGGTVFR.E
120 - 132	1437.8934	1436.8862	1436.8867	-0.0005	0	R.LVSGWVKPIIIGR.H
133 - 140	1009.4427	1008.4354	1008.4413	-0.0059	0	R.HAYGDQYR.A
223 - 233	1445.7199	1444.7126	1444.7238	-0.0112	1	R.FKDIFQEIYDK.Q
322 - 338	1878.9588	1877.9515	1877.9271	0.0244	0	K.GQETSTNPIASIFAWTR.G
389 - 400	1509.6339	1508.6266	1508.6493	-0.0227	0	R.SDYLNTFEFMDK.L
401 - 408	914.5246	913.5174	913.5596	-0.0423	1	K.LGENLKIK.L

No match to: 1790.9201

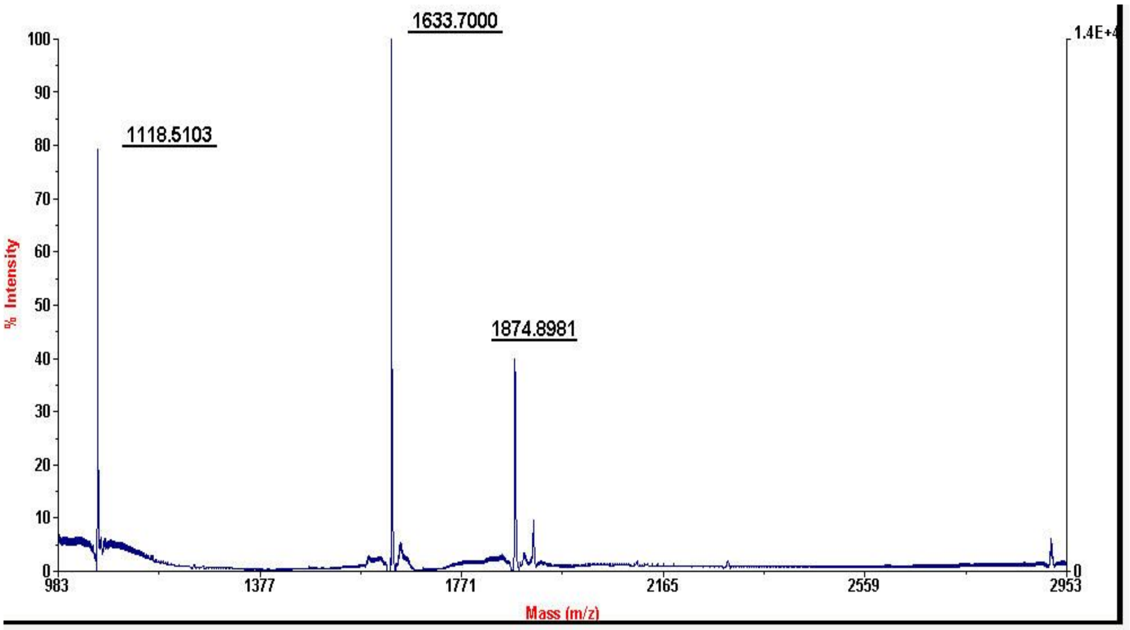
227) Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2) (PRP 2)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
11 - 21	1312.6425	1311.6352	1311.5956	0.0396	0	R.HGESAWNLENR.F
22 - 39	1979.9416	1978.9343	1978.8697	0.0646	0	R.FSGWYDADLSPAGHEEAK.R
22 - 40	2136.0692	2135.0619	2134.9708	0.0911	1	R.FSGWYDADLSPAGHEEAKR.G
118 - 138	2417.1892	2416.1819	2416.1045	0.0774	0	R.SYDVPPPPMEPDHPFYSNISK.D
142 - 162	2425.2687	2424.2614	2424.1478	0.1136	1	R.YADLTEDQLPSCESLKDTIAR.A
163 - 176	1683.9378	1682.9305	1682.9031	0.0274	0	R.ALPFWNEEIVPQIK.E
196 - 222	3023.6305	3022.6232	3022.5572	0.0660	0	K.HLEGLSEEAIMELNLPTGIPIVYELDK.N
223 - 240	2115.2043	2114.1970	2114.1193	0.0777	0	K.NLKPIKPMQFLGDEETVR.K

No match to: 1060.0786

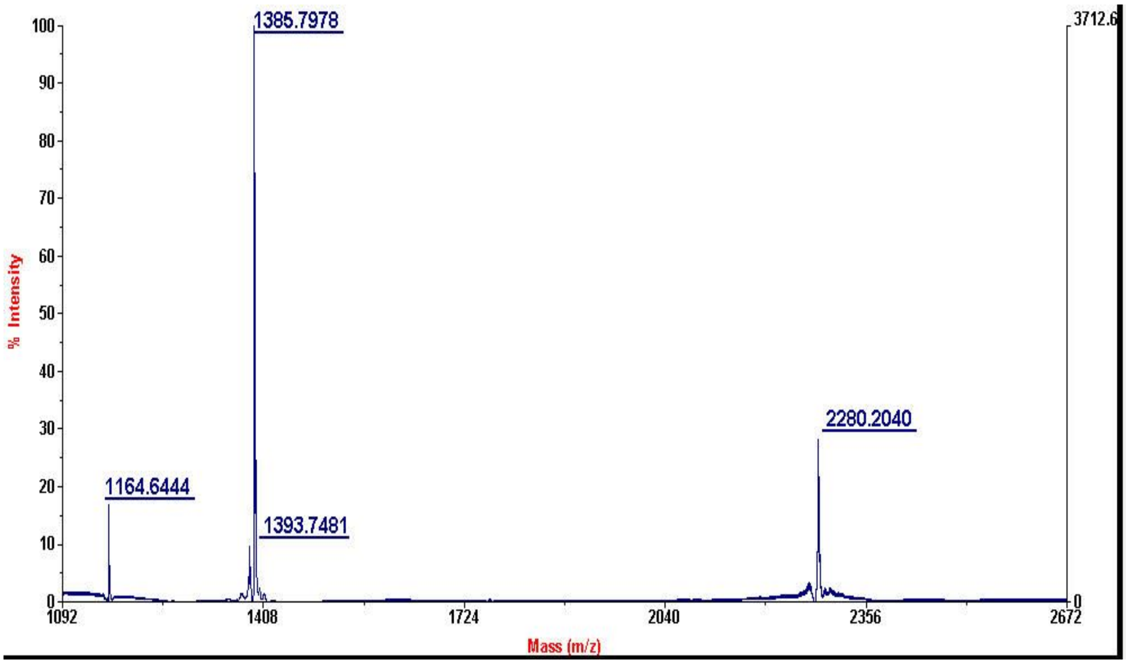
229) L-lactate dehydrogenase A chain (EC 1.1.1.27)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
58 - 73	1874.8981	1873.8909	1873.9542	-0.0633	1	K.LKGEMMDLQHGSLFLR.T
60 - 73	1633.7000	1632.6927	1632.7752	-0.0825	0	K.GEMMDLQHGSLFLR.T
91 - 99	913.5445	912.5372	912.5756	-0.0384	0	K.LVIITAGAR.Q
319 - 328	1118.5103	1117.5031	1117.5768	-0.0737	0	K.SADTLWGIQK.E

No match to: 1910.8809

230) Malate dehydrogenase

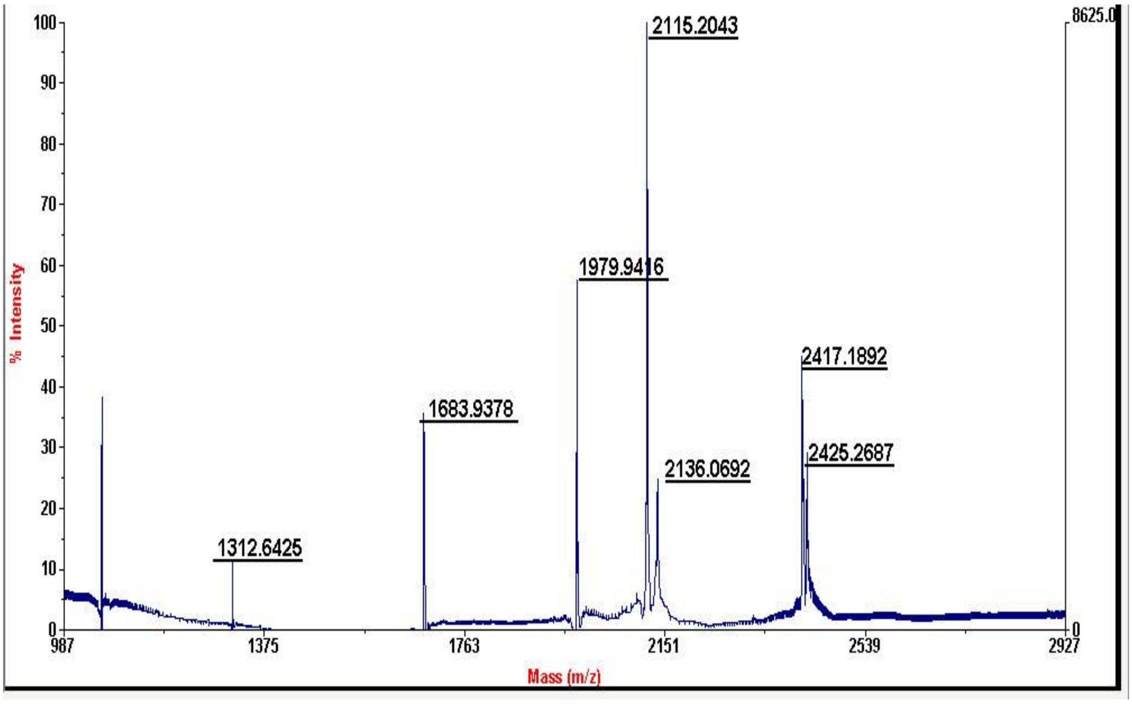


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

80 - 92	1385.7978	1384.7905	1384.7384	0.0521	0	K.DLDVAILVGSMPR.R
180 - 199	2280.2040	2279.1967	2279.1083	0.0884	0	K.NVIIWGNHSSTQYPDVNHAK.V
221 - 230	1164.6444	1163.6371	1163.5934	0.0437	0	K.GEFVTTVQQR.G
299 - 310	1393.7481	1392.7408	1392.7037	0.0371	0	K.FVEGLPINDFSR.E

No match to: 1763.8559

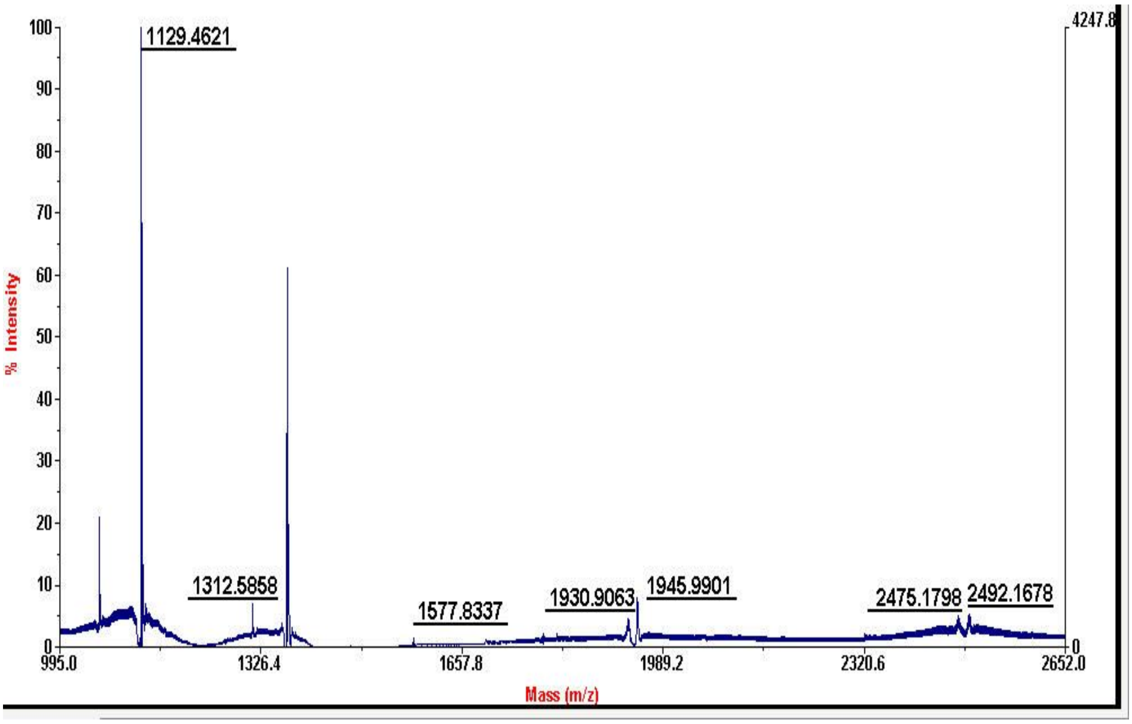
231) Phosphoglycerate mutase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
11 - 21	1312.6425	1311.6352	1311.5956	0.0396	0	R.HGESAWNLENR.F
22 - 39	1979.9416	1978.9343	1978.8697	0.0646	0	R.FSGWYDADLSPAGHEEAK.R
22 - 40	2136.0692	2135.0619	2134.9708	0.0911	1	R.FSGWYDADLSPAGHEEAKR.G
118 - 138	2417.1892	2416.1819	2416.1045	0.0774	0	R.SYDVPPPPMEPDHPFYSNISK.D
142 - 162	2425.2687	2424.2614	2424.1478	0.1136	1	R.YADLTEDQLPSCESLKDTIAR.A
163 - 176	1683.9378	1682.9305	1682.9031	0.0274	0	R.ALPFWNEEIVPQIK.E
196 - 222	3023.6305	3022.6232	3022.5572	0.0660	0	K.HLEGLSEEAIMELNLPTGIPIVYELDK.N
223 - 240	2115.2043	2114.1970	2114.1193	0.0777	0	K.NLKPIKPMQFLGDEETVR.K

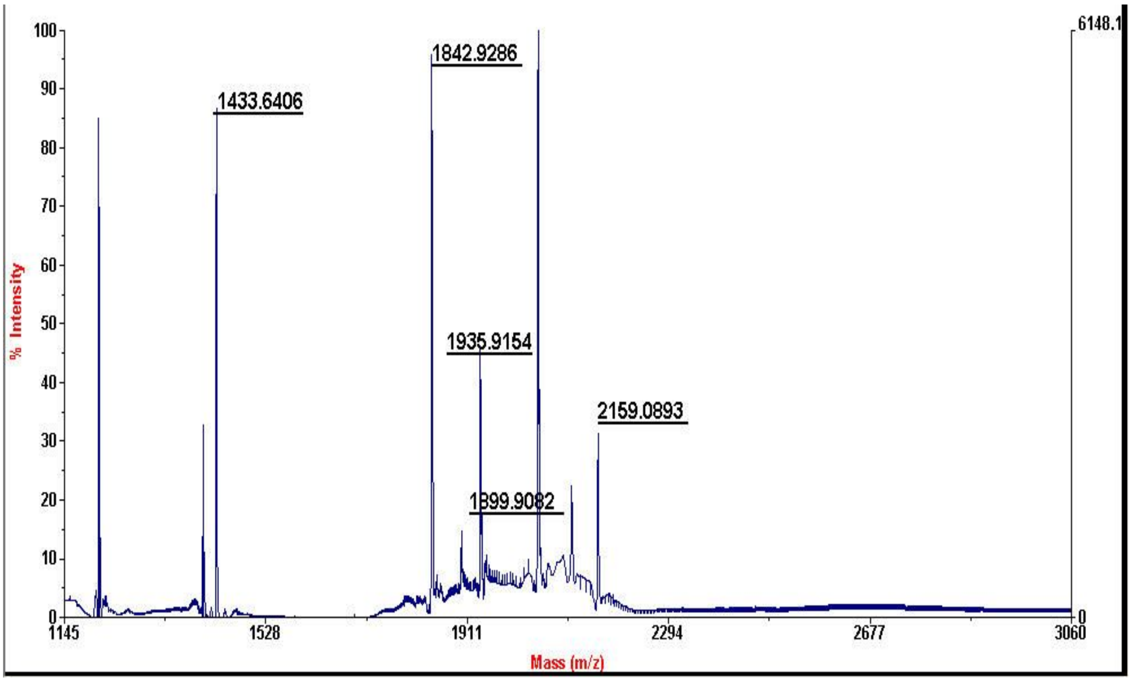
No match to: 1060.0786

232 ）Carbonic anhydrase 3 (EC 4.2.1.1) (Carbonic anhydrase III) (Carbonate dehydratase III) (CA-III)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
4 - 24	2492.1678	2491.1605	2491.1093	0.0511	0	K.EWGYASHNGPDHWHELFPNAK.G
40 - 57	1930.9063	1929.8990	1929.8857	0.0133	0	R.HDPSLQPWSVSYDGGSAK.T
68 - 76	1129.4621	1128.4548	1128.5087	-0.0540	0	R.VVFDDTYDR.S
81 - 89	913.4232	912.4159	912.4817	-0.0658	0	R.GGPLPGPYR.L
92 - 113	2475.1798	2474.1725	2474.0999	0.0726	0	R.QFHLHWGSSDDHGSEHTVDGVK.Y
114 - 126	1577.8337	1576.8264	1576.8150	0.0114	0	K.YAAELHLVHWNPK.Y
149 - 165	1945.9901	1944.9829	1944.9581	0.0248	0	K.IGHENGEFQIFLDALDK.I
178 - 188	1312.5858	1311.5785	1311.5740	0.0045	0	K.FDPSCLFPACR.D
178 - 188	1369.5742	1368.5669	1368.5955	-0.0285	0	K.FDPSCLFPACR.D 2
227 - 253	3011.7293	3010.7221	3010.5624	0.1597	0	R.SLLSSAENEPPVPLVSNWRPPQPINNR.V

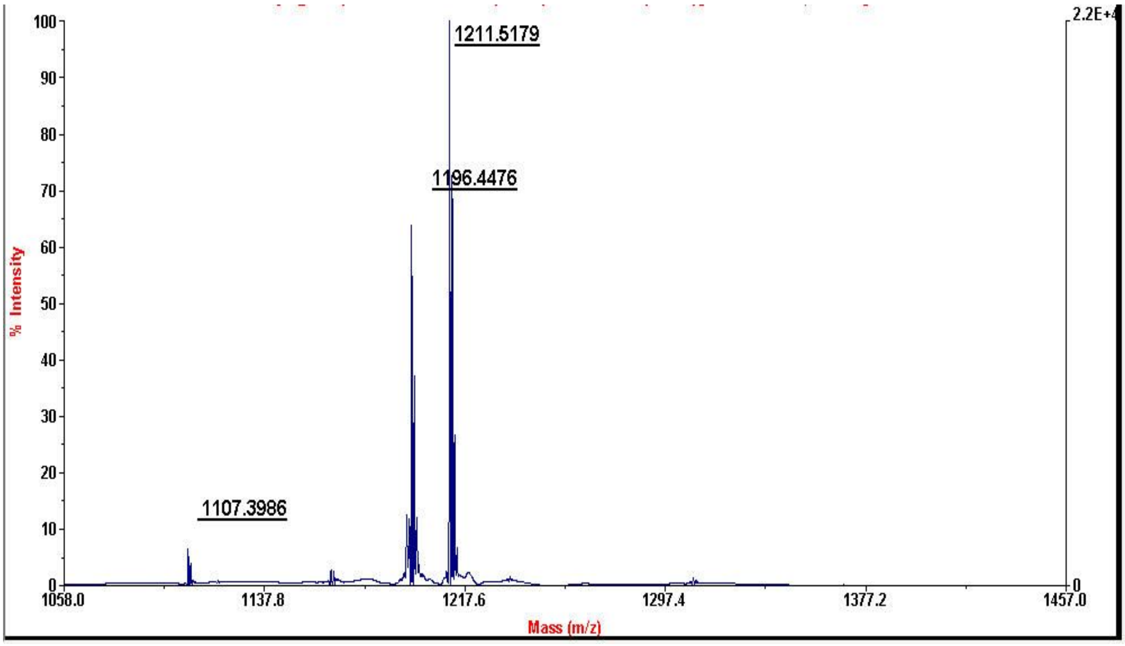
233 ） Cysteine and glycine-rich protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
16 - 32	2044.9417	2043.9344	2043.8996	0.0349	0	K.TVYFAEEVQCEGNSFHK.S
43 - 59	1935.9154	1934.9082	1934.9043	0.0038	0	K.NLDSTTVAVHGEEIYCK.S
70 - 91	2159.0893	2158.0820	2158.0541	0.0279	1	K.GYGYGQGAGTLSTDKGESLGIK.H
92 - 108	1842.9286	1841.9213	1841.8768	0.0445	0	K.HEEAPGHRPTTNPNASK.F
152 - 168	1899.9082	1898.9009	1898.8931	0.0078	1	K.GLESTTLADKDGEIYCK.G
179 - 193	1433.6406	1432.6334	1432.6734	-0.0401	0	K.GFGFGQGAGALVHSE.-

No match to: 1059.9851, 1210.5147, 1408.6522, 2109.1015

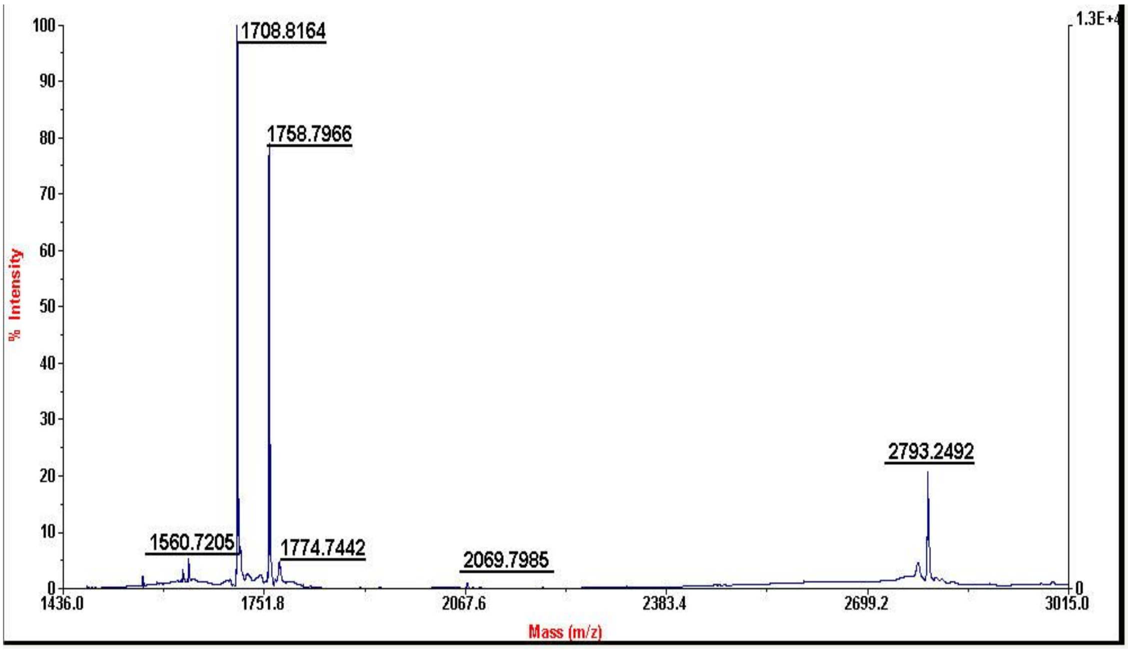
234 ） Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase 2)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 16	980.2871	979.2798	979.5239	-0.2441	0	K.IGHPAPNFK.A
111 - 120	1107.3986	1106.3914	1106.5971	-0.2058	0	R.TIAQDYGVLK.A
141 - 151	1211.5179	1210.5107	1210.6669	-0.1563	0	R.QITVNDLPVGR.S
159 - 168	1196.4476	1195.4403	1195.6237	-0.1834	0	R.LVQAFQFTDK.H

No match to: 908.7372, 1194.4832, 2406.5587

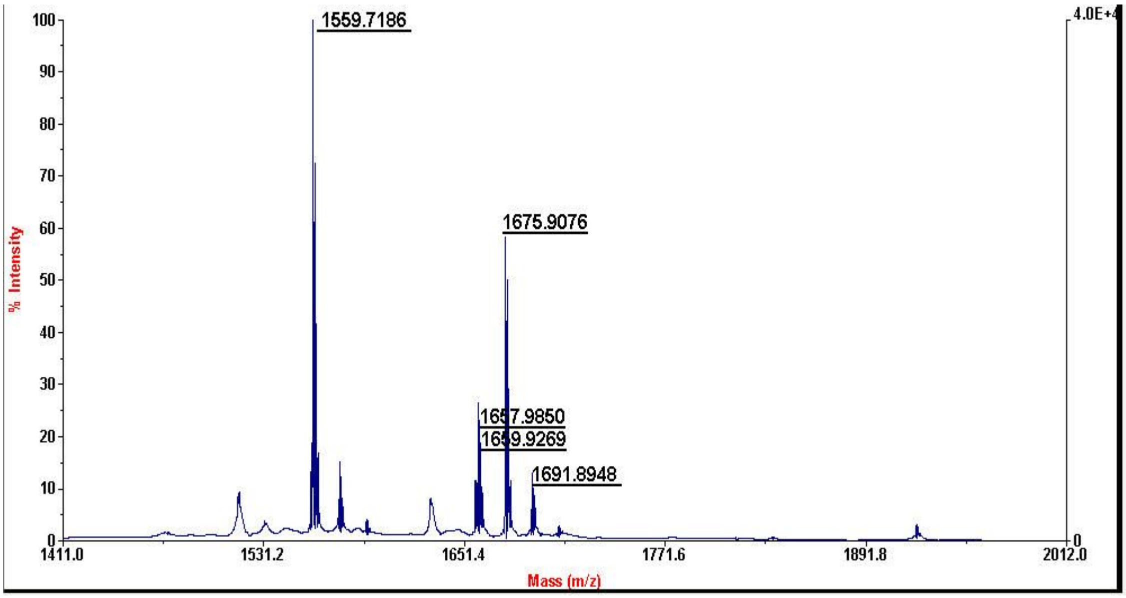
235 ） Phosphatidylethanolamine-binding protein 1 (PEBP-1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
63 - 76	1560.7205	1559.7133	1559.8195	-0.1062	0	K.LYTLVLTDPDAPSR.K
81 - 93	1758.7966	1757.7893	1757.8824	-0.0931	1	K.YREWHHFLVVNMK.G
81 - 93	1774.7442	1773.7369	1773.8773	-0.1404	1	K.YREWHHFLVVNMK.G Oxidation (M)
120 - 132	1708.8164	1707.8091	1707.8984	-0.0893	0	R.YVWLVYEQDRPLK.C
120 - 141	2793.2492	2792.2419	2792.3955	-0.1536	1	R.YVWLVYEQDRPLKCDEPILSNR.S
162 - 179	2069.7985	2068.7912	2068.9200	-0.1288	0	R.APVAGTCYQAEWDDYVPK.L
162 - 187	2988.2324	2987.2252	2987.4010	-0.1759	1	R.APVAGTCYQAEWDDYVPKLYEQLSGK.-

No match to: 1714.7740

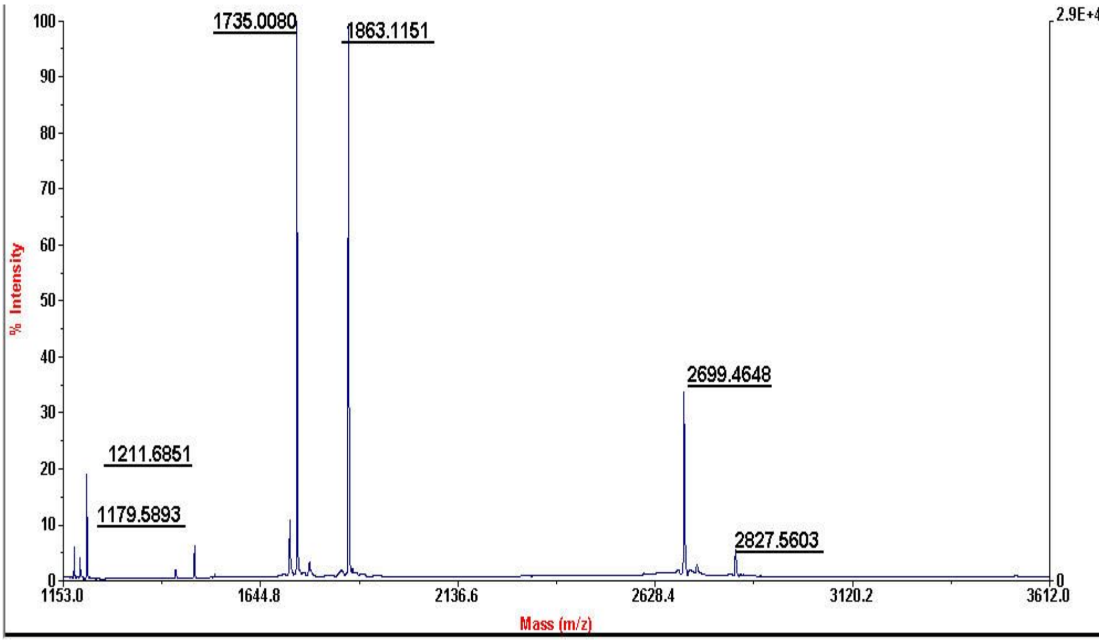
236 ）Protein DJ-1 (Oncogene DJ1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
13 - 27	1675.9076	1674.9003	1674.7956	0.1047	0	K.GAEEMETVIPVDVMR.R
13 - 27	1691.8948	1690.8876	1690.7905	0.0970	0	K.GAEEMETVIPVDVMR.R Oxidation (M)
33 - 48	1657.9850	1656.9777	1656.8617	0.1160	1	K.VTVAGLAGKDPVQCSR.D
49 - 63	1659.9269	1658.9196	1658.8185	0.1011	1	R.DVVICPDASLEDAKK.E
133 - 145	1559.7186	1558.7113	1558.6292	0.0820	0	K.MMNGGHYTYSENR.V

No match to: 1560.7024

237 ）Peroxiredoxin-2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
68 - 91	2699.4648	2698.4575	2698.3537	0.1039	0	K.LGCEVLGVSVDSQFTHLAWINTPR.K
68 - 92	2827.5603	2826.5530	2826.4486	0.1044	1	K.LGCEVLGVSVDSQFTHLAWINTPRK.E
92 - 109	1863.1151	1862.1078	1862.0625	0.0453	1	R.KEGGLGPLNIPLLADVTR.R
93 - 109	1735.0080	1734.0007	1733.9675	0.0332	0	K.EGGLGPLNIPLLADVTR.R
110 - 119	1179.5893	1178.5820	1178.6295	-0.0474	1	R.RLSEDYGVLK.T
140 - 150	1211.6851	1210.6779	1210.6669	0.0109	0	R.QITVNDLPVGR.S

No match to: 964.4978, 1479.7470, 1716.9998

238 ） Heat-shock protein beta-6 (HspB6)

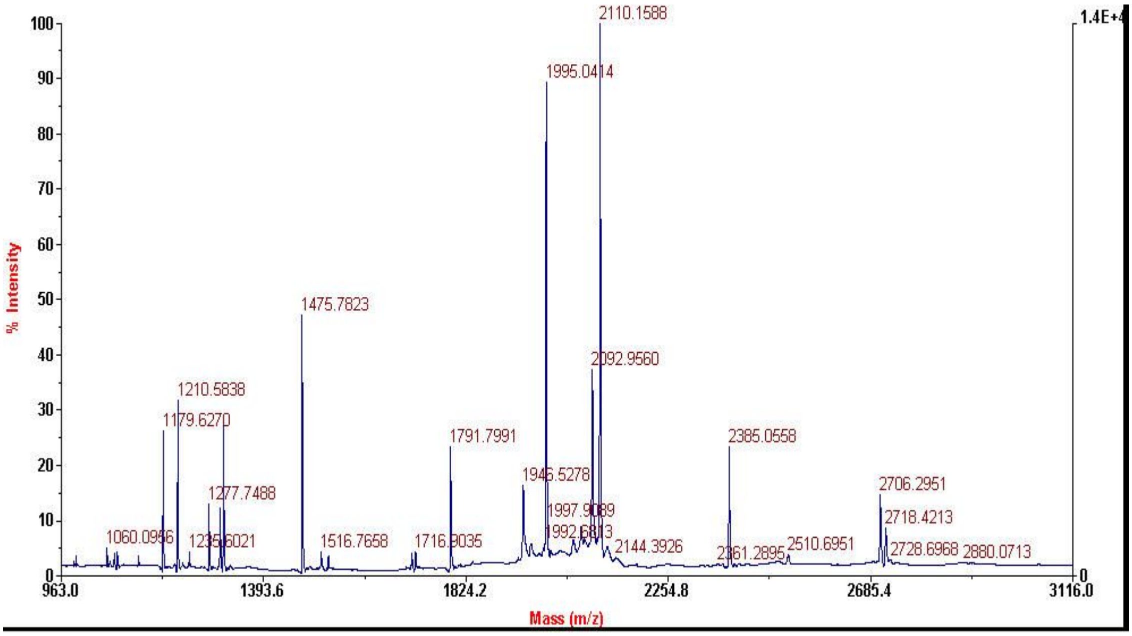
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
15 - 27	1193.6699	1192.6626	1192.6564	0.0063	0	R.ASAPLPGLSAPGR.L
33 - 56	2668.3717	2667.3644	2667.3617	0.0027	0	R.FGEGLLEAELAALCPTTLAPYYLR.A
57 - 81	2557.3497	2556.3424	2556.3951	-0.0527	0	R.APSVALPVAQVPTDPGHFSVLLDVK.H
92 - 102	1231.6512	1230.6439	1230.6469	-0.0029	0	K.VVGEHVEVHAR.H
103 - 115	1578.7363	1577.7291	1577.7334	-0.0044	0	R.HEERPDEHGFVAR.E

121 - 160	3837.0671	3836.0598	3836.0471	0.0127	1

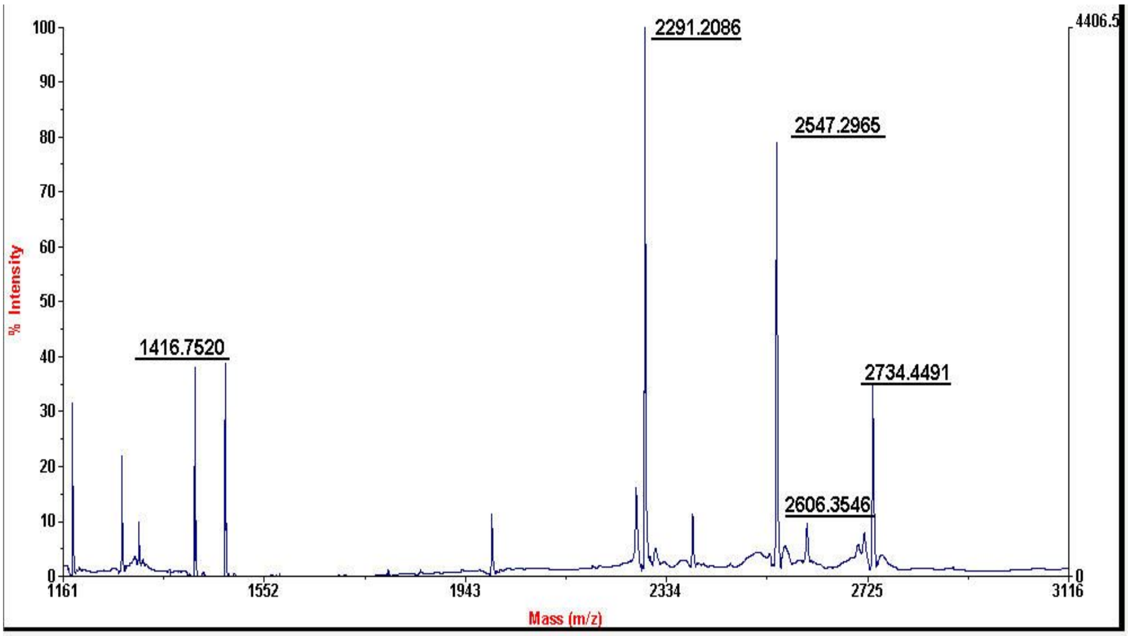
R.YRLPPGVDPAAVTSALSPEGVLSIQAAPASAQAPPPAAAK.-

No match to: 1593.8570, 1609.8133, 2109.0702

239 ）Casein kinase I isoform alpha (EC 2.7.11.1)



240 ） Histidine triad nucleotide-binding protein 1

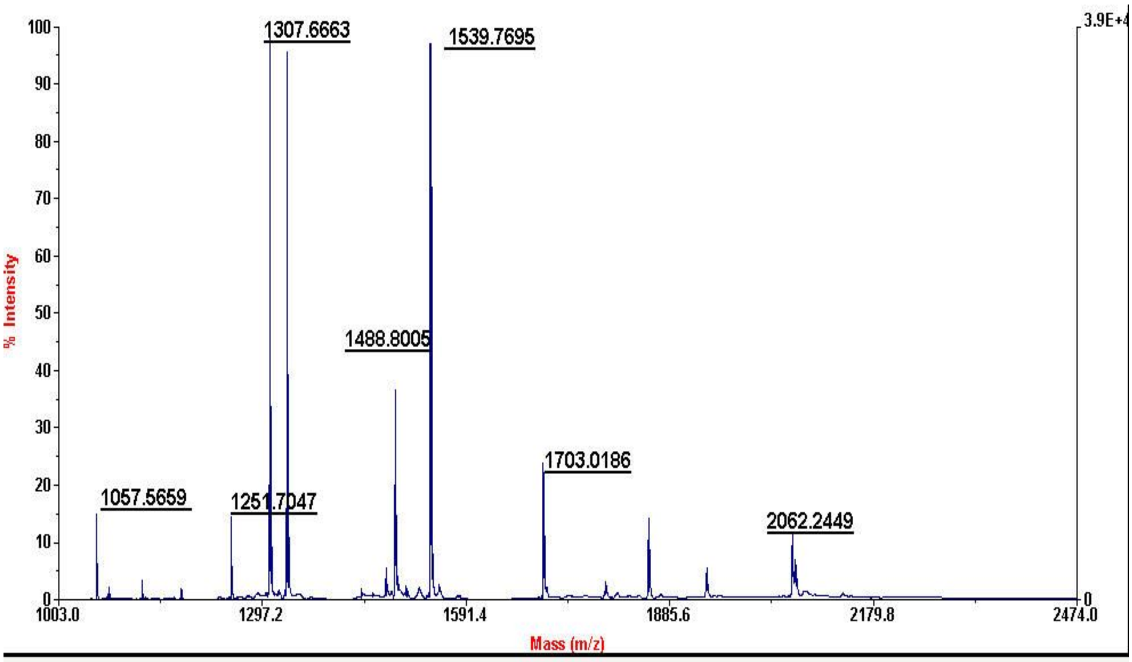


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 21	1416.7520	1415.7447	1415.7520	-0.0073	0	K.AQVARPGGDTIFGK.I
31 - 37	907.4774	906.4701	906.4447	0.0255	0	K.IIFEDDR.C
38 - 57	2291.2086	2290.2014	2290.1932	0.0082	0	R.CLAFHDISPQAPTHFLVIPK.K

59 - 82	2606.3546	2605.3473	2605.3057	0.0416	0	K.HISQISVAEDDDESLLGHLMIVGK.K
59 - 83	2734.4491	2733.4419	2733.4007	0.0412	1	K.HISQISVAEDDDESLLGHLMIVGKK.C
96 - 119	2547.2965	2546.2892	2546.2447	0.0445	0	R.MVVNEGSDGGQSVYHVHLHVLGGR.Q

No match to: 1179.6240, 1274.7542, 1475.7862, 1993.9724, 2274.2064, 2383.9918, 2546.2295

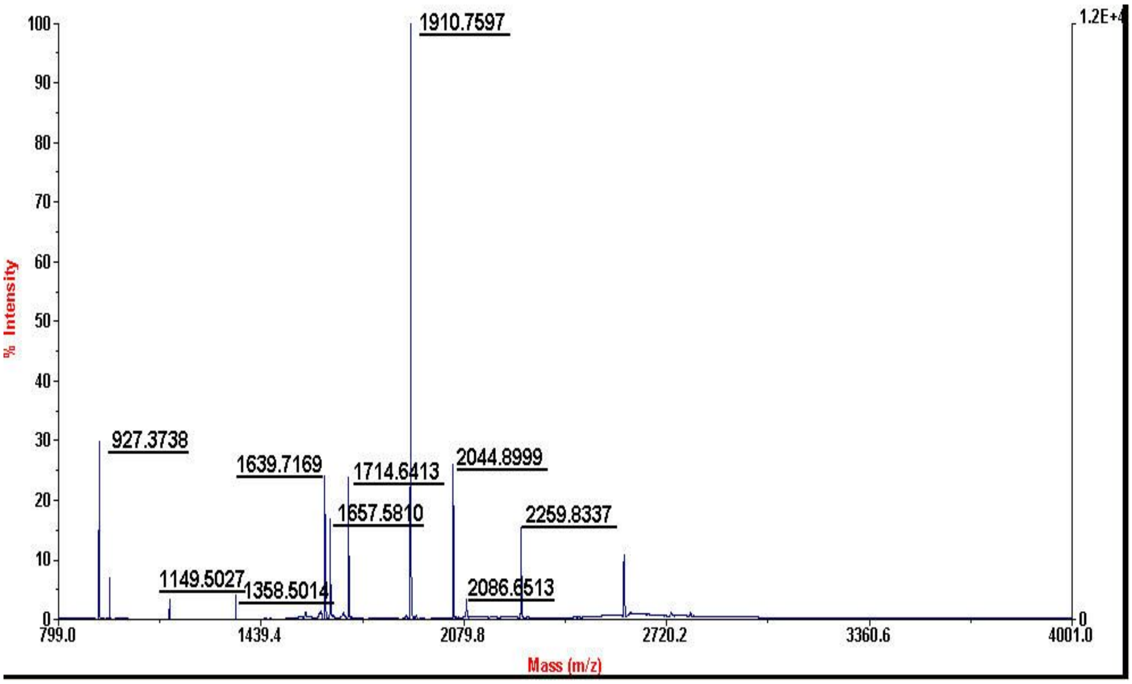
241 ） Destrin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 45	1251.7047	1250.6975	1250.6692	0.0282	1	K.AVIFCLSADKK.C
54 - 69	1703.0186	1702.0113	1701.9188	0.0924	0	K.EILVGDVGVTITDPFK.H
70 - 78	1057.5659	1056.5586	1056.5426	0.0160	0	K.HFVGMLPEK.D
70 - 81	1488.8005	1487.7933	1487.7013	0.0920	1	K.HFVGMLPEKDCR.Y
82 - 92	1307.6663	1306.6591	1306.6081	0.0510	0	R.YALYDASFETK.E
96 - 112	2062.2449	2061.2377	2061.1008	0.1368	1	R.KEELMFFLWAPELAPLK.S
133 - 145	1539.7695	1538.7622	1538.6532	0.1091	0	K.HECQANGPEDLNR.A

No match to: 1332.6849, 1855.0556

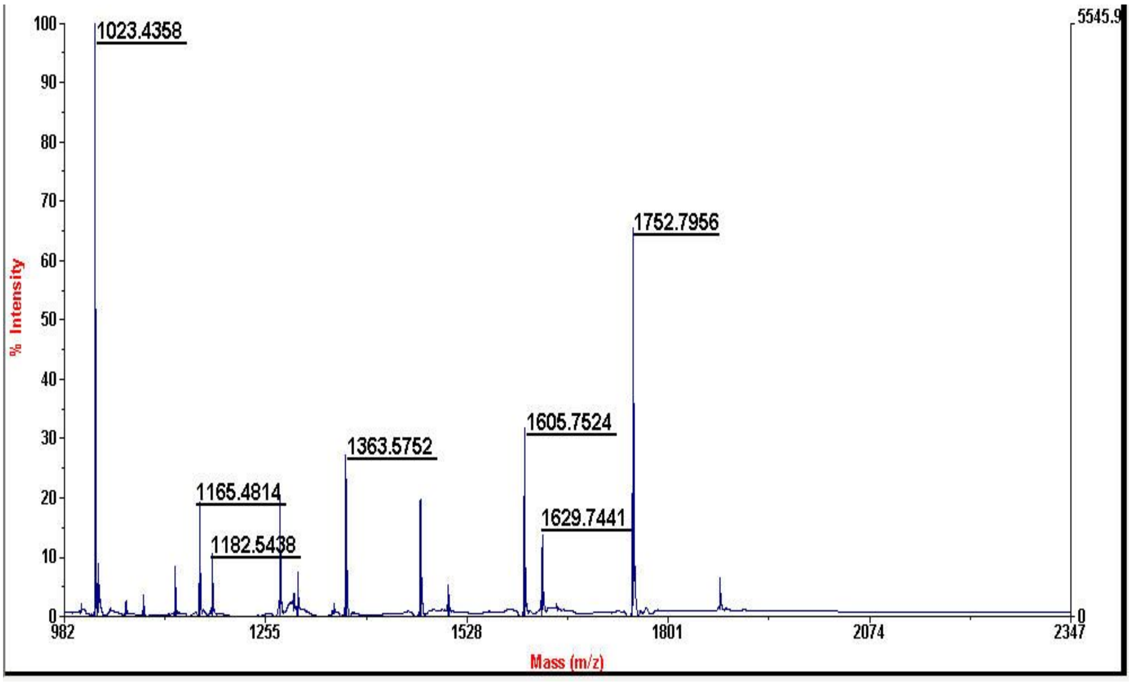
242 ） Serum albumin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
25 - 34	1149.5027	1148.4954	1148.5686	-0.0732	1	R.DAHKSEVAHR.F	
118 - 130	1714.6413	1713.6340	1713.7893	-0.1553	1	K.QEPERNECFLQHK.D	
162 - 168	927.3738	926.3665	926.4861	-0.1196	0	K.YLYEIAR.R	
265 - 281	2086.6513	2085.6441	2085.8303	-0.1862	0	K.VHTECCHGDLLECADDR.A	3
348 - 360	1639.7169	1638.7096	1638.7752	-0.0656	0	K.DVFLGMFLYEYAR.R	Oxidation (M)
397 - 413	2044.8999	2043.8927	2044.0881	-0.1954	0	K.VFDEFKPLVEEPQNLIK.Q	
414 - 426	1657.5810	1656.5738	1656.7453	-0.1716	0	K.QNCELFEQLGEYK.F	
427 - 434	960.4481	959.4409	959.5552	-0.1144	0	K.FQNALLVR.Y	
509 - 524	1910.7597	1909.7525	1909.9244	-0.1719	0	R.RPCFSALEVDETYVPK.E	
525 - 543	2259.8337	2258.8264	2259.0154	-0.1890	0	K.EFNAETFTFHADICTLSEK.E	
570 - 581	1358.5014	1357.4941	1357.6224	-0.1283	0	K.AVMDDFAAFVEK.C	Oxidation (M)

No match to: 2584.8715, 2794.0957

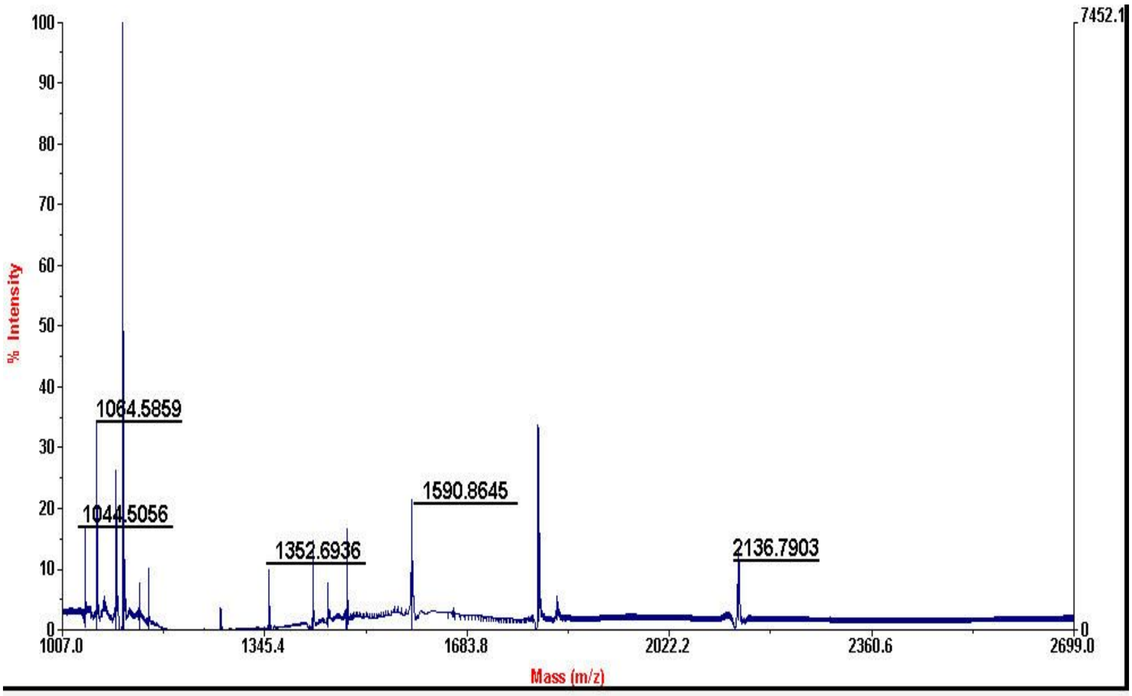
243 ） Lamin-A/C



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
29 - 41	1629.7441	1628.7368	1628.8005	-0.0638	1	R.LQEKEDLQELNDR.L
157 - 166	1182.5438	1181.5365	1181.6040	-0.0675	0	R.TLEGELHDLR.G
209 - 216	1023.4358	1022.4286	1022.5032	-0.0747	0	K.NIYSEELR.E
281 - 296	1752.7956	1751.7883	1751.8550	-0.0668	0	R.NSNLVGAAHEELQQSR.I
428 - 435	919.3992	918.3919	918.4308	-0.0389	0	R.SSFSQHAR.T
440 - 453	1605.7524	1604.7452	1604.8046	-0.0594	1	R.VAVEEVDEEGKFVR.L
516 - 527	1363.5752	1362.5679	1362.6099	-0.0419	0	K.AQNTWGCGNSLR.T
655 - 664	1165.4814	1164.4741	1164.4903	-0.0162	0	R.TQSPQNCSIM.-

No match to: 1132.5912, 1274.5562, 1298.5668, 1464.6705, 1870.7912, 2899.1743

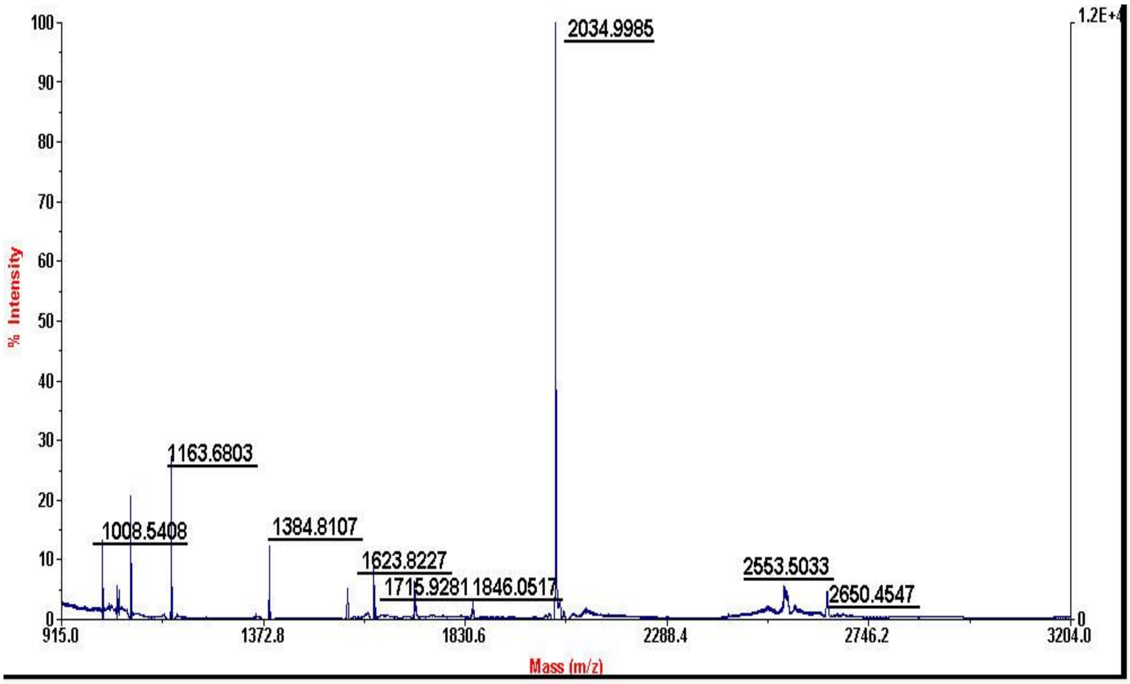
244 ） Prolargin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
76 - 92	2136.7903	2135.7830	2135.8387	-0.0557	0	R.ECYCPPDFPSALYCDSR.N	3
130 - 137	1044.5056	1043.4984	1043.5148	-0.0165	0	R.WINLDNNR.I	
160 - 171	1352.6936	1351.6863	1351.7095	-0.0232	0	K.NQLEEVPSALPR.N	
194 - 206	1590.8645	1589.8573	1589.8889	-0.0316	0	K.LENLLLLDLQHNR.L	
264 - 272	1064.5859	1063.5786	1063.5815	-0.0028	0	K.SFPNLAFIR.L	

No match to: 1096.4923, 1150.5586, 1425.7871, 1482.7074, 1802.7915

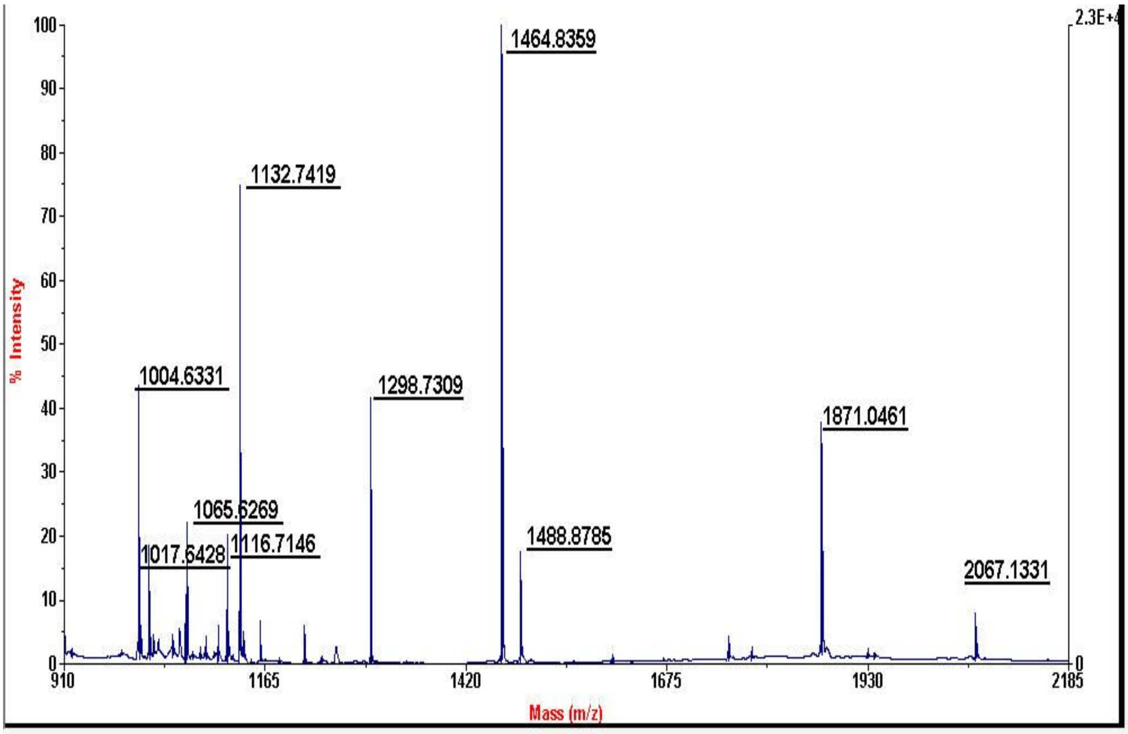
245 ） Bifunctional purine biosynthesis protein PURH



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
50 - 64	1623.8227	1622.8154	1622.7610	0.0544	0	R.DVSELTGFPEMLGGR.V Oxidation (M)
109 - 133	2553.5033	2552.4960	2552.3698	0.1263	0	K.TVASPGVTVEEAVEQIDIGGVTLLR.A
178 - 194	2034.9985	2033.9912	2033.9119	0.0793	0	K.AFTHTAQYDEAISDYFR.K
295 - 305	1163.6803	1162.6730	1162.6346	0.0384	0	K.TLTPISAAYAR.A
438 - 451	1384.8107	1383.8035	1383.7219	0.0816	0	K.NGQVIGIGAGQQSR.I
462 - 468	1008.5408	1007.5335	1007.4977	0.0358	0	K.ANYWWLR.H
484 - 507	2650.4547	2649.4474	2649.3133	0.1341	1	K.RAEISNAIDQYVTGTIGEDEDLIK.W
510 - 525	1846.0517	1845.0444	1844.9771	0.0673	1	K.ALFEEVPELLTEAEKK.E
531 - 545	1715.9281	1714.9208	1714.8566	0.0641	0	K.LTEVSISSDAFFPFR.D

No match to: 1023.5531, 1040.5391, 1072.5272

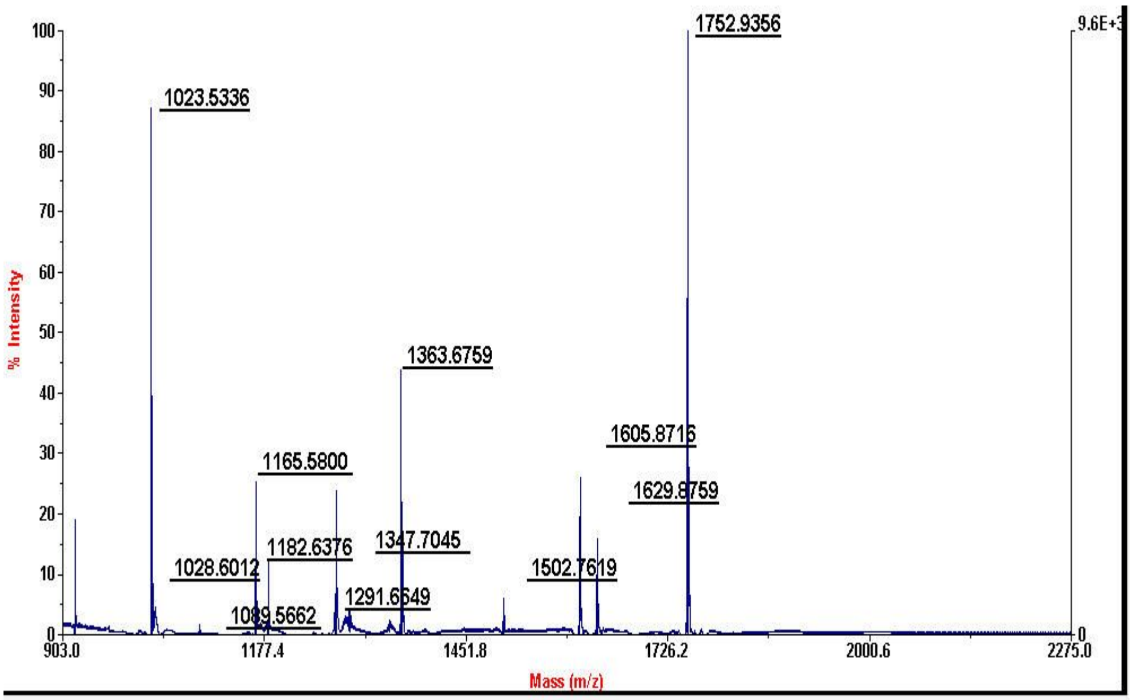
246 ） Stress-induced-phosphoprotein 1 (STI1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
14 - 32	2067.1331	2066.1258	2065.9990	0.1268	0	K.ALSVGNIDDALQCYSEAIK.L	
33 - 44	1464.8359	1463.8286	1463.7269	0.1017	0	K.LDPHNHVLYSNR.S	
78 - 87	1132.7419	1131.7346	1131.6400	0.0946	1	R.KAAALEFLNR.F	
79 - 87	1004.6331	1003.6258	1003.5450	0.0808	0	K.AAALEFLNR.F	
94 - 109	1871.0461	1870.0388	1869.9220	0.1168	1	R.TYEEGLKHEANNPQLK.E	
145 - 153	1065.6269	1064.6196	1064.5502	0.0694	0	R.TLLSDPTYR.E	
154 - 160	900.5847	899.5774	899.5076	0.0698	0	R.ELIEQLR.N	
230 - 237	909.4850	908.4777	908.4239	0.0538	0	K.ELGNDAYK.K	
316 - 325	1298.7309	1297.7236	1297.6455	0.0781	1	K.YKDAIHFYNK.S	
352 - 364	1488.8785	1487.8713	1487.7871	0.0841	0	R.LAYINPDLALEEK.N	
382 - 389	1017.6428	1016.6355	1016.5403	0.0952	1	K.HYTEAIKR.N	
534 - 543	1116.7146	1115.7073	1115.6373	0.0701	0	K.LMDVGLIAIR.-	Oxidation (M)

No match to: 1254.9619

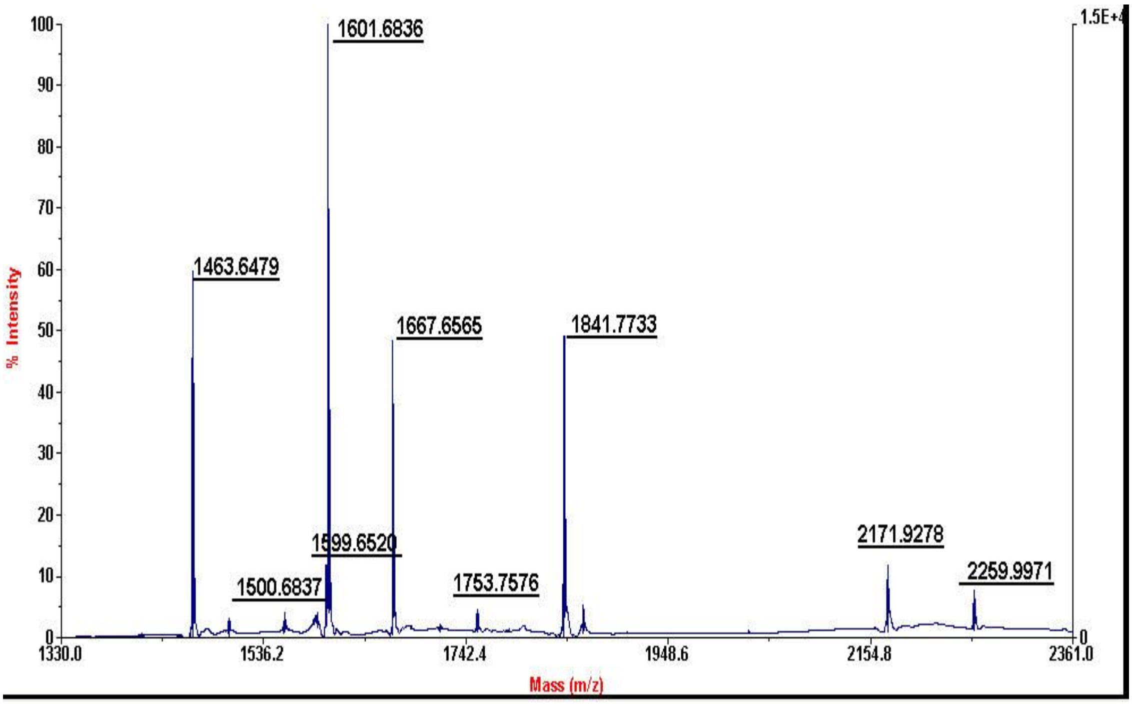
247 ） Lamin-A/C



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
29 - 41	1629.8759	1628.8686	1628.8005	0.0681	1	R.LQEKEDLQELNDR.L	
42 - 48	849.5141	848.5068	848.4756	0.0312	0	R.LAVYIDR.V	
51 - 60	1089.5662	1088.5589	1088.5462	0.0128	0	R.SLETENAGLR.L	
79 - 89	1165.5800	1164.5727	1164.5411	0.0316	0	K.AAYEAELGDAR.K	
157 - 166	1182.6376	1181.6303	1181.6040	0.0263	0	R.TLEGELHDLR.G	
209 - 216	1023.5336	1022.5264	1022.5032	0.0231	0	K.NIYSEELR.E	
241 - 249	1028.6012	1027.5939	1027.5662	0.0277	0	R.LADALQELR.A	
250 - 261	1502.7619	1501.7547	1501.7161	0.0386	1	R.AQHEDQVEQYKK.E	
281 - 296	1752.9356	1751.9283	1751.8550	0.0733	0	R.NSNLVGAAHEELQQSR.I	
367 - 377	1347.7045	1346.6972	1346.6652	0.0320	0	K.LALDMEIHAYR.K	Oxidation (M)
428 - 435	919.4619	918.4546	918.4308	0.0239	0	R.SSFSQHAR.T	
440 - 453	1605.8716	1604.8644	1604.8046	0.0598	1	R.VAVEEVDEEGKFVR.L	
472 - 482	1291.6649	1290.6577	1290.6204	0.0372	0	R.QNGDDPLLTYR.F	
516 - 527	1363.6759	1362.6686	1362.6099	0.0587	0	K.AQNTWGCGNSLR.T	

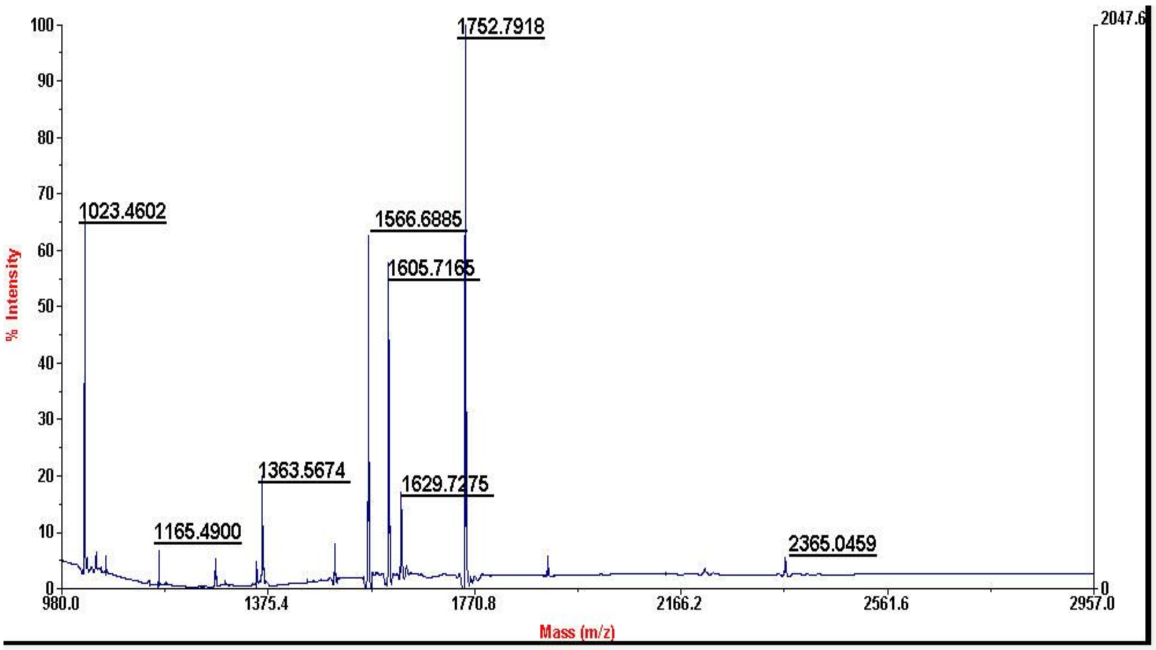
No match to: 1274.6472, 2899.4096

248 ） Aconitate hydratase, mitochondrial precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
69 - 84	1841.7733	1840.7660	1840.8955	-0.1295	0	K.IVYGHLDDPASQEIER.G	
118 - 138	2259.9971	2258.9898	2259.1318	-0.1420	0	K.VAVPSTIHCDHLIEAQVGGEK.D	
145 - 160	1753.7576	1752.7503	1752.8682	-0.1179	0	K.DINQEVYNFLATAGAK.Y	
371 - 378	985.4378	984.4305	984.5029	-0.0723	0	K.EGWPLDIR.V	
379 - 395	1861.6783	1860.6710	1860.7982	-0.1272	0	R.VGLIGSCTNSSYEDMGR.S	; Oxidation (M)
412 - 424	1463.6479	1462.6406	1462.7416	-0.1010	0	K.SQFTITPGSEQIR.A	
430 - 437	935.4128	934.4055	934.4872	-0.0817	0	R.DGYAQILR.D	
438 - 457	2171.9278	2170.9206	2171.0252	-0.1046	0	R.DLGGIVLANACGPCIGQWDR.K	2
522 - 534	1500.6837	1499.6765	1499.7620	-0.0855	1	K.FRLEAPDADELPK.G	
550 - 564	1599.6520	1598.6447	1598.7285	-0.0838	0	K.DSSGQHVDVSPTSQR.L	
634 - 648	1601.6836	1600.6763	1600.7845	-0.1083	0	R.NAVTQEFGPVPDTAR.Y	
657 - 671	1667.6565	1666.6492	1666.7587	-0.1095	0	R.WVVIGDENYGEGSSR.E	
744 - 767	2925.3256	2924.3183	2924.4205	-0.1022	0	K.HPNGTQETILLNHTFNETQIEWFR.A	

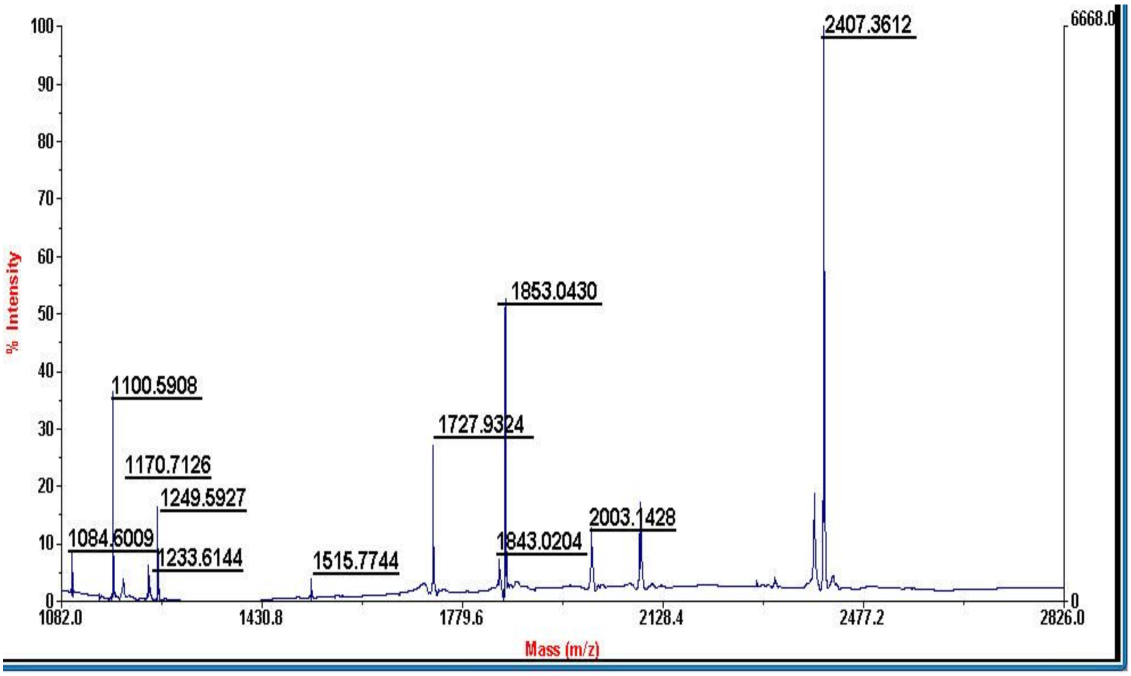
249 ） Lamin-A/C



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
29 - 41	1629.7275	1628.7202	1628.8005	-0.0803	1	R.LQEKEDLQELNDR.L
209 - 216	1023.4602	1022.4530	1022.5032	-0.0503	0	K.NIYSEELR.E
250 - 261	1502.6661	1501.6588	1501.7161	-0.0573	1	R.AQHEDQVEQYKK.E
281 - 296	1752.7918	1751.7845	1751.8550	-0.0705	0	R.NSNLVGAAHEELQQSR.I
428 - 435	919.3606	918.3533	918.4308	-0.0775	0	R.SSFSQHAR.T
440 - 453	1605.7165	1604.7092	1604.8046	-0.0954	1	R.VAVEEVDEEGKFVR.L
516 - 527	1363.5674	1362.5601	1362.6099	-0.0498	0	K.AQNTWGCGNSLR.T
598 - 624	2365.0459	2364.0386	2364.1517	-0.1132	0	K.ASASGSGAQVGGPISSGSSASSVTVTR.S
628 - 644	1566.6885	1565.6813	1565.7434	-0.0622	0	R.SVGGSGGGSFGDNLVTR.S
655 - 664	1165.4900	1164.4827	1164.4903	-0.0076	0	R.TQSPQNCSIM.-

No match to: 1064.5439, 1274.5279, 1352.6465

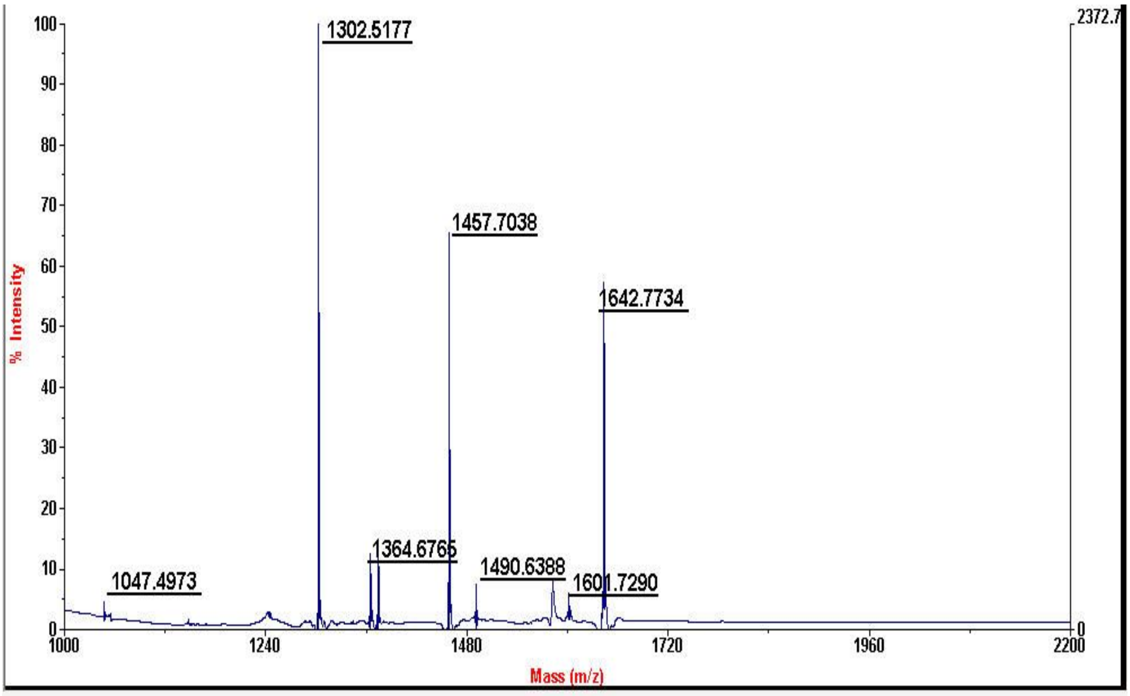
250 ） Iron-responsive element-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
57 - 72	2003.1428	2002.1356	2002.0384	0.0971	1	K.KQDIENILHWNVTQHK.N	
73 - 82	1170.7126	1169.7053	1169.6557	0.0497	0	K.NIEVPFKPAR.V	
142 - 149	1050.5396	1049.5323	1049.4778	0.0545	0	K.NQDLEFER.N	
159 - 168	1233.6144	1232.6071	1232.5509	0.0562	0	K.WGSQAFHNMR.I	
159 - 168	1249.5927	1248.5854	1248.5458	0.0396	0	K.WGSQAFHNMR.I	Oxidation (M)
277 - 293	1853.0430	1852.0358	1851.9519	0.0838	0	K.FVEFFGPGVAQLSIADR.A	
336 - 344	1084.6009	1083.5936	1083.5535	0.0401	0	K.YLQAVGMFR.D	
336 - 344	1100.5908	1099.5835	1099.5484	0.0351	0	K.YLQAVGMFR.D	Oxidation (M)
401 - 413	1515.7744	1514.7672	1514.7015	0.0657	0	K.GFQVAPEHHNDHK.T	
588 - 601	1727.9324	1726.9252	1726.8638	0.0613	1	K.DIWPTRDEIQAVER.Q	
594 - 601	959.4579	958.4506	958.4720	-0.0214	0	R.DEIQAVER.Q	
633 - 639	941.5063	940.4990	940.4807	0.0183	0	K.LFFWNSK.S	
645 - 660	1843.0204	1842.0132	1841.9563	0.0568	0	K.SPPFFENLTLDLQPPK.S	
737 - 758	2407.3612	2406.3540	2406.2179	0.1360	0	K.QAPQTIHLPSGEILDVFDAAER.Y	
794 - 802	1037.5772	1036.5699	1036.5189	0.0510	0	K.AVLAESYER.I	

No match to: 1189.1426, 2087.1645

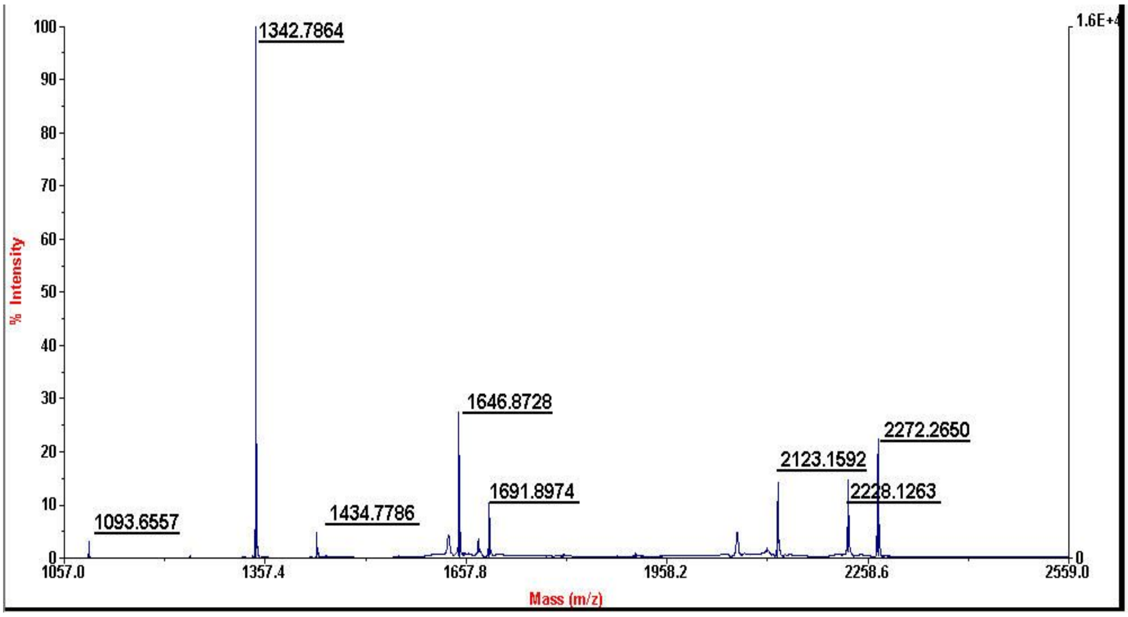
251 ） Peptidyl-prolyl cis-trans isomerase B precursor



Matched peptides shown in **Bold Red**

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
64 - 76	1364.6765	1363.6692	1363.6983	-0.0291	0	K.TVDNFVALATGEK.G	
88 - 101	1642.7734	1641.7661	1641.8185	-0.0524	1	R.VIKDFMIQGGDFTR.G	Oxidation (M)
91 - 101	1302.5177	1301.5104	1301.5711	-0.0607	0	K.DFMIQGGDFTR.G	Oxidation (M)
109 - 121	1601.7290	1600.7218	1600.7522	-0.0304	1	K.SIYGERFPDENFK.L	
124 - 137	1490.6388	1489.6315	1489.6772	-0.0457	0	K.HYGPGWVSMANAGK.D	Oxidation (M)
138 - 150	1457.7038	1456.6965	1456.7198	-0.0233	0	K.DTNGSQFFITTVK.T	
164 - 172	1047.4973	1046.4900	1046.5430	-0.0530	0	K.VLEGMEVVR.K	Oxidation (M)
197 - 208	1373.7278	1372.7205	1372.7602	-0.0397	1	K.IEVEKPFAIAKE.-	

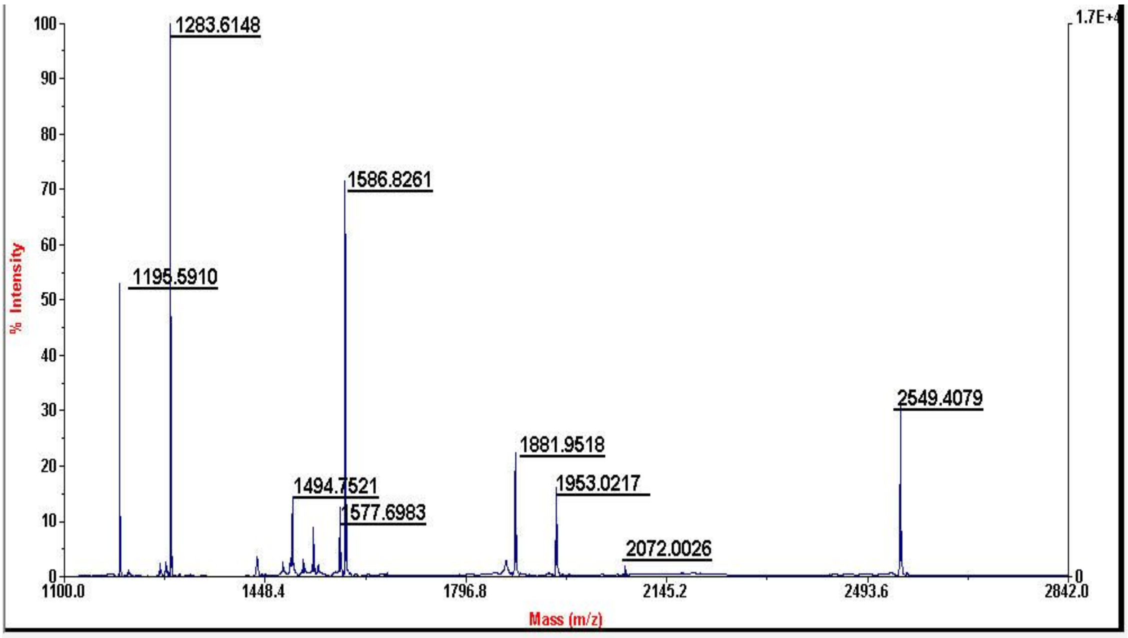
252 ） Fructose-bisphosphate aldolase A



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 13	1434.7786	1433.7714	1433.7191	0.0523	0	M.PYQYPALTPEQK.K
44 - 57	1646.8728	1645.8655	1645.8019	0.0636	1	R.LQSIGTENTEENRR.F
88 - 99	1342.7864	1341.7791	1341.7041	0.0750	0	K.ADDGRPFPQVIK.S
112 - 134	2272.2650	2271.2577	2271.1343	0.1234	0	K.GVVPLAGTNGETTTQGLDGLSER.C
154 - 173	2123.1592	2122.1519	2122.0840	0.0678	0	K.IGEHTPSALAIMENANVLAR.Y Oxidation (M)
244 - 258	1691.8974	1690.8901	1690.8348	0.0553	0	K.FSHEEIAMATVTALR.R Oxidation (M)
323 - 331	1093.6557	1092.6484	1092.5563	0.0921	1	K.AAQEEYVKR.A
343 - 364	2228.1263	2227.1191	2227.0182	0.1009	0	K.YTPSGQAGAAASESLFVSNHAY.-

No match to: 2062.4837

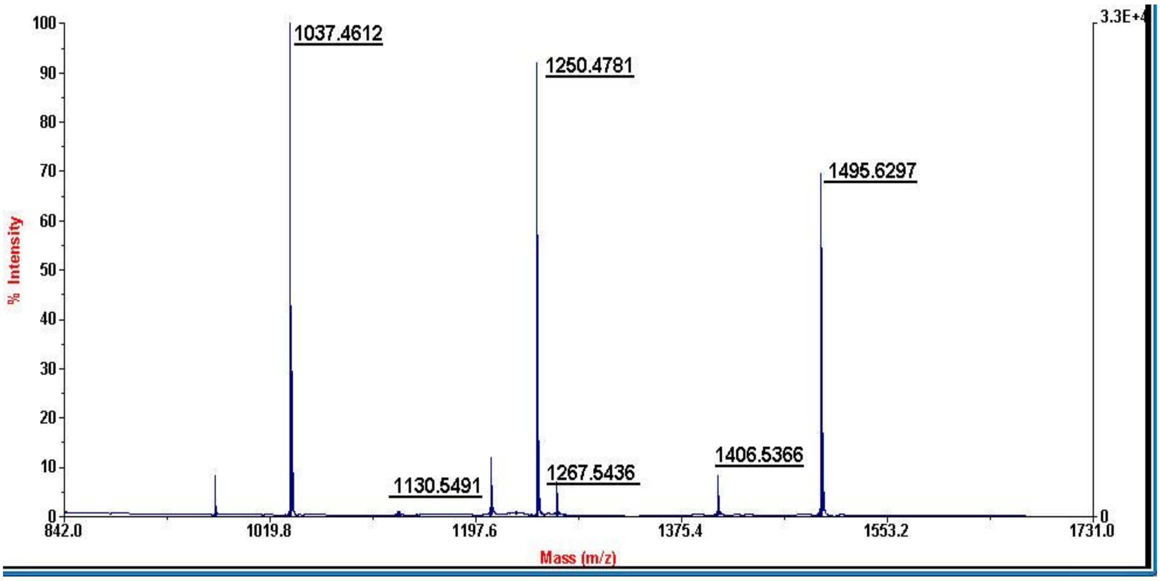
253 ） Serotransferrin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
123 - 132	1195.5910	1194.5838	1194.5452	0.0386	0	K.DSGFQMNQLR.G	
237 - 251	1881.9518	1880.9445	1880.8687	0.0759	1	K.ADRDQYELLCLDNTR.K	
252 - 273	2549.4079	2548.4006	2548.2856	0.1150	1	R.KPVDEYKDCHLAQVPSHTVVAR.S	
332 - 343	1494.7521	1493.7448	1493.7224	0.0224	0	K.MYLGYEYVTAIR.N	Oxidation (M)
434 - 452	2072.0026	2070.9953	2070.9204	0.0749	0	K.SDNCEDTPEAGYFAVAVVK.K	
495 - 508	1577.6983	1576.6910	1576.6504	0.0406	0	R.FDEFFSEGCAPGSK.K	
531 - 541	1283.6148	1282.6076	1282.5618	0.0457	0	K.EGYYGYTGAFR.C	
572 - 587	1953.0217	1952.0145	1951.9309	0.0836	1	K.NLNEKDYELLCLDGTR.K	
588 - 600	1586.8261	1585.8189	1585.7671	0.0518	0	R.KPVEEYANCHLAR.A	
684 - 696	1531.7458	1530.7385	1530.6807	0.0579	0	K.CSTSSLLEACTFR.R	2

No match to: 1514.7110

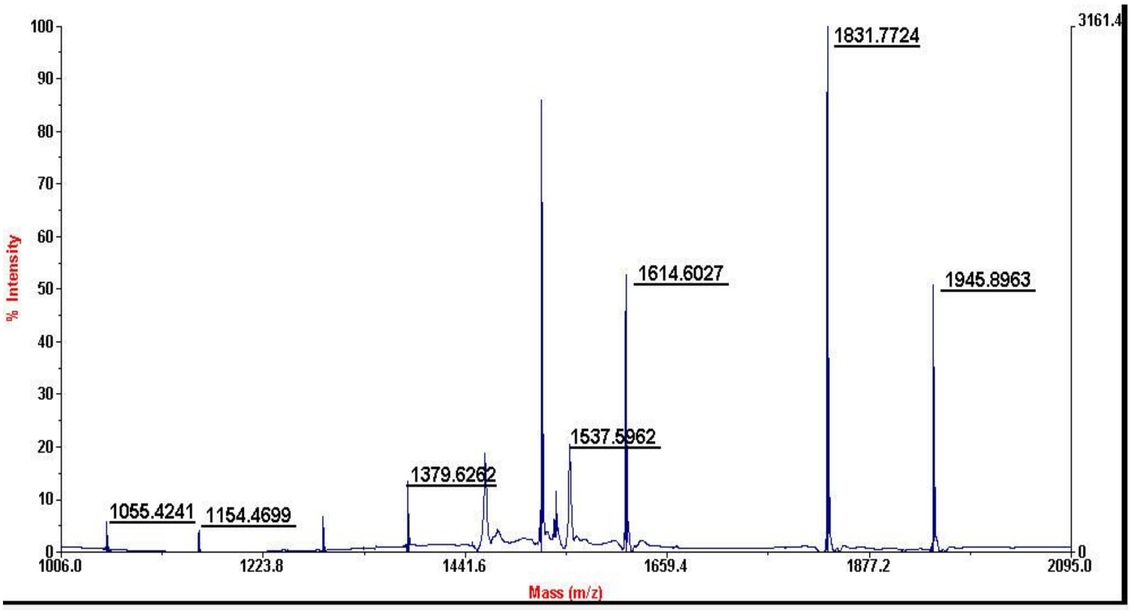
254 ） Adenylate kinase isoenzyme 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
10 - 21	1130.5491	1129.5418	1129.6496	-0.1077	0	K.IIFVVGGPGSGK.G
32 - 44	1495.6297	1494.6225	1494.7467	-0.1242	0	K.YGYTHLSTGDLLR.S
89 - 97	1037.4612	1036.4539	1036.5342	-0.0803	0	K.GFLIDGYPR.E
98 - 107	1250.4781	1249.4708	1249.5575	-0.0867	0	R.EVQQGEEFER.R
98 - 108	1406.5366	1405.5293	1405.6586	-0.1293	1	R.EVQQGEEFERR.I
149 - 155	972.4559	971.4486	971.5076	-0.0590	1	K.RLETYYK.A
156 - 166	1267.5436	1266.5363	1266.6496	-0.1133	0	K.ATEPVIAFYEK.R

No match to: 1210.4547

255 ） Peptidyl-prolyl cis-trans isomerase A

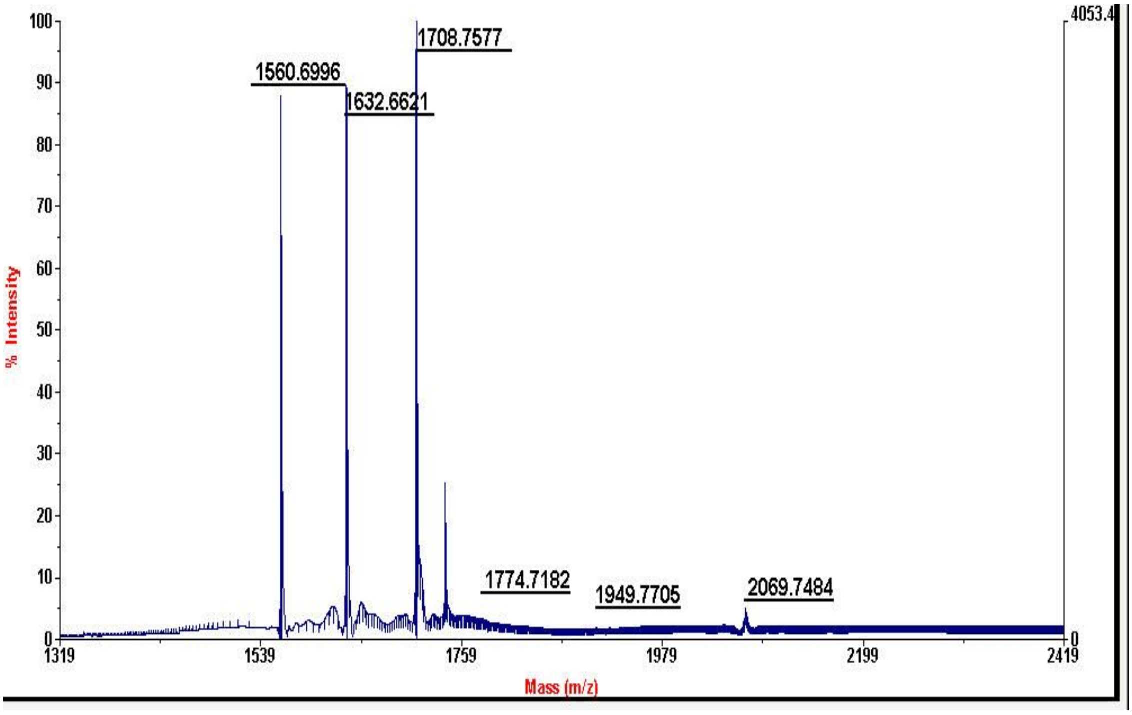


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

2 - 19	1945.8963	1944.8890	1944.9946	-0.1056	0	M.VNPTVFFDIAVDGEPLGR.V	
20 - 28	1055.4241	1054.4169	1054.5335	-0.1166	0	R.VSFELFADK.V	
20 - 31	1379.6262	1378.6189	1378.7496	-0.1307	1	R.VSFELFADKVPK.T	
56 - 69	1614.6027	1613.5954	1613.7331	-0.1376	0	R.IIPGFMCQGGDFTR.H	; Oxidation (M)
77 - 91	1831.7724	1830.7651	1830.9039	-0.1389	1	K.SIYGEKFEDENFILK.H	
83 - 91	1154.4699	1153.4626	1153.5655	-0.1029	0	K.FEDENFILK.H	
132 - 144	1537.5962	1536.5889	1536.7276	-0.1386	1	K.VKEGMNIVEAMER.F	2 Oxidation (M)

No match to: 1288.5646, 1462.9226, 1523.6125, 1553.7968

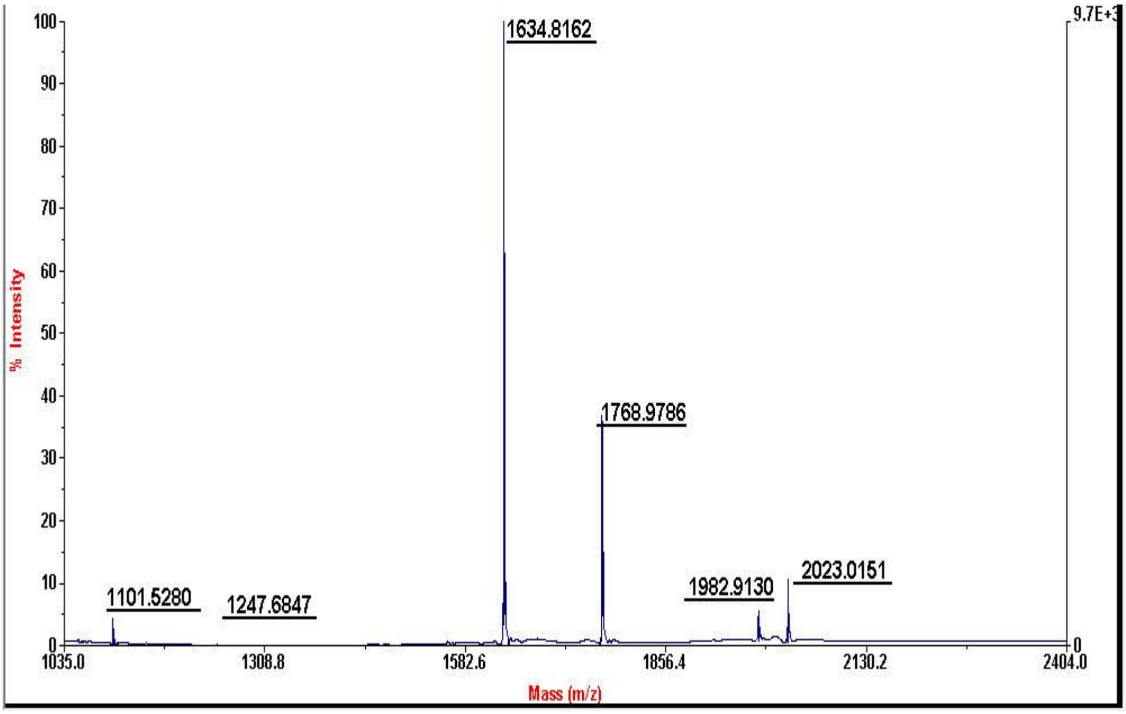
256 ） Phosphatidylethanolamine-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
48 - 62	1632.6621	1631.6548	1631.7903	-0.1355	0	K.NRPTSISWDGLDSGK.L	
63 - 76	1560.6996	1559.6924	1559.8195	-0.1272	0	K.LYTLVLTDPDAPSR.K	
81 - 93	1774.7182	1773.7109	1773.8773	-0.1664	1	K.YREWHHFLVVNMK.G	Oxidation (M)
94 - 113	1949.7705	1948.7632	1948.9378	-0.1746	0	K.GNDISSGTVLSDYVGSGPPK.G	
120 - 132	1708.7577	1707.7504	1707.8984	-0.1480	0	R.YVWLVYEQDRPLK.C	
162 - 179	2069.7484	2068.7412	2068.9200	-0.1789	0	R.APVAGTCYQAEWDDYVPK.L	

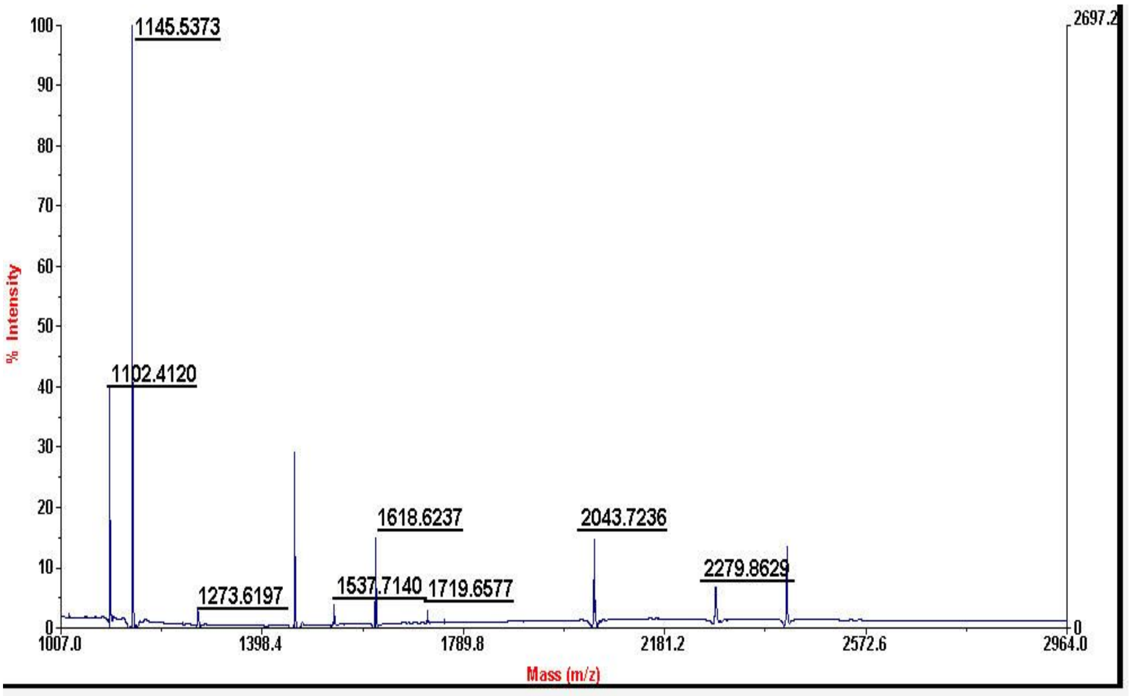
No match to: 1648.6736, 1664.6380, 1740.7480

257 ） Phosphoglycerate kinase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 39	1101.5280	1100.5207	1100.5323	-0.0116	0	K.NNQITNNQR.I
76 - 86	1247.6847	1246.6774	1246.6809	-0.0035	0	K.YSLEPVAVELK.S
157 - 171	1634.8162	1633.8089	1633.7849	0.0241	0	K.LGDVYVNDAFGTAHR.A
200 - 216	1768.9786	1767.9714	1767.9883	-0.0169	0	K.ALESPERPFLAILGGAK.V
247 - 264	1982.9130	1981.9058	1981.9303	-0.0245	0	K.VLNNMEIGTSLFDEEGAK.I
Oxidation (M)						
280 - 297	2023.0151	2022.0078	2022.0310	-0.0231	1	K.ITLPVDFVTADKFDENAK.T

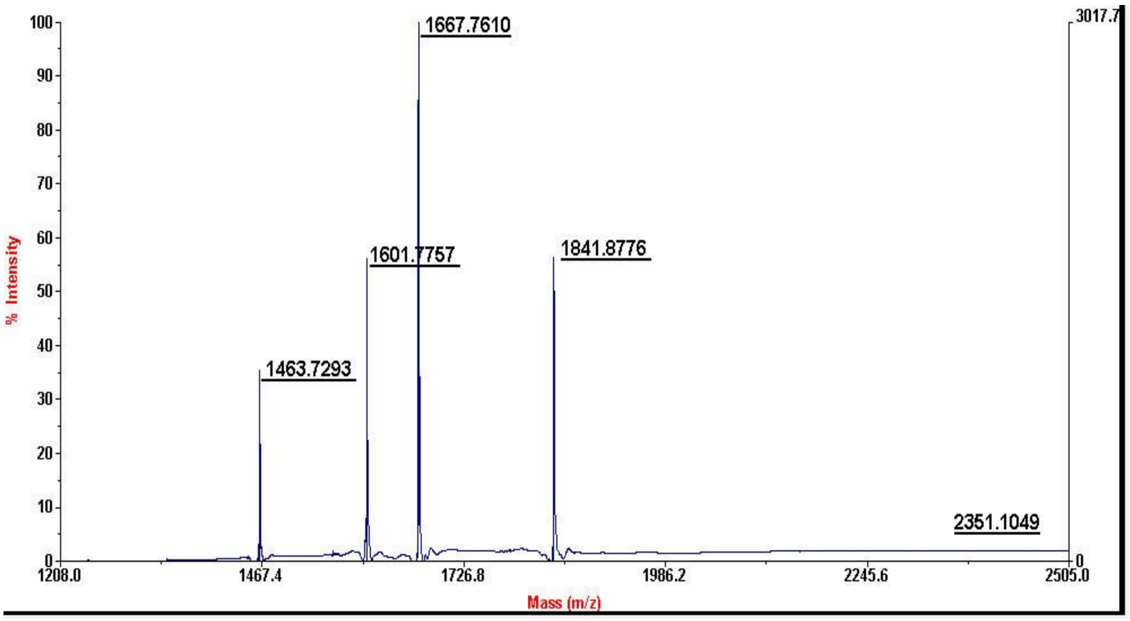
258 ） WD repeat protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 17	1273.6197	1272.6124	1272.7190	-0.1066	1	K.KVFASLPQVER.G
8 - 17	1145.5373	1144.5300	1144.6241	-0.0940	0	K.VFASLPQVER.G
66 - 81	1618.6237	1617.6165	1617.7675	-0.1510	0	K.YAPSGFYIASGDVSGK.L
84 - 90	891.3900	890.3827	890.4498	-0.0671	0	R.IWDTTQK.E
96 - 104	1102.4120	1101.4048	1101.5131	-0.1083	0	K.YEYQPFAGK.I
162 - 180	2043.7236	2042.7163	2042.9044	-0.1881	0	R.LATGSDDNCAAFFEGPPFK.F
204 - 219	1719.6577	1718.6504	1718.8152	-0.1647	0	R.FATASADGQIYIYDGK.T
471 - 484	1537.7140	1536.7067	1536.8399	-0.1332	1	R.LYSILGTTLKDEGK.L
490 - 511	2279.8629	2278.8557	2279.0529	-0.1972	0	K.GPVTDVAYSHDGAFLAVCDASK.V

No match to: 918.3681, 1023.4512, 1461.6547, 1752.7174, 2418.0330, 2584.9940, 3397.3271

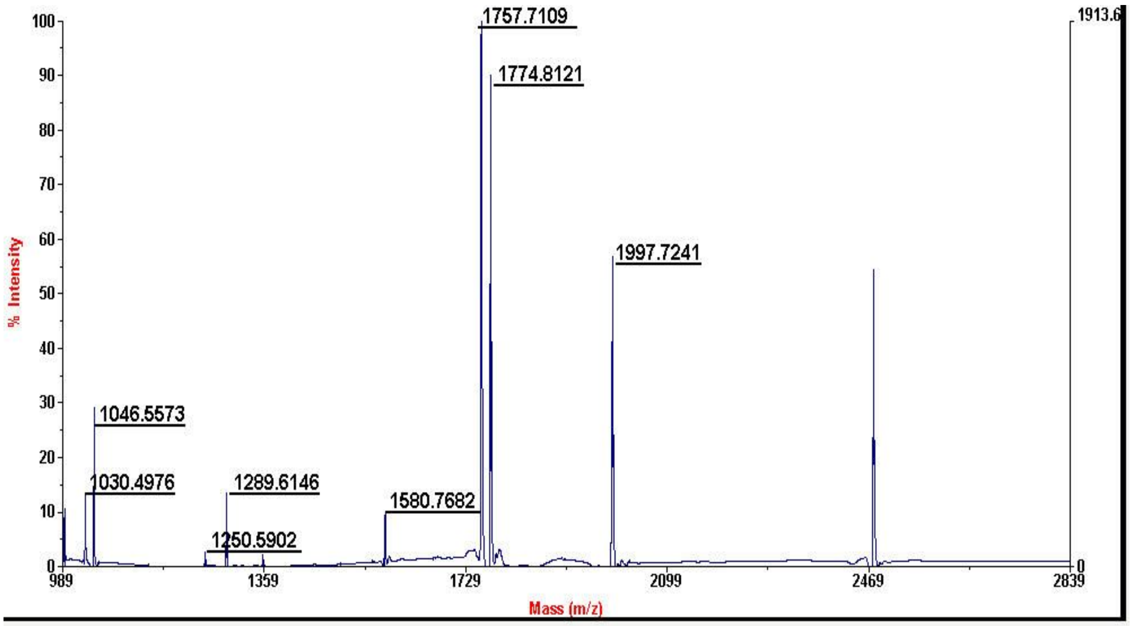
259 ） Aconitate hydratase, mitochondrial precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
32 - 50	2351.1049	2350.0977	2350.0939	0.0037	0	K.VAMSHFEPNEYIHYDLLEK.N	Oxidation (M)
69 - 84	1841.8776	1840.8703	1840.8955	-0.0252	0	K.IVYGHLDDPASQEIER.G	
371 - 378	985.4893	984.4820	984.5029	-0.0209	0	K.EGWPLDIR.V	
412 - 424	1463.7293	1462.7220	1462.7416	-0.0196	0	K.SQFTITPGSEQIR.A	
430 - 437	935.4417	934.4344	934.4872	-0.0528	0	R.DGYAQILR.D	
634 - 648	1601.7757	1600.7684	1600.7845	-0.0162	0	R.NAVTQEFGPVPDTAR.Y	
657 - 671	1667.7610	1666.7537	1666.7587	-0.0050	0	R.WVVIGDENYGEGSSR.E	

No match to: 3197.7325

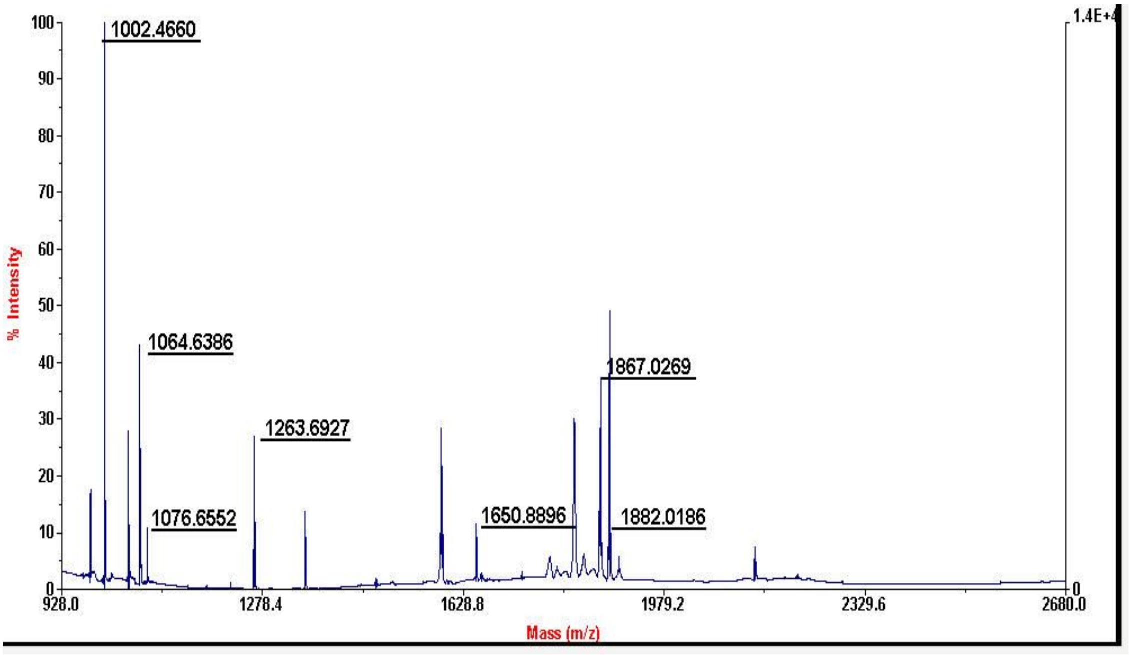
260 ） Collagen alpha-1(VI) chain precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
186 - 199	1580.7682	1579.7610	1579.8358	-0.0749	0	K.VFSVAITPDHLEPR.L	
200 - 210	1289.6146	1288.6073	1288.6775	-0.0702	0	R.LSIIATDHTYR.R	
241 - 256	1997.7241	1996.7169	1996.8190	-0.1021	0	K.NNVEQVCCSFECQPAR.G	3
712 - 722	1250.5902	1249.5829	1249.6415	-0.0586	0	R.DQLLPPSPNNR.I	
873 - 888	1774.8121	1773.8048	1773.9122	-0.1074	0	R.VAVVQYSGTGQQRPER.A	
977 - 984	992.4831	991.4758	991.5199	-0.0441	0	R.QVNEPHIR.V	
991 - 1005	1757.7109	1756.7036	1756.8056	-0.1020	0	K.TAEYDVAYGESHLFR.V	
1006 - 1014	1046.5573	1045.5500	1045.5920	-0.0420	0	R.VPSYQALLR.G	
1015 - 1023	1030.4976	1029.4903	1029.5356	-0.0453	0	R.GVFHQTVSR.K	

No match to: 1356.5078, 2477.9811

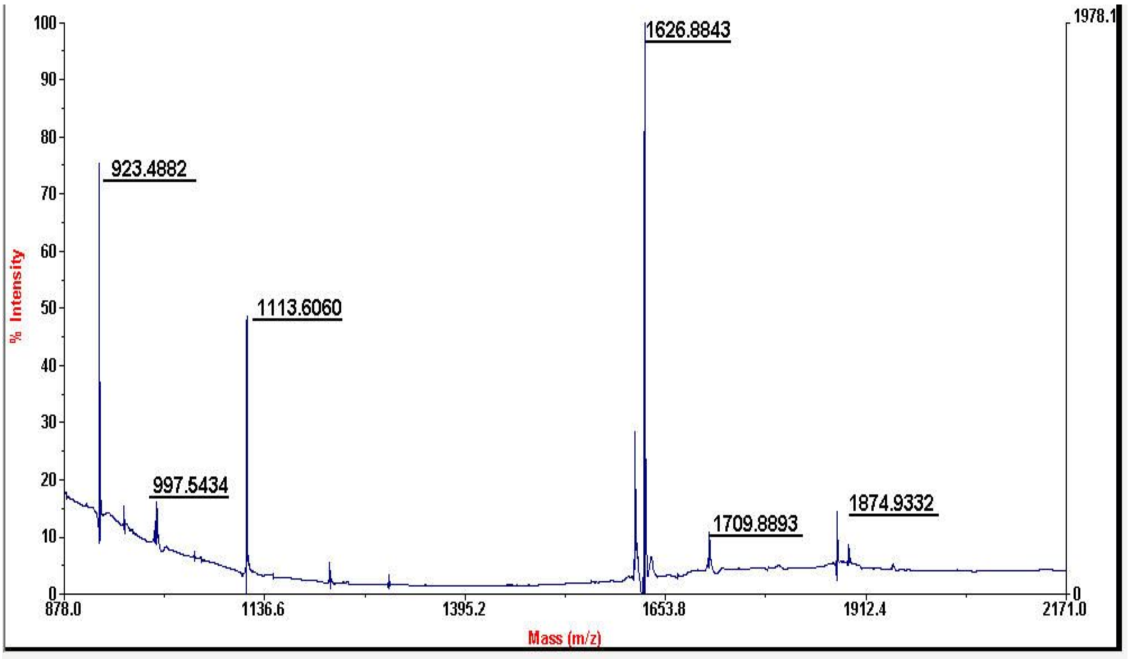
261 ） Heterogeneous nuclear ribonucleoprotein L



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
16 - 25	1002.4660	1001.4587	1001.4203	0.0385	0	R.YYGGGSEGGR.A	
67 - 76	1076.6552	1075.6479	1075.6138	0.0341	0	K.TPASPVVHIR.G	
199 - 215	1882.0186	1881.0113	1880.8687	0.1426	0	K.NGVQAMVEFDSVQSAQR.A	Oxidation (M)
234 - 241	977.5878	976.5806	976.5341	0.0464	0	K.IEYAKPTR.L	
404 - 417	1650.8896	1649.8823	1649.7984	0.0839	0	R.AITHLNNNFMFGQK.L	Oxidation (M)
522 - 537	1867.0269	1866.0196	1865.8982	0.1215	0	K.SDALETLGFLNHYQMK.N	
538 - 548	1263.6927	1262.6854	1262.6295	0.0559	0	K.NPNGPYPYTLK.L	
549 - 558	1064.6386	1063.6313	1063.4757	0.1557	0	K.LCFSTAQHAS.-	

No match to: 1044.5780, 1352.8119, 1590.9767, 1820.1687, 2137.0359, 2890.5699

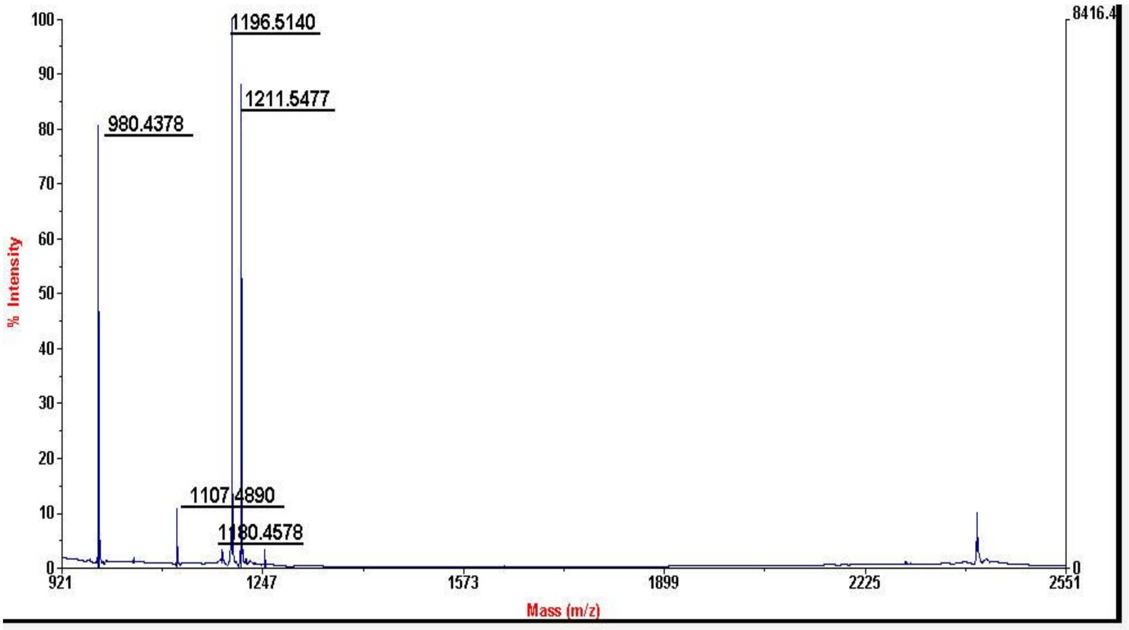
262) GTP:AMP phosphotransferase mitochondrial



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 43	997.5434	996.5361	996.5352	0.0009	0	K.HLSSGDLLR.D
81 - 94	1709.8893	1708.8820	1708.8573	0.0247	0	K.NLTQYSWLLDGFPR.T
95 - 104	1113.6060	1112.5987	1112.5826	0.0161	0	R.TLPQAEALDR.A
129 - 136	923.4882	922.4809	922.4773	0.0036	0	R.WIHPASGR.V
147 - 161	1626.8843	1625.8770	1625.8625	0.0145	0	K.TVGIDDLTGEPLIQR.E
175 - 189	1874.9332	1873.9259	1873.9098	0.0162	0	K.AYEDQTKPVLEYYQK.K

No match to: 1296.6691, 1614.9120, 1889.9315, 1946.0120

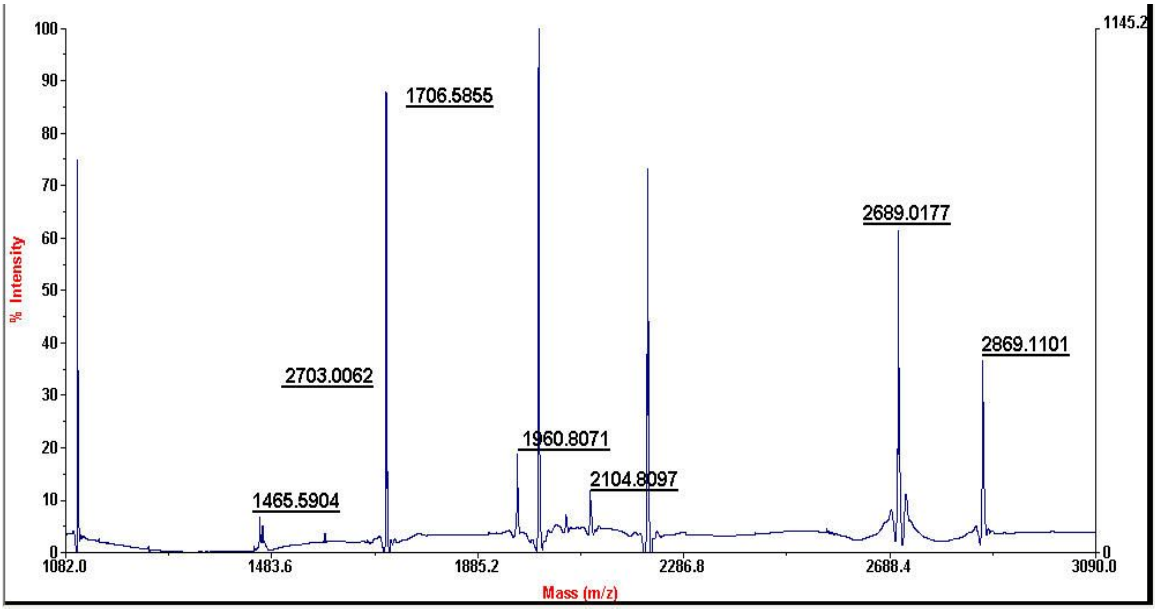
263) Peroxiredoxin-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
8 - 16	980.4378	979.4305	979.5239	-0.0934	0	K.IGHPAPNFK.A	
17 - 27	1180.4578	1179.4505	1179.5594	-0.1089	0	K.ATAVMPDGQFK.D	Oxidation (M)
111 - 120	1107.4890	1106.4817	1106.5972	-0.1155	0	R.TIAQDYGVLK.A	
141 - 151	1211.5477	1210.5404	1210.6670	-0.1266	0	R.QITVNDLPVGR.S	
159 - 168	1196.5140	1195.5067	1195.6237	-0.1170	0	R.LVQAFQFTDK.H	

No match to: 1250.4710, 2405.9575

264) WD repeat protein 17 - Homo sapiens

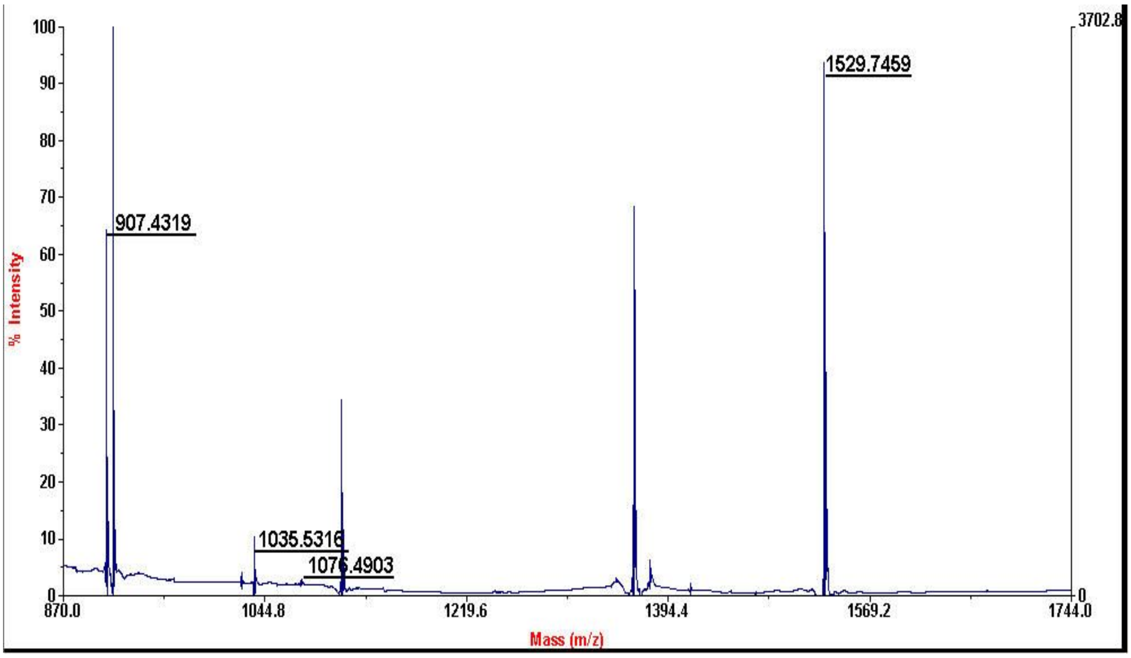


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

1 - 22	2869.1101	2868.1028	2868.2312	-0.1284	0	-.MAWMTYISNWFEQDDWYEGLQR.A	
475 - 491	1960.8071	1959.7998	1959.9050	-0.1052	0	R.FNEHGTNGIFCIAWSHK.D	
574 - 592	2104.8097	2103.8025	2104.0008	-0.1983	1	K.WSPLREGILCSGSDDGTVR.I	
579 - 592	1465.5904	1464.5831	1464.6515	-0.0684	0	R.EGILCSGSDDGTVR.I	
1014 - 1036	2703.0062	2701.9989	2702.2010	-0.2021	1	R.KCMMISVCFPCVGYSVPFCYVNR.N	
1015 - 1036	2689.0177	2688.0104	2688.1490	-0.1386	0	K.CMMISVCFPCVGYSVPFCYVNR.N	3
1076 - 1090	1706.5855	1705.5782	1705.8015	-0.2233	0	K.LPTVEECMQLAETAR.A	Oxidation (M)

No match to: 2215.8159, 2718.9014

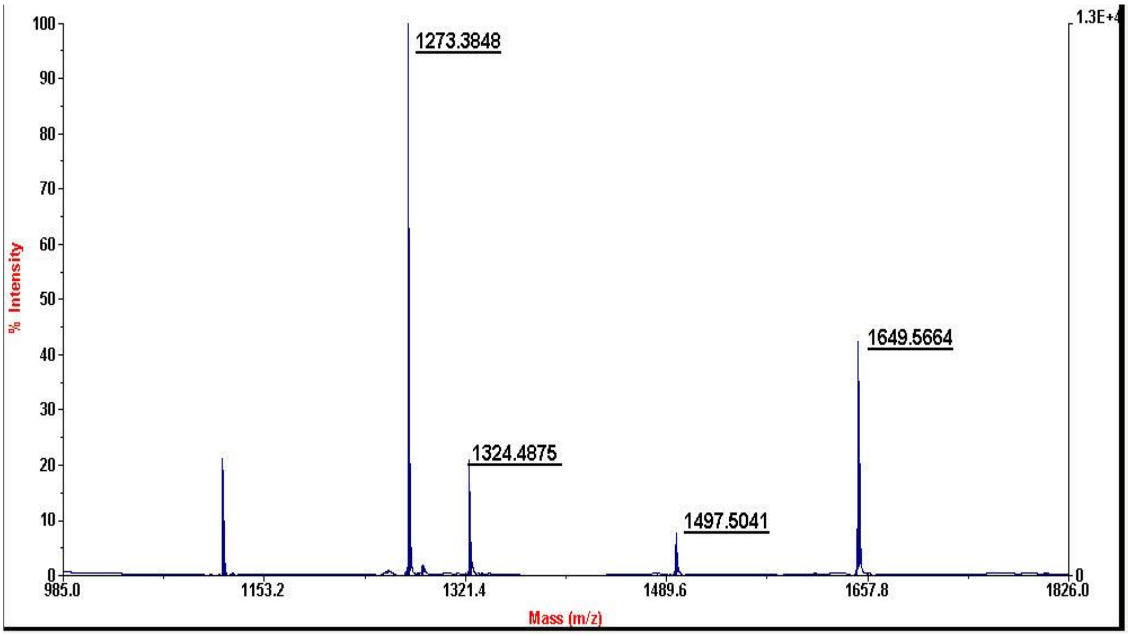
265) 10 kDa heat shock protein, mitochondrial



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 15	1035.5316	1034.5243	1034.5913	-0.0670	1	R.KFLPLFDR.V
9 - 15	907.4319	906.4246	906.4963	-0.0717	0	K.FLPLFDR.V
71 - 80	1076.4903	1075.4830	1075.5914	-0.1083	0	K.VLLPEYGGTK.V
81 - 92	1529.7459	1528.7386	1528.7926	-0.0540	1	K.VVLDDKDYFLFR.D

No match to: 1111.4807, 1364.6360, 1378.6190, 1413.6386

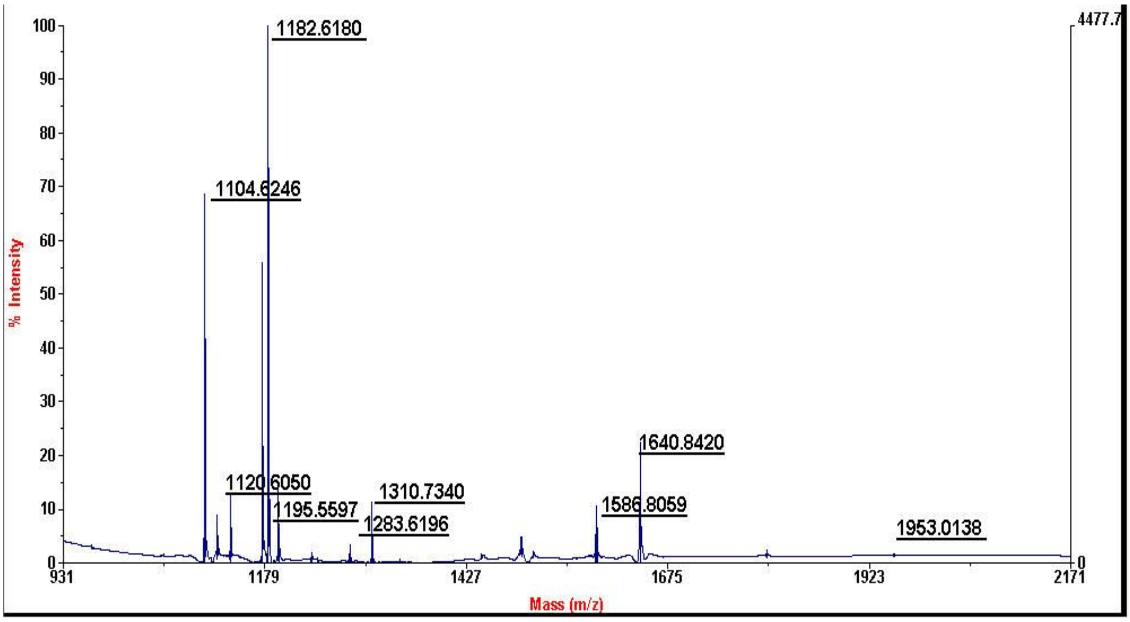
266) Galectin-3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
152 - 162	1273.3848	1272.3775	1272.6000	-0.2225	0	R.GNDVAFHFNPR.F
187 - 199	1497.5041	1496.4969	1496.7664	-0.2695	0	R.QSVFPFESGKPFK.I
200 - 210	1324.4875	1323.4802	1323.7187	-0.2385	0	K.IQVLVEPDHFK.V
211 - 224	1649.5664	1648.5591	1648.8434	-0.2842	0	K.VAVNDAHLLQYNHR.V

No match to: 1118.4811

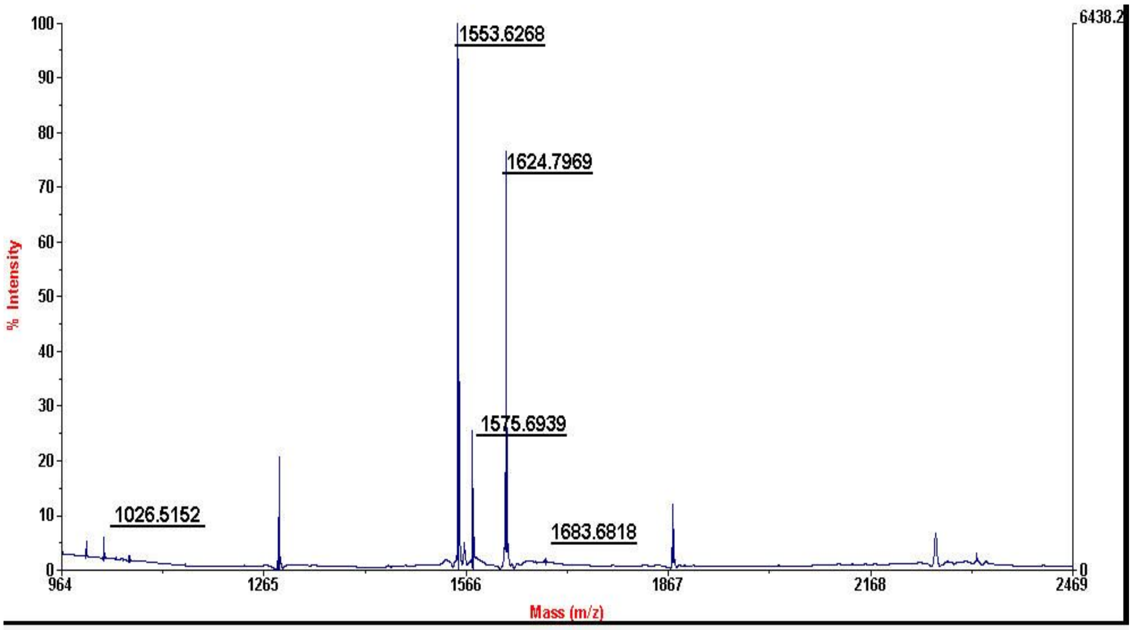
267) Tudor domain-containing protein 7



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
110 - 120	1310.7340	1309.7268	1309.6740	0.0527	0	K.TMPFFLEGKPK.A	Oxidation (M)
189 - 205	1953.0138	1952.0065	1952.0302	-0.0237	1	R.FSPKASLQPPLQMHLSR.T	Oxidation (M)
563 - 576	1640.8420	1639.8347	1639.8392	-0.0045	1	K.LNPKFCSLSFQATK.C	
685 - 693	1182.6180	1181.6107	1181.5539	0.0568	1	R.KIEDYFHCK.H	
747 - 756	1195.5597	1194.5524	1194.6720	-0.1196	1	K.VSELREIPPR.F	
793 - 804	1283.6196	1282.6123	1282.5533	0.0590	0	R.DSVLNCSDCSIK.V	
1005 - 1013	1104.6246	1103.6173	1103.5798	0.0376	0	K.VQPLVDMFR.K	
1005 - 1013	1120.6050	1119.5978	1119.5747	0.0231	0	K.VQPLVDMFR.K	Oxidation (M)
1029 - 1041	1586.8059	1585.7986	1585.6653	0.1333	0	K.CNQWSEEASMVFR.N	

No match to: 1136.6057, 1175.6177, 1235.5166, 1509.6975, 2549.4011

268) ATP synthase subunit alpha, mitochondrial precursor

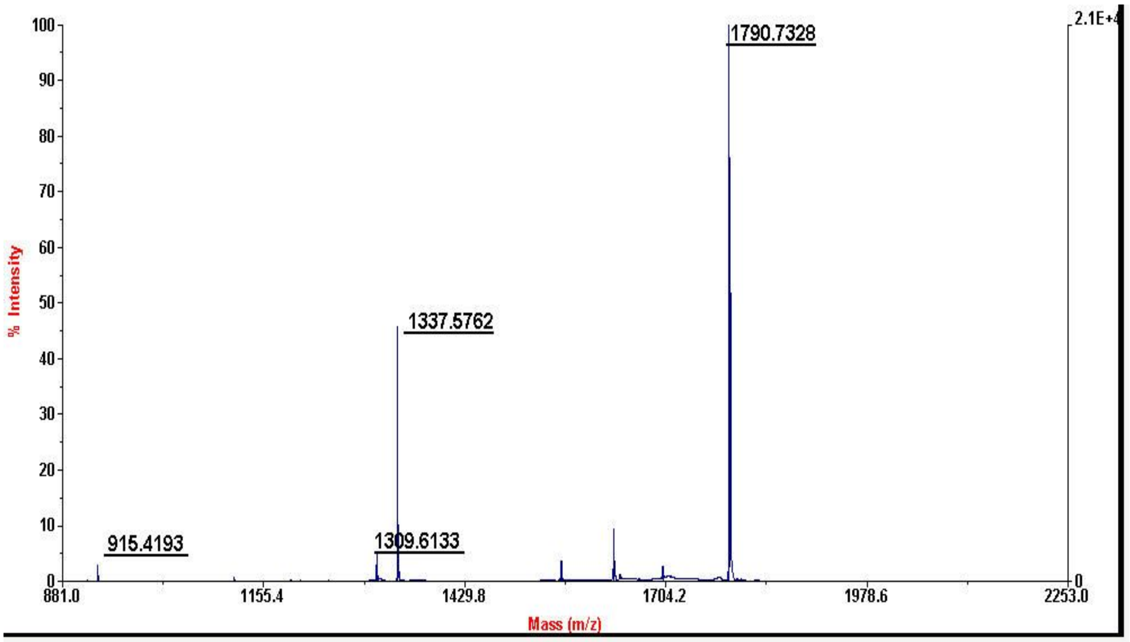


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
59 - 73	1575.6939	1574.6866	1574.7788	-0.0922	0	R.ILGADTSVDLEETGR.V	
89 - 103	1683.6818	1682.6745	1682.7821	-0.1076	0	R.NVQAEEMVEFSSGLK.G	Oxidation (M)
134 - 149	1624.7969	1623.7896	1623.8832	-0.0936	0	R.TGAIVDVPVGEELLGR.V	

195 - 204	1026.5152	1025.5080	1025.5869	-0.0790	0	K.AVDSLVPIGR.G
335 - 347	1553.6268	1552.6195	1552.7310	-0.1115	0	R.EAYPGDVFYLHSR.L

No match to: 1286.5830, 1677.6846, 1872.8488

269) Cofilin-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 45	1309.6133	1308.6060	1308.6748	-0.0687	1	K.AVLFCLSEDKK.N
46 - 53	915.4193	914.4120	914.5073	-0.0953	0	K.NIILEEGK.E
82 - 92	1337.5762	1336.5690	1336.6187	-0.0497	0	R.YALYDATYETK.E
133 - 146	1790.7328	1789.7256	1789.8053	-0.0798	1	K.HELQANCYEEVKDR.C

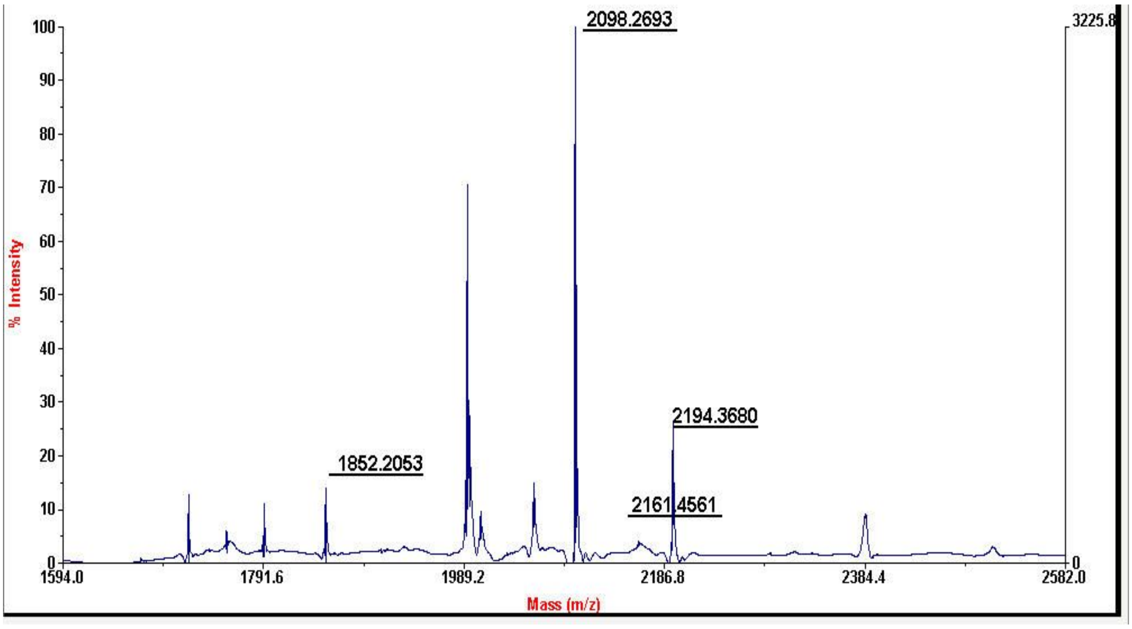
No match to: 1560.7615, 1699.7393

270 Collagen alpha-1(VI) chain precursor

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
28 - 51	2699.4666	2698.4593	2698.3313	0.1280	0	R.AVAFQDCPVDLFFVLDTSESVALR.L
83 - 105	2598.5156	2597.5083	2597.3238	0.1845	0	R.NLVWNAGALHYSDEVEIIQGLTR.M
186 - 199	1580.9418	1579.9345	1579.8358	0.0986	0	K.VFSVAITPDHLEPR.L
873 - 888	1775.0736	1774.0663	1773.9122	0.1541	0	R.VAVVQYSGTGQQRPER.A
991 - 1005	1757.9520	1756.9447	1756.8056	0.1391	0	K.TAEYDVAYGESHLFR.V

1006 - 1014	1046.6268	1045.6196	1045.5920	0.0275	0	R.VPSYQALLR.G

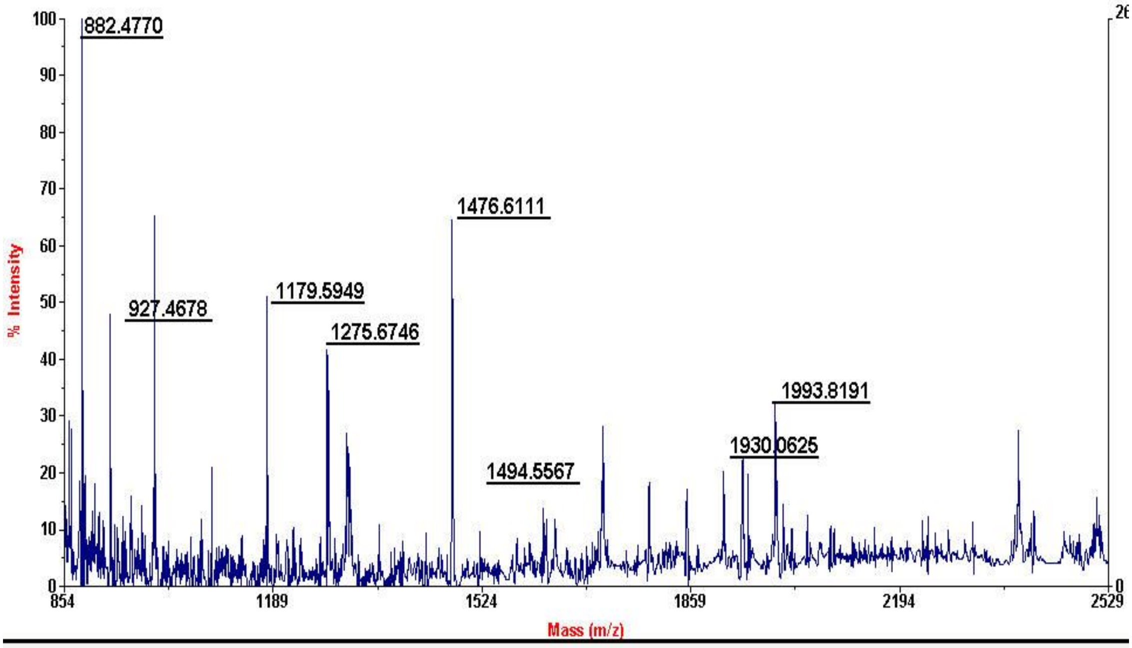
271 Probable lipid phosphate phosphatase PPAPDC3 (EC 3.1.3.-)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
79 - 95	1852.2053	1851.1981	1850.9746	0.2234	1	K.GIAFNSLLAIDICMSKR.L
115 - 135	2161.4561	2160.4488	2160.2493	0.1995	0	K.LIGITGHGIPWIGGTILCLVK.S
216 - 234	2098.2693	2097.2620	2097.2319	0.0301	1	R.VLLVLWALCVGLSRVMIGR.H
253 - 271	2194.3680	2193.3607	2193.0672	0.2935	0	R.LVELVWMPSSTCQMLISAW.-

No match to: 1717.1430, 1991.3859

272 Kinesin-like protein KIF14

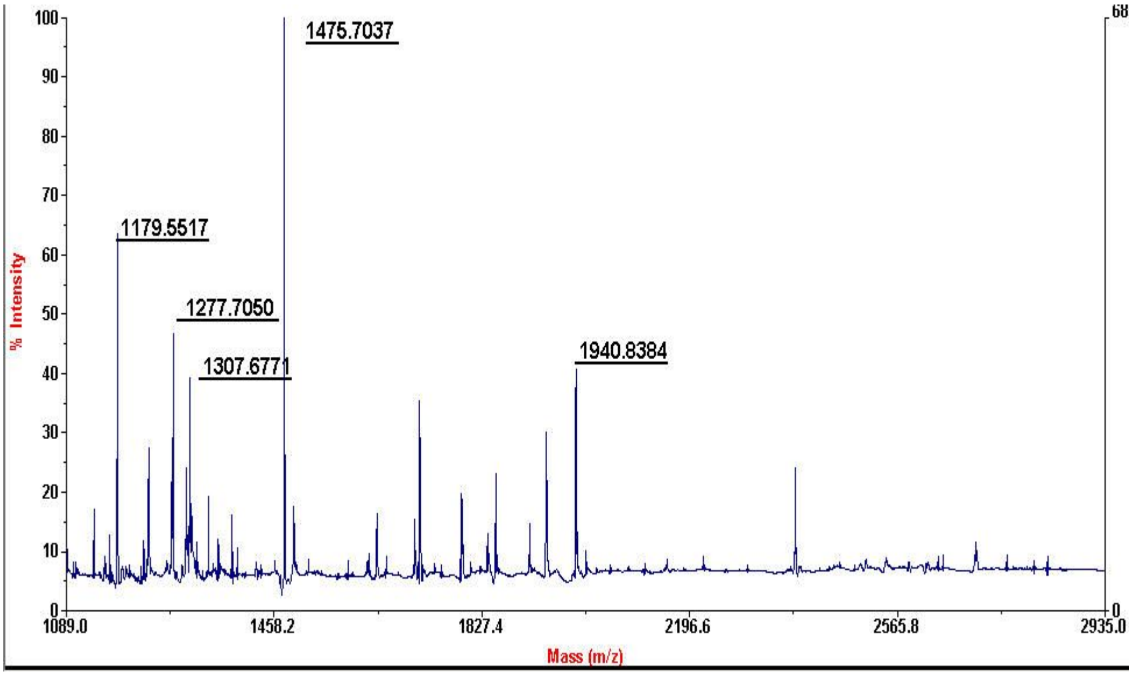


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
319 - 328	1179.5949	1178.5877	1178.6044	-0.0167	1	K.SSFLANKQER.S	
354 - 370	1930.0625	1929.0552	1929.0796	-0.0244	1	K.VENSQVTVAVRVRPFTK.R	
427 - 434	882.4770	881.4697	881.5334	-0.0637	0	K.LAAPLLER.A	
570 - 582	1494.5567	1493.5495	1493.7548	-0.2054	0	R.SHSVFTLVMTQTK.T	Oxidation (M)
743 - 752	1275.6746	1274.6673	1274.6765	-0.0092	1	R.LCRQEITSLR.M	
950 - 962	1476.6111	1475.6038	1475.7476	-0.1438	1	K.AKEEMMQGIQIAK.E	
1458 - 1475	1993.8191	1992.8118	1993.0302	-0.2184	1	K.TNAMGLIRSLENIFAESK.I	
1506 - 1512	927.4678	926.4605	926.5007	-0.0402	1	K.LKHCLEK.A	

No match to: 998.4712

273

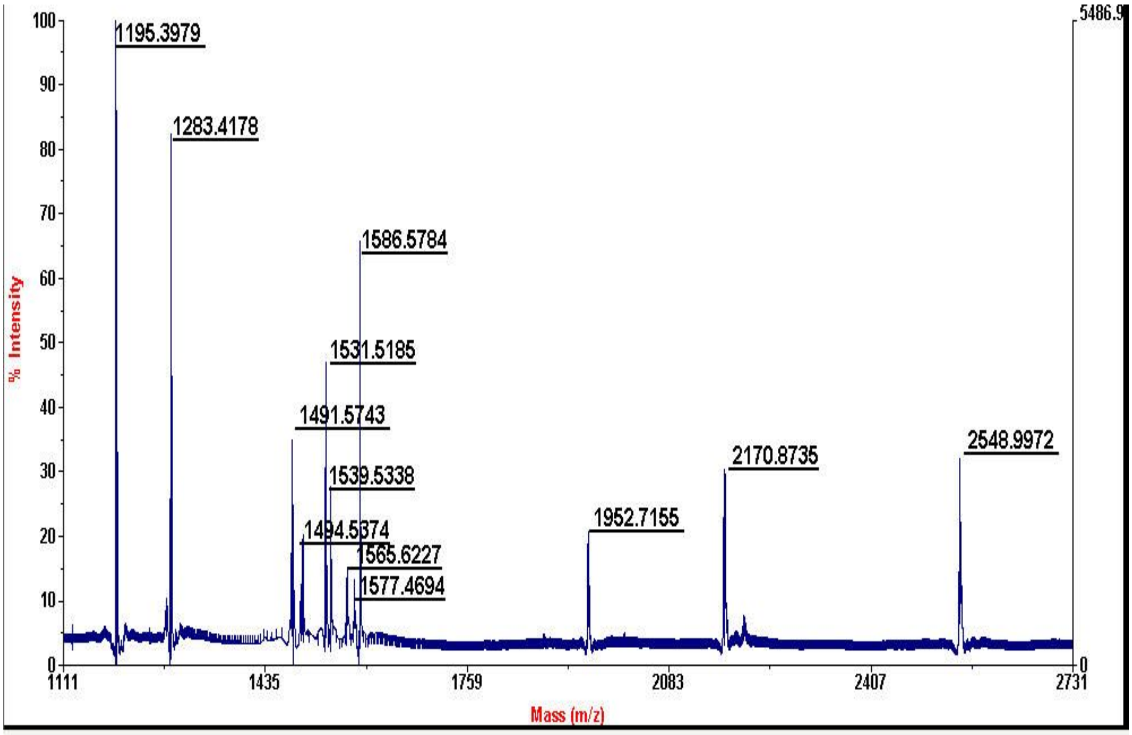
PH and SEC7 domain-containing protein 3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
208 - 218	1277.7050	1276.6977	1276.7390	-0.0413	1	K.DLLKALYNSIK.N
330 - 347	1940.8384	1939.8311	1939.9752	-0.1441	1	K.NAVSVHHALASKATDYEK.K
480 - 493	1475.7037	1474.6964	1474.7151	-0.0186	0	K.ELLSNDESEAAGLK.K
520 - 530	1307.6771	1306.6698	1306.6993	-0.0295	1	R.KDHRPETPSIK.Q
521 - 530	1179.5517	1178.5444	1178.6044	-0.0599	0	K.DHRPETPSIK.Q

No match to: 1716.8051, 1993.9218

274 Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal-binding globulin)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
144 - 162	2170.8735	2169.8663	2170.0881	-0.2218	0	R.SAGWNIPIGLLYCDLPEPR.K	
240 - 251	1539.5338	1538.5266	1538.7035	-0.1769	0	R.DQYELLCLDNTR.K	
252 - 273	2548.9972	2547.9899	2548.2856	-0.2958	1	R.KPVDEYKDCHLAQVPSHTVVAR.S	
298 - 310	1491.5743	1490.5670	1490.7518	-0.1848	1	K.SKEFQLFSSPHGK.D	
332 - 343	1478.5719	1477.5646	1477.7275	-0.1629	0	K.MYLGYEYVTAIR.N	
332 - 343	1494.5374	1493.5302	1493.7224	-0.1923	0	K.MYLGYEYVTAIR.N	Oxidation (M)
363 - 371	1195.3979	1194.3906	1194.5352	-0.1446	0	K.WCALSHHER.L	
495 - 508	1577.4694	1576.4621	1576.6504	-0.1883	0	R.FDEFFSEGCAPGSK.K	
531 - 541	1283.4178	1282.4105	1282.5618	-0.1513	0	K.EGYYGYTGAFR.C	
572 - 587	1952.7155	1951.7083	1951.9309	-0.2227	1	K.NLNEKDYELLCLDGTR.K	
588 - 600	1586.5784	1585.5712	1585.7671	-0.1959	0	R.KPVEEYANCHLAR.A	
647 - 659	1565.6227	1564.6154	1564.7919	-0.1766	1	K.DLLFRDDTVCLAK.L	
684 - 696	1531.5185	1530.5112	1530.6807	-0.1695	0	K.CSTSSLLEACTFR.R	2

275 Lamin-A/C

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
134 - 144	1243.6969	1242.6896	1242.7183	-0.0287	1	R.LKDLEALLNSK.E

157 - 171	1665.9763	1664.9690	1664.8846	0.0844	1	R.TLEGELHDLRGQVAK.L
241 - 260	2384.0632	2383.0559	2383.1768	-0.1208	1	R.LADALQELRAQHEDQVEQYK.K
281 - 296	1752.9778	1751.9705	1751.8550	0.1155	0	R.NSNLVGAAHEELQQSR.I
428 - 435	919.4975	918.4902	918.4308	0.0594	0	R.SSFSQHAR.T
440 - 453	1605.9434	1604.9361	1604.8046	0.1315	1	R.VAVEEVDEEGKFVR.L
516 - 527	1363.7224	1362.7152	1362.6099	0.1053	0	K.AQNTWGCGNSLR.T

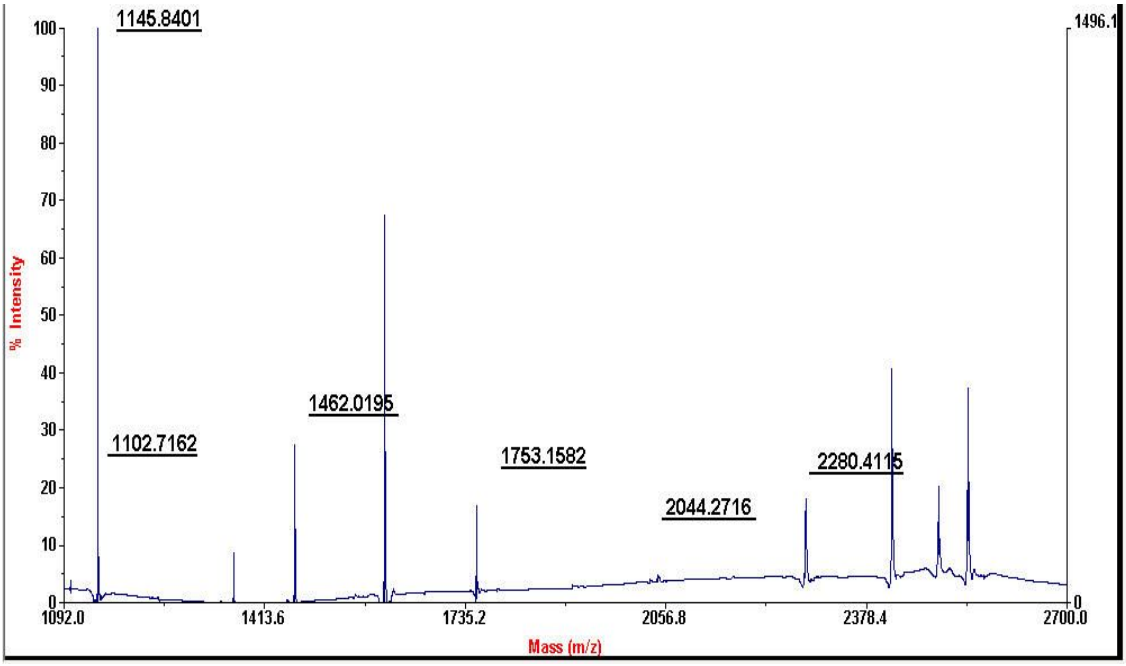
No match to: 1064.6515, 1307.7382, 1461.7441, 1565.8321, 1590.9968, 1638.9194, 2501.3924

276 WD repeat protein 1

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 17	1145.7110	1144.7037	1144.6241	0.0796	0	K.VFASLPQVER.G
44 - 65	2418.4317	2417.4244	2417.2339	0.1905	0	R.NIDNPALADIYTEHAHQVVVAK.Y
96 - 104	1102.6057	1101.5984	1101.5131	0.0853	0	K.YEYQPFAGK.I
156 - 161	806.4965	805.4892	805.4195	0.0698	0	K.QSRPYR.L
162 - 180	2044.0503	2043.0430	2042.9044	0.1386	0	R.LATGSDDNCAAFFEGPPFK.F
197 - 219	2493.3508	2492.3435	2492.1608	0.1827	1	R.FSPDGNRFATASADGQIYIYDGK.T
232 - 256	2585.4754	2584.4681	2584.2194	0.2487	0	K.AHDGGIYAISWSPDSTHLLSASGDK.T
438 - 470	3397.8940	3396.8868	3396.6045	0.2822	0	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L
490 - 511	2280.2182	2279.2109	2279.0529	0.1581	0	K.GPVTDVAYSHDGAFLAVCDASK.V
512 - 534	2540.4276	2539.4204	2539.2132	0.2072	0	K.VVTVFSVADGYSENNVFYGHHAK.I

No match to: 882.6521, 918.5258, 1461.8791, 1605.9309, 1752.9806, 3382.8614, 3526.9284, 3822.5162

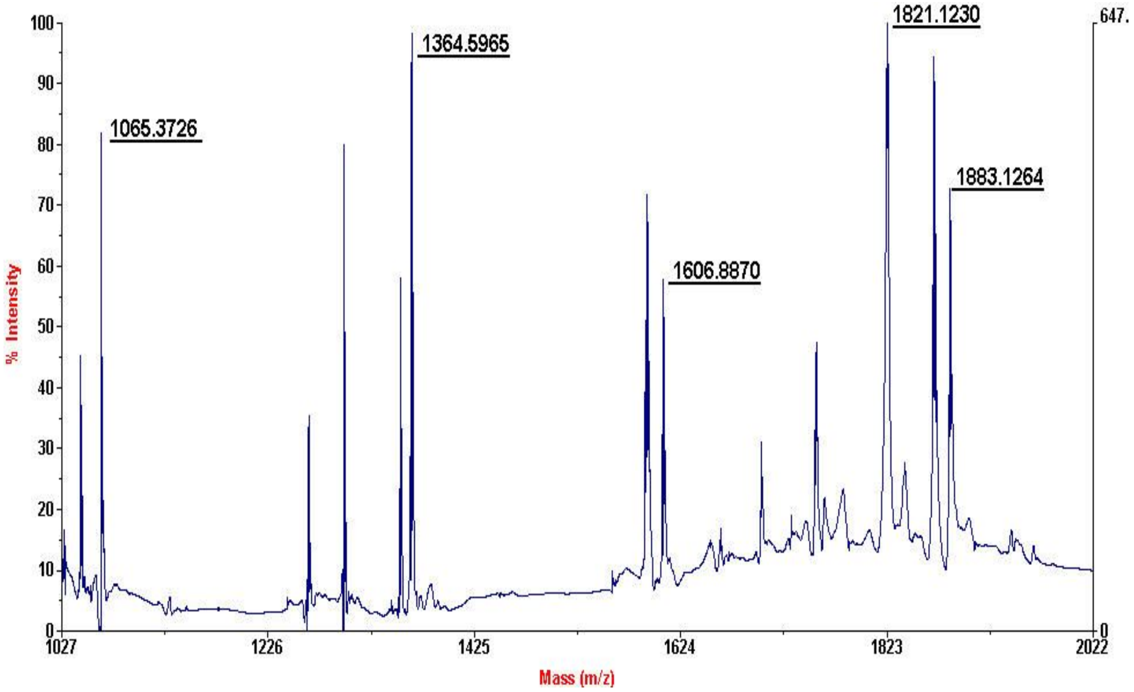
277 Cullin-associated NEDD8-dissociated protein 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
15 - 23	1102.7162	1101.7089	1101.4761	0.2328	1	K.MTSSDKDFR.F	Oxidation (M)
129 - 142	1462.0195	1461.0122	1460.8463	0.1659	1	R.LPGPRVPTSPTAIR.T	
143 - 158	1753.1582	1752.1509	1751.9213	0.2296	1	R.TLIQCLGSVGRQAGHR.L	
319 - 346	3136.8494	3135.8421	3135.5845	0.2576	1	K.GWLEAMEEPTQTGSNLHMLRGQVPLVVK.A	Oxidation (M)
458 - 466	1145.8401	1144.8328	1144.6618	0.1710	0	R.ALWPLHRPR.M	
467 - 486	2280.4115	2279.4042	2279.1290	0.2752	1	R.MLDPEPYVGEMSAVTLARLR.A	2 Oxidation (M)
953 - 970	2044.2716	2043.2643	2042.9732	0.2912	1	R.EVEMGPFKHTVDDGLDVR.K	

No match to: 1363.8679, 1538.0787, 1606.0870

278 Fructose-bisphosphate aldolase C



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
29 - 42	1364.5965	1363.5892	1363.6653	-0.0761	0	K.GILAADESVGSMAK.R Oxidation (M)
72 - 87	1883.1264	1882.1191	1881.9811	0.1380	1	K.KCIGGVIFFHETLYQK.D
141 - 149	1065.3726	1064.3653	1064.5039	-0.1387	1	K.DGADFAKWR.C
290 - 304	1821.1230	1820.1157	1819.9192	0.1965	0	R.CPLPRPWALTFSYGR.A
316 - 330	1606.8870	1605.8797	1605.7747	0.1051	1	R.GQRDNAGAATEEFIK.R

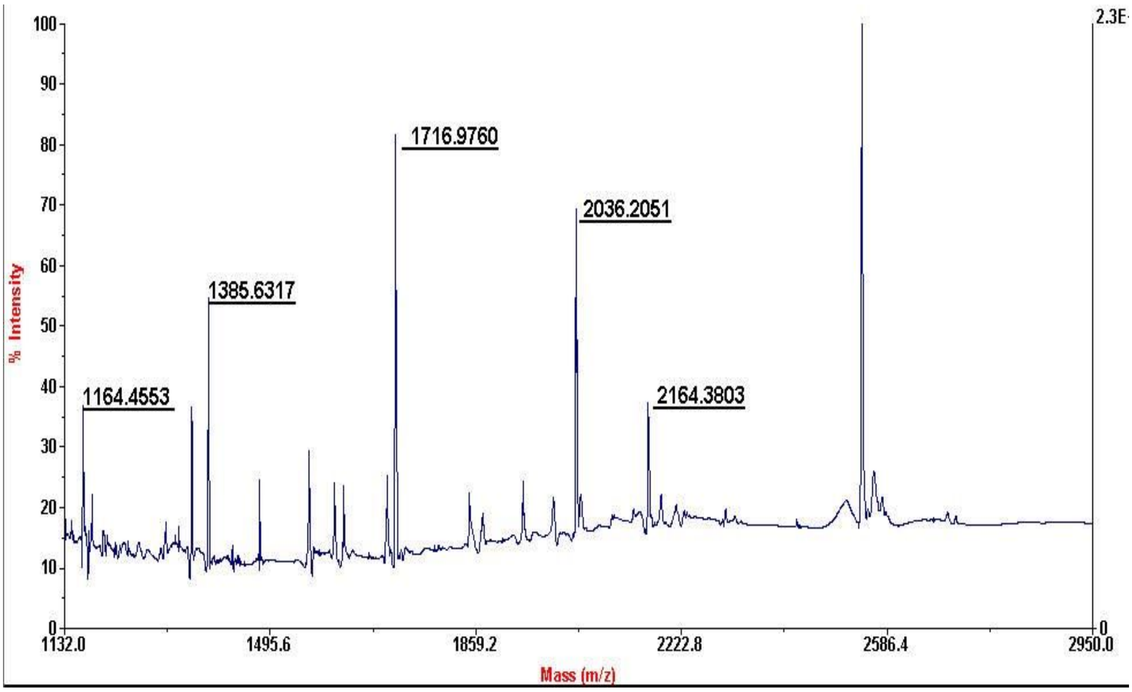
No match to: 1299.5356, 1353.6505, 1363.6288, 1867.1179

279

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
104 - 113	1385.6317	1384.6244	1384.5798	0.0446	0	R.YFFDEWMFGK.V Oxidation (M)
142 - 159	2036.2051	2035.1978	2035.0343	0.1635	1	R.YRAIVNPMDMQTSGALLR.T
144 - 159	1716.9760	1715.9687	1715.8698	0.0989	0	R.AIVNPMDMQTSGALLR.T
144 - 163	2164.3803	2163.3730	2163.0850	0.2880	1	R.AIVNPMDMQTSGALLRTCVK.A Oxidation (M)
334 - 343	1164.4553	1163.4481	1163.4964	-0.0484	0	R.HFNSQLCCGR.K

No match to: 1040.1290, 1476.7675, 2540.9390

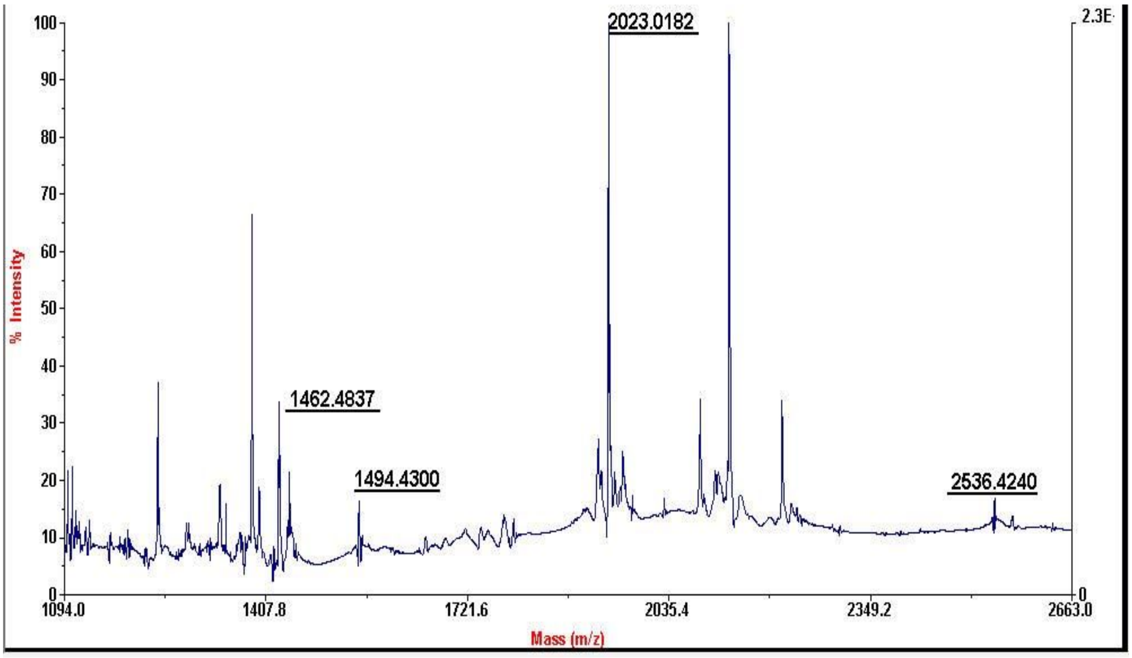
280 Psoriasis susceptibility 1 candidate gene 1 protein



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 12	1494.4300	1493.4228	1493.6351	-0.2124	1	-.MTCTDQKSHSQR.A ; Oxidation (M)
46 - 67	2536.4240	2535.4167	2535.1609	0.2557	0	R.LCHMEPANHFWHAGDLQAMISK.E
68 - 79	1462.4837	1461.4764	1461.6307	-0.1542	0	K.EFHLAATQDDCR.K
111 - 129	2023.0182	2022.0109	2022.1010	-0.0901	0	R.LQQPQPLPPPSGIHLSASR.T

No match to: 1120.1442, 1293.2546, 1482.4808, 1683.6845, 1715.7020, 1813.7861

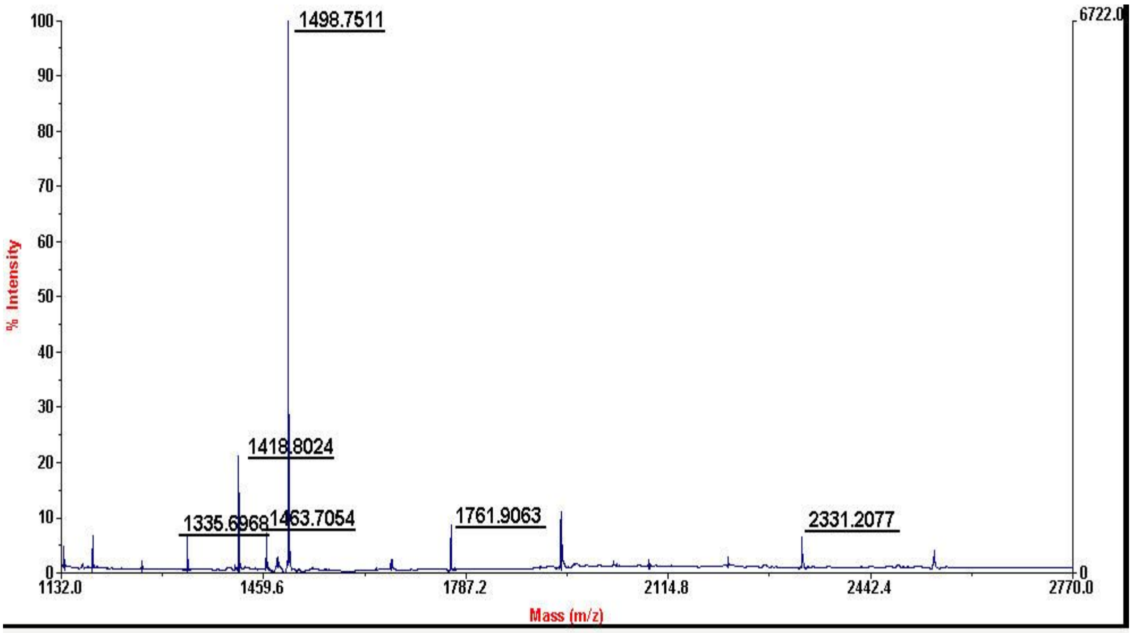
281 Hcp beta-lactamase-like protein C1orf163



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
33 - 39	882.4480	881.4407	881.3338	0.1069	0	K.DPDGCYR.L	
33 - 48	1940.7454	1939.7381	1939.9098	-0.1717	1	K.DPDGCYRLVDYLEGIR.K	
95 - 106	1427.7267	1426.7195	1426.6771	0.0424	1	R.CFLMACEKPGKK.S	; Oxidation (M)
178 - 195	2082.8041	2081.7968	2081.9233	-0.1265	1	K.ACDLGHIWACANASRMYK.L	; Oxidation (M)

No match to: 1385.5364, 2128.6678

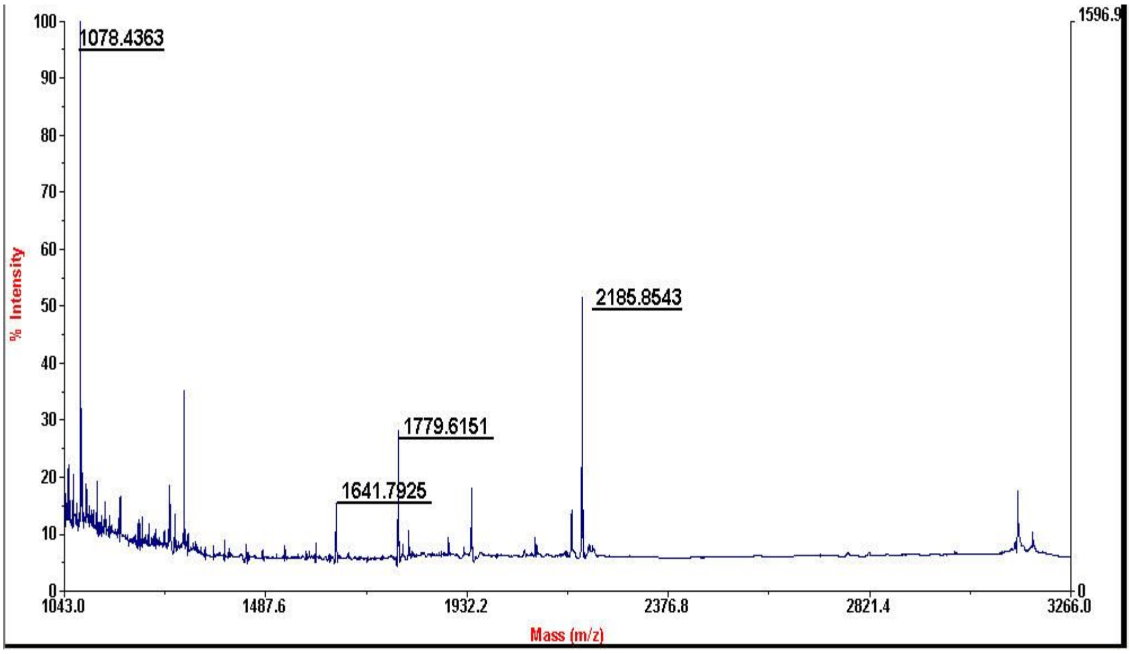
282 T-complex protein 1 subunit zeta (TCP-1-zeta)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
59 - 79	2331.2077	2330.2004	2330.2052	-0.0049	0	K.DGNVLLHEMQIQHPTASLIAK.V	Oxidation (M)
105 - 117	1498.7511	1497.7438	1497.7576	-0.0137	0	K.QADLYISEGLHPR.I	
118 - 129	1335.6968	1334.6895	1334.7081	-0.0186	1	R.IITEGFEAAKEK.A	
130 - 141	1418.8024	1417.7951	1417.7929	0.0022	1	K.ALQFLEEVKVSR.E	
142 - 153	1463.7054	1462.6981	1462.7086	-0.0105	1	R.EMDRETLIDVAR.T	Oxidation (M)
450 - 465	1761.9063	1760.8991	1760.9309	-0.0318	0	K.VLAQNSGFDLQETLVK.I	

No match to: 882.5355, 996.5641, 1182.5953, 1940.9360, 2543.4054

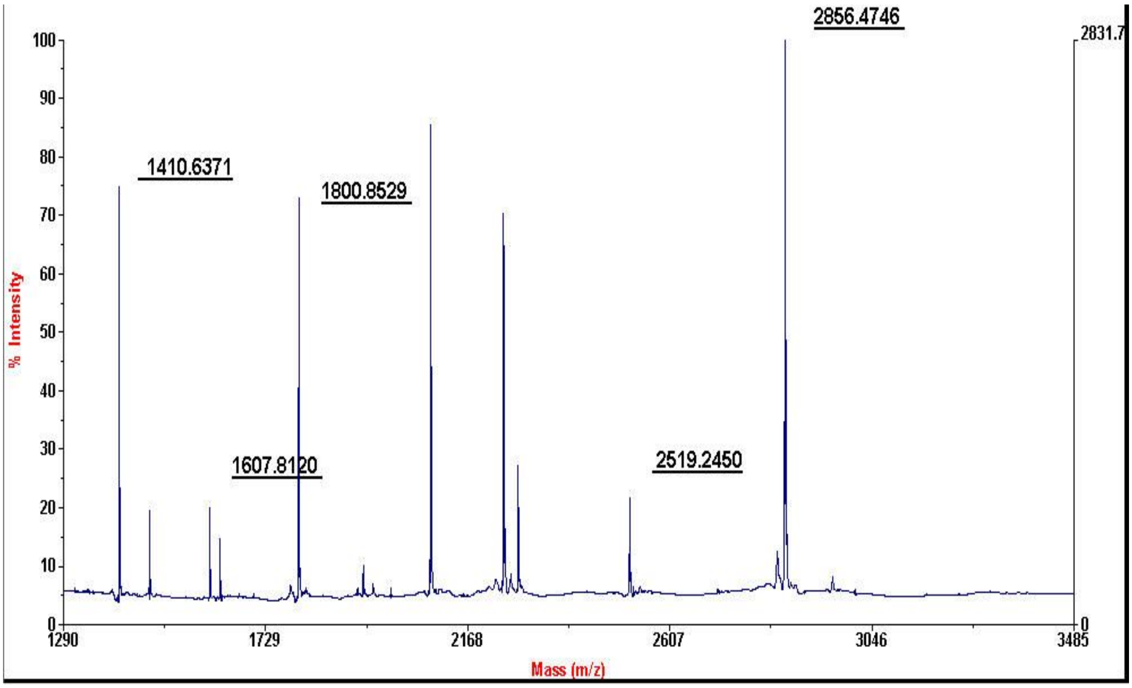
283 Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) - Homo sapiens (Human)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 49	1779.6151	1778.6078	1778.7609	-0.1530	0	K.TDTSHHDQDHPTFNK.I
50 - 63	1641.7925	1640.7853	1640.8562	-0.0710	0	K.ITPNLAEFAFSLYR.Q
161 - 179	2185.8543	2184.8470	2185.0327	-0.1858	1	K.LYHSEAFTVNFGDTEEAKK.Q
299 - 306	1078.4363	1077.4290	1077.5203	-0.0913	1	K.FLENEDRR.S

No match to: 1940.7366

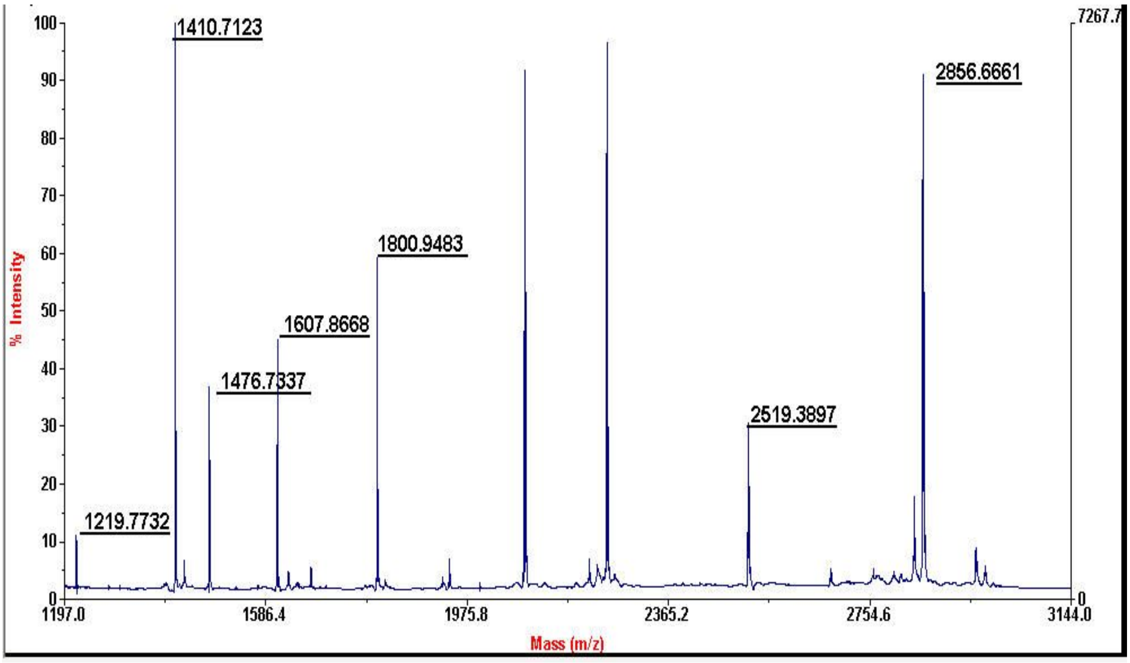
284 Calreticulin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 36	1410.6371	1409.6298	1409.6212	0.0086	0	K.EQFLDGDGWTSR.W
74 - 87	1607.8120	1606.8047	1606.7667	0.0380	0	R.FYALSASFEPFSNK.G
163 - 185	2856.4746	2855.4673	2855.3800	0.0873	1	R.CKDDEFTHLYTLIVRPDNTYEVK.I
186 - 207	2519.2450	2518.2377	2518.1864	0.0514	1	K.IDNSQVESGSLEDDWDFLPPKK.I
208 - 222	1800.8529	1799.8456	1799.8326	0.0131	1	K.IKDPDASKPEDWDER.A

No match to: 845.1194, 861.0781, 1629.7850, 2086.9801, 2245.0828, 2277.0773

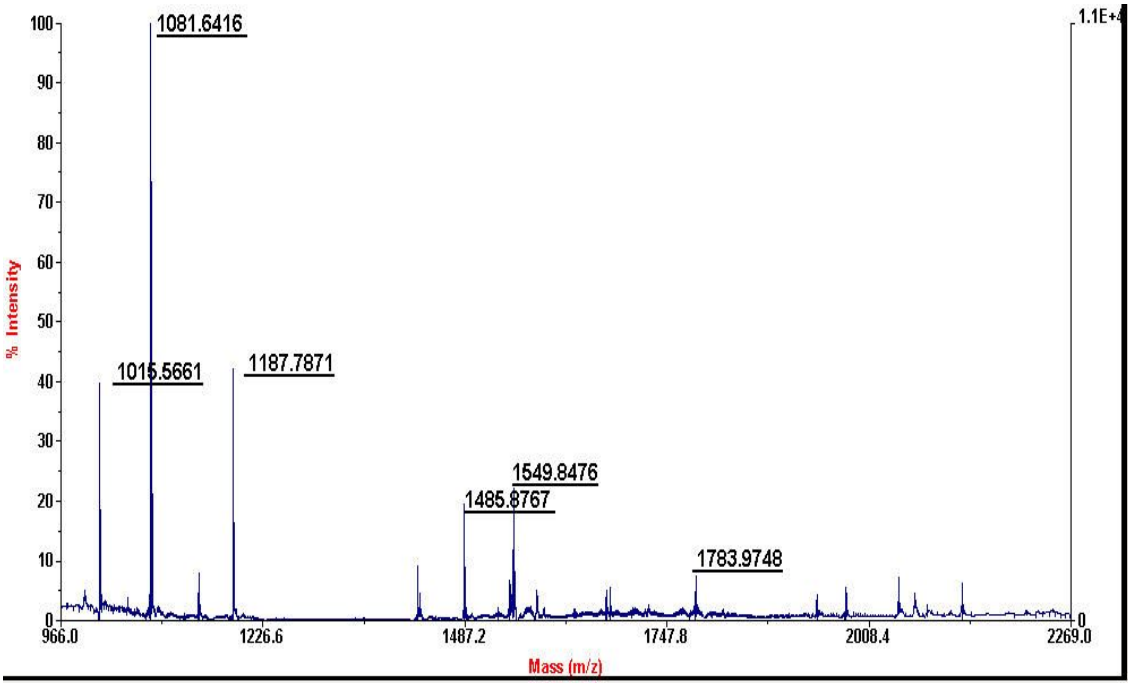
285 Calreticulin precursor (CRP55)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 36	1410.7123	1409.7050	1409.6212	0.0839	0	K.EQFLDGDGWTSR.W
74 - 87	1607.8668	1606.8596	1606.7667	0.0928	0	R.FYALSASFEPFSNK.G
88 - 98	1219.7732	1218.7659	1218.6972	0.0686	0	K.GQTLVVQFTVK.H
99 - 111	1476.7337	1475.7264	1475.6463	0.0800	0	K.HEQNIDCGGGYVK.L
144 - 151	1019.6150	1018.6077	1018.5600	0.0477	0	K.VHVIFNYK.G
163 - 185	2856.6661	2855.6588	2855.3800	0.2788	1	R.CKDDEFTHLYTLIVRPDNTYEVK.I
186 - 207	2519.3897	2518.3825	2518.1864	0.1961	1	K.IDNSQVESGSLEDDWDFLPPKK.I
208 - 222	1800.9483	1799.9410	1799.8326	0.1085	1	K.IKDPDASKPEDWDER.A

No match to: 882.6053, 1941.0829, 2087.1189, 2245.2439, 2959.6990

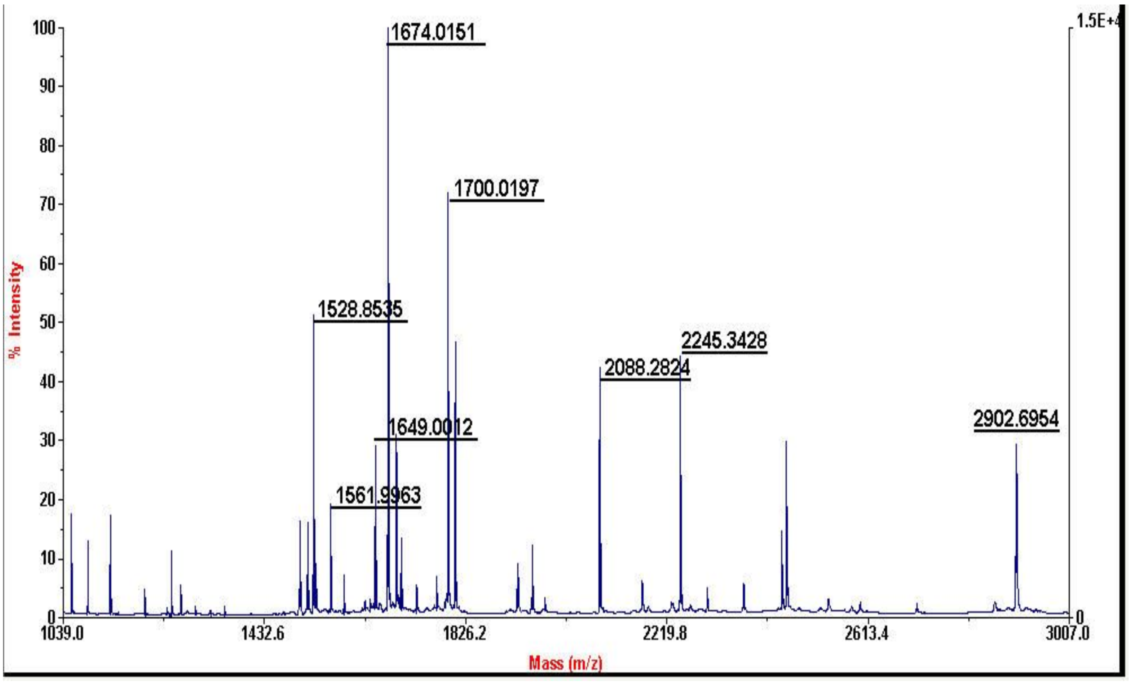
286 Endoplasmin precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
76 - 84	1081.6416	1080.6343	1080.5352	0.0990	0	K.FAFQAEVNR.M	
96 - 102	919.6249	918.6176	918.5287	0.0890	1	K.NKEIFLR.E	
385 - 395	1187.7871	1186.7798	1186.6710	0.1088	0	K.SILFVPTSAPR.G	
396 - 404	1015.5661	1014.5588	1014.4658	0.0930	0	R.GLFDEYGSK.K	
415 - 428	1783.9748	1782.9675	1782.8069	0.1606	1	R.RVFITDDFHDMMPK.Y	2 Oxidation (M)
614 - 625	1549.8476	1548.8403	1548.7646	0.0757	1	K.EFEPLLNWMKDK.A	
742 - 754	1485.8767	1484.8694	1484.8021	0.0673	1	R.MLRLSLNIDPDAK.V	

No match to: 1978.0847, 2067.2642

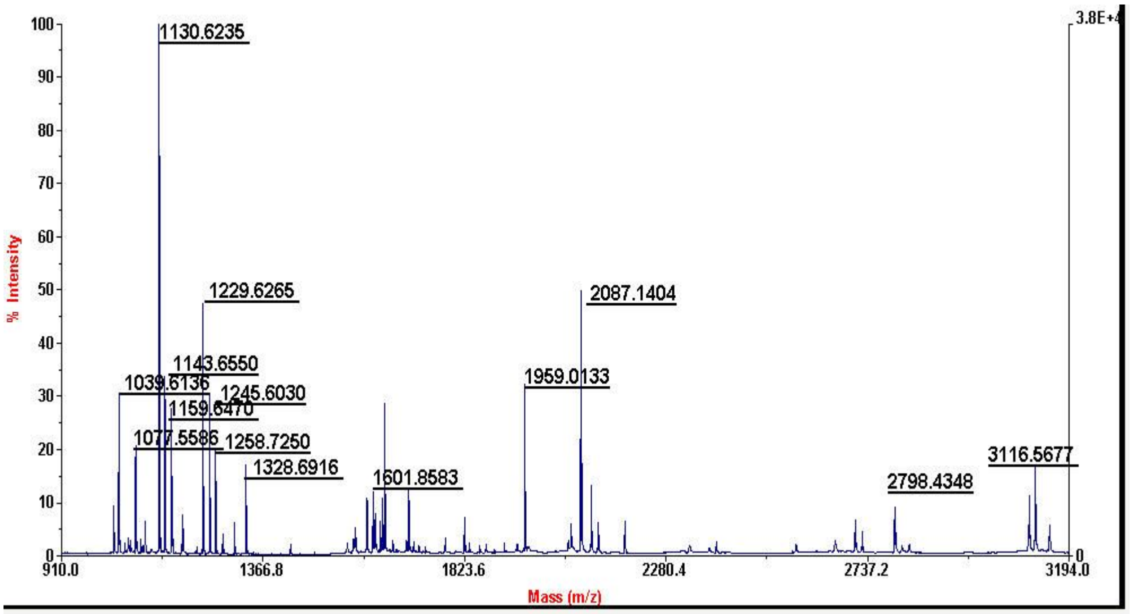
287 Desmin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
17 - 37	2088.2824	2087.2751	2087.0840	0.1911	0	R.TFGGAPGFPLGSPLSSPVFPR.A
79 - 105	2902.6954	2901.6881	2901.4032	0.2848	0	R.TPSSYGAGELLDFSLADAVNQEFLTTR.T
128 - 142	1674.0151	1673.0078	1672.8532	0.1546	0	R.FLEQQNAALAAEVNR.L
151 - 163	1649.0012	1647.9940	1647.8467	0.1472	1	R.VAELYEEELRELR.R
176 - 189	1700.0197	1699.0124	1698.8537	0.1588	1	R.VDVERDNLLDDLQR.L
194 - 212	2245.3428	2244.3355	2244.1386	0.1970	1	K.LQEEIQLKEEAENNLAAFR.A
228 - 240	1561.9963	1560.9890	1560.8511	0.1379	1	R.RIESLNEEIAFLK.K
356 - 369	1528.8535	1527.8463	1527.6954	0.1509	0	R.FASEASGYQDNIAR.L

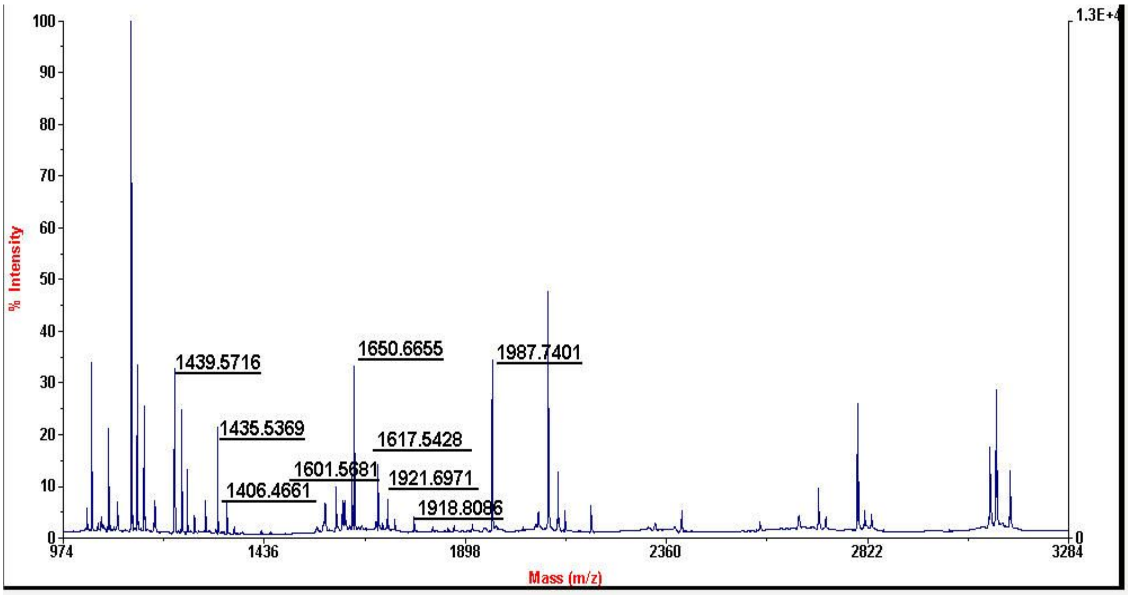
No match to: 1055.5682, 1501.8546, 1690.0887, 1791.0493, 1805.1089, 2444.4930, 2453.4763

288 Tubulin beta-2C chain



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
20 - 46	3116.5677	3115.5604	3115.4159	0.1445	0	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	
47 - 58	1328.6916	1327.6843	1327.6408	0.0435	0	R.INVYYNEATGGK.Y	
63 - 77	1601.8583	1600.8510	1600.8131	0.0379	0	R.AVLVDLEPGTMDSVR.S	
78 - 103	2798.4348	2797.4275	2797.3361	0.0914	0	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	
104 - 121	1959.0133	1958.0060	1957.9745	0.0315	0	K.GHYTEGAELVDSVLDVVR.K	
104 - 122	2087.1404	2086.1331	2086.0695	0.0636	1	K.GHYTEGAELVDSVLDVVRK.E	
155 - 162	1077.5586	1076.5513	1076.5250	0.0263	1	K.IREEYPDR.I	
242 - 251	1130.6235	1129.6162	1129.5880	0.0282	0	R.FPGQLNADLR.K	
242 - 252	1258.7250	1257.7177	1257.6830	0.0348	1	R.FPGQLNADLRK.L	
253 - 262	1143.6550	1142.6477	1142.6270	0.0207	0	K.LAVNMVPFPR.L	
253 - 262	1159.6470	1158.6398	1158.6219	0.0178	0	K.LAVNMVPFPR.L	Oxidation (M)
310 - 318	1039.6136	1038.6064	1038.5862	0.0201	0	R.YLTVAAVFR.G	
381 - 390	1229.6265	1228.6192	1228.5910	0.0282	0	R.ISEQFTAMFR.R	
381 - 390	1245.6030	1244.5957	1244.5860	0.0097	0	R.ISEQFTAMFR.R	Oxidation (M)

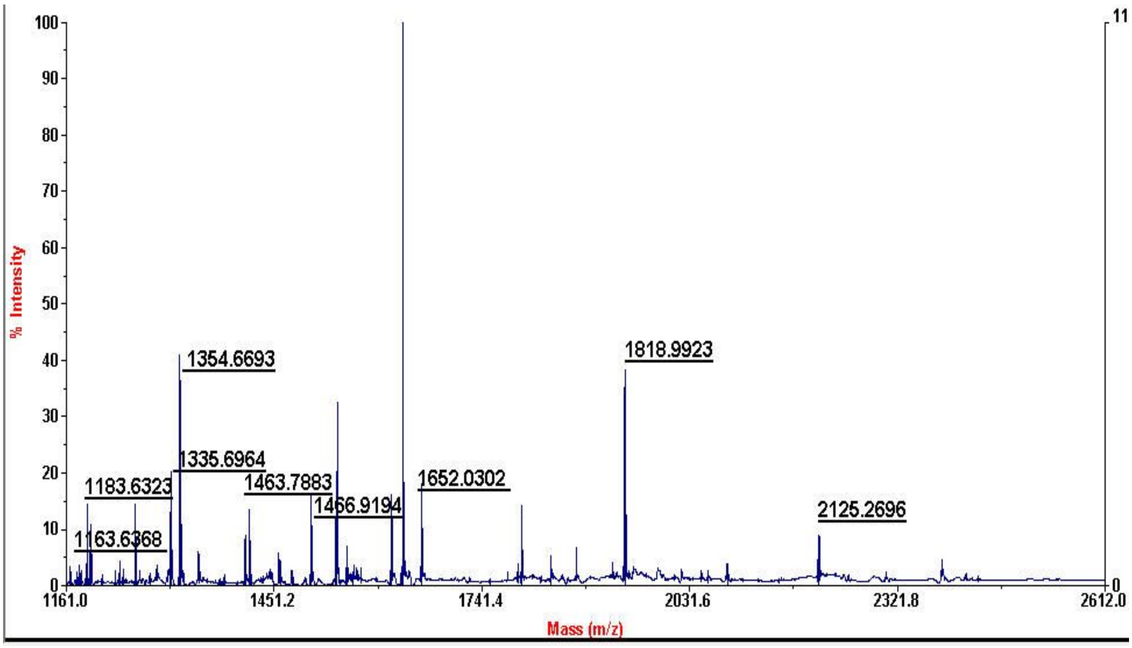
289 ATP synthase subunit beta



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
95 - 109	1650.6655	1649.6582	1649.9101	-0.2519	0	R.LVLEVAQHLGESTVR.T
125 - 143	1918.8086	1917.8013	1918.0888	-0.2875	1	K.VLDSGAPIKIPVGPETLGR.I
226 - 239	1406.4661	1405.4588	1405.6739	-0.2151	0	K.AHGGYSVFAGVGER.T
265 - 279	1601.5681	1600.5609	1600.8031	-0.2423	0	K.VALVYGQMNEPPGAR.A
265 - 279	1617.5428	1616.5355	1616.7981	-0.2625	0	K.VALVYGQMNEPPGAR.A Oxidation (M)
282 - 294	1439.5716	1438.5643	1438.7820	-0.2177	0	R.VALTGLTVAEYFR.D
295 - 310	1921.6971	1920.6898	1920.9581	-0.2683	0	R.DQEGQDVLLFIDNIFR.F
311 - 324	1435.5369	1434.5296	1434.7467	-0.2171	0	R.FTQAGSEVSALLGR.I
388 - 406	1987.7401	1986.7329	1987.0262	-0.2933	0	R.AIAELGIYPAVDPLDSTSR.I

No match to: 1483.4655, 1556.7165, 1831.5580, 2690.9711

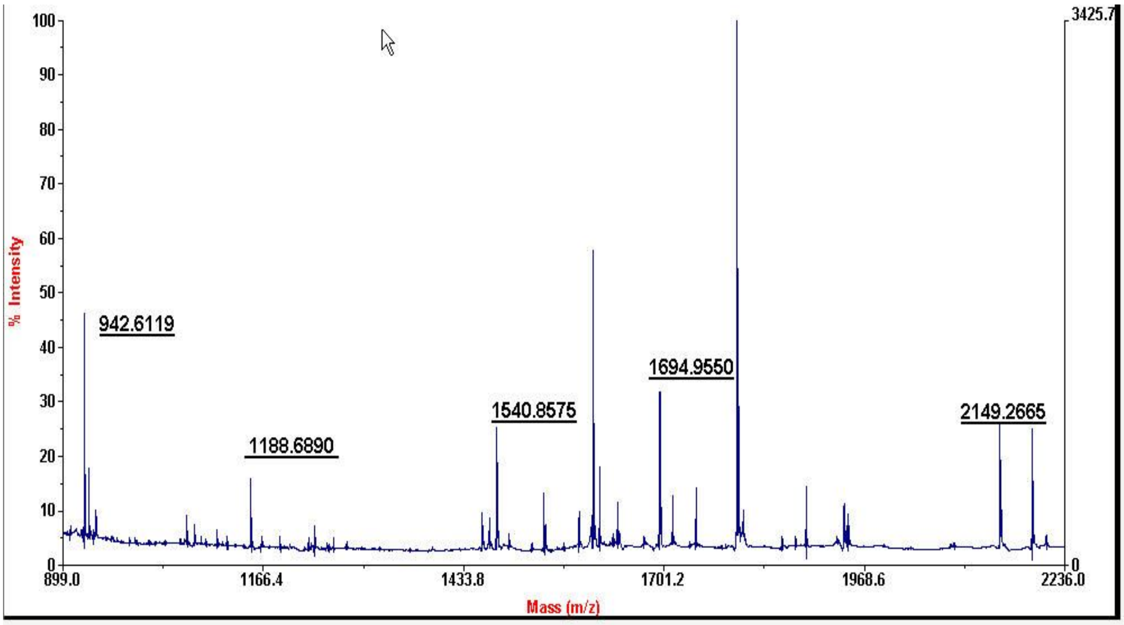
290 Enoyl-CoA hydratase, mitochondrial precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
42 - 56	1652.0302	1651.0230	1650.9529	0.0701	1	R.GKNNTVGLIQLNRPK.A	
44 - 56	1466.9194	1465.9121	1465.8365	0.0756	0	K.NNTVGLIQLNRPK.A	
75 - 92	1818.9923	1817.9850	1817.9047	0.0803	0	K.TFEEDPAVGAIVLTGGDK.A	
119 - 127	1163.6368	1162.6295	1162.5883	0.0412	0	K.HWDHLTQVK.K	
158 - 178	2125.2696	2124.2623	2124.1328	0.1296	0	K.AQFAQPEILIGTIPGAGGTQR.L	
186 - 197	1354.6693	1353.6620	1353.6268	0.0352	0	K.SLAMEMVLTGDR.I	2 Oxidation (M)
262 - 272	1335.6964	1334.6891	1334.6143	0.0749	0	K.LFYSTFATDDR.K	
262 - 273	1463.7883	1462.7810	1462.7092	0.0717	1	K.LFYSTFATDDRK.E	
274 - 283	1183.6323	1182.6250	1182.5703	0.0547	1	K.EGMTAFVEKR.K	Oxidation (M)

No match to: 1293.9213, 1412.7435, 1568.8855, 1591.9106

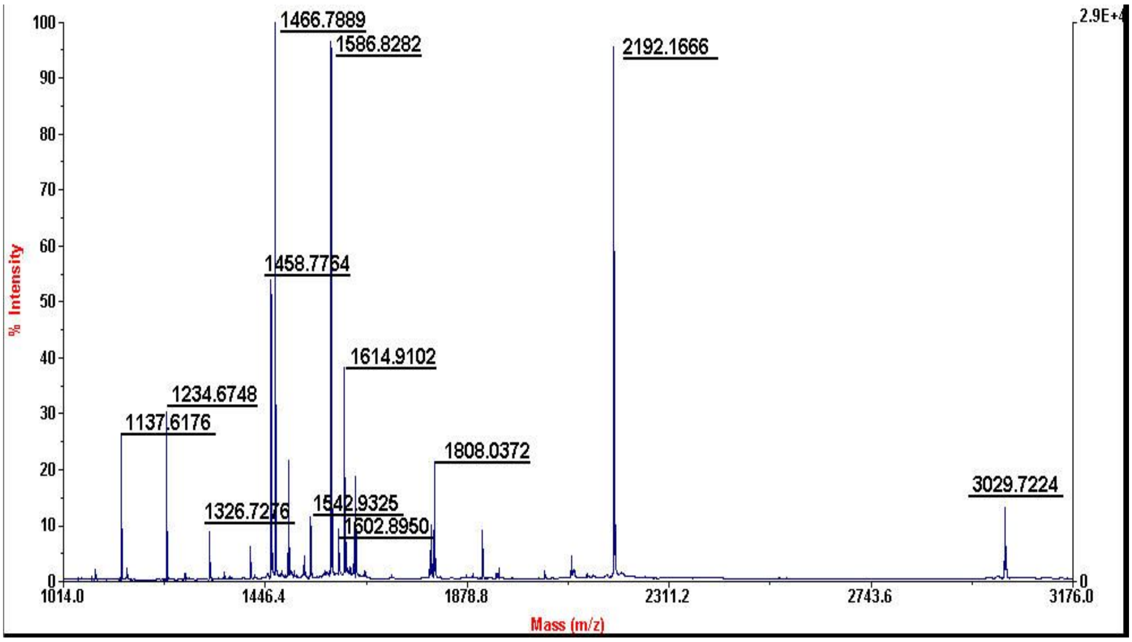
291 Protein-L-isoaspartate(D-aspartate) O-methyltransferase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
25 - 37	1540.8575	1539.8502	1539.7603	0.0899	1	K.TDKVFEVMLATDR.S	Oxidation (M)
82 - 98	1694.9550	1693.9477	1693.8458	0.1019	0	K.ALDVGSGSGILTACFAR.M	
106 - 124	2149.2665	2148.2592	2148.1539	0.1054	1	K.VIGIDHIKELVDDSINNVR.K	
125 - 135	1188.6890	1187.6817	1187.6146	0.0671	1	R.KDDPTLLSSGR.V	
136 - 144	942.6119	941.6046	941.5294	0.0751	0	R.VQLVVGDGR.M	

No match to: 1234.7121, 1604.9159, 1798.0038, 2192.1961

292 Triosephosphate isomerase

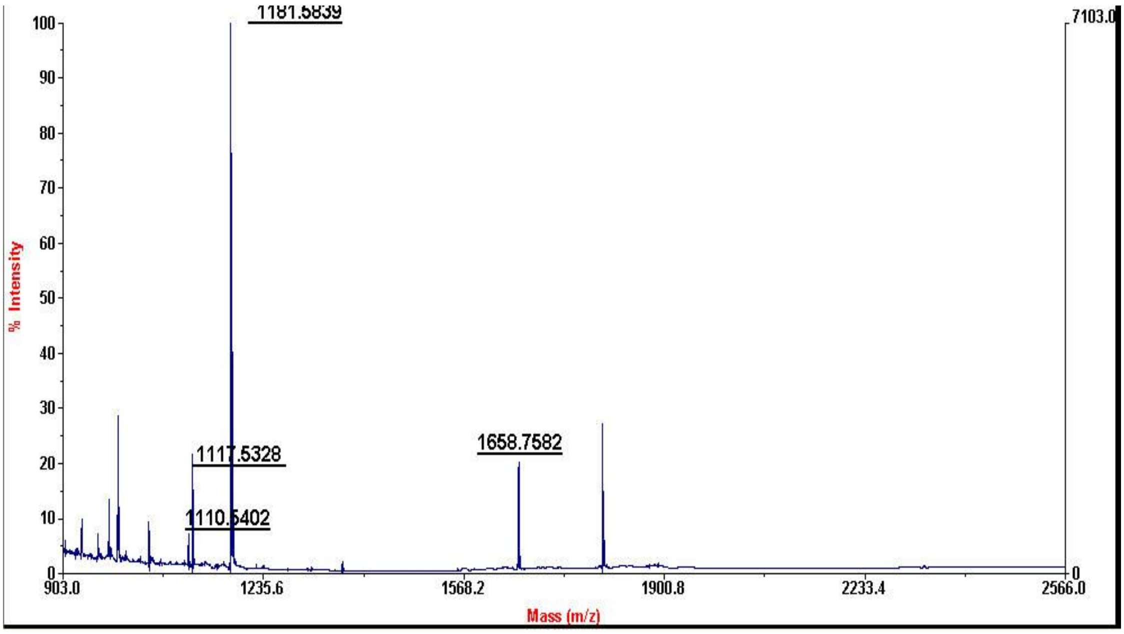


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

7 - 14	954.5298	953.5226	953.4760	0.0466	0	K.FFVGGNWK.M
19 - 33	1542.9325	1541.9252	1541.8777	0.0475	1	R.KQSLGELIGTLNAAK.V
34 - 53	2192.1666	2191.1594	2191.0620	0.0974	0	K.VPADTEVVCAPPTAYIDFAR.Q
60 - 69	1137.6176	1136.6103	1136.5648	0.0455	0	K.IAVAAQNCYK.V
86 - 99	1586.8282	1585.8209	1585.7307	0.0902	0	K.DCGATWVVLGHSER.R
100 - 113	1614.9102	1613.9029	1613.8162	0.0868	1	R.RHVFGESDELIGQK.V
101 - 113	1458.7764	1457.7691	1457.7151	0.0541	0	R.HVFGESDELIGQK.V
114 - 131	1808.0372	1807.0299	1806.9662	0.0638	0	K.VAHALAEGLGVIACIGEK.L
161 - 175	1602.8950	1601.8877	1601.8817	0.0059	0	K.VVLAYEPVWAIGTGK.T
176 - 188	1466.7889	1465.7816	1465.7161	0.0655	0	K.TATPQQAQEVHEK.L
195 - 206	1234.6748	1233.6675	1233.5949	0.0726	0	K.SNVSDAVAQSTR.I
207 - 219	1326.7276	1325.7203	1325.6649	0.0554	0	R.IIYGGSVTGATCK.E
220 - 248	3029.7224	3028.7151	3028.5757	0.1394	0	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q

No match to: 1495.8023, 1638.8637, 1911.0293

293 L-xylulose reductase

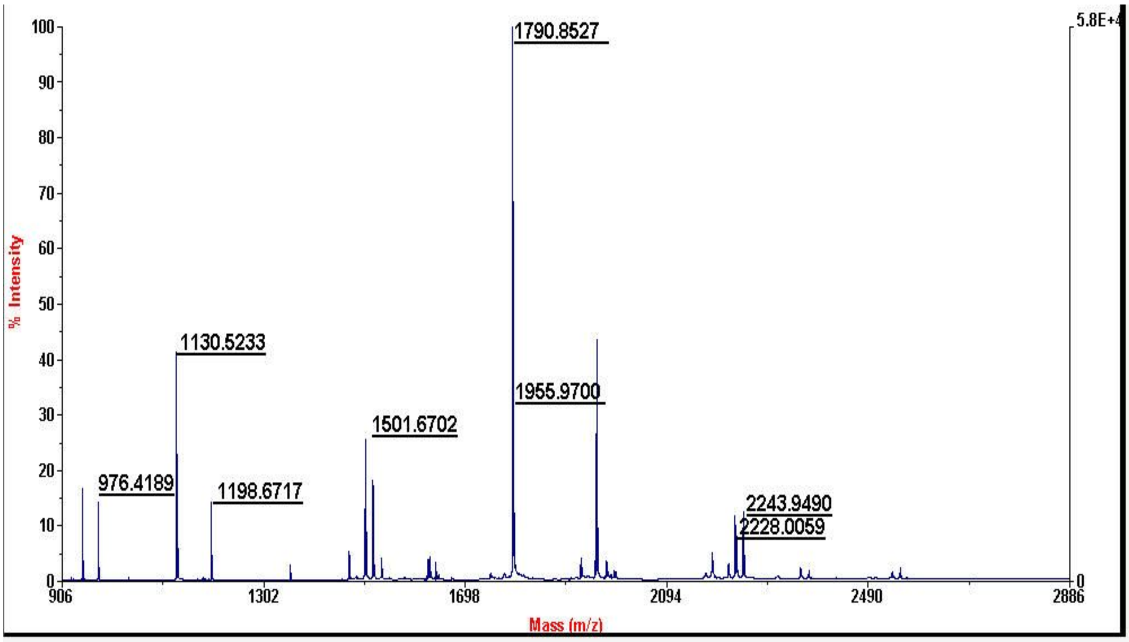


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
22 - 33	1181.5839	1180.5766	1180.6313	-0.0547	0	R.GTVQALHATGAR.V
40 - 49	1117.5328	1116.5255	1116.5775	-0.0520	0	R.TQADLDSLVR.E

126 - 141	1658.7582	1657.7509	1657.8206	-0.0697	0	R.GVPGAIVNVSSQCSQR.A
162 - 171	1110.5402	1109.5329	1109.5903	-0.0574	0	K.VMALELGPHK.I Oxidation (M)

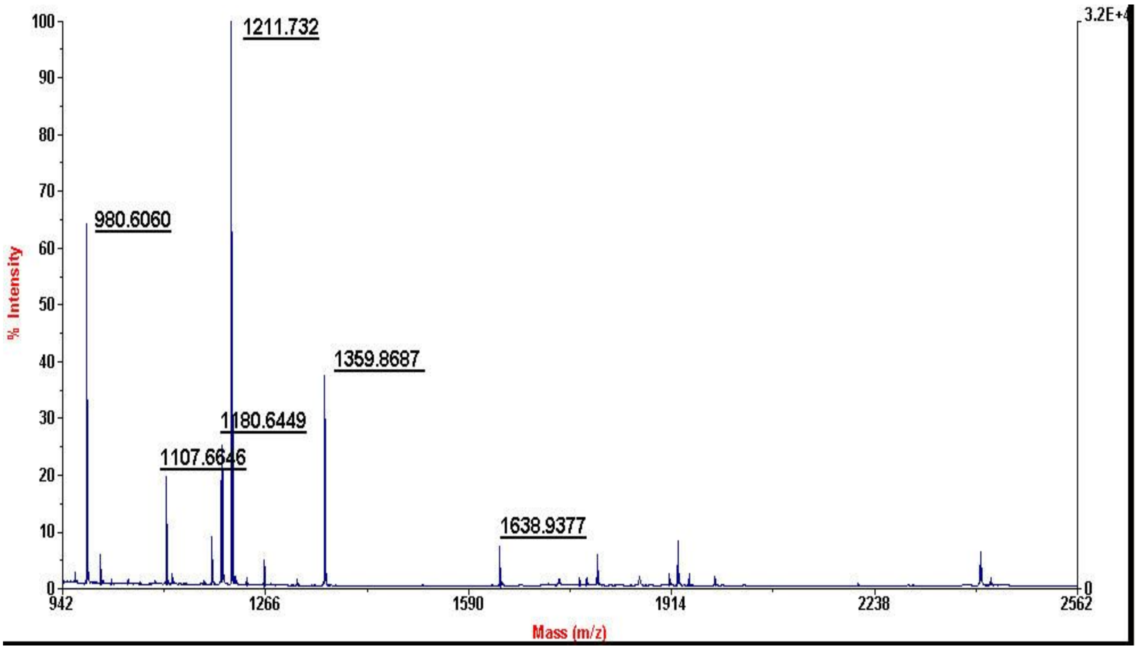
No match to: 979.5130, 994.4676, 1797.7968

294 Actin, gamma-enteric smooth muscle



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 29	976.4189	975.4116	975.4410	-0.0294	0	K.AGFAGDDAPR.A
30 - 40	1198.6717	1197.6644	1197.6982	-0.0338	0	R.AVFPSIVGRPR.H
86 - 96	1501.6702	1500.6629	1500.7262	-0.0633	0	K.IWHHSFYNELR.V
97 - 114	1955.9700	1954.9627	1955.0364	-0.0737	0	R.VAPEEHPTLLTEAPLNPK.A
149 - 178	3196.5423	3195.5350	3195.6023	-0.0673	0	R.TTGIVLDSGDGVTHNVPIYEGYALPHAIMR.L
198 - 207	1130.5233	1129.5160	1129.5404	-0.0244	0	R.GYSFVTTAER.E
240 - 255	1790.8527	1789.8454	1789.8846	-0.0392	0	K.SYELPDGQVITIGNER.F
293 - 313	2228.0059	2226.9987	2227.0579	-0.0592	0	K.DLYANNVLSGGTTMYPGIADR.M
293 - 313	2243.9490	2242.9417	2243.0528	-0.1111	0	K.DLYANNVLSGGTTMYPGIADR.M Oxidation (M)

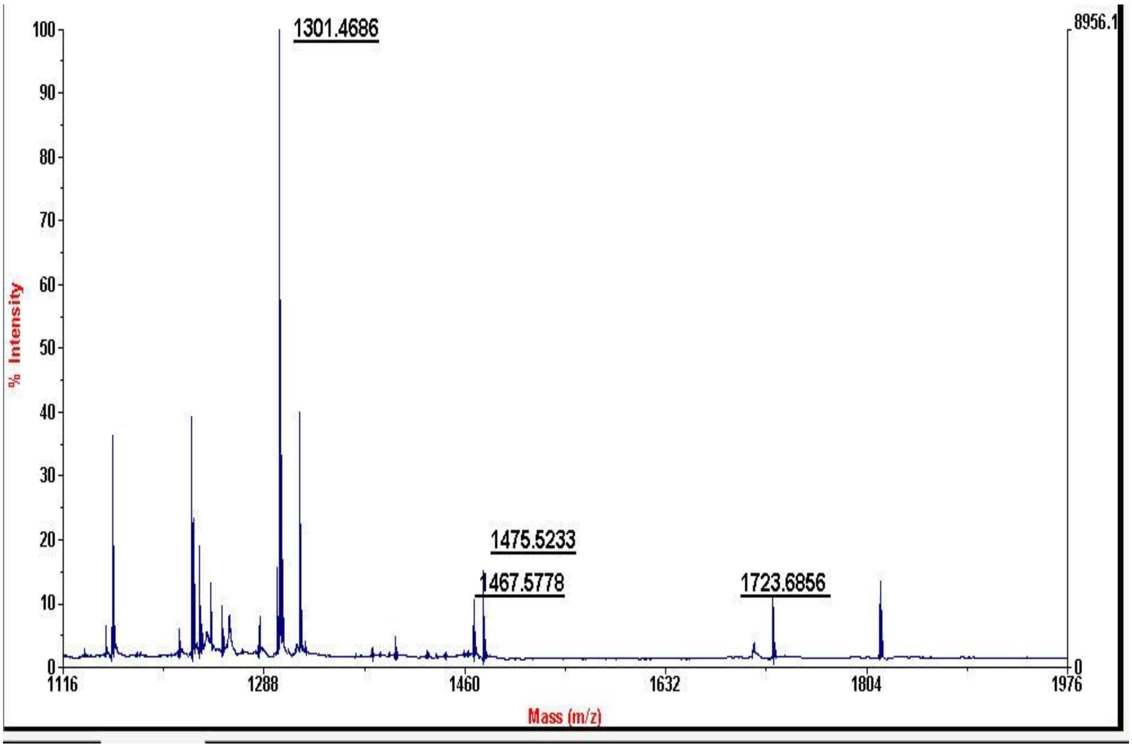
295 Peroxiredoxin-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
8 - 16	980.6060	979.5987	979.5239	0.0747	0	K.IGHPAPNFK.A	
17 - 27	1180.6449	1179.6377	1179.5594	0.0782	0	K.ATAVMPDGQFK.D	Oxidation (M)
94 - 109	1638.9377	1637.9305	1637.8447	0.0858	0	K.QGGLGPMNIPLVSDPK.R	Oxidation (M)
111 - 120	1107.6646	1106.6573	1106.5972	0.0602	0	R.TIAQDYGVLK.A	
129 - 140	1359.8687	1358.8614	1358.7922	0.0692	1	R.GLFIIDDKGILR.Q	
141 - 151	1211.7328	1210.7255	1210.6670	0.0585	0	R.QITVNDLPVGR.S	

No match to: 1002.5594, 1194.7041, 1639.9985, 1794.0713, 1862.1850, 1923.1324, 2405.3781

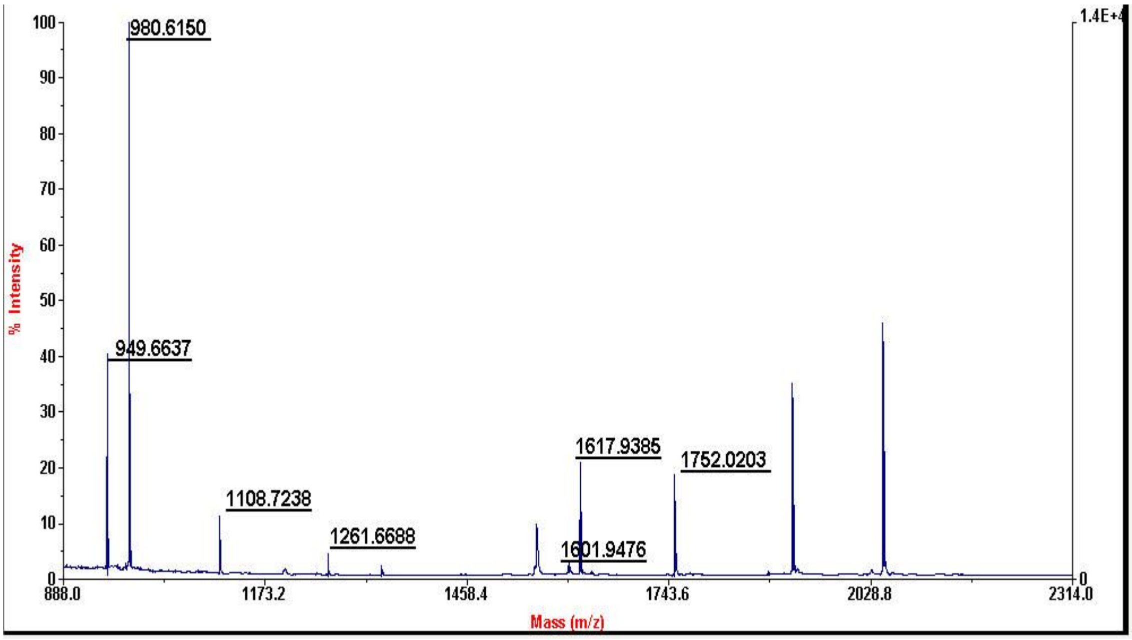
296 Melanoma antigen recognized by T-cells 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 14	1723.6856	1722.6783	1722.8188	-0.1404	1	-.MPREDAHFIYGYPK.K
4 - 15	1467.5778	1466.5705	1466.7194	-0.1488	1	R.EDAHFIYGYPKK.G
73 - 82	1301.4686	1300.4613	1300.5731	-0.1118	1	R.RCPQEGFDHR.D
74 - 85	1475.5233	1474.5160	1474.6259	-0.1099	1	R.CPQEGFDHRDSK.V

No match to: 1012.4647, 1157.4787, 1226.3770, 1232.4459, 1318.4441, 1815.5837

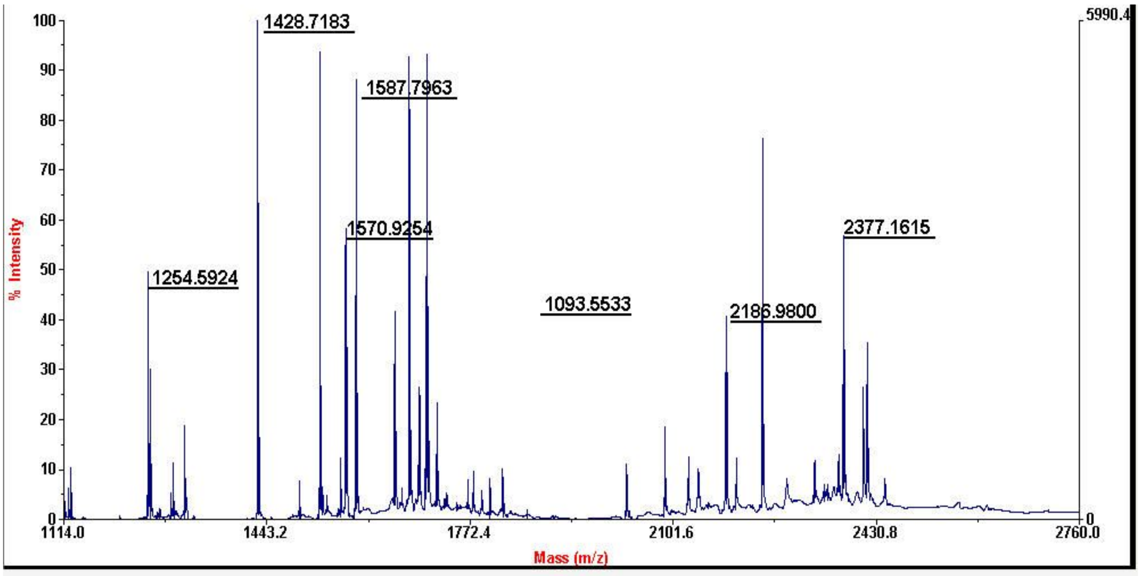
297 Rho GDP-dissociation inhibitor 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
51 - 58	949.6637	948.6564	948.5392	0.1172	1	K.YKEALLGR.V	
128 - 134	980.6150	979.6078	979.4875	0.1202	0	K.YIQHTYR.K	
128 - 135	1108.7238	1107.7165	1107.5825	0.1340	1	K.YIQHTYRK.G	
139 - 152	1601.9476	1600.9403	1600.7555	0.1847	1	K.IDKTDYMVGSYGPR.A	
139 - 152	1617.9385	1616.9313	1616.7505	0.1808	1	K.IDKTDYMVGSYGPR.A	Oxidation (M)
142 - 152	1261.6688	1260.6616	1260.5445	0.1171	0	K.TDYMVGSYGPR.A	Oxidation (M)
153 - 167	1752.0203	1751.0130	1750.8301	0.1829	0	R.AEEYEFLTPVEEAPK.G	

No match to: 1201.8115, 1557.1211, 1918.1466, 2046.2275

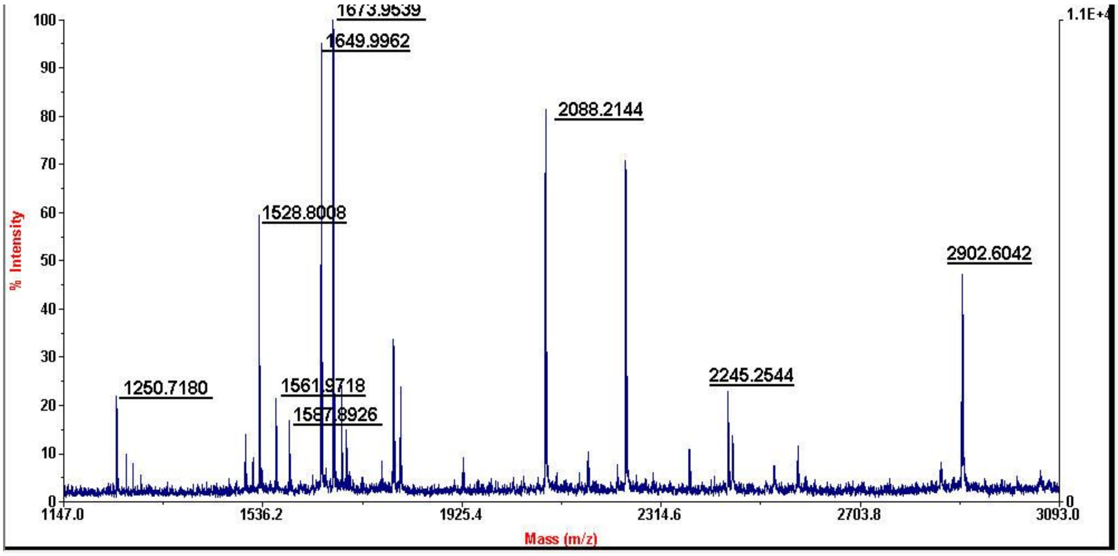
298 Vimentin - Homo sapiens (Human)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
51 - 64	1428.7183	1427.7110	1427.7045	0.0065	0	R.SLYASSPGGVYATR.S
101 - 113	1587.7963	1586.7890	1586.7900	-0.0010	1	R.TNEKVELQELNDR.F
146 - 155	1254.5924	1253.5851	1253.5598	0.0253	0	R.LGDLYEEEMR.E
295 - 304	1093.5533	1092.5460	1092.5200	0.0260	0	K.FADLSEAANR.N
322 - 342	2377.1615	2376.1543	2376.1591	-0.0048	1	R.QVQSLTCEVDALKGTNESLER.Q
346 - 364	2186.9800	2185.9727	2185.9586	0.0141	0	R.EMEENFAVEAANYQDTIGR.L
411 - 424	1570.9254	1569.9181	1569.8878	0.0303	0	R.ISLPLPNFSSLNLR.E

No match to: 1250.6418, 1528.7029, 1648.8830, 1673.8660, 1689.9334, 1701.9140, 1718.8870, 2245.1295, 2306.7200, 2415.2084

299 Desmin

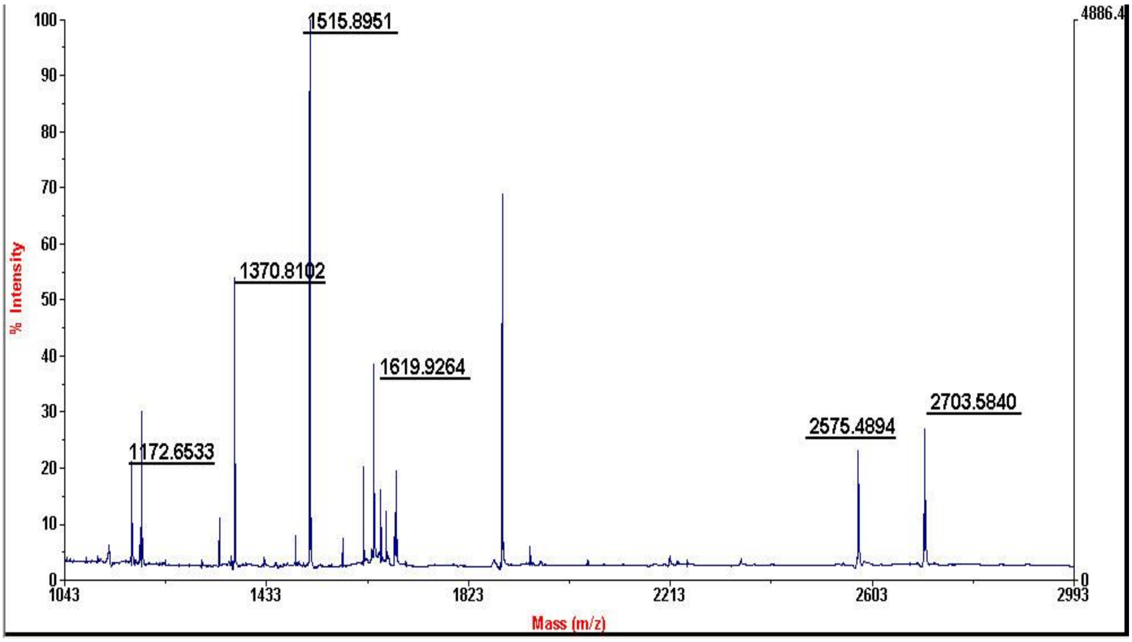


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

17 - 37	2088.2144	2087.2071	2087.0840	0.1231	0	R.TFGGAPGFPLGSPLSSPVFPR.A
79 - 105	2902.6042	2901.5969	2901.4032	0.1937	0	R.TPSSYGAGELLDFSLADAVNQEFLTTR.T
106 - 118	1587.8926	1586.8853	1586.7900	0.0953	1	R.TNEKVELQELNDR.F
128 - 142	1673.9539	1672.9466	1672.8532	0.0934	0	R.FLEQQNAALAAEVNR.L
151 - 160	1250.7180	1249.7107	1249.6190	0.0917	0	R.VAELYEEELR.E
194 - 212	2245.2544	2244.2471	2244.1386	0.1086	1	K.LQEEIQLKEEAENNLAAFR.A
228 - 240	1561.9718	1560.9645	1560.8511	0.1134	1	R.RIESLNEEIAFLK.K
356 - 369	1528.8008	1527.7936	1527.6954	0.0982	0	R.FASEASGYQDNIAR.L
416 - 429	1649.9962	1648.9889	1648.8937	0.0952	0	R.INLPIQTYSALNFR.E

No match to: 1055.5620, 1690.0594, 1791.0010, 1805.0525, 2444.4119

300 Protein disulfide-isomerase A3 precursor

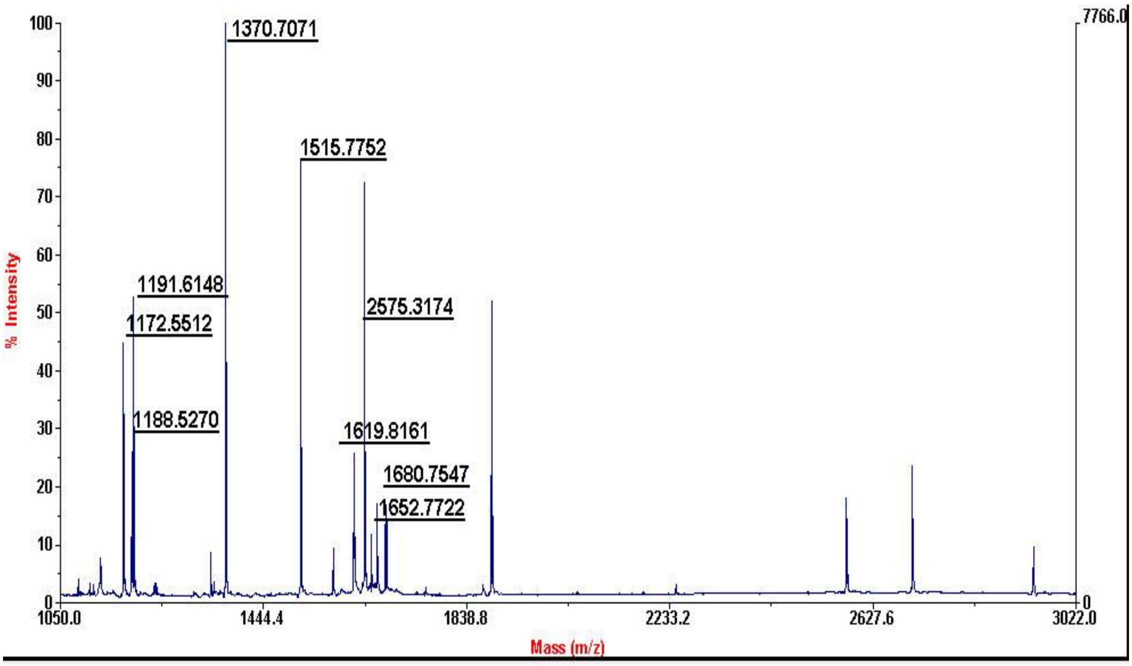


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
259 - 271	1619.9264	1618.9191	1618.7766	0.1425	0	K.DLLIAYYDVDYEK.N
305 - 329	2703.5840	2702.5768	2702.3915	0.1852	1	R.KTFSHELSDFGLESTAGEIPVVAIR.T
306 - 329	2575.4894	2574.4821	2574.2966	0.1855	0	K.TFSHELSDFGLESTAGEIPVVAIR.T

336 - 344	1172.6533	1171.6460	1171.5332	0.1128	0	K.FVMQEEFSR.D
352 - 363	1515.8951	1514.8879	1514.7518	0.1361	1	R.FLQDYFDGNLKR.Y
472 - 482	1370.8102	1369.8029	1369.6878	0.1152	0	R.ELSDFISYLQR.E

No match to: 882.6447, 1190.6483, 1639.8918, 1887.1332

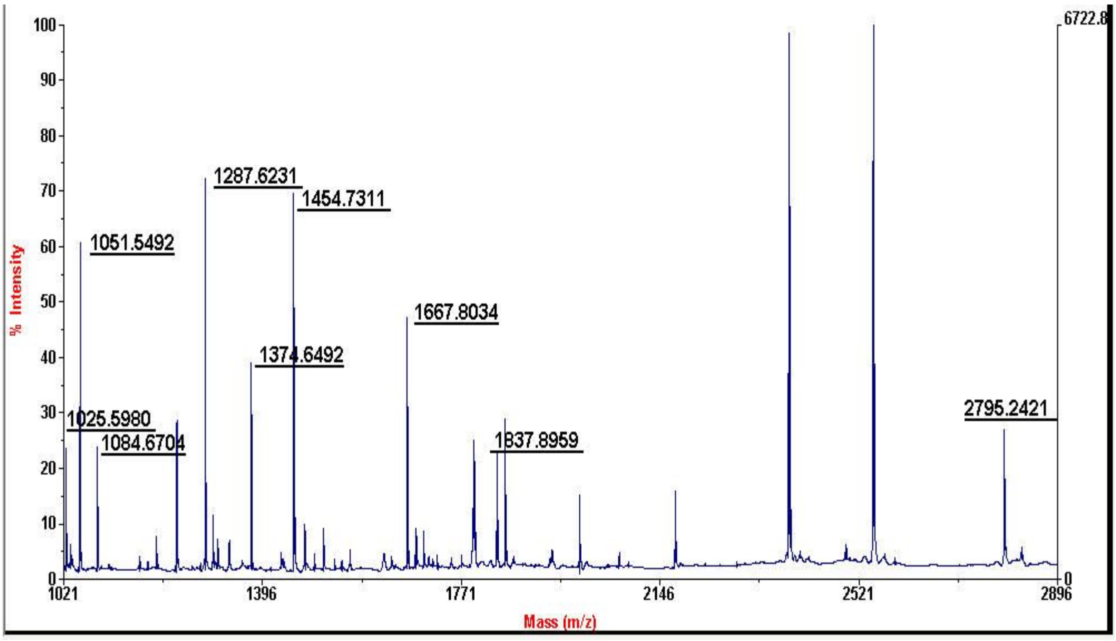
301 Protein disulfide-isomerase A3 precursor (EC 5.3.4.1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
63 - 73	1191.6148	1190.6075	1190.5931	0.0144	0	R.LAPEYEAAATR.L	
105 - 119	1652.7722	1651.7650	1651.7590	0.0059	1	K.IFRDGEEAGAYDGPR.T	
259 - 271	1619.8161	1618.8088	1618.7766	0.0322	0	K.DLLIAYYDVDYEK.N	
306 - 329	2575.3174	2574.3101	2574.2966	0.0135	0	K.TFSHELSDFGLESTAGEIPVVAIR.T	
336 - 344	1172.5512	1171.5439	1171.5332	0.0107	0	K.FVMQEEFSR.D	
336 - 344	1188.5270	1187.5198	1187.5281	-0.0084	0	K.FVMQEEFSR.D	Oxidation (M)
352 - 363	1515.7752	1514.7679	1514.7518	0.0162	1	R.FLQDYFDGNLKR.Y	
434 - 448	1680.7547	1679.7475	1679.7461	0.0014	0	K.MDATANDVPSPYEVR.G	Oxidation (M)
472 - 482	1370.7071	1369.6999	1369.6878	0.0121	0	R.ELSDFISYLQR.E	

No match to: 1127.8829, 1639.7720, 1887.0049, 2702.4085

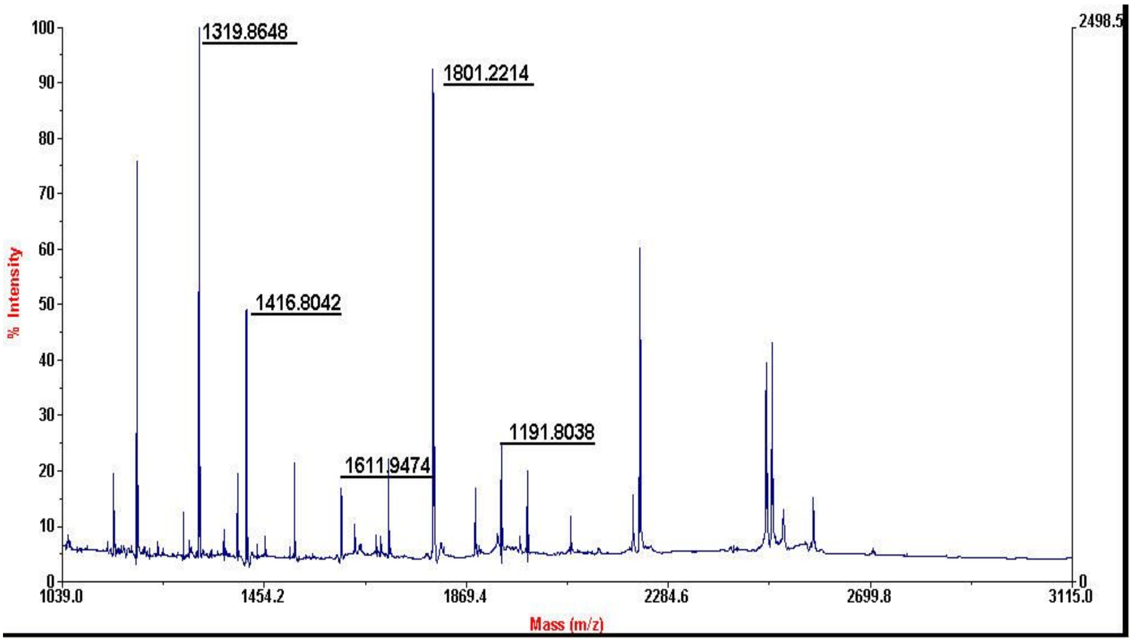
302 Selenium-binding protein 1 –



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
24 - 34	1454.7311	1453.7239	1453.7275	-0.0037	0	R.EEIVYLPCIYR.N
53 - 62	1287.6231	1286.6159	1286.6190	-0.0031	0	K.SPQYCQVIHR.L
94 - 103	1084.6704	1083.6631	1083.6652	-0.0021	0	K.LVLPSLISSR.I
196 - 211	1837.8959	1836.8886	1836.9305	-0.0419	0	R.HNVMISTEWAAPNVLR.D
212 - 235	2795.2421	2794.2348	2794.2776	-0.0428	0	R.DGFNPADVEAGLYGSHLYVWDWQR.H
246 - 254	1025.5980	1024.5907	1024.5917	-0.0010	0	K.DGLIPLEIR.F
321 - 333	1667.8034	1666.7962	1666.8256	-0.0294	0	R.FLYFSNWLHGDLR.Q
334 - 344	1374.6492	1373.6419	1373.6688	-0.0269	0	R.QYDISDPQRPR.L
412 - 419	1051.5492	1050.5420	1050.5498	-0.0079	0	K.QFYPDLIR.E

No match to: 1050.4935, 1233.6409, 1792.9402, 1852.9382, 1993.9445, 2389.1240, 2547.3186

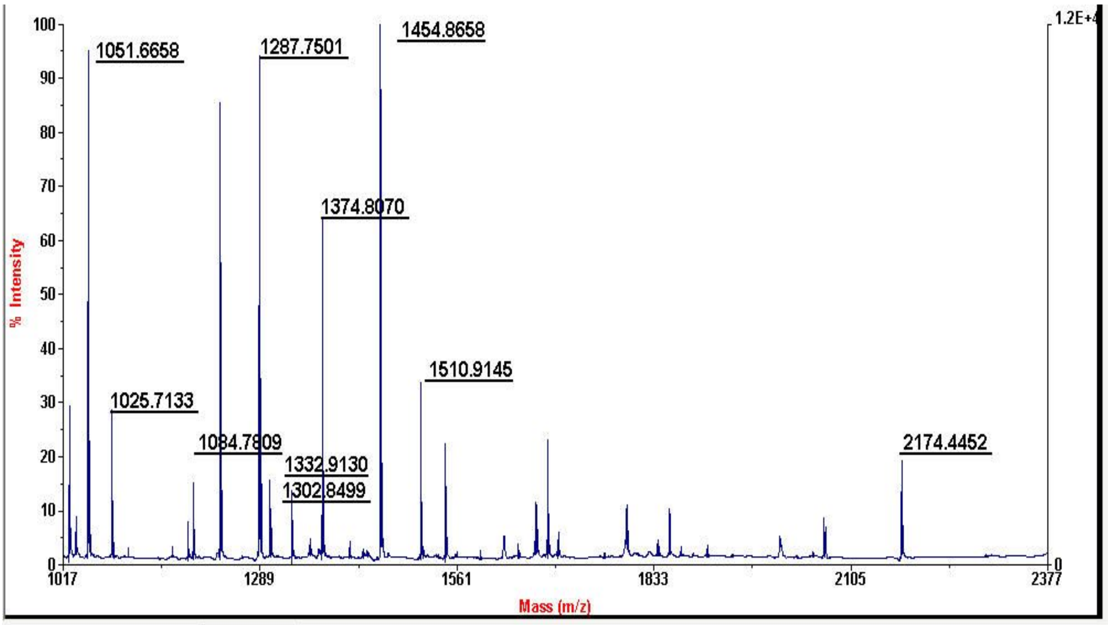
303 Tryptophanyl-tRNA synthetase, cytoplasmic



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
97 - 106	1191.8038	1190.7965	1190.6659	0.1306	1	K.GIDYDKLIVR.F
123 - 133	1319.8648	1318.8575	1318.7007	0.1568	0	R.ATGQRPHHFLR.R
257 - 264	972.6428	971.6355	971.5189	0.1167	0	K.HVTFNQVK.G
265 - 277	1416.8042	1415.7970	1415.6391	0.1578	0	K.GIFGFTDSDCIGK.I
375 - 388	1611.9474	1610.9401	1610.7550	0.1852	1	K.HAFSGGRDTIEEHR.Q
433 - 448	1801.2214	1800.2141	1800.0257	0.1884	0	K.ALIEVLQPLIAEHQAR.R

No match to: 1817.4960, 1941.1535, 2225.2916, 2485.5710, 2497.5064, 2884.7486

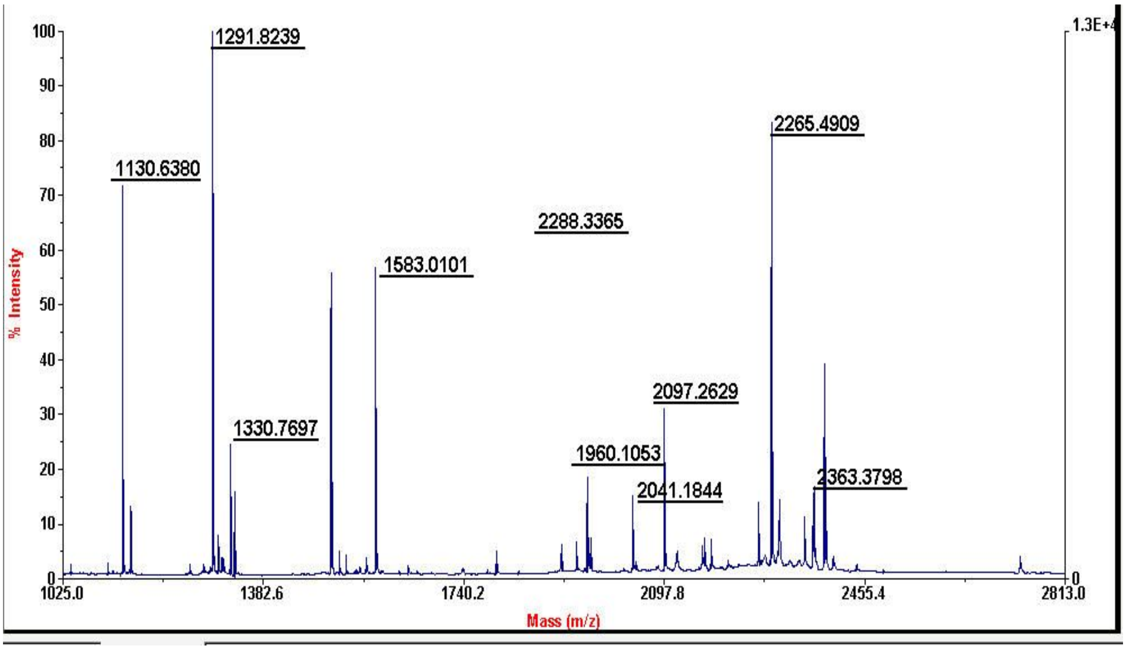
304 Selenium-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
24 - 34	1454.8658	1453.8585	1453.7275	0.1310	0	R.EEIVYLPCIYR.N
53 - 62	1287.7501	1286.7429	1286.6190	0.1239	0	K.SPQYCQVIHR.L
94 - 103	1084.7809	1083.7736	1083.6652	0.1084	0	K.LVLPSLISSR.I
161 - 174	1510.9145	1509.9073	1509.7715	0.1357	0	K.GGFVLLDGETFEVK.G
236 - 254	2174.4452	2173.4379	2173.2470	0.1909	1	R.HEIVQTLSLKDGLIPLEIR.F
246 - 254	1025.7133	1024.7061	1024.5917	0.1144	0	K.DGLIPLEIR.F
334 - 344	1374.8070	1373.7997	1373.6688	0.1310	0	R.QYDISDPQRPR.L
345 - 357	1332.9130	1331.9057	1331.7813	0.1244	0	R.LTGQLFLGGSIVK.G
412 - 419	1051.6658	1050.6586	1050.5498	0.1087	0	K.QFYPDLIR.E
449 - 460	1302.8499	1301.8427	1301.7092	0.1335	0	K.EPLGPALAHELR.Y

No match to: 1024.6773, 1233.7809, 1544.8767, 1794.1485, 2389.3680, 2459.2942, 2547.6053

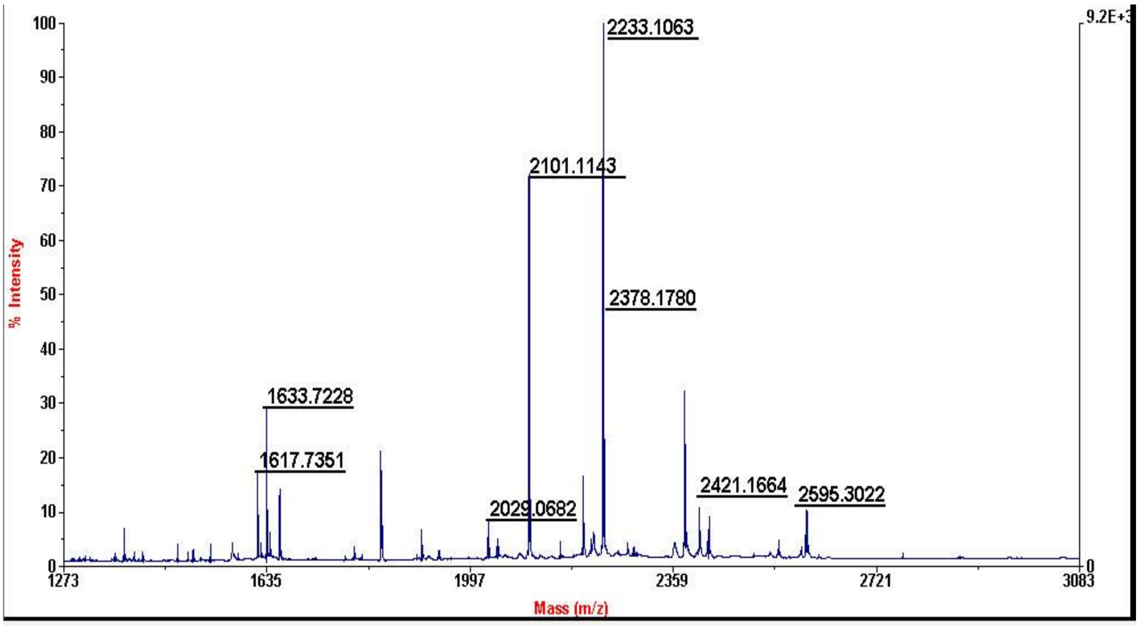
305 T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta) - Homo sapiens (Human)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
90 - 111	2288.3365	2287.3292	2287.1544	0.1748	0	R.VQDDEVGDGTTSVTVLAAELLR.E
121 - 131	1291.8239	1290.8167	1290.7197	0.0970	0	K.IHPQTIIAGWR.E
139 - 156	1960.1053	1959.0980	1958.9698	0.1283	1	R.EALLSSAVDHGSDEVKFR.Q
205 - 223	2041.1844	2040.1771	2040.0415	0.1356	1	K.LGGSLADSYLDEGFLLDKK.I
285 - 293	1130.6380	1129.6307	1129.5451	0.0856	0	K.HGINCFINR.Q
323 - 342	2097.2629	2096.2556	2096.1154	0.1402	0	R.LALVTGGEIASTFDHPELVK.L
377 - 388	1330.7697	1329.7625	1329.6524	0.1100	0	R.GATQQILDEAER.S
445 - 466	2363.3798	2362.3725	2362.1838	0.1887	0	R.MLPTIIADNAGYDSADLVAQLR.A
Oxidation (M)						
502 - 516	1583.0101	1582.0028	1581.9090	0.0938	0	R.QVLLSAAEAAEVILR.V
502 - 522	2265.4909	2264.4836	2264.3103	0.1733	1	R.QVLLSAAEAAEVILRVDNIIK.A

No match to: 1323.8287, 1502.8708, 2302.2760, 2383.2739

306 Succinyl-CoA:3-ketoacid-coenzyme A transferase 1

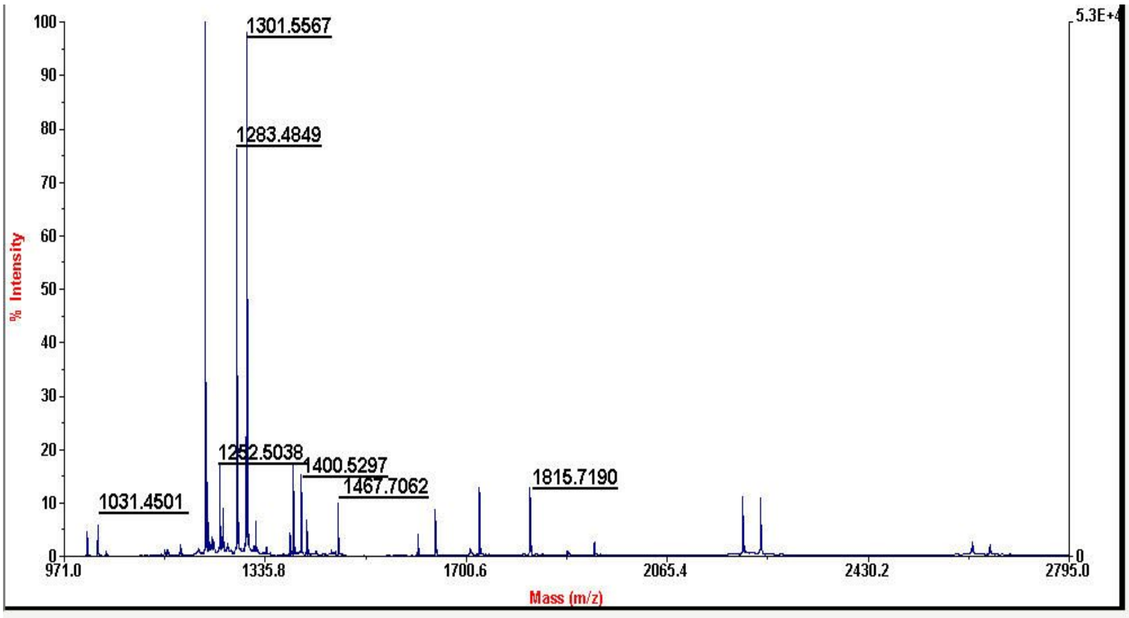


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
84 - 104	2101.1143	2100.1071	2100.1328	-0.0257	0	K.GLTAVSNNAGVDNFGLGLLLR.S
111 - 124	1617.7351	1616.7278	1616.7141	0.0138	0	R.MVSSYVGENAEFER.Q
111 - 124	1633.7228	1632.7156	1632.7090	0.0066	0	R.MVSSYVGENAEFER.Q Oxidation (M)
125 - 144	2233.1063	2232.0991	2232.1274	-0.0283	0	R.QYLSGELEVELTPQGTLAER.I
147 - 173	2595.3022	2594.2949	2594.3017	-0.0068	0	R.AGGAGVPAFYTPTGYGTLVQEGGSPIK.Y
191 - 211	2378.1780	2377.1707	2377.1954	-0.0247	0	R.EFNGQHFILEEAITGDFALVK.A
237 - 268	3560.8074	3559.8001	3559.8199	-0.0197	0	K.AAETTVVEVEEIVDIGAFAPEDIHIPQIYVHR.L
369 - 390	2421.1664	2420.1592	2420.1570	0.0022	0	K.ETVTILPGASFFSSDESFAMIR.G Oxidation (M)
483 - 500	2029.0682	2028.0609	2028.0779	-0.0170	0	K.GLTLIELWEGLTVDDVQK.S

No match to: 1656.8658, 1838.0517, 2198.1634

307

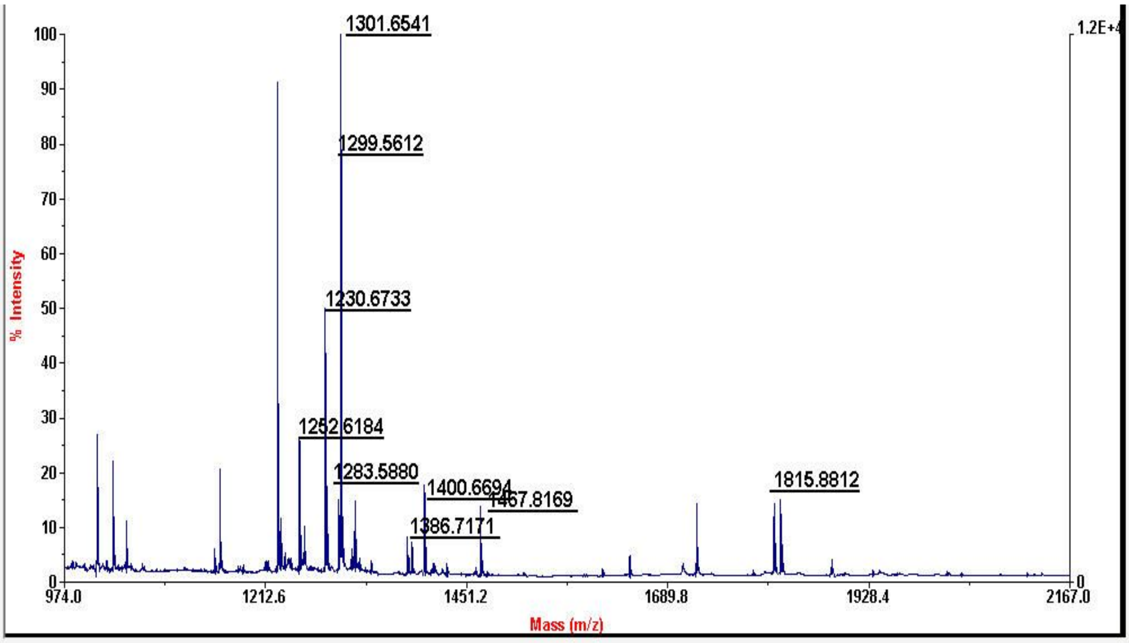
Apolipoprotein A-I precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
48 - 64	1815.7190	1814.7117	1814.8435	-0.1318	1	K.DSGRDYVSQFEGSALGK.Q
52 - 64	1400.5297	1399.5225	1399.6620	-0.1395	0	R.DYVSQFEGSALGK.Q
121 - 130	1252.5038	1251.4965	1251.6136	-0.1170	0	K.VQPYLDDFQK.K
132 - 140	1283.4849	1282.4776	1282.5652	-0.0875	0	K.WQEEMELYR.Q
143 - 155	1467.7062	1466.6990	1466.7841	-0.0851	1	K.VEPLRAELQEGAR.Q
165 - 173	1031.4501	1030.4429	1030.5117	-0.0688	0	K.LSPLGEEMR.D
185 - 195	1301.5567	1300.5494	1300.6411	-0.0917	0	R.THLAPYSDELR.Q

No match to: 1226.4522, 1644.6477, 1723.8209, 1823.7850, 2170.8224

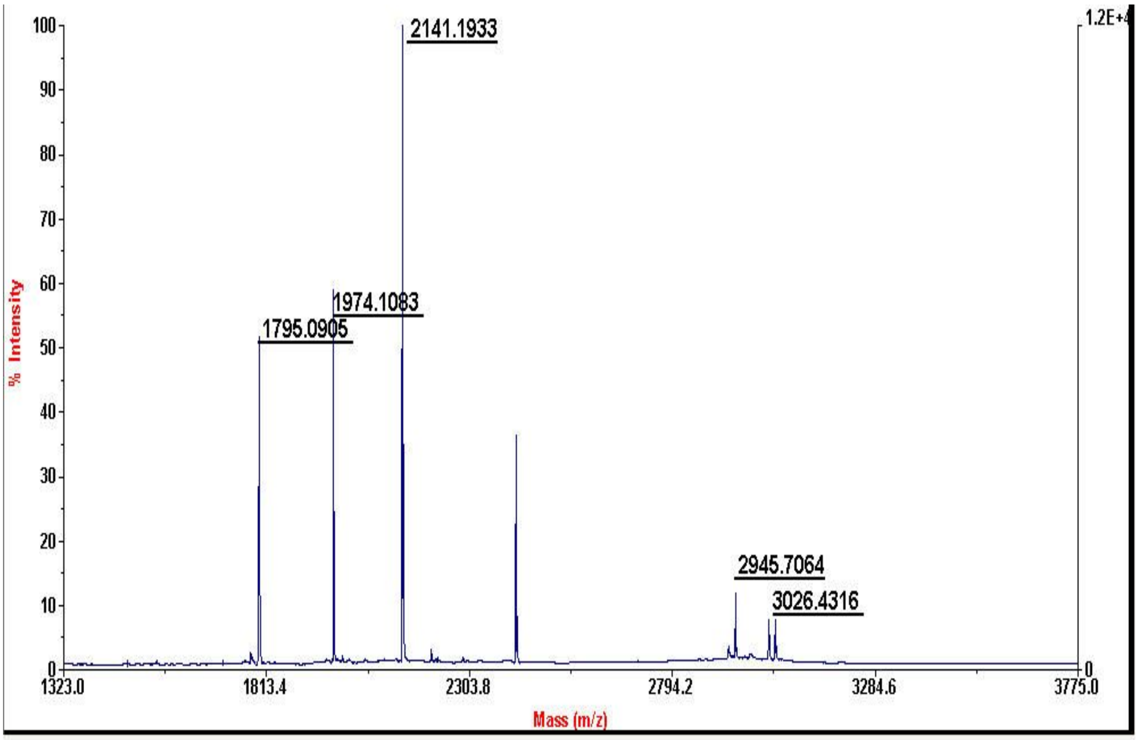
308 Apolipoprotein A-I precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
48 - 64	1815.8812	1814.8739	1814.8435	0.0304	1	K.DSGRDYVSQFEGSALGK.Q	
52 - 64	1400.6694	1399.6621	1399.6620	0.0002	0	R.DYVSQFEGSALGK.Q	
84 - 101	2202.1559	2201.1486	2201.1117	0.0369	1	K.LREQLGPVTQEFWDNLEK.E	
121 - 130	1252.6184	1251.6111	1251.6136	-0.0025	0	K.VQPYLDDFQK.K	
132 - 140	1283.5880	1282.5807	1282.5652	0.0155	0	K.WQEEMELYR.Q	
132 - 140	1299.5612	1298.5539	1298.5601	-0.0062	0	K.WQEEMELYR.Q	Oxidation (M)
143 - 155	1467.8169	1466.8096	1466.7841	0.0255	1	K.VEPLRAELQEGAR.Q	
185 - 195	1301.6541	1300.6468	1300.6411	0.0057	0	R.THLAPYSDELR.Q	
240 - 250	1230.6733	1229.6661	1229.7020	-0.0359	0	R.QGLLPVLESFK.V	
251 - 262	1386.7171	1385.7098	1385.7078	0.0020	0	K.VSFLSALEEYTK.K	

No match to: 1226.5516, 1644.7983, 1723.9666, 2234.1630

309 Inosine triphosphate pyrophosphatase

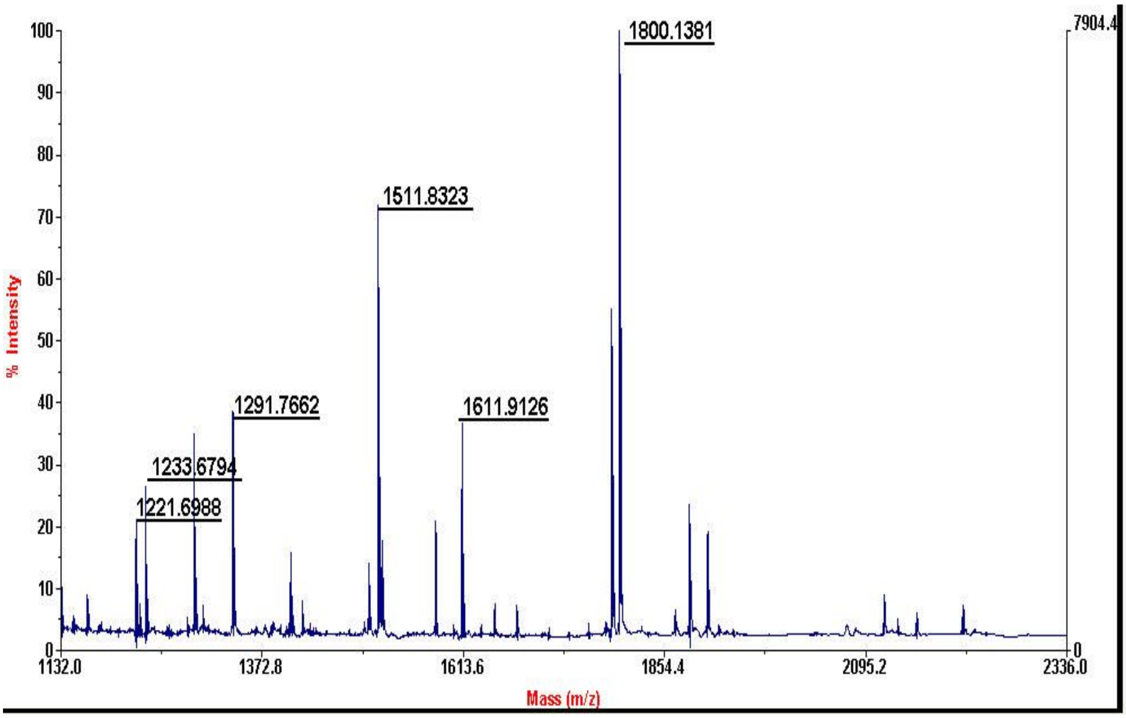


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
40 - 56	1974.1083	1973.1011	1972.9629	0.1381	0	K.IDLPEYQGEPDEISIQK.C

63 - 89	2945.7064	2944.6991	2944.4827	0.2164	0	R.QVQGPVLVEDTCLCFNALGGLPGPYIK.W 2
95 - 110	1795.0905	1794.0832	1793.9676	0.1157	0	K.LKPEGLHQLLAGFEDK.S
111 - 130	2141.1933	2140.1860	2140.0259	0.1601	0	K.SAYALCTFALSTGDPSQPVR.L
145 - 169	3026.4316	3025.4243	3025.1994	0.2250	0	R.GCQDFGWDPCFQPDGYEQTYAEMPK.A 2

No match to: 1941.6862, 2415.5070

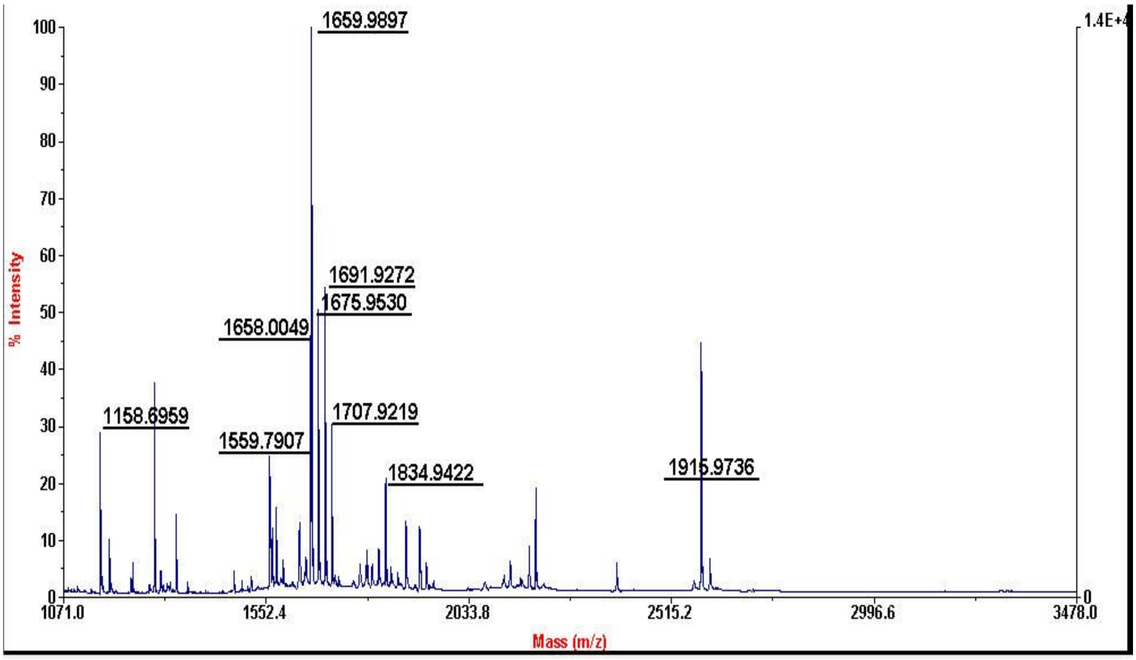
310 Protein-glutamine gamma-glutamyltransferase 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
541 - 550	1221.6988	1220.6915	1220.6475	0.0440	0	K.SVPLCILYEK.Y
551 - 562	1511.8323	1510.8250	1510.7449	0.0801	1	K.YRDCLTESNLIK.V
565 - 580	1800.1381	1799.1308	1799.0192	0.1116	0	R.ALLVEPVINSYLLAER.D
581 - 590	1233.6794	1232.6721	1232.6288	0.0433	0	R.DLYLENPEIK.I
635 - 649	1611.9126	1610.9053	1610.8039	0.1014	0	K.TVEIPDPVEAGEEVK.V
664 - 674	1291.7662	1290.7589	1290.7183	0.0406	1	K.LVVNFESDKLK.A

No match to: 1337.8052, 1500.7771, 1516.8400, 1790.9977, 1884.0707

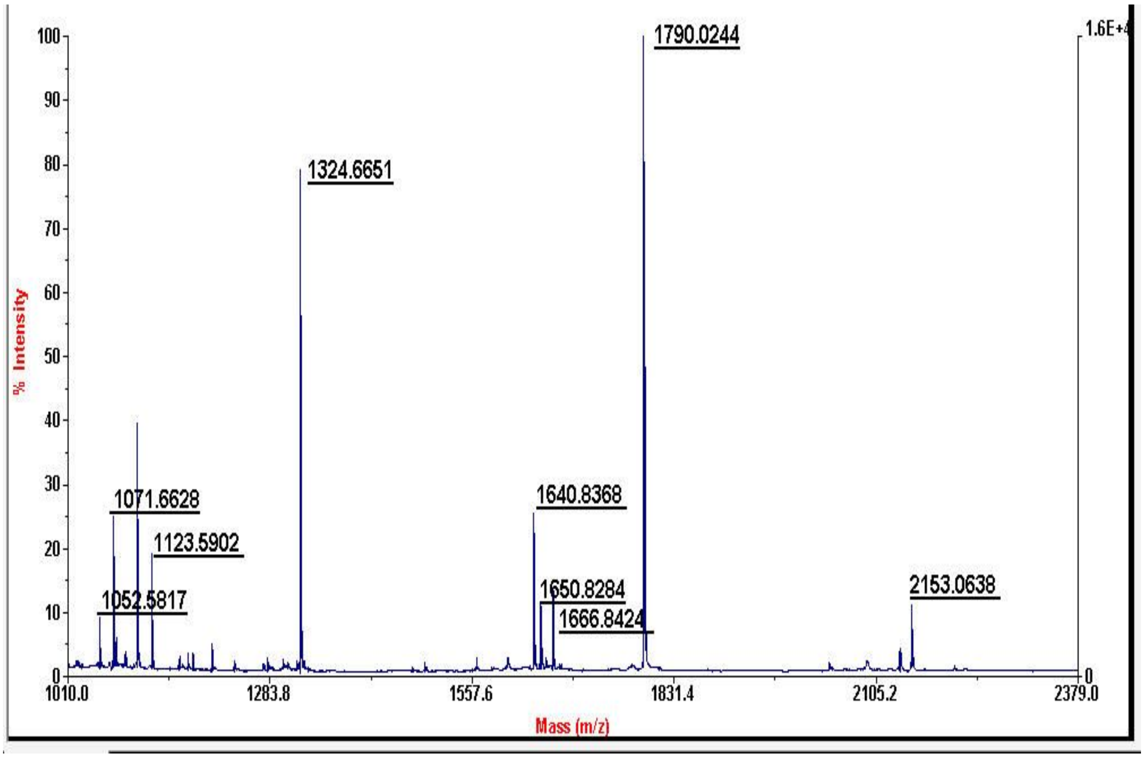
311 Protein DJ-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
13 - 27	1675.9530	1674.9457	1674.7957	0.1500	0	K.GAEEMETVIPVDVMR.R
13 - 27	1691.9272	1690.9199	1690.7906	0.1293	0	K.GAEEMETVIPVDVMR.R Oxidation (M)
13 - 27	1707.9219	1706.9146	1706.7855	0.1291	0	K.GAEEMETVIPVDVMR.R 2 Oxidation (M)
33 - 48	1658.0049	1656.9976	1656.8618	0.1358	1	K.VTVAGLAGKDPVQCSR.D
49 - 63	1659.9897	1658.9824	1658.8185	0.1639	1	R.DVVICPDASLEDAKK.E
90 - 98	1158.6959	1157.6886	1157.6040	0.0846	1	K.EILKEQENR.K
131 - 145	1834.9422	1833.9349	1833.7410	0.1939	1	K.DKMMNGGHYTYSENR.V 2 Oxidation (M)
133 - 145	1559.7907	1558.7834	1558.6293	0.1541	0	K.MMNGGHYTYSENR.V
133 - 148	1915.9736	1914.9663	1914.8352	0.1311	1	K.MMNGGHYTYSENRVEK.D

No match to: 1286.7776, 1337.8561, 1560.7556, 1631.1474, 1690.8460, 1835.8773, 1884.1276, 2071.8029, 2192.1176, 2584.5565

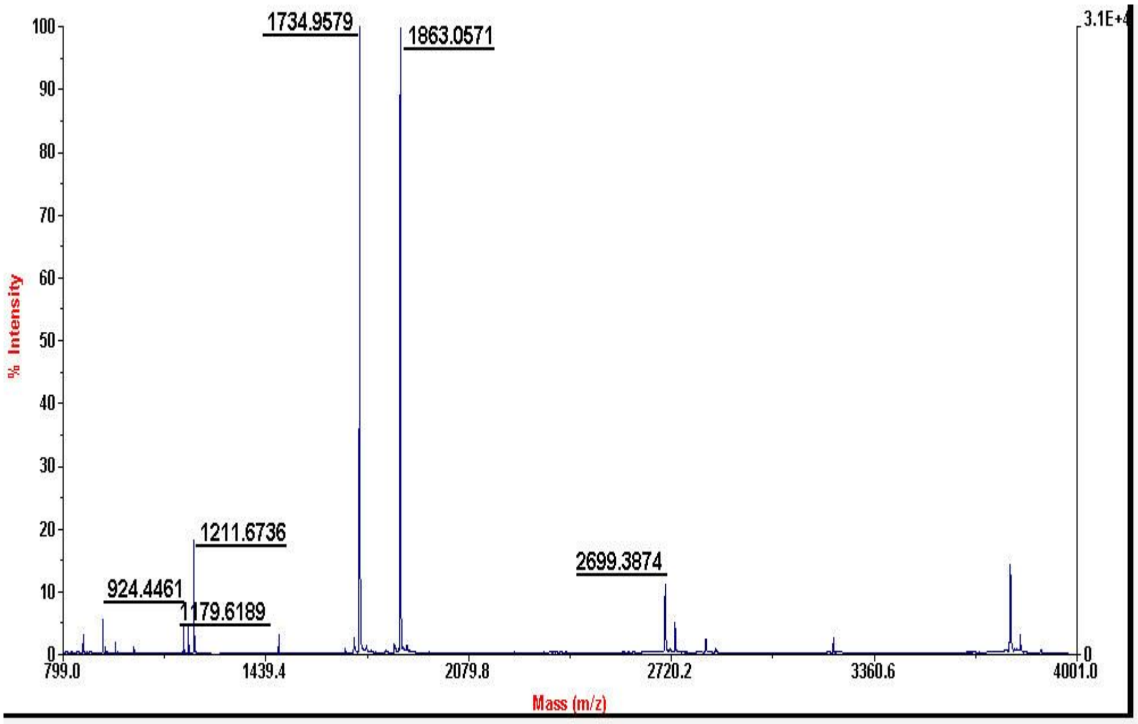
312 Heme-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
24 - 34	1324.6651	1323.6578	1323.5942	0.0636	1	K.GDKEEVAYEER.A
41 - 56	1790.0244	1789.0171	1788.9258	0.0914	0	K.FATVEVTDKPVDEALR.E
62 - 72	1123.5902	1122.5829	1122.5669	0.0160	1	K.VAKYAGGTNDK.G
104 - 118	1640.8368	1639.8295	1639.7842	0.0453	0	R.IPNQFQSDPPAPSDK.S
126 - 140	1650.8284	1649.8211	1649.7759	0.0451	0	R.EGITVYSMQFGGYAK.E
126 - 140	1666.8424	1665.8351	1665.7709	0.0642	0	R.EGITVYSMQFGGYAK.E Oxidation (M)
153 - 162	1052.5817	1051.5744	1051.5298	0.0446	0	R.AALEGTATYR.G
163 - 180	2153.0638	2152.0566	2151.9394	0.1172	0	R.GDIYFCTGYDPPMKPYGR.R ; Oxidation (M)
181 - 188	1071.6628	1070.6556	1070.6236	0.0319	1	R.RNEIWLLK.T

No match to: 988.4994, 1103.6719, 1204.7390, 1649.8310, 2093.6726

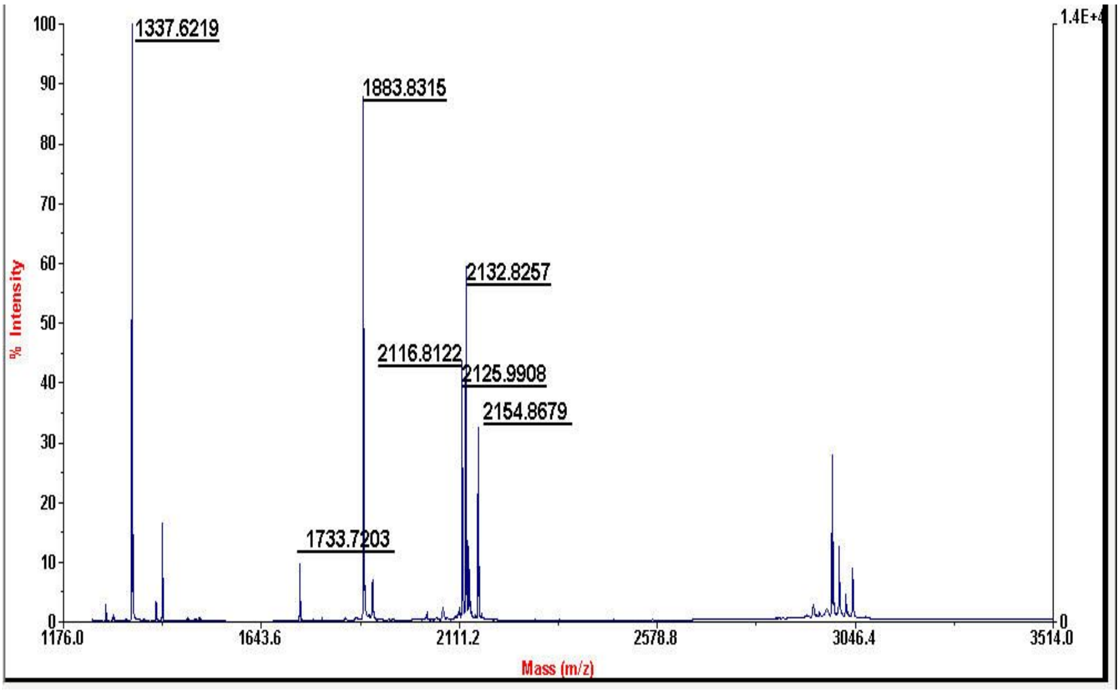
313 Peroxiredoxin-2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
68 - 91	2699.3874	2698.3801	2698.3537	0.0263	0	K.LGCEVLGVSVDSQFTHLAWINTPR.K
92 - 109	1863.0571	1862.0498	1862.0625	-0.0127	1	R.KEGGLGPLNIPLLADVTR.R
93 - 109	1734.9579	1733.9506	1733.9676	-0.0169	0	K.EGGLGPLNIPLLADVTR.R
110 - 119	1179.6189	1178.6116	1178.6295	-0.0179	1	R.RLSEDYGVLK.T
120 - 127	924.4461	923.4388	923.4348	0.0040	0	K.TDEGIAYR.G
140 - 150	1211.6736	1210.6663	1210.6670	-0.0007	0	R.QITVNDLPVGR.S

No match to: 1194.6230, 2731.3888

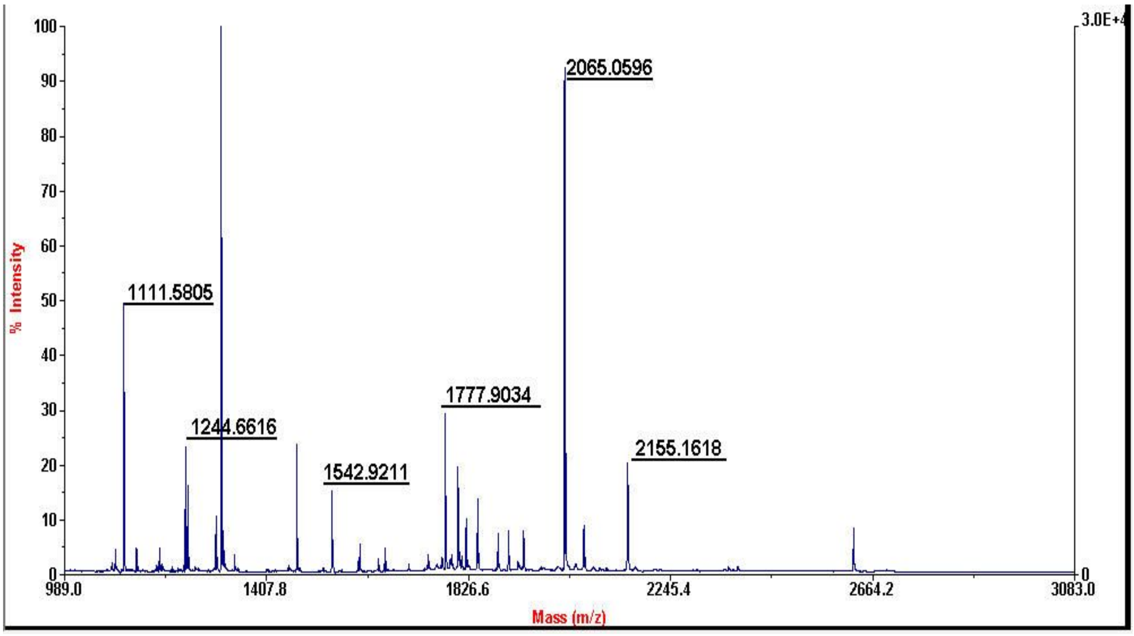
314 Glutathione S-transferase P



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 12	1337.6219	1336.6146	1336.7180	-0.1034	0	M.PPYTVVYFPVR.G
31 - 45	1733.7203	1732.7130	1732.8519	-0.1389	0	K.EEVVTVETWQEGSLK.A
56 - 71	1883.8315	1882.8242	1882.9425	-0.1183	0	K.FQDGDLTLYQSNTILR.H
83 - 101	2116.8122	2115.8049	2115.9743	-0.1693	0	K.DQQEAALVDMVNDGVEDLR.C
83 - 101	2132.8257	2131.8185	2131.9692	-0.1507	0	K.DQQEAALVDMVNDGVEDLR.C
Oxidation (M)						
104 - 121	2154.8679	2153.8606	2154.0521	-0.1914	1	K.YISLIYTNYEAGKDDYVK.A
122 - 141	2125.9908	2124.9835	2125.1531	-0.1697	0	K.ALPGQLKPFETLLSQNQGGK.T

No match to: 1408.6463, 1904.8148, 2948.1962, 2991.2528

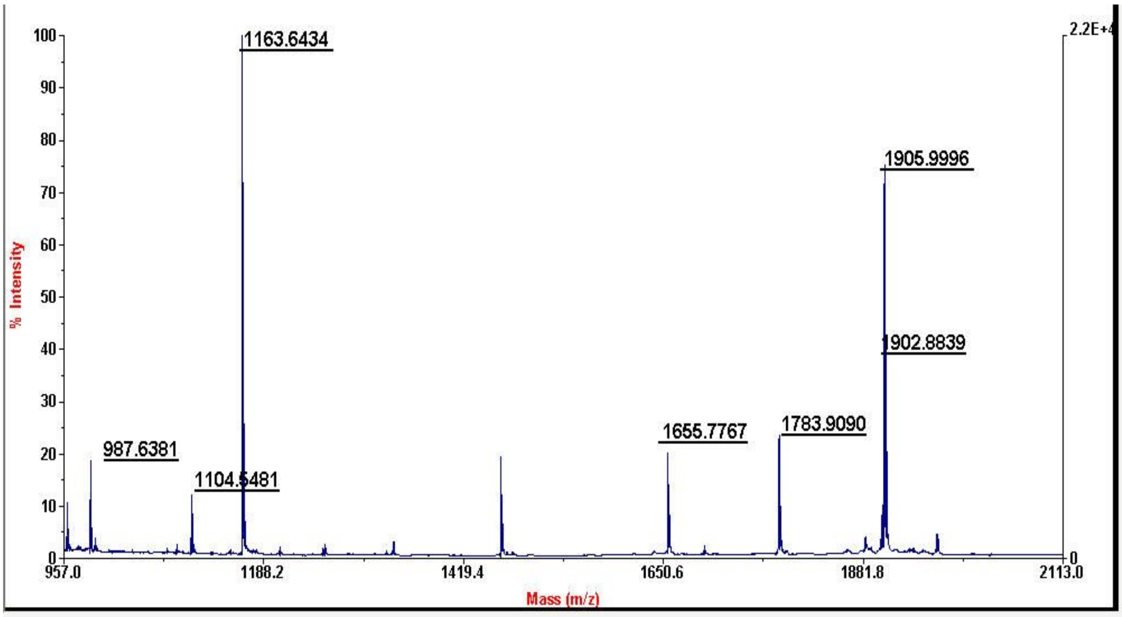
315 Annexin A2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
29 - 47	2155.1618	2154.1545	2154.0593	0.0952	1	K.AYTNFDAERDALNIETAIK.T
50 - 63	1542.9211	1541.9138	1541.8413	0.0725	0	K.GVDEVTIVNILTNR.S
69 - 77	1111.5805	1110.5733	1110.5458	0.0275	0	R.QDIAFAYQR.R
120 - 135	1777.9034	1776.8962	1776.8564	0.0398	0	K.GLGTDEDSLIEIICSR.T
136 - 145	1244.6616	1243.6543	1243.6156	0.0387	0	R.TNQELQEINR.V
179 - 196	2065.0596	2064.0523	2063.9760	0.0763	1	R.RAEDGSVIDYELIDQDAR.D

No match to: 1239.6332, 1302.6840, 1313.7809, 1469.8793, 1804.9165, 1820.9023, 1887.0702, 2025.1821, 2623.3790

316 Heat-shock protein beta-1

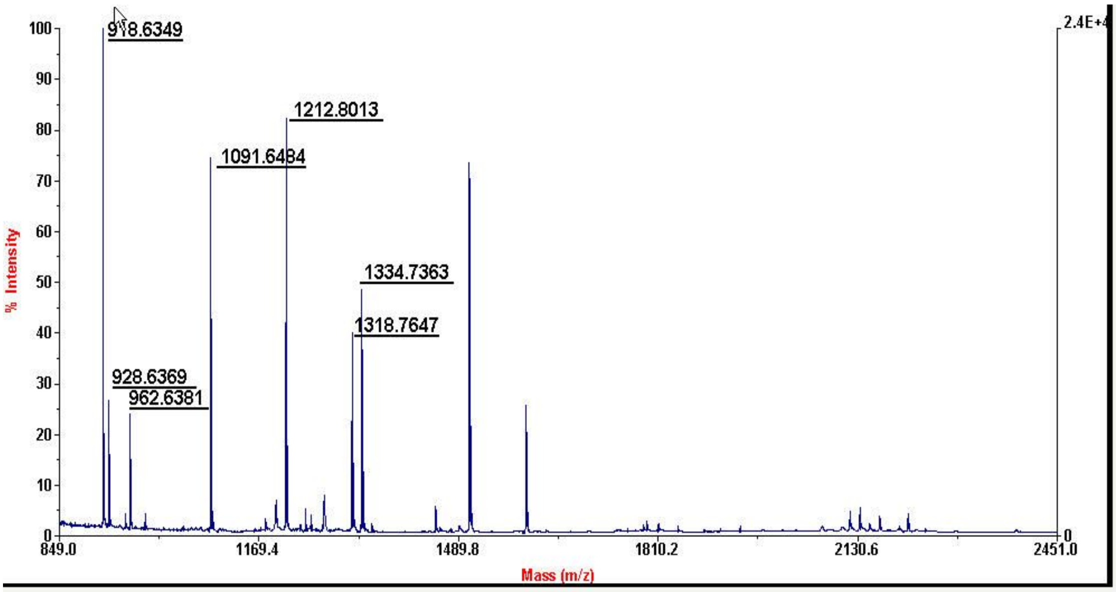


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

5 - 12	987.6381	986.6309	986.6025	0.0283	1	R.RVPFSLLR.G
13 - 27	1902.8839	1901.8766	1901.8598	0.0168	1	R.GPSWDPFRDWYPHSR.L
21 - 27	960.4469	959.4396	959.4250	0.0146	0	R.DWYPHSR.L
28 - 37	1163.6434	1162.6361	1162.6135	0.0226	0	R.LFDQAFGLPR.L
97 - 112	1783.9090	1782.9018	1782.9152	-0.0135	0	R.VSLDVNHFAPDELTVK.T
124 - 136	1655.7767	1654.7694	1654.7448	0.0247	1	K.HEERQDEHGYISR.C
128 - 136	1104.5481	1103.5409	1103.4996	0.0413	0	R.QDEHGYISR.C
172 - 188	1905.9996	1904.9923	1904.9843	0.0079	0	K.LATQSNEITIPVTFESR.A

No match to: 1462.8064

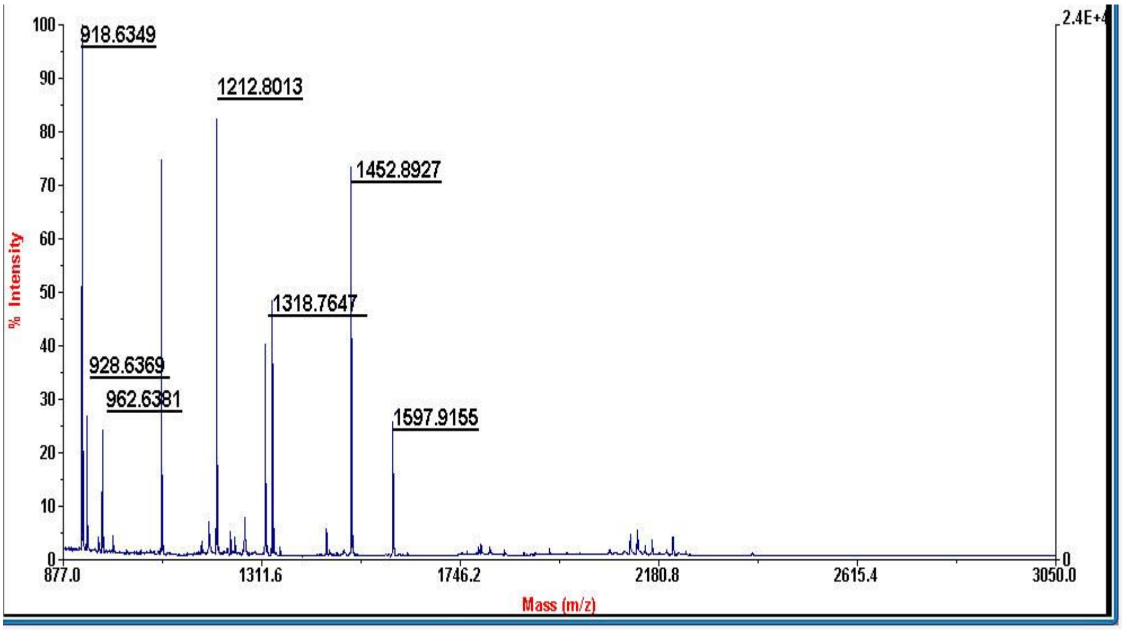
317 Growth factor receptor-bound protein 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
70 - 78	1091.6484	1090.6411	1090.5441	0.0971	1	K.AEEMLSKQR.H	
77 - 86	1212.8013	1211.7940	1211.6523	0.1417	1	K.QRHDGAFLIR.E	
79 - 86	928.6369	927.6296	927.4926	0.1370	0	R.HDGAFLIR.E	
143 - 149	918.6349	917.6277	917.5083	0.1194	0	R.NQQIFLR.D	
196 - 207	1318.7647	1317.7574	1317.5707	0.1867	0	K.GACHGQTGMFPR.N	
196 - 207	1334.7363	1333.7290	1333.5656	0.1634	0	K.GACHGQTGMFPR.N	; Oxidation (M)
208 - 215	962.6381	961.6308	961.4981	0.1327	0	R.NYVTPVNR.N	

No match to: 1195.7212, 1274.2056, 1452.8927, 1506.9538, 1597.9155, 2211.3992

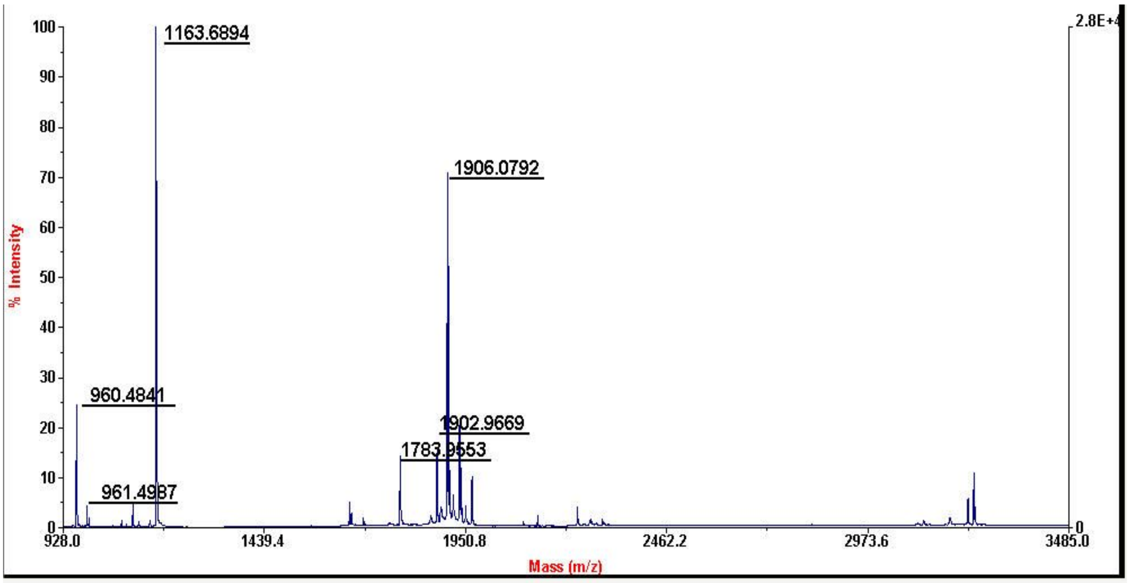
318 CRSP complex subunit 6



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
151 - 162	1212.8013	1211.7940	1211.7601	0.0339	1	K.KSLAGAAQILLK.G	
407 - 415	962.6381	961.6308	961.4869	0.1439	0	R.LSGPQAFDK.N	
437 - 443	928.6369	927.6296	927.5403	0.0893	1	K.HIFLRSR.A	
442 - 454	1318.7647	1317.7574	1317.7000	0.0574	1	R.SRAAATIDSLASR.I	
607 - 614	918.6349	917.6277	917.4454	0.1822	0	K.SDVLQDNK.W	
607 - 619	1597.9155	1596.9082	1596.8008	0.1074	1	K.SDVLQDNKWSHLR.G	
639 - 651	1452.8927	1451.8854	1451.7074	0.1780	0	K.MELLMSALSPCLL.-	2 Oxidation (M)

No match to: 1091.6484, 1195.7212, 1274.2056, 1334.7363, 1506.9538, 2211.3992

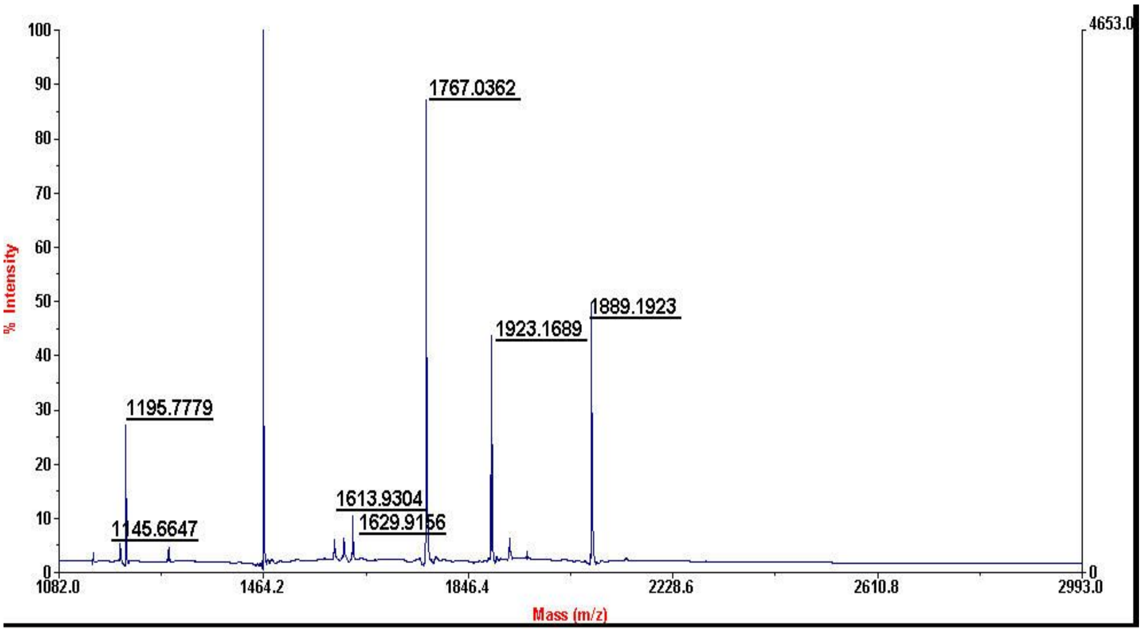
319 Heat-shock protein beta-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
13 - 20	961.4987	960.4914	960.4454	0.0461	0	R.GPSWDPFR.D
13 - 27	1902.9669	1901.9596	1901.8598	0.0998	1	R.GPSWDPFRDWYPHSR.L
21 - 27	960.4841	959.4768	959.4250	0.0518	0	R.DWYPHSR.L
28 - 37	1163.6894	1162.6821	1162.6135	0.0686	0	R.LFDQAFGLPR.L
97 - 112	1783.9553	1782.9480	1782.9152	0.0328	0	R.VSLDVNHFAPDELTVK.T
172 - 188	1906.0792	1905.0719	1904.9843	0.0876	0	K.LATQSNEITIPVTFESR.A

No match to: 1165.6920, 1878.0678, 1934.8966, 1938.8909, 1966.8783

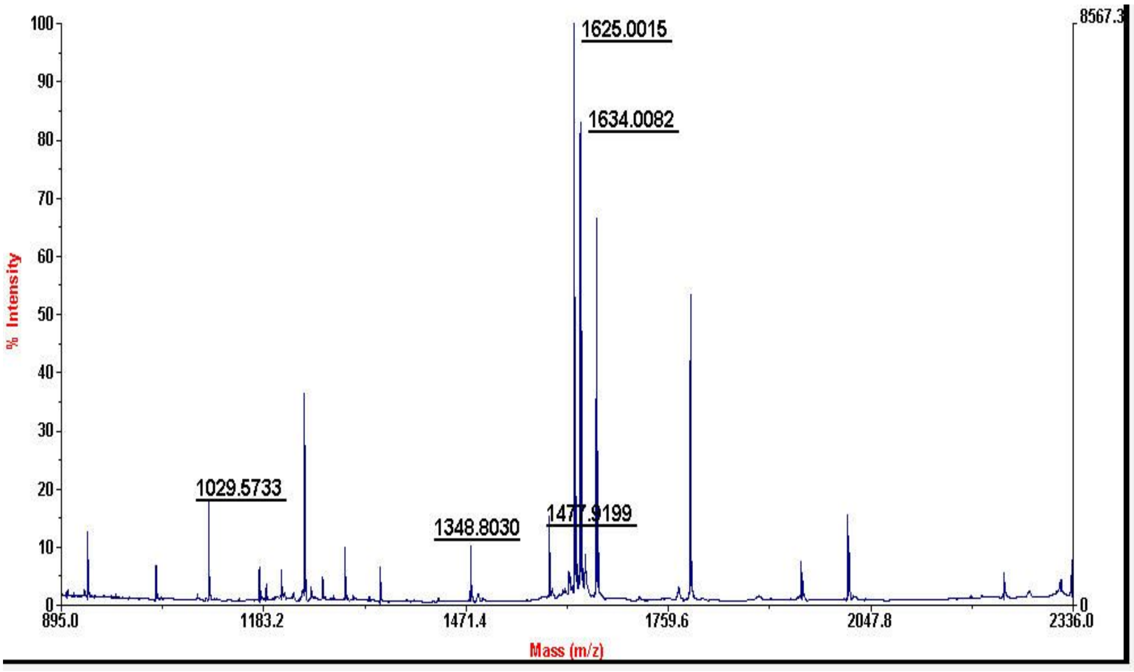
320 Proteasome subunit beta type 3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
18 - 27	1145.6647	1144.6574	1144.5771	0.0803	1	K.NCVAIAADRR.F	
28 - 41	1613.9304	1612.9231	1612.7919	0.1311	0	R.FGIQAQMVTTDFQK.I	
28 - 41	1629.9156	1628.9083	1628.7869	0.1215	0	R.FGIQAQMVTTDFQK.I	Oxidation (M)
49 - 66	1889.1923	1888.1850	1888.0418	0.1432	0	R.LYIGLAGLATDVQTVAQR.L	
69 - 77	1195.7779	1194.7706	1194.6761	0.0946	1	K.FRLNLYELK.E	
99 - 115	1923.1689	1922.1617	1921.9938	0.1679	1	K.RFGPYYTEPVIAGLDPK.T	
100 - 115	1767.0362	1766.0289	1765.8927	0.1362	0	R.FGPYYTEPVIAGLDPK.T	

No match to: 1206.7533, 1285.8473, 1462.8997, 1595.9515, 2076.1171

321 5'(3')-deoxyribonucleotidase, cytosolic type

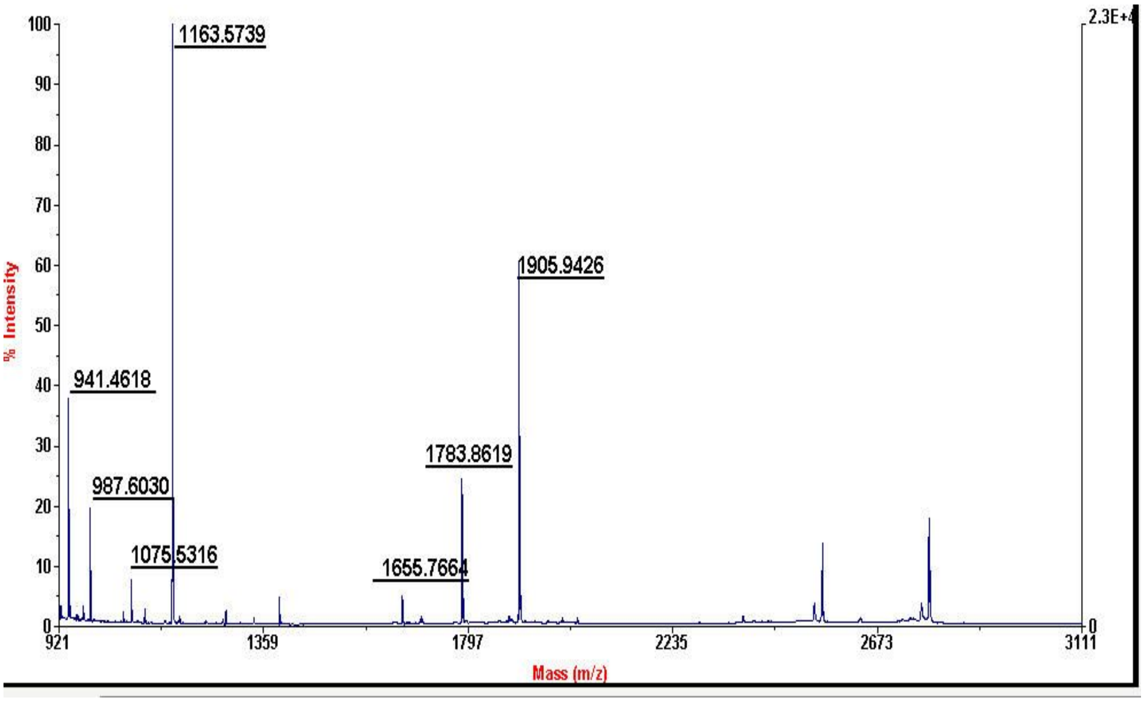


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
30 - 41	1477.9199	1476.9126	1476.7361	0.1765	0	R.FPEEPHVPLEQR.R
30 - 42	1634.0082	1633.0010	1632.8372	0.1637	1	R.FPEEPHVPLEQRR.G
105 - 112	1029.5733	1028.5661	1028.4498	0.1163	0	K.YHHCVGEK.Y
105 - 114	1348.8030	1347.7957	1347.6142	0.1815	1	K.YHHCVGEKYR.W

115 - 127	1625.0015	1623.9942	1623.8158	0.1784	0	R.WVEQHLGPQFVER.I
170 - 177	932.6794	931.6722	931.5603	0.1118	0	R.HLVLPPTR.R

No match to: 1104.7897, 1240.6811, 1298.7444, 1589.9355, 1617.7851, 1643.7245, 1656.9720, 1690.8802, 1790.1230, 2015.2956, 2401.2871, 2433.2553

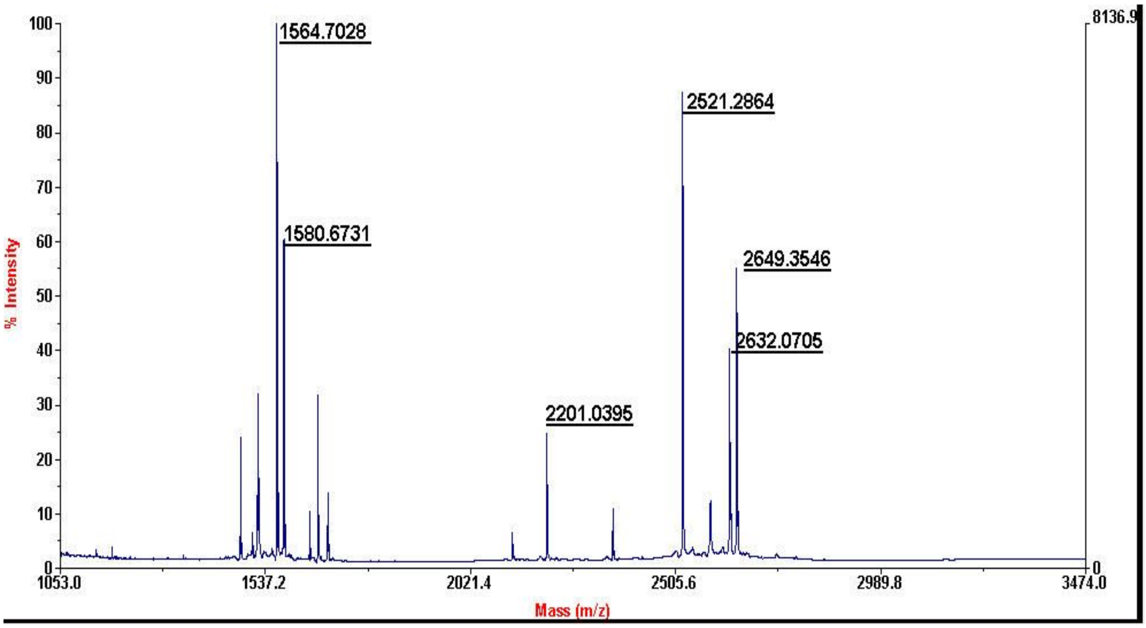
322 Heat-shock protein beta-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
5 - 12	987.6030	986.5957	986.6025	-0.0068	1	R.RVPFSLLR.G
28 - 37	1163.5739	1162.5666	1162.6135	-0.0469	0	R.LFDQAFGLPR.L
80 - 89	1075.5316	1074.5244	1074.5669	-0.0426	0	R.QLSSGVSEIR.H
90 - 96	941.4618	940.4545	940.4627	-0.0083	1	R.HTADRWR.V
97 - 112	1783.8619	1782.8546	1782.9152	-0.0606	0	R.VSLDVNHFAPDELTVK.T
124 - 136	1655.7664	1654.7591	1654.7448	0.0144	1	K.HEERQDEHGYISR.C
172 - 188	1905.9426	1904.9354	1904.9843	-0.0490	0	K.LATQSNEITIPVTFESR.A

No match to: 1365.1378, 2537.9265, 2553.1977, 2554.1631, 2637.0182, 2782.3704, 2783.3224

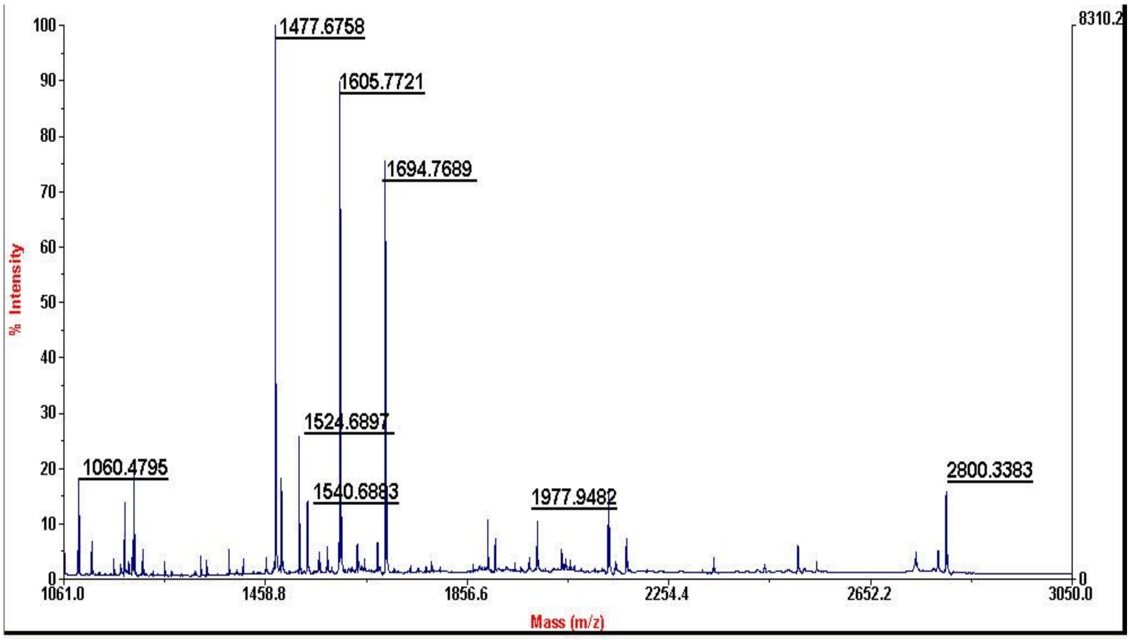
323 Proteasome subunit alpha type 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
71 - 84	1564.7028	1563.6955	1563.7504	-0.0549	0	K.HIGLVYSGMGPDYR.V	
71 - 84	1580.6731	1579.6658	1579.7453	-0.0795	0	K.HIGLVYSGMGPDYR.V	Oxidation (M)
92 - 113	2649.3546	2648.3473	2648.4326	-0.0853	1	R.KLAQQYYLVYQEPIPTAQLVQR.V	
93 - 113	2521.2864	2520.2792	2520.3376	-0.0585	0	K.LAQQYYLVYQEPIPTAQLVQR.V	
178 - 196	2201.0395	2200.0322	2200.1263	-0.0941	0	R.YNEDLELEDAIHTAILTLK.E	
197 - 219	2632.0705	2631.0632	2631.1217	-0.0585	0	K.ESFEGQMTEDNIEVGICNEAGFR.R	

No match to: 1519.9430, 1660.8762, 1684.7236, 2186.8565, 2505.1791, 2546.4503, 2587.1067

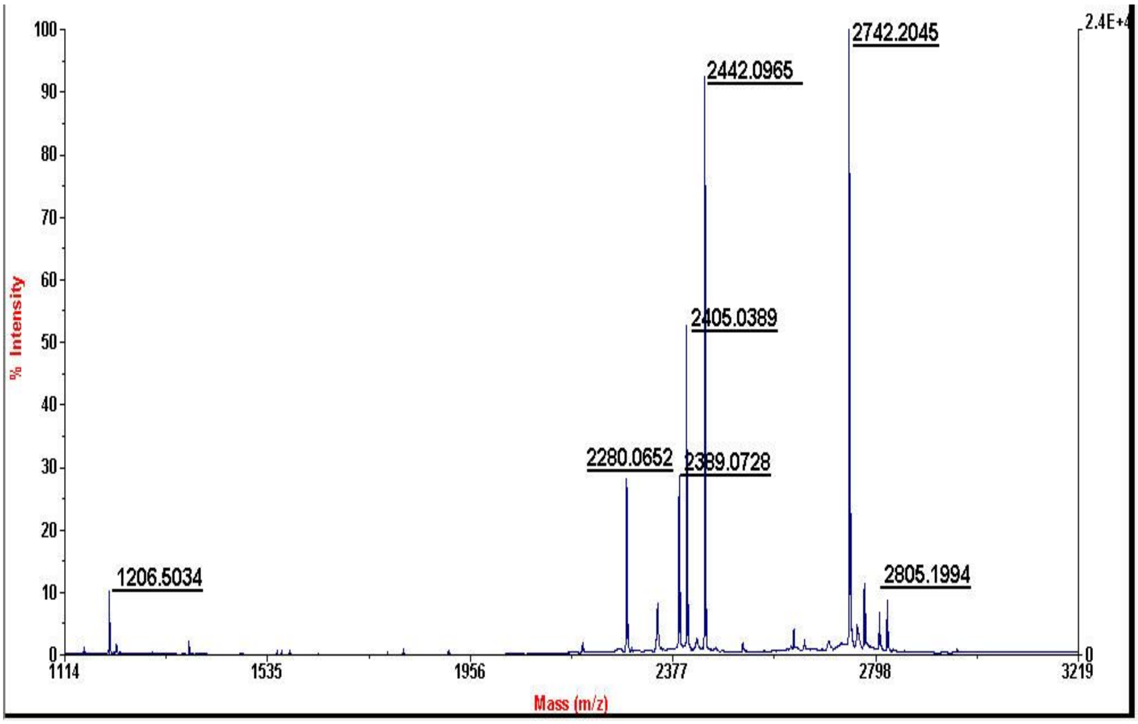
324 Protein-L-isoaspartate(D-aspartate) O-methyltransferase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
5 - 18	1477.6758	1476.6685	1476.7433	-0.0748	0	K.SGGASHSELIHNLR.K
5 - 19	1605.7721	1604.7648	1604.8383	-0.0735	1	K.SGGASHSELIHNLRK.N
25 - 37	1524.6897	1523.6824	1523.7654	-0.0830	1	K.TDKVFEVMLATDR.S
25 - 37	1540.6883	1539.6810	1539.7603	-0.0793	1	K.TDKVFEVMLATDR.S Oxidation (M)
82 - 98	1694.7689	1693.7616	1693.8458	-0.0841	0	K.ALDVGSGSGILTACFAR.M
126 - 135	1060.4795	1059.4722	1059.5197	-0.0475	0	K.DDPTLLSSGR.V
179 - 204	2800.3383	2799.3310	2799.4477	-0.1166	1	R.LILPVGPAGGNQMLEQYDKLQDGSIK.M Oxidation (M)
205 - 221	1977.9482	1976.9409	1977.0679	-0.1270	1	K.MKPLMGVIYVPLTDKEK.Q Oxidation (M)

No match to: 952.4784, 972.4159, 1090.4688, 1198.5725, 1489.6165, 1896.8150, 2134.9705

325 ES1 protein homolog, mitochondrial precursor

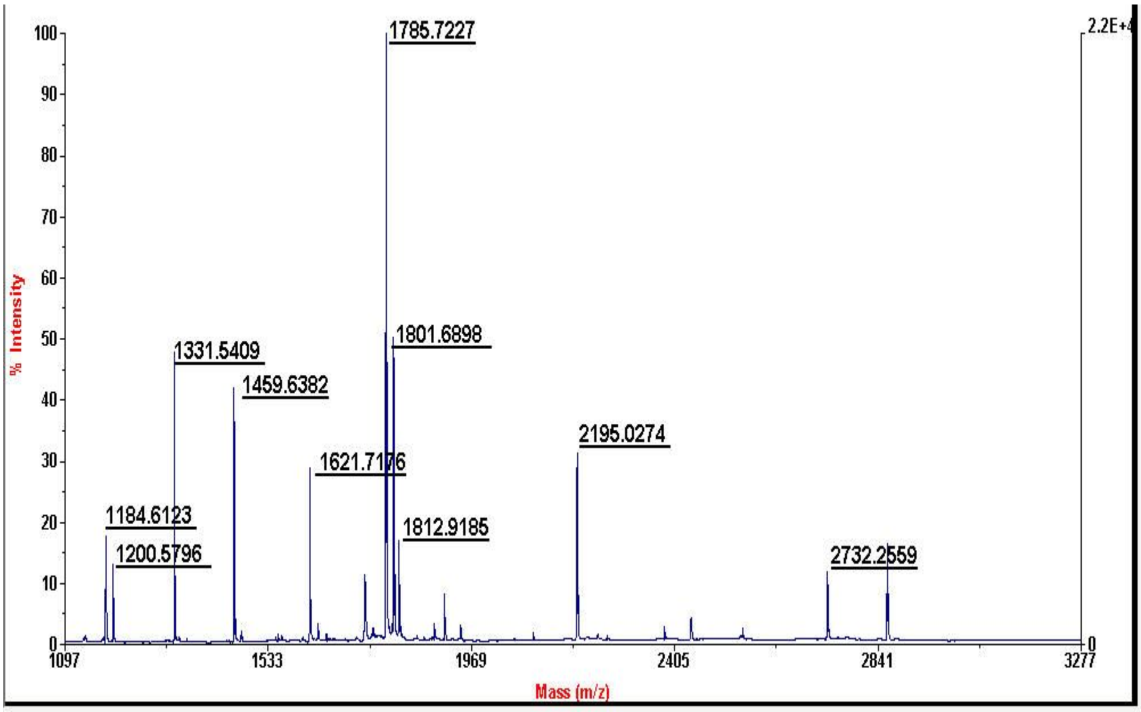


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
73 - 94	2389.0728	2388.0655	2388.1896	-0.1241	0	R.GGAEVQIFAPDVPQMHVIDHTK.G
73 - 94	2405.0389	2404.0316	2404.1846	-0.1530	0	R.GGAEVQIFAPDVPQMHVIDHTK.G Oxidation (M)
117 - 141	2442.0965	2441.0892	2441.2339	-0.1447	0	K.ITDLANLSAANHDAAIFPGGFGAAK.N

165 - 185	2280.0652	2279.0580	2279.1918	-0.1339	0	K.EFHQAGKPIGLCCIAPVLAAK.V	2
189 - 214	2742.2045	2741.1972	2741.3297	-0.1325	1	R.GVEVTVGHEQEEGGKWPYAGTAEAIK.A	
204 - 214	1206.5034	1205.4962	1205.6080	-0.1119	0	K.WPYAGTAEAIK.A	
236 - 260	2805.1994	2804.1921	2804.3448	-0.1527	0	K.VVTTPAFMCETALHYIHDGIGAMVR.K	; Oxidation (M)

No match to: 2344.1367, 2345.9678, 2701.1171, 2762.1342, 2774.1865

326 3-hydroxyacyl-CoA dehydrogenase type-2

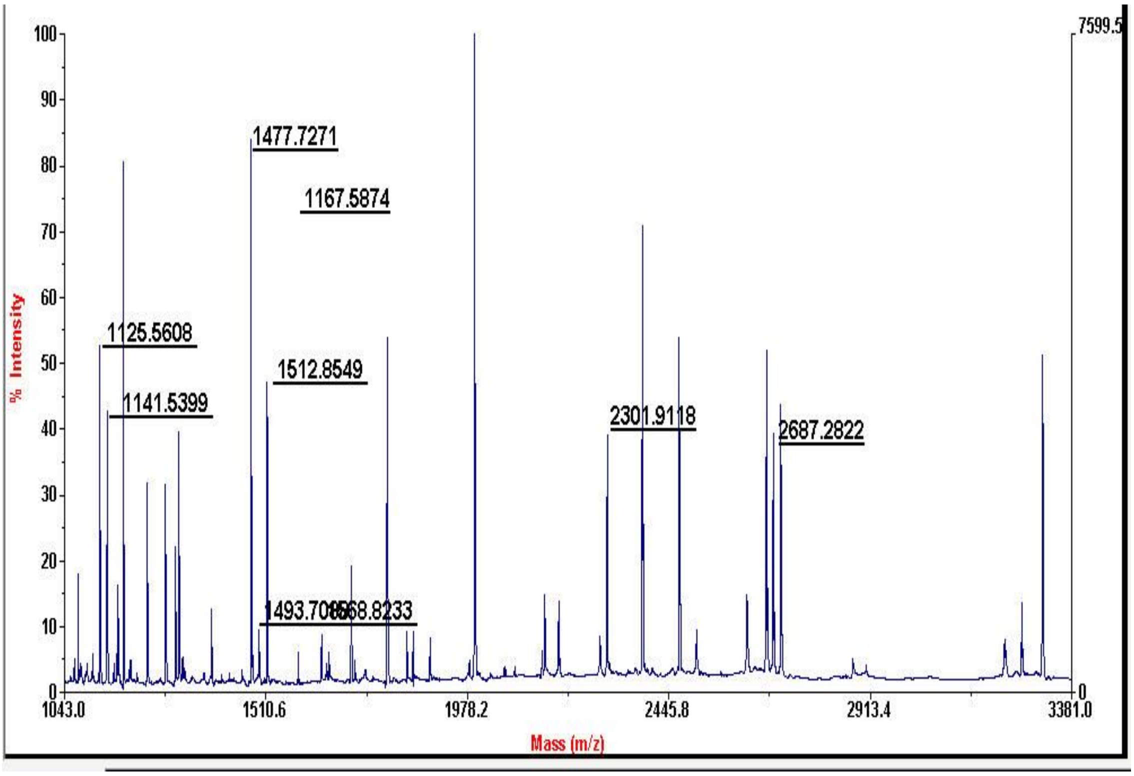


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
10 - 29	1812.9185	1811.9112	1812.0105	-0.0993	0	K.GLVAVITGGASGLGLATAER.L
30 - 52	2195.0274	2194.0202	2194.1593	-0.1392	0	R.LVGQGASAVLLDLPNSGGEAQAK.K
54 - 79	2732.2559	2731.2486	2731.3851	-0.1365	1	K.LGNNCVFAPADVTSEKDVQTALALAK.G
105 - 116	1459.6382	1458.6310	1458.7215	-0.0906	1	K.KGQTHTLEDFQR.V
106 - 116	1331.5409	1330.5336	1330.6266	-0.0930	0	K.GQTHTLEDFQR.V
131 - 147	1785.7227	1784.7154	1784.8112	-0.0957	0	R.LVAGEMGQNEPDQGGQR.G

131 - 147	1801.6898	1800.6825	1800.8061	-0.1235	0	R.LVAGEMGQNEPDQGGQR.G	Oxidation (M)
173 - 184	1184.6123	1183.6050	1183.6747	-0.0697	0	K.GGIVGMTLPIAR.D	
173 - 184	1200.5796	1199.5723	1199.6696	-0.0973	0	K.GGIVGMTLPIAR.D	Oxidation (M)
213 - 226	1621.7176	1620.7104	1620.8083	-0.0979	0	K.VCNFLASQVPFPSR.L	

No match to: 1740.9711, 1910.8380, 2860.3627

327 Flavin reductase

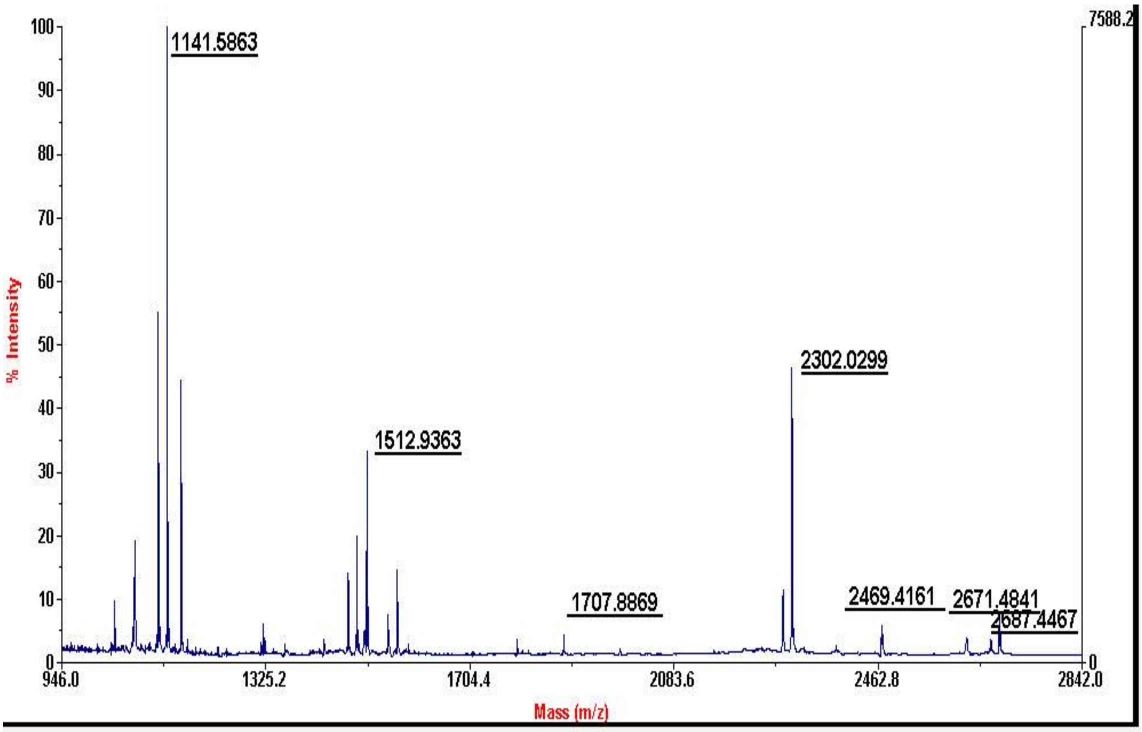


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
64 - 78	1512.8549	1511.8477	1511.8672	-0.0195	0	K.TVAGQDAVIVLLGTR.N	
79 - 92	1477.7271	1476.7199	1476.6879	0.0320	0	R.NDLSPTTVMSEGAR.N	
79 - 92	1493.7088	1492.7015	1492.6828	0.0187	0	R.NDLSPTTVMSEGAR.N	Oxidation (M)
125 - 134	1167.5874	1166.5801	1166.6044	-0.0243	0	R.LQAVTDDHIR.M	
146 - 170	2687.2822	2686.2749	2686.3425	-0.0676	0	K.YVAVMPPHIGDQPLTGAYTVTLDGR.G	Oxidation (M)

175 - 187	1568.8233	1567.8161	1567.8293	-0.0133	1	R.VISKHDLGHFMLR.C	Oxidation (M)
179 - 187	1125.5608	1124.5535	1124.5549	-0.0014	0	K.HDLGHFMLR.C	
179 - 187	1141.5399	1140.5326	1140.5499	-0.0173	0	K.HDLGHFMLR.C	Oxidation (M)
188 - 206	2301.9118	2300.9045	2300.9281	-0.0235	0	R.CLTTDEYDGHSTYPSHQYQ.-	

No match to: 1043.5468, 1081.1604, 1123.4862, 1508.6701, 2284.9419, 2286.8224, 2627.8323

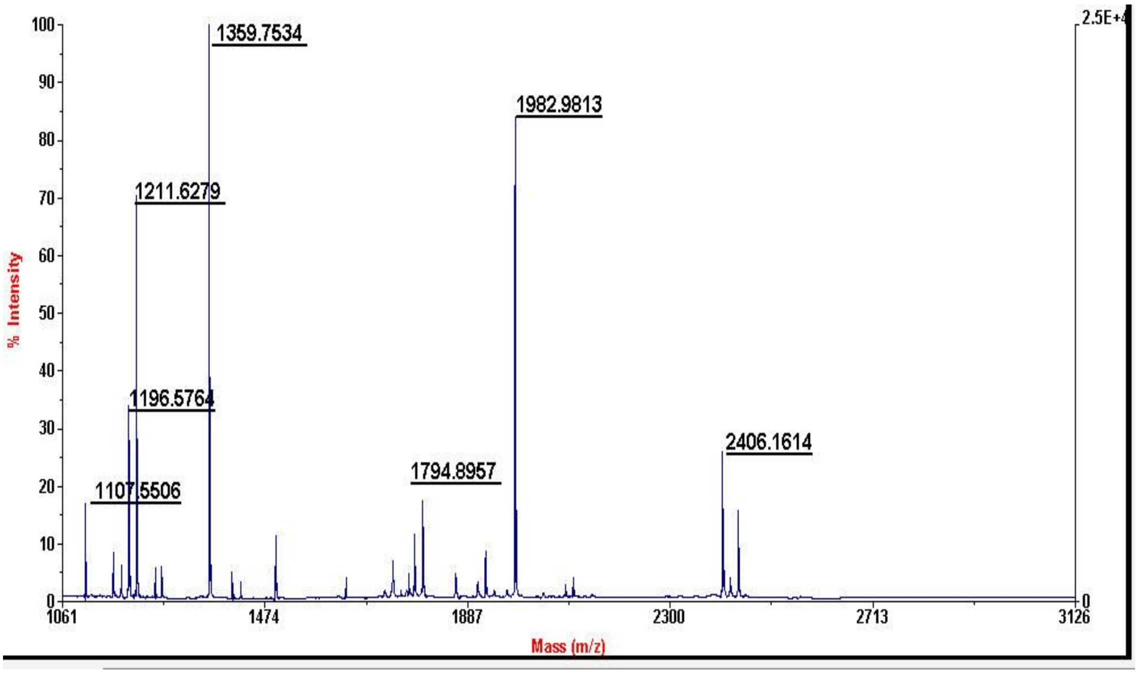
328 Flavin reductase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
40 - 63	2469.4161	2468.4088	2468.3024	0.1065	0	R.LPSEGPRPAHVVVGDVLQAADVDK.T	
64 - 78	1512.9363	1511.9291	1511.8672	0.0619	0	K.TVAGQDAVIVLLGTR.N	
106 - 120	1707.8869	1706.8797	1706.8702	0.0095	0	K.VVACTSAFLLWDPTK.V	
146 - 170	2671.4841	2670.4768	2670.3476	0.1292	0	K.YVAVMPPHIGDQPLTGAYTVTLDGR.G	
146 - 170	2687.4467	2686.4395	2686.3425	0.0969	0	K.YVAVMPPHIGDQPLTGAYTVTLDGR.G	Oxidation (M)
179 - 187	1141.5863	1140.5790	1140.5499	0.0291	0	K.HDLGHFMLR.C	Oxidation (M)
188 - 206	2302.0299	2301.0226	2300.9281	0.0945	0	R.CLTTDEYDGHSTYPSHQYQ.-	

No match to: 1179.6662, 1235.6311, 1277.7813, 1307.7537, 1475.8208, 1791.8164, 1852.0231, 1994.0541, 2384.0524, 2627.5374, 2705.3035

329 Peroxiredoxin-1

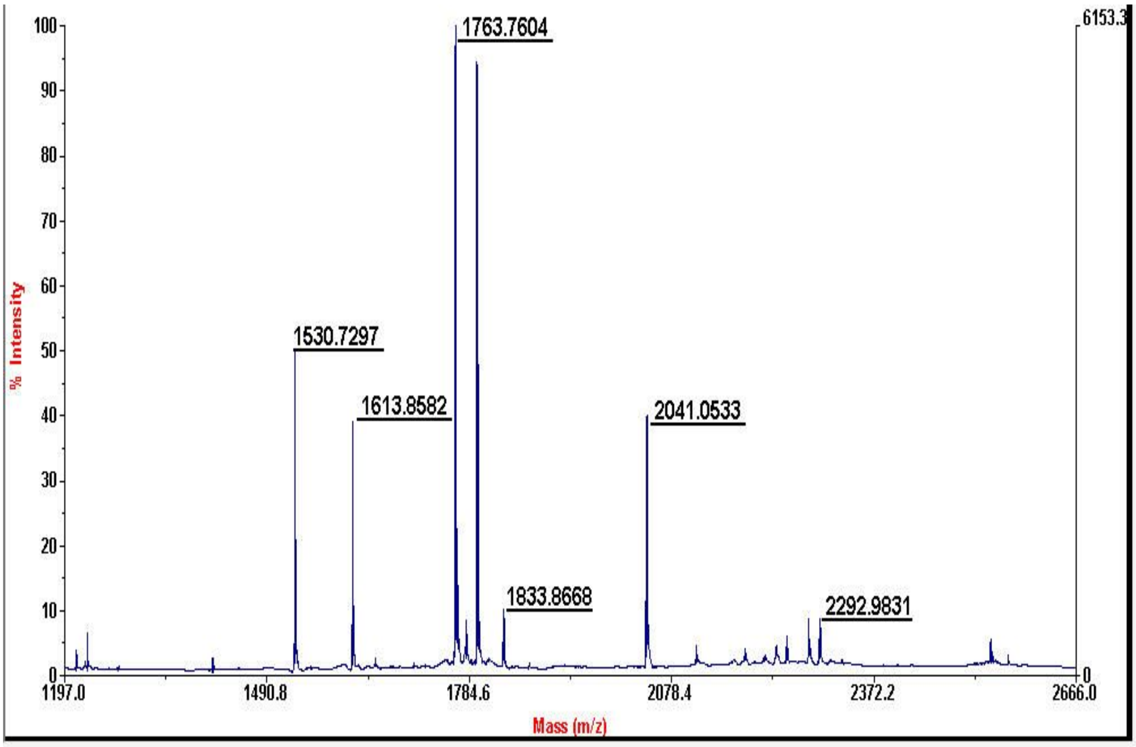


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 16	980.4847	979.4775	979.5239	-0.0465	0	K.IGHPAPNFK.A
94 - 110	1794.8957	1793.8884	1793.9458	-0.0574	1	K.QGGLGPMNIPLVSDPKR.T
Oxidation (M)						
111 - 120	1107.5506	1106.5433	1106.5972	-0.0539	0	R.TIAQDYGVLK.A
111 - 128	1982.9813	1981.9740	1982.0109	-0.0369	1	R.TIAQDYGVLKADEGISFR.G
129 - 140	1359.7534	1358.7462	1358.7922	-0.0460	1	R.GLFIIDDKGILR.Q
141 - 151	1211.6279	1210.6206	1210.6670	-0.0463	0	R.QITVNDLPVGR.S
159 - 168	1196.5764	1195.5691	1195.6237	-0.0546	0	R.LVQAFQFTDK.H
169 - 190	2406.1614	2405.1541	2405.1798	-0.0256	0	K.HGEVCPAGWKPGSDTIKPDVQK.S

No match to: 1194.6024, 1495.7237, 1718.0263, 1734.9255, 1922.9755, 2438.1194

330

Glyceraldehyde-3-phosphate dehydrogenase

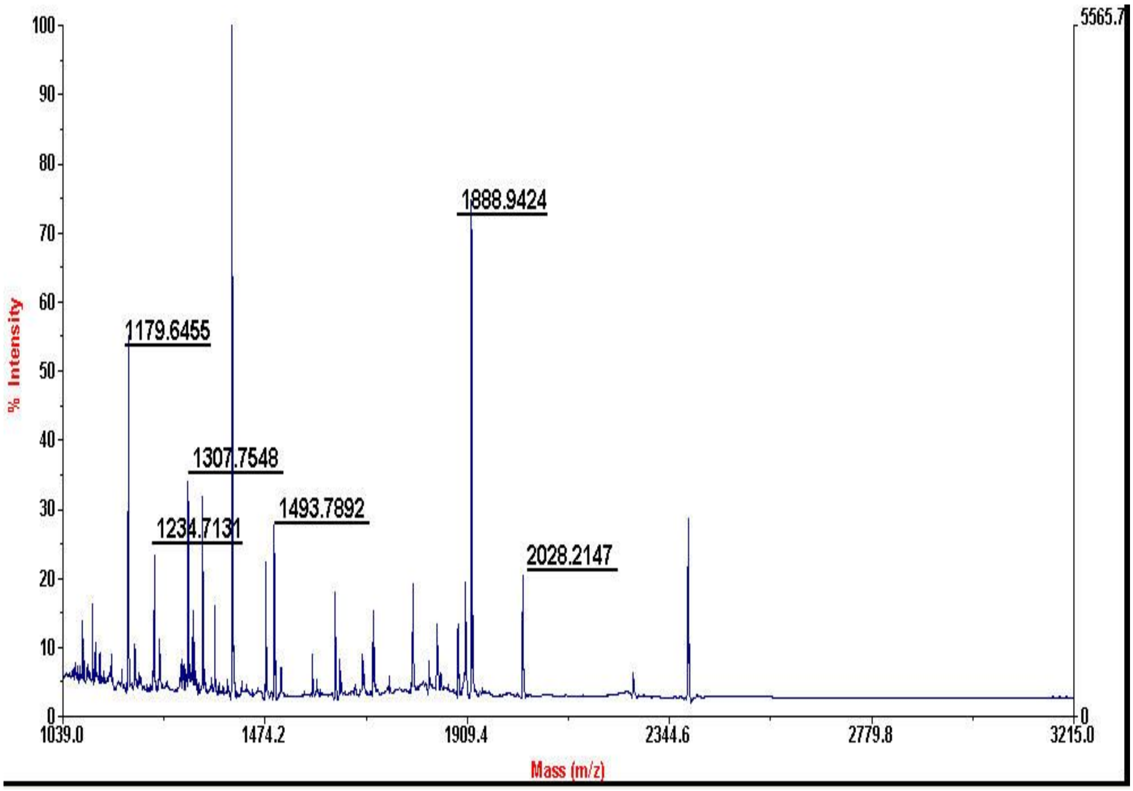


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
67 - 80	1613.8582	1612.8510	1612.8937	-0.0427	0	K.LVINGNPITIFQER.D	
67 - 84	2041.0533	2040.0460	2040.1004	-0.0544	1	K.LVINGNPITIFQERDPSK.I	
87 - 107	2292.9831	2291.9759	2292.0257	-0.0498	0	K.WGDAGAEYVVESTGVFTTMEK.A	
Oxidation (M)							
146 - 162	1833.8668	1832.8595	1832.9124	-0.0529	0	K.IISNASCTTNCLAPLAK.V	2
235 - 248	1530.7297	1529.7224	1529.7872	-0.0648	0	R.VPTANVSVVDLTCR.L	
310 - 323	1763.7604	1762.7531	1762.7951	-0.0419	0	K.LISWYDNEFGYSNR.V	

No match to: 1492.7649, 1599.9716, 1614.8425, 1778.7573, 1795.7544, 1813.6603, 2042.0332, 2045.7264

331

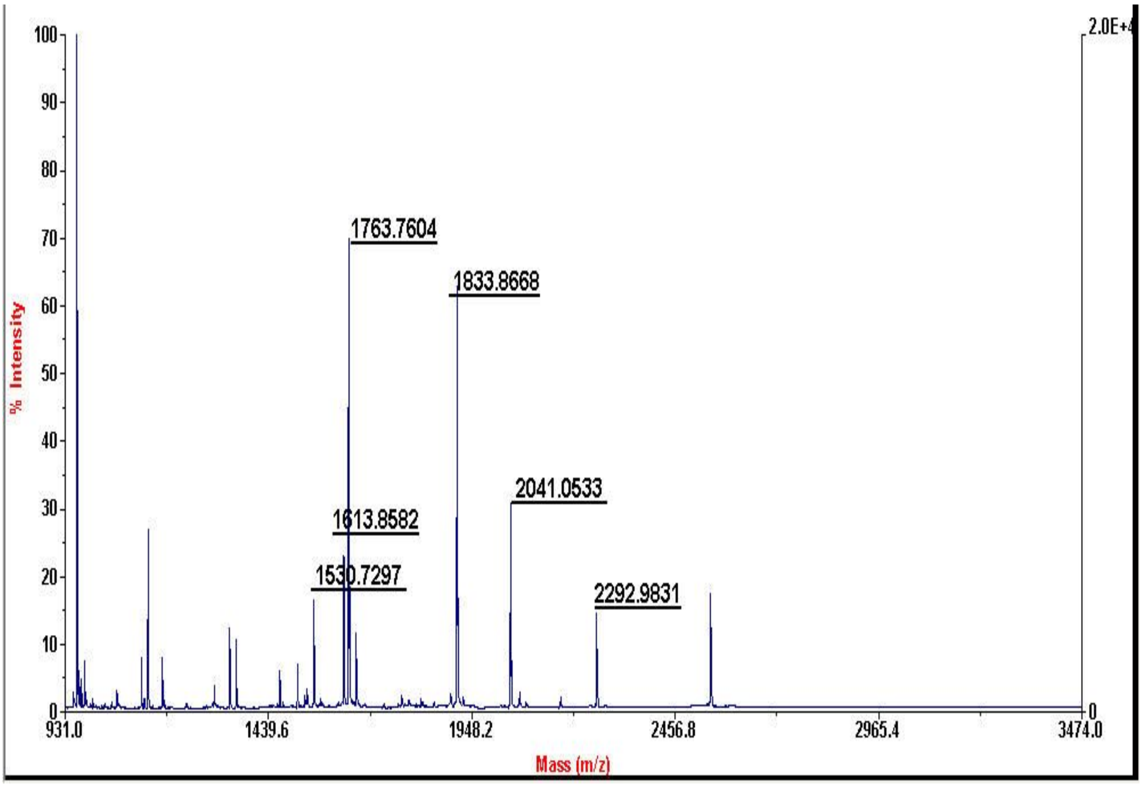
WD repeat protein 25 - Homo sapiens



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
67 - 77	1234.7131	1233.7058	1233.4833	0.2225	0	K.HGSCEDPGGYR.L
78 - 95	2028.2147	2027.2074	2027.0007	0.2068	1	R.LPLAQLGRSDWGSCPSQR.L
86 - 95	1179.6455	1178.6382	1178.4775	0.1607	0	R.SDWGSCPSQR.L
86 - 101	1888.9424	1887.9351	1887.8686	0.0665	1	R.SDWGSCPSQRLQWPGK.E
146 - 159	1493.7892	1492.7819	1492.6794	0.1025	0	K.SSFHAQSESETVGK.N
194 - 206	1307.7548	1306.7475	1306.6630	0.0845	1	K.GKDVEPQGPPAGR.A

No match to: 1339.7688, 1403.7850, 1705.9493, 1918.0149

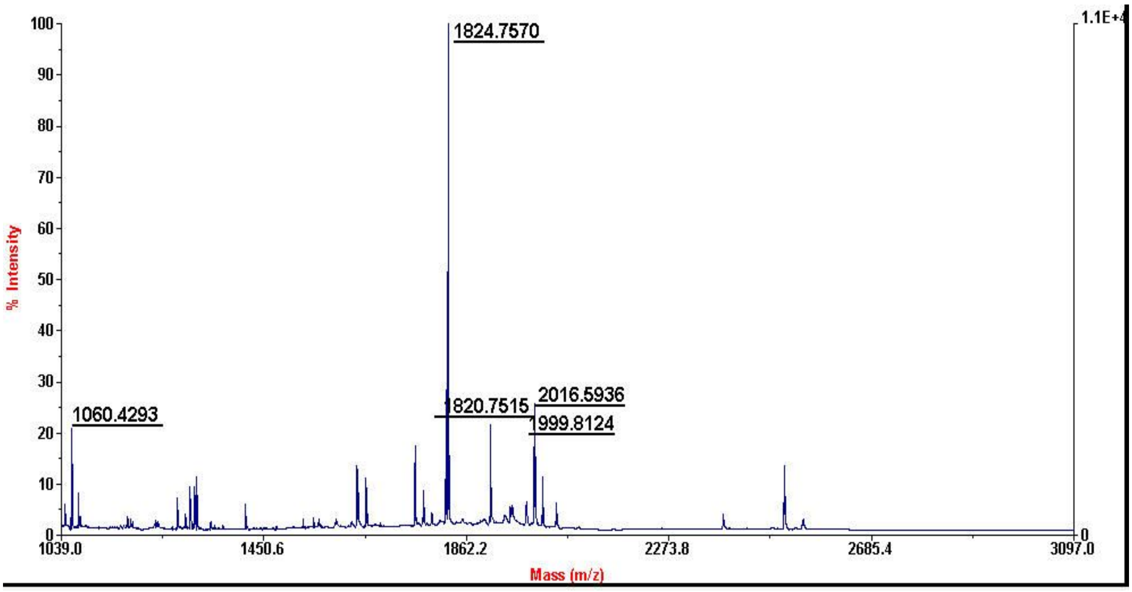
332 Glyceraldehyde-3-phosphate dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
67 - 80	1613.8582	1612.8510	1612.8937	-0.0427	0	K.LVINGNPITIFQER.D	
67 - 84	2041.0533	2040.0460	2040.1004	-0.0544	1	K.LVINGNPITIFQERDPSK.I	
87 - 107	2292.9831	2291.9759	2292.0257	-0.0498	0	K.WGDAGAEYVVESTGVFTTMEK.A	
Oxidation (M)							
146 - 162	1833.8668	1832.8595	1832.9124	-0.0529	0	K.IISNASCTTNCLAPLAK.V	2
235 - 248	1530.7297	1529.7224	1529.7872	-0.0648	0	R.VPTANVSVVDLTCR.L	
310 - 323	1763.7604	1762.7531	1762.7951	-0.0419	0	K.LISWYDNEFGYSNR.V	

No match to: 1492.7649, 1599.9716, 1614.8425, 1778.7573, 1795.7544, 1813.6603, 2042.0332, 2045.7264

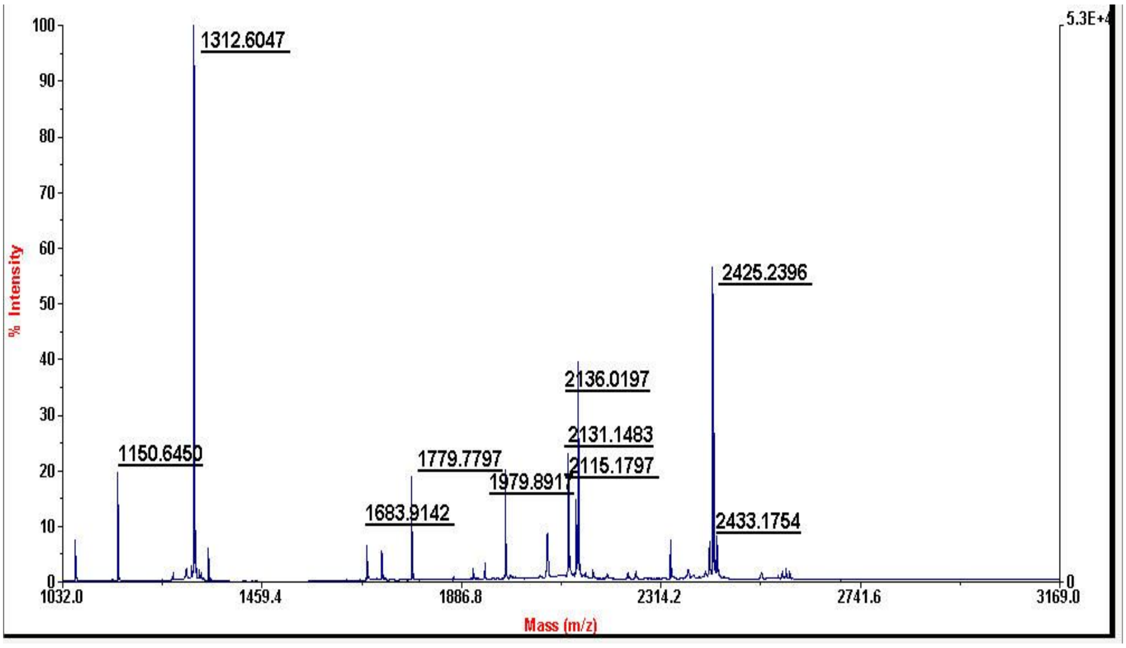
333 S-methyl-5-thioadenosine phosphorylase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
12 - 29	1824.7570	1823.7498	1823.9629	-0.2131	0	K.IGIIGGTGLDDPEILEGR.T
33 - 49	1820.7515	1819.7442	1819.9720	-0.2278	0	K.YVDTPFGKPSDALILGK.I
100 - 116	1999.8124	1998.8051	1999.0262	-0.2211	0	R.EEIQPGDIVIIDQFIDR.T
117 - 133	2016.5936	2015.5863	2015.8578	-0.2715	0	R.TTMRPQSFYDGSHSCAR.G ; Oxidation (M)
167 - 176	1060.4293	1059.4220	1059.5383	-0.1162	0	K.GTMVTIEGPR.F
181 - 187	903.2523	902.2450	902.3956	-0.1506	0	R.AESFMFR.T Oxidation (M)

No match to: 960.4260, 1059.4522, 1639.7348, 1757.6175, 1898.2372, 1910.7127, 1962.2760

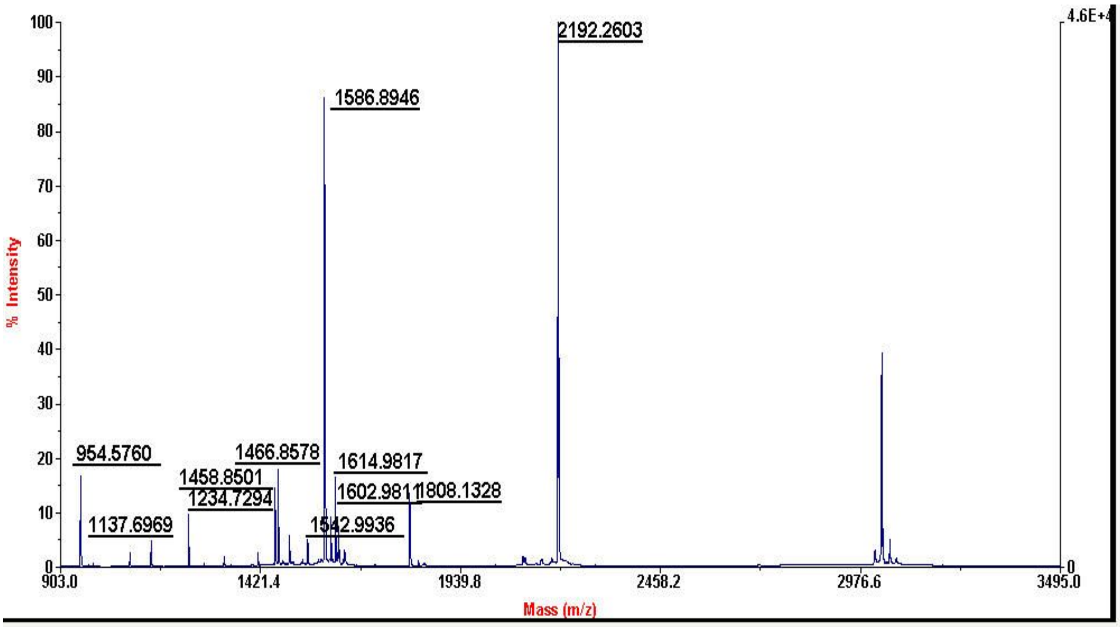
334 Phosphoglycerate mutase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
11 - 21	1312.6047	1311.5974	1311.5956	0.0018	0	R.HGESAWNLENR.F
22 - 39	1979.8917	1978.8845	1978.8697	0.0148	0	R.FSGWYDADLSPAGHEEAK.R
22 - 40	2136.0197	2135.0124	2134.9708	0.0416	1	R.FSGWYDADLSPAGHEEAKR.G
47 - 61	1779.7797	1778.7724	1778.7822	-0.0097	0	R.DAGYEFDICFTSVQK.R
118 - 138	2433.1754	2432.1682	2432.0995	0.0687	0	R.SYDVPPPPMEPDHPFYSNISK.D
Oxidation (M)						
142 - 162	2425.2396	2424.2323	2424.1478	0.0845	1	R.YADLTEDQLPSCESLKDTIAR.A
163 - 176	1683.9142	1682.9069	1682.9032	0.0037	0	R.ALPFWNEEIVPQIK.E
181 - 191	1150.6450	1149.6377	1149.6618	-0.0241	0	R.VLIAAHGNSLR.G
223 - 240	2115.1797	2114.1724	2114.1194	0.0530	0	K.NLKPIKPMQFLGDEETVR.K
223 - 240	2131.1483	2130.1410	2130.1143	0.0267	0	K.NLKPIKPMQFLGDEETVR.K
Oxidation (M)						

No match to: 2070.2378

335 Triosephosphate isomerase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 14	954.5760	953.5687	953.4760	0.0928	0	K.FFVGGNWK.M

19 - 33	1542.9936	1541.9863	1541.8777	0.1086	1	R.KQSLGELIGTLNAAK.V
34 - 53	2192.2603	2191.2531	2191.0620	0.1911	0	K.VPADTEVVCAPPTAYIDFAR.Q
60 - 69	1137.6969	1136.6897	1136.5648	0.1248	0	K.IAVAAQNCYK.V
86 - 99	1586.8946	1585.8873	1585.7307	0.1566	0	K.DCGATWVVLGHSER.R
100 - 113	1614.9817	1613.9745	1613.8162	0.1583	1	R.RHVFGESDELIGQK.V
101 - 113	1458.8501	1457.8428	1457.7151	0.1277	0	R.HVFGESDELIGQK.V
114 - 131	1808.1328	1807.1255	1806.9662	0.1594	0	K.VAHALAEGLGVIACIGEK.L
161 - 175	1602.9811	1601.9738	1601.8817	0.0921	0	K.VVLAYEPVWAIGTGK.T
176 - 188	1466.8578	1465.8505	1465.7161	0.1344	0	K.TATPQQAQEVHEK.L
195 - 206	1234.7294	1233.7221	1233.5949	0.1272	0	K.SNVSDAVAQSTR.I

No match to: 2107.8306

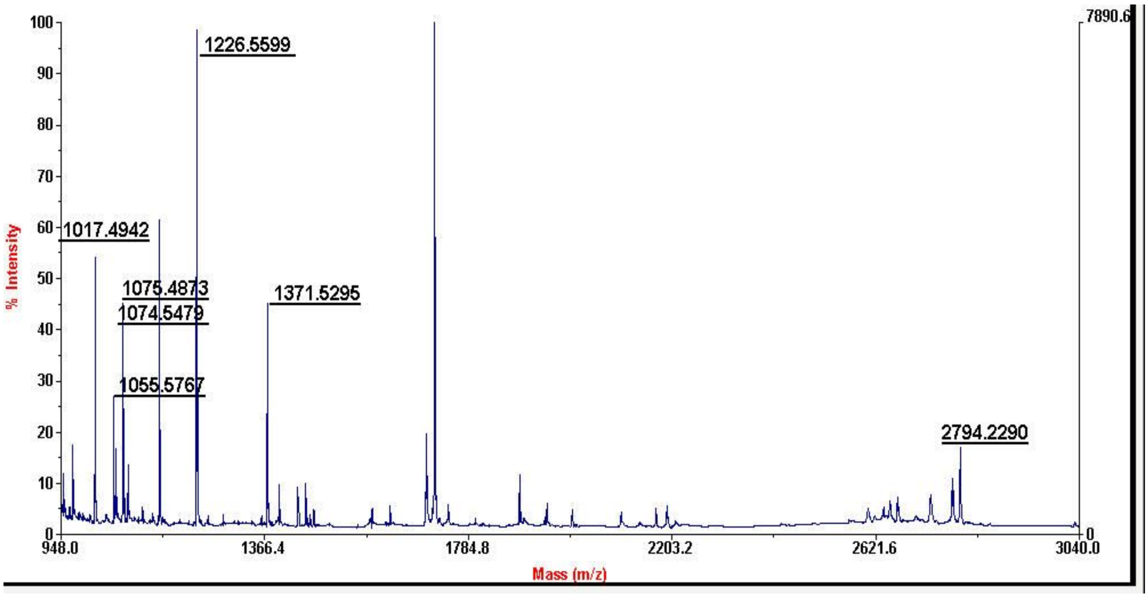
336

Triosephosphate isomerase

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 14	954.3618	953.3545	953.4760	-0.1214	0	K.FFVGGNWK.M
86 - 99	1586.5029	1585.4956	1585.7307	-0.2351	0	K.DCGATWVVLGHSER.R
100 - 113	1614.5671	1613.5599	1613.8162	-0.2563	1	R.RHVFGESDELIGQK.V
101 - 113	1458.4737	1457.4664	1457.7151	-0.2487	0	R.HVFGESDELIGQK.V
161 - 175	1602.6047	1601.5974	1601.8817	-0.2843	0	K.VVLAYEPVWAIGTGK.T

No match to: 986.3295, 1495.5311, 1618.5019, 1634.5922, 1807.6714, 2191.7170

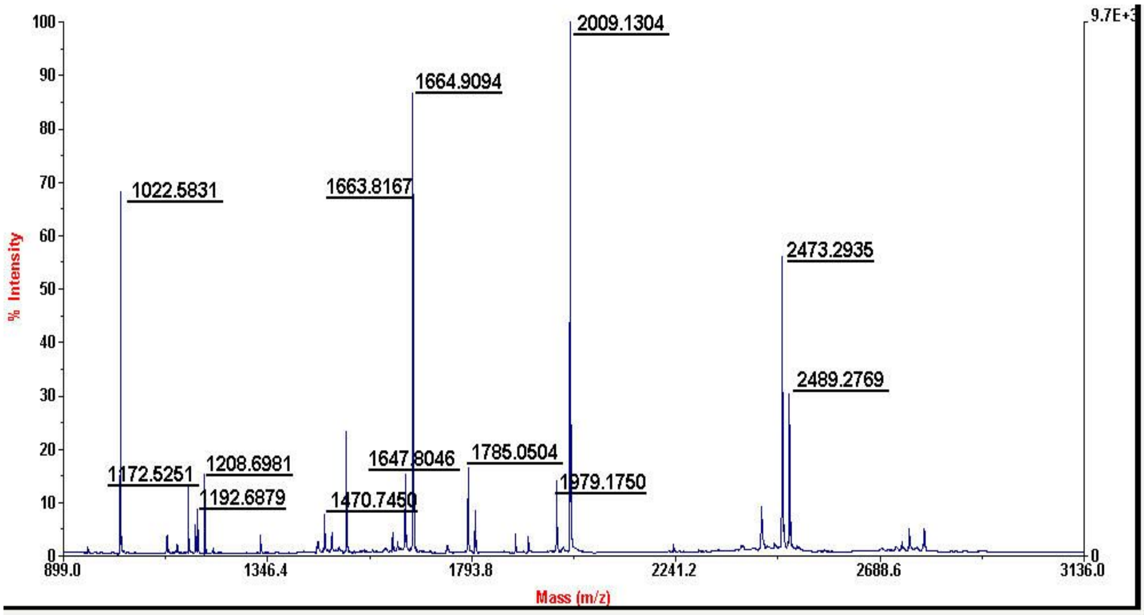
337 Serum albumin precursor - Homo sapiens



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 34	1149.5711	1148.5638	1148.5686	-0.0049	1	R.DAHKSEVAHR.F
35 - 44	1226.5599	1225.5526	1225.5979	-0.0453	1	R.FKDLGEENFK.A
89 - 97	1017.4942	1016.4869	1016.5291	-0.0422	0	K.SLHTLFGDK.L
98 - 105	933.4966	932.4893	932.5113	-0.0220	0	K.LCTVATLR.E
118 - 130	1714.7645	1713.7572	1713.7893	-0.0321	1	K.QEPERNECFLQHK.D
123 - 130	1075.4873	1074.4801	1074.4917	-0.0116	0	R.NECFLQHK.D
131 - 138	940.4369	939.4296	939.4410	-0.0114	0	K.DDNPNLPR.L
139 - 161	2794.2290	2793.2217	2793.3466	-0.1249	1	R.LVRPEVDVMCTAFHDNEETFLKK.Y ; Oxidation (M)
161 - 168	1055.5767	1054.5695	1054.5811	-0.0116	1	K.KYLYEIAR.R
162 - 168	927.4944	926.4871	926.4861	0.0010	0	K.YLYEIAR.R
187 - 198	1371.5295	1370.5222	1370.5595	-0.0373	0	K.AAFTECCQAADK.A 2
206 - 214	1074.5479	1073.5406	1073.5353	0.0053	1	K.LDELRDEGK.A

No match to: 1697.7581, 2734.9902

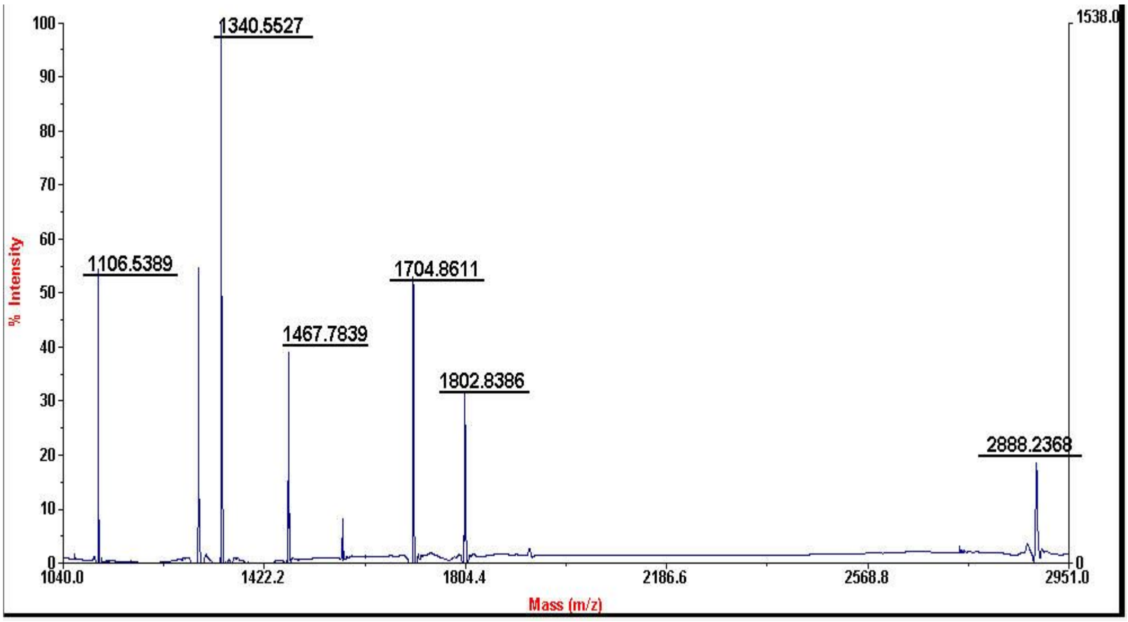
338 Purine nucleoside phosphorylase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 41	1979.1750	1978.1678	1978.0418	0.1259	0	K.HRPQVAIICGSGLGGLTDK.L
42 - 58	2009.1304	2008.1231	2008.0054	0.1177	0	K.LTQAQIFDYGEIPNFPR.S
68 - 76	1022.5831	1021.5758	1021.5709	0.0049	0	R.LVFGFLNGR.A
85 - 95	1470.7450	1469.7377	1469.6802	0.0576	0	R.FHMYEGYPLWK.V
124 - 133	1192.6879	1191.6806	1191.6322	0.0485	0	K.FEVGDIMLIR.D
124 - 133	1208.6981	1207.6908	1207.6271	0.0637	0	K.FEVGDIMLIR.D Oxidation (M)
155 - 168	1647.8046	1646.7973	1646.7147	0.0825	1	R.FGDRFPAMSDAYDR.T
155 - 168	1663.8167	1662.8094	1662.7097	0.0998	1	R.FGDRFPAMSDAYDR.T Oxidation (M)
159 - 168	1172.5251	1171.5178	1171.4968	0.0210	0	R.FPAMSDAYDR.T
186 - 207	2473.2935	2472.2862	2472.1301	0.1561	0	R.ELQEGTYVMVAGPSFETVAECR.V
186 - 207	2489.2769	2488.2696	2488.1250	0.1446	0	R.ELQEGTYVMVAGPSFETVAECR.V ; Oxidation (M)
212 - 229	1785.0504	1784.0432	1783.9502	0.0929	0	K.LGADAVGMSTVPEVIVAR.H
255 - 270	1664.9094	1663.9021	1663.8641	0.0380	1	K.ANHEEVLAAGKQAAQK.L

No match to: 1023.5752, 1518.7437, 2429.3880

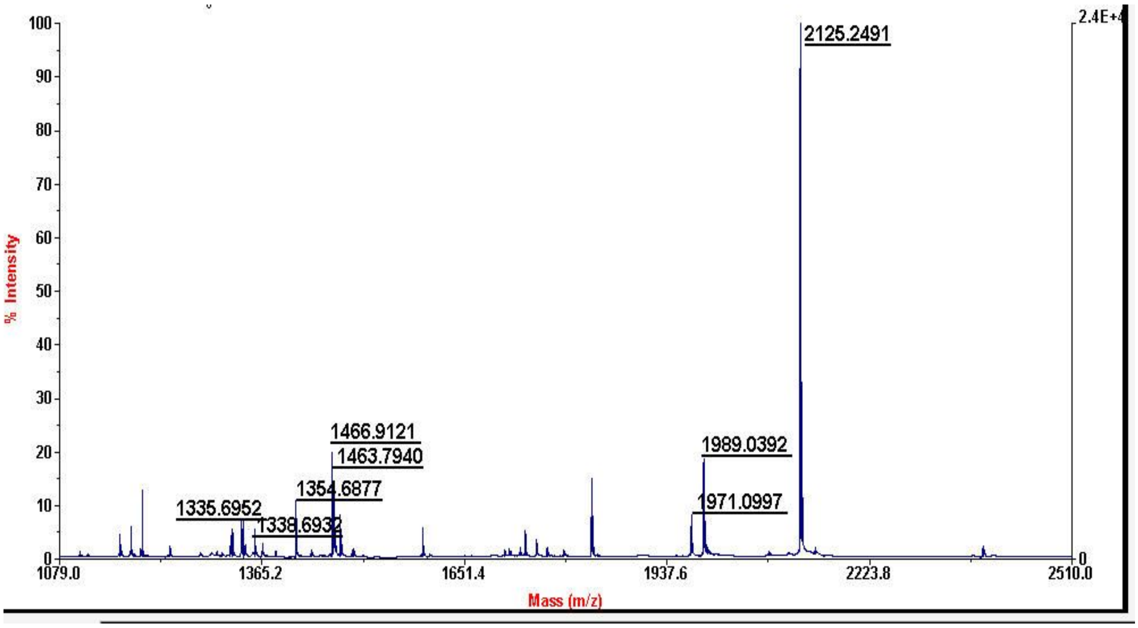
339 Phosphoglycerate mutase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
11 - 21	1312.5873	1311.5800	1311.5956	-0.0155	0	R.HGESAWNLENR.F
22 - 39	1979.8618	1978.8546	1978.8697	-0.0152	0	R.FSGWYDADLSPAGHEEAK.R
22 - 40	2135.9409	2134.9336	2134.9708	-0.0372	1	R.FSGWYDADLSPAGHEEAKR.G
47 - 61	1779.7725	1778.7652	1778.7822	-0.0169	0	R.DAGYEFDICFTSVQK.R
91 - 100	1059.5491	1058.5418	1058.5509	-0.0091	0	R.HYGGLTGLNK.A
118 - 138	2433.0867	2432.0795	2432.0995	-0.0200	0	R.SYDVPPPPMEPDHPFYSNISK.D
Oxidation (M)						
142 - 162	2425.1266	2424.1193	2424.1478	-0.0285	1	R.YADLTEDQLPSCESLKDTIAR.A
181 - 191	1150.6715	1149.6642	1149.6618	0.0024	0	R.VLIAAHGNSLR.G
223 - 240	2115.1216	2114.1144	2114.1194	-0.0050	0	K.NLKPIKPMQFLGDEETVR.K
223 - 240	2131.0870	2130.0797	2130.1143	-0.0346	0	K.NLKPIKPMQFLGDEETVR.K
Oxidation (M)						

No match to: 2070.1526, 2072.0240, 2373.0369

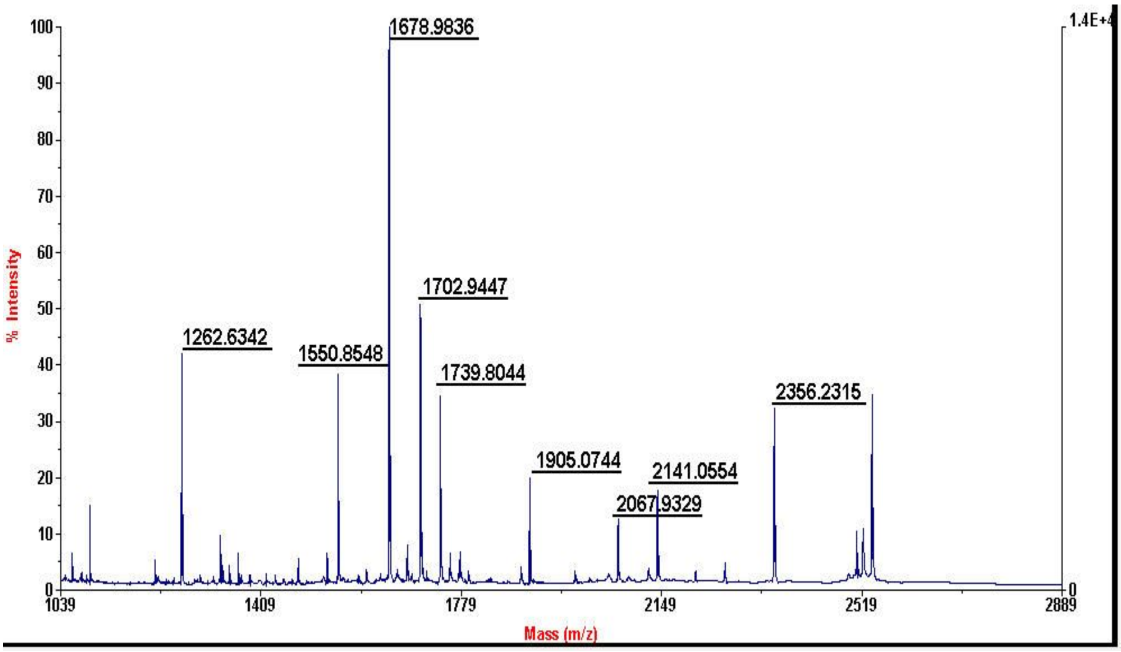
340 Enoyl-CoA hydratase, mitochondrial precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
44 - 56	1466.9121	1465.9048	1465.8365	0.0683	0	K.NNTVGLIQLNRPK.A	
57 - 74	1971.0997	1970.0924	1970.0142	0.0782	0	K.ALNALCDGLIDELNQALK.T	
158 - 178	2125.2491	2124.2419	2124.1328	0.1091	0	K.AQFAQPEILIGTIPGAGGTQR.L	
186 - 197	1338.6932	1337.6860	1337.6319	0.0541	0	K.SLAMEMVLTGDR.I	Oxidation (M)
186 - 197	1354.6877	1353.6804	1353.6268	0.0536	0	K.SLAMEMVLTGDR.I	2 Oxidation (M)
212 - 228	1989.0392	1988.0319	1987.9594	0.0725	0	K.ICPVETLVEEAIQCAEK.I	2
262 - 272	1335.6952	1334.6879	1334.6143	0.0736	0	K.LFYSTFATDDR.K	
262 - 273	1463.7940	1462.7867	1462.7092	0.0775	1	K.LFYSTFATDDRK.E	

No match to: 1195.6078, 1412.7595, 1475.8085, 1831.0081

341 Annexin A1

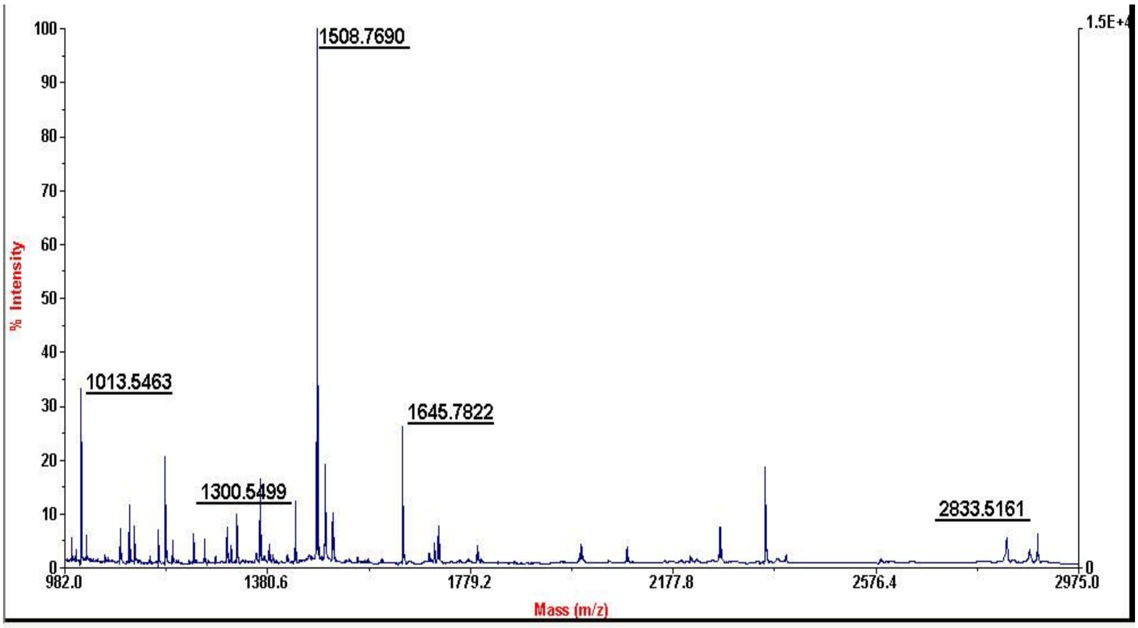


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
10 - 26	2141.0554	2140.0481	2140.0113	0.0369	0	K.QAWFIENEEQEYVQTVK.S
30 - 53	2356.2315	2355.2243	2355.1495	0.0747	0	K.GGPGSAVSPYPTFNPSSDVAALHK.A
82 - 98	1905.0744	1904.0672	1904.0255	0.0417	1	K.AAYLQETGKPLDETLKK.A
114 - 124	1262.6342	1261.6269	1261.5939	0.0330	0	K.TPAQFDADELR.A
129 - 144	1702.9447	1701.9374	1701.8785	0.0589	0	K.GLGTDEDTLIEILASR.T
186 - 204	2067.9329	2066.9256	2066.8777	0.0479	1	K.GDRSEDFGVNEDLADSDAR.A
189 - 204	1739.8044	1738.7971	1738.7282	0.0689	0	R.SEDFGVNEDLADSDAR.A
214 - 228	1678.9836	1677.9763	1677.9050	0.0713	1	R.KGTDVNVFNTILTTR.S
215 - 228	1550.8548	1549.8476	1549.8100	0.0375	0	K.GTDVNVFNTILTTR.S

No match to: 926.4785, 972.5301, 1092.6316, 1644.8739, 2537.2449

342

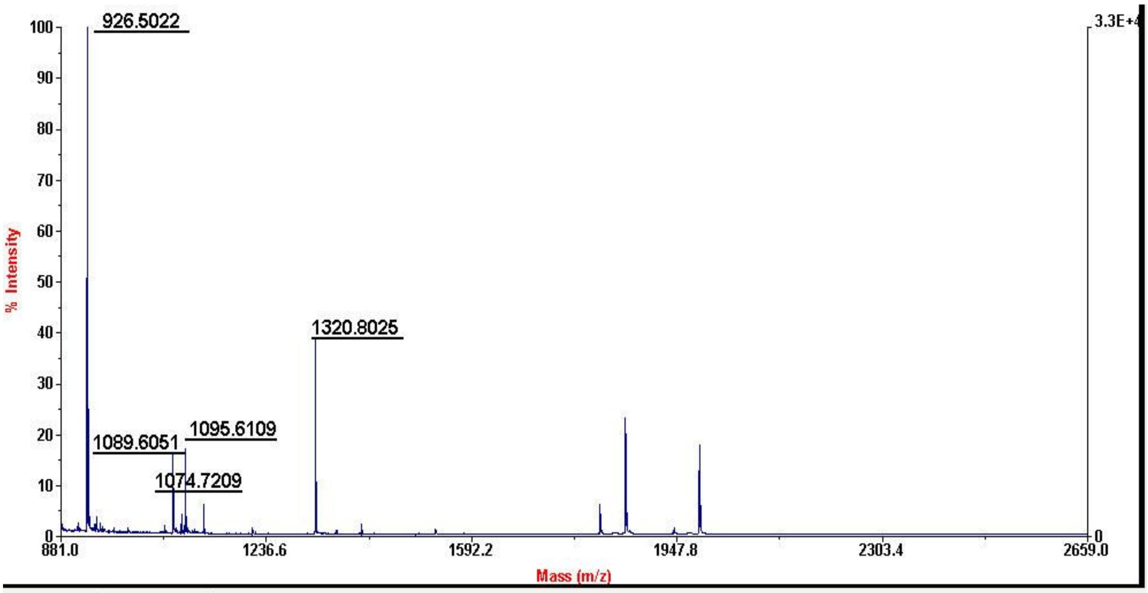
D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
45 - 73	2833.5161	2832.5089	2832.4004	0.1085	1	R.TYASAAEPVGSKAVLVTGCDSGFGFSLAK.H	
200 - 212	1508.7690	1507.7617	1507.7275	0.0342	1	R.MANPARSPYCITK.F	
213 - 223	1300.5499	1299.5426	1299.5918	-0.0491	0	K.FGVEAFSDCLR.Y	
276 - 283	1013.5463	1012.5390	1012.5229	0.0161	1	K.YFDEKIAK.M	
315 - 325	1645.7822	1644.7750	1644.7184	0.0566	0	R.YHPMDYYWWLR.M	Oxidation (M)

No match to: 1365.6449, 1434.7310, 1477.6980, 1493.7019, 2270.0582, 2358.1232

343 Glutathione transferase omega-1

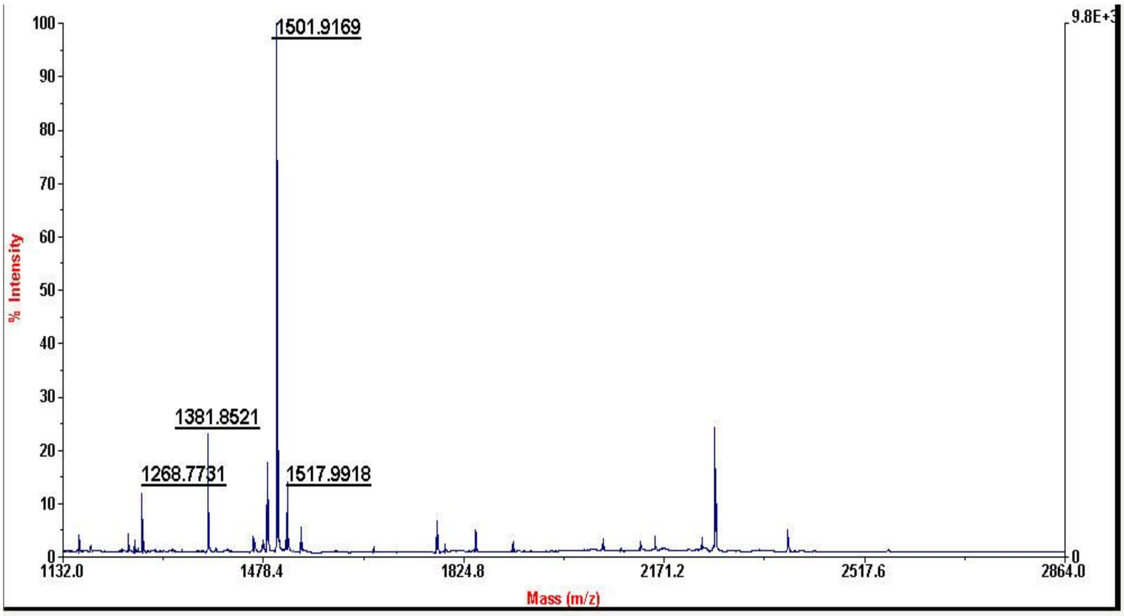


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
12 - 25	1320.8025	1319.7952	1319.6834	0.1118	0	K.GSAPPGPVPEGSIR.I

31 - 37	926.5022	925.4950	925.4116	0.0833	0	R.FCPFAER.T
58 - 65	1095.6109	1094.6036	1094.5549	0.0487	0	K.NKPEWFFK.K
102 - 110	1089.6051	1088.5978	1088.5390	0.0588	0	K.LLPDDPYEK.A
123 - 132	1074.7209	1073.7136	1073.6233	0.0903	0	K.VPSLVGSFIR.S

No match to: 1813.9972, 1857.9886, 1866.2566, 1968.1782, 1986.0891

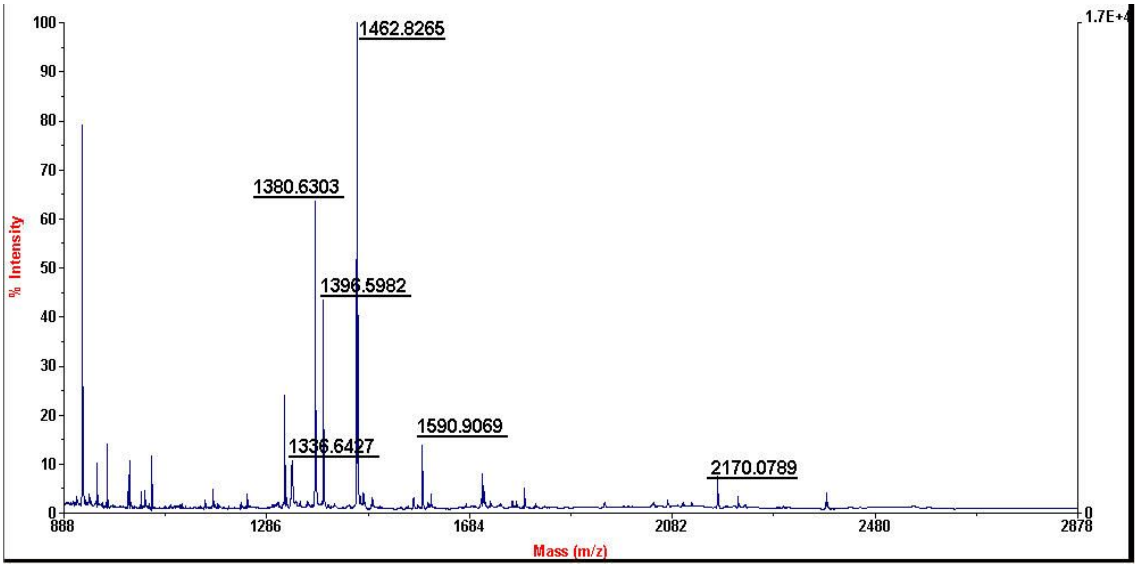
344 Proteasome activator complex subunit 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
14 - 24	1381.8521	1380.8448	1380.6708	0.1741	1	K.VDVFREDLCTK.T
25 - 35	1268.7731	1267.7658	1267.6448	0.1210	0	K.TENLLGSYFPK.K
59 - 72	1517.9918	1516.9846	1516.8501	0.1345	1	K.APLDIPVPDPVKEK.E
191 - 198	971.5868	970.5795	970.4621	0.1174	0	K.QPHVGDYR.Q
199 - 210	1501.9169	1500.9097	1500.7208	0.1888	0	R.QLVHELDEAEYR.D

No match to: 1111.7005, 1484.8978, 2258.2733

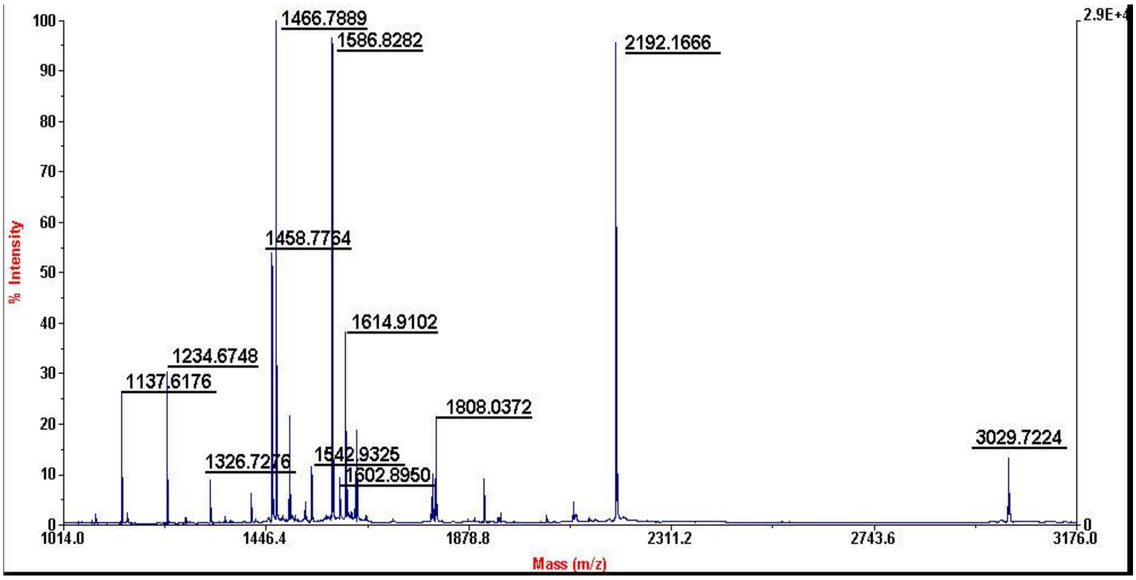
345 Proteasome subunit beta type 7 precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
2 - 21	2170.0789	2169.0716	2169.0426	0.0290	1	M.AAVSVYAPPVGGFSFDNCRR.N	
185 - 195	1380.6303	1379.6230	1379.6027	0.0203	0	K.FRPDMEEEEAK.N	
185 - 195	1396.5982	1395.5909	1395.5976	-0.0067	0	K.FRPDMEEEEAK.N	Oxidation (M)
226 - 237	1462.8265	1461.8193	1461.7980	0.0213	0	K.LDFLRPYTVPNK.K	
226 - 238	1590.9069	1589.8996	1589.8929	0.0067	1	K.LDFLRPYTVPNKK.G	
247 - 258	1336.6427	1335.6354	1335.6704	-0.0350	1	R.CEKGTTAVLTEK.I	

No match to: 923.5151, 972.4783, 1014.6009, 1060.5647, 1320.6975, 1708.8095

346 6-phosphogluconolactonase



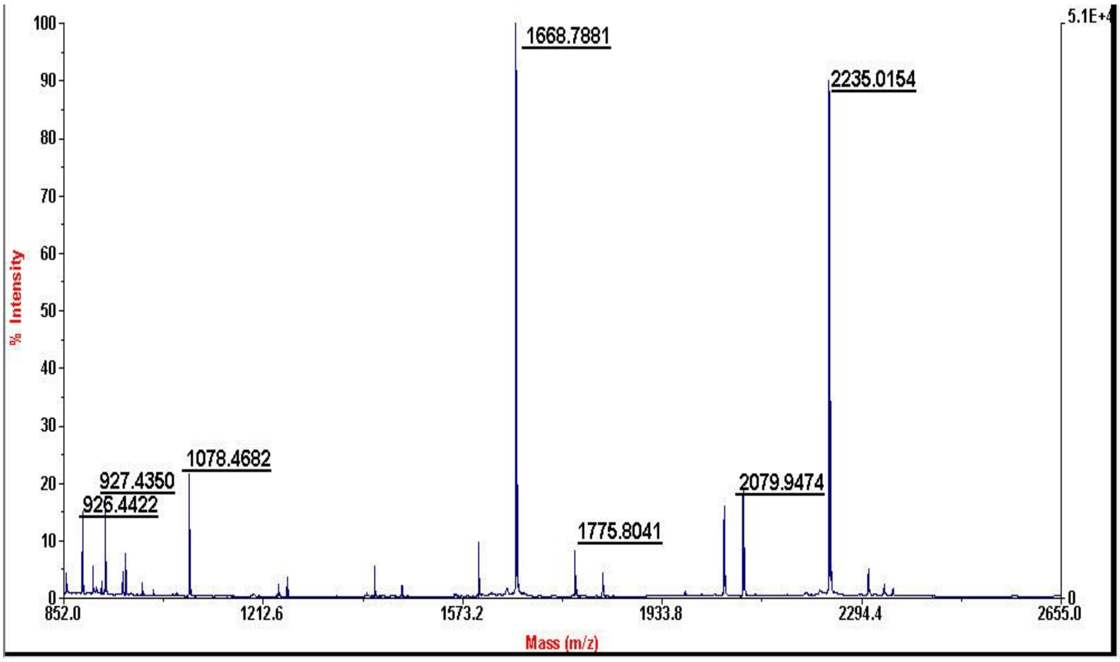
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
57 - 72	1491.0201	1490.0128	1489.8252	0.1875	0	R.ELPAAVAPAGPASLAR.W

73 - 81	1183.6755	1182.6682	1182.5128	0.1554	0	R.WTLGFCDER.L
82 - 96	1768.0843	1767.0770	1766.8628	0.2143	0	R.LVPFDHAESTYGLYR.T
171 - 185	1602.1037	1601.0965	1600.8937	0.2028	0	K.IVAPISDSPKPPPQR.V
236 - 246	1351.8167	1350.8094	1350.6390	0.1704	0	K.LCWFLDEAAAR.L

No match to: 913.6140, 1734.0173, 2485.7129, 2530.5795, 2546.5592, 2555.4946, 2794.8234

347

NG,NG-dimethylarginine dimethylaminohydrolase 2

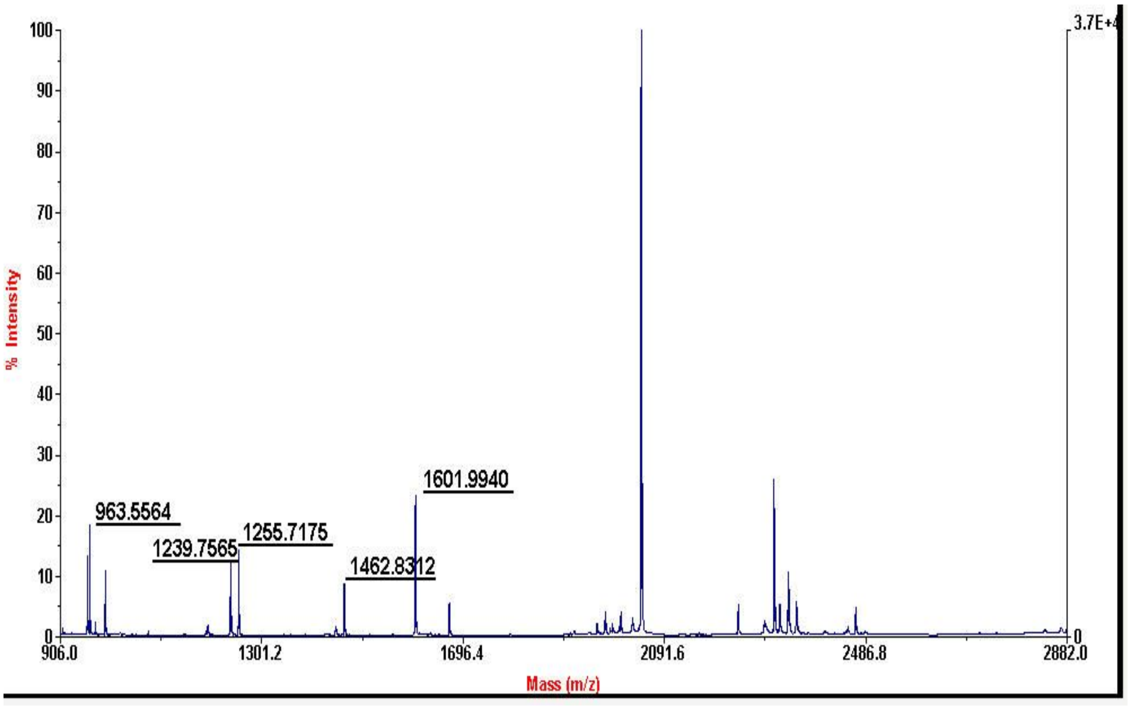


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
18 - 40	2079.9474	2078.9402	2079.0848	-0.1446	0	R.GVPESLASGEGAGAGLPALDLAK.A
97 - 104	927.4350	926.4277	926.4934	-0.0657	0	R.RPEVDGVR.K
114 - 134	2235.0154	2234.0081	2234.1067	-0.0986	0	R.IVEIGDENATLDGTDVLFTGR.E
135 - 142	926.4422	925.4349	925.4909	-0.0560	0	R.EFFVGLSK.W
148 - 157	1078.4682	1077.4609	1077.5455	-0.0845	0	R.GAEIVADTFR.D
158 - 173	1668.7881	1667.7808	1667.8631	-0.0823	0	R.DFAVSTVPVSGPSHLR.G
252 - 267	1775.8041	1774.7968	1774.9023	-0.1055	0	K.LSDVTLVPVSCSELEK.A

No match to: 963.4061, 1601.7504, 2044.9446, 2219.6829

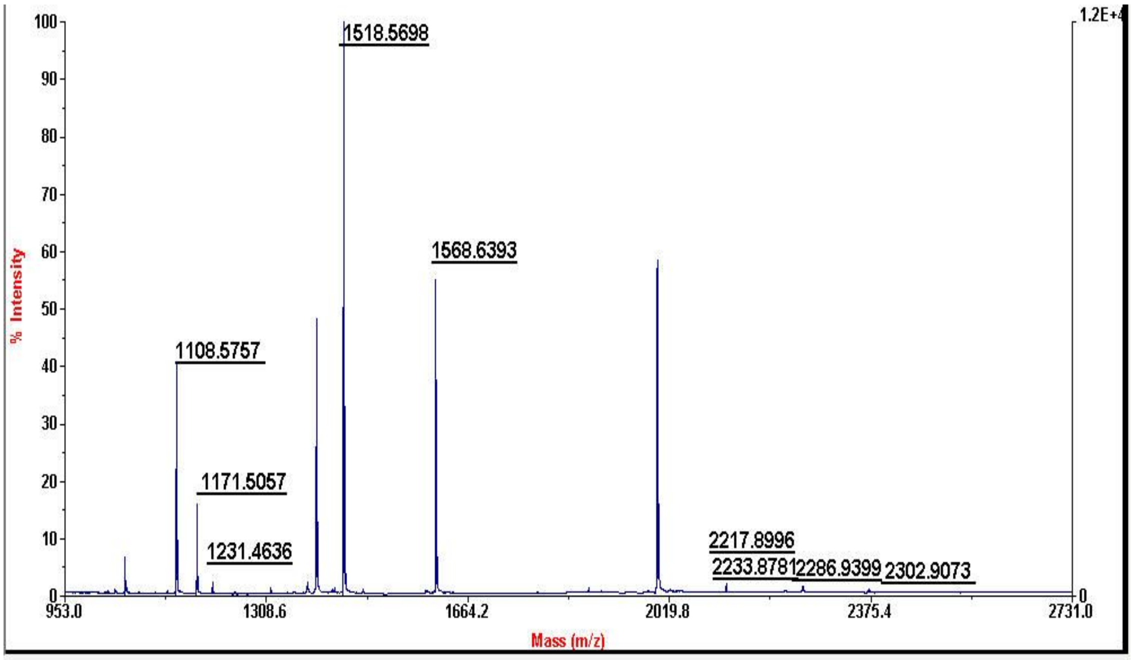
348

Cathepsin D precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
195 - 205	1239.7565	1238.7492	1238.6118	0.1374	0	K.FDGILGMAYPR.I	
195 - 205	1255.7175	1254.7102	1254.6067	0.1035	0	K.FDGILGMAYPR.I	Oxidation (M)
223 - 235	1601.9940	1600.9867	1600.8249	0.1618	0	K.LVDQNIFSFYLSR.D	
393 - 399	963.5564	962.5491	962.4498	0.0993	0	R.YYTVFDR.D	
393 - 403	1462.8312	1461.8239	1461.6637	0.1602	1	R.YYTVFDRDNNR.V	

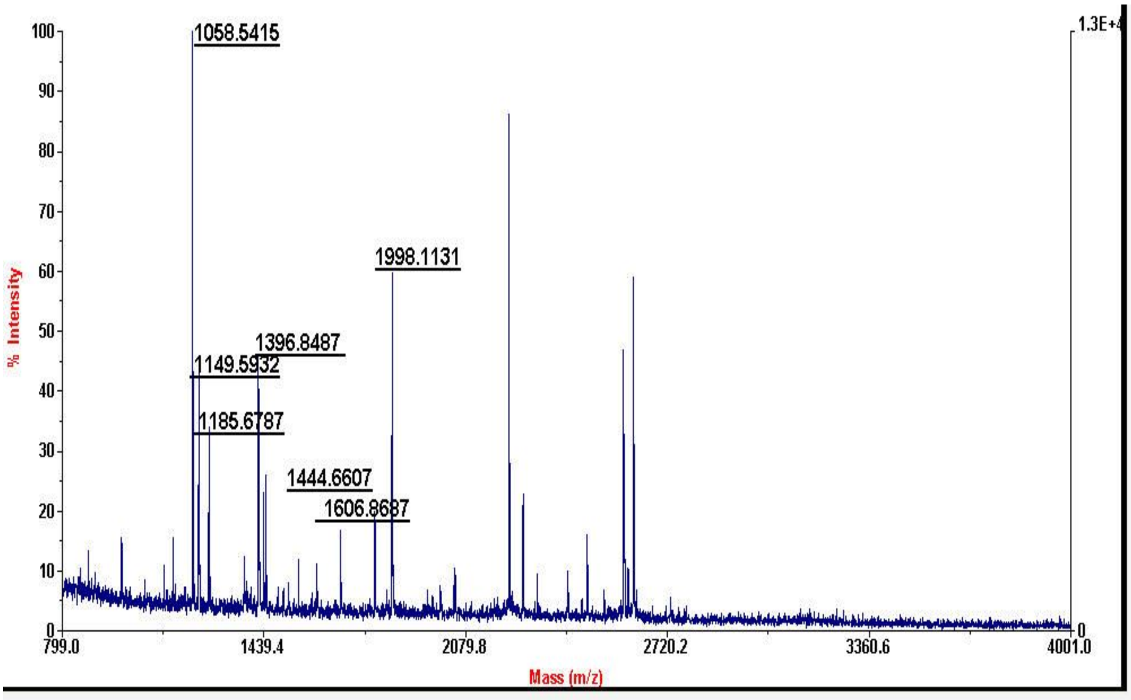
349 F-actin capping protein subunit beta



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
15 - 23	1108.5757	1107.5684	1107.6400	-0.0716	1	R.RLPPQQIEK.N
58 - 66	1231.4636	1230.4563	1230.5339	-0.0776	0	K.DYLLCDYNR.D
73 - 92	2217.8996	2216.8923	2217.0160	-0.1238	1	R.SPWSNKYDPPLEDGAMPSAR.L
73 - 92	2233.8781	2232.8709	2233.0110	-0.1401	1	R.SPWSNKYDPPLEDGAMPSAR.L
Oxidation (M)						
79 - 92	1518.5698	1517.5625	1517.6820	-0.1195	0	K.YDPPLEDGAMPSAR.L
95 - 108	1696.7380	1695.7307	1695.8216	-0.0909	1	R.KLEVEANNAFDQYR.D
96 - 108	1568.6393	1567.6321	1567.7267	-0.0946	0	K.LEVEANNAFDQYR.D
146 - 159	1685.6864	1684.6791	1684.7879	-0.1088	0	K.GCWDSIHVVEVQEK.S
196 - 215	2286.9399	2285.9326	2286.0369	-0.1043	1	R.QMEKDETVSDCSPHIANIGR.L
196 - 215	2302.9073	2301.9000	2302.0318	-0.1318	1	R.QMEKDETVSDCSPHIANIGR.L ;
Oxidation (M)						
226 - 235	1171.5057	1170.4984	1170.5921	-0.0936	0	R.STLNEIYFGK.T

No match to: 1561.7091, 1606.6195, 1622.5874, 2285.9427

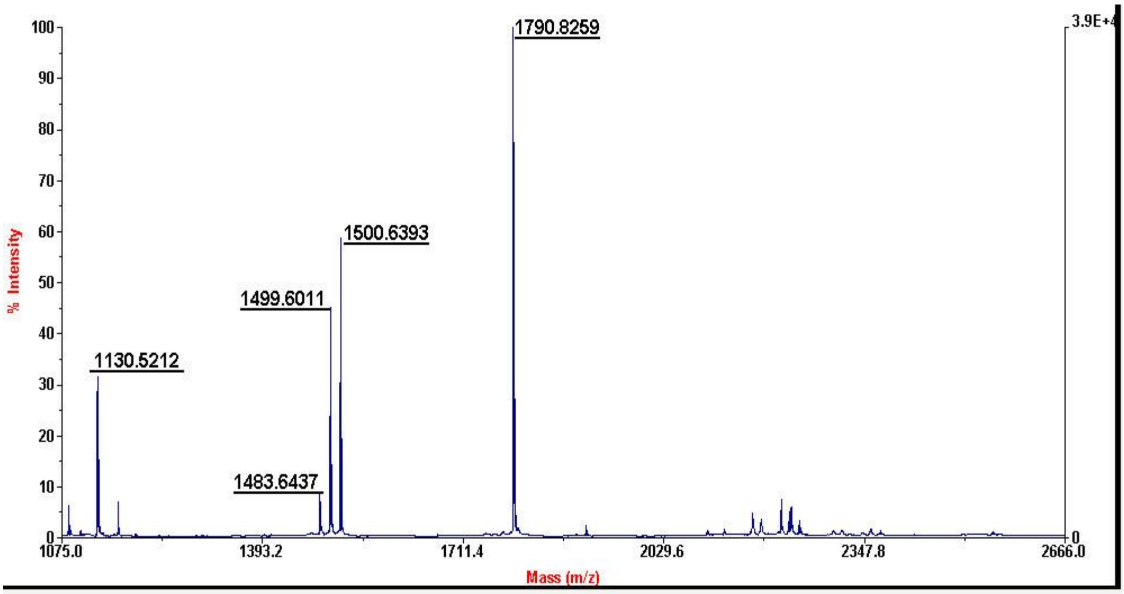
350 Prohibitin - Homo sapiens



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
84 - 93	1185.6787	1184.6714	1184.6513	0.0201	0	K.DLQNVNITLR.I
94 - 105	1396.8487	1395.8414	1395.8350	0.0064	0	R.ILFRPVASQLPR.I
106 - 117	1444.6607	1443.6534	1443.6518	0.0017	0	R.IFTSIGEDYDER.V
134 - 143	1149.5932	1148.5860	1148.5826	0.0034	0	R.FDAGELITQR.E
187 - 195	1058.5415	1057.5342	1057.5152	0.0190	0	K.QVAQQEAER.A
220 - 239	1998.1131	1997.1058	1997.0793	0.0265	0	K.AAELIANSLATAGDGLIELR.K
240 - 253	1606.8687	1605.8614	1605.8362	0.0252	1	R.KLEAAEDIAYQLSR.S

No match to: 1379.6959, 1394.7854, 1637.7559, 1982.5520, 2007.4528

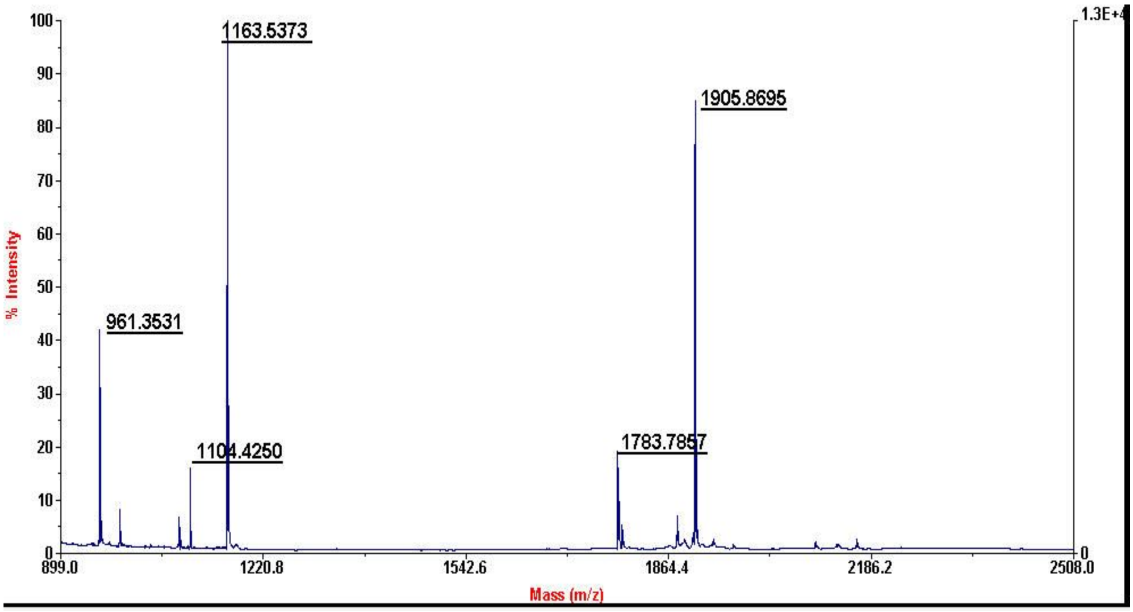
351 Netrin-1 precursor - Homo sapiens



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
66 - 76	1130.5212	1129.5139	1129.5662	-0.0523	0	R.VSSTCGRPPAR.Y	
88 - 100	1500.6393	1499.6320	1499.6973	-0.0653	1	R.LRSCHLCNASDPK.K	
170 - 183	1790.8259	1789.8186	1789.8610	-0.0424	1	R.TWVPFQFYSTQCRK.M	
184 - 195	1499.6011	1498.5938	1498.7827	-0.1888	1	K.MYNRPHRAPITK.Q	Oxidation (M)
352 - 358	960.4040	959.3967	959.4422	-0.0455	0	R.FNMELYK.L	Oxidation (M)
373 - 384	1483.6437	1482.6364	1482.6357	0.0007	1	R.HNTAGRHCHYCK.E	

No match to: 1132.4907, 1163.5954, 1516.6416

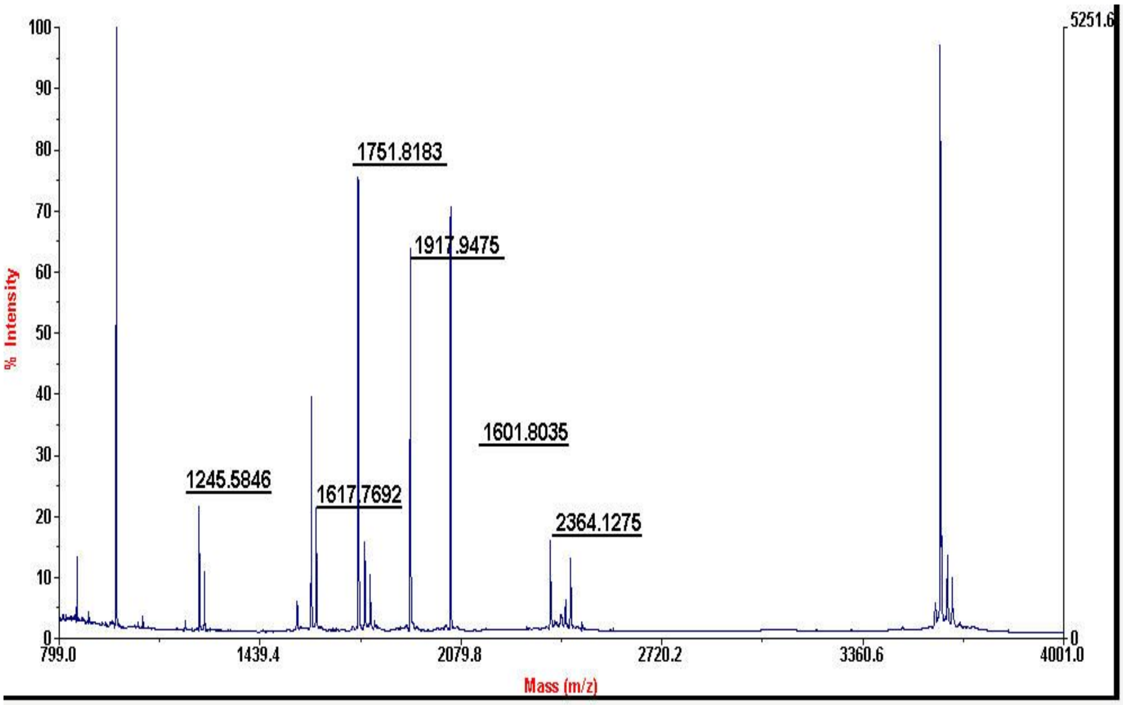
352 Heat-shock protein beta-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
13 - 20	961.3531	960.3458	960.4454	-0.0996	0	R.GPSWDPFR.D
21 - 27	960.3557	959.3484	959.4250	-0.0766	0	R.DWYPHSR.L
28 - 37	1163.5373	1162.5300	1162.6135	-0.0835	0	R.LFDQAFGLPR.L
97 - 112	1783.7857	1782.7784	1782.9152	-0.1368	0	R.VSLDVNHFAPDELTVK.T
128 - 136	1104.4250	1103.4178	1103.4996	-0.0818	0	R.QDEHGYISR.C
172 - 188	1905.8695	1904.8622	1904.9843	-0.1222	0	K.LATQSNEITIPVTFESR.A

No match to: 993.3502, 1087.4316, 1865.4597, 1877.8835, 1904.8251

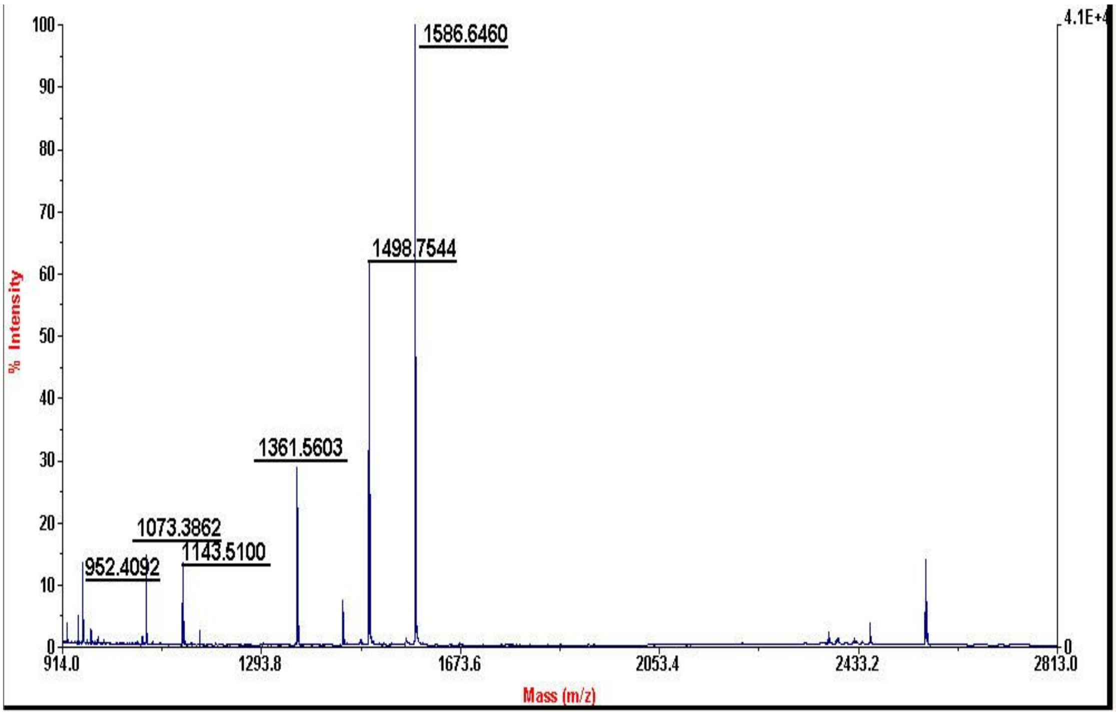
353 Rho GDP-dissociation inhibitor 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
34 - 49	1917.9475	1916.9402	1916.9327	0.0075	1	K.SIQEIQELDKDDESLR.K	
128 - 134	980.5050	979.4977	979.4875	0.0102	0	K.YIQHTYR.K	
139 - 152	1601.8035	1600.7962	1600.7555	0.0407	1	K.IDKTDYMVGSYGPR.A	
139 - 152	1617.7692	1616.7619	1616.7505	0.0115	1	K.IDKTDYMVGSYGPR.A	Oxidation (M)
142 - 152	1245.5846	1244.5773	1244.5496	0.0277	0	K.TDYMVGSYGPR.A	
153 - 167	1751.8183	1750.8110	1750.8301	-0.0191	0	R.AEEYEFLTPVEEAPK.G	
181 - 199	2364.1275	2363.1202	2363.1070	0.0133	1	R.FTDDDKTDHLSWEWNLTIK.K	

No match to: 1557.2394, 2046.0488, 2428.1168

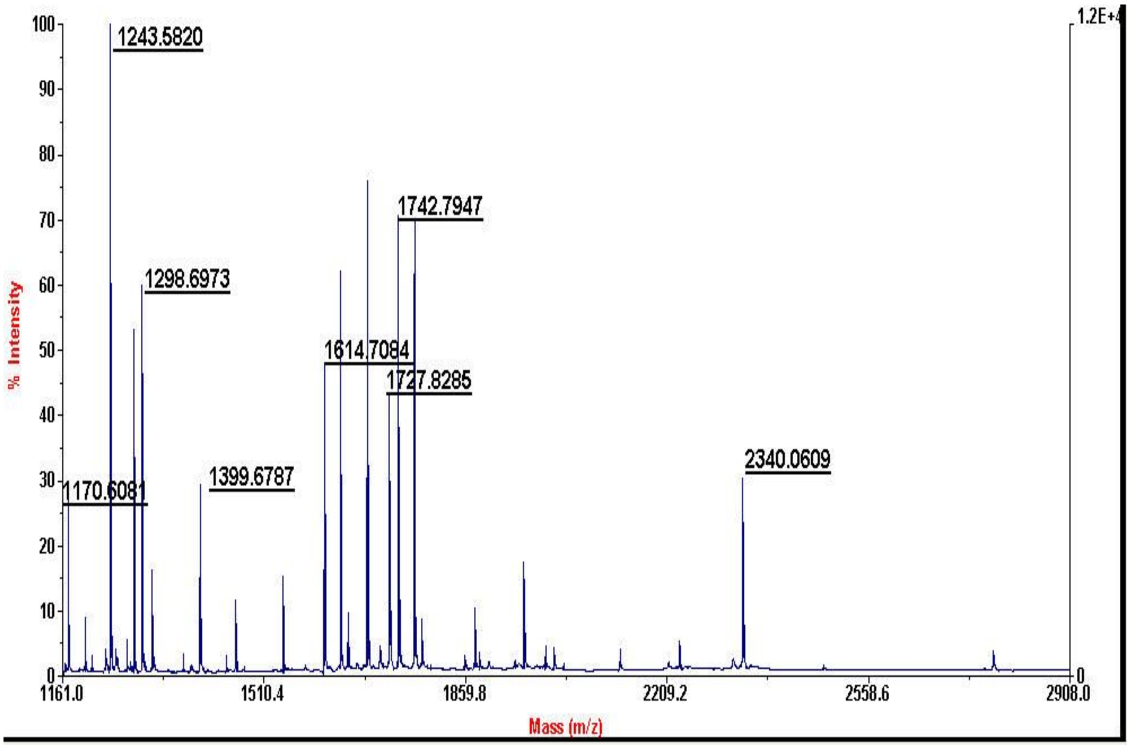
354 Heme-binding protein 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
27 - 41	1586.6460	1585.6387	1585.7372	-0.0985	0	K.APEDAGPQPGSYEIR.H
133 - 140	952.4092	951.4020	951.4848	-0.0828	0	R.AEMTVFVR.S
141 - 150	1073.3862	1072.3789	1072.4825	-0.1036	0	R.SFDGFSSAQK.N
151 - 163	1498.7544	1497.7471	1497.8515	-0.1044	0	K.NQEQLLTLASILR.E
173 - 184	1361.5603	1360.5530	1360.6663	-0.1133	0	K.VYYYTAGYNSPVK.L
189 - 197	1143.5100	1142.5027	1142.6084	-0.1056	0	R.NNEVWLIQK.N

No match to: 943.4850, 1449.5172, 2561.0736

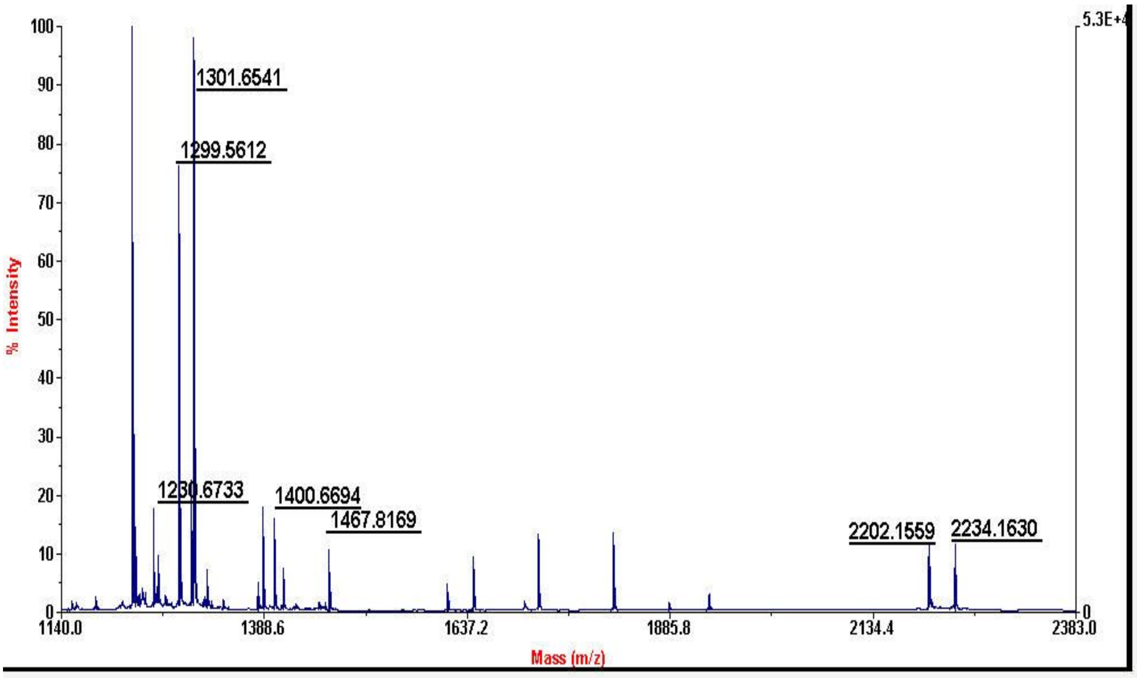
355 Tropomyosin alpha-4 chain



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
13 - 27	1742.7947	1741.7875	1741.8595	-0.0720	1	R.KIQALQQQADEAEDR.A
14 - 27	1614.7084	1613.7011	1613.7645	-0.0634	0	K.IQALQQQADEAEDR.A
55 - 65	1399.6787	1398.6714	1398.7467	-0.0752	1	R.RIQLVEEELDR.A
56 - 65	1243.5820	1242.5748	1242.6456	-0.0708	0	R.IQLVEEELDR.A
56 - 69	1727.8285	1726.8212	1726.8849	-0.0637	1	R.IQLVEEELDRAQER.L
132 - 142	1298.6973	1297.6900	1297.7605	-0.0705	1	R.KLVILEGELER.A
133 - 142	1170.6081	1169.6009	1169.6656	-0.0647	0	K.LVILEGELER.A
229 - 248	2340.0609	2339.0536	2339.1063	-0.0527	0	K.EENVGLHQTLDQTLNELNCI.-

No match to: 1284.6673, 1543.6975, 1642.7373, 1688.7293, 1689.7067, 1770.8102, 1960.9501

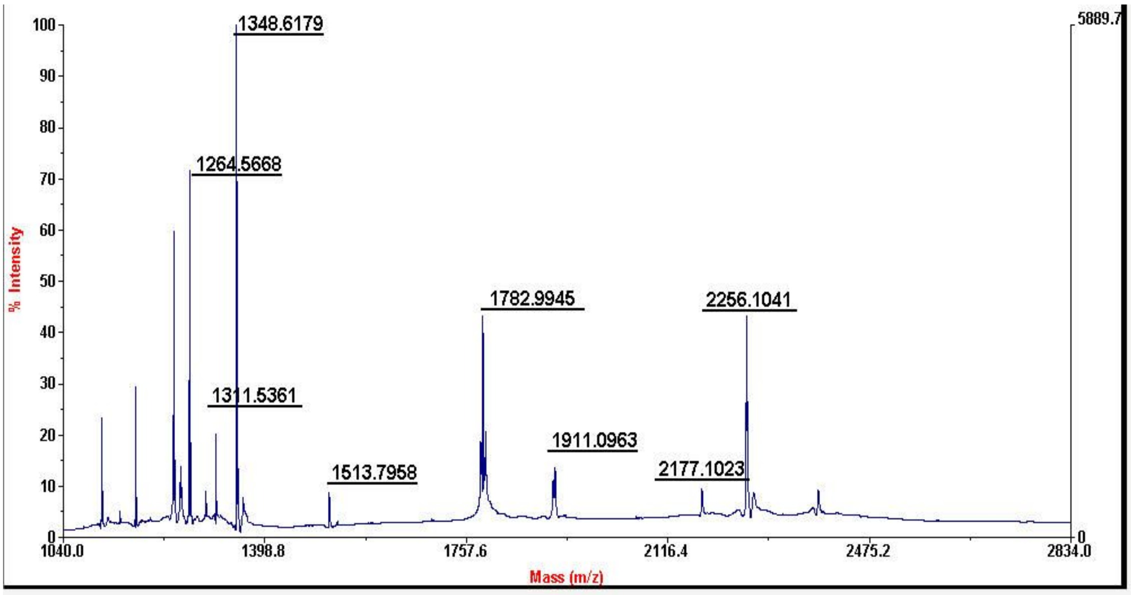
356 Guanine nucleotide-binding protein alpha-15 subunit



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
100 - 110	1301.6541	1300.6468	1300.7139	-0.0671	0	R.LQIPFSRPESK.H
111 - 129	2234.1630	2233.1557	2233.0838	0.0719	1	K.HHASLVMSQDPYKVTTFEK.R Oxidation (M)
130 - 140	1467.8169	1466.8096	1466.7241	0.0856	1	K.RYAAAMQWLWR.D Oxidation (M)
187 - 205	2202.1559	2201.1486	2201.0609	0.0877	1	R.MPTTGINEYCFSVQKTNLR.I
202 - 213	1299.5612	1298.5539	1298.7307	-0.1767	1	K.TNLRIVDVGGQK.S
310 - 318	1230.6733	1229.6661	1229.6227	0.0434	1	K.RFILDMYTR.M Oxidation (M)
319 - 331	1400.6694	1399.6621	1399.5748	0.0873	0	R.MYTGCVDGPEGSK.K

No match to: 1226.5516, 1252.6184, 1283.5880, 1386.7171, 1644.7983, 1723.9666, 1815.8812

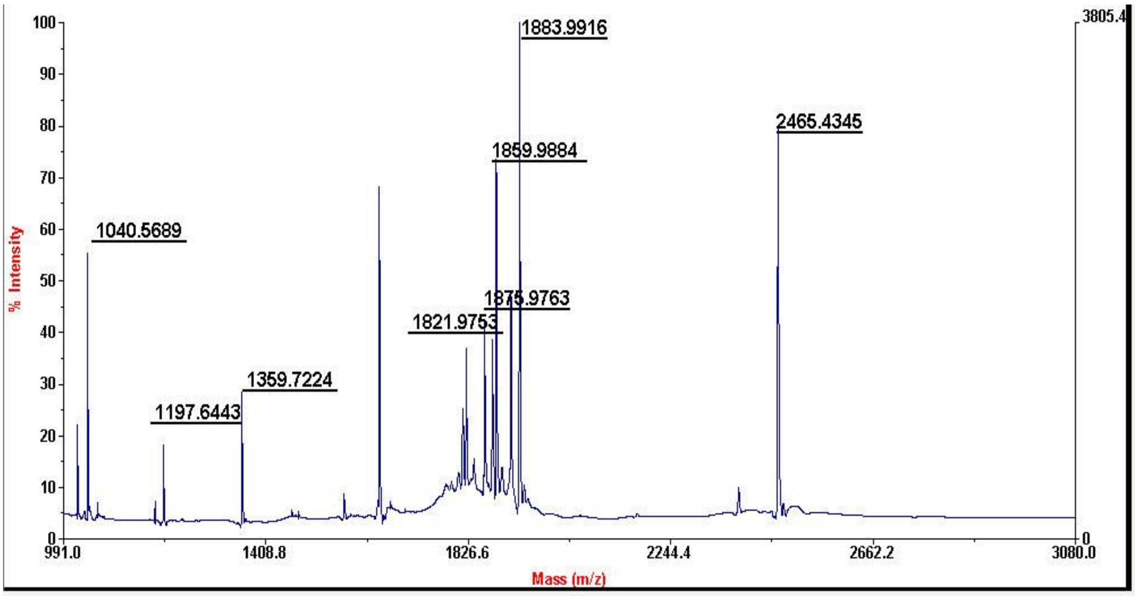
357 Heat shock protein HSP 90-beta



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
149 - 168	2256.1041	2255.0968	2254.9515	0.1453	0	K.HNDDEQYAWESSAGGSFTVR.A
187 - 196	1311.5361	1310.5289	1310.5626	-0.0338	0	K.EDQTEYLEER.R
320 - 330	1348.6179	1347.6106	1347.6571	-0.0465	0	K.HFSVEGQLEFR.A
379 - 392	1513.7958	1512.7885	1512.7783	0.0102	0	R.GVVDSEDLPLNISR.E
457 - 475	2177.1023	2176.0950	2175.9378	0.1571	0	R.YHTSQSGDEMTSLSEYVSR.M
613 - 623	1264.5668	1263.5595	1263.4933	0.0661	0	R.DNSTMGYMMAK.K Oxidation (M)
624 - 639	1911.0963	1910.0890	1910.0374	0.0516	1	K.KHLEINPDHPIVETLR.Q
625 - 639	1782.9945	1781.9872	1781.9424	0.0448	0	K.HLEINPDHPIVETLR.Q

No match to: 1108.4895, 1168.4961, 1235.5470, 1786.9979

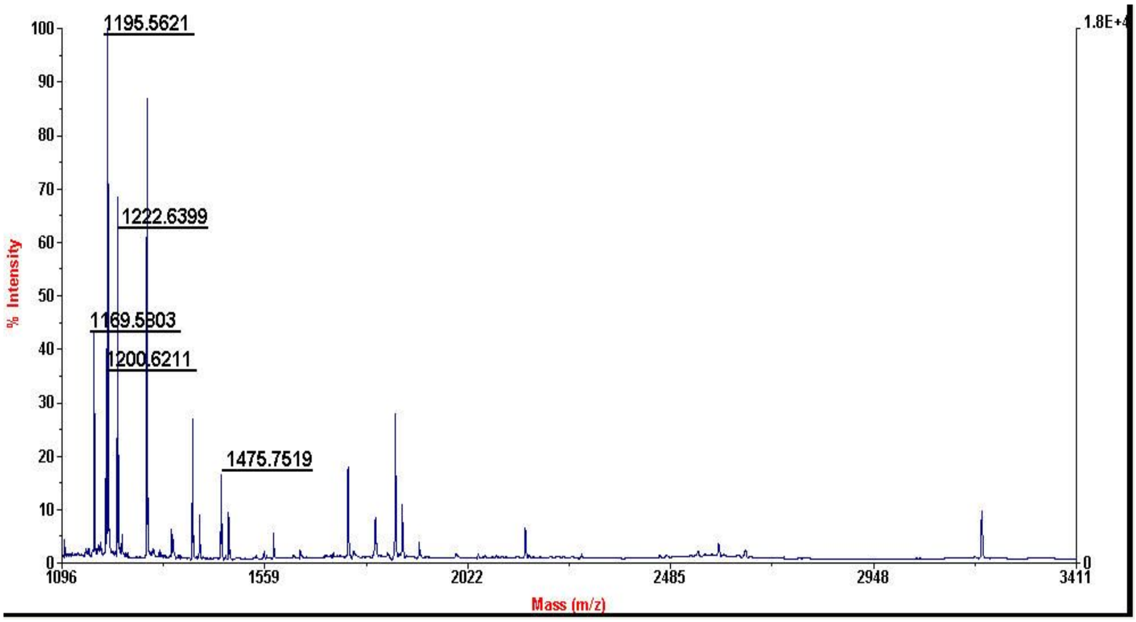
358 Kaptin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
33 - 43	1197.6443	1196.6370	1196.6401	-0.0031	0	R.LDIDSPPITAR.N
44 - 56	1359.7224	1358.7151	1358.6976	0.0175	0	R.NTGIICTIGPASR.S
74 - 89	1883.9916	1882.9843	1882.8962	0.0881	0	R.LNFSHGTHEYHAETIK.N
93 - 115	2465.4345	2464.4272	2464.2849	0.1423	0	R.TATESFASDPILYRPVAVALDTK.G
231 - 246	1859.9884	1858.9811	1858.8923	0.0888	0	K.FGVEQDVDMVFASFIR.K
231 - 246	1875.9763	1874.9690	1874.8872	0.0818	0	K.FGVEQDVDMVFASFIR.K Oxidation (M)
248 - 256	1040.5689	1039.5616	1039.5410	0.0206	1	K.ASDVHEVRK.V
271 - 278	953.4893	952.4820	952.4726	0.0094	0	K.IENHEGVR.R
279 - 294	1821.9753	1820.9680	1820.9090	0.0590	1	R.RFDEILEASDGIMVAR.G
279 - 294	1837.9696	1836.9623	1836.9039	0.0584	1	R.RFDEILEASDGIMVAR.G Oxidation (M)
280 - 294	1665.8717	1664.8644	1664.8079	0.0565	0	R.FDEILEASDGIMVAR.G
368 - 376	1019.5242	1018.5170	1018.5083	0.0086	0	K.GDYPLEAVR.M
384 - 399	1932.0815	1931.0742	1930.9788	0.0954	0	R.EAEAAIYHLQLFEELR.R
476 - 489	1642.8189	1641.8116	1641.7634	0.0482	0	K.DPVQEAWAEDVDLR.V

No match to: 1033.6079, 1179.6230, 1570.7916, 1914.0799

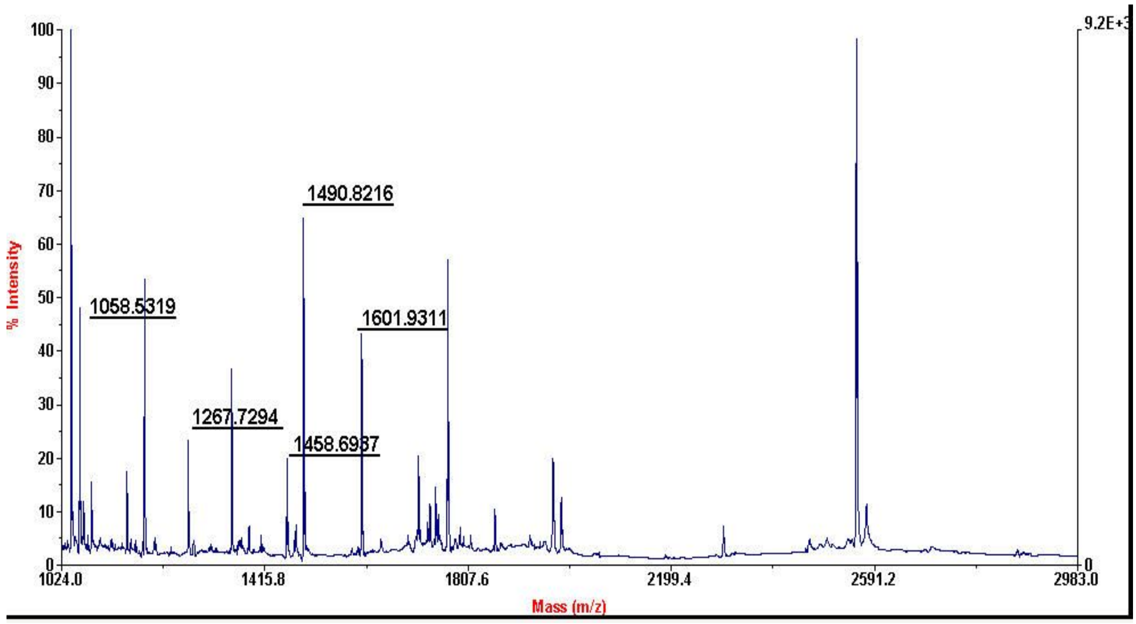
359 Nicotinate-nucleotide pyrophosphorylase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
92 - 102	1222.6399	1221.6327	1221.6288	0.0039	0	R.GPAHCLLLGER.V
111 - 126	1475.7519	1474.7446	1474.7198	0.0249	0	R.CSGIASAAAAAVEAAR.G
127 - 138	1169.5803	1168.5730	1168.5737	-0.0007	0	R.GAGWTGHVAGTR.K
150 - 161	1200.6211	1199.6139	1199.6410	-0.0272	0	K.YGLLVGGAASHR.Y
172 - 183	1195.5621	1194.5549	1194.5992	-0.0444	0	K.DNHVVAAGGVEK.A

No match to: 1289.5931, 1393.5964, 1458.7245, 1748.9066, 1855.9294, 1871.9182

360 Integrin-linked protein kinase

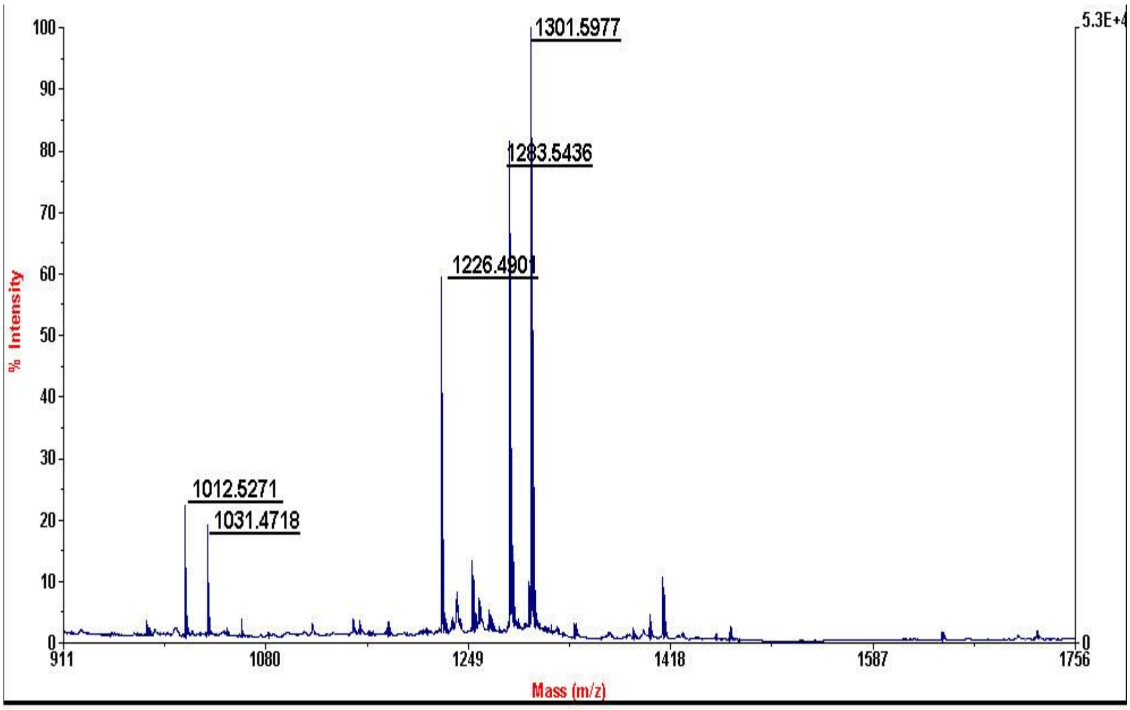


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 56	1490.8216	1489.8143	1489.7744	0.0399	1	R.EGRSAVVEMLIMR.G

212 - 220	1058.5319	1057.5246	1057.5556	-0.0310	0	R.WQGNDIVVK.V	
324 - 334	1267.7294	1266.7221	1266.5584	0.1637	0	R.SVMIDEDMTAR.I	
342 - 349	998.2748	997.2675	997.4440	-0.1764	0	K.FSFQCPGR.M	
427 - 438	1458.6937	1457.6865	1457.7119	-0.0254	1	K.ICMNEDPAKRPK.F	
436 - 448	1601.9311	1600.9238	1600.9010	0.0228	1	K.RPKFDMIVPILEK.M	Oxidation (M)

No match to: 913.4206, 1042.5545, 1183.4828, 1351.6520, 1767.9243, 1971.0707, 2555.4199

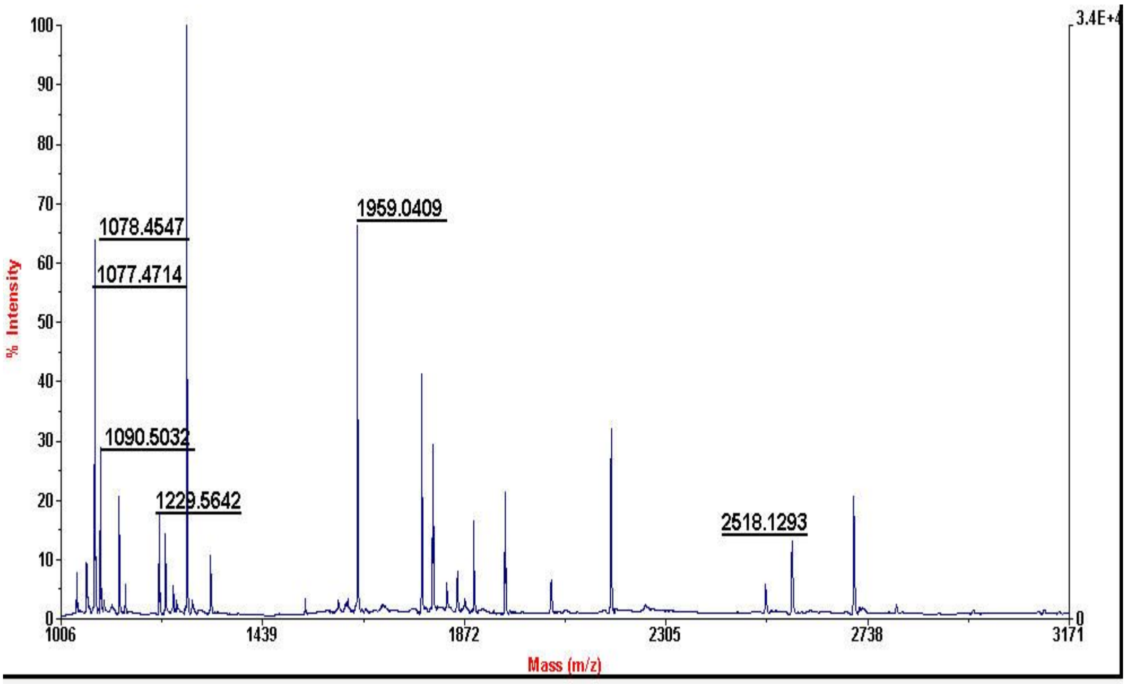
361 Kelch-like protein 15



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
58 - 67	1301.5977	1300.5904	1300.5904	0.0001	1	R.IMFTADMRER.D	2 Oxidation (M)
119 - 127	1031.4718	1030.4646	1030.4980	-0.0334	0	K.FCCSFLLAK.I	
474 - 482	1226.4901	1225.4828	1225.5484	-0.0657	1	K.MNYARCFHK.M	
533 - 542	1012.5271	1011.5198	1011.5349	-0.0151	0	R.SGHGVTVLDK.Q	
572 - 581	1283.5436	1282.5363	1282.5322	0.0042	1	K.EDEYPRMPCK.L	Oxidation (M)

No match to: 1252.5429, 1411.6308

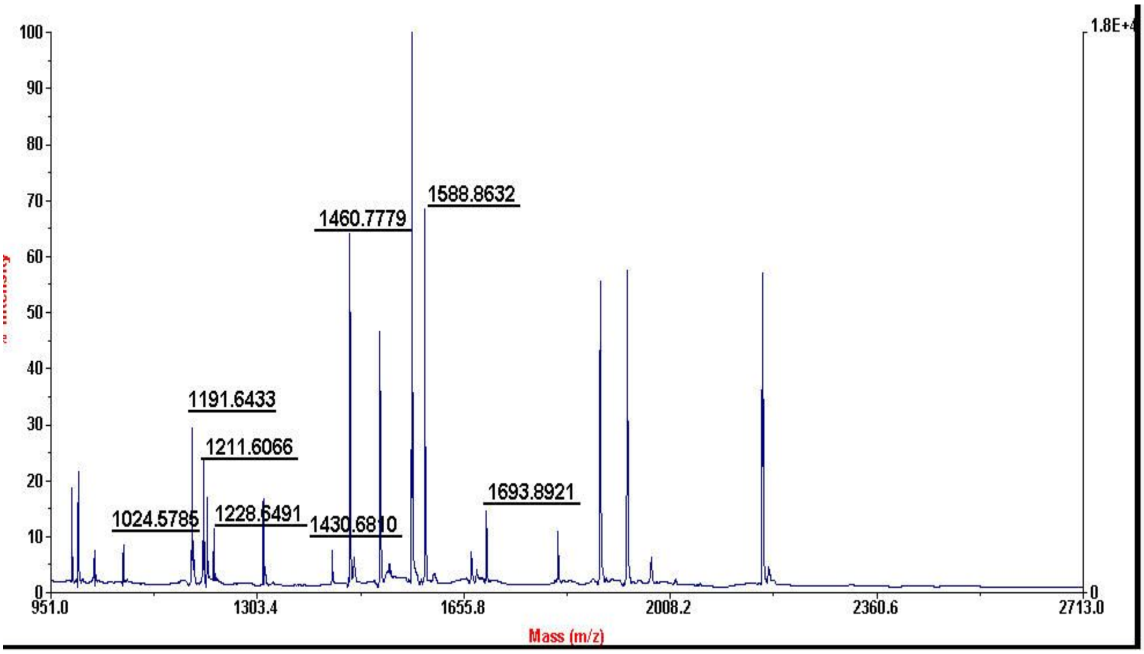
362 Proteasome activator complex subunit



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 12	1229.5642	1228.5569	1228.7027	-0.1458	1	M.ASLLKVDQEVK.L
38 - 46	1077.4714	1076.4641	1076.6117	-0.1476	0	K.LLELDSFLK.E
89 - 110	2518.1293	2517.1220	2517.1589	-0.0369	1	R.LDECEEAFQGTKVFVMPNGMLK.S
2 Oxidation (M)						
196 - 203	1078.4547	1077.4475	1077.4879	-0.0405	0	K.YPHVEDYR.R
204 - 212	1090.5032	1089.4959	1089.5666	-0.0707	1	R.RTVTEIDEK.E
226 - 241	1959.0409	1958.0336	1958.0295	0.0041	1	R.NQYVTLHDMILKNIEK.I

No match to: 922.3591, 1060.0781, 1130.5310, 1143.5737, 1216.5976, 1275.6383, 1326.7217, 1641.8707, 1779.7589, 1803.9518, 1855.9754, 1891.8696

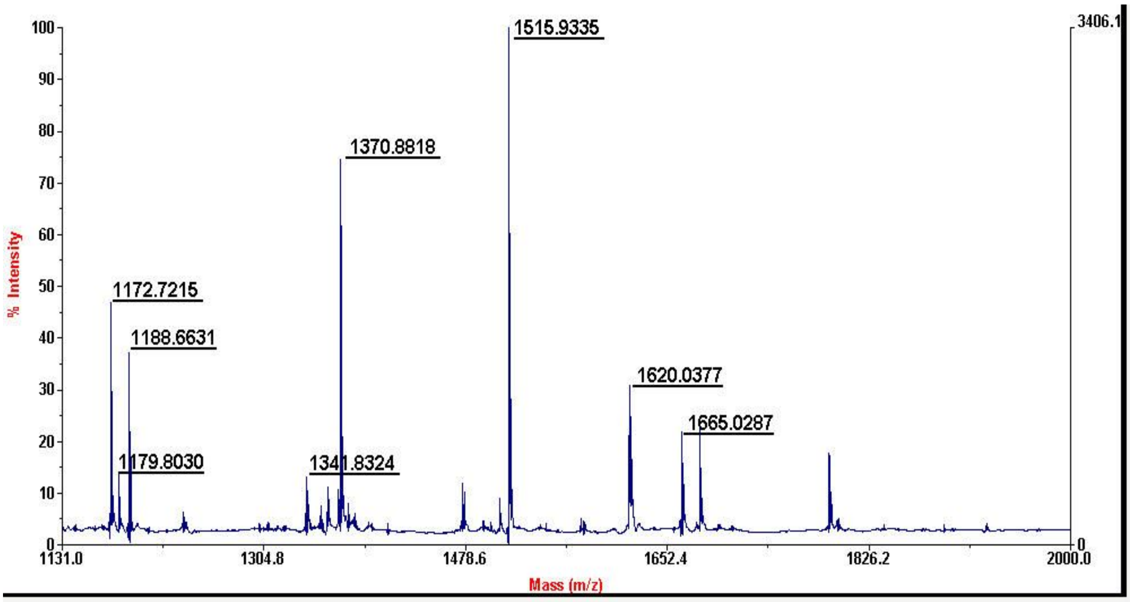
363 Rho GTPase-activating protein 25



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
142 - 153	1191.6433	1190.6360	1190.5866	0.0494	0	R.VAGTPCGVFGQR.L	
327 - 340	1693.8921	1692.8848	1692.8473	0.0375	1	R.GTPQIQRVMTMMIR.D	2 Oxidation (M)
417 - 426	1211.6066	1210.5993	1210.6458	-0.0465	1	K.VPREKPGDWK.M	
440 - 454	1588.8632	1587.8559	1587.7715	0.0844	1	R.KCFLTSAFQGANSSK.M	
441 - 454	1460.7779	1459.7706	1459.6765	0.0941	0	K.CFLTSAFQGANSSK.M	
521 - 535	1430.6810	1429.6737	1429.6685	0.0053	0	K.GDTLASPNSETGPGK.K	
574 - 581	1024.5785	1023.5712	1023.4661	0.1051	0	K.ENYDVWAK.V	
582 - 591	1228.6491	1227.6418	1227.6822	-0.0404	1	K.VVRLNEELEK.E	

No match to: 986.5365, 997.5420, 1074.5835, 1217.6602, 1313.6607, 1512.7829, 1566.8087, 1816.0262, 1888.0091, 1934.0573, 2165.0424

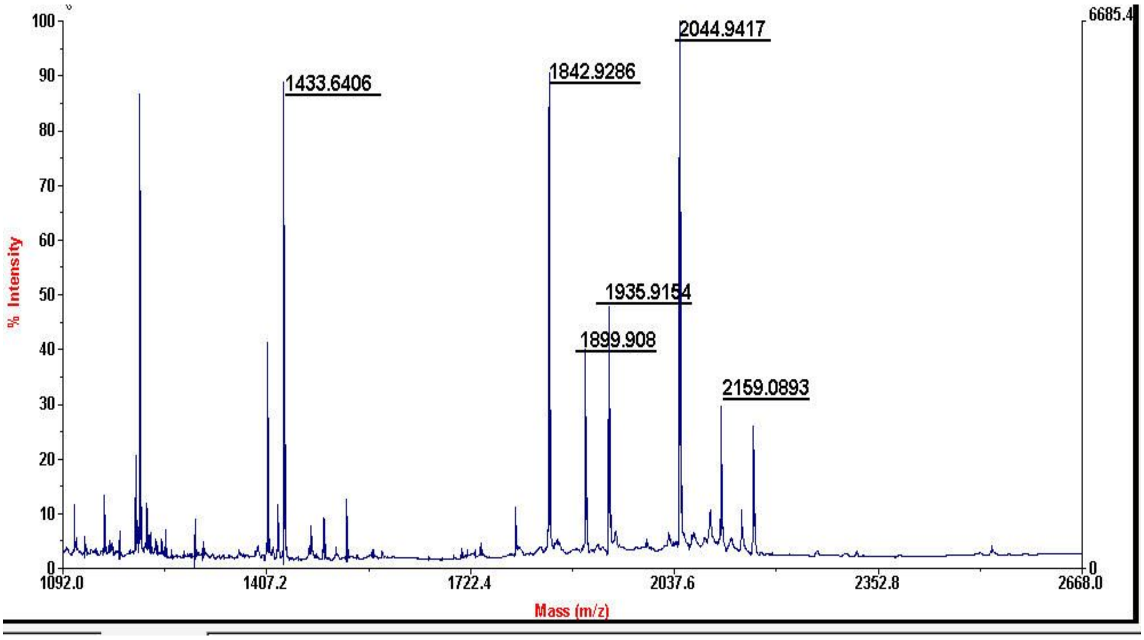
364 Rho-related GTP-binding protein RhoQ



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 22	2126.1435	2125.1362	2125.0845	0.0517	1	-.MAHGPGALMLKCVVVGDGAVGK.T	
Oxidation (M)							
140 - 153	1570.9359	1569.9286	1569.8548	0.0738	1	K.EKPICVEQGQKLAK.E	
154 - 172	2187.0828	2186.0756	2186.0169	0.0586	1	K.EIGACCYVECSALTQKGLK.T	3
194 - 205	1295.6677	1294.6604	1294.6196	0.0409	1	R.IGSRCINCCLIT.-	

No match to: 1093.4995, 1254.5586, 1323.6140

365 Cysteine and glycine-rich protein 2

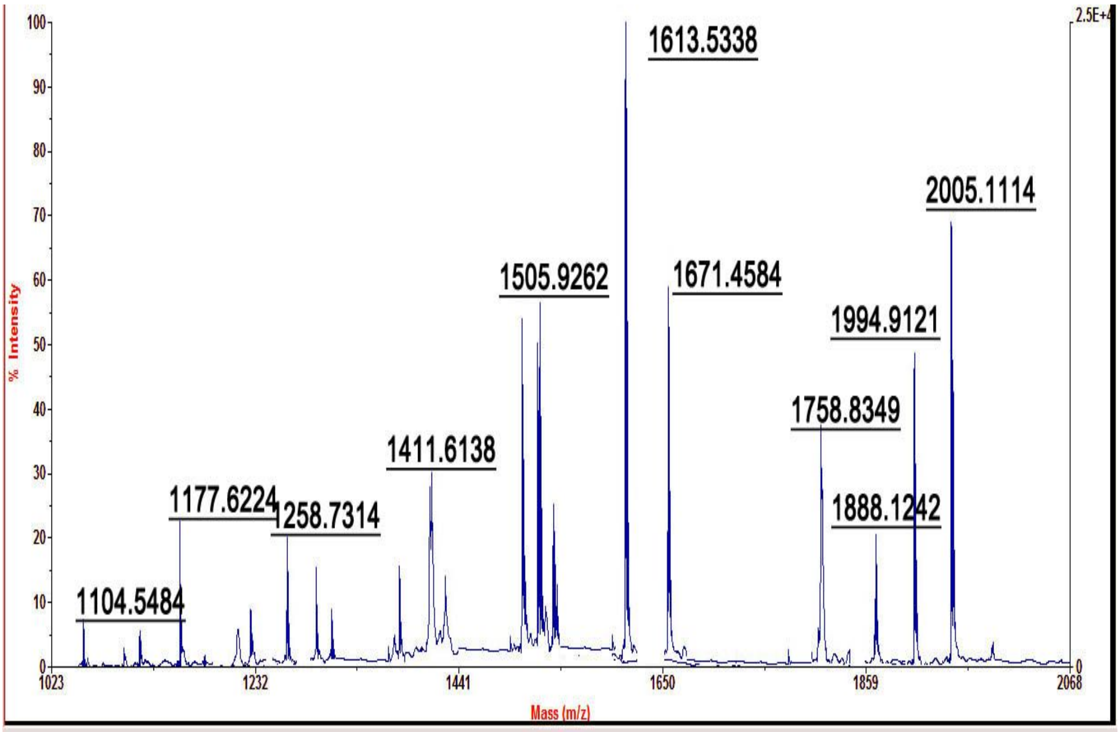


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

16 - 32	2044.9417	2043.9344	2043.8996	0.0349	0	K.TVYFAEEVQCEGNSFHK.S
43 - 59	1935.9154	1934.9082	1934.9043	0.0038	0	K.NLDSTTVAVHGEEIYCK.S
70 - 91	2159.0893	2158.0820	2158.0541	0.0279	1	K.GYGYGQGAGTLSTDKGESLGIK.H
92 - 108	1842.9286	1841.9213	1841.8768	0.0445	0	K.HEEAPGHRPTTNPNASK.F
152 - 168	1899.9082	1898.9009	1898.8931	0.0078	1	K.GLESTTLADKDGEIYCK.G
179 - 193	1433.6406	1432.6334	1432.6734	-0.0401	0	K.GFGFGQGAGALVHSE.-

No match to: 1059.9851, 1210.5147, 1408.6522, 2109.1015

367 Adenylate cyclase type 5

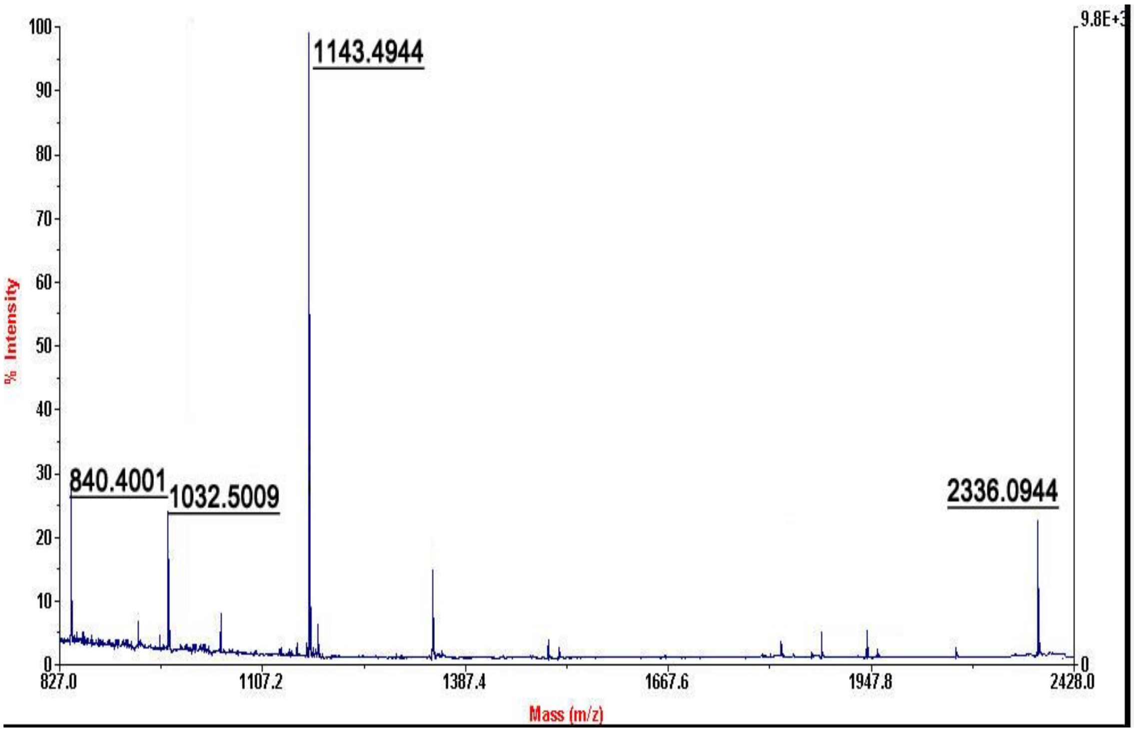


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
6 - 16	1104.5484	1103.5411	1103.5611	-0.0200	0	K.SVSPPGYAAQK.T
75 - 98	2499.1758	2498.1685	2498.0510	0.1175	0	R.SDDDDDPPLSGDDPLAGGFGFSFR.S
130 - 154	2093.0282	2092.0209	2092.0410	-0.0200	0	R.APPAGGGGGSAAAAASAGGTEVRPR.S
324 - 346	2762.5692	2761.5619	2761.4520	0.1100	0	R.SASEGIWWTVFFIYTIYTLLPVR.M
349 - 367	1888.1242	1887.1169	1887.1669	-0.0500	0	R.AAVLSGVLLSALHLAIALR.T
368 - 377	1177.6224	1176.6151	1176.6139	0.0012	0	R.TNAQDQFLLK.Q

815 - 825	1258.7314	1257.7241	1257.7081	0.0160	0	K.LFPSPLQTLSR.K
988 - 1013	2867.8393	2866.8320	2866.6321	0.2000	0	K.VVTPIIISVFVLALYLHAQQVESTAR.L
1027 - 1037	1411.6138	1410.6065	1410.6085	-0.0020	0	K.EEMEELQAYNR.R
1099 - 1115	2005.1114	2004.1041	2004.0051	0.0990	0	R.LLNEIIADFDEIISEDR.F
1124 - 1142	1994.9121	1993.9048	1993.8939	0.0109	0	K.TIGSTYMAASGLNDSTYDK.V
1164 - 1176	1671.4584	1670.4511	1670.7511	-0.3000	0	K.YINEHSFNNFQMK.I
1177 - 1192	1505.9262	1504.9189	1504.9090	0.0100	0	K.IGLNIGPVVAGVIGAR.K
1247 - 1261	1613.5338	1612.5265	1612.7265	-0.2000	0	K.GEMMTYFLNGGPPLS.-

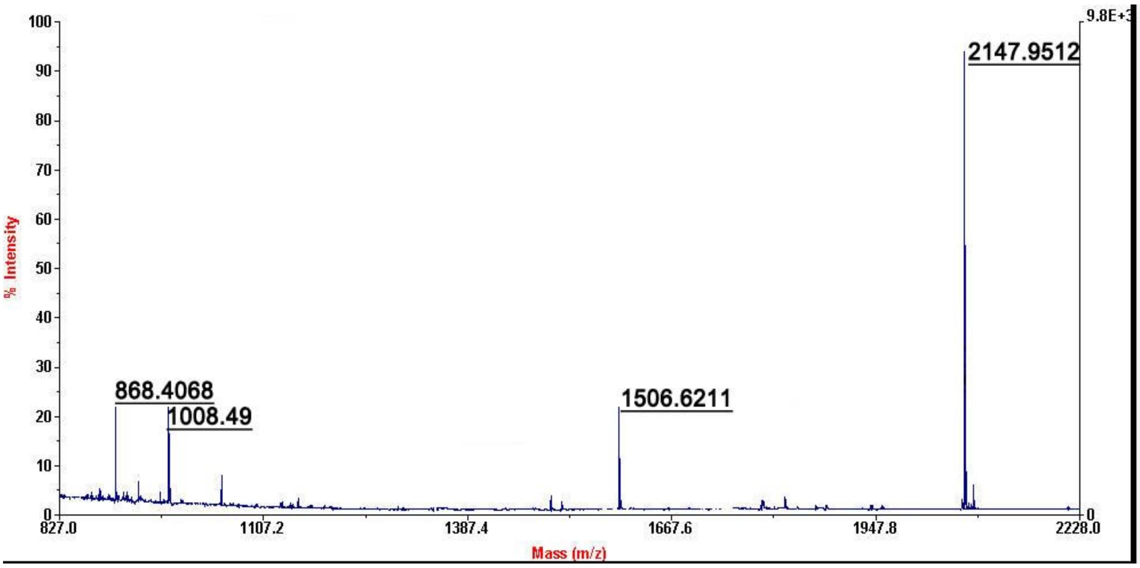
No match to: 1758.8349, 2156.8553, 2431.2195

368 Beta-defensin 104



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
29 - 36	840.4001	839.3928	839.3960	-0.0031	0	R.ICGYGTAR.C
51 - 60	1143.4944	1142.4871	1142.4671	0.0200	0	R.CPNTYACCLR.K
62 - 69	1032.5009	1031.4936	1031.5036	-0.0100	0	K.WDESLLNR.T

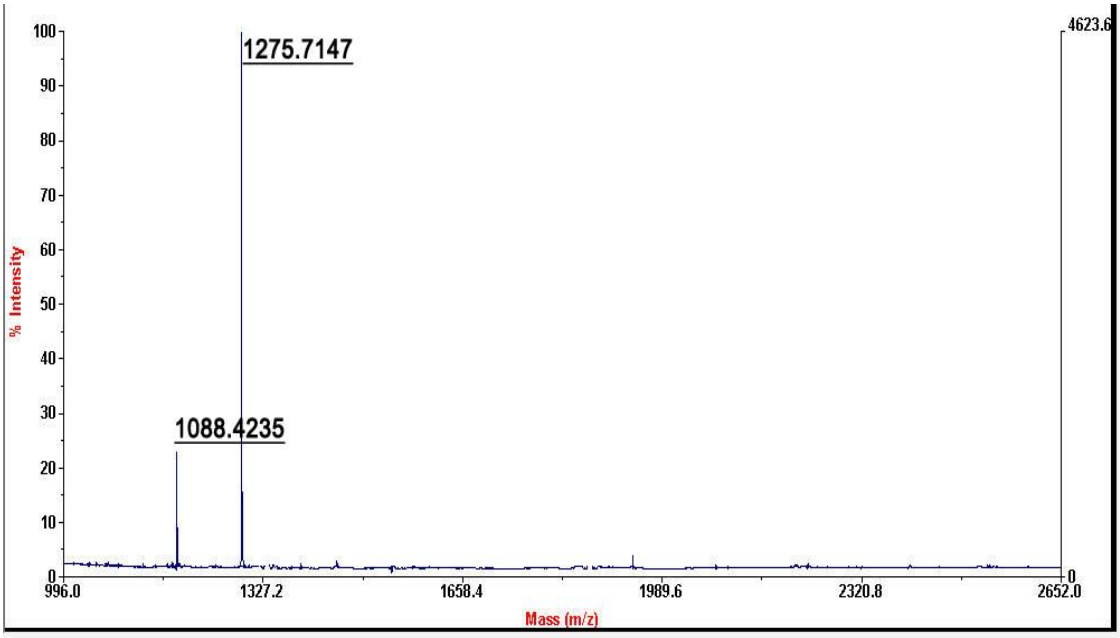
369 Beta-defensin 105



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
55 - 68	1634.7271	1633.7198	1633.7188	0.0010	1	R.KECLENEKPDGNCR.L
56 - 68	1506.6341	1505.6268	1505.6238	0.0030	0	K.ECLENEKPDGNCR.L
69 - 75	868.4138	867.4065	867.4095	-0.0030	0	R.LNFLCCR.Q
69 - 77	1152.5700	1151.5627	1151.5692	-0.0065	1	R.LNFLCCRQR.I

No match to: 2147.9462

370 Beta-defensin 118

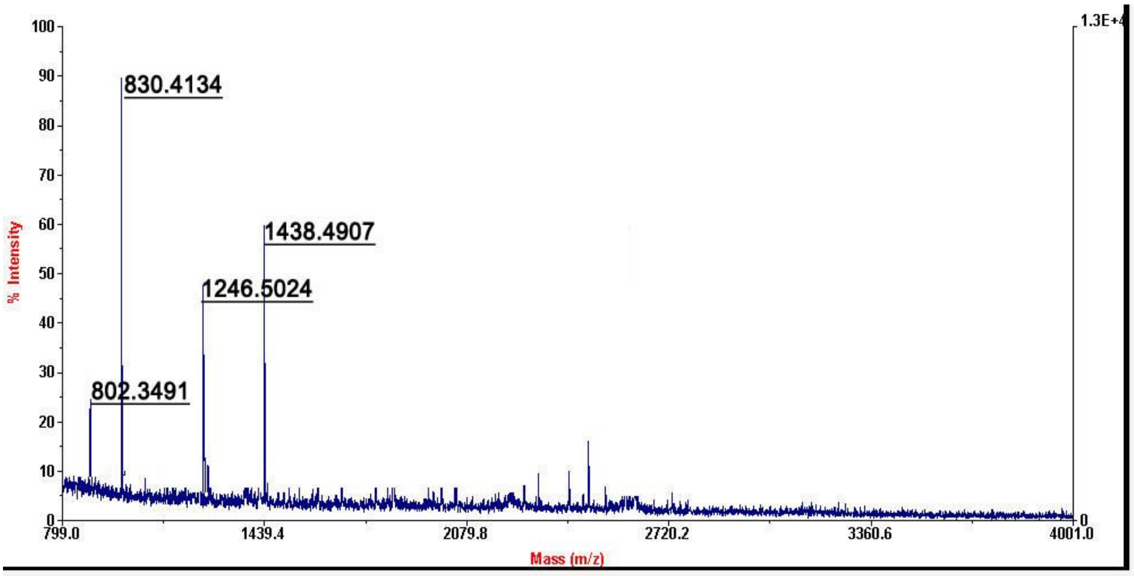


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
27 - 35	1118.4751	1117.4678	1117.4658	0.0020	1	K.CWNRSGHCR.K
37 - 45	977.4722	976.4649	976.4648	0.0002	1	K.QCKDGEAVK.D
40 - 49	1065.4883	1064.4810	1064.4808	0.0002	1	K.DGEAVKDTCK.N

46 - 52	849.4242	848.4169	848.4174	-0.0005	1	K.DTCKNLR.A

No match to: 1088.4139

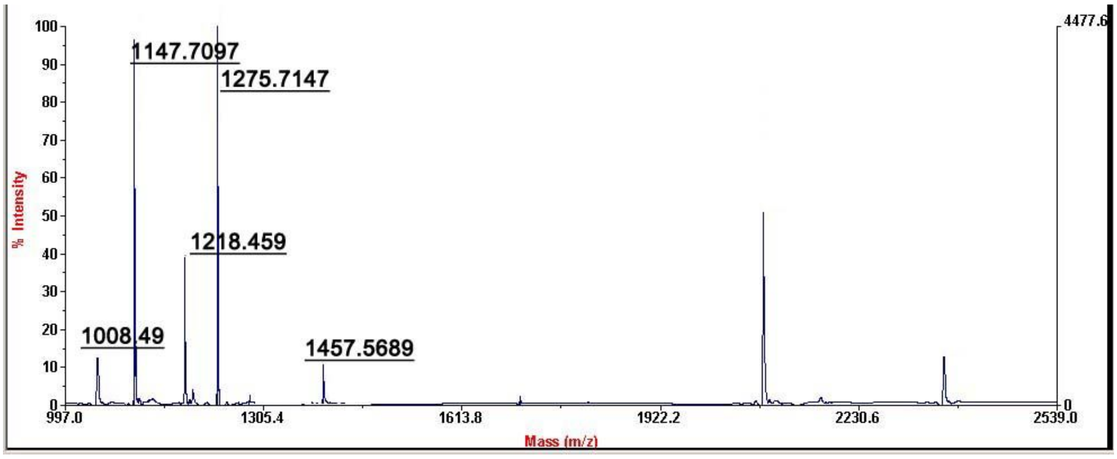
371 Beta-defensin 121



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
36 - 45	1246.6074	1245.6001	1245.5951	0.0050	0	K.ESEVYYILCK.T
56 - 62	830.5184	829.5111	829.5062	0.0050	0	K.YVPVKPK.L
63 - 76	1438.6967	1437.6894	1437.6835	0.0059	0	K.LTDTNTSLESTSAV.-

No match to: 802.4495

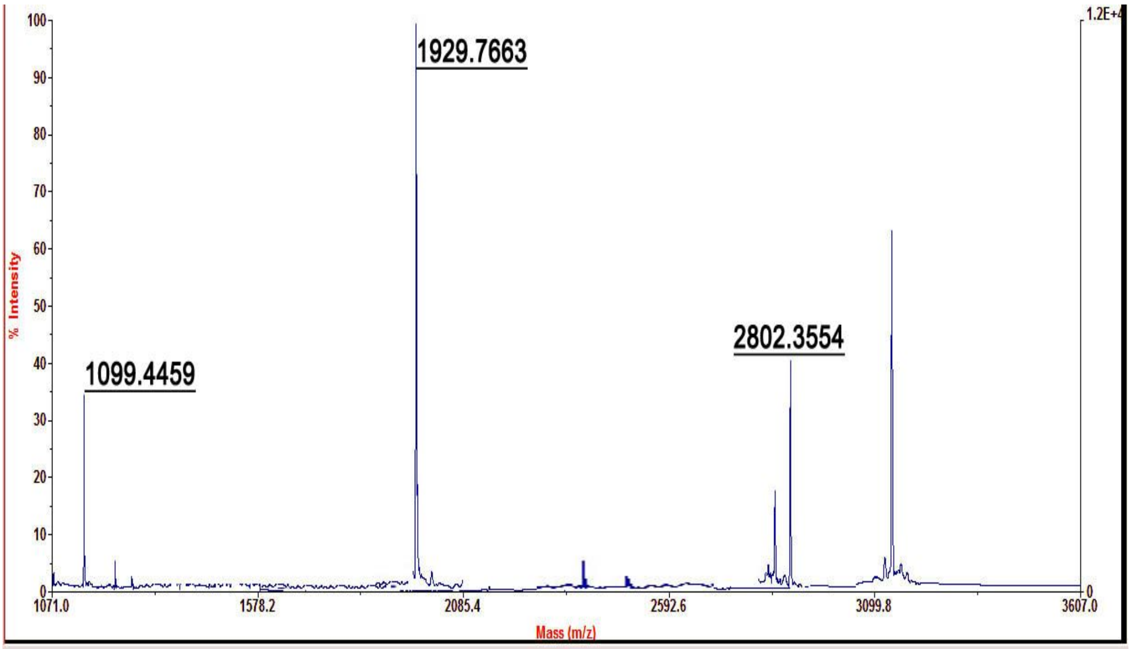
372 Beta-defensin 129



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

27 - 35	1008.4900	1007.4827	1007.4827	0.0000	1	R.CLMGLGRCR.D
34 - 43	1218.4590	1217.4517	1217.4917	-0.0400	1	R.CRDHCNVDEK.E
36 - 43	959.5887	958.5814	958.3814	0.2000	0	R.DHCNVDEK.E
36 - 47	1457.5689	1456.5616	1456.6616	-0.1000	1	R.DHCNVDEKEIQK.C
65 - 87	2664.3237	2663.3164	2663.3265	-0.0100	0	K.NYLQYGTPNVLNEDVQEMLKPAK.N
96 - 106	1275.7147	1274.7074	1274.8074	-0.1000	1	R.KHILSVLPQIK.S
97 - 106	1147.7097	1146.7024	1146.7125	-0.0100	0	K.HILSVLPQIK.S

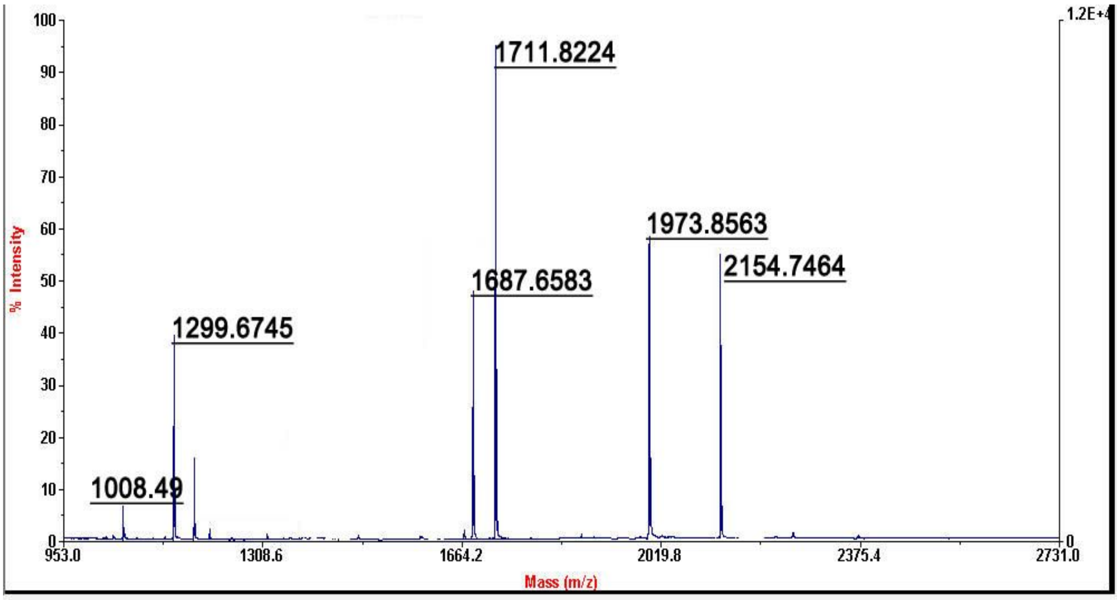
373 Beta-defensin 132



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
27 - 36	1099.4459	1098.4386	1098.4586	-0.0200	0	K.CVSNTPGYCR.T
37 - 53	1929.7663	1928.7590	1928.7790	-0.0200	0	R.TCCHWGETALFMCNASR.K
55 - 78	2802.3554	2801.3481	2801.3781	-0.0300	0	K.CCISYSFLPKPDLPQLIGNHWQSR.R

No match to: 3101.1232

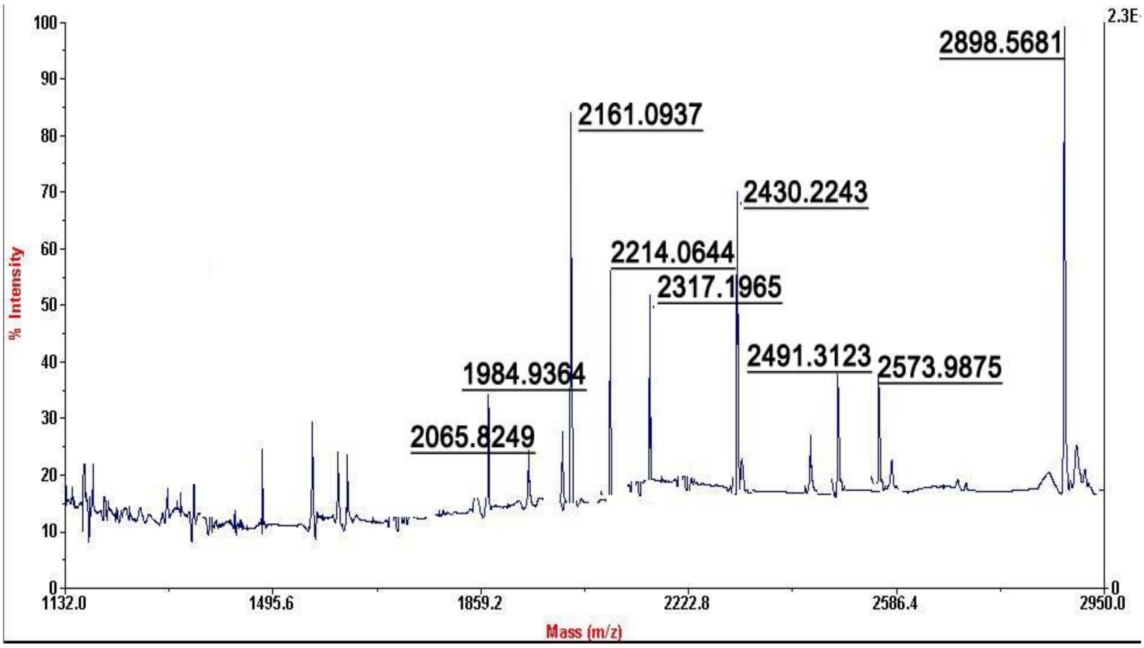
374 Cadherin-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
382 - 397	1711.8224	1710.8151	1710.9152	-0.1001	0	K.GQVPENEANVVITTLK.V
528 - 545	1973.8563	1972.8490	1972.9490	-0.1000	0	R.DTANWLEINPDTGAISTR.A
785 - 796	1299.6745	1298.6672	1298.6653	0.0020	0	R.NDVAPTLMSVPR.Y
856 - 868	1687.6583	1686.6510	1686.6910	-0.0400	0	K.DQDYDYLNEWGNR.F

No match to: 1008.4900, 2154.7464

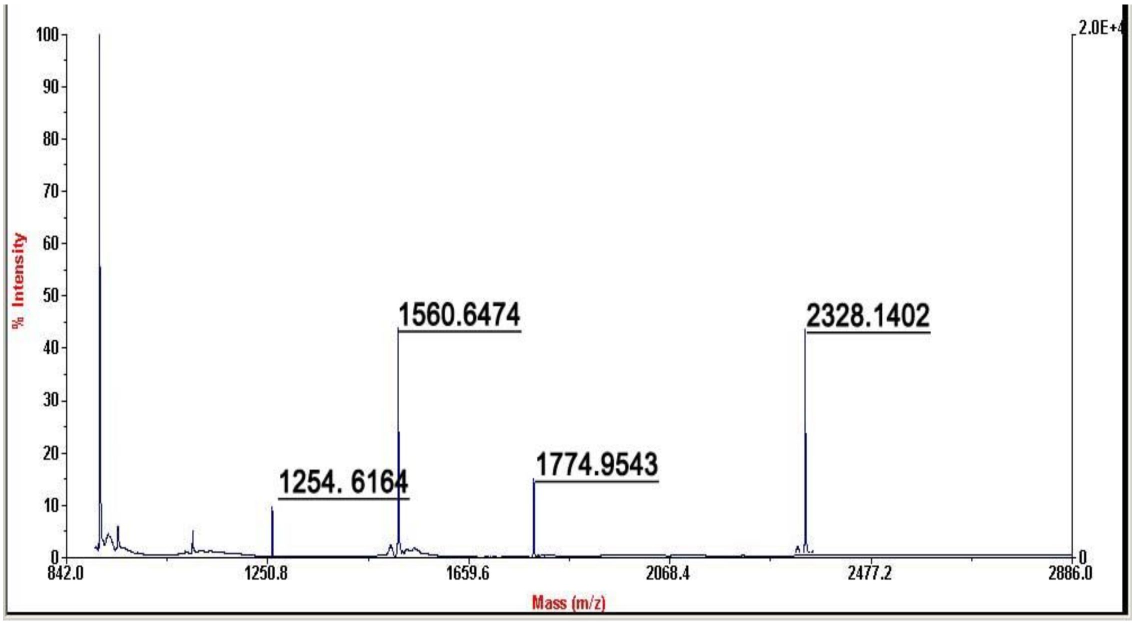
375 A-kinase anchor protein 4



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 18	2214.0644	2213.0571	2212.8785	0.1786	0	-.MMAYSDTTMMSDDIDWLR.S 2 Oxidation (M)
270 - 287	1984.9364	1983.9291	1983.9281	0.0010	0	K.IASEMAYEAVELTAAEMR.G
332 - 353	2430.2243	2429.2170	2429.2190	-0.0020	1	K.GLMVYANQVASDMMVSLMKTLK.V
389 - 408	2161.0937	2160.0864	2160.0885	-0.0021	0	K.NLHNITGVLMTDSDFVSAVK.R
389 - 409	2317.1965	2316.1892	2316.1896	-0.0004	1	K.NLHNITGVLMTDSDFVSAVKR.N
624 - 644	2491.3123	2490.3050	2490.3048	0.0002	1	K.MDMSNIVLMLIQKLLNENPFK.C
773 - 797	2898.5681	2897.5608	2897.4608	0.1000	0	K.QLQAVLQWIAASQFNVPMLYFMGDK.D

No match to: 2065.8249, 2573.9875

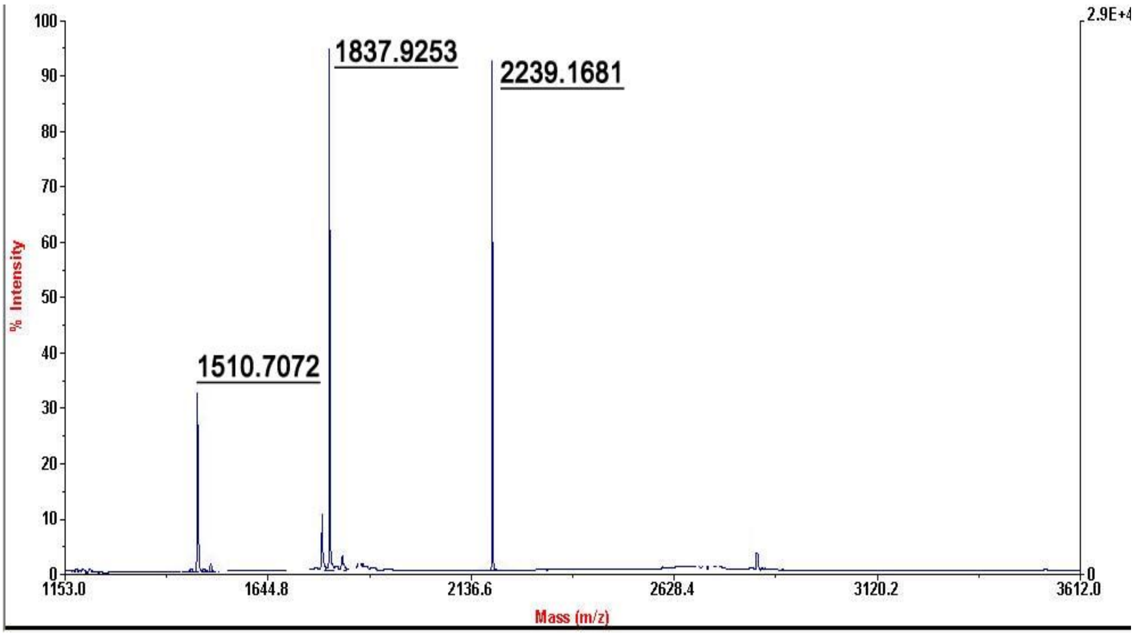
376 Cystatin-8



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
47 - 58	1560.6474	1559.6401	1559.6901	-0.0500	0	K.QCLWFAMQEYNK.E
97 - 112	1774.9543	1773.9470	1773.8931	0.0540	0	R.KPLSTNEICAIQENSK.L
117 - 137	2328.1402	2327.1329	2327.1330	-0.0001	0	K.LSCSFLVGALPWNGEFTVMEK.K

No match to: 1008.4900, 1254.0000, 1299.6745

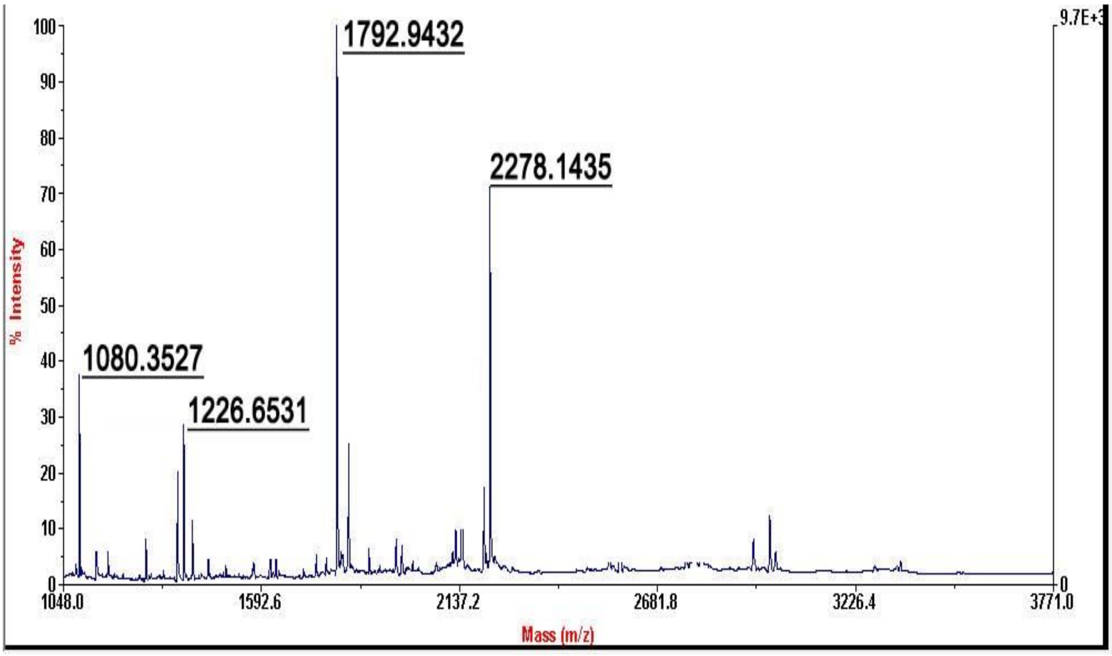
377 Cystatin-11



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
30 - 45	1837.9253	1836.9180	1836.9080	0.0100	0	K.TFLSVHEVMAVENYAK.D
46 - 57	1510.7072	1509.6999	1509.7100	-0.0100	0	K.DSLQWITDQYNK.E
76 - 107	3857.7780	3856.7707	3856.7607	0.0100	0	R.QVTDHLEYHLNVEMQWTTCQKPETTNCVPQER.E
112 - 129	2239.1681	2238.1608	2238.0609	0.1000	0	K.QVNCFFSVFAVPWFEQYK.I

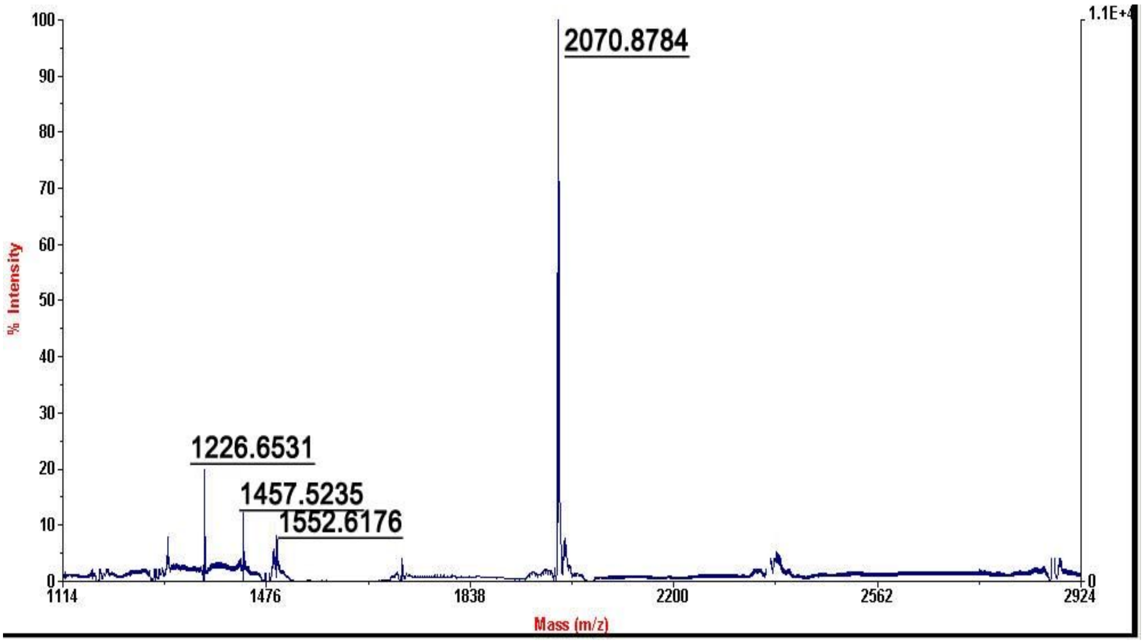
No match to: 1008.2314

378 Cystatin-C



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
52 - 62	1226.6531	1225.6458	1225.5979	0.0479	0	R.ALDFAVGEYNK.A
63 - 71	1080.3527	1079.3454	1079.4454	-0.1000	0	K.ASNDMYHSR.A
81 - 96	1792.9432	1791.9359	1791.9519	-0.0160	0	K.QIVAGVNYFLDVELGR.T
121 - 140	2278.1435	2277.1362	2277.0962	0.0400	0	K.AFCSFQIYAVPWQGTMTLSK.S

379 Cysteine-rich secretory protein 1

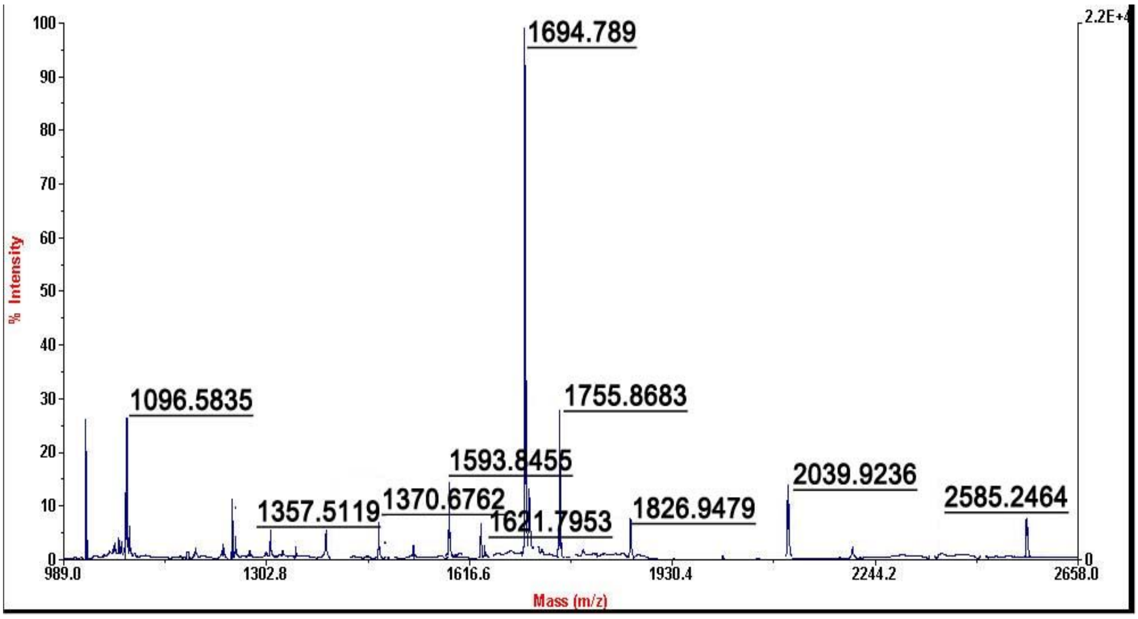


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
55 - 64	1055.5547	1054.5474	1054.5845	-0.0371	0	R.VVPPASNMLK.M

81 - 92	1457.5235	1456.5162	1456.5962	-0.0800	0	K.YCDMTESNPLER.R
169 - 185	2070.8784	2069.8711	2069.8611	0.0100	0	R.YLYVCHYCHEGNDPETK.N
191 - 205	1552.6176	1551.6103	1551.6004	0.0100	0	K.TGVPCEACPSNCEDK.L

No match to: 1080.3527, 1226.6531

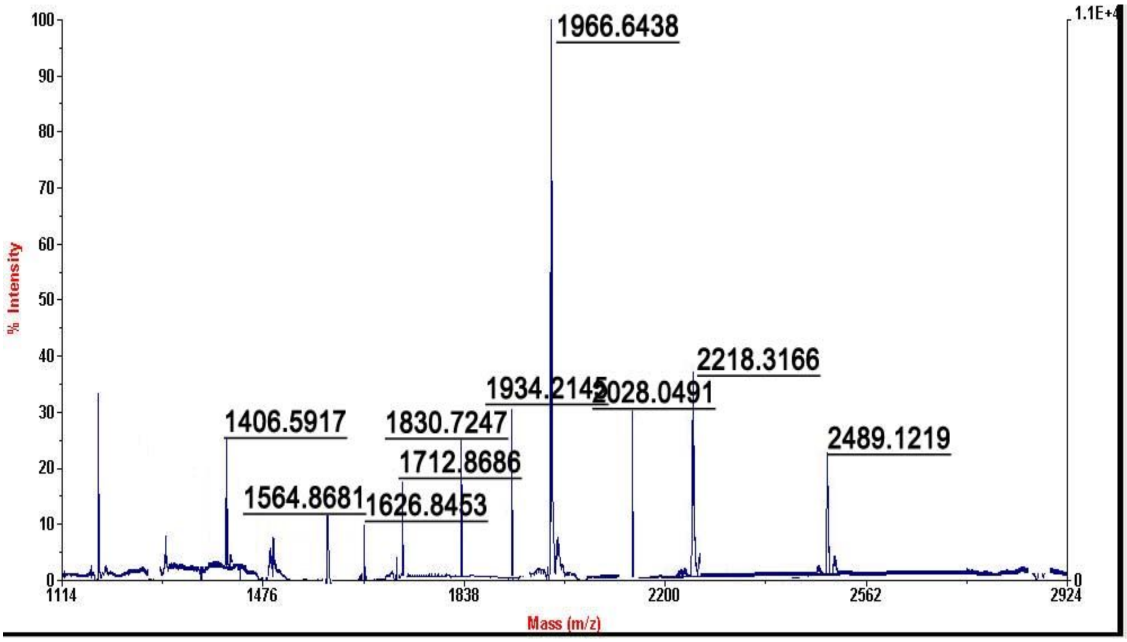
380 Disintegrin and metalloproteinase domain-containing protein 28



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
231 - 243	1621.7953	1620.7880	1620.7680	0.0200	0	R.VFEMANYVNMLYK.K
245 - 260	1826.9479	1825.9406	1825.9397	0.0010	0	K.LNTHVALVGMEIWTDK.D
333 - 355	2585.2464	2584.2391	2584.0392	0.1999	0	R.VAGTMAHEMGHNFGMFHDDYSCK.C
356 - 365	1096.5835	1095.5762	1095.4763	0.1000	0	K.CPSTICVMDK.A
443 - 455	1402.6799	1401.6726	1401.5727	0.0999	0	K.ATFQCALGECCEK.C
490 - 501	1370.6762	1369.6689	1369.6350	0.0339	0	R.FQVNGFPCHHGK.G
587 - 605	2039.9236	2038.9163	2038.9154	0.0010	0	K.TFDPEDTSQEIGMVANGTK.C
698 - 711	1593.8455	1592.8382	1592.8383	-0.0001	0	K.DQRPLSTTGTRPHK.Q

No match to: 1357.5119, 1694.7890, 1755.8683

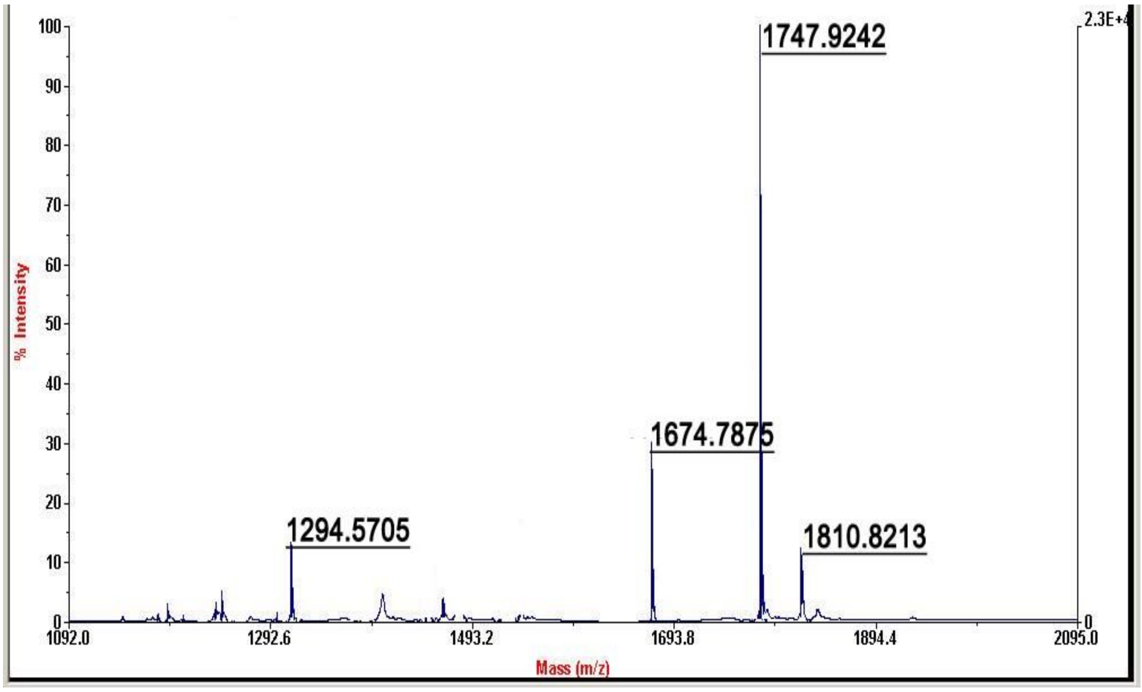
381 Disintegrin and metalloproteinase domain-containing protein 7



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
179 - 191	1406.5917	1405.5844	1405.5845	-0.0001	0	K.TVPGDNESEEDSK.I
239 - 257	2218.3166	2217.3093	2217.1794	0.1300	0	K.TLNIHVTLVGIEIWTHEDK.I
258 - 270	1564.8681	1563.8608	1563.8508	0.0100	0	K.IELYSNIETTLLR.F
357 - 369	1335.6253	1334.6180	1334.6210	-0.0030	0	K.CVMDSDGSIPALK.F
465 - 482	1966.6438	1965.6365	1965.7365	-0.1000	0	K.DECDFPEMCTGHSPACPK.D
494 - 503	1135.4567	1134.4494	1134.4474	0.0020	0	K.NSEGYCFMGK.C
508 - 528	2489.1219	2488.1146	2488.0046	0.1100	0	R.EDQCSELFDDEAIESHDICYK.M
610 - 626	1830.7247	1829.7174	1829.6875	0.0300	0	K.CGEGMVCNNGECLNMEK.V
700 - 714	1626.8453	1625.8380	1625.8261	0.0120	0	K.QVQSPPTETLGVENK.G
715 - 724	1212.5653	1211.5580	1211.5571	0.0009	0	K.GYFGDEQQIR.T
725 - 741	1934.2145	1933.2072	1933.0673	0.1400	0	R.TEPILPEIHFLNKPASK.D

No match to: 1712.8686, 2028.0491

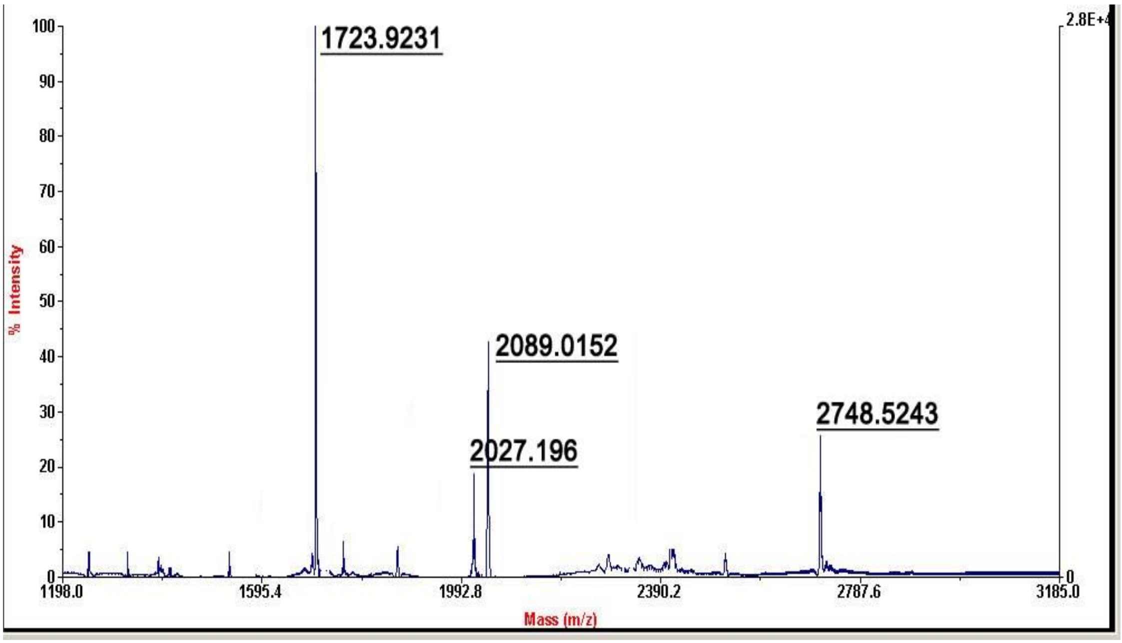
382 Diamine acetyltransferase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
4 - 19	1747.9242	1746.9169	1746.9087	0.0082	0	K.FVIRPATAADCSDILR.L
27 - 39	1674.7875	1673.7802	1673.7858	-0.0056	0	K.YEYMEEQVILTEK.D
88 - 101	1810.8213	1809.8140	1809.8647	-0.0507	0	K.LLYLEDFFVMSDYR.G
102 - 111	1020.4354	1019.4281	1019.5651	-0.1370	0	R.GFGIGSEILK.N
122 - 141	2402.0932	2401.0859	2401.0871	-0.0012	0	R.CSSMHFLVAEWNEPSINFYK.R

No match to: 1294.5705

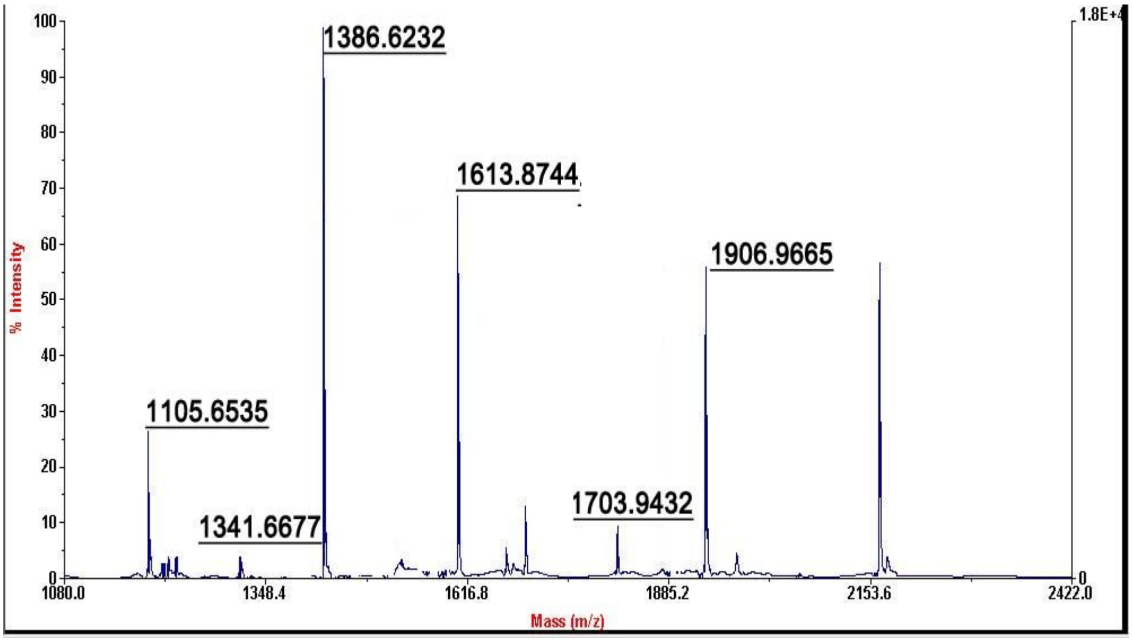
383 Epididymal-specific lipocalin-6



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
26 - 43	2027.1960	2026.1887	2026.0887	0.1000	0	R.LDPEQLLGPWYVLAVASR.E
55 - 70	1723.9231	1722.9158	1722.9628	-0.0470	0	K.NVVGVVVTLTPENNLR.T
71 - 90	2089.0152	2088.0079	2087.9980	0.0099	0	R.TLSSQHGLGGCDQSVMDLIK.R
92 - 115	2748.5243	2747.5170	2747.4071	0.1099	0	R.NSGWVFENPSIGVLELWVLATNFR.D

No match to: 1055.5547, 1080.3527

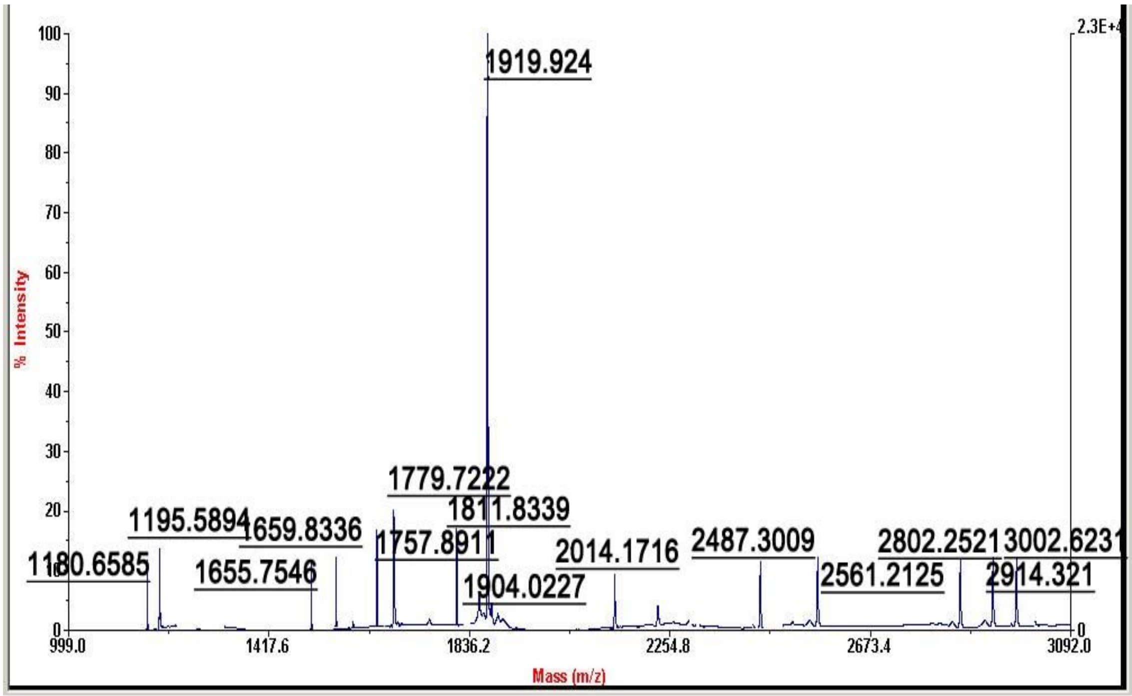
384 Epididymal-specific lipocalin-8



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
38 - 53	1613.8744	1612.8671	1612.8672	-0.0001	0	R.EVGVASDQSLVLTAPK.R
71 - 83	1386.6232	1385.6159	1385.6133	0.0027	0	K.VAYNSSGSCEIEK.I
84 - 94	1105.6535	1104.6462	1104.5663	0.0800	0	K.IVGSEIDSTGK.F
102 - 117	1906.9665	1905.9592	1905.9472	0.0120	0	R.EIHVLDTDYEGYAILR.V
150 - 165	1703.9432	1702.9359	1702.9002	0.0357	0	R.ELTADTGLYLAARPGR.C

No match to: 1341.6677, 2165.0424

385 Epididymis-specific alpha-mannosidase

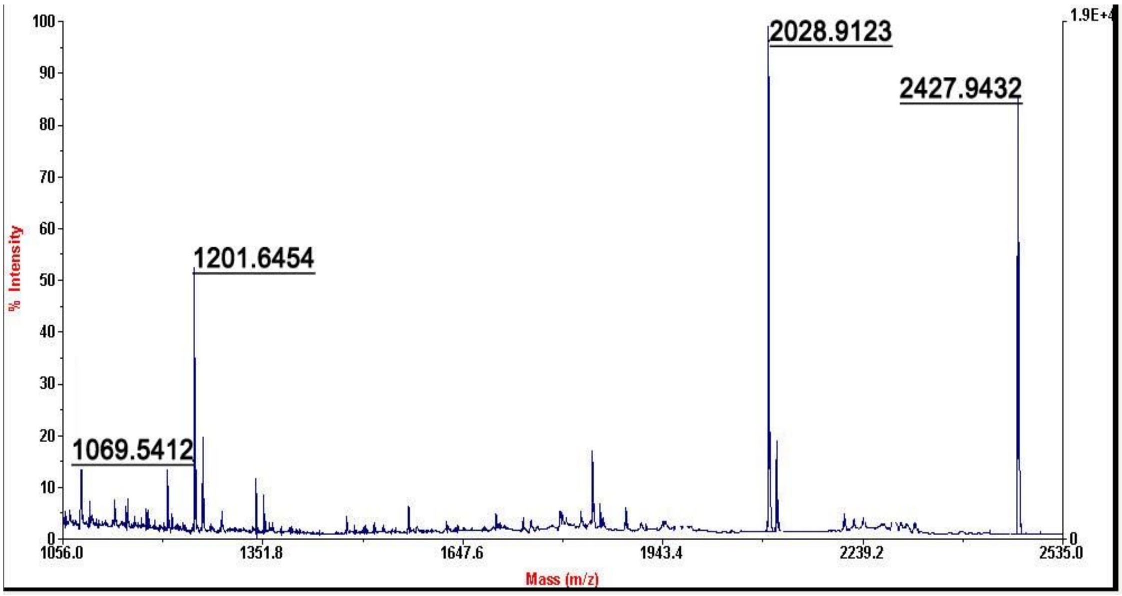


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
204 - 227	2914.3210	2913.3137	2913.3214	-0.0077	0	R.QEIFTHIMDQYSYCTPSHIPFSNR.S
331 - 340	1180.6585	1179.6512	1179.6513	-0.0000	0	R.ALHALNVTWR.V
343 - 365	2802.2521	2801.2448	2801.2511	-0.0062	0	R.DHHDFLPYSTEPFQAWTGFYTSR.S
396 - 411	1904.0227	1903.0154	1903.0064	0.0090	0	R.GHLDPTWALQQLQQLR.W
684 - 699	1811.8339	1810.8266	1810.8897	-0.0631	0	R.LTHVPQGHDGELLCHR.I
700 - 713	1659.8336	1658.8263	1658.8264	-0.0000	0	R.IEQEYQAGPLELNR.E
719 - 740	2561.2125	2560.2052	2560.1612	0.0440	0	R.TSTNLNSQQVIYSDNNGYQMQR.R
754 - 768	1779.7222	1778.7149	1778.7644	-0.0495	0	R.NYYPMVQSAFMEDGK.S

778 - 795	1919.9240	1918.9167	1918.9432	-0.0265	0	R.AHGISSQGNGQVEVMLHR.R
860 - 886	3002.6231	3001.6158	3001.6501	-0.0343	0	K.LPGPQQQEAVTLPPNLHLQILSIPGWR.Y
978 - 997	2014.1716	2013.1643	2013.0644	0.1000	0	R.GDTTSPSRPPGGPIITVHPK.E
1001 - 1009	1195.5894	1194.5821	1194.5822	-0.0001	0	R.TFFIHFQQQ.-

No match to: 1655.7546, 1757.8911, 2487.3009

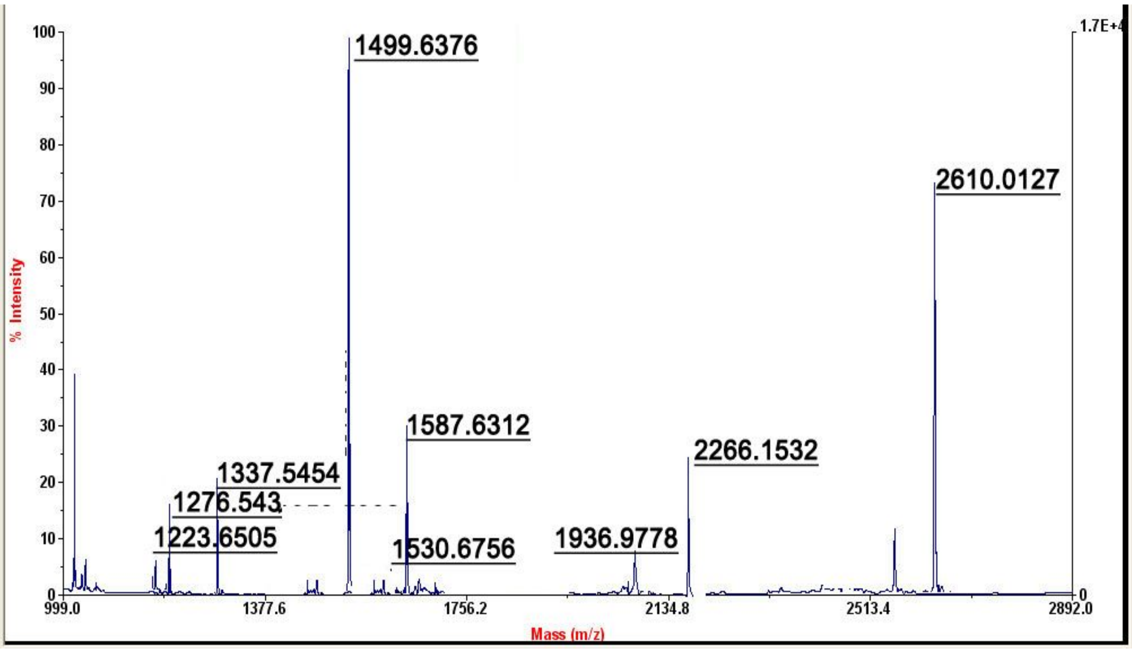
386 Eppin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
38 - 45	1069.5412	1068.5339	1068.4182	0.1157	0	R.EECEFQER.D
82 - 97	2028.9123	2027.9050	2027.9240	-0.0190	0	K.ETGPCLAYFLHWWYDK.K
99 - 120	2427.9432	2426.9359	2426.9678	-0.0319	0	K.DNTCSMFVYGGCQGNNNNFQSK.A

No match to: 1201.6454

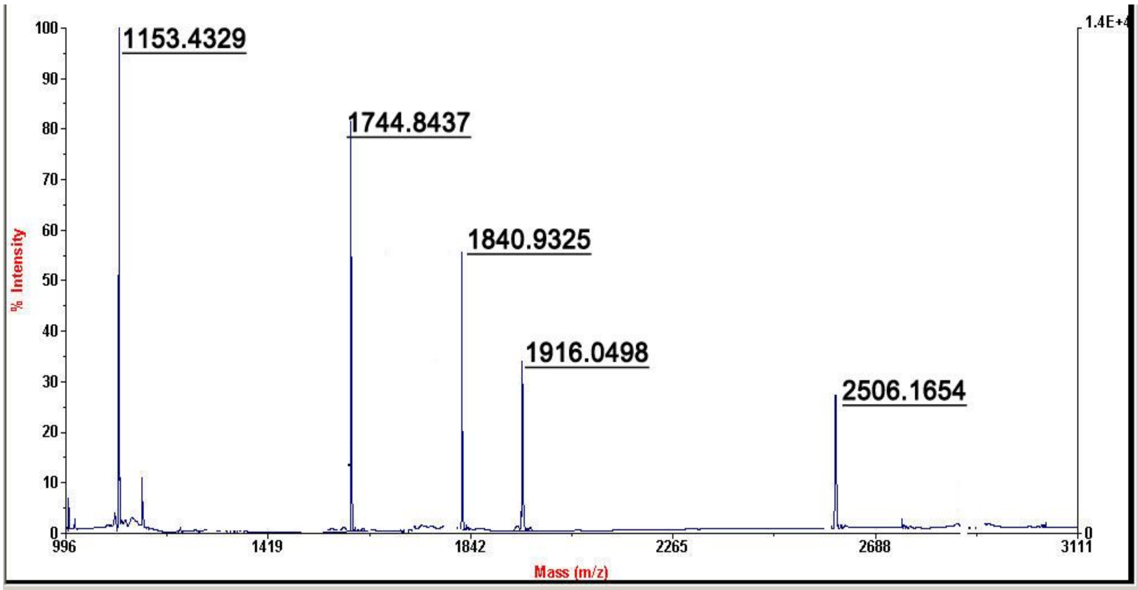
387 Epididymal sperm-binding protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
37 - 56	2266.1532	2265.1459	2265.0459	0.1000	0	K.GSVYFTCTHIHSLSPWCATR.A
74 - 81	1058.5392	1057.5319	1057.5419	-0.0100	0	R.CIFPFIYR.G
127 - 136	1223.6505	1222.6432	1222.6532	-0.0100	0	R.KPCIFPSIYR.N
151 - 161	1337.5454	1336.5381	1336.5791	-0.0410	0	K.LWCPTTENMDK.D
173 - 189	1936.9778	1935.9705	1935.9706	-0.0000	0	R.ISALVPGFPCHFPFNYK.N
192 - 202	1276.5430	1275.5357	1275.5190	0.0167	0	K.NYFNCTNEGSK.E
203 - 223	2610.0127	2609.0054	2609.0628	-0.0573	0	K.ENLVWCATSYNYDQDHTWVYC.-

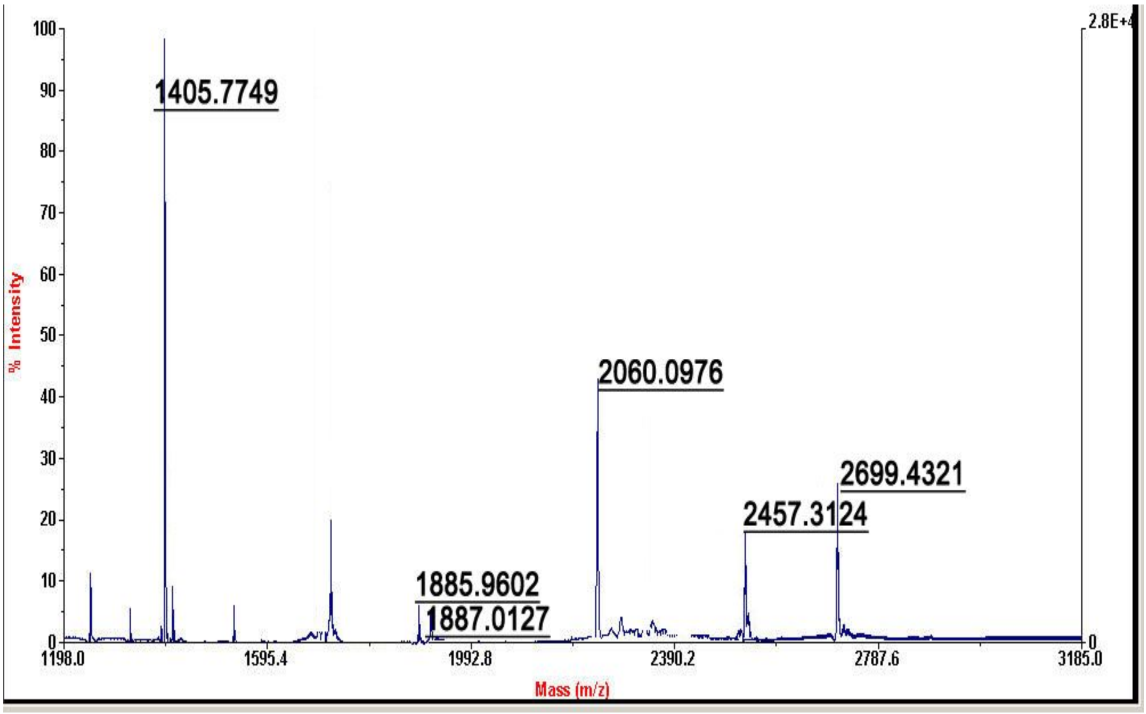
No match to: 1499.6376, 1530.6756, 1587.6312

388 Epididymal-specific lipocalin-12



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
59 - 75	1840.9325	1839.9252	1839.9003	0.0249	0	R.ALLNAFTATFELSDDGR.F
76 - 84	1153.4329	1152.4256	1152.5386	-0.1130	0	R.FEVWNAMTR.G
121 - 135	1744.8437	1743.8364	1743.8502	-0.0138	0	R.VVDSDYTQFALMLSR.R
152 - 168	1916.0498	1915.0425	1915.0026	0.0399	0	R.SWLLPPGTLDQFICLGR.A
169 - 192	2506.1654	2505.1581	2505.1482	0.0099	0	R.AQGLSDDNIVFPDVTGWSPQASVC.-

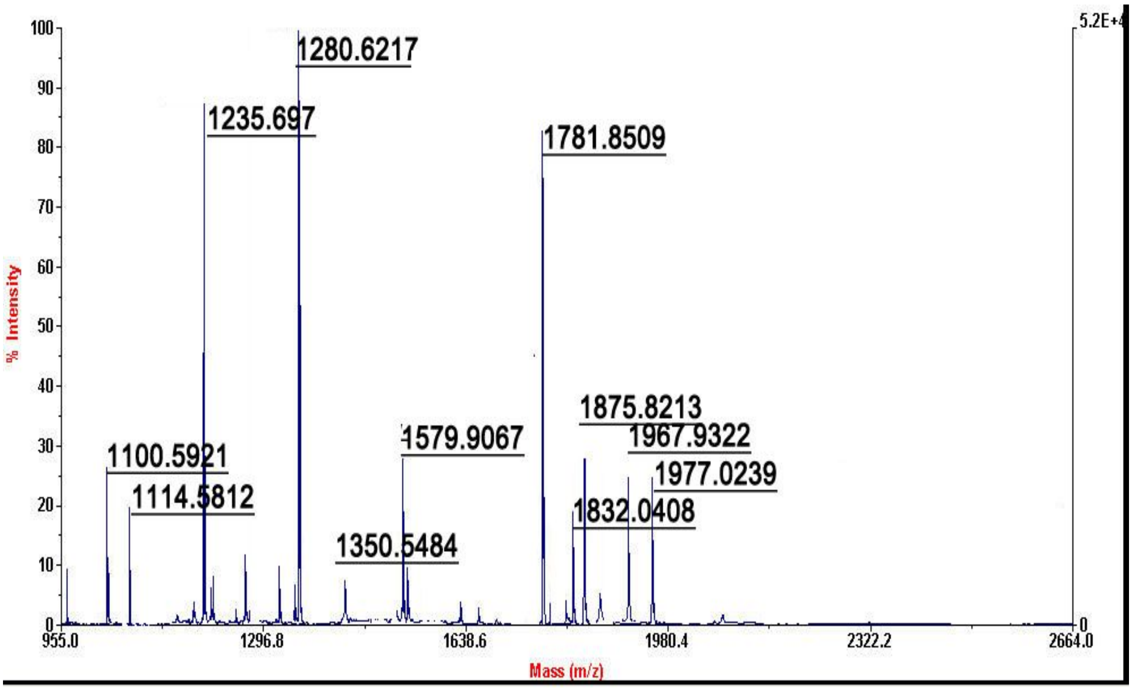
389 F-actin-capping protein subunit alpha-3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
18 - 39	2457.3124	2456.3051	2456.3137	-0.0086	0	R.LLLQAPPGEFVNAFDDLCLLIR.D
59 - 82	2699.4321	2698.4248	2698.2996	0.1252	0	K.YSVPLCIDGNPVLLSHHNVMGDYR.F
94 - 102	1134.6154	1133.6081	1133.6080	0.0001	0	K.YDLLQNQLK.D
103 - 118	1885.9602	1884.9529	1884.9330	0.0200	0	K.DIQSHGIIQNEAEYLR.V
198 - 207	1155.6590	1154.6517	1154.6118	0.0400	0	R.CVNLHIEISK.D
236 - 253	2060.0976	2059.0903	2059.0585	0.0318	0	K.FQAAVLEELQELSNEALR.K
272 - 283	1405.7749	1404.7676	1404.7686	-0.0010	0	R.ILSDLNLVMYPK.L

No match to: 1887.0127

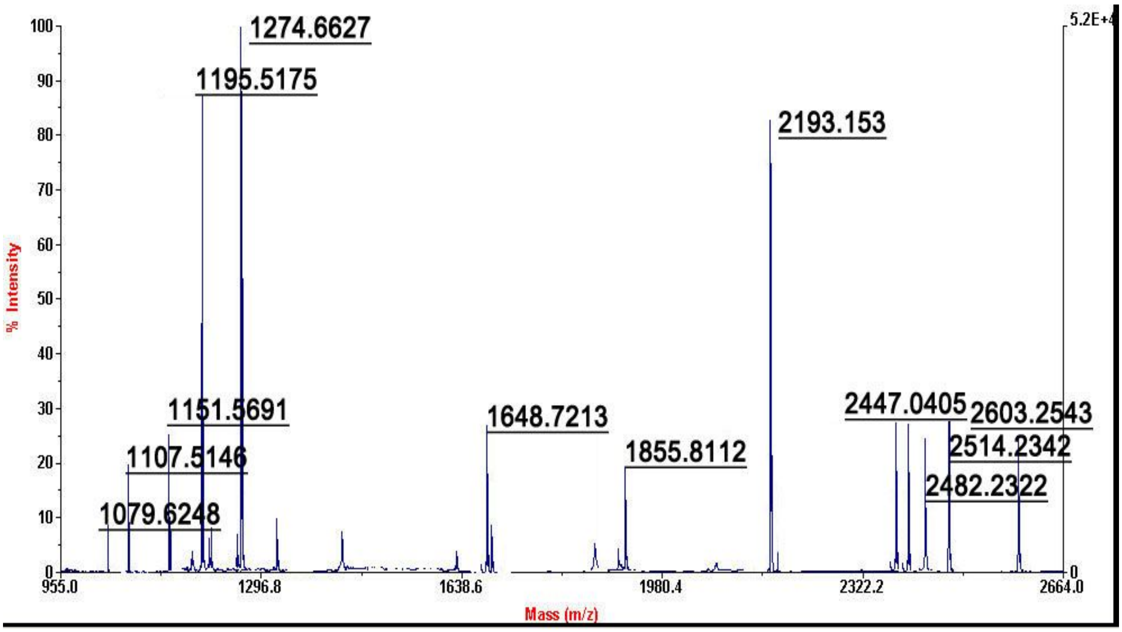
390 Thioredoxin domain-containing protein 3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
110 - 118	1100.5921	1099.5848	1099.5873	-0.0025	0	K.VINLIDEER.K
180 - 189	1114.5812	1113.5739	1113.5818	-0.0079	0	K.AGFIIEAEHK.T
252 - 268	1875.8213	1874.8140	1874.8390	-0.0250	0	R.SEDQPEVEAQVTPGMMK.N
271 - 280	1280.6217	1279.6144	1279.6044	0.0100	0	K.QDSLQEYLER.Q
281 - 298	1967.9322	1966.9249	1966.9418	-0.0169	0	R.QHLAQLCDIEEDAANVAK.F
318 - 330	1579.9067	1578.8994	1578.8994	0.0000	0	K.TLALLRPNLFHER.K
364 - 373	1350.5484	1349.5411	1349.5411	-0.0000	0	K.EYENEDYFNK.L
475 - 485	1235.6970	1234.6897	1234.6557	0.0340	1	K.EAGFDLTQVKK.M
508 - 525	1977.0239	1976.0166	1976.0396	-0.0230	0	K.DLLEMLSVGPSMVMILTK.W

No match to: 1781.8509, 1832.0408

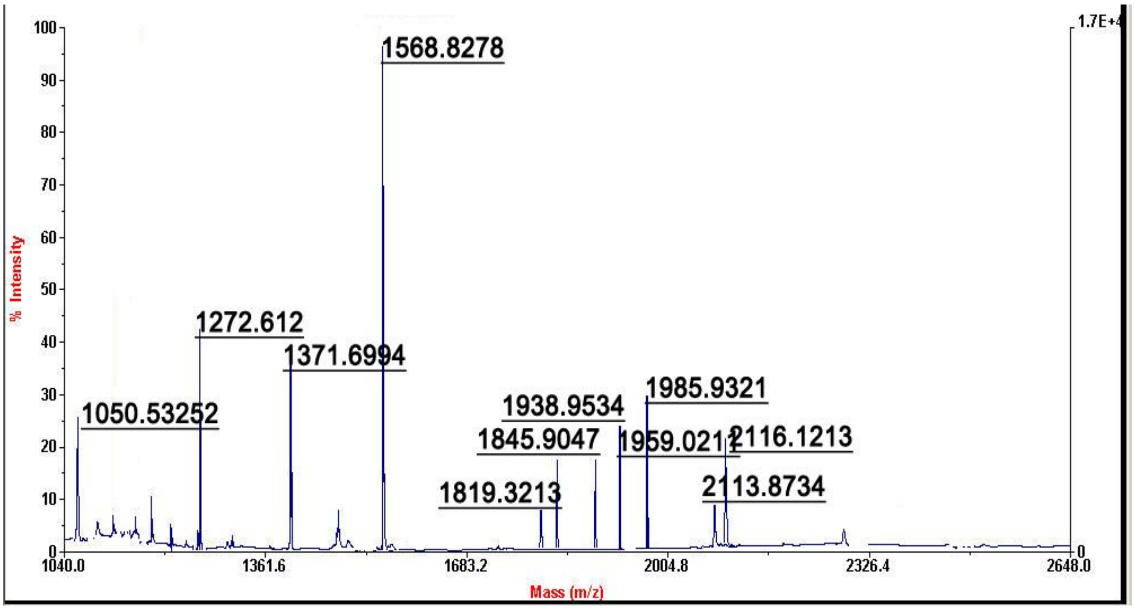
391 Thioredoxin domain-containing protein 5



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
38 - 63	2447.0405	2446.0332	2446.0633	-0.0300	0	R.AQEAAAAAADGPPAADGEDGQDPHSK.H
189 - 211	2603.2543	2602.2470	2602.2816	-0.0346	0	K.QGLYELSASNFELHVAQGDHFIK.F
212 - 221	1195.5175	1194.5102	1194.5103	-0.0001	0	K.FFAPWCGHCK.A
222 - 241	2193.1530	2192.1457	2192.1477	-0.0020	0	K.ALAPTWEQLALGLEHSETVK.I
288 - 296	1151.5691	1150.5618	1150.5618	-0.0000	0	R.EYVESQLQR.T
297 - 321	2514.2342	2513.2269	2513.2021	0.0249	0	R.TETGATETVTPSEAPVLAAEPEADK.G
322 - 344	2482.2322	2481.2249	2481.2639	-0.0390	0	K.GTVLALTENNFDDTIAEGITFIK.F
355 - 365	1274.6627	1273.6554	1273.6554	0.0000	0	K.TLAPTWEELSK.K
395 - 403	1079.6248	1078.6175	1078.6175	0.0000	0	R.GYPTLLLFR.G

No match to: 1107.5146, 1648.7213, 1855.8112

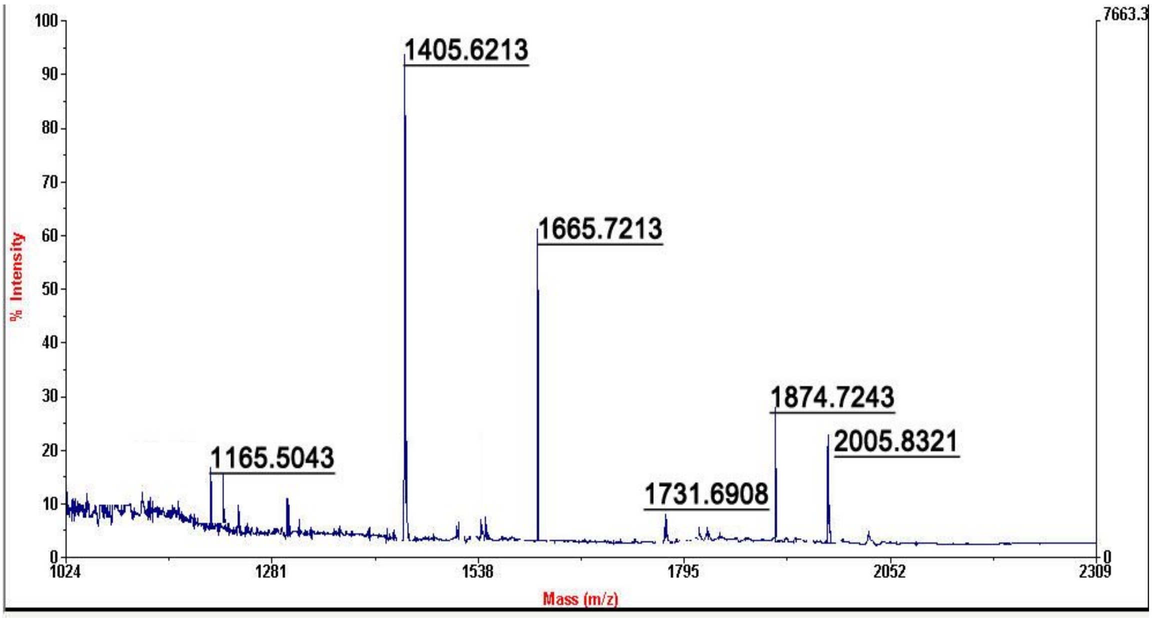
392 WD repeat-containing protein 8



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
71 - 86	1938.9534	1937.9461	1937.9458	0.0003	0	R.GLVQVWSLEQPEWHCK.I
116 - 124	1050.5325	1049.5252	1049.5580	-0.0327	0	R.ITVWSLCTK.S
228 - 246	1985.9321	1984.9248	1984.9531	-0.0282	0	K.SVAWSPSSQFLAVGSYDGK.V
281 - 295	1568.8278	1567.8205	1567.8181	0.0024	0	K.SPQLGLGCLSFPPPR.A
308 - 326	2116.1213	2115.1140	2115.1576	-0.0435	0	K.YEIASVPVSLQTLKPVTDR.A
331 - 348	1959.0211	1958.0138	1957.9972	0.0167	0	K.IGIGMLAFSPDSYFLATR.N
349 - 363	1811.9432	1810.9359	1810.9002	0.0357	0	R.NDNIPNAVWVWDIQK.L
366 - 377	1371.6994	1370.6921	1370.7922	-0.1001	0	R.LFAVLEQLSPVR.A
378 - 387	1272.6120	1271.6047	1271.6047	0.0000	0	R.AFQWDPQQPR.L
436 - 454	2113.8734	2112.8661	2112.9431	-0.0770	0	K.DHFCLCFLETEAVVGTACR.Q

No match to: 1819.3213, 1845.9047

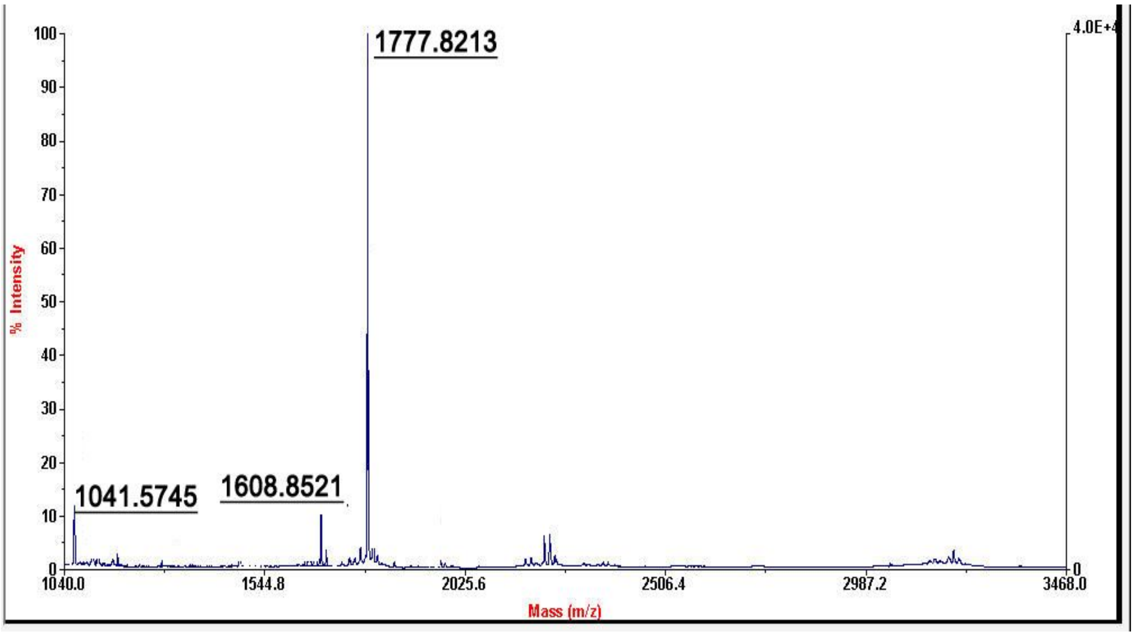
393 WAP four-disulfide core domain protein 8



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
56 - 73	2005.8321	2004.8248	2004.8115	0.0133	0	R.LTCTTELPDSCNTDFDCK.E
87 - 100	1665.7213	1664.7140	1664.7183	-0.0043	0	K.CMDPFQEPCMLPVR.H
101 - 110	1165.5043	1164.4970	1164.4843	0.0128	0	R.HGNCNHEAQR.W
164 - 180	1874.7243	1873.7170	1873.7281	-0.0111	0	K.ECPPSCHSDIDCPQTDK.C
216 - 227	1405.6213	1404.6140	1404.6265	-0.0125	0	K.CLQDEECPLVEK.C

No match to: 1731.6908

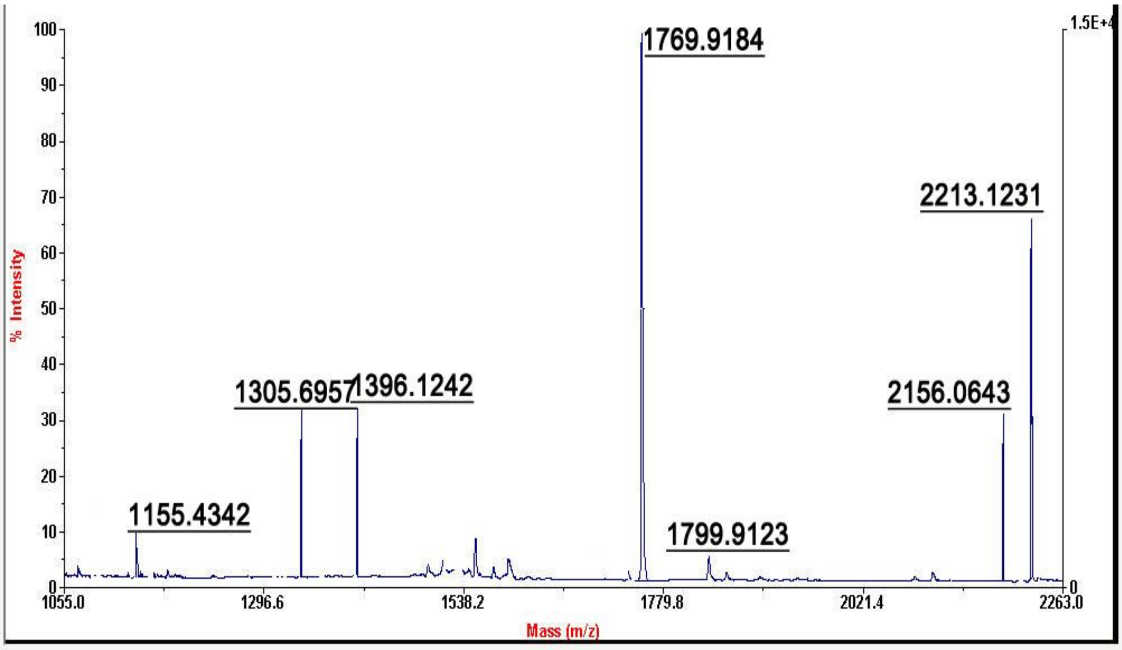
394 WAP four-disulfide core domain protein 6



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
36 - 52	2018.9892	2017.9819	2017.9812	0.0007	1	K.IKVECEVEEIDQCTKPR.D
38 - 52	1777.8083	1776.8010	1776.8022	-0.0012	0	K.VECEVEEIDQCTKPR.D
75 - 82	1017.5403	1016.5330	1016.5338	-0.0008	1	K.IYAVCHRR.L
83 - 97	1608.8524	1607.8451	1607.8460	-0.0009	0	R.LAPAWPPYHTGGTIK.K

No match to: 1041.5754, 1282.7542

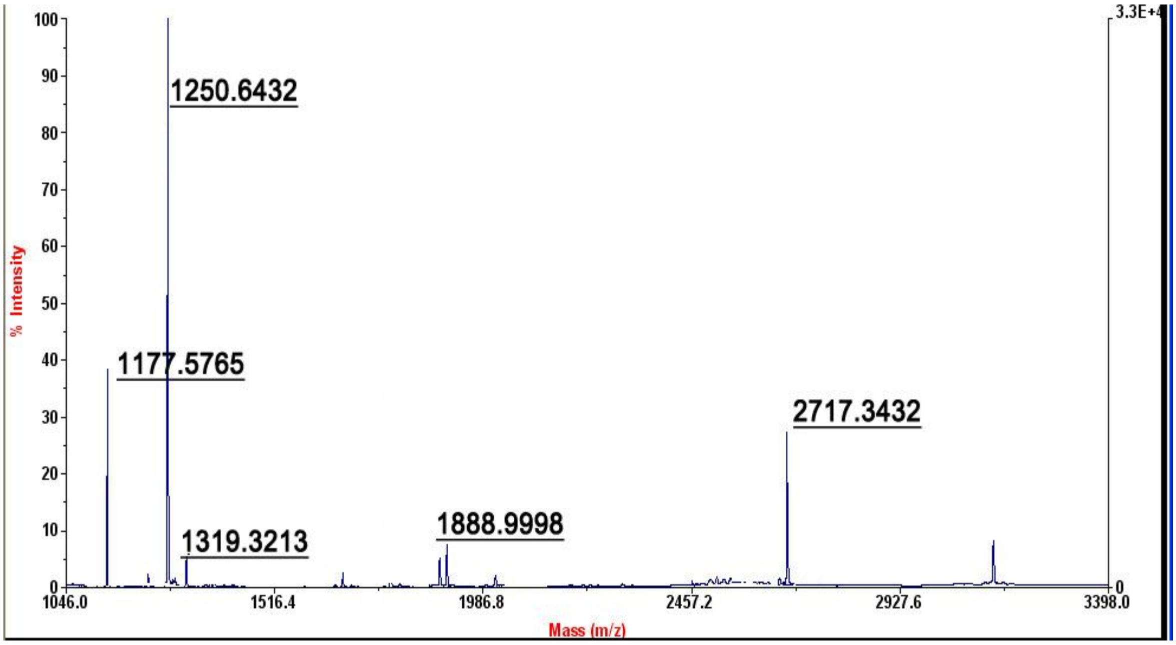
395 Ribonuclease-like protein 9



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
42 - 50	1155.4342	1154.4269	1154.4801	-0.0532	0	K.EEFEECLEK.F
51 - 62	1305.6957	1304.6884	1304.6877	0.0007	0	K.FFSTGPARPPTK.E
98 - 114	2213.1231	2212.1158	2212.0663	0.0495	0	R.WVAEHYFLLMQYDELQK.I
135 - 154	2156.0643	2155.0570	2155.0329	0.0241	0	K.GLVEGVYCNLTEAFEIPACK.Y
162 - 176	1799.9123	1798.9050	1798.8382	0.0668	0	K.GYVLITCSWQNEMQK.R

No match to: 1396.1242, 1713.7213, 1769.9184

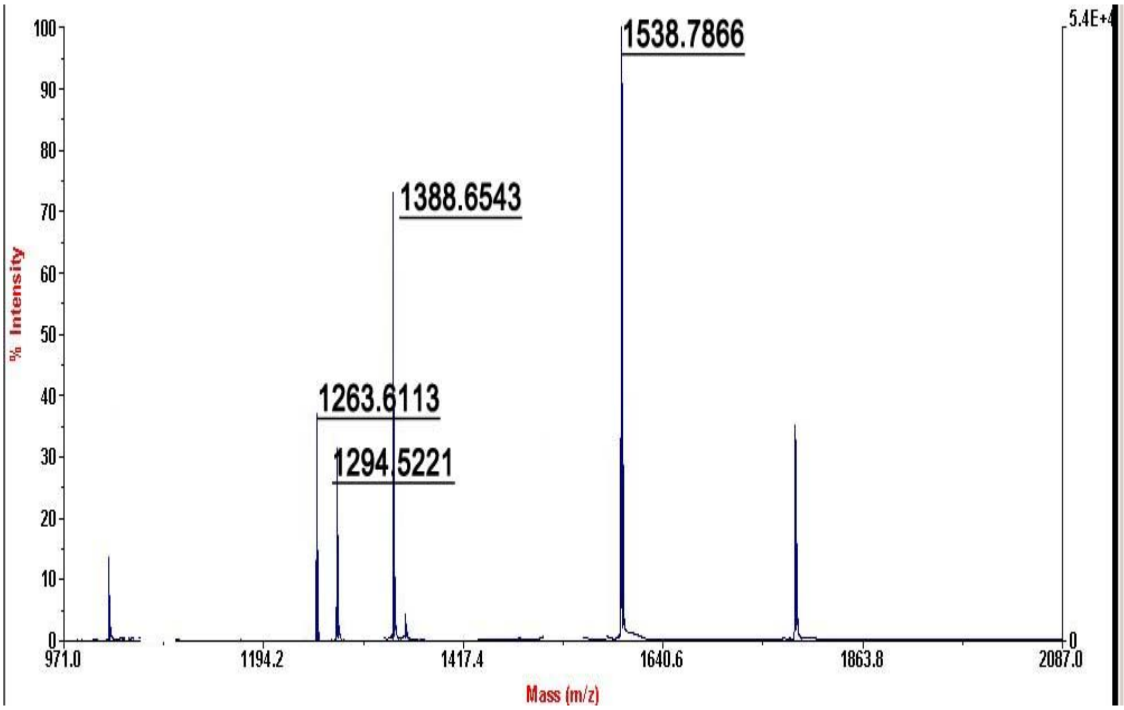
396 Ribonuclease-like protein 12



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
45 - 53	1177.5765	1176.5692	1176.5532	0.0160	0	R.YCNHMIIQR.V
86 - 102	1888.9998	1887.9925	1887.8859	0.1066	0	K.VACQNLSAIFCFQSETK.F
105 - 115	1250.6432	1249.6359	1249.6159	0.0200	0	K.MTVCQLIEGTR.Y

No match to: 1319.3213, 2717.3432

397 Ribonuclease-like protein 13

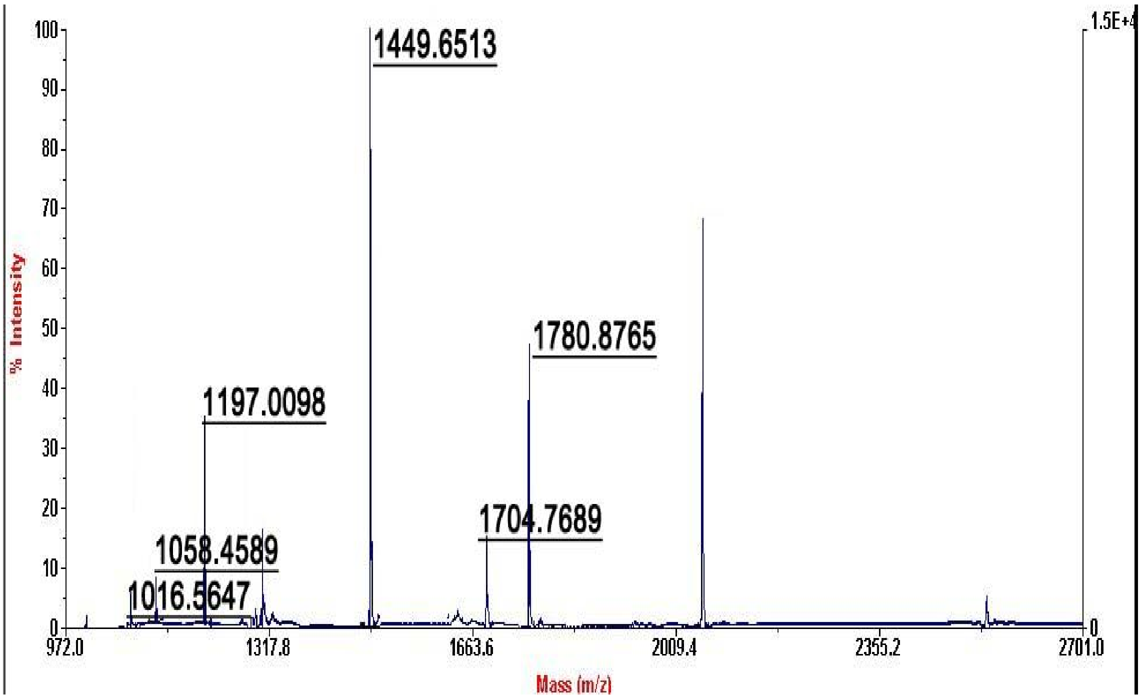


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

31 - 41	1388.6543	1387.6470	1387.6772	-0.0302	0	R.NFYTLSIDYPR.V
50 - 60	1294.5221	1293.5148	1293.5304	-0.0156	0	R.GYCNGLMSYMR.G
71 - 80	1263.6113	1262.6040	1262.6924	-0.0884	0	K.IHYVIHAPWK.A
142 - 156	1538.7866	1537.7793	1537.7664	0.0129	0	K.YEADPIGIAGLYSGI.-

No match to: 1675.4532

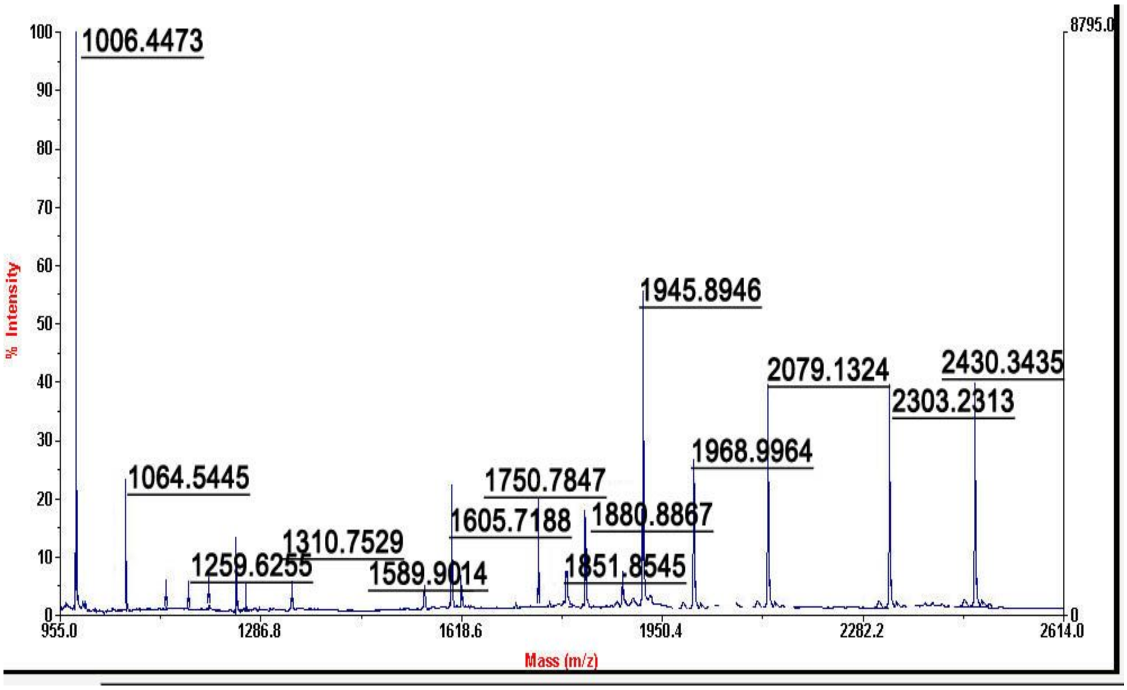
398 Ribonuclease 4



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
52 - 59	1058.4589	1057.4516	1057.4507	0.0009	0	R.YCNLMMQR.R
70 - 82	1704.7689	1703.7616	1703.8420	-0.0804	0	R.FNTFIHEDIWNIR.S
97 - 105	1016.5647	1015.5574	1015.4579	0.0995	0	K.MNCHEGVVK.V
131 - 147	1780.8765	1779.8692	1779.8614	0.0078	0	R.VVIACEGNPQVPVHFDG.-

No match to: 1197.0098, 1449.6513, 2103.3321

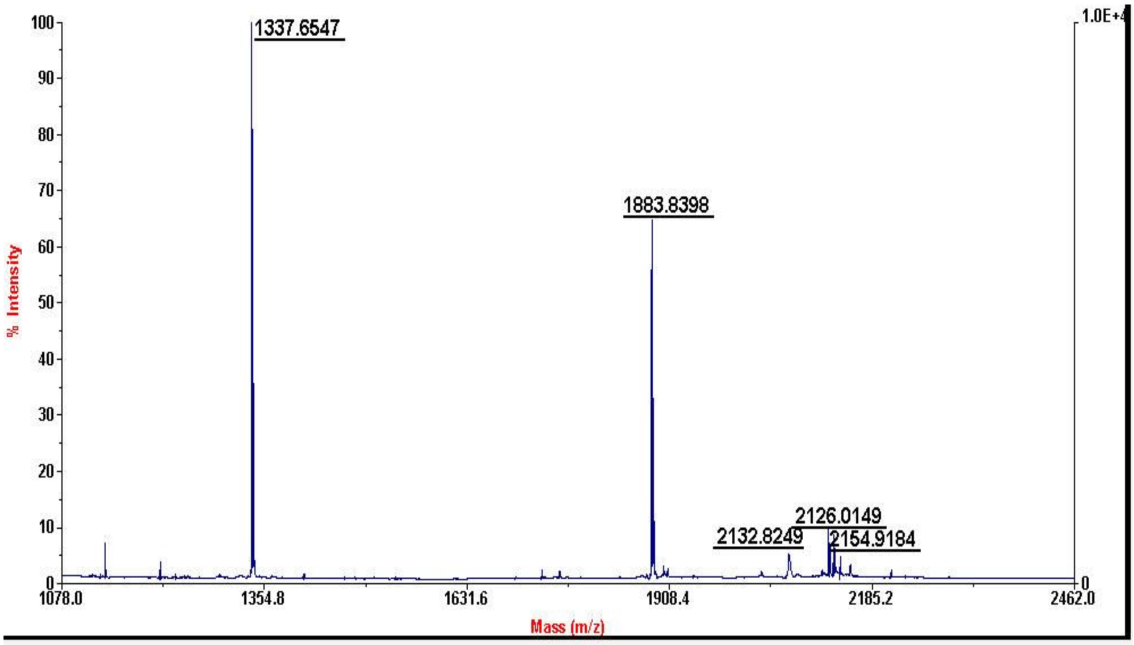
399 Sperm-associated antigen 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
48 - 63	1880.8867	1879.8794	1879.7822	0.0972	0	R.SGEEGYYPELTEFCEK.H
78 - 94	1851.8545	1850.8472	1850.8686	-0.0214	0	K.DKPAATAASFTAEEWEK.I
113 - 125	1605.7188	1604.7115	1604.7116	-0.0000	0	K.MHFHETETFPAMK.D
255 - 267	1582.6434	1581.6361	1581.6882	-0.0520	0	K.LQNWNSAFQDCEK.V
422 - 449	2303.2313	2302.2240	2302.1050	0.1190	0	R.ASAAAAAGGGATGHPGGGQGAENPAGLK.S
580 - 599	2079.1324	2078.1251	2078.1677	-0.0425	0	K.LSPIPAVPASVPLQAWHPAK.E
798 - 819	2430.3435	2429.3362	2429.3066	0.0296	0	K.LPIAKPNNAYEFGQIINALSTR.K
845 - 858	1589.9001	1588.8929	1588.9076	-0.0147	0	K.LEGDTFLLLIQSLK.N

No match to: 1750.7847, 1945.8946, 1968.9964

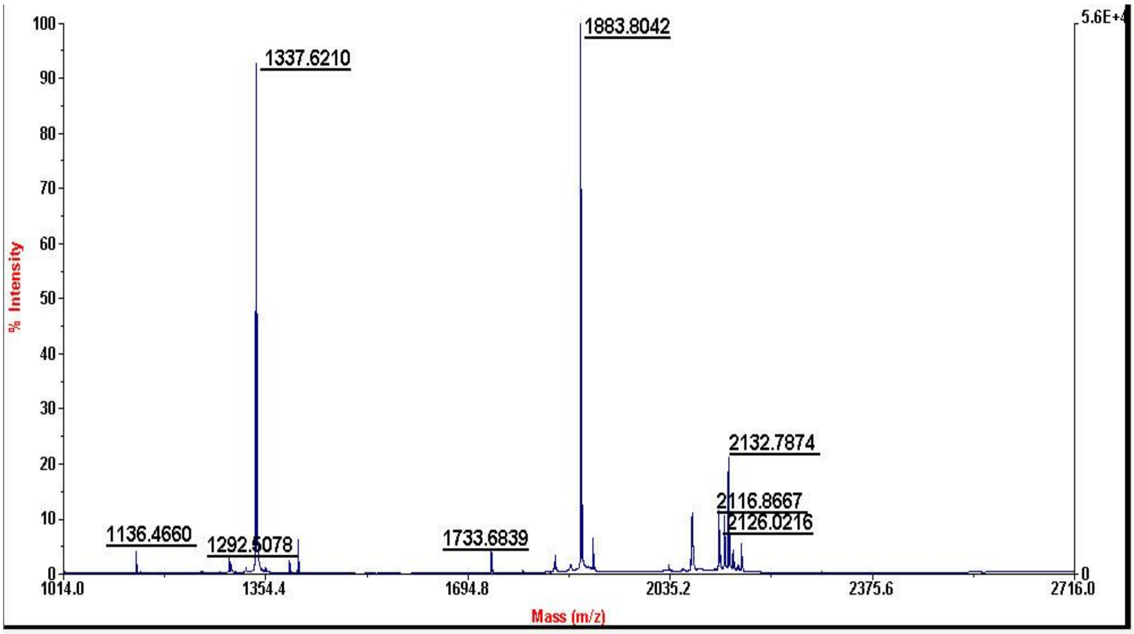
400 Glutathione S-transferase P



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 12	1337.6547	1336.6474	1336.7180	-0.0705	0	M.PPYTVVYFPVR.G
56 - 71	1883.8398	1882.8325	1882.9425	-0.1100	0	K.FQDGDLTLYQSNTILR.H
83 - 101	2132.8249	2131.8177	2131.9692	-0.1515	0	K.DQQEAALVDMVNDGVEDLR.C
Oxidation (M)						
104 - 121	2154.9184	2153.9112	2154.0521	-0.1409	1	K.YISLIYTNYEAGKDDYVK.A
122 - 141	2126.0149	2125.0076	2125.1531	-0.1456	0	K.ALPGQLKPFETLLSQNQGGK.T

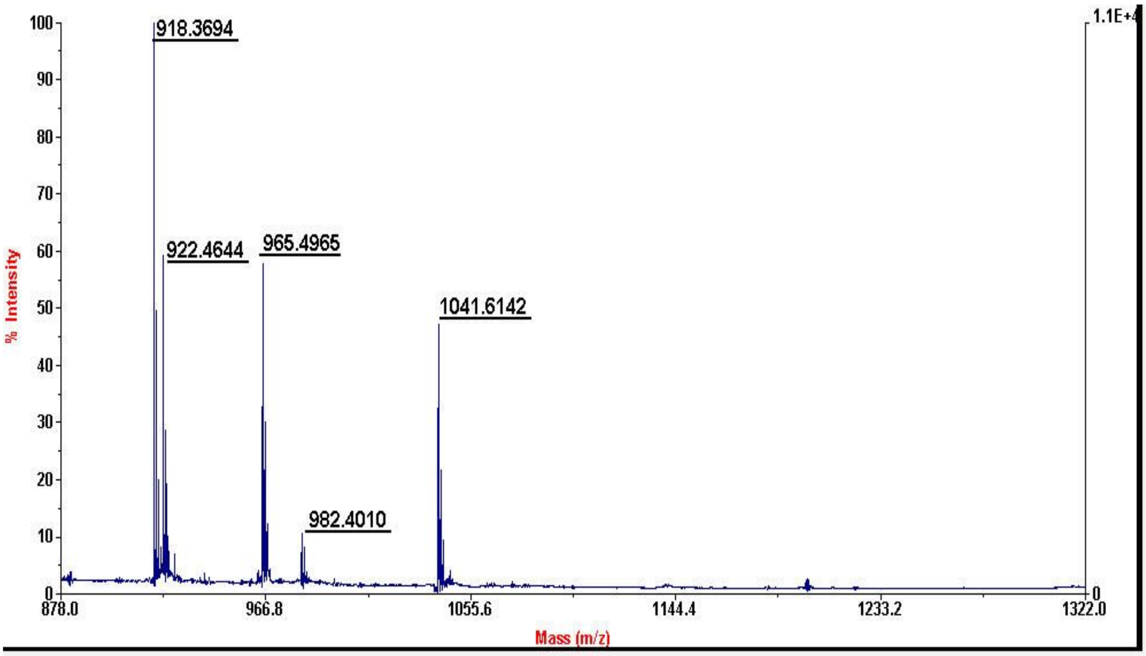
No match to: 1135.5812, 1212.6012, 2072.8229, 2140.8687

401 Glutathione S-transferase P



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
2 - 12	1337.6210	1336.6137	1336.7180	-0.1042	0	M.PPYTVVYFPVR.G	
20 - 30	1292.5078	1291.5005	1291.6231	-0.1226	0	R.MLLADQGQSWK.E	Oxidation (M)
31 - 45	1733.6839	1732.6766	1732.8519	-0.1753	0	K.EEVVTVETWQEGSLK.A	
46 - 55	1136.4660	1135.4587	1135.5696	-0.1108	0	K.ASCLYGQLPK.F	
56 - 71	1883.8042	1882.7970	1882.9425	-0.1455	0	K.FQDGDLTLYQSNTILR.H	
83 - 101	2116.8667	2115.8595	2115.9743	-0.1148	0	K.DQQEAALVDMVNDGVEDLR.C	
83 - 101	2132.7874	2131.7801	2131.9692	-0.1890	0	K.DQQEAALVDMVNDGVEDLR.C	Oxidation (M)
122 - 141	2126.0216	2125.0143	2125.1531	-0.1389	0	K.ALPGQLKPFETLLSQNQGGK.T	

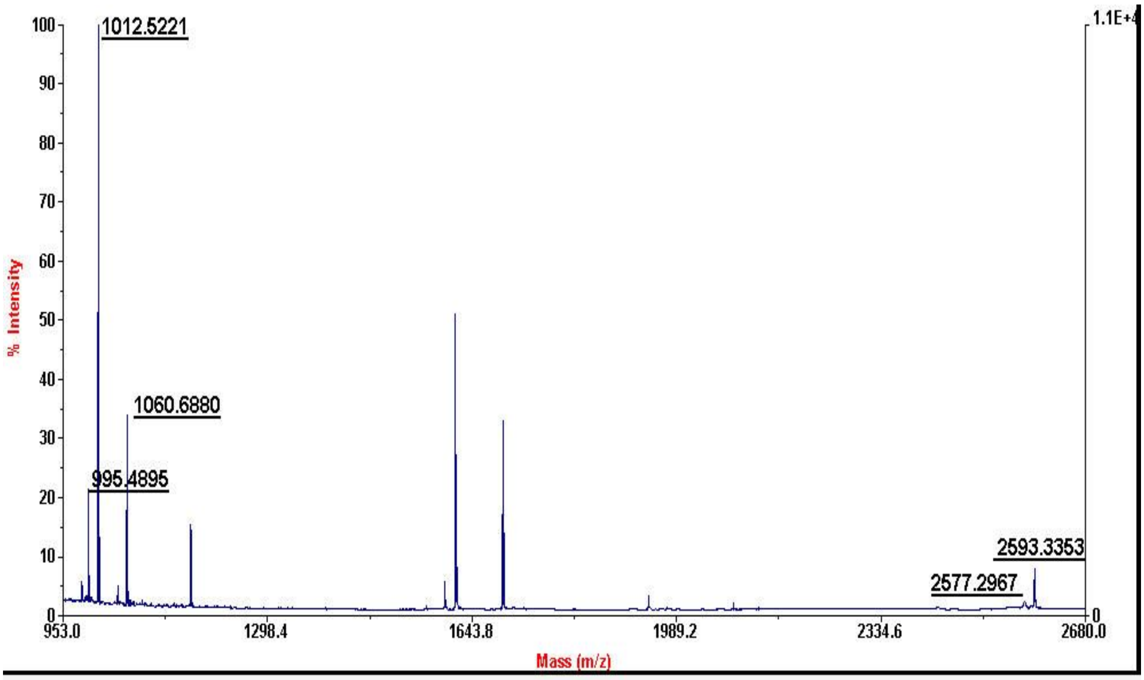
402 Platelet-activating factor acetylhydrolase IB subunit gamma



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
23 - 29	982.4010	981.3937	981.4603	-0.0666	0	R.WMSLHHR.F	Oxidation (M)
119 - 127	1041.6142	1040.6069	1040.5978	0.0091	0	K.AIVQLVNER.Q	
142 - 149	918.3694	917.3621	917.4831	-0.1210	0	R.GQHPNPLR.E	
199 - 206	965.4965	964.4893	964.4800	0.0092	0	R.LGYTPVCR.A	
207 - 214	922.4644	921.4571	921.5760	-0.1188	0	R.ALHSLLLR.L	

No match to: 1200.8224, 1331.9398, 1435.1645, 1460.1562, 1798.7453, 1813.8400, 2211.3875

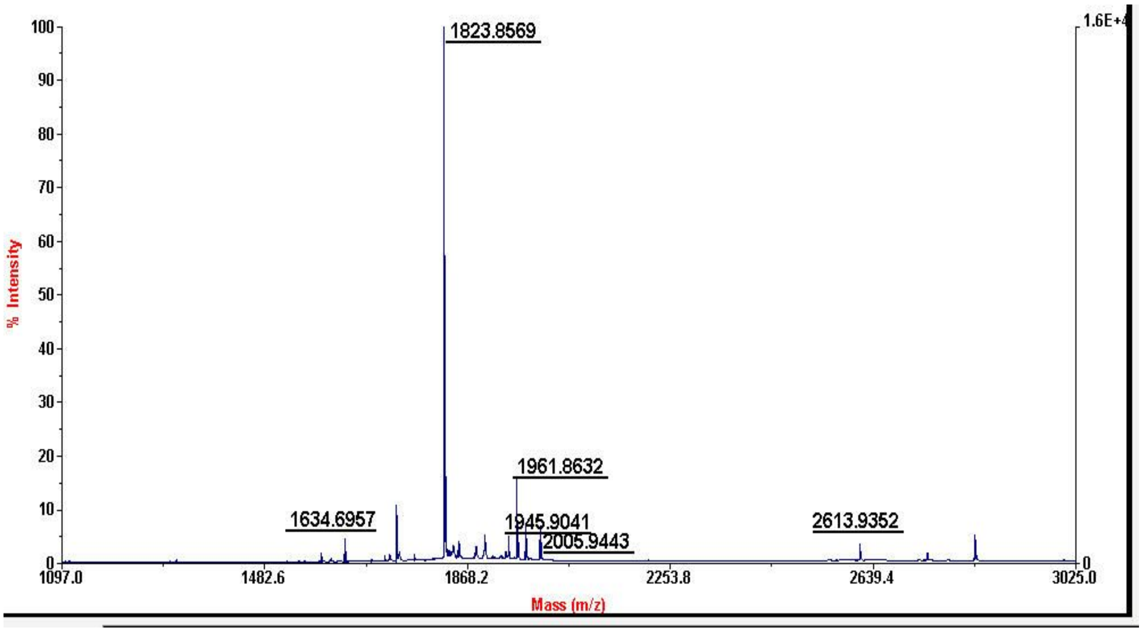
403 Ubiquinol-cytochrome c reductase iron-sulfur subunit



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
85 - 92	1012.5221	1011.5149	1011.4662	0.0487	0	K.VPDFSEYR.R
93 - 101	1060.6880	1059.6807	1059.5924	0.0883	1	R.RLEVLDSTK.S
131 - 155	2593.3353	2592.3280	2592.3833	-0.0552	1	K.NAVTQFVSSMSASADVLALAKIEIK.L
197 - 204	995.4895	994.4822	994.4468	0.0354	0	R.DPQHDLDR.V
251 - 274	2577.2967	2576.2894	2576.2720	0.0174	0	R.LGPAPLNLEVPTYEFTSDDMVIVG.-

No match to: 1168.7806, 1597.5697, 1615.5572, 1694.6455, 1942.1067

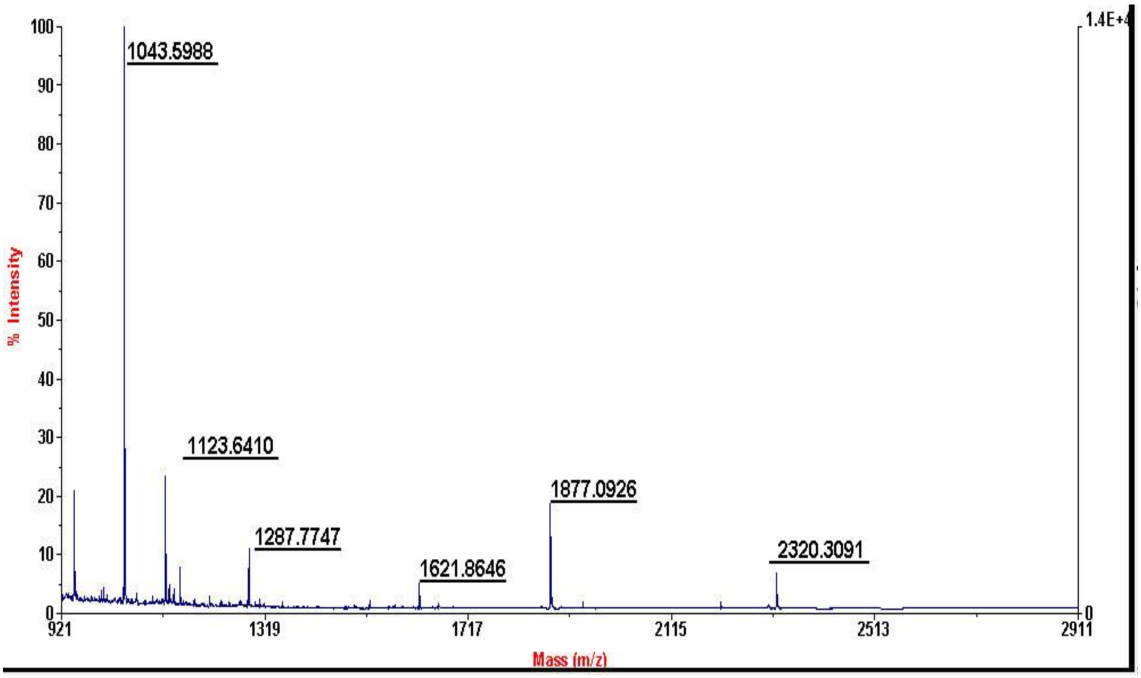
404 Cathepsin B precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
224 - 237	1634.6957	1633.6884	1633.7008	-0.0124	0	K.HYGYNSYSVSNSEK.D	
224 - 245	2613.9352	2612.9280	2613.1693	-0.2413	1	K.HYGYNSYSVSNSEKDIMAEIYK.N	
Oxidation (M)							
246 - 263	2005.9443	2004.9371	2004.9833	-0.0462	0	K.NGPVEGAFSVYSDFLLYK.S	
264 - 281	1945.9041	1944.8968	1944.8935	0.0034	0	K.SGVYQHVTGEMMGGHAIR.I	
Oxidation (M)							
264 - 281	1961.8632	1960.8559	1960.8884	-0.0325	0	K.SGVYQHVTGEMMGGHAIR.I	2
Oxidation (M)							
315 - 331	1823.8569	1822.8496	1822.8632	-0.0136	0	R.GQDHCGIESEVVAGIPR.T	

No match to: 1732.8483, 1850.8702, 1899.9442, 1977.9029, 2741.2953, 2832.2365

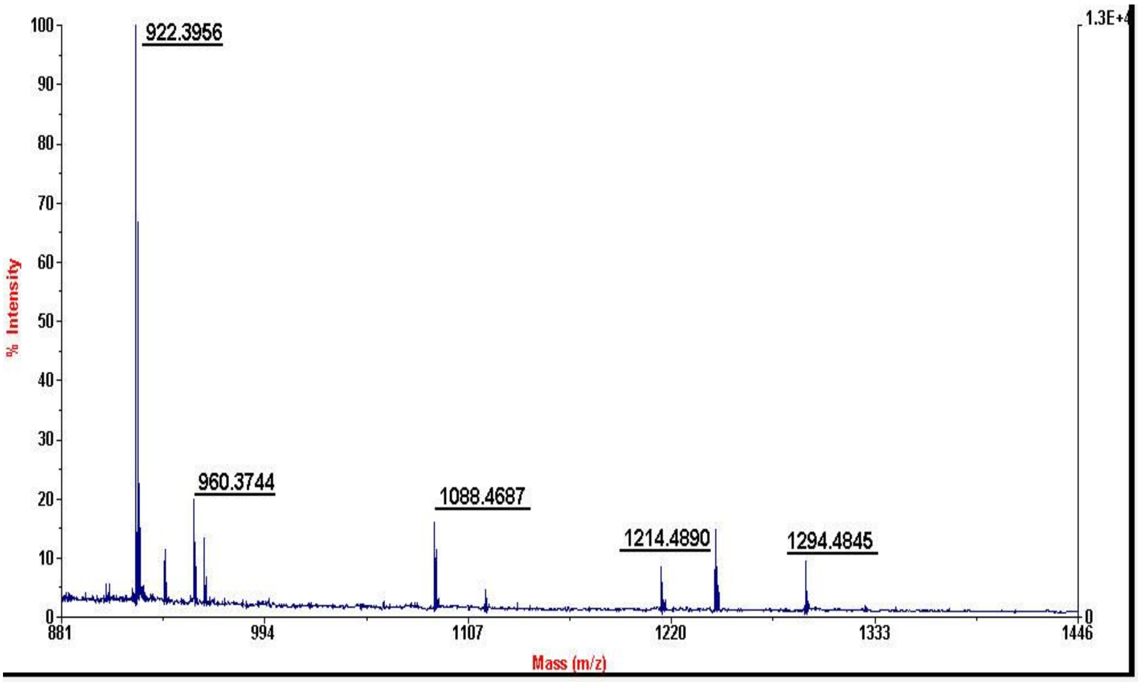
405 arginine/serine-rich 3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
12 - 28	1877.0926	1876.0853	1875.9439	0.1414	1	K.VYVGNLGNNGNKTELER.A
29 - 37	1043.5988	1042.5915	1042.5236	0.0679	0	R.AFGYYGPLR.S
38 - 57	2320.3091	2319.3018	2319.1437	0.1582	1	R.SVWVARNPPGFAFVEFEDPR.D
44 - 57	1621.8646	1620.8573	1620.7573	0.1000	0	R.NPPGFAFVEFEDPR.D
58 - 69	1287.7747	1286.7674	1286.6215	0.1459	1	R.DAADAVRELDGR.T
89 - 98	1123.6410	1122.6337	1122.5683	0.0654	1	R.NRGPPPSWGR.R

No match to: 945.5402, 1152.8452, 1286.7904, 2304.4842

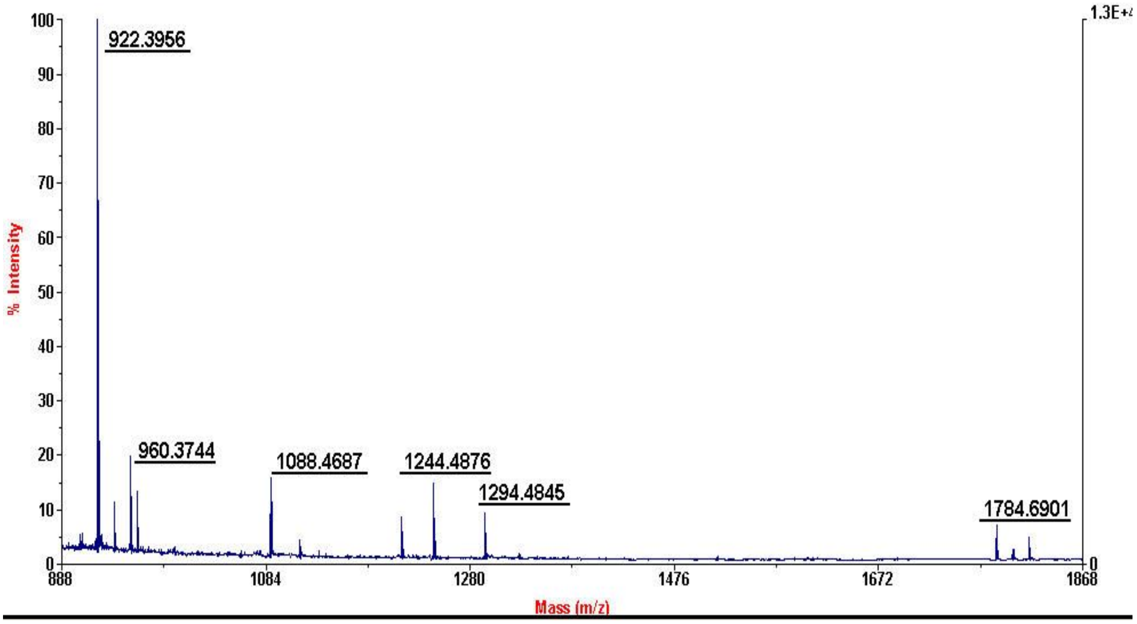
406 GTP-binding nuclear protein Ran



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
30 - 37	960.3744	959.3671	959.4712	-0.1041	0	R.HLTGEFEK.K
30 - 38	1088.4687	1087.4614	1087.5662	-0.1048	1	R.HLTGEFEKK.Y
61 - 71	1294.4845	1293.4772	1293.5990	-0.1217	0	K.FNVWDTAGQEK.F
100 - 106	922.3956	921.3883	921.4569	-0.0686	0	K.NVPNWHR.D
143 - 152	1214.4890	1213.4817	1213.5979	-0.1162	0	K.NLQYYDISAK.S

No match to: 954.3745, 1244.4876, 1784.6901, 1800.7127, 1816.6979

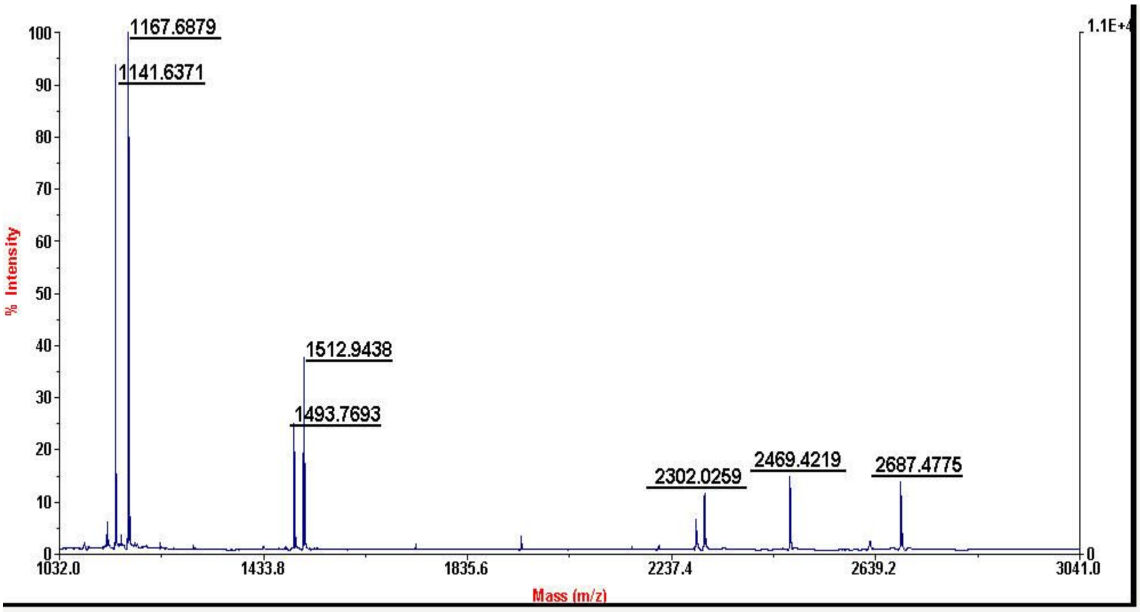
407 Huntingtin-associated protein 1 (HAP-1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
6 - 14	922.3956	921.3883	921.4273	-0.0390	1	R.LGRCCAGSR.L	
139 - 147	954.3745	953.3672	953.5043	-0.1371	0	R.RPGVSGPER.A	
168 - 175	960.3744	959.3671	959.5287	-0.1616	1	K.KITQEDVK.V	
217 - 227	1294.4845	1293.4772	1293.5871	-0.1098	0	K.QNSVLMEENSK.L	Oxidation (M)
398 - 407	1244.4876	1243.4804	1243.5325	-0.0522	1	R.CRMYGAETEK.L	
535 - 550	1784.6901	1783.6829	1783.8120	-0.1292	0	R.GFEAEEGLMLAADIMR.G	2 Oxidation (M)

No match to: 1088.4687, 1214.4890, 1800.7127, 1816.6979

408 Flavin reductase

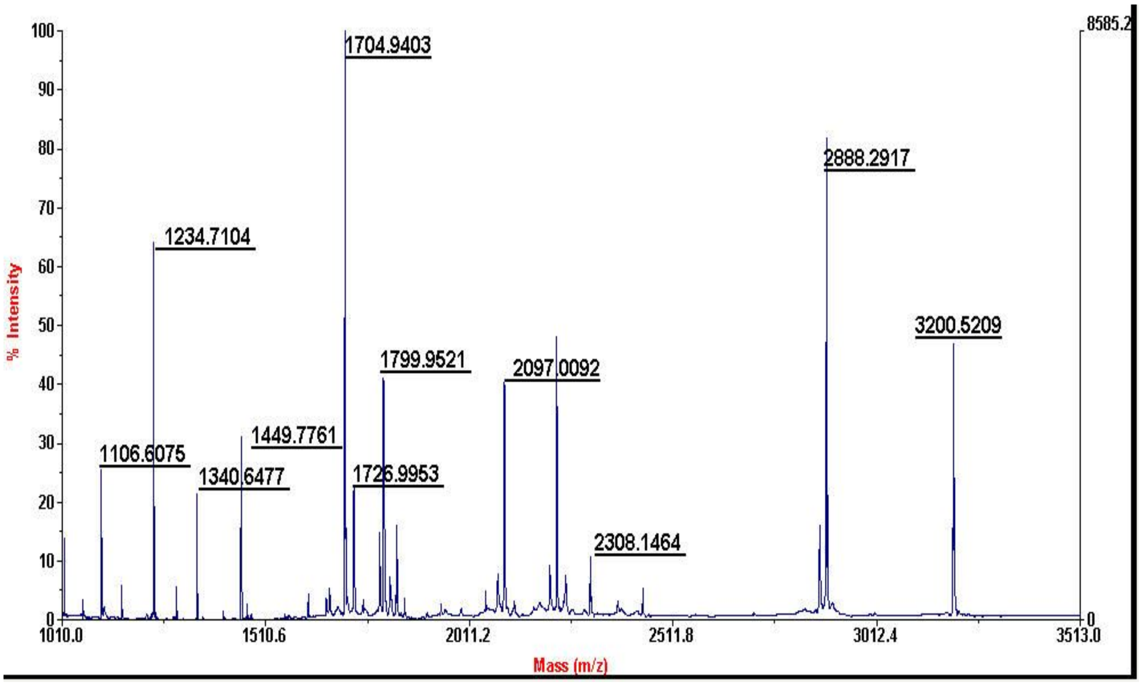


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

40 - 63	2469.4219	2468.4146	2468.3024	0.1122	0	R.LPSEGPRPAHVVVGDVLQAADVDK.T	
64 - 78	1512.9438	1511.9365	1511.8672	0.0694	0	K.TVAGQDAVIVLLGTR.N	
79 - 92	1493.7693	1492.7620	1492.6828	0.0792	0	R.NDLSPTTVMSEGAR.N	Oxidation (M)
125 - 134	1167.6879	1166.6806	1166.6044	0.0762	0	R.LQAVTDDHIR.M	
146 - 170	2687.4775	2686.4702	2686.3425	0.1277	0	K.YVAVMPPHIGDQPLTGAYTVTLDGR.G	Oxidation (M)
179 - 187	1141.6371	1140.6298	1140.5499	0.0800	0	K.HDLGHFMLR.C	Oxidation (M)
188 - 206	2302.0259	2301.0186	2300.9281	0.0906	0	R.CLTTDEYDGHSTYPSHQYQ.-	

No match to: 1166.7295, 1941.0442, 2285.0308, 2627.2849

409 Annexin A5

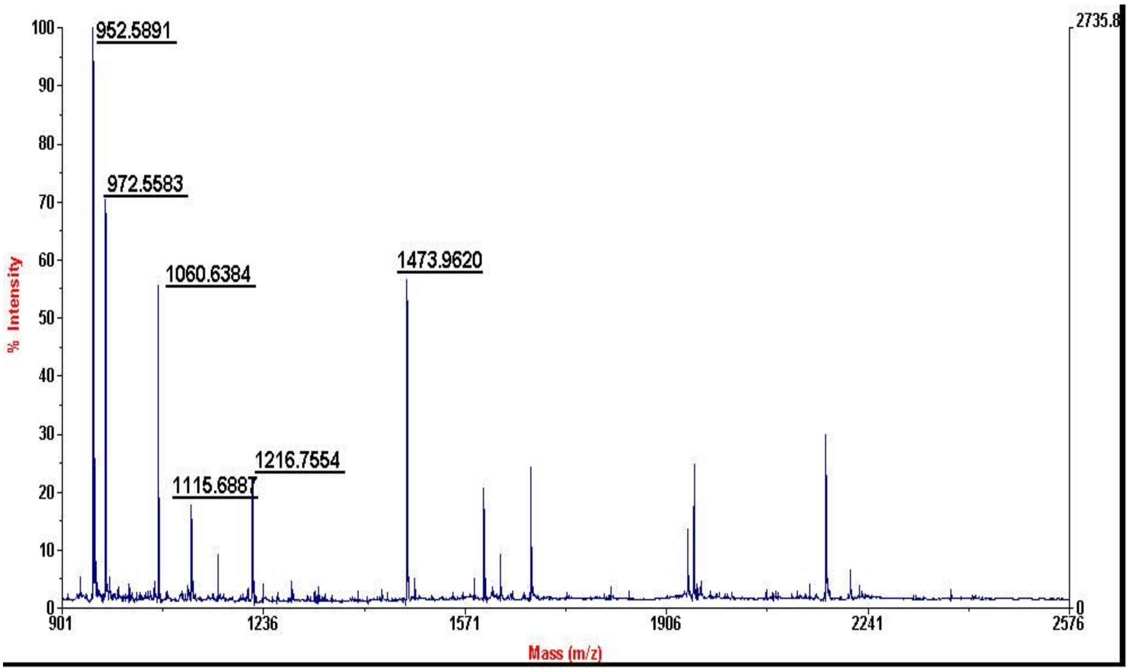


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 18	1340.6477	1339.6404	1339.6045	0.0359	0	R.GTVTDFPGFDER.A
7 - 25	2097.0092	2096.0019	2095.9811	0.0209	1	R.GTVTDFPGFDERADAETLR.K
30 - 45	1704.9403	1703.9331	1703.8941	0.0389	0	K.GLGTDEESILTLLTSR.S
46 - 58	1449.7761	1448.7688	1448.7372	0.0317	1	R.SNAQRQEISAAFK.T
109 - 123	1726.9953	1725.9880	1725.9625	0.0256	1	K.VLTEIIASRTPEELR.A

124 - 151	3200.5209	3199.5136	3199.4469	0.0667	1	R.AIKQVYEEEYGSSLEDDVVGDTSGYYQR.M
127 - 151	2888.2917	2887.2844	2887.2308	0.0536	0	K.QVYEEEYGSSLEDDVVGDTSGYYQR.M
187 - 201	1799.9521	1798.9448	1798.8890	0.0558	1	K.WGTDEEKFITIFGTR.S
209 - 227	2308.1464	2307.1391	2307.1093	0.0298	1	K.VFDKYMTISGFQIEETIDR.E Oxidation (M)
277 - 285	1106.6075	1105.6003	1105.5768	0.0235	0	R.SEIDLFNIR.K
277 - 286	1234.7104	1233.7031	1233.6717	0.0314	1	R.SEIDLFNIRK.E

No match to: 1790.9447, 1831.9190, 2225.0803

410 Mimecan precursor



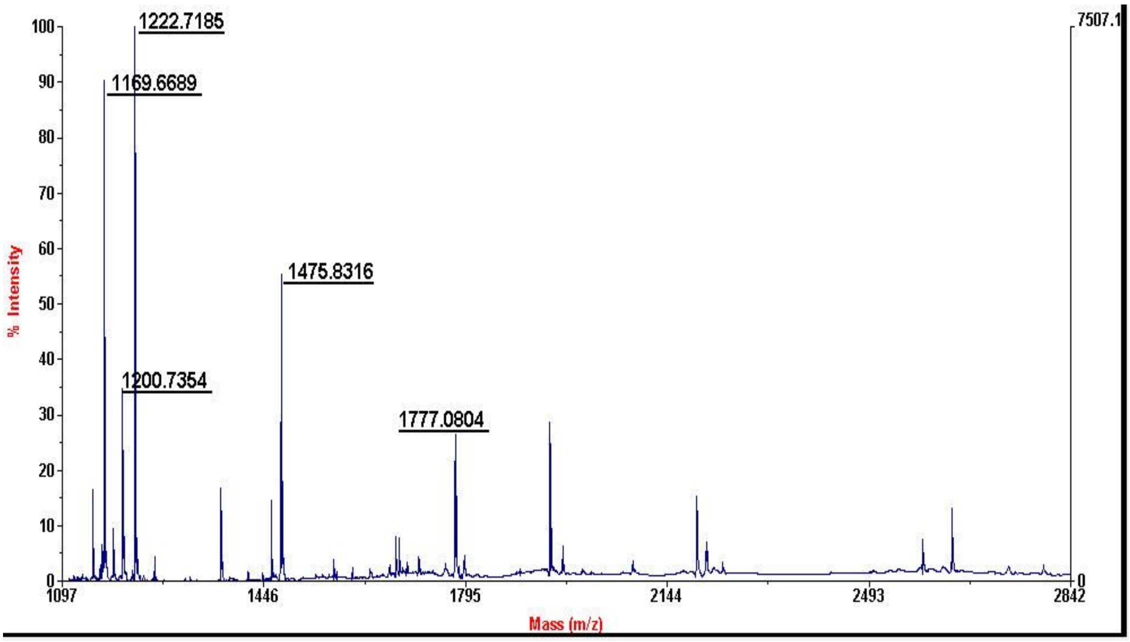
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
120 - 127	972.5583	971.5510	971.4712	0.0798	0	K.ESAYLYAR.F
134 - 146	1473.9620	1472.9548	1472.7987	0.1560	1	K.LTAKDFADIPNLR.R
138 - 146	1060.6384	1059.6311	1059.5349	0.0962	0	K.DFADIPNLR.R
138 - 147	1216.7554	1215.7481	1215.6360	0.1121	1	K.DFADIPNLRR.L
282 - 290	1115.6887	1114.6814	1114.5593	0.1221	0	K.HPNSFICLK.R

291 - 298	952.5891	951.5818	951.5178	0.0640	1	K.RLPIGSYF.-

No match to: 1630.1013, 1680.1820, 1941.1836, 1951.2983, 2170.3899

411

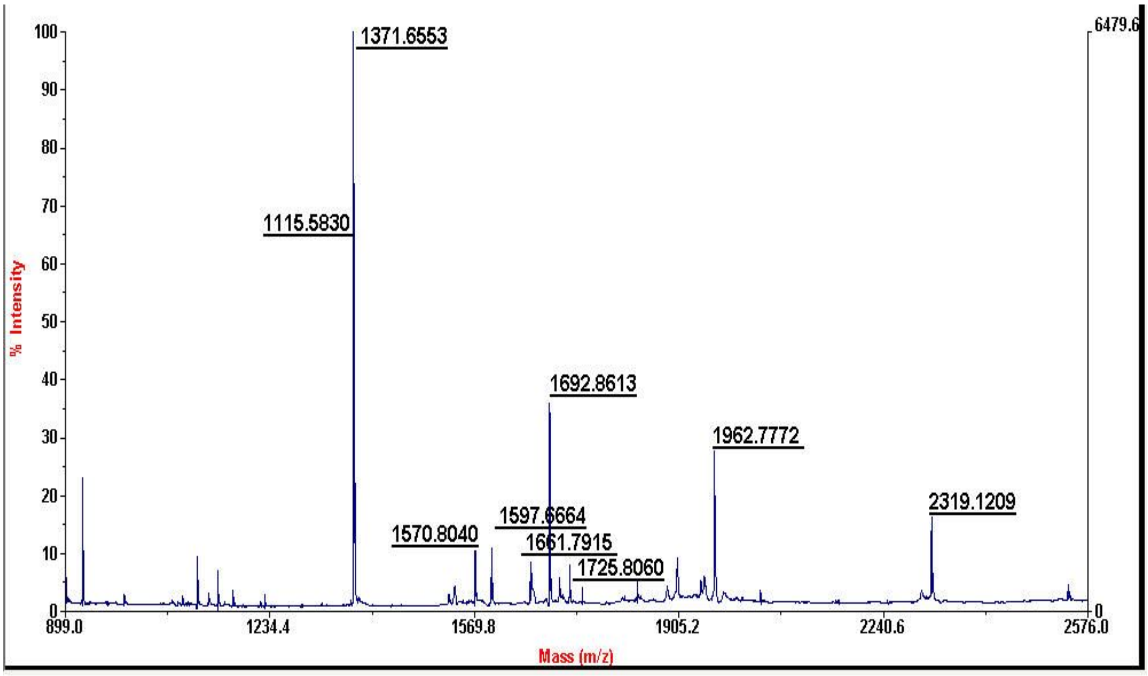
Nicotinate-nucleotide pyrophosphorylase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
87 - 102	1777.0804	1776.0731	1775.9465	0.1266	1	R.VAEVRGPAHCLLLGER.V
92 - 102	1222.7185	1221.7112	1221.6288	0.0824	0	R.GPAHCLLLGER.V
111 - 126	1475.8316	1474.8244	1474.7198	0.1046	0	R.CSGIASAAAAAVEAAR.G
127 - 138	1169.6689	1168.6616	1168.5738	0.0878	0	R.GAGWTGHVAGTR.K
150 - 161	1200.7354	1199.7281	1199.6411	0.0870	0	K.YGLLVGGAASHR.Y

No match to: 1018.6349, 1149.6703, 1185.6635, 1371.7683, 1458.8040

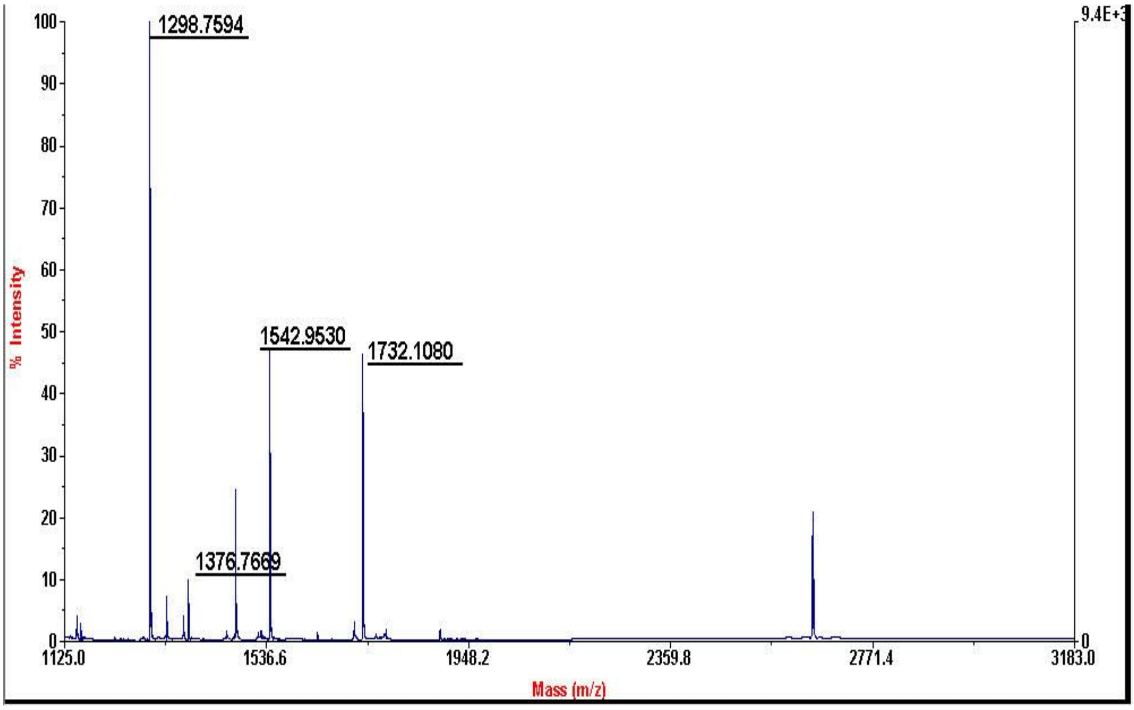
412 Annexin A4 (Annexin IV)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
10 - 24	1597.6664	1596.6591	1596.7202	-0.0611	0	K.AASGFNAMEDAQTLR.K Oxidation (M)
10 - 25	1725.8060	1724.7987	1724.8152	-0.0165	1	K.AASGFNAMEDAQTLRK.A Oxidation (M)
29 - 44	1692.8613	1691.8540	1691.8730	-0.0190	0	K.GLGTDEDAIISVLAYR.N
45 - 53	1115.5830	1114.5757	1114.5843	-0.0086	1	R.NTAQRQEIR.T
101 - 116	1661.7915	1660.7842	1660.8090	-0.0248	0	K.GAGTDEGCLIEILASR.T
124 - 134	1371.6553	1370.6481	1370.6579	-0.0098	0	R.ISQTYQQQYGR.S
135 - 150	1962.7772	1961.7699	1961.8789	-0.1090	1	R.SLEDDIRSDTSFMFQR.V Oxidation (M)
151 - 172	2319.1209	2318.1136	2318.1866	-0.0730	1	R.VLVSLSAGGRDEGNYLDDALVR.Q
203 - 214	1570.8040	1569.7967	1569.8052	-0.0085	1	R.NHLLHVFDEYKR.I

No match to: 1149.5820

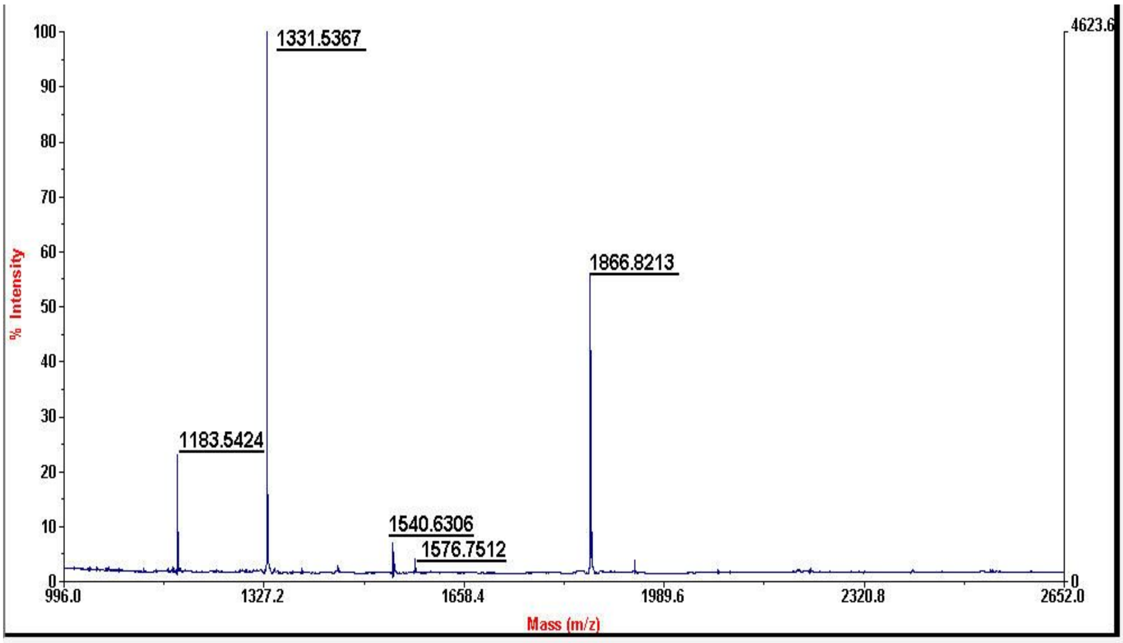
413 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
96 - 103	992.6241	991.6168	991.4505	0.1663	1	K.ISRDADCR.A
149 - 158	1298.7594	1297.7521	1297.6302	0.1219	0	R.YQETFNVIER.C
186 - 196	1376.7669	1375.7596	1375.6231	0.1365	0	R.YCAQDAFFQVK.E
197 - 211	1542.9530	1541.9458	1541.8049	0.1408	0	K.EVDVGLAADVGTLQR.L
215 - 230	1732.1080	1731.1007	1730.9315	0.1692	0	K.VIGNQSLVNELAFTAR.K

No match to: 1149.6959, 1157.7777, 1366.7884, 1472.8203, 1518.8623, 2648.4377

414 Sialic acid synthase

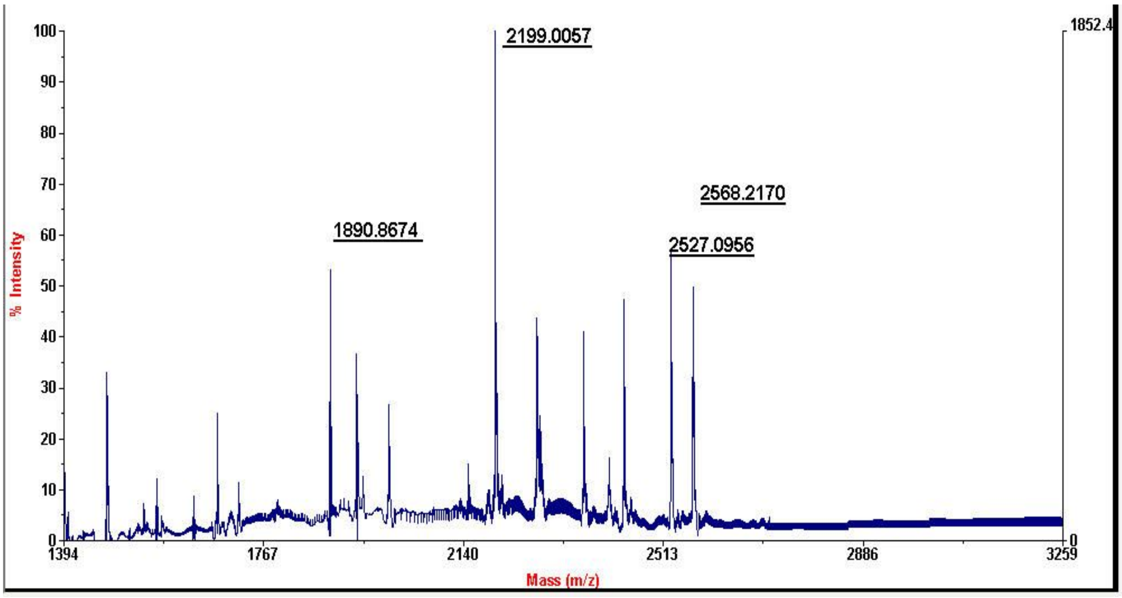


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

42 - 52	1183.5424	1182.5351	1182.4831	0.0520	1	R.MAKECGADCAK.F
80 - 86	890.4253	889.4180	889.4406	-0.0226	1	K.TYGEHKR.H
87 - 96	1331.5367	1330.5294	1330.6054	-0.0760	0	R.HLEFSHDQYR.E
132 - 145	1540.6306	1539.6233	1539.7205	-0.0972	0	K.VGSGDTNNFPYLEK.T
247 - 264	1866.8213	1865.8140	1865.9119	-0.0979	0	K.GSDHSASLEPGELAELVR.S
321 - 334	1576.7512	1575.7439	1575.8297	-0.0858	1	K.GYPPEDIFNLVGKK.V

No match to: 1050.4893

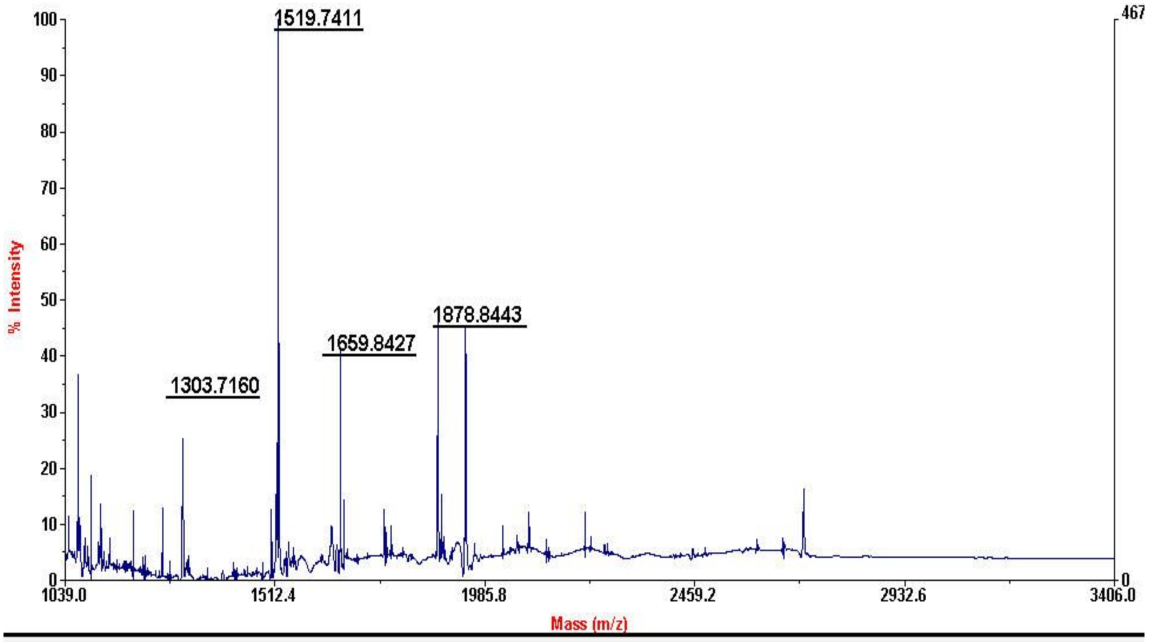
415 Thioredoxin-like protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 23	2199.0057	2197.9984	2198.0968	-0.0983	0	M.VGVKPVGSDPDFQPELSGAGSR.L
86 - 102	1890.8674	1889.8601	1889.9483	-0.0882	1	K.VRIDQYQGADAVGLEEK.I
212 - 234	2568.2170	2567.2097	2567.2966	-0.0869	1	R.SEPTQALELTEDDIKEDGIVPLR.Y
238 - 259	2527.0956	2526.0883	2526.1987	-0.1103	0	K.FQNVNSVTIFVQSNQGEEETTR.I

No match to: 1060.4992, 1283.5925, 1999.8223, 2276.8515

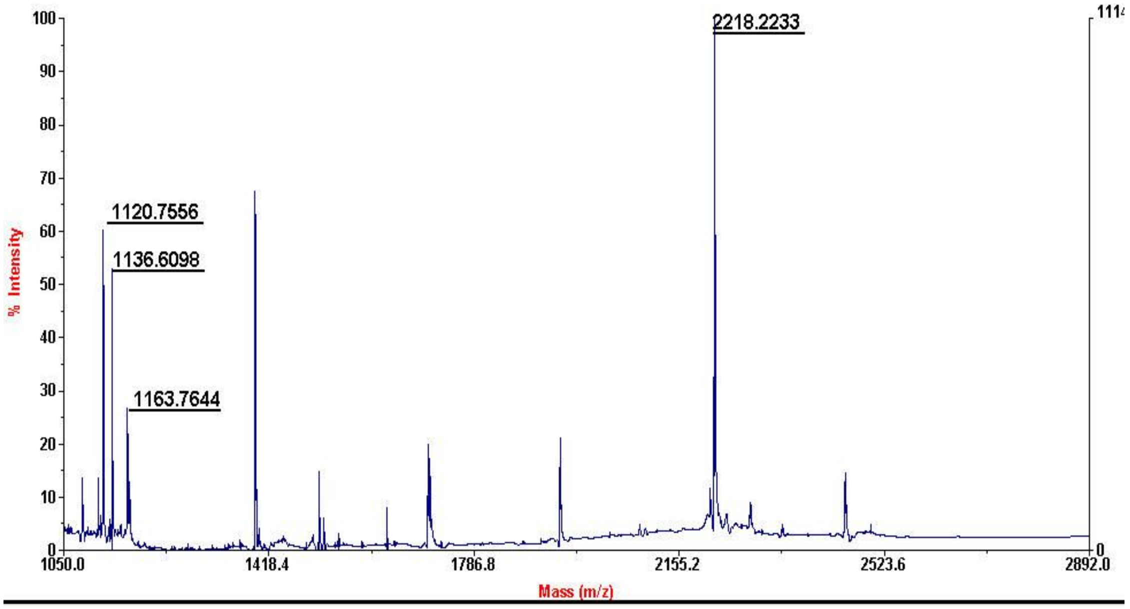
416 Scavenger mRNA decapping enzyme DcpS



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
229 - 242	1659.8427	1658.8354	1658.9468	-0.1114	1	R.SLRDLTPEHLPLLR.N
232 - 242	1303.7160	1302.7088	1302.7296	-0.0208	0	R.DLTPEHLPLLR.N
243 - 255	1519.7411	1518.7338	1518.8266	-0.0928	0	R.NILHQGQEAILQR.Y
295 - 310	1878.8443	1877.8370	1877.9305	-0.0935	0	R.AHLLAEVIENLECDPR.H

No match to: 1066.0622, 1940.8027

417 Aldose reductase

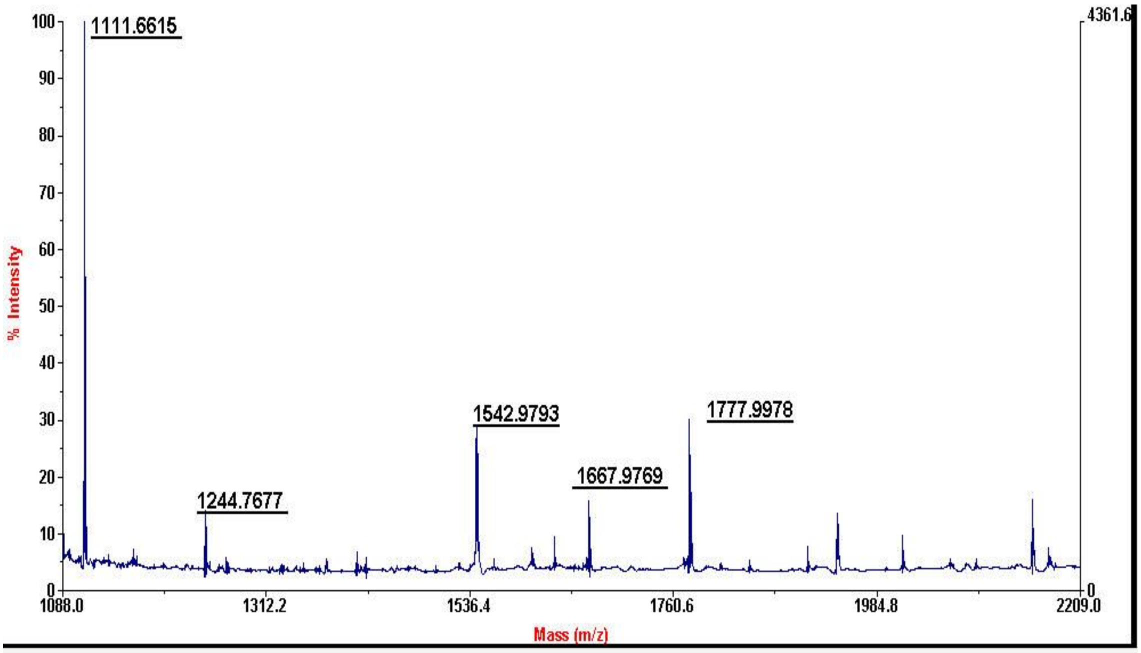


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
34 - 41	892.6052	891.5979	891.4814	0.1165	0	K.VAIDVGYR.H
70 - 78	1120.7556	1119.7484	1119.6288	0.1196	1	K.REELFIVSK.L

79 - 86	1136.6098	1135.6025	1135.5121	0.0904	0	K.LWCTYHEK.G
91 - 101	1163.7644	1162.7572	1162.6016	0.1556	1	K.GACQKTLSDLK.L
178 - 195	2218.2233	2217.2160	2217.0888	0.1272	0	K.YKPAVNQIECHPYLTQEK.L

No match to: 1393.8529, 1508.8061

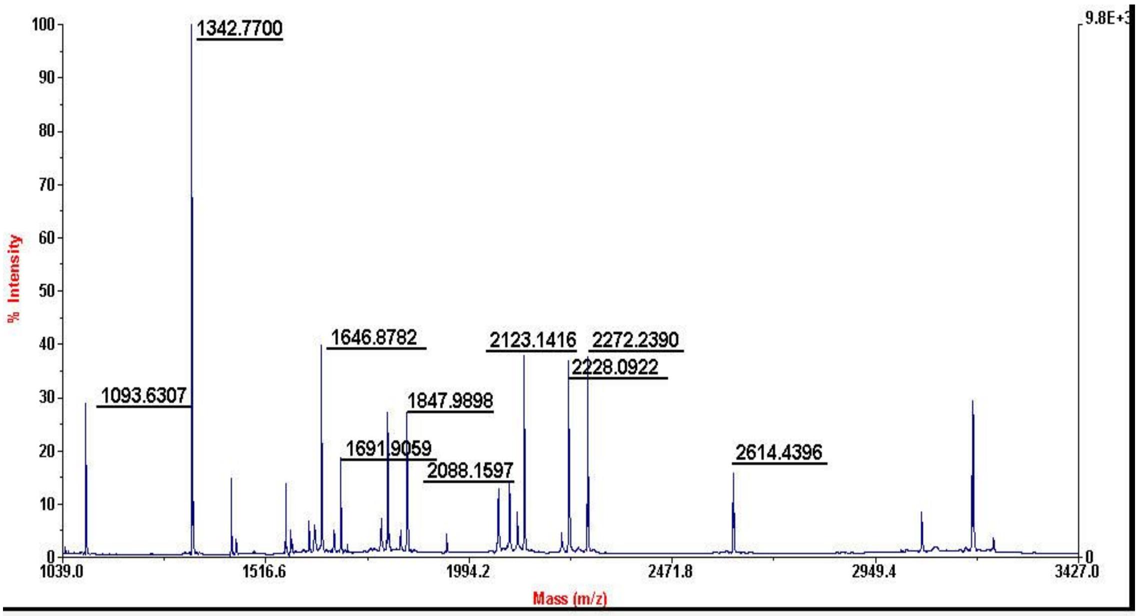
418 Annexin A2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
50 - 63	1542.9793	1541.9721	1541.8413	0.1307	0	K.GVDEVTIVNILTNR.S
64 - 77	1667.9769	1666.9696	1666.8175	0.1521	1	R.SNAQRQDIAFAYQR.R
69 - 77	1111.6615	1110.6543	1110.5458	0.1085	0	R.QDIAFAYQR.R
120 - 135	1777.9978	1776.9905	1776.8564	0.1341	0	K.GLGTDEDSLIEIICSR.T
136 - 145	1244.7677	1243.7604	1243.6156	0.1448	0	R.TNQELQEINR.V
228 - 233	827.5206	826.5133	826.4337	0.0796	1	K.VFDRYK.S

No match to: 1940.0790, 2155.2687

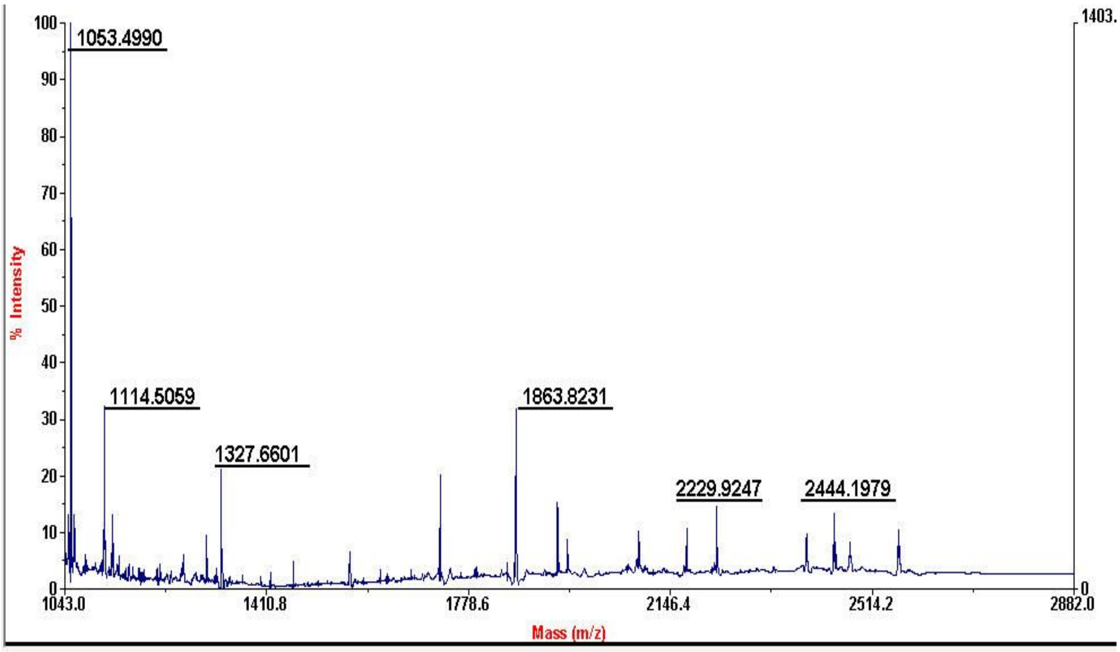
419 Fructose-bisphosphate aldolase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 57	1646.8782	1645.8709	1645.8019	0.0690	1	R.LQSIGTENTEENRR.F
70 - 87	2088.1597	2087.1525	2087.0874	0.0651	0	R.VNPCIGGVILFHETLYQK.A
88 - 99	1342.7700	1341.7627	1341.7041	0.0586	0	K.ADDGRPFPQVIK.S
109 - 134	2614.4396	2613.4323	2613.3246	0.1077	1	K.VDKGVVPLAGTNGETTTQGLDGLSER.C
112 - 134	2272.2390	2271.2318	2271.1343	0.0975	0	K.GVVPLAGTNGETTTQGLDGLSER.C
154 - 173	2123.1416	2122.1343	2122.0840	0.0503	0	K.IGEHTPSALAIMENANVLAR.Y Oxidation (M)
244 - 258	1691.9059	1690.8986	1690.8348	0.0638	0	K.FSHEEIAMATVTALR.R Oxidation (M)
244 - 259	1847.9898	1846.9825	1846.9359	0.0465	1	K.FSHEEIAMATVTALRR.T Oxidation (M)
323 - 331	1093.6307	1092.6235	1092.5563	0.0671	1	K.AAQEEYVKR.A
343 - 364	2228.0922	2227.0849	2227.0182	0.0667	0	K.YTPSGQAGAAASESLFVSNHAY.-

No match to: 1802.9870, 2062.4017, 3175.7207

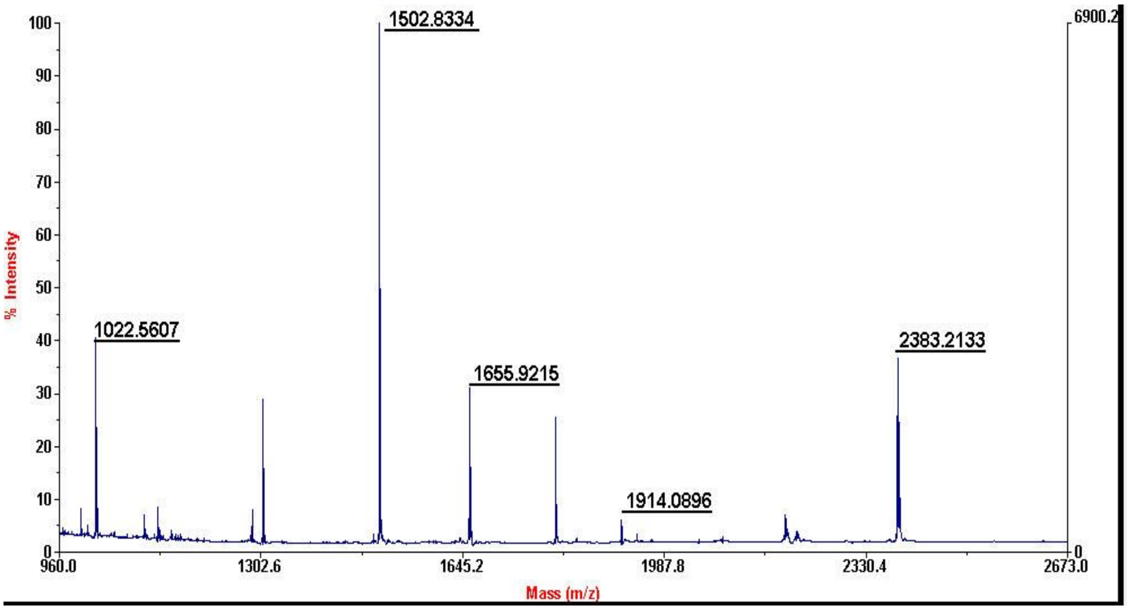
420 Inorganic pyrophosphatase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
10 - 18	1053.4990	1052.4917	1052.5291	-0.0373	0	R.AAPFSLEYR.V
26 - 41	1863.8231	1862.8159	1862.9203	-0.1044	0	K.GQYISPFHDIPIYADK.D
42 - 52	1327.6601	1326.6529	1326.6755	-0.0226	0	K.DVFHMVVEVPR.W
80 - 88	1114.5059	1113.4986	1113.5859	-0.0873	0	R.YVANLFPYK.G
156 - 177	2444.1979	2443.1906	2443.1979	-0.0073	1	K.VIAINVDDPDAANYNDINDVKR.L
193 - 211	2229.9247	2228.9174	2229.0742	-0.1568	1	R.YKVPDGKPENEFAFNAEFK.D

No match to: 954.3945, 1561.6852

421 Beta-2-glycoprotein 1 precursor

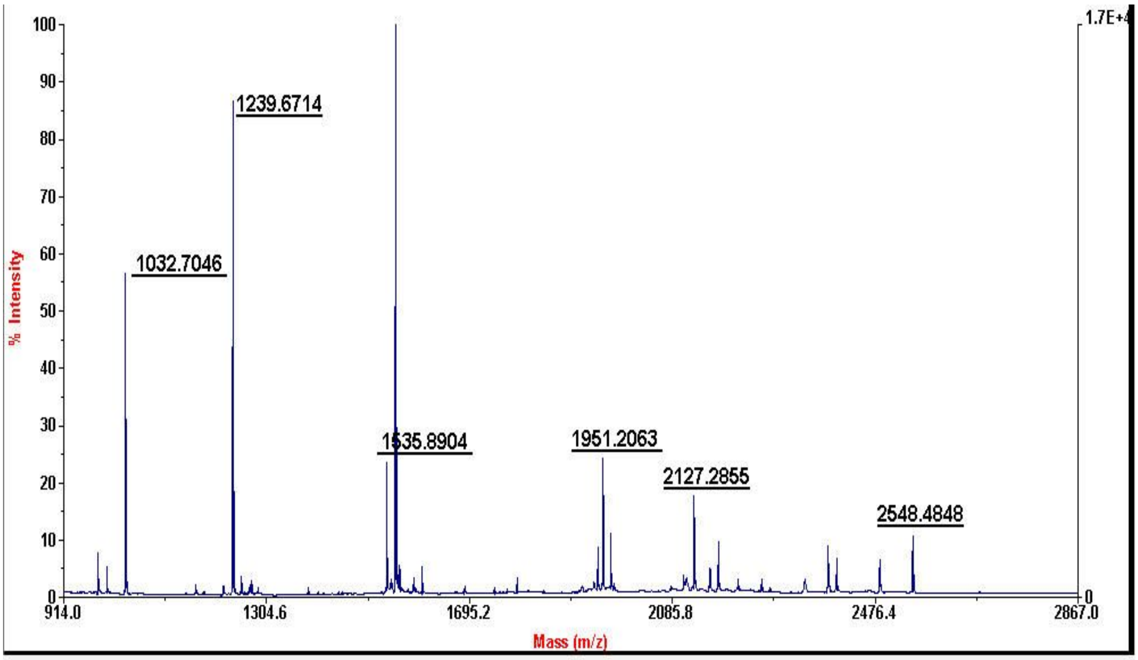


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

22 - 38	1914.0896	1913.0823	1912.9969	0.0854	0	R.TCPKPDDLPFSTVVPLK.T	
39 - 58	2383.2133	2382.2060	2382.0838	0.1222	0	K.TFYEPGEEITYSCKPGYVSR.G	
83 - 96	1502.8334	1501.8261	1501.7711	0.0550	0	R.VCPFAGILENGAVR.Y	
271 - 279	1022.5607	1021.5535	1021.5193	0.0342	0	K.ATVVYQGER.V	
288 - 301	1655.9215	1654.9143	1654.7596	0.1547	1	K.NGMLHGDKVSFFCK.N	; Oxidation (M)

No match to: 1305.7659, 1656.9171, 1802.9974

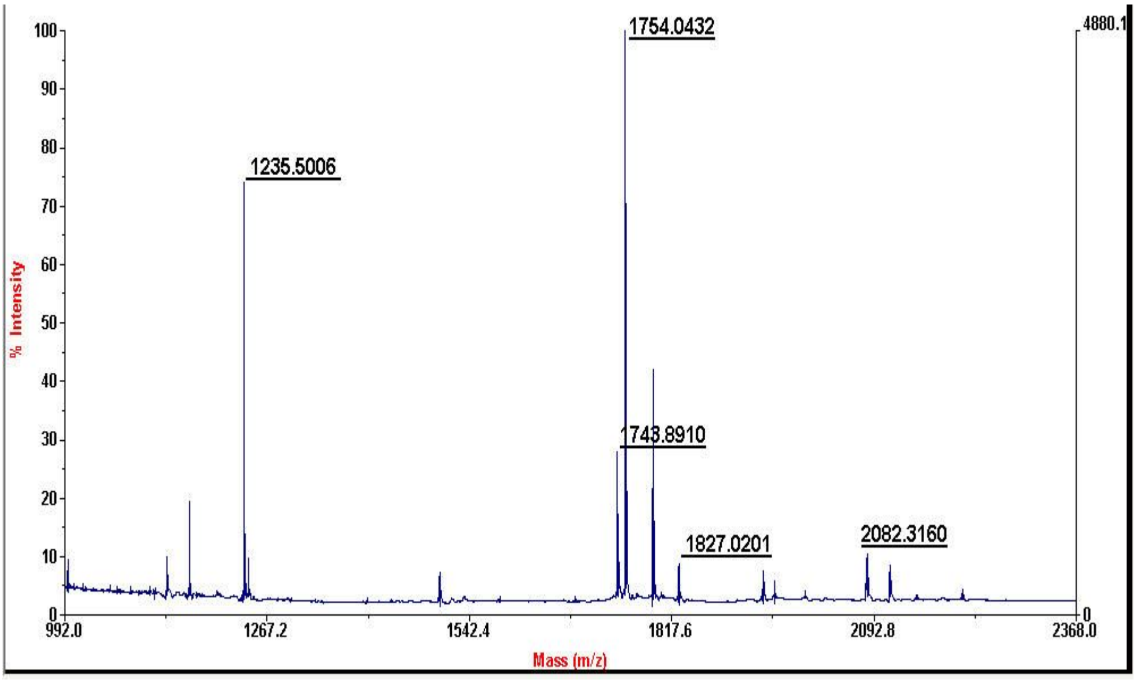
422 Fibrinogen beta chain precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
54 - 72	1951.2063	1950.1990	1949.9959	0.2031	0	R.EEAPSLRPAPPPISGGGYR.A	
179 - 196	2127.2855	2126.2782	2126.0756	0.2026	0	K.HQLYIDETVNSNIPTNLR.V	
225 - 246	2548.4848	2547.4775	2547.2131	0.2644	1	R.TPCTVSCNIPVVSGKECEEIIR.K	3
354 - 367	1535.8904	1534.8832	1534.7164	0.1667	0	K.AHYGGFTVQNEANK.Y	
427 - 436	1239.6714	1238.6641	1238.5105	0.1537	0	K.EDGGGWWYNR.C	
484 - 491	1032.7046	1031.6973	1031.5553	0.1421	0	K.IRPFFPQQ.-	

No match to: 1552.8549, 1967.2303, 2384.4039

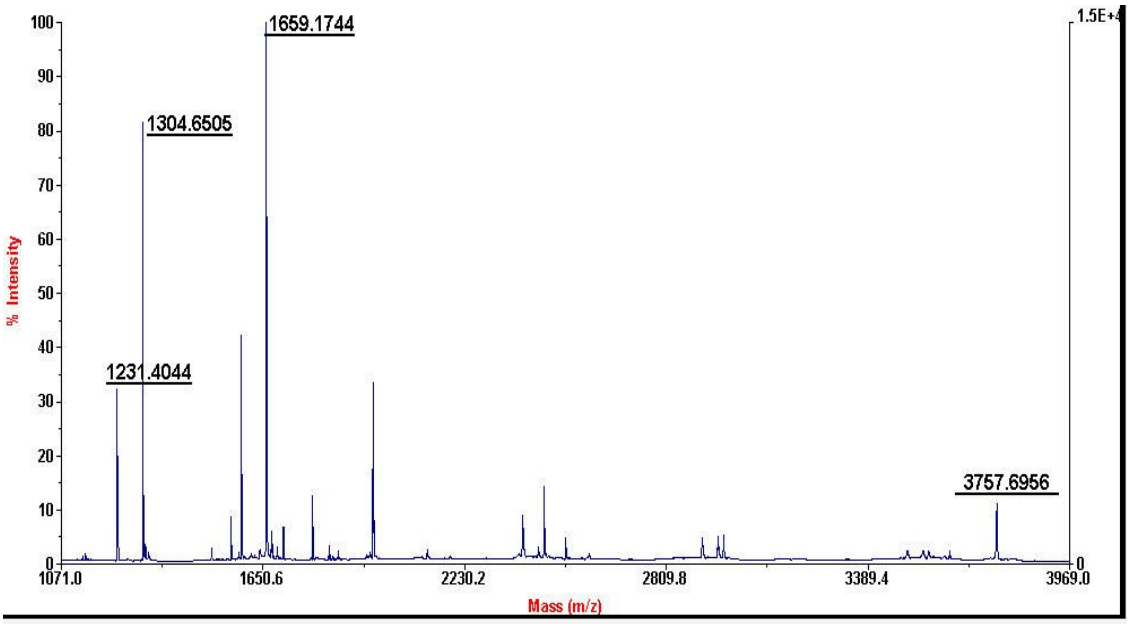
423 Exostosin-like 3



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
69 - 84	1827.0201	1826.0128	1825.9179	0.0950	1	R.VGNELCEVKHVLDLCR.I	
85 - 99	1743.8910	1742.8838	1742.9414	-0.0576	1	R.IRESVSEELLQLEAK.R	
144 - 158	1754.0432	1753.0359	1752.9556	0.0803	1	K.ELMAQNQPKLSLPIR.L	Oxidation (M)
538 - 556	2082.3160	2081.3087	2081.1381	0.1706	1	R.IQIPAAPIREEAAAEIPHR.S	
673 - 682	1235.5006	1234.4934	1234.5863	-0.0930	0	R.EEVLMNSLER.L	Oxidation (M)

No match to: 1942.1022

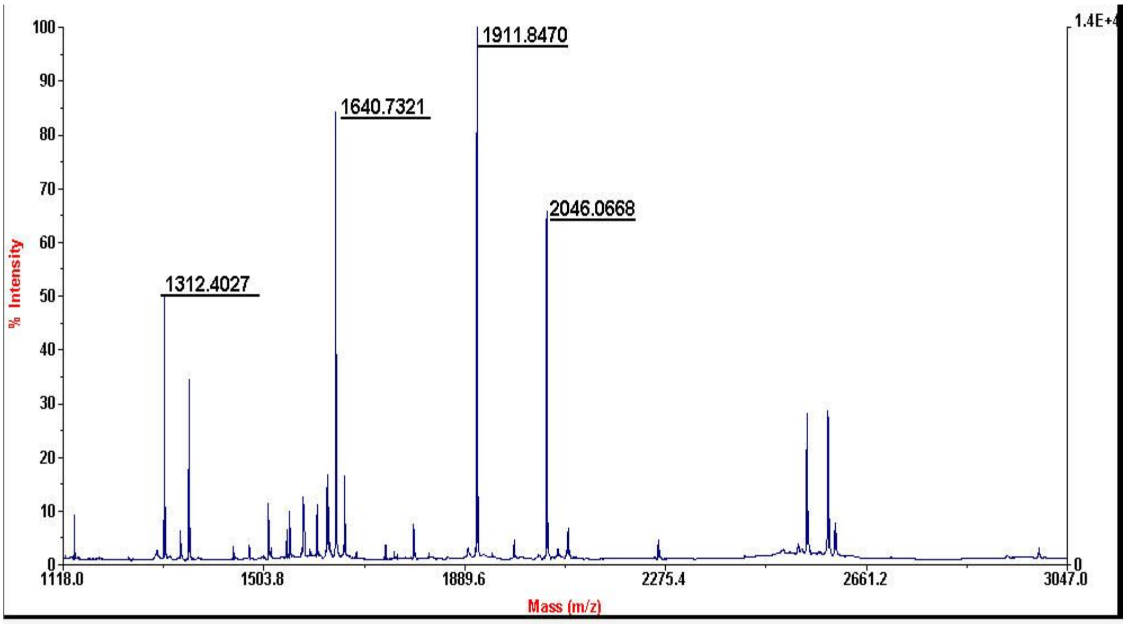
424 Argininosuccinate synthase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
109 - 121	1304.6505	1303.6432	1303.6521	-0.0089	1	R.EGAKYVSHGATGK.G
147 - 155	1231.4044	1230.3971	1230.5855	-0.1884	1	R.MPEFYNRFK.G
177 - 209	3757.6956	3756.6883	3756.7915	-0.1033	1	K.NPWSMDENLMHISYEAGILENPKNQAPPGLYTK.T
349 - 363	1659.1744	1658.1672	1657.9879	0.1792	1	K.VQVSVLKGQVYILGR.E

No match to: 1588.0922, 1966.6215

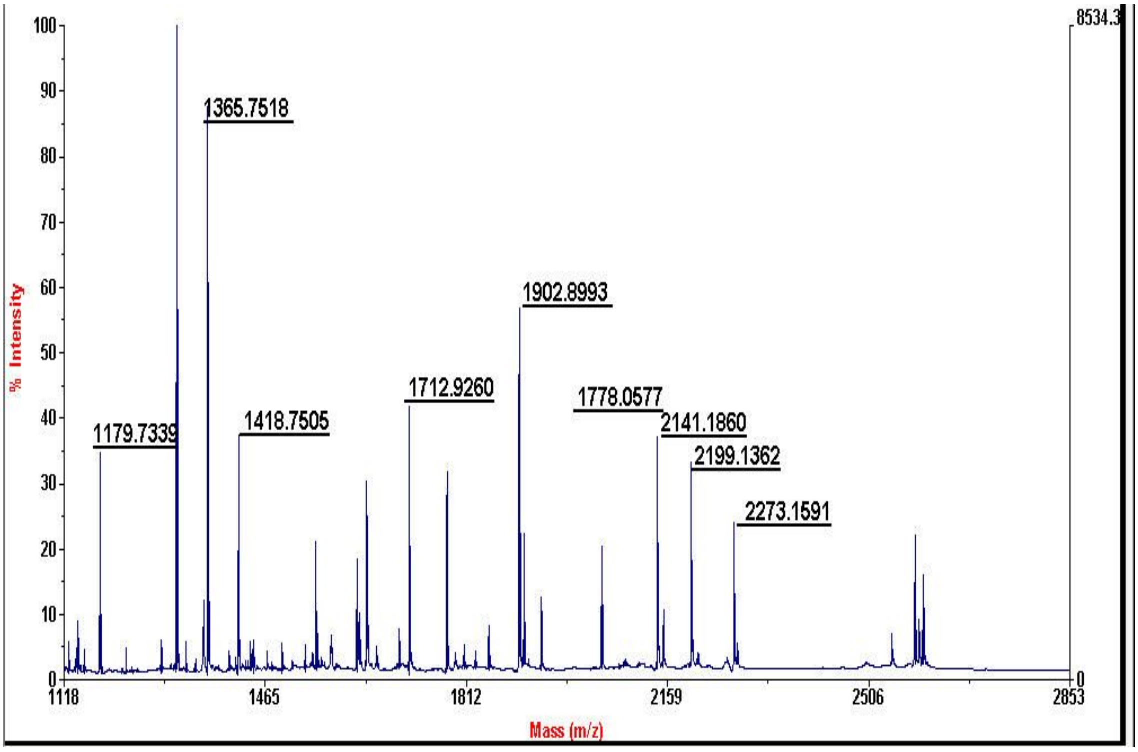
425 Torsin-3A precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
174 - 186	1640.7321	1639.7249	1639.8504	-0.1255	1	K.NFVARMLVENLYR.D Oxidation (M)
179 - 195	2046.0668	2045.0595	2044.9380	0.1215	1	R.MLVENLYRDGLMSDCVR.M 2 Oxidation (M)
360 - 375	1911.8470	1910.8397	1910.9005	-0.0608	0	K.EETLDEIAQMMVYVPK.E Oxidation (M)
376 - 386	1312.4027	1311.3954	1311.5765	-0.1811	0	K.EEQLFSSQGCK.S

No match to: 2586.3341

426 Rab GDP dissociation inhibitor beta

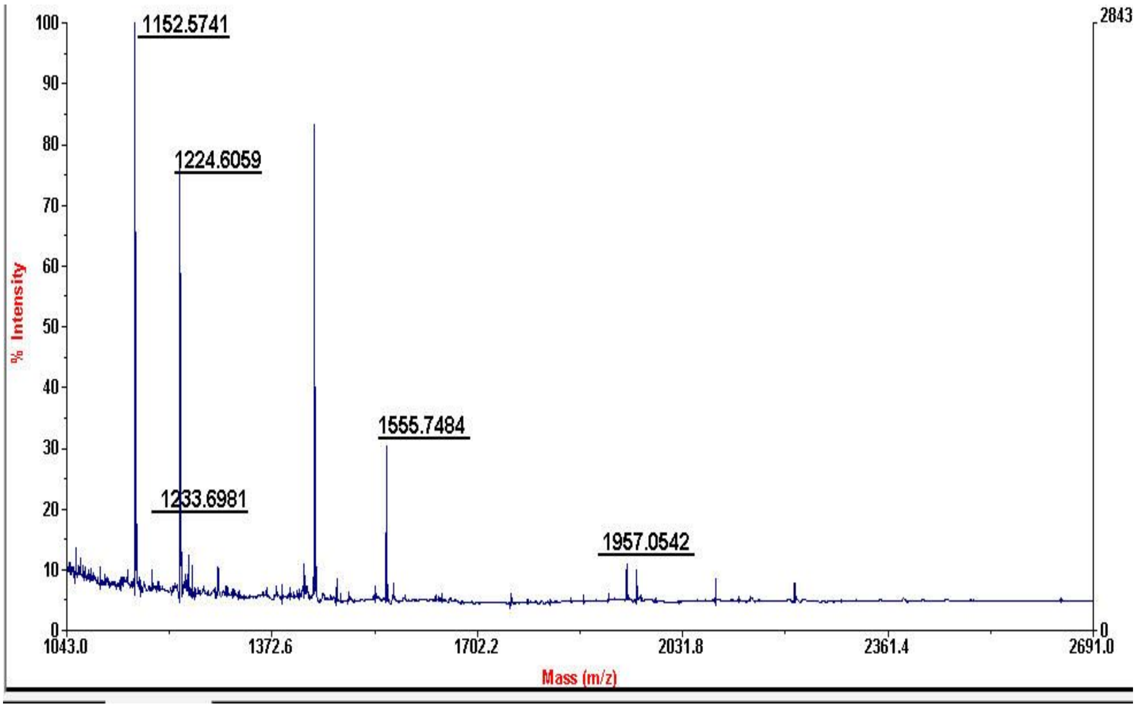


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
36 - 55	2273.1591	2272.1518	2272.1011	0.0507	1	R.NPYYGGESASITPLEDLYKR.F
56 - 68	1418.7505	1417.7432	1417.7024	0.0409	1	R.FKIPGSPPESMGR.G Oxidation (M)
143 - 156	1712.9260	1711.9187	1711.8570	0.0618	1	K.FLVYVANFDEKDPR.T
194 - 208	1902.8993	1901.8921	1901.8102	0.0819	0	R.TDDYLDQPCYETINR.I
222 - 240	2141.1860	2140.1788	2140.0993	0.0795	0	K.SPYLYPLYGLGELPQGFAR.L

300 - 309	1179.7339	1178.7266	1178.6845	0.0421	0	R.VICILSHPIK.N
310 - 328	2199.1362	2198.1289	2198.0498	0.0791	0	K.NTNDANSCQIIIPQNQVNR.K
365 - 379	1778.0577	1777.0505	1776.9985	0.0520	0	K.EIRPALELLEPIEQK.F
391 - 402	1365.7518	1364.7445	1364.6936	0.0509	0	K.DLGTESQIFISR.T

No match to: 1311.7865, 1552.6430, 1639.8896, 1911.0156, 2045.1422, 2585.2097

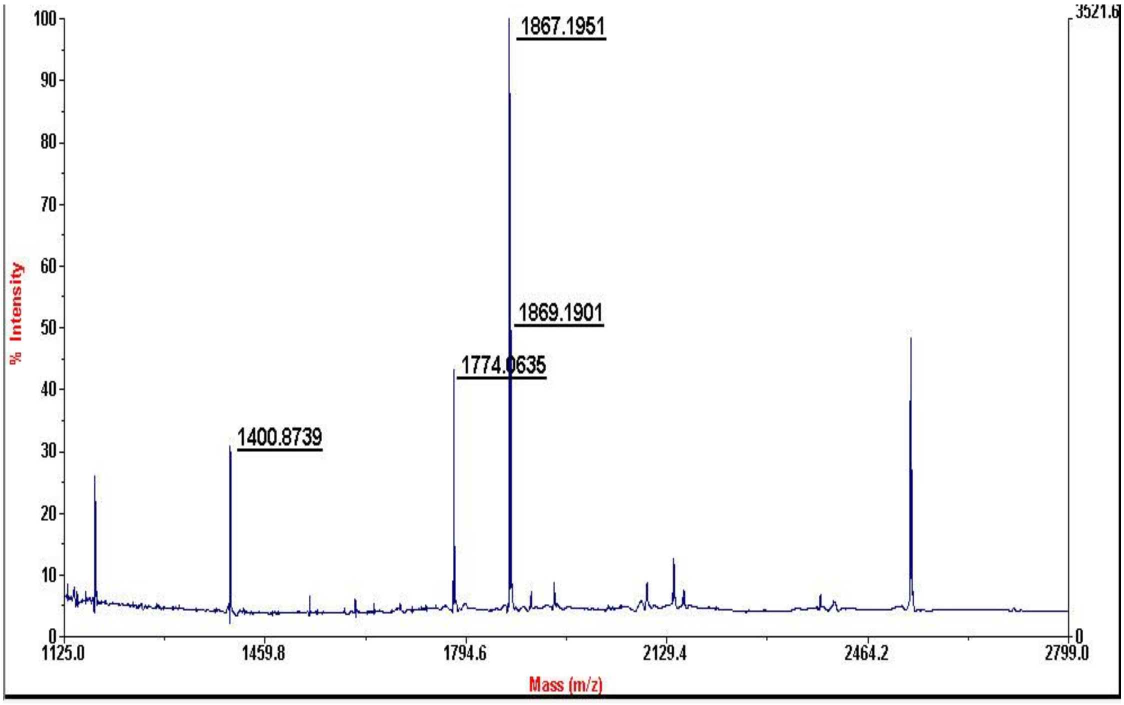
427 Septin-11



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
66 - 79	1555.7484	1554.7412	1554.7063	0.0349	0	K.FESDPATHNEPGVR.L	
84 - 93	1224.6059	1223.5987	1223.5782	0.0205	0	R.SYELQESNVR.L	
138 - 146	1152.5741	1151.5668	1151.5360	0.0308	0	R.SLFNYHDTR.I	
273 - 279	946.5624	945.5551	945.5429	0.0121	1	K.LREMLIR.V	Oxidation (M)
293 - 298	880.4600	879.4527	879.4239	0.0288	0	R.HYELYR.R	
327 - 336	1233.6981	1232.6909	1232.6513	0.0396	1	K.RNEFLGELQK.K	
400 - 418	1957.0542	1956.0469	1956.0024	0.0444	0	K.AAAQLLQSQAQQSGAQQTK.K	

No match to: 1361.8020, 1439.8018, 1634.8589, 1940.9965

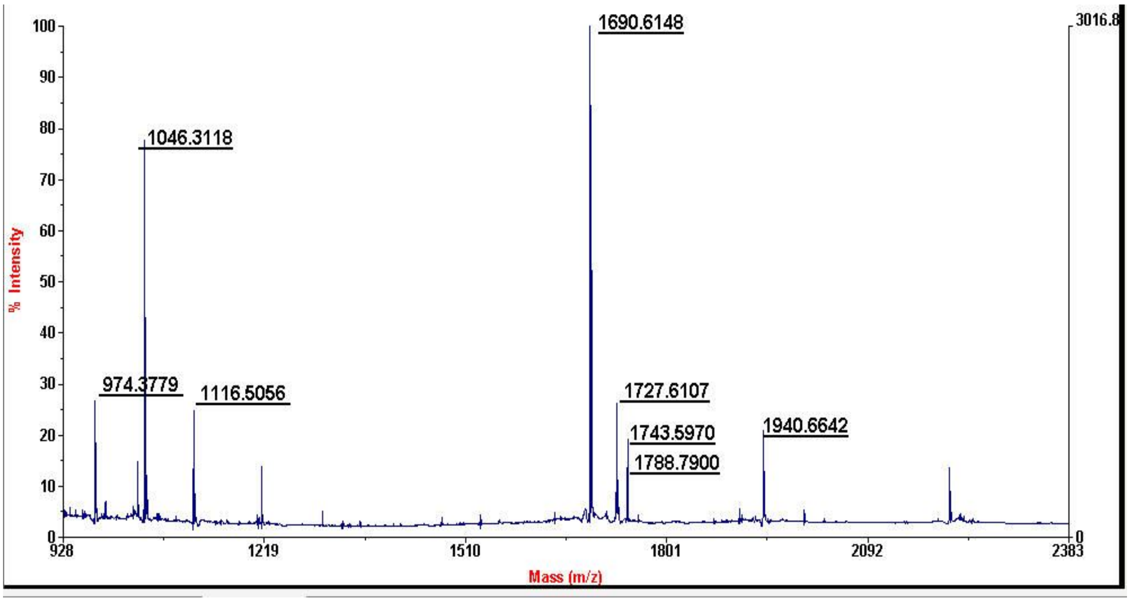
428 Alpha-centractin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
33 - 43	1400.8739	1399.8667	1399.6707	0.1960	0	K.YCFPNYVGRPK.H
201 - 215	1774.0635	1773.0563	1772.7893	0.2669	0	K.EGYDFHSSSEFEIVK.A
239 - 255	1867.1951	1866.1878	1865.9159	0.2719	0	K.AQYYLPDGSTIEIGPSR.F
362 - 369	1869.1901	967.5217	967.3883	0.1334	0	K.EYEEDGAR.S

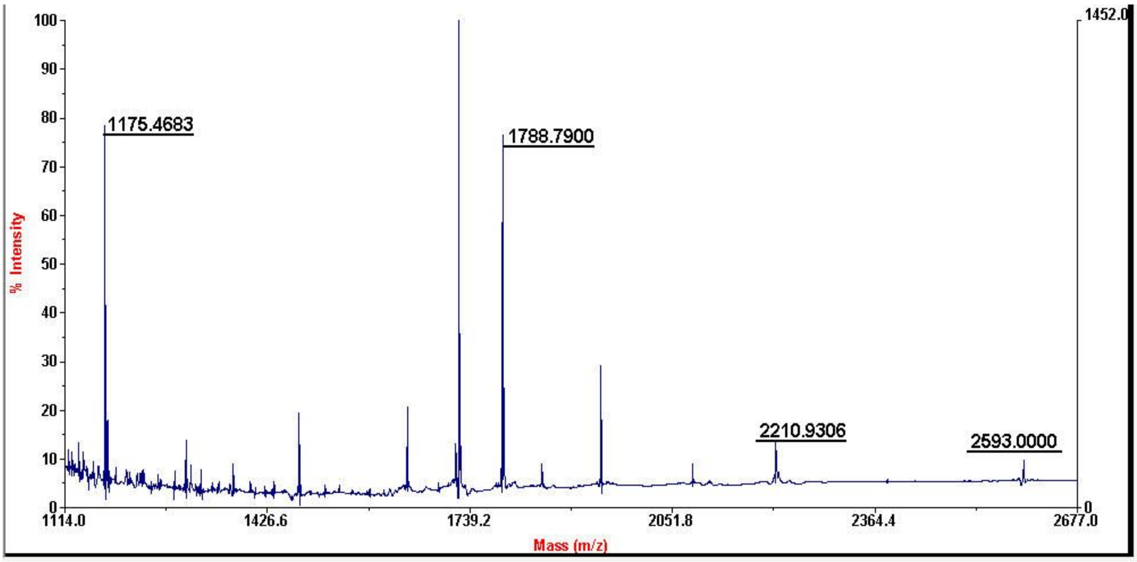
No match to: 2534.7155

429 Nebulin-related-anchoring protein (N-RAP)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
255 - 263	974.3779	973.3706	973.4828	-0.1123	0	R.ANELASDVR.Y	
611 - 619	1116.5056	1115.4983	1115.5168	-0.0186	1	K.MSSEVEYKK.G	Oxidation (M)
917 - 931	1727.6107	1726.6034	1726.8274	-0.2240	1	K.AYGLQSDNQYRADVK.W	
975 - 983	1046.3118	1045.3045	1045.4862	-0.1817	0	K.DTPEMVQAR.I	
1298 - 1314	1940.6642	1939.6569	1939.9428	-0.2859	1	R.ASGDIASDFLYRHDFVK.E	
1383 - 1396	1690.6148	1689.6075	1689.8726	-0.2651	1	R.TQYHKFTALPEDLK.M	
1429 - 1436	893.3530	892.3457	892.3960	-0.0503	0	R.SPQMESAK.K	Oxidation (M)
1598 - 1613	1743.5970	1742.5897	1742.8588	-0.2690	0	R.SQFHSSTDQPGLLQAK.R	

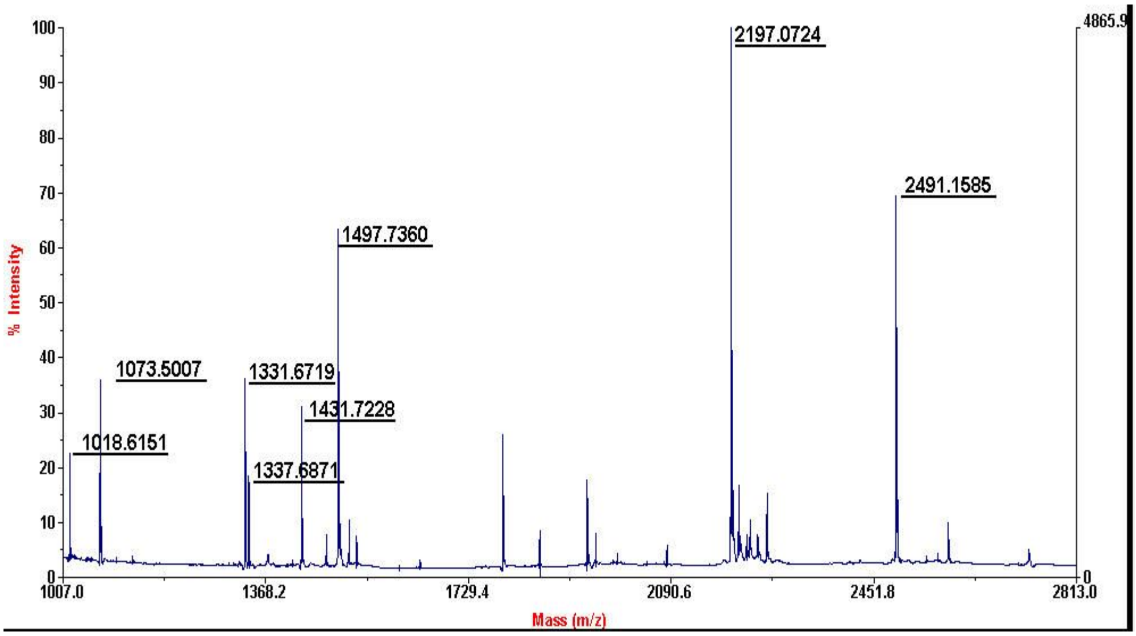
430 T-cell surface glycoprotein CD5 precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
70 - 79	1175.4683	1174.4610	1174.5255	-0.0645	0	K.QWEDPSQASK.V
122 - 137	1788.7900	1787.7827	1787.8004	-0.0177	0	R.NDMCHSLGLTCLEPQK.T
339 - 356	2210.9306	2209.9233	2210.0513	-0.1280	1	R.GLFCPHQKLSQCHELWER.N
439 - 461	2593.0000	2591.9927	2592.1701	-0.1774	1	R.SHAENPTASHVDNEYSQPPRNSR.L

No match to: 1721.6813

431 Aminoacylase-1

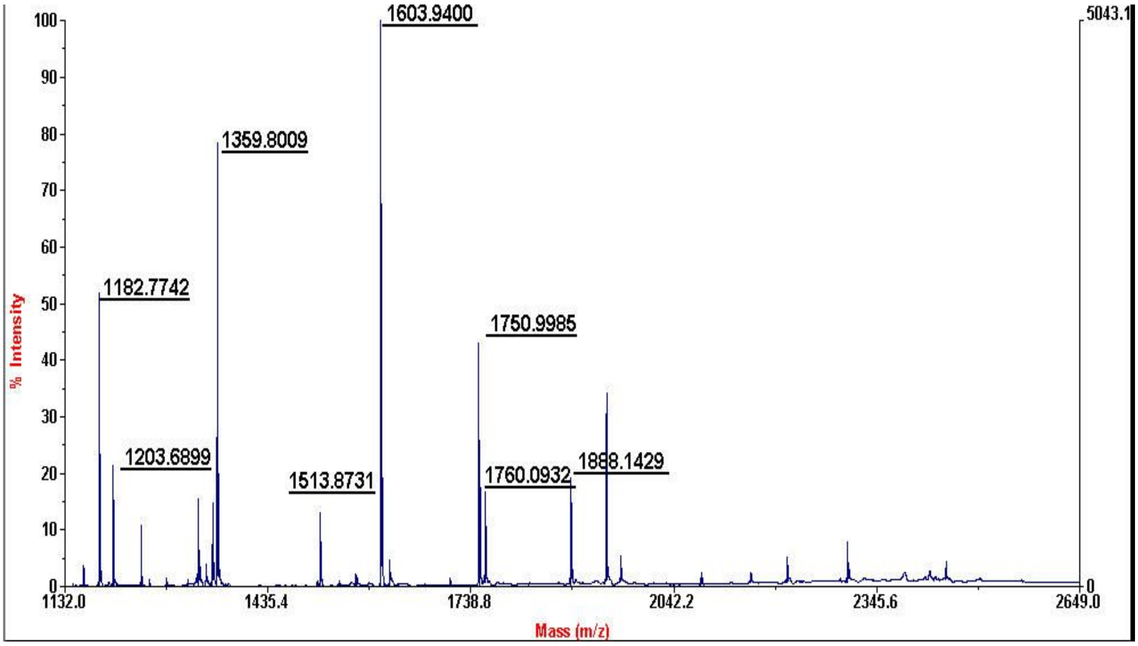


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
5 - 17	1497.7360	1496.7287	1496.7260	0.0027	0	K.GPEEEHPSVTLFR.Q	
24 - 43	2197.0724	2196.0651	2196.0851	-0.0200	0	R.TVQPKPDYGAAVAFFEETAR.Q	
101 - 109	1073.5007	1072.4935	1072.4825	0.0109	0	K.DSEGYIYAR.G	
116 - 126	1337.6871	1336.6798	1336.6809	-0.0011	0	K.CVSIQYLEAVR.R	
169 - 191	2491.1585	2490.1512	2490.1703	-0.0191	0	R.AGFALDEGIANPTDAFTVFYSER.S	
192 - 197	830.4568	829.4495	829.4235	0.0260	0	R.SPWWVR.V	
222 - 230	1018.6151	1017.6079	1017.5971	0.0107	0	K.VVNSILAFR.E	
354 - 367	1431.7228	1430.7155	1430.7340	-0.0185	0	R.AVGVPALGFSPMNR.T	Oxidation (M)
368 - 378	1331.6719	1330.6646	1330.6630	0.0017	0	R.TPVLLHDHDER.L	

379 - 386	984.5595	983.5522	983.5552	-0.0030	0	R.LHEAVFLR.G

No match to: 1790.8924, 1940.9300

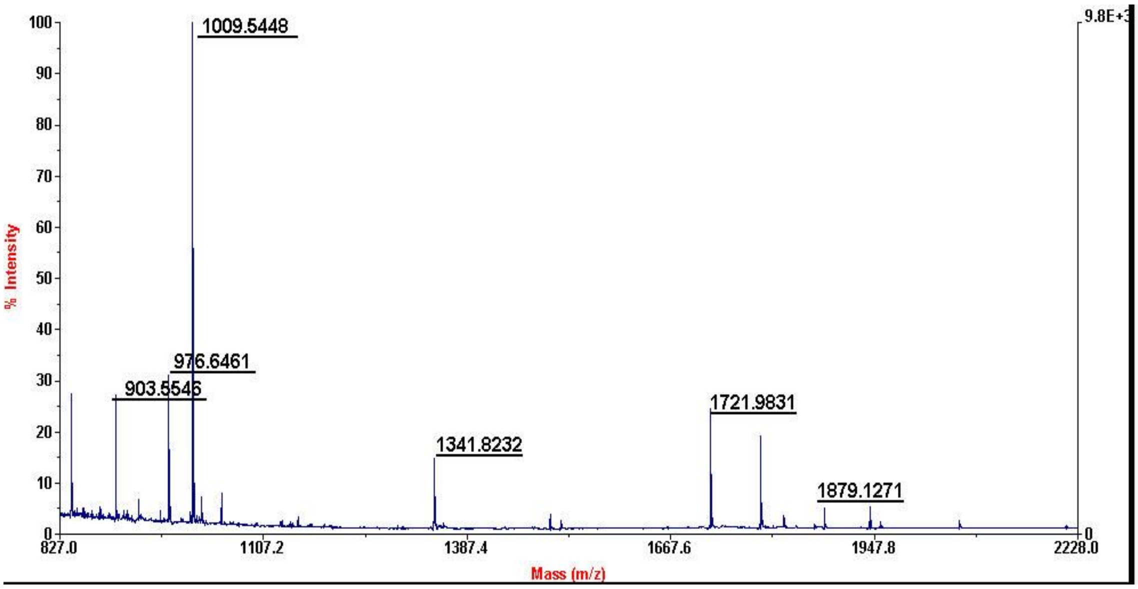
432 Septin-2 (Protein NEDD5)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
67 - 77	1182.7742	1181.7669	1181.6768	0.0901	1	R.VIPGAAEKIER.T
78 - 91	1603.9400	1602.9327	1602.8101	0.1226	0	R.TVQIEASTVEIEER.G
78 - 94	1888.1429	1887.1356	1886.9949	0.1407	1	R.TVQIEASTVEIEERGVK.L
97 - 112	1750.9985	1749.9912	1749.8356	0.1556	0	R.LTVVDTPGYGDAINCR.D
117 - 128	1513.8731	1512.8658	1512.7460	0.1198	0	K.TIISYIDEQFER.Y
129 - 138	1203.6899	1202.6826	1202.5680	0.1146	0	R.YLHDESGLNR.R
129 - 139	1359.8009	1358.7936	1358.6691	0.1245	1	R.YLHDESGLNRR.H
233 - 249	1760.0932	1759.0860	1758.9516	0.1344	0	K.ASIPFSVVGSNQLIEAK.G

No match to: 1045.7046, 1331.8498, 1941.0829

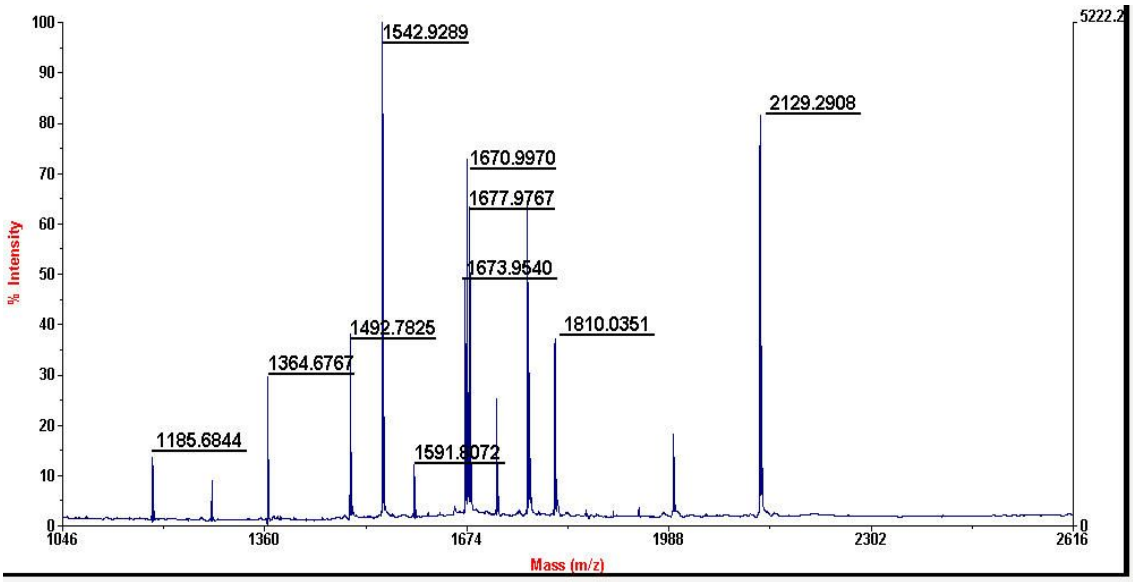
433 Isocitrate dehydrogenase [NADP] cytoplasmic



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
101 - 109	976.6461	975.6388	975.5502	0.0887	0	R.NILGGTVFR.E
133 - 140	1009.5448	1008.5375	1008.4413	0.0962	0	R.HAYGDQYR.A
237 - 249	1721.9831	1720.9758	1720.8321	0.1437	1	K.SQFEAQKIWYEHR.L
244 - 249	903.5546	902.5473	902.4399	0.1075	0	K.IWYEHR.L
302 - 314	1341.8232	1340.8159	1340.6684	0.1475	0	K.TVEAEAAHGTVTR.H
322 - 338	1879.1271	1878.1198	1877.9272	0.1926	0	K.GQETSTNPIASIFAWTR.G

No match to: 1791.0236, 1941.0713

434 Elongation factor Tu, mitochondrial precursor (EF-Tu)

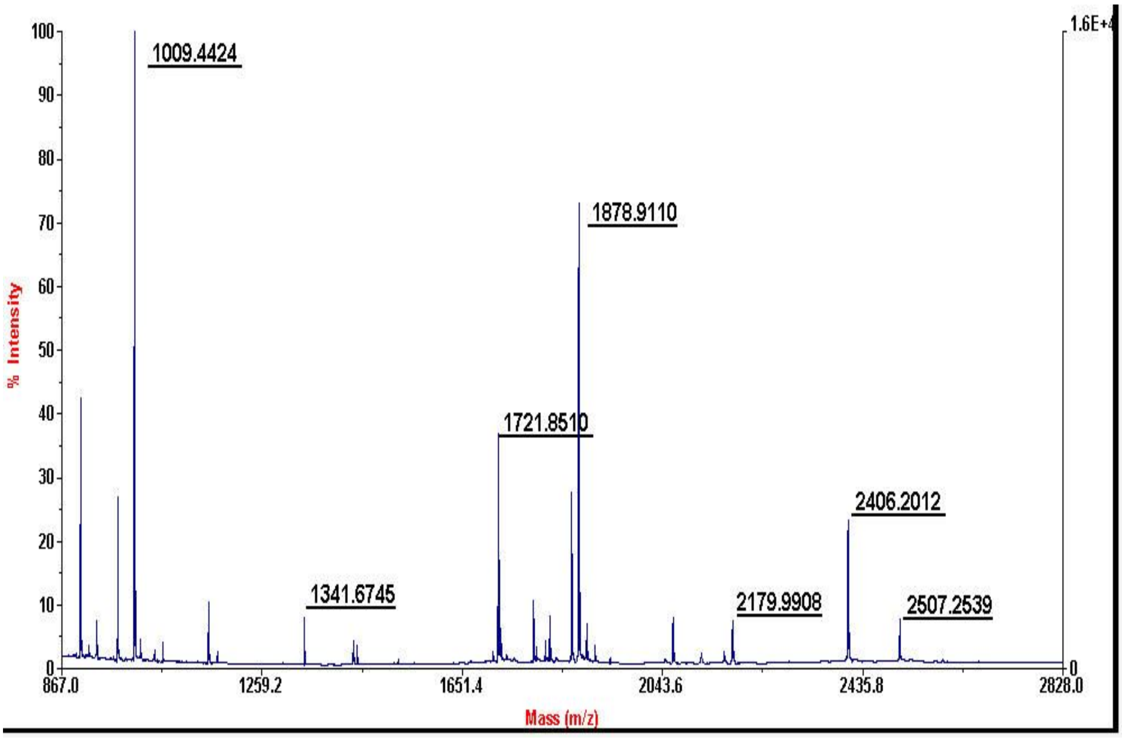


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

54 - 70	1810.0351	1809.0278	1808.9282	0.0996	0	R.DKPHVNVGTIGHVDHGK.T
91 - 102	1492.7825	1491.7752	1491.6841	0.0911	1	K.KYEEIDNAPEER.A
92 - 102	1364.6767	1363.6694	1363.5891	0.0803	0	K.YEEIDNAPEER.A
92 - 104	1591.8072	1590.7999	1590.7274	0.0726	1	K.YEEIDNAPEERAR.G
105 - 120	1673.9540	1672.9467	1672.8533	0.0935	0	R.GITINAAHVEYSTAAR.H
163 - 169	851.5704	850.5631	850.5025	0.0607	0	R.EHLLLAR.Q
239 - 252	1542.9289	1541.9216	1541.8453	0.0762	0	K.LLDAVDTYIPVPAR.D
253 - 271	2129.2908	2128.2835	2128.1568	0.1267	0	R.DLEKPFLLPVEAVYSVPGR.G
312 - 327	1670.9970	1669.9898	1669.8747	0.1151	1	K.SLERAEAGDNLGALVR.G
316 - 327	1185.6844	1184.6771	1184.6149	0.0622	0	R.AEAGDNLGALVR.G
352 - 366	1677.9767	1676.9694	1676.8733	0.0961	1	K.VEAQVYILSKEEGGR.H
422 - 429	978.5886	977.5813	977.5043	0.0770	1	R.FTLRDGNR.T

No match to: 1719.9393, 1767.9653

435 Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42)



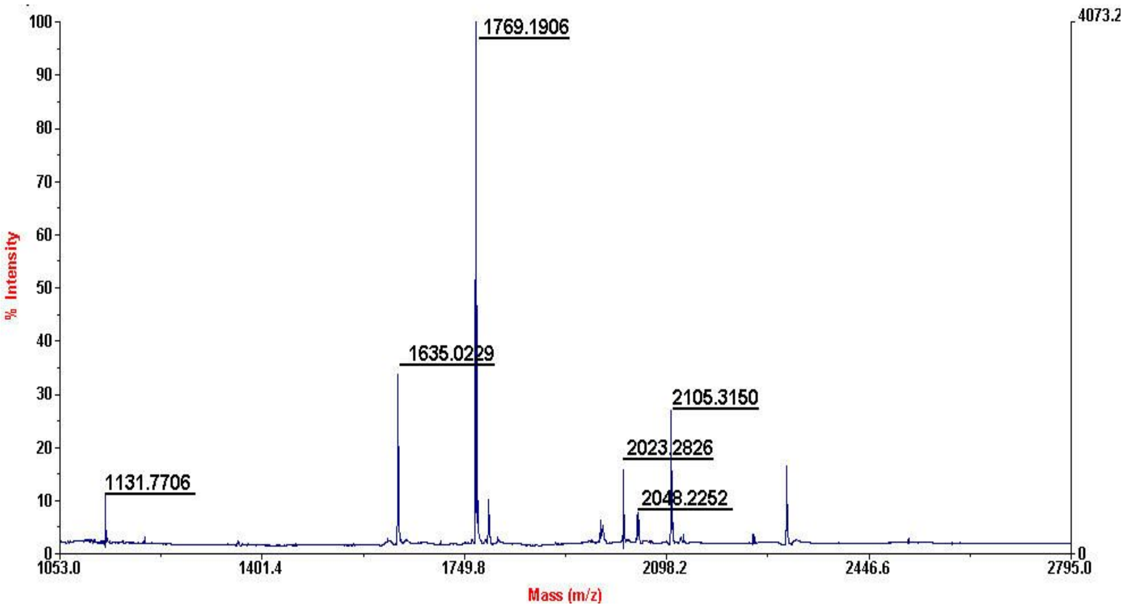
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
30 - 49	2406.2012	2405.1939	2405.2267	-0.0328	0	K.LIFPYVELDLHSYDLGIENR.D

101 - 109	976.5585	975.5512	975.5502	0.0010	0	R.NILGGTVFR.E
133 - 140	1009.4424	1008.4351	1008.4413	-0.0062	0	R.HAYGDQYR.A
141 - 164	2507.2539	2506.2466	2506.2592	-0.0126	1	R.ATDFVVPGPGKVEITYTPSDGTQK.V
237 - 249	1721.8510	1720.8437	1720.8321	0.0116	1	K.SQFEAQKIWYEHR.L
244 - 249	903.4531	902.4458	902.4399	0.0060	0	K.IWYEHR.L
302 - 314	1341.6745	1340.6672	1340.6684	-0.0013	0	K.TVEAEAAHGTVTR.H
322 - 338	1878.9110	1877.9038	1877.9272	-0.0234	0	K.GQETSTNPIASIFAWTR.G
389 - 406	2179.9908	2178.9836	2179.0143	-0.0308	1	R.SDYLNTFEFMDKLGENLK.I

Oxidation (M)

No match to: 1790.8926, 1864.9403, 2064.0618

436 Phosphoglycerate kinase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 39	2048.2252	2047.2180	2046.9905	0.2274	1	R.VDFNVPMKNNQITNNQR.I

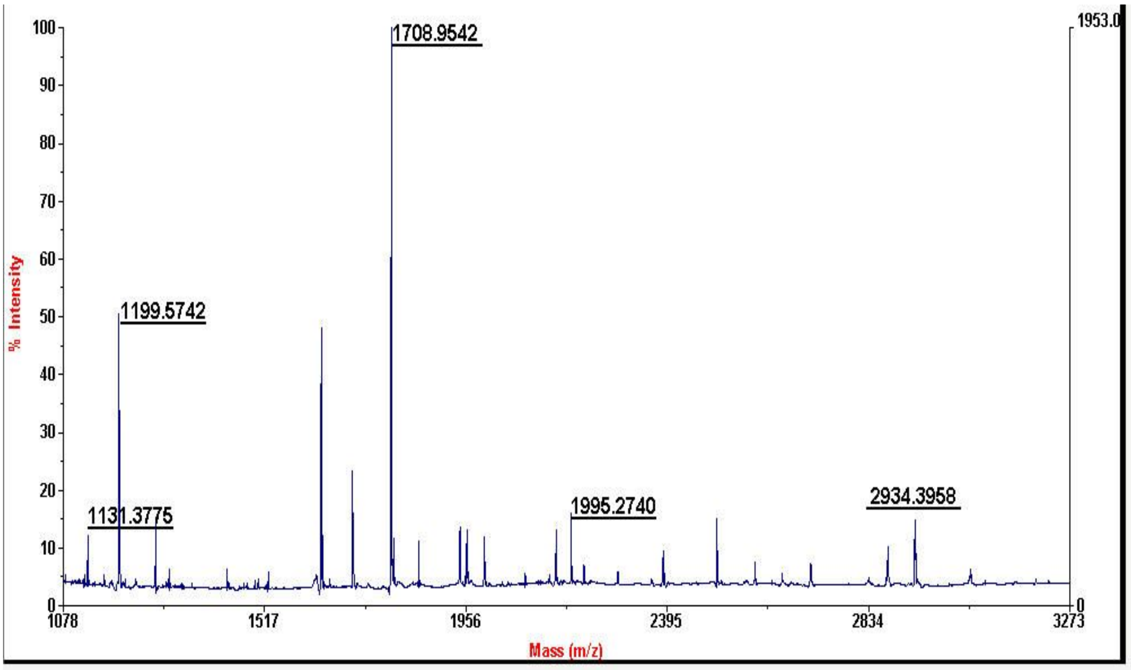
Oxidation (M)

142 - 151	1131.7706	1130.7633	1130.6084	0.1549	1	K.AEPAKIEAFR.A
157 - 171	1635.0229	1634.0156	1633.7849	0.2307	0	K.LGDVYVNDAFGTAHR.A
200 - 216	1769.1906	1768.1833	1767.9883	0.1950	0	K.ALESPERPFLAILGGAK.V
280 - 297	2023.2826	2022.2754	2022.0310	0.2444	1	K.ITLPVDFVTADKFDENAK.T

333 - 350	2105.3150	2104.3077	2104.0531	0.2547	0	K.QIVWNGPVGVFEWEAFAR.G

No match to: 882.6376, 1791.0985, 2246.4691, 2304.5063, 3281.2667, 3351.5392

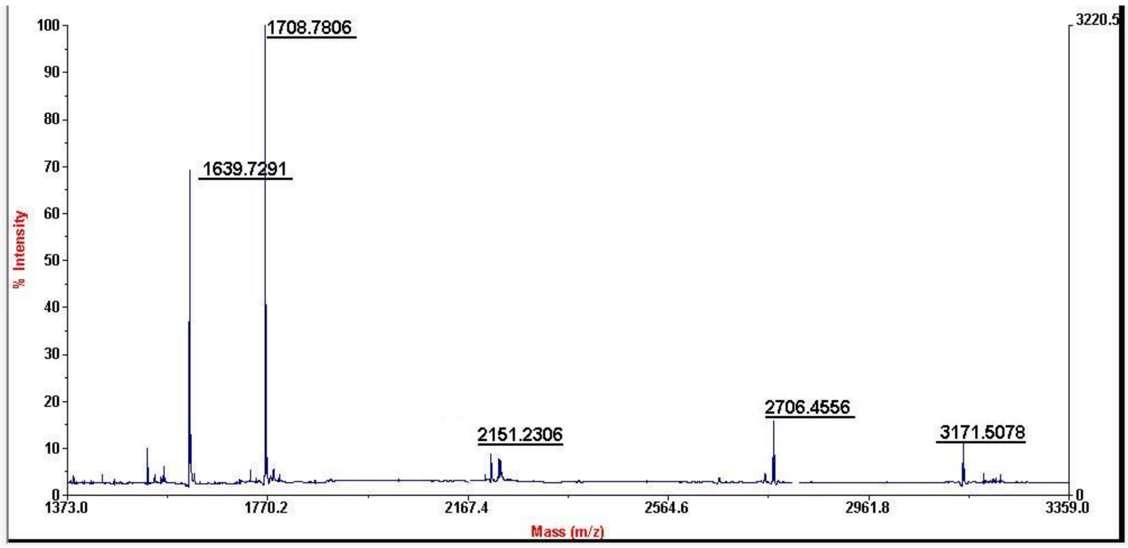
437 Zinc finger protein 559



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
167 - 176	1199.5742	1198.5669	1198.6128	-0.0459	0	K.TSQNLHLVCK.K
178 - 186	1131.3775	1130.3702	1130.5720	-0.2018	0	K.THTQEKPYK.C
245 - 261	1995.2740	1994.2667	1993.9680	0.2987	0	K.ACGKPFTESSYLTQHLR.T
374 - 388	1708.9542	1707.9469	1707.7709	0.1760	1	R.THTGEKPYQCKECGK.A
514 - 538	2934.3958	2933.3885	2933.2630	0.1255	1	R.SHSVEKPYKECGQTFSNSSCLTECV.- 3

No match to: 2185.5149

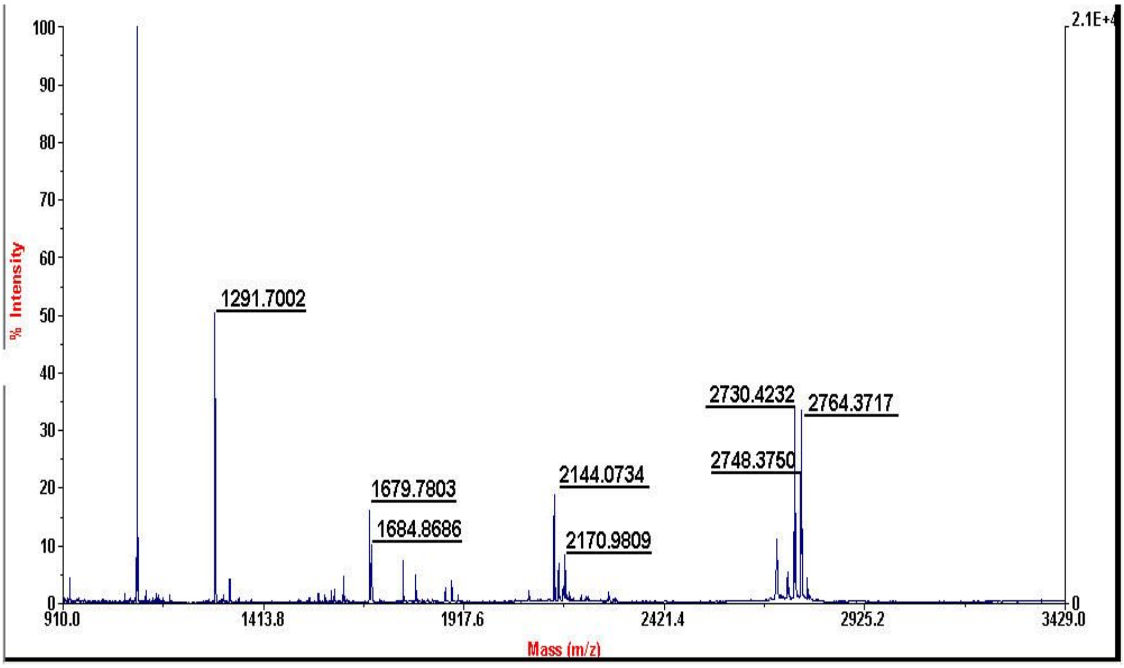
438 Leucine-zipper-like transcriptional regulator 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 21	1639.7291	1638.7218	1638.8438	-0.1220	0	M.AGPGSTGGQIGAAALAGGAR.S
157 - 170	1708.7806	1707.7733	1707.8369	-0.0636	1	K.FATGQWTEWKIEGR.L
363 - 388	2706.4556	2705.4484	2705.3297	0.1187	1	R.DVFGLDFGTTSAKQPTQPASELPSGR.L
419 - 435	2151.2306	2150.2233	2149.9350	0.2883	1	R.FQFSCYPKCTLHEDYGR.L
698 - 725	3171.5078	3170.5006	3170.4835	0.0171	1	R.SFMPEDGQVNISIGEMVPSRQAFESMLR.Y Oxidation (M)

No match to: 2175.2498

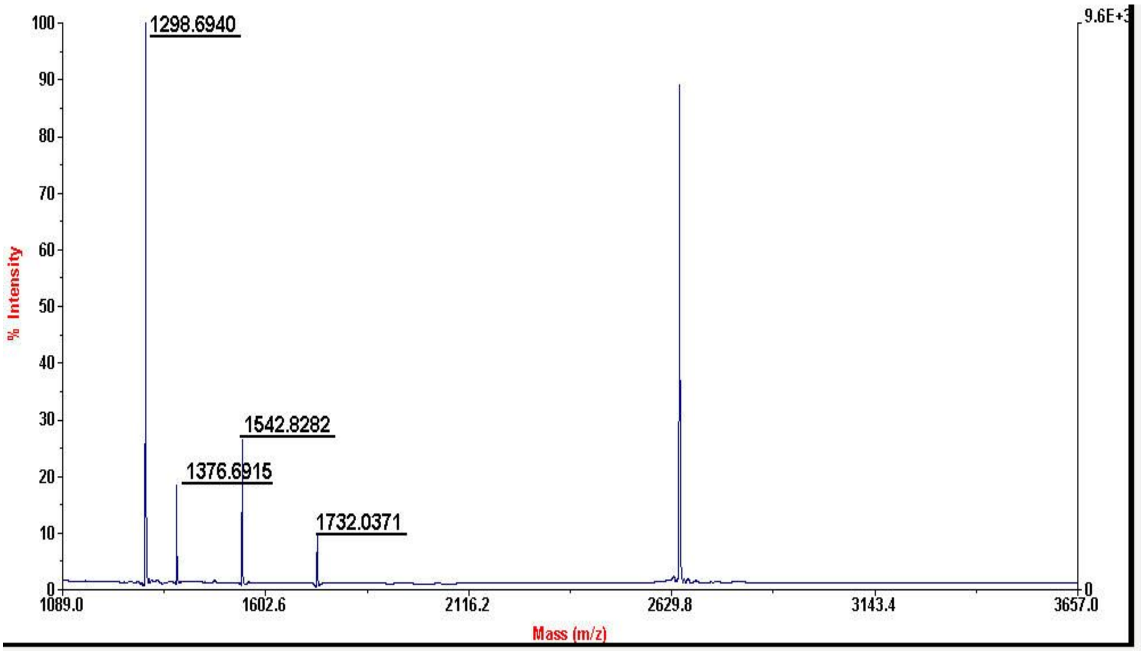
439 NG,NG-dimethylarginine dimethylaminohydrolase 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 31	1291.7002	1290.6929	1290.7044	-0.0115	0	R.ALPESLGQHALR.S
112 - 136	2748.3750	2747.3677	2747.3800	-0.0123	1	K.LQLNIVEMKDENATLDGGDVLFTGR.E
112 - 136	2764.3717	2763.3644	2763.3749	-0.0105	1	K.LQLNIVEMKDENATLDGGDVLFTGR.E Oxidation (M)
121 - 136	1679.7803	1678.7730	1678.7799	-0.0069	0	K.DENATLDGGDVLFTGR.E
150 - 175	2730.4232	2729.4159	2729.4276	-0.0117	1	R.GAEILADTFKDYAVSTVPVADGLHLK.S
160 - 175	1684.8686	1683.8613	1683.8832	-0.0219	0	K.DYAVSTVPVADGLHLK.S
176 - 196	2170.9809	2169.9736	2170.0034	-0.0298	0	K.SFCSMAGPNLIAIGSSESAQK.A ; Oxidation (M)
212 - 230	2144.0734	2143.0661	2143.0983	-0.0322	0	K.LTVPDDIAANCIYLNIPNK.G

No match to: 1095.5587, 1763.8011, 2703.3304

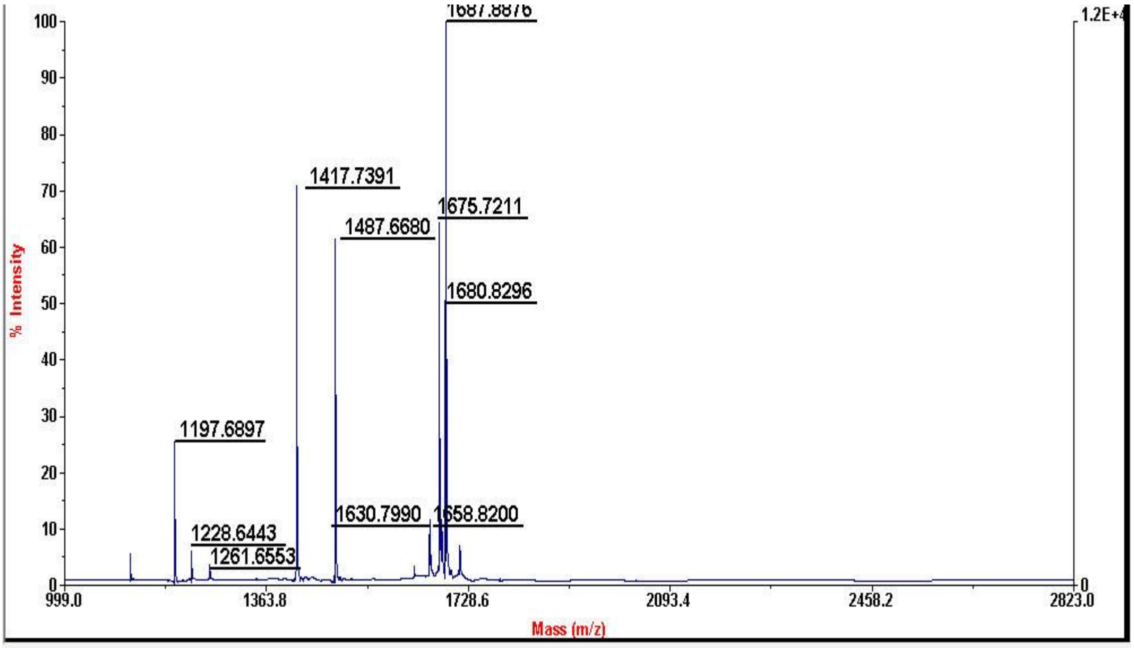
440 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
149 - 158	1298.6940	1297.6867	1297.6302	0.0565	0	R.YQETFNVIER.C
186 - 196	1376.6915	1375.6843	1375.6231	0.0612	0	R.YCAQDAFFQVK.E
197 - 211	1542.8282	1541.8209	1541.8049	0.0160	0	K.EVDVGLAADVGTLQR.L
215 - 230	1732.0371	1731.0298	1730.9315	0.0983	0	K.VIGNQSLVNELAFTAR.K

No match to: 2648.3011

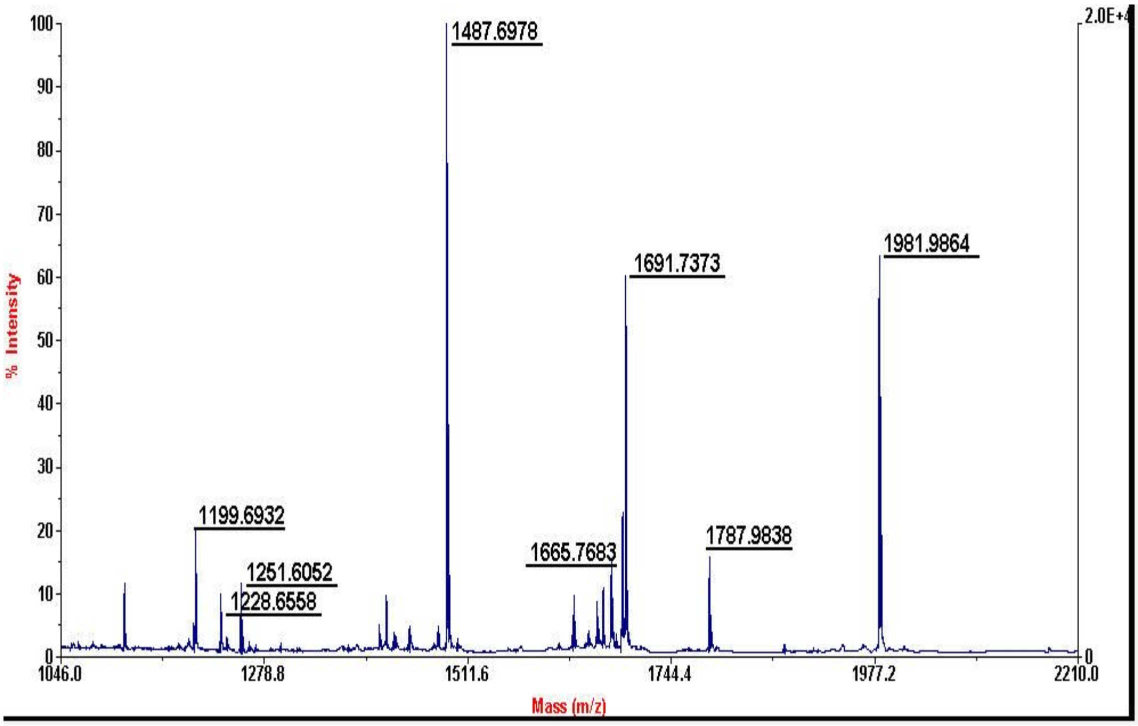
441 Heat shock 70 kDa protein 1 (HSP70.1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

26 - 36	1228.6443	1227.6370	1227.6207	0.0162	0	K.VEIIANDQGNR.T	
37 - 49	1487.6680	1486.6607	1486.6940	-0.0333	0	R.TTPSYVAFTDTER.L	
57 - 71	1658.8200	1657.8127	1657.8424	-0.0297	0	K.NQVALNPQNTVFDAK.R	
89 - 102	1680.8296	1679.8223	1679.8420	-0.0197	0	K.HWPFQVINDGDKPK.V	
113 - 126	1630.7990	1629.7917	1629.7960	-0.0043	0	K.AFYPEEISSMVLTK.M	Oxidation (M)
160 - 171	1197.6897	1196.6824	1196.6877	-0.0053	0	K.DAGVIAGLNVLR.I	
172 - 187	1687.8876	1686.8803	1686.8940	-0.0137	0	R.IINEPTAAAIAYGLDR.T	
221 - 236	1675.7211	1674.7138	1674.7234	-0.0096	0	K.ATAGDTHLGGEDFDNR.L	
237 - 246	1261.6553	1260.6480	1260.6503	-0.0023	0	R.LVNHFVEEFK.R	
237 - 247	1417.7391	1416.7318	1416.7514	-0.0196	1	R.LVNHFVEEFKR.K	

442 Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)

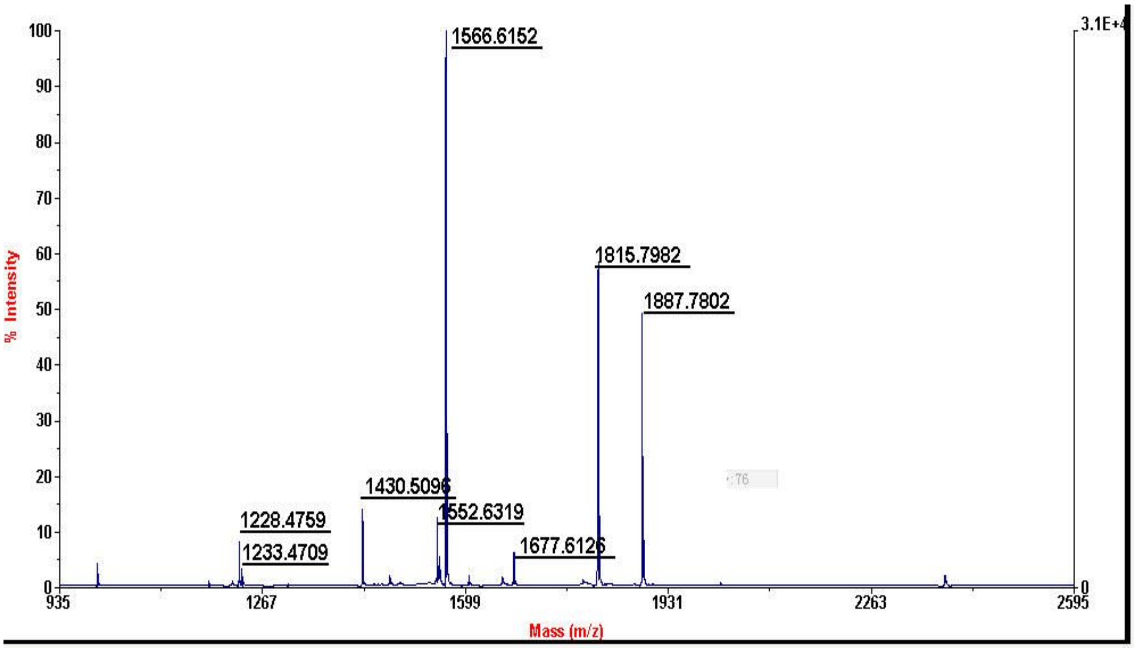


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
26 - 36	1228.6558	1227.6485	1227.6207	0.0277	0	K.VEIIANDQGNR.T	
37 - 49	1487.6978	1486.6905	1486.6940	-0.0035	0	R.TTPSYVAFTDTER.L	
57 - 71	1665.7683	1664.7610	1664.7828	-0.0218	0	K.NQVAMNPTNTVFDAK.R	Oxidation (M)
138 - 155	1981.9864	1980.9791	1980.9905	-0.0114	0	K.TVTNAVVTVPAYFNDSQR.Q	

160 - 171	1199.6932	1198.6859	1198.6670	0.0190	0	K.DAGTIAGLNVLR.I	
172 - 188	1787.9838	1786.9765	1786.9828	-0.0064	1	R.IINEPTAAAIAYGLDKK.V	
221 - 236	1691.7373	1690.7300	1690.7183	0.0117	0	K.STAGDTHLGGEDFDNR.M	
237 - 246	1251.6052	1250.5979	1250.6118	-0.0138	0	R.MVNHFIAEFK.R	Oxidation (M)

No match to: 1118.5318, 1417.8086, 1675.7505, 1687.9149

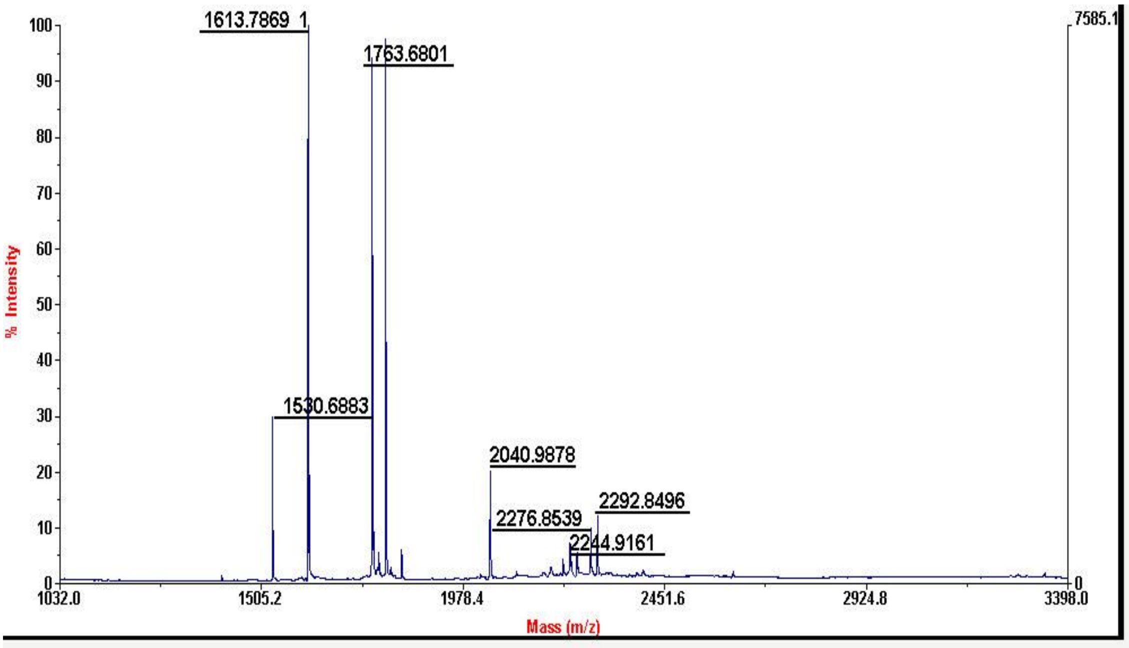
443 78 kDa glucose-regulated protein precursor (GRP 78)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
50 - 60	1228.4759	1227.4687	1227.6207	-0.1521	0	R.VEIIANDQGNR.I	
61 - 74	1566.6152	1565.6080	1565.7726	-0.1646	0	R.ITPSYVAFTPEGER.L	
82 - 96	1677.6126	1676.6054	1676.8006	-0.1952	0	K.NQLTSNPENTVFDAK.R	
102 - 113	1430.5096	1429.5023	1429.6838	-0.1815	0	R.TWNDPSVQQDIK.F	
139 - 152	1552.6319	1551.6246	1551.7854	-0.1608	0	K.TFAPEEISAMVLTK.M	Oxidation (M)
165 - 181	1887.7802	1886.7729	1886.9639	-0.1910	0	K.VTHAVVTVPAYFNDAQR.Q	
186 - 197	1233.4709	1232.4636	1232.6183	-0.1547	0	K.DAGTIAGLNVMR.I	Oxidation (M)
198 - 214	1815.7982	1814.7909	1814.9890	-0.1981	1	R.IINEPTAAAIAYGLDKR.E	
298 - 306	997.4124	996.4051	996.5101	-0.1050	0	R.ALSSQHQAR.I	

No match to: 1814.7187, 2383.7650

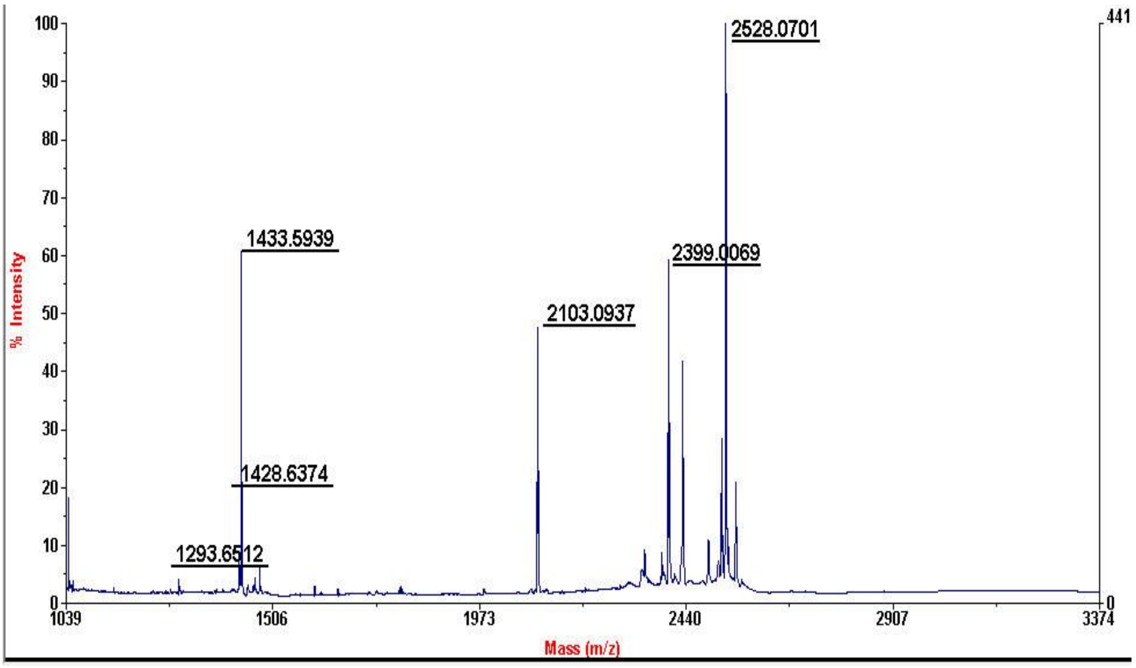
444 Glyceraldehyde-3-phosphate dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
67 - 80	1613.7869	1612.7797	1612.8937	-0.1140	0	K.LVINGNPITIFQER.D	
67 - 84	2040.9878	2039.9805	2040.1004	-0.1198	1	K.LVINGNPITIFQERDPSK.I	
87 - 107	2276.8539	2275.8466	2276.0307	-0.1841	0	K.WGDAGAEYVVESTGVFTTMEK.A	
87 - 107	2292.8496	2291.8423	2292.0257	-0.1833	0	K.WGDAGAEYVVESTGVFTTMEK.A	
Oxidation (M)							
119 - 139	2244.9161	2243.9088	2244.0919	-0.1830	0	R.VIISAPSADAPMFVMGVNHEK.Y	2
Oxidation (M)							
235 - 248	1530.6883	1529.6811	1529.7872	-0.1061	0	R.VPTANVSVVDLTCR.L	
310 - 323	1763.6801	1762.6728	1762.7951	-0.1223	0	K.LISWYDNEFGYSNR.V	

No match to: 1614.7771, 1747.8372, 1795.6830

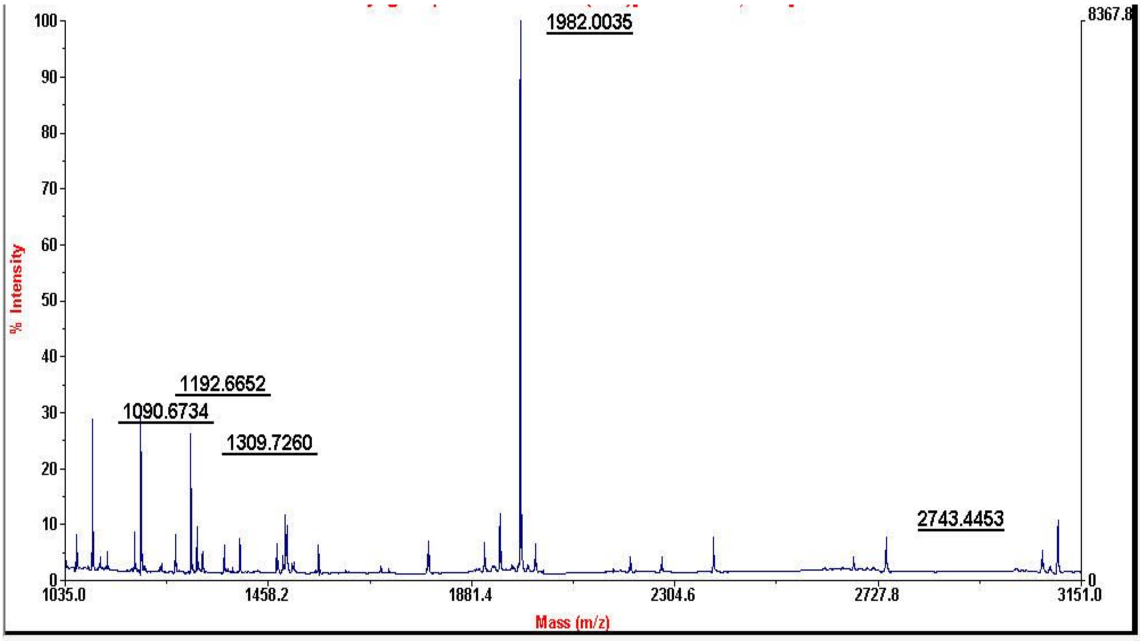
445 Voltage-dependent anion-selective channel protein 2 (VDAC-2)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
90 - 100	1433.5939	1432.5866	1432.6333	-0.0467	0	K.WCEYGLTFTEK.W	
123 - 135	1428.6374	1427.6302	1427.6933	-0.0631	0	K.LTFDTTFSPNTGK.K	
193 - 200	940.4512	939.4439	939.4563	-0.0124	0	R.NNFAVGYR.T	
201 - 223	2528.0701	2527.0629	2527.1616	-0.0987	0	R.TGDFQLHTNVNDGTEFGGSIYQK.V	
224 - 244	2399.0069	2397.9996	2398.0529	-0.0533	0	K.VCEDLDTSVNLAWTSGTNCTR.F	2
251 - 262	1293.6512	1292.6439	1292.6612	-0.0173	0	K.YQLDPTASISAK.V	
263 - 282	2103.0937	2102.0864	2102.1484	-0.0620	0	K.VNNSSLIGVGYTQTLRPGVK.L	

No match to: 1043.4333, 1449.6286, 1464.6207, 2429.0471

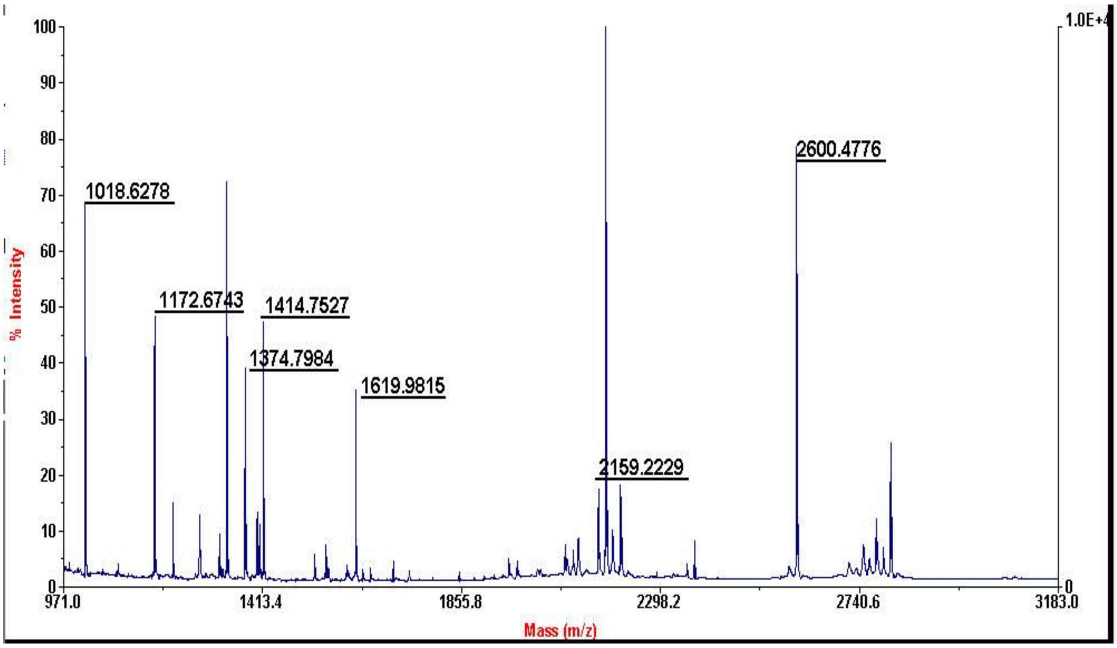
446 Guanine nucleotide-binding protein subunit beta 2-like 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
48 - 57	1192.6652	1191.6579	1191.5520	0.1059	0	R.DETNYGIPQR.A
131 - 139	1090.6734	1089.6661	1089.5641	0.1020	0	K.LWNTLGVCK.Y
140 - 155	1982.0035	1980.9962	1980.8636	0.1326	0	K.YTVQDESHSEWVSCVR.F
186 - 212	2743.4453	2742.4380	2742.3032	0.1348	0	K.TNHIGHTGYLNTVTVSPDGSLCASGGK.D
246 - 257	1309.7260	1308.7187	1308.6536	0.0651	0	R.YWLCAATGPSIK.I

No match to: 1091.6548, 1296.7336, 1493.8292, 1496.7948, 1939.9688, 2384.1259

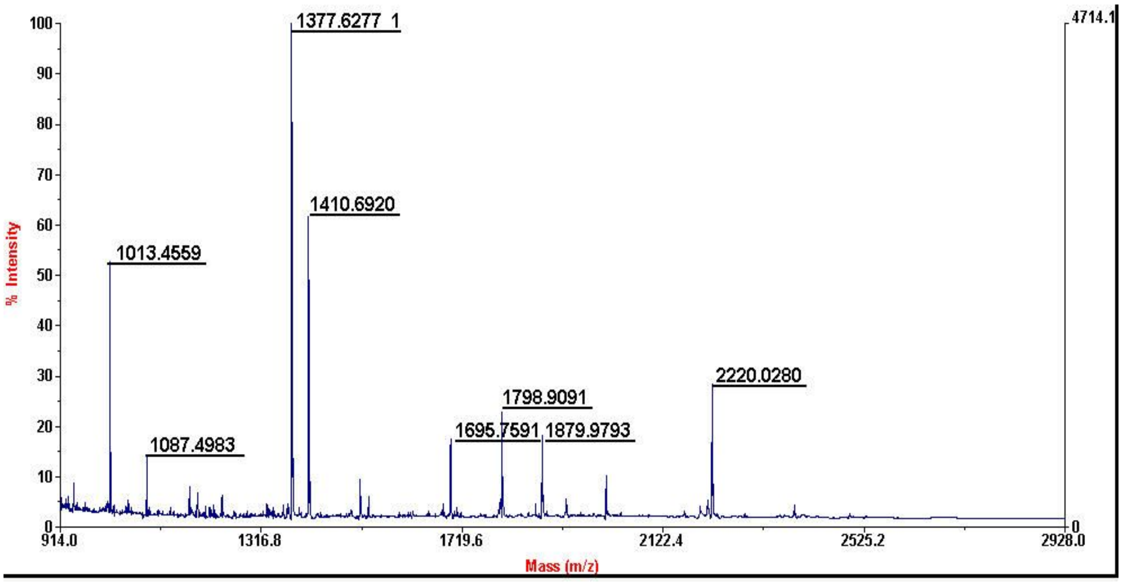
447 Potassium-transporting ATPase alpha chain 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 25	2600.4776	2599.4703	2599.1934	0.2769	1	-.MGKAENYELYSVELGPGPGGDMAAK.M Oxidation (M)
224 - 238	1619.9815	1618.9742	1618.7435	0.2308	0	K.VDNSSLTGESEPQTR.S
362 - 370	1018.6278	1017.6205	1017.5641	0.0564	1	R.LASKNCVVK.N
442 - 455	1414.7527	1413.7454	1413.7616	-0.0162	1	R.AAFKSGQDAVPVPK.R
608 - 618	1172.6743	1171.6670	1171.6383	0.0287	1	R.ATVPDAVLKCR.T
637 - 658	2159.2229	2158.2156	2158.1117	0.1039	0	K.AIAASVGIISEGSETVEDIAAR.L
683 - 694	1374.7984	1373.7911	1373.6497	0.1415	0	K.DMDPSELVEALR.T

No match to: 1333.8606, 2176.2541, 2208.2765, 2809.5728

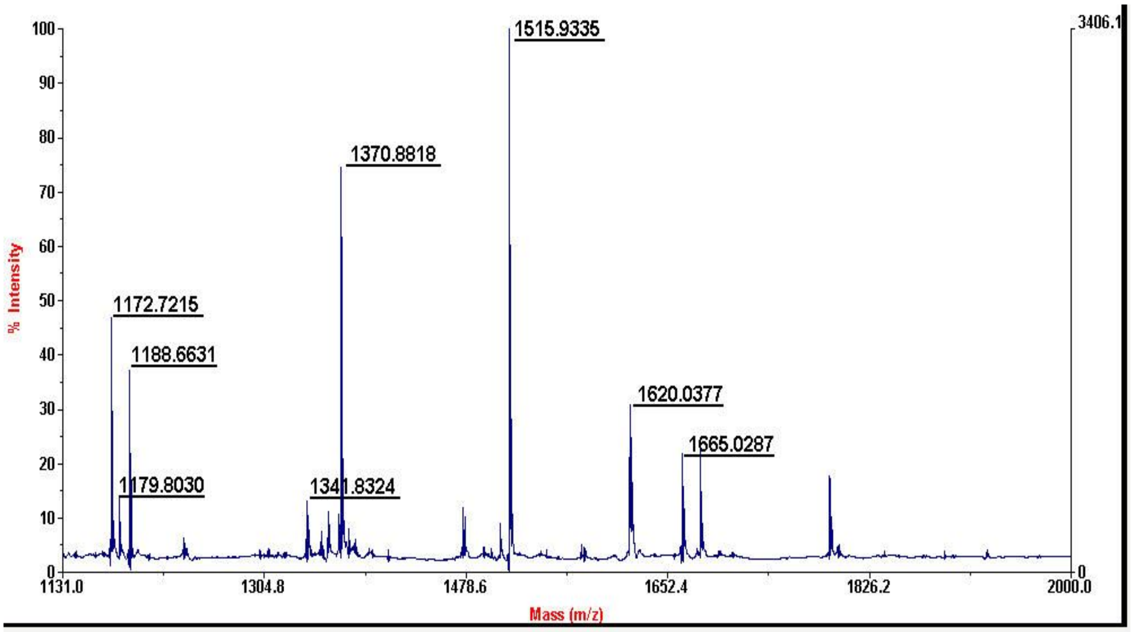
448 Heterogeneous nuclear ribonucleoproteins A2/B1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 38	1798.9091	1797.9018	1797.9149	-0.0131	0	K.LFIGGLSFETTEESLR.N
39 - 46	1087.4983	1086.4910	1086.4770	0.0140	0	R.NYYEQWGK.L
114 - 129	1879.9793	1878.9721	1878.9588	0.0133	1	K.LFVGGIKEDTEEHHLR.D
130 - 147	2220.0280	2219.0207	2219.0634	-0.0426	1	R.DYFEEYGKIDTIEIITDR.Q
154 - 168	1695.7591	1694.7518	1694.7577	-0.0059	0	R.GFGFVTFDDHDPVDK.I
174 - 185	1410.6920	1409.6848	1409.6800	0.0048	0	K.YHTINGHNAEVR.K
204 - 213	1013.4559	1012.4486	1012.4363	0.0123	0	R.GGNFGFGDSR.G
214 - 228	1377.6277	1376.6204	1376.6222	-0.0018	0	R.GGGGNFGPGPGSNFR.G

No match to: 1411.6784, 2008.0264

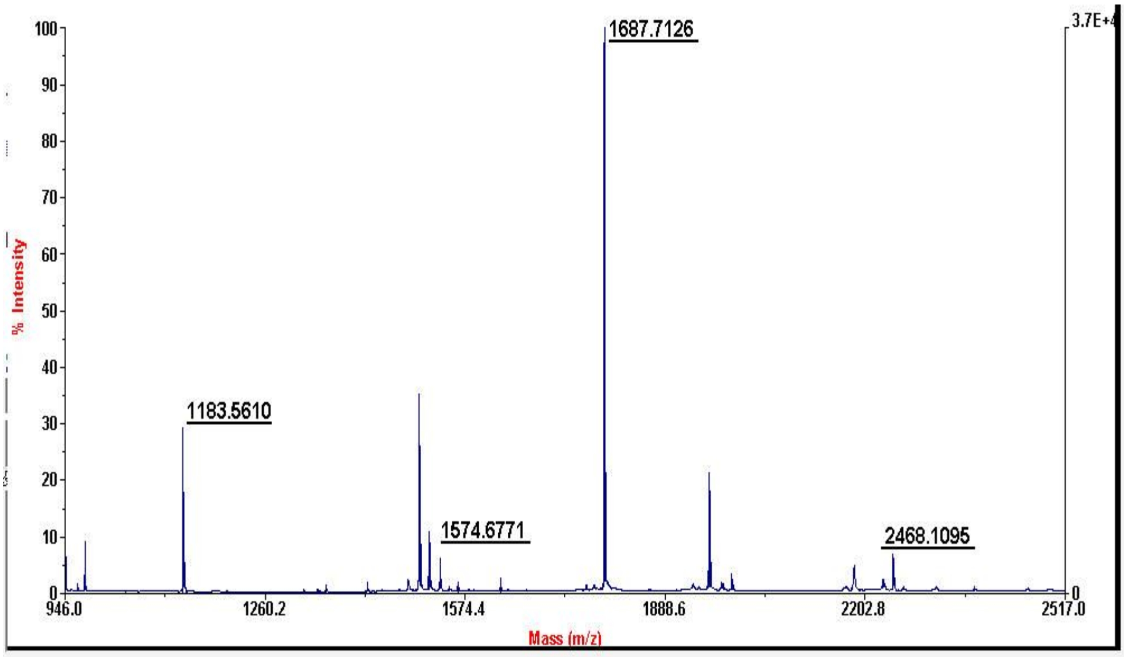
449 Protein disulfide-isomerase A3 precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
174 - 183	1179.8030	1178.7958	1178.5792	0.2166	1	K.AASNLRDNYR.F	
259 - 271	1620.0377	1619.0304	1618.7766	0.2538	0	K.DLLIAYYDVDYEK.N	
336 - 344	1172.7215	1171.7143	1171.5332	0.1811	0	K.FVMQEEFSR.D	
336 - 344	1188.6631	1187.6558	1187.5281	0.1277	0	K.FVMQEEFSR.D	Oxidation (M)
352 - 363	1515.9335	1514.9262	1514.7518	0.1745	1	R.FLQDYFDGNLKR.Y	
434 - 448	1665.0287	1664.0215	1663.7512	0.2703	0	K.MDATANDVPSPYEVR.G	
449 - 460	1341.8324	1340.8251	1340.6765	0.1487	0	R.GFPTIYFSPANK.K	
472 - 482	1370.8818	1369.8745	1369.6878	0.1867	0	R.ELSDFISYLQR.E	

No match to: 1235.7030, 2575.6118, 2703.7733

450 Glyoxylate reductase/hydroxypyruvate reductase

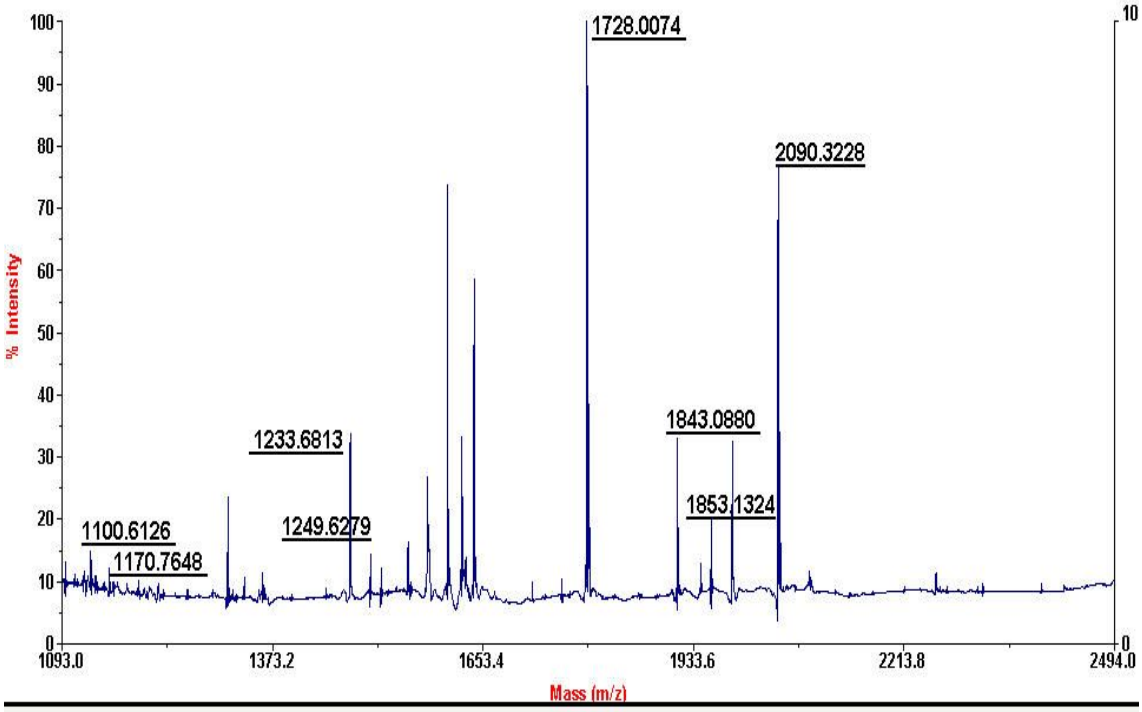


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 8	1046.4115	1045.4043	1045.5889	-0.1846	1	-.MRPVRLMK.V	Oxidation (M)
26 - 47	2586.8919	2585.8846	2586.1544	-0.2698	1	R.AADCEVEQWDSDEPIPAKELER.G	
125 - 134	1183.5610	1182.5537	1182.6608	-0.1071	1	R.RLPEAIEEVK.N	
172 - 179	944.4934	943.4861	943.5603	-0.0743	0	R.LKPFGVQR.F	
263 - 286	2468.1095	2467.1022	2467.3686	-0.2664	0	K.IAAAGLDVTSPEPLPTNHPLLTLK.N	
287 - 300	1574.6771	1573.6698	1573.8147	-0.1449	0	K.NCVILPHIGSATHR.T	

303 - 318	1687.7126	1686.7053	1686.9086	-0.2034	0	R.NTMSLLAANNLLAGLR.G	Oxidation (M)

No match to: 1364.4979, 1377.5388, 1411.5571, 1790.7267

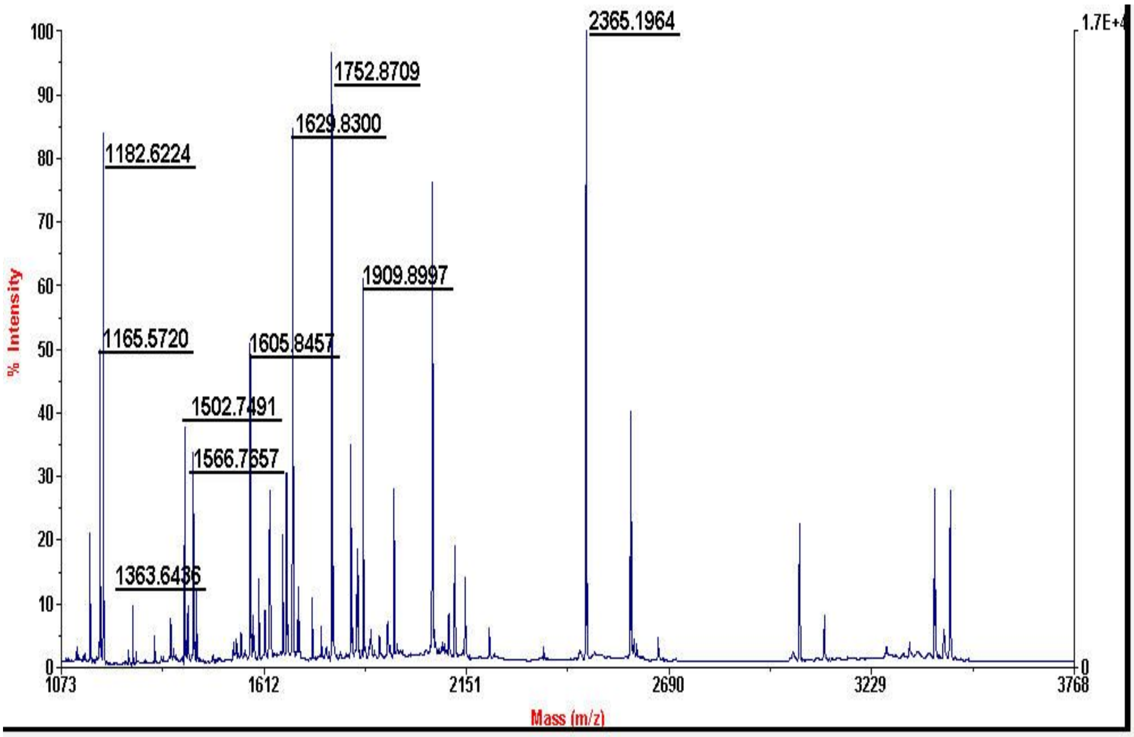
451 Iron-responsive element-binding protein 1 (IRE-BP 1)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
57 - 72	2003.1868	2002.1796	2002.0384	0.1411	1	K.KQDIENILHWNVTQHK.N	
73 - 82	1170.7648	1169.7576	1169.6557	0.1019	0	K.NIEVPFKPAR.V	
142 - 149	1050.5759	1049.5686	1049.4778	0.0908	0	K.NQDLEFER.N	
159 - 168	1233.6813	1232.6740	1232.5509	0.1231	0	K.WGSQAFHNMR.I	
159 - 168	1249.6279	1248.6206	1248.5458	0.0748	0	K.WGSQAFHNMR.I	Oxidation (M)
169 - 187	2090.3228	2089.3156	2089.1684	0.1472	0	R.IIPPGSGIIHQVNLEYLAR.V	
277 - 293	1853.1324	1852.1251	1851.9519	0.1732	0	K.FVEFFGPGVAQLSIADR.A	
336 - 344	1100.6126	1099.6053	1099.5484	0.0569	0	K.YLQAVGMFR.D	Oxidation (M)
588 - 601	1728.0074	1727.0001	1726.8638	0.1363	1	K.DIWPTRDEIQAVER.Q	
594 - 601	959.5148	958.5076	958.4720	0.0356	0	R.DEIQAVER.Q	
645 - 660	1843.0880	1842.0807	1841.9563	0.1244	0	K.SPPFFENLTLDLQPPK.S	

No match to: 1189.5531, 2087.2491, 2390.4313, 2407.4304, 2969.8731, 2970.3727

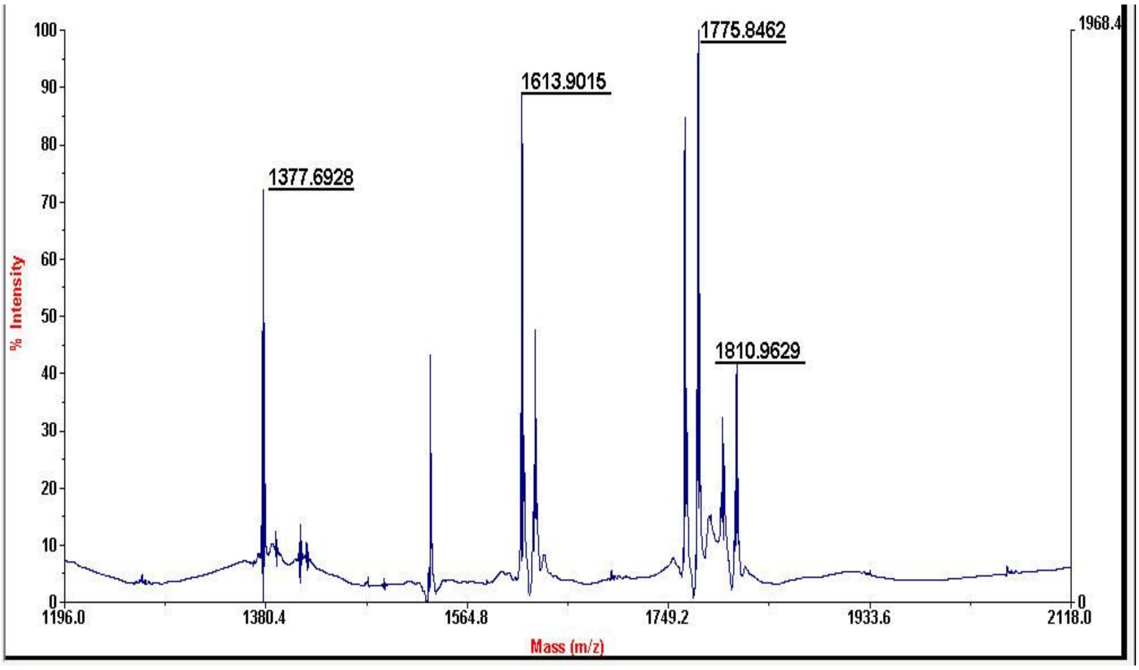
452 Lamin-A/C



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
29 - 41	1629.8300	1628.8227	1628.8005	0.0222	1	R.LQEKEDLQELNDR.L
79 - 89	1165.5720	1164.5647	1164.5411	0.0236	0	K.AAYEAELGDAR.K
157 - 166	1182.6224	1181.6152	1181.6040	0.0111	0	R.TLEGELHDLR.G
209 - 216	1023.5126	1022.5053	1022.5032	0.0021	0	K.NIYSEELR.E
250 - 261	1502.7491	1501.7418	1501.7161	0.0257	1	R.AQHEDQVEQYKK.E
281 - 296	1752.8709	1751.8637	1751.8550	0.0086	0	R.NSNLVGAAHEELQQSR.I
352 - 366	1909.8997	1908.8925	1908.9139	-0.0214	0	R.MQQQLDEYQELLDIK.L Oxidation (M)
440 - 453	1605.8457	1604.8384	1604.8046	0.0338	1	R.VAVEEVDEEGKFVR.L
516 - 527	1363.6436	1362.6363	1362.6099	0.0264	0	K.AQNTWGCGNSLR.T
598 - 624	2365.1964	2364.1891	2364.1517	0.0373	0	K.ASASGSGAQVGGPISSGSSASSVTVTR.S
628 - 644	1566.7657	1565.7584	1565.7434	0.0150	0	R.SVGGSGGGSFGDNLVTR.S

No match to: 1274.6034, 1639.8666, 1910.9199, 2045.0828, 2364.1739

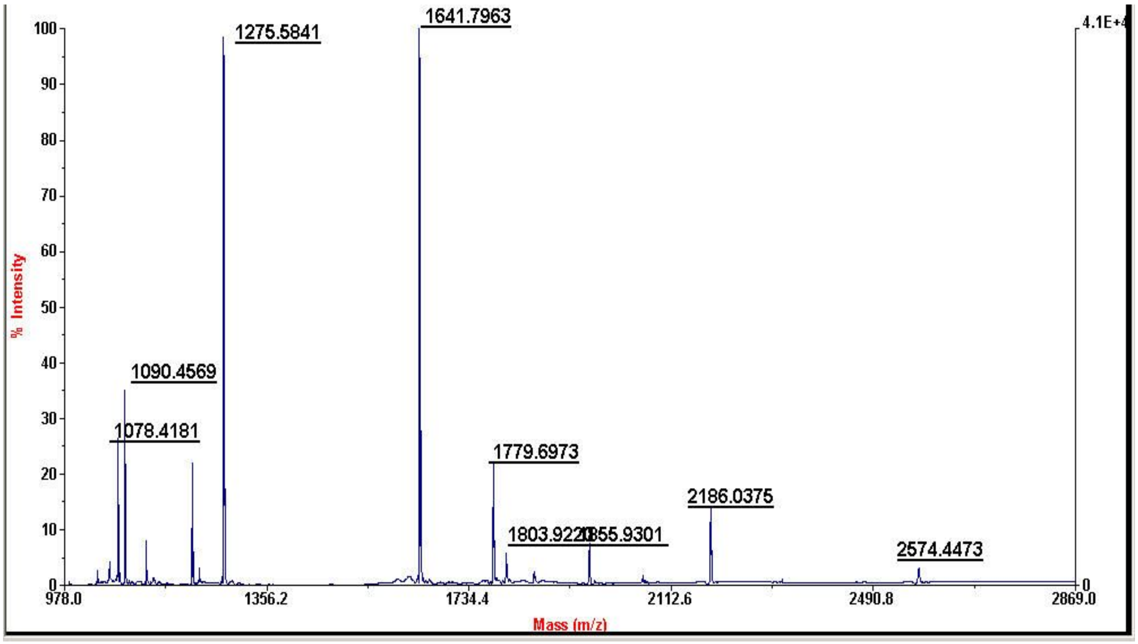
453 WD repeat protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 17	1273.6197	1272.6124	1272.7190	-0.1066	1	K.KVFASLPQVER.G
8 - 17	1145.5373	1144.5300	1144.6241	-0.0940	0	K.VFASLPQVER.G
66 - 81	1618.6237	1617.6165	1617.7675	-0.1510	0	K.YAPSGFYIASGDVSGK.L
96 - 104	1102.4120	1101.4048	1101.5131	-0.1083	0	K.YEYQPFAGK.I
162 - 180	2043.7236	2042.7163	2042.9044	-0.1881	0	R.LATGSDDNCAAFFEGPPFK.F
204 - 219	1719.6577	1718.6504	1718.8152	-0.1647	0	R.FATASADGQIYIYDGK.T
471 - 484	1537.7140	1536.7067	1536.8399	-0.1332	1	R.LYSILGTTLKDEGK.L
490 - 511	2279.8629	2278.8557	2279.0529	-0.1972	0	K.GPVTDVAYSHDGAFLAVCDASK.V

No match to: 918.3681, 1101.4142, 1461.6547, 1752.7174, 2418.0330, 3397.3271

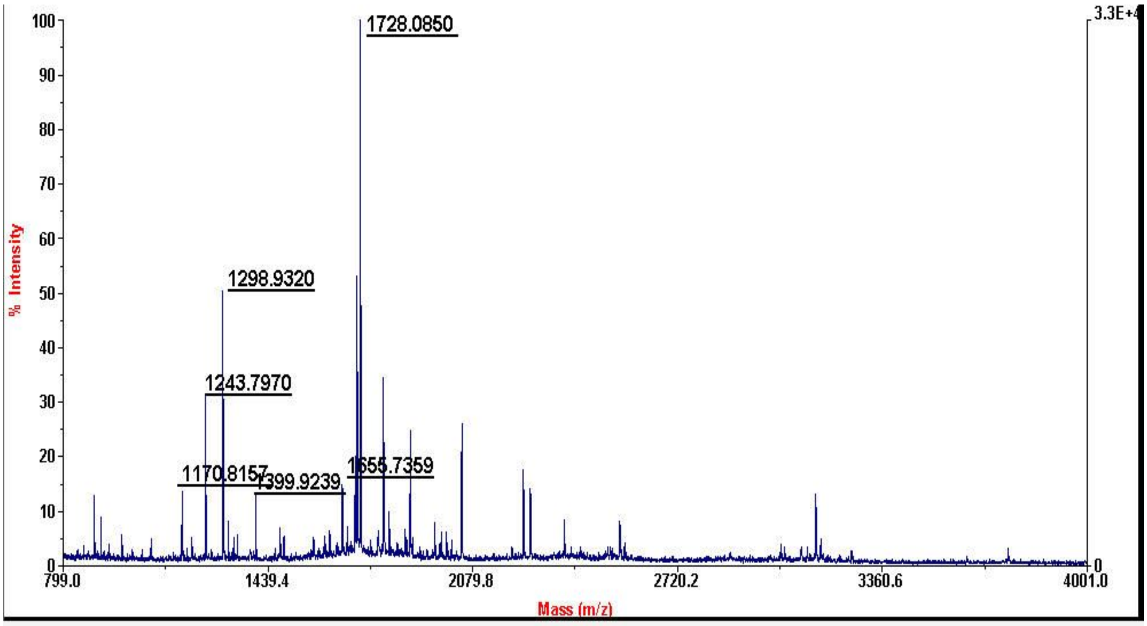
454 Olfactory receptor 10X1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 9	1104.6246	1103.6173	1103.6372	-0.0199	1	-.MKINQTILK.E	Oxidation (M)
122 - 130	1103.5446	1102.5373	1102.5957	-0.0584	0	R.FLAICNPLR.Y	
165 - 174	1235.5166	1234.5093	1234.6128	-0.1035	0	R.DSFCRPNLVK.H	
165 - 185	2549.4011	2548.3939	2548.2654	0.1285	1	R.DSFCRPNLVKHFFCHMLAVIR.L	Oxidation (M)
299 - 308	1120.6050	1119.5978	1119.5892	0.0085	1	R.RMMGNTVALK.K	
299 - 308	1136.6057	1135.5984	1135.5842	0.0142	1	R.RMMGNTVALK.K	Oxidation (M)

No match to: 1195.5597, 1283.6196, 1509.6975, 1586.8059, 1640.8420

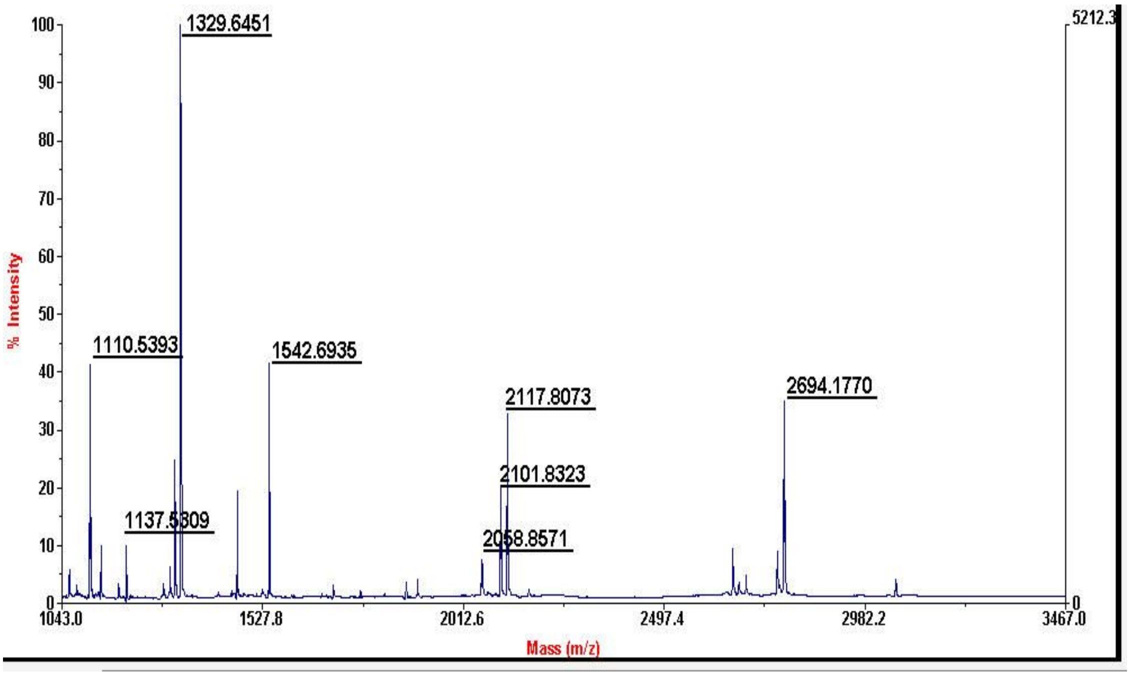
455 Tropomyosin alpha-4 chain (Tropomyosin-4)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
55 - 65	1399.9239	1398.9167	1398.7467	0.1700	1	R.RIQLVEEELDR.A
56 - 65	1243.7970	1242.7897	1242.6456	0.1442	0	R.IQLVEEELDR.A
56 - 69	1728.0850	1727.0777	1726.8849	0.1928	1	R.IQLVEEELDRAQER.L
132 - 142	1298.9320	1297.9247	1297.7605	0.1642	1	R.KLVILEGELER.A
133 - 142	1170.8157	1169.8084	1169.6656	0.1429	0	K.LVILEGELER.A
133 - 146	1655.7359	1654.7286	1654.8889	-0.1603	1	K.LVILEGELERAEER.A

No match to: 1582.3723, 1710.9294, 1717.0244, 1800.1930, 1884.1920, 2044.2554, 2237.3960, 2259.3760

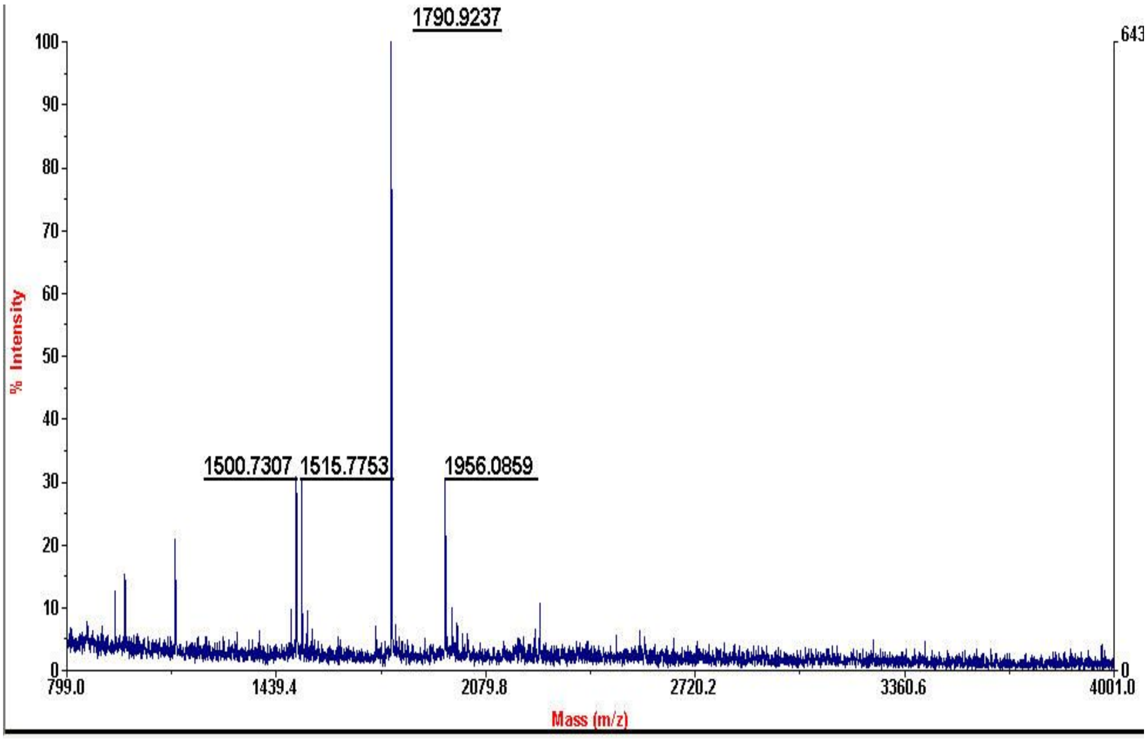
456 Zinc finger protein 57 - Homo sapiens (Human)



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
175 - 197	2694.1770	2693.1697	2693.2438	-0.0741	1	K.QACICPSHLHSHGRTDTEEKPYK.R
189 - 197	1110.5393	1109.5320	1109.5240	0.0080	0	R.TDTEEKPYK.R
199 - 209	1329.6451	1328.6379	1328.6044	0.0334	0	R.QACGQTFQHPR.Y
270 - 287	2101.8323	2100.8251	2100.9292	-0.1041	1	R.HMTTHTGEKPYKCQHCGK.A
Oxidation (M)						
312 - 324	1542.6935	1541.6862	1541.7297	-0.0435	1	K.QCGKTFSWSETLR.V
335 - 343	1137.5309	1136.5236	1136.5107	0.0130	1	K.LYKCEHCGK.A
350 - 367	2117.8073	2116.8000	2117.0112	-0.2113	1	R.SFQGHLRTHTGEKPYECK.Q
480 - 496	2058.8571	2057.8499	2057.9854	-0.1355	1	K.QCGKTFTWSSTLHNHVR.M

No match to: 943.5523, 1109.5607, 1315.5724, 1465.7681, 2769.3093, 2786.2987

457 Actin, alpha cardiac muscle 1

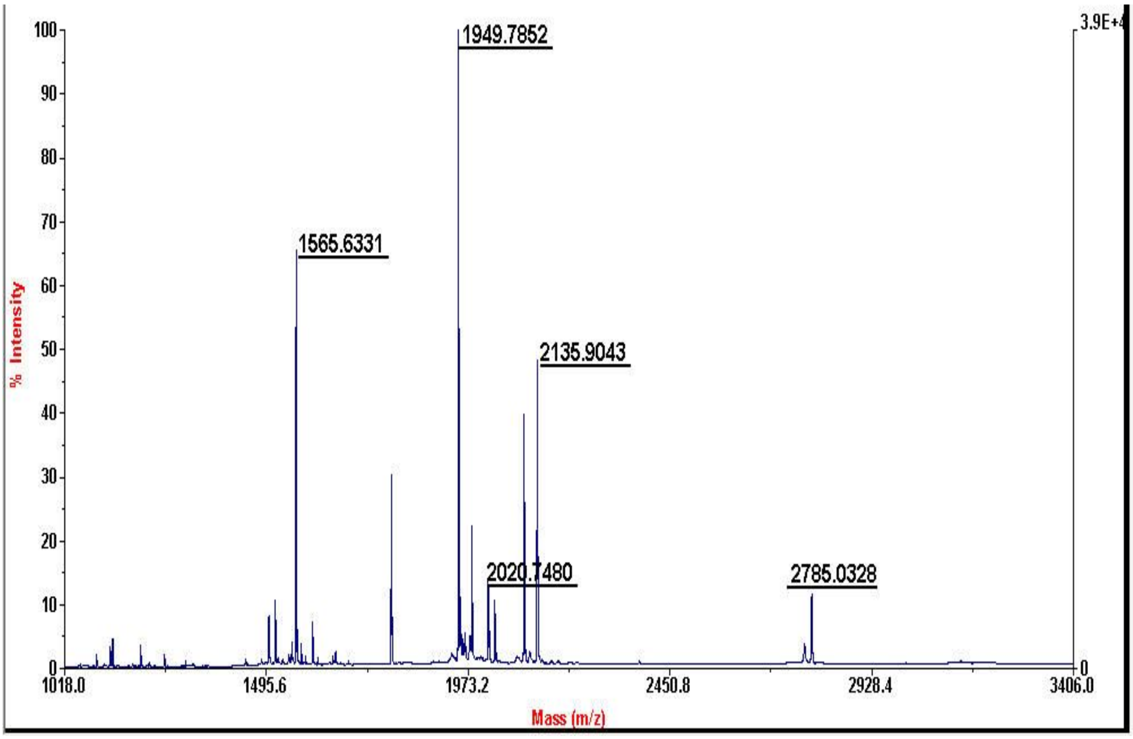


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
21 - 30	976.4800	975.4728	975.4410	0.0317	0	K.AGFAGDDAPR.A
87 - 97	1515.7753	1514.7680	1514.7419	0.0261	0	K.IWHHTFYNELR.V
98 - 115	1956.0859	1955.0786	1955.0364	0.0423	0	R.VAPEEHPTLLTEAPLNPK.A

199 - 208	1130.5803	1129.5730	1129.5404	0.0326	0	R.GYSFVTTAER.E
241 - 256	1790.9237	1789.9164	1789.8846	0.0318	0	K.SYELPDGQVITIGNER.F
362 - 374	1500.7307	1499.7234	1499.7005	0.0230	0	K.QEYDEAGPSIVHR.K

No match to: 1132.5628, 1499.7053, 1516.7246, 1954.1219, 1955.1143

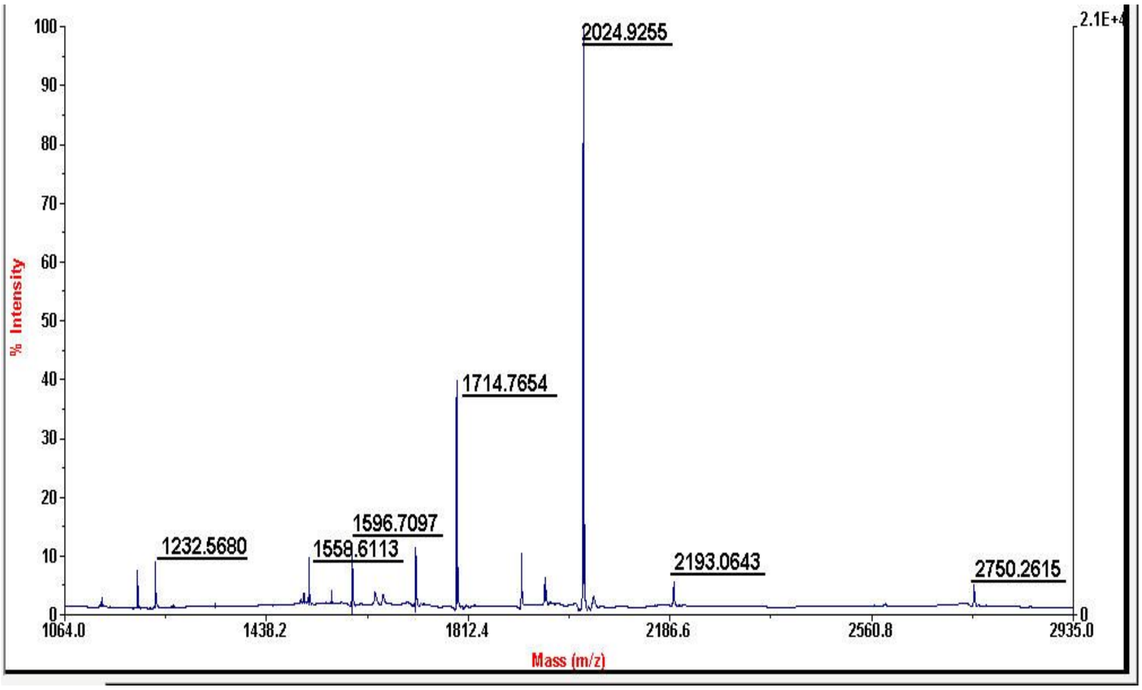
458 Reticulocalbin-1 precursor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
71 - 83	1565.6331	1564.6259	1564.7369	-0.1110	1	K.TFDQLTPDESKER.L
87 - 105	2135.9043	2134.8970	2135.0383	-0.1412	1	K.IVDRIDNDGDGFVTTEELK.T
123 - 129	981.3931	980.3858	980.4716	-0.0857	1	K.VWKDYDR.D
142 - 165	2785.0328	2784.0255	2784.2205	-0.1949	0	K.QATYGYYLGNPAEFHDSSDHHTFK.K
189 - 204	2020.7480	2019.7407	2019.9036	-0.1629	0	R.EEFTAFLHPEEFEHMK.E
250 - 256	969.3785	968.3713	968.4352	-0.0639	0	R.EQFNEFR.D
271 - 286	1949.7852	1948.7780	1948.9180	-0.1400	0	R.HWILPQDYDHAQAEAR.H

No match to: 951.3513, 1790.7575, 1948.7040, 1981.7625, 2104.7934

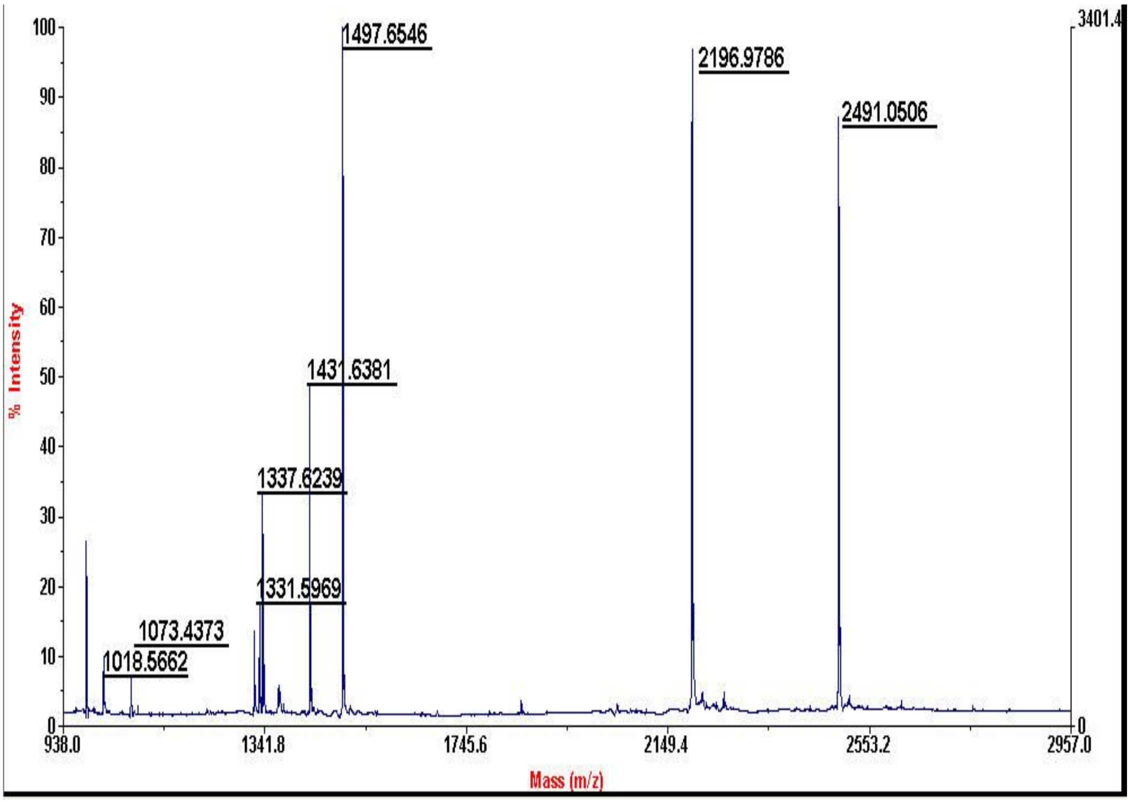
459 Secernin-2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
32 - 56	2750.2615	2749.2543	2749.3532	-0.0990	1	K.NSDRPRDEVQEVVFVPAGTHTPGSR.L	
38 - 56	2024.9255	2023.9182	2023.9964	-0.0782	0	R.DEVQEVVFVPAGTHTPGSR.L	
57 - 69	1596.7097	1595.7024	1595.7865	-0.0841	0	R.LQCTYIEVEQVSK.T	
104 - 119	1714.7654	1713.7582	1713.8607	-0.1026	0	K.EPVGEGEALLGMDLLR.L	Oxidation (M)
167 - 177	1232.5680	1231.5607	1231.6197	-0.0590	0	R.TEAWVLETAGR.L	
190 - 209	2193.0643	2192.0571	2192.1185	-0.0615	0	R.NISNQLSIGTDISAQHPELR.T	
271 - 284	1558.6113	1557.6040	1557.6552	-0.0511	1	R.DKESGICMDSGGFR.T	
361 - 371	1198.5938	1197.5865	1197.5924	-0.0059	0	R.GHQAALGLMER.D	Oxidation (M)

No match to: 1516.6230, 1639.8499, 1790.8185, 1910.8635, 1953.9697, 2705.5450

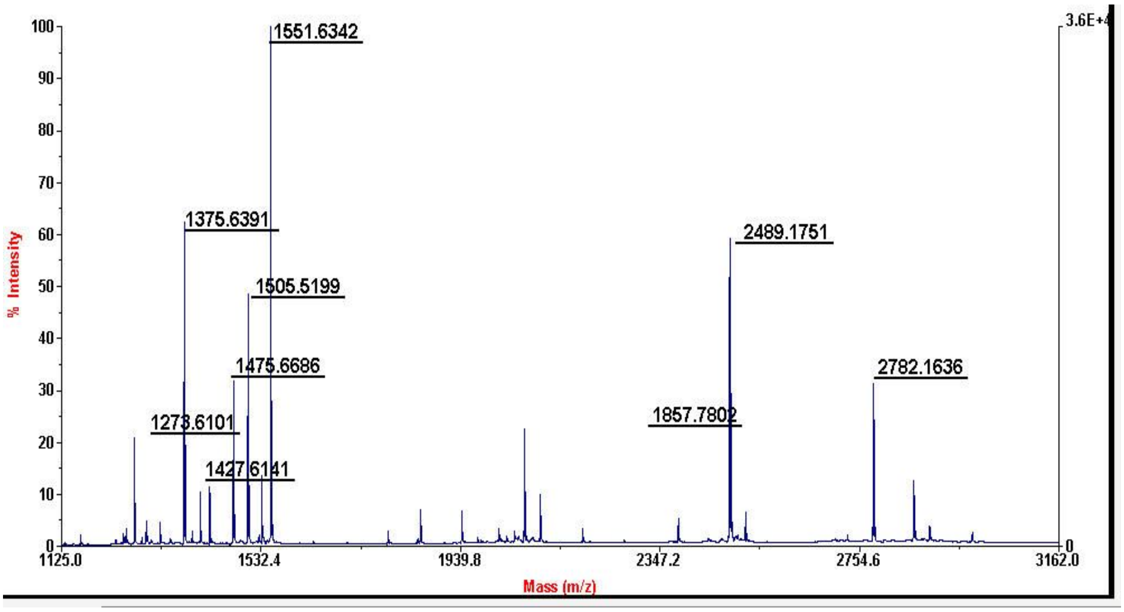
460 Aminoacylase-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
5 - 17	1497.6546	1496.6474	1496.7260	-0.0786	0	K.GPEEEHPSVTLFR.Q	
24 - 43	2196.9786	2195.9713	2196.0851	-0.1139	0	R.TVQPKPDYGAAVAFFEETAR.Q	
101 - 109	1073.4373	1072.4300	1072.4825	-0.0525	0	K.DSEGYIYAR.G	
116 - 126	1337.6239	1336.6166	1336.6809	-0.0643	0	K.CVSIQYLEAVR.R	
169 - 191	2491.0506	2490.0433	2490.1703	-0.1270	0	R.AGFALDEGIANPTDAFTVFYSER.S	
222 - 230	1018.5662	1017.5589	1017.5971	-0.0382	0	K.VVNSILAFR.E	
354 - 367	1431.6381	1430.6308	1430.7340	-0.1032	0	R.AVGVPALGFSPMNR.T	Oxidation (M)
368 - 378	1331.5969	1330.5896	1330.6630	-0.0734	0	R.TPVLLHDHDER.L	
379 - 386	984.5106	983.5034	983.5552	-0.0519	0	R.LHEAVFLR.G	

No match to: 1320.6066, 1371.2427

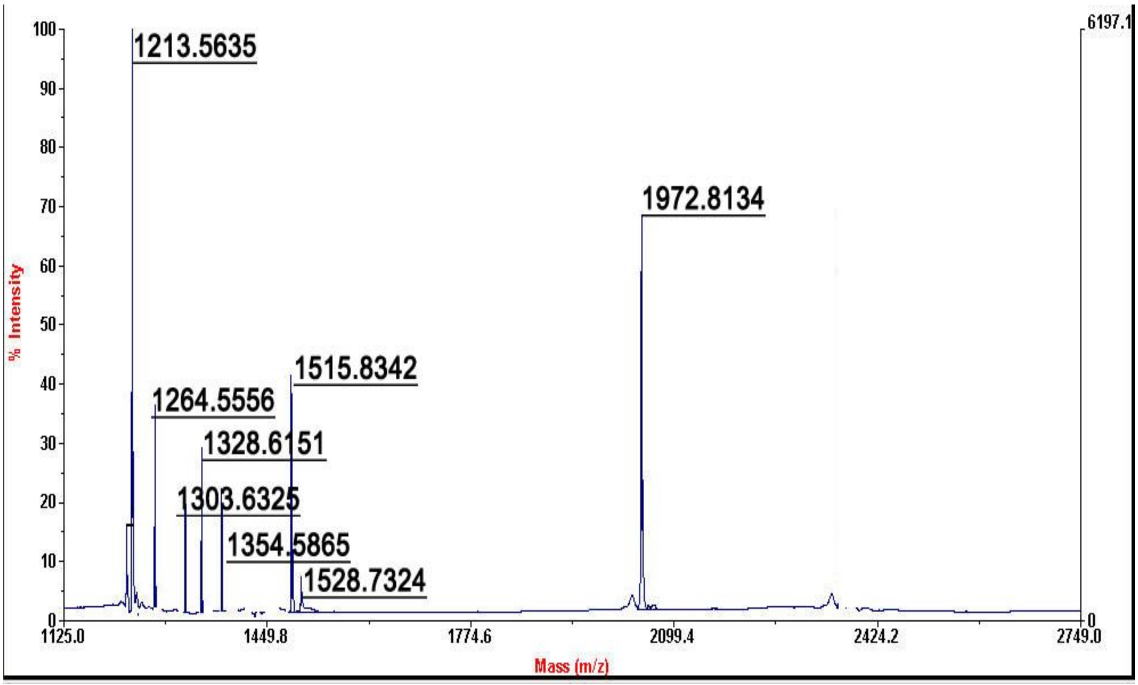
461 Alcohol dehydrogenase [NADP+]



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
35 - 42	928.3831	927.3759	927.4814	-0.1055	0	K.YALSVGYR.H
43 - 68	2782.1636	2781.1563	2781.3279	-0.1716	1	R.HIDCAAIYGNEPEIGEALKEDVGPGK.A
69 - 80	1375.6391	1374.6319	1374.7507	-0.1188	1	K.AVPREELFVTSK.L
86 - 97	1427.6141	1426.6068	1426.7317	-0.1249	1	K.HHPEDVEPALRK.T
154 - 167	1475.6686	1474.6613	1474.7892	-0.1279	0	K.GLVQALGLSNFNSR.Q
204 - 218	1551.6342	1550.6269	1550.7576	-0.1307	0	R.GLEVTAYSPLGSSDR.A
219 - 240	2489.1751	2488.1678	2488.3213	-0.1535	1	R.AWRDPDEPVLLEEPVVLALAEK.Y
241 - 251	1273.6101	1272.6029	1272.7302	-0.1274	1	K.YGRSPAQILLR.W
310 - 325	1857.7802	1856.7729	1856.8846	-0.1117	1	R.VPRDAGHPLYPFNDPY.-
313 - 325	1505.5199	1504.5126	1504.6623	-0.1497	0	R.DAGHPLYPFNDPY.-

No match to: 1533.6352, 2069.9316, 2101.9281, 2865.3492

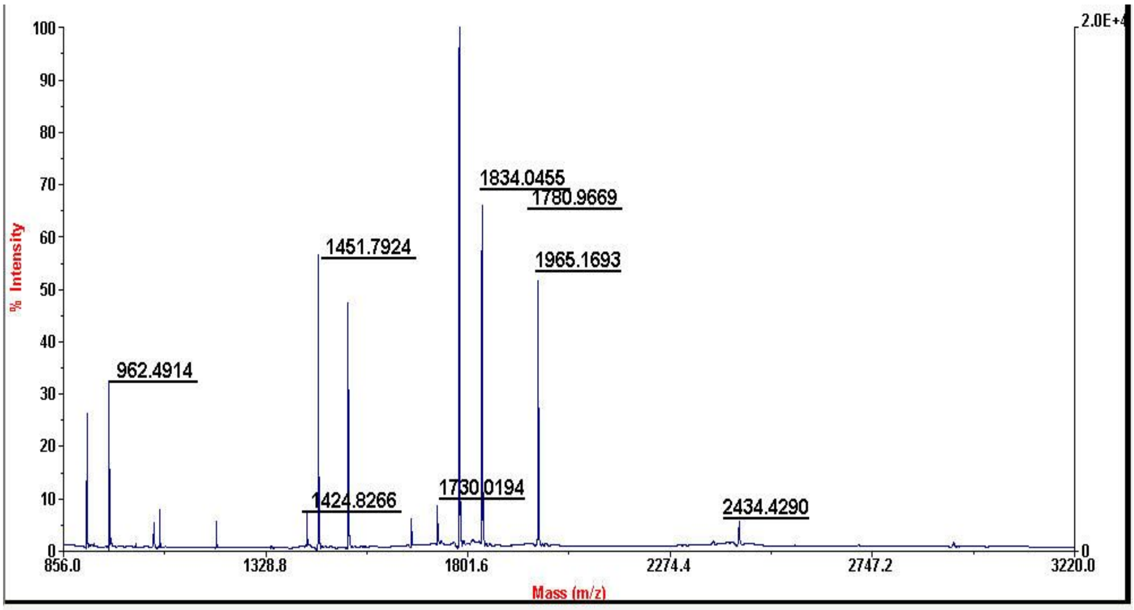
462 Transcription elongation factor A protein 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
33 - 45	1515.8342	1514.8269	1514.8126	0.0143	0	K.NIPMTLELLQSTR.I
209 - 222	1528.7324	1527.7251	1527.7868	-0.0617	0	K.NVLCGNIPPDLFAR.M
223 - 234	1354.5865	1353.5792	1353.5792	0.0000	0	R.MTAEEMASDELK.E
253 - 265	1328.6151	1327.6078	1327.6078	-0.0000	0	K.TGGTQTDLFTCGK.C
270 - 279	1213.5635	1212.5562	1212.5557	0.0005	0	K.NCTYTQVQTR.S
280 - 297	1972.8134	1971.8061	1971.8125	-0.0064	0	R.SADEPMTTFVVCNECGNR.W

No match to: 1070.5105, 1264.5556, 1303.6325

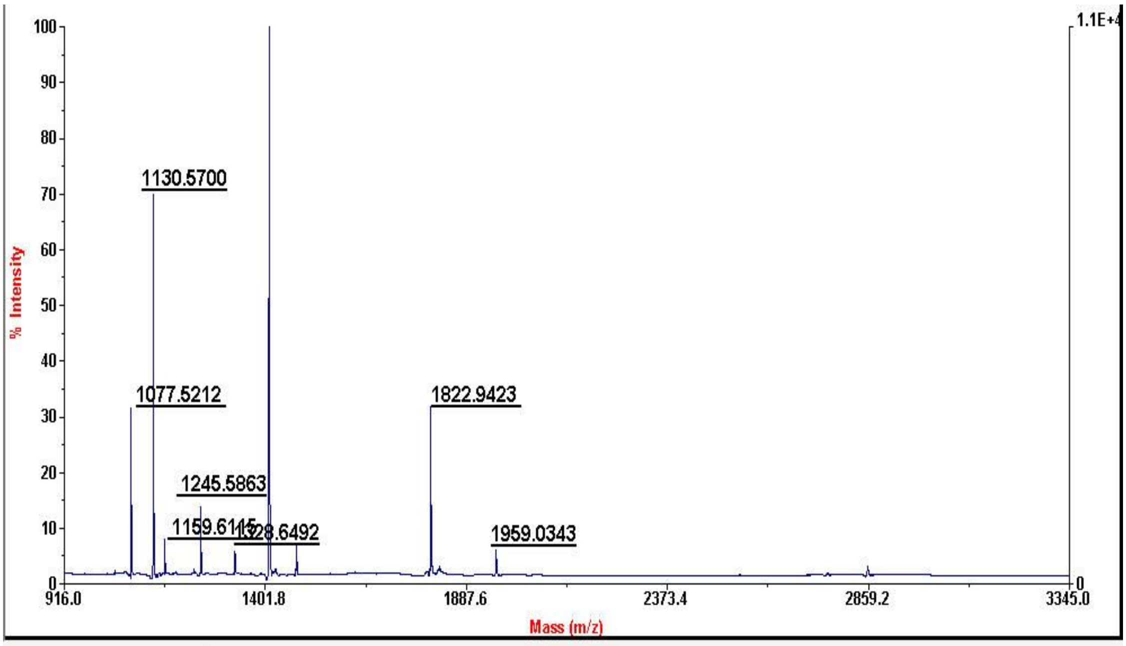
463 Protein disulfide-isomerase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
82 - 97	1780.9669	1779.9597	1779.8275	0.1321	0	K.VDATEESDLAQQYGVR.G
196 - 207	1424.8266	1423.8193	1423.7711	0.0482	1	K.YQLDKDGVVLFK.K
231 - 247	1965.1693	1964.1620	1964.0367	0.1253	0	K.HNQLPLVIEFTEQTAPK.I
286 - 300	1834.0455	1833.0382	1832.9057	0.1325	0	K.ILFIFIDSDHTDNQR.I
327 - 338	1451.7924	1450.7851	1450.6939	0.0912	0	K.YKPESEELTAER.I
339 - 345	962.4914	961.4841	961.4440	0.0401	0	R.ITEFCHR.F
351 - 370	2434.4290	2433.4217	2433.2362	0.1855	1	K.IKPHLMSQELPEDWDKQPVK.V
Oxidation (M)						
410 - 424	1730.0194	1729.0121	1728.9046	0.1075	1	K.LGETYKDHENIVIAK.M
445 - 452	910.4555	909.4483	909.4345	0.0138	0	K.FFPASADR.T

No match to: 1080.6237, 1521.8388, 1668.9680

464 Tubulin beta-2C chain

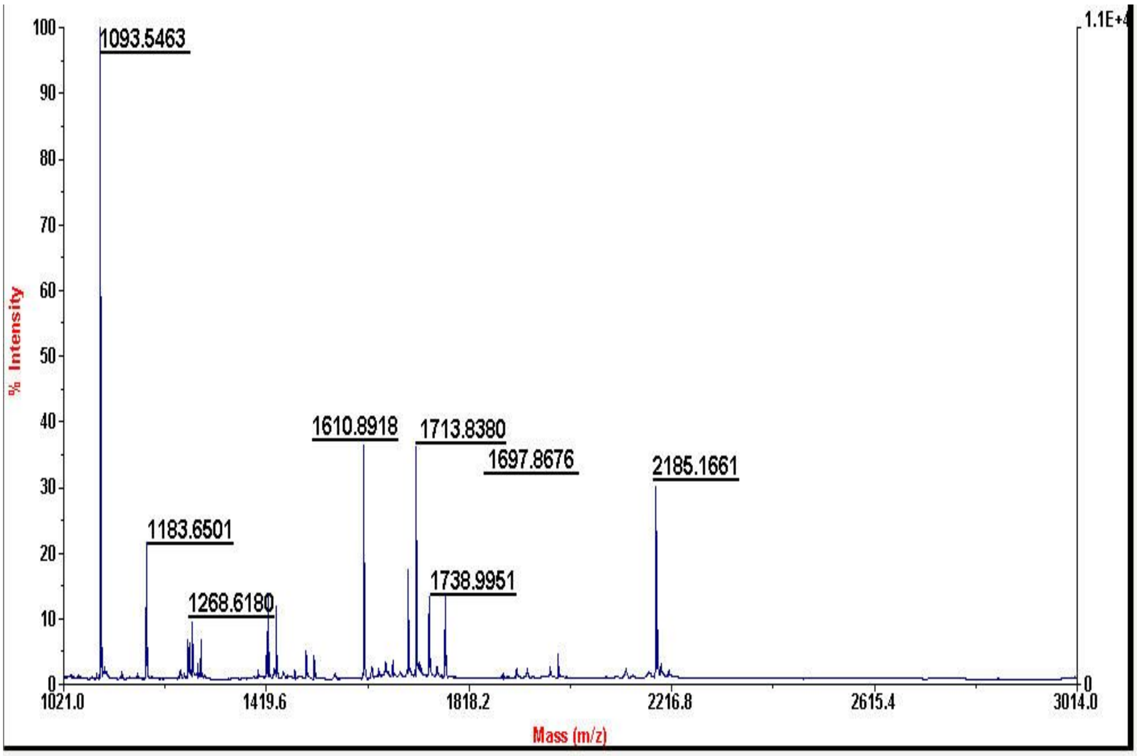


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
3 - 19	1822.9423	1821.9351	1821.9156	0.0195	0	R.EIVHLQAGQCGNQIGAK.F
47 - 58	1328.6492	1327.6420	1327.6408	0.0012	0	R.INVYYNEATGGK.Y
104 - 121	1959.0343	1958.0271	1957.9745	0.0525	0	K.GHYTEGAELVDSVLDVVR.K
155 - 162	1077.5212	1076.5140	1076.5250	-0.0111	1	K.IREEYPDR.I
242 - 251	1130.5700	1129.5627	1129.5880	-0.0253	0	R.FPGQLNADLR.K
253 - 262	1159.6115	1158.6043	1158.6219	-0.0177	0	K.LAVNMVPFPR.L Oxidation (M)

381 - 390	1245.5863	1244.5790	1244.5860	-0.0069	0	R.ISEQFTAMFR.R	Oxidation (M)

No match to: 1410.6431, 1475.6616, 1800.8638, 2856.5326

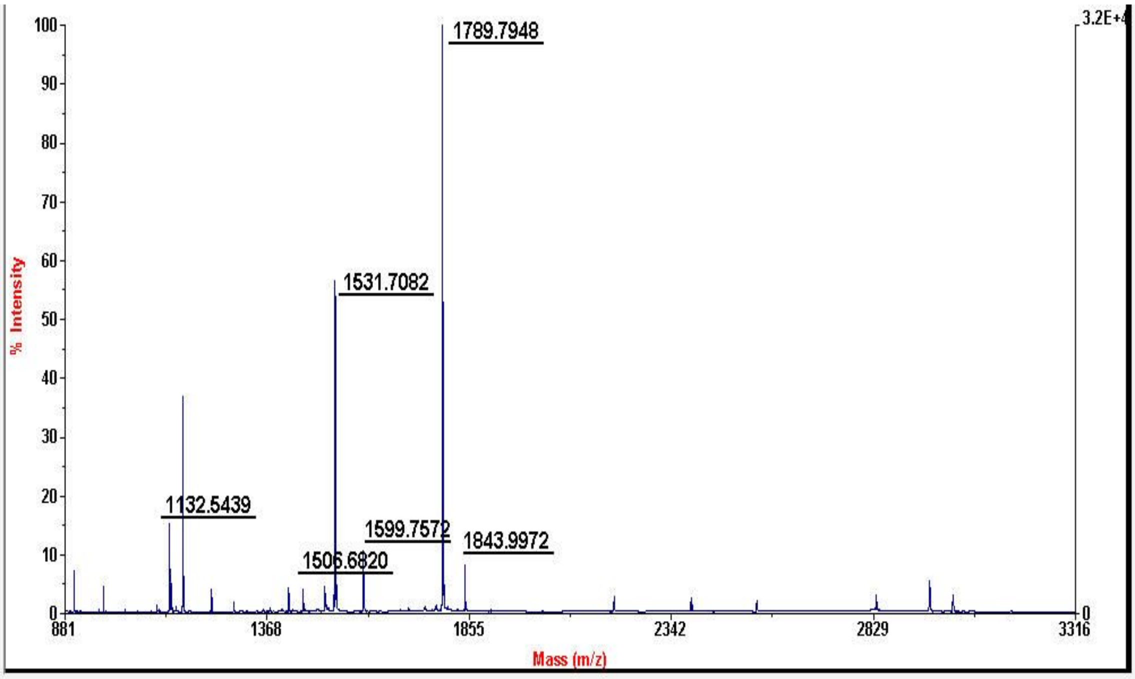
465 T-complex protein 1 subunit epsilon



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
133 - 142	1093.5463	1092.5390	1092.5200	0.0191	0	R.IADGYEQAAR.V	
151 - 170	2185.1661	2184.1589	2184.1889	-0.0300	1	K.ISDSVLVDIKDTEPLIQTAK.T	
227 - 241	1697.8676	1696.8603	1696.8607	-0.0003	1	K.GVIVDKDFSHPQMPK.K	
227 - 241	1713.8380	1712.8307	1712.8556	-0.0249	1	K.GVIVDKDFSHPQMPK.K	Oxidation (M)
248 - 261	1610.8918	1609.8846	1609.8902	-0.0056	0	K.IAILTCPFEPPKPK.T	
324 - 340	1738.9951	1737.9879	1737.9414	0.0465	0	R.WVGGPEIELIAIATGGR.I	
401 - 410	1183.6501	1182.6428	1182.6179	0.0249	0	R.SLHDALCVIR.N	
440 - 449	1268.6180	1267.6107	1267.5689	0.0418	0	K.CPTLEQYAMR.A	

No match to: 1770.9710, 2126.7558

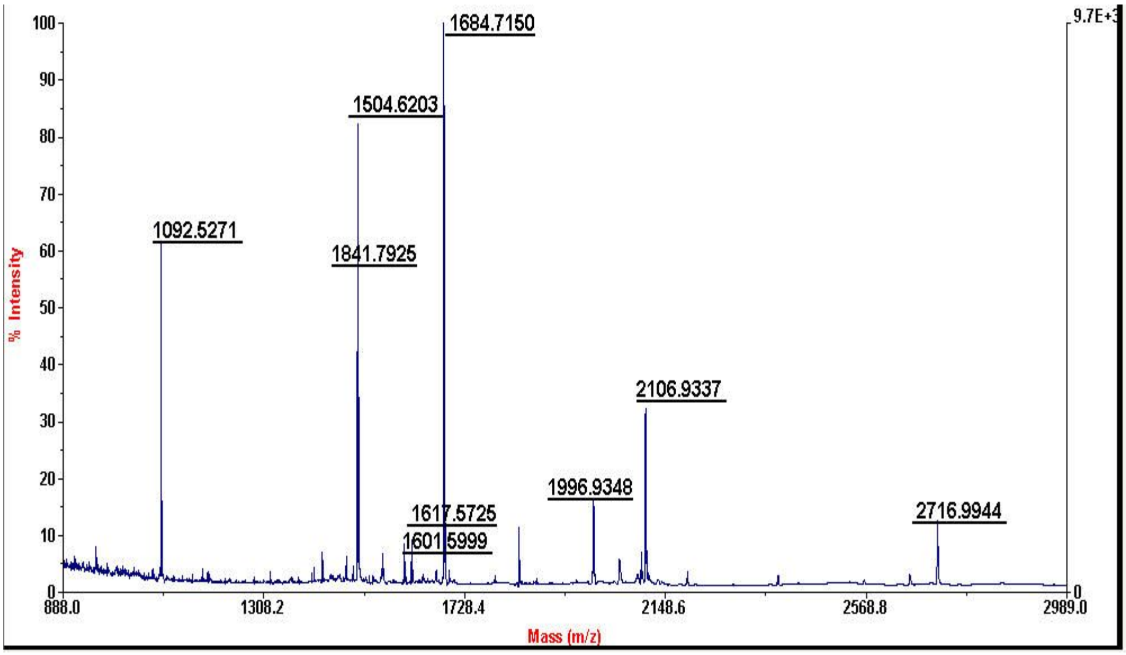
466Aldehyde dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
85 - 94	1132.5439	1131.5366	1131.5825	-0.0459	0	R.AAFQLGSPWR.R
160 - 172	1531.7082	1530.7009	1530.7355	-0.0345	0	K.TIPIDGDFFSYTR.H
210 - 226	1843.9972	1842.9899	1843.0455	-0.0555	0	K.VAEQTPLTALYVANLIK.E
325 - 338	1789.7948	1788.7875	1788.8206	-0.0332	0	R.TFVQEDIYDEFVER.S
356 - 368	1506.6820	1505.6748	1505.6998	-0.0251	0	K.TEQGPQVDETQFK.K
493 - 506	1599.7572	1598.7499	1598.7828	-0.0329	0	R.ELGEYGLQAYTEVK.T

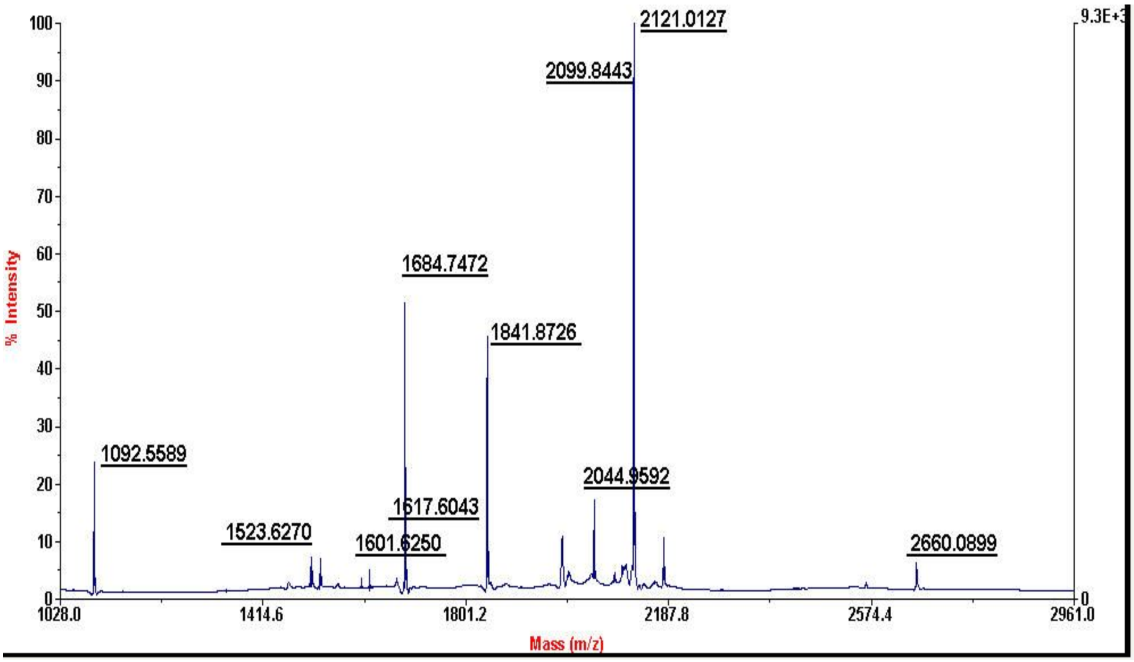
No match to: 1164.5422, 2963.4603, 3809.8500

467 Heterogeneous nuclear ribonucleoprotein H



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
17 - 29	1504.6203	1503.6130	1503.6776	-0.0646	0	R.GLPWSCSADEVQR.F	
50 - 68	2106.9337	2105.9264	2105.9753	-0.0489	0	R.EGRPSGEAFVELESEDEVK.L	
99 - 114	1684.7150	1683.7077	1683.7601	-0.0524	0	K.HTGPNSPDTANDGFVR.L	
151 - 167	1841.7925	1840.7852	1840.8843	-0.0991	0	R.STGEAFVQFASQEIAEK.A	
234 - 259	2716.9944	2715.9871	2716.0375	-0.0504	0	R.GAYGGGYGGYDDYNGYNDGYGFGSDR.F	
263 - 275	1601.5999	1600.5926	1600.6399	-0.0472	0	R.DLNYCFSGMSDHR.Y	
263 - 275	1617.5725	1616.5652	1616.6348	-0.0695	0	R.DLNYCFSGMSDHR.Y	Oxidation (M)
300 - 316	1996.9348	1995.9275	1995.9690	-0.0415	0	R.ATENDIYNFFSPLNPVR.V	
317 - 326	1092.5271	1091.5198	1091.5724	-0.0525	0	R.VHIEIGPDGR.V	

468 Heterogeneous nuclear ribonucleoprotein H2

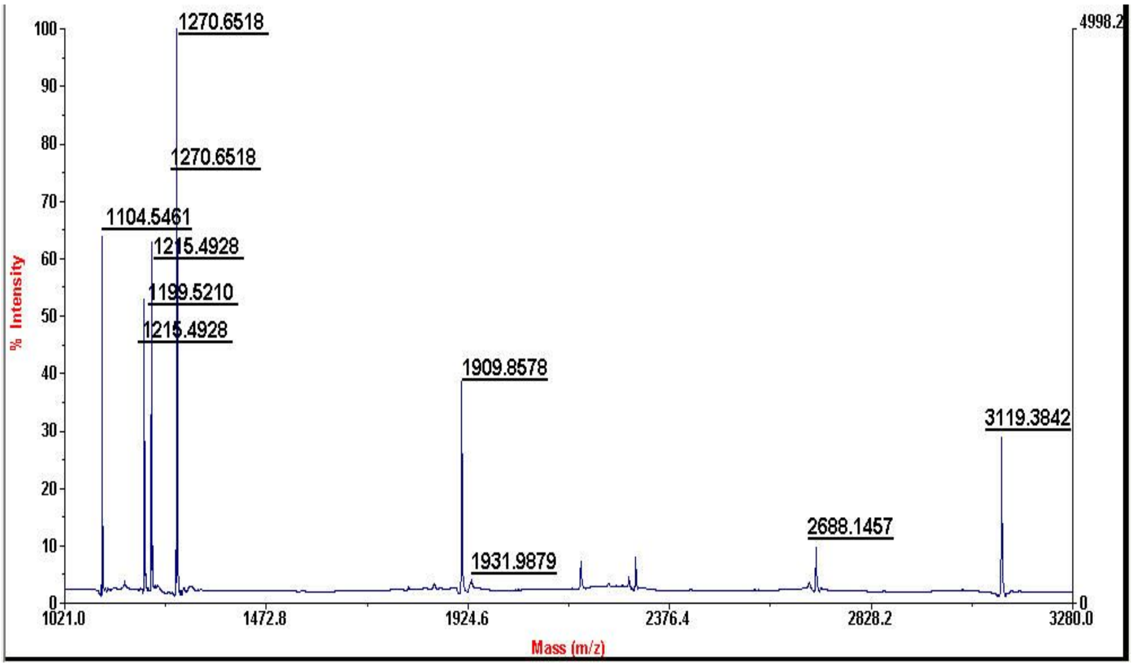


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
17 - 29	1523.6270	1522.6197	1522.6544	-0.0347	0	R.GLPWSCSADEVMR.F	Oxidation (M)
50 - 68	2121.0127	2120.0054	2119.9909	0.0145	0	R.EGRPSGEAFVELESEEEVK.L	
99 - 114	1684.7472	1683.7399	1683.7601	-0.0202	0	K.HTGPNSPDTANDGFVR.L	
151 - 167	1841.8726	1840.8654	1840.8843	-0.0189	0	R.STGEAFVQFASQEIAEK.A	
234 - 259	2660.0899	2659.0826	2659.0160	0.0666	0	R.GAYGGGYGGYDDYGGYNDGYGFGSDR.F	

263 - 275	1601.6250	1600.6177	1600.6399	-0.0221	0	R.DLNYCFSGMSDHR.Y
263 - 275	1617.6043	1616.5971	1616.6348	-0.0377	0	R.DLNYCFSGMSDHR.Y Oxidation (M)
276 - 294	2083.8725	2082.8652	2082.8636	0.0015	0	R.YGDGGSSFQSTTGHCVHMR.G
276 - 294	2099.8443	2098.8370	2098.8586	-0.0216	0	R.YGDGGSSFQSTTGHCVHMR.G Oxidation (M)
300 - 316	2044.9592	2043.9519	2043.9360	0.0159	0	R.ATENDIYNFFSPLNPMR.V Oxidation (M)
317 - 326	1092.5589	1091.5516	1091.5724	-0.0207	0	R.VHIEIGPDGR.V

No match to: 1877.9535, 1997.0158, 2563.3415

469 Non-specific lipid-transfer protein

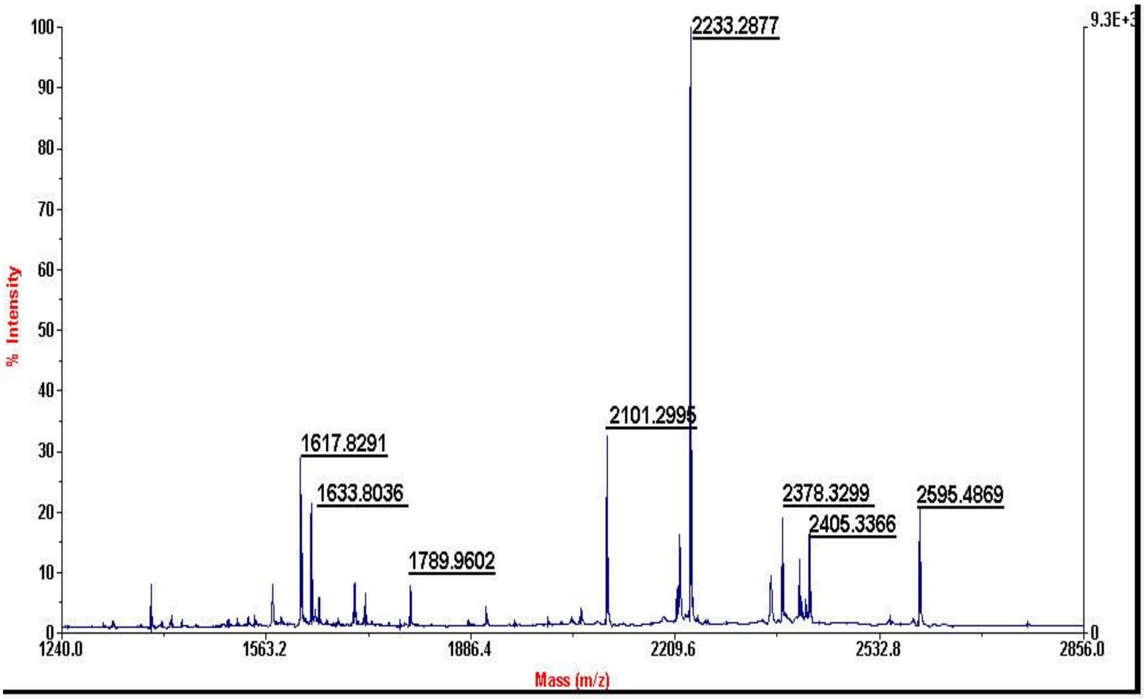


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
24 - 33	1104.5461	1103.5388	1103.5723	-0.0335	0	K.FVKPGAENSR.D
46 - 74	3119.3842	3118.3769	3118.4125	-0.0355	0	K.ALADAQIPYSAVDQACVGYVFGDSTCGQR.A
106 - 123	1931.9879	1930.9806	1931.0186	-0.0380	0	R.QLIQGGVAECVLALGFEK.M
151 - 168	1909.8578	1908.8505	1908.9192	-0.0688	0	K.YGLSAHPVAPQMFGYAGK.E Oxidation (M)

191 - 213	2688.1457	2687.1384	2687.1809	-0.0425	0	K.HSVNNPYSQFQDEYSLDEVMASK.E	
191 - 213	2704.1134	2703.1061	2703.1759	-0.0697	0	K.HSVNNPYSQFQDEYSLDEVMASK.E	Oxidation (M)
251 - 270	2299.9940	2298.9867	2299.0599	-0.0732	0	K.AVEILAQEMMTDLPSSFEEK.S	2 Oxidation (M)
405 - 415	1199.5210	1198.5137	1198.5441	-0.0304	0	K.MGFPEAASSFR.T	
405 - 415	1215.4928	1214.4855	1214.5390	-0.0535	0	K.MGFPEAASSFR.T	Oxidation (M)
512 - 522	1270.6518	1269.6445	1269.5812	0.0633	0	K.MNPQSAFFQGK.L	Oxidation (M)

No match to: 1272.5919, 1849.0081, 1908.8087, 2176.8919

470 3-ketoacid-coenzyme A transferase 1

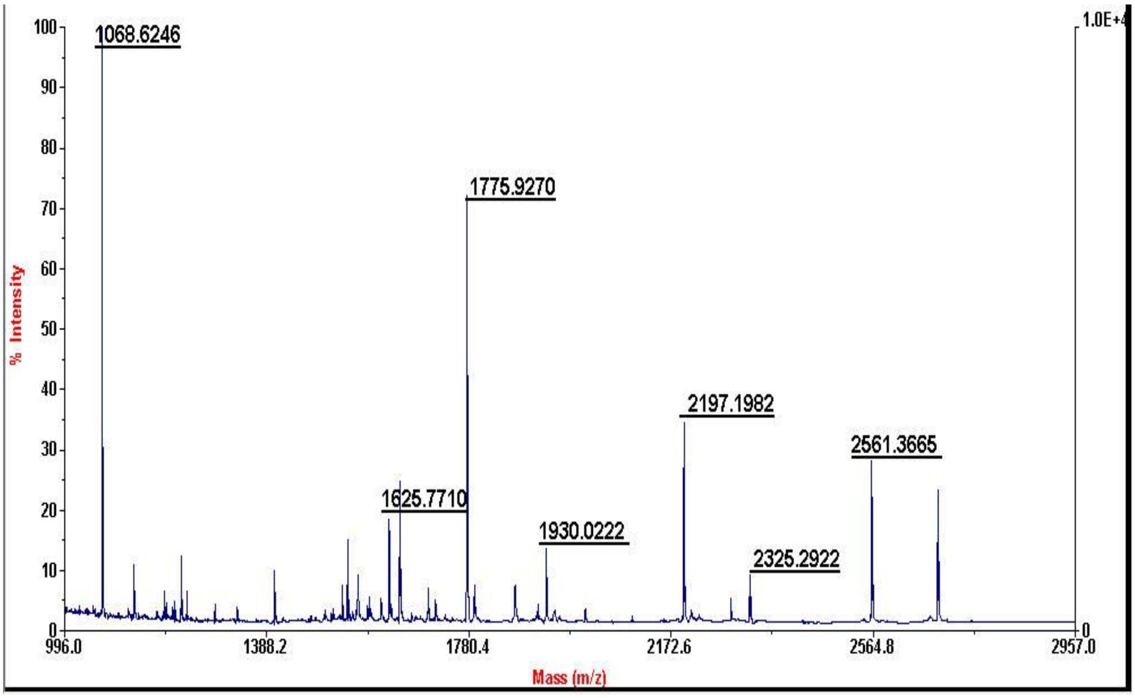


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
84 - 104	2101.2995	2100.2922	2100.1328	0.1595	0	K.GLTAVSNNAGVDNFGLGLLLR.S	
110 - 124	1789.9602	1788.9529	1788.8101	0.1428	1	K.RMVSSYVGENAEFER.Q	Oxidation (M)
111 - 124	1617.8291	1616.8219	1616.7141	0.1078	0	R.MVSSYVGENAEFER.Q	
111 - 124	1633.8036	1632.7964	1632.7090	0.0874	0	R.MVSSYVGENAEFER.Q	Oxidation (M)

125 - 144	2233.2877	2232.2804	2232.1274	0.1530	0	R.QYLSGELEVELTPQGTLAER.I
147 - 173	2595.4869	2594.4796	2594.3017	0.1779	0	R.AGGAGVPAFYTPTGYGTLVQEGGSPIK.Y
191 - 211	2378.3299	2377.3226	2377.1954	0.1272	0	R.EFNGQHFILEEAITGDFALVK.A
369 - 390	2405.3366	2404.3293	2404.1621	0.1673	0	K.ETVTILPGASFFSSDESFAMIR.G
369 - 390	2421.3487	2420.3414	2420.1570	0.1845	0	K.ETVTILPGASFFSSDESFAMIR.G Oxidation (M)

No match to: 1573.9493, 1702.0257, 2216.2279, 2362.2674

471 Aldehyde dehydrogenase X



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
52 - 73	2325.2922	2324.2849	2324.1761	0.1088	1	K.KTFPTVNPTTGEVIGHVAEGDR.A
53 - 73	2197.1982	2196.1909	2196.0811	0.1098	0	K.TFPTVNPTTGEVIGHVAEGDR.A
148 - 155	957.4552	956.4479	956.4392	0.0087	0	R.YFAGWADK.W
160 - 172	1625.7710	1624.7637	1624.7127	0.0511	0	K.TIPMDGQHFCFTR.H Oxidation (M)
325 - 338	1775.9270	1774.9197	1774.8414	0.0784	0	R.TFVEESIYNEFLER.T
348 - 369	2561.3665	2560.3592	2560.2194	0.1398	1	K.VGNPFELDTQQGPQVDKEQFER.V

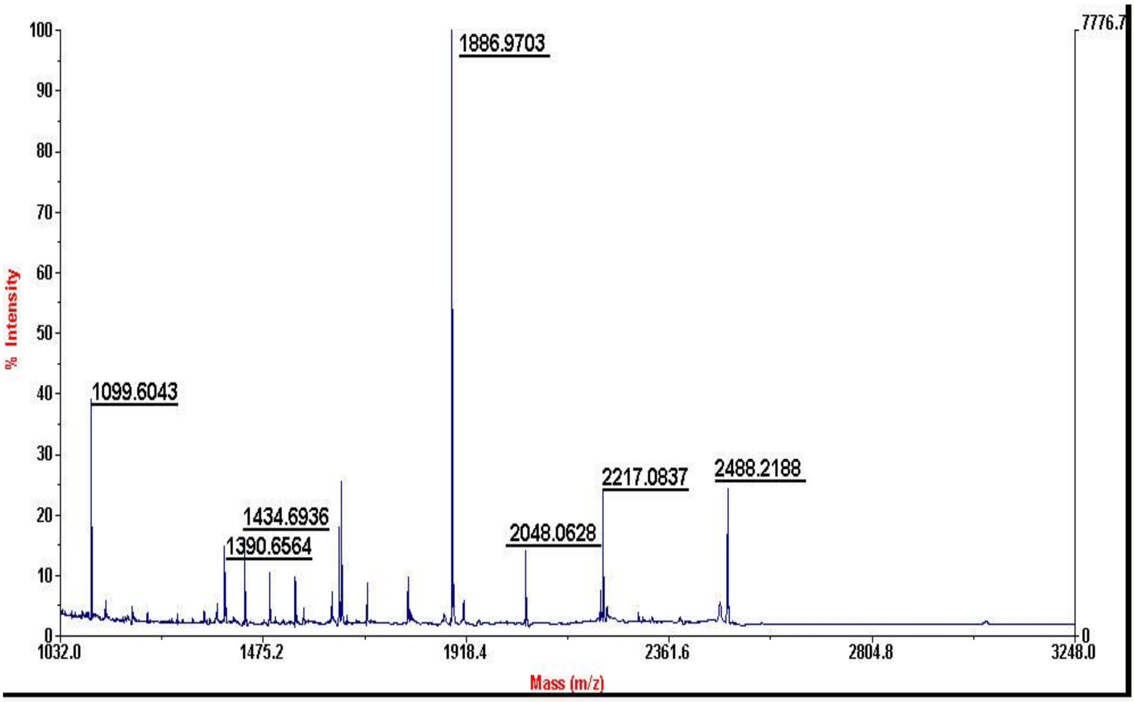
395 - 411	1930.0222	1929.0149	1928.9455	0.0694	0	R.GFFIKPTVFGGVQDDMR.I

Oxidation (M)

442 - 451	1068.6246	1067.6173	1067.5764	0.0409	0	R.YGLAAAVFTR.D

No match to: 1130.5873, 1544.8498, 1645.8777, 1870.0274, 2689.4880

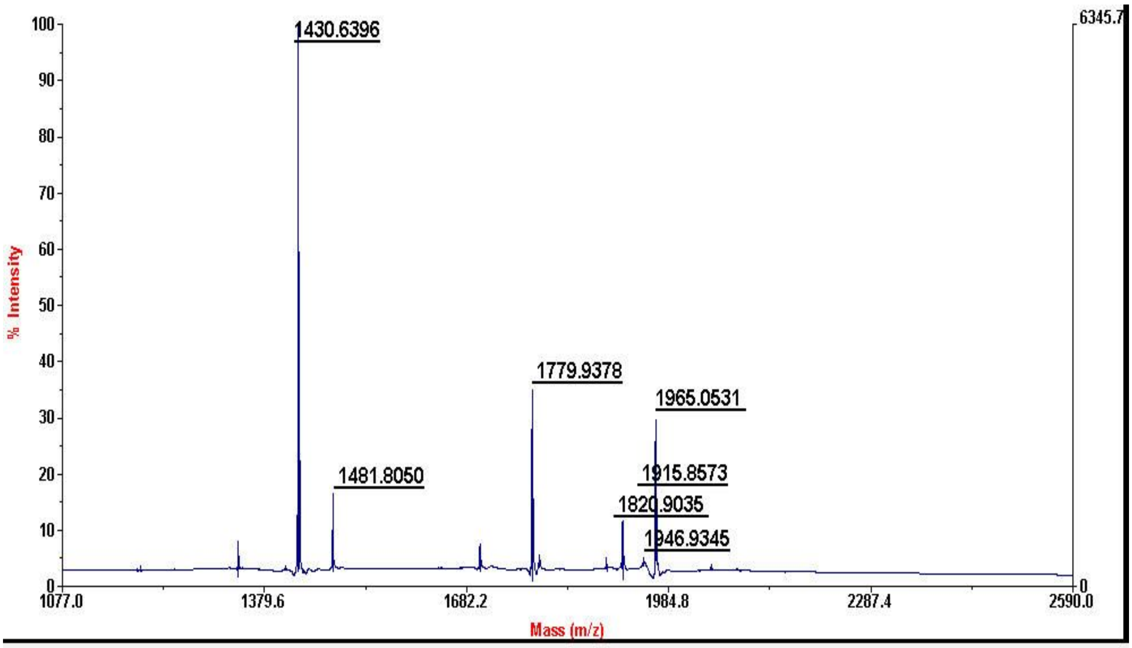
472 D-3-phosphoglycerate dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
9 - 20	1434.6936	1433.6864	1433.6643	0.0221	0	K.VLISDSLDPCCR.K
39 - 54	1886.9703	1885.9631	1885.9455	0.0176	0	K.EELIAELQDCEGLIVR.S
237 - 247	1099.6043	1098.5970	1098.6033	-0.0063	0	R.GGIVDEGALLR.A
248 - 268	2217.0837	2216.0764	2216.0532	0.0232	0	R.ALQSGQCAGAALDVFTEEPPR.D
248 - 270	2488.2188	2487.2115	2487.1812	0.0303	1	R.ALQSGQCAGAALDVFTEEPPRDR.A
271 - 289	2048.0628	2047.0556	2047.0157	0.0399	0	R.ALVDHENVISCPHLGASTK.E
462 - 469	986.5895	985.5822	985.5960	-0.0138	0	R.DLPLLLFR.T
523 - 533	1390.6564	1389.6491	1389.6466	0.0025	0	K.QHVTEAFQFHF.-

No match to: 1544.7668, 1645.8181, 1700.7848, 2472.2010

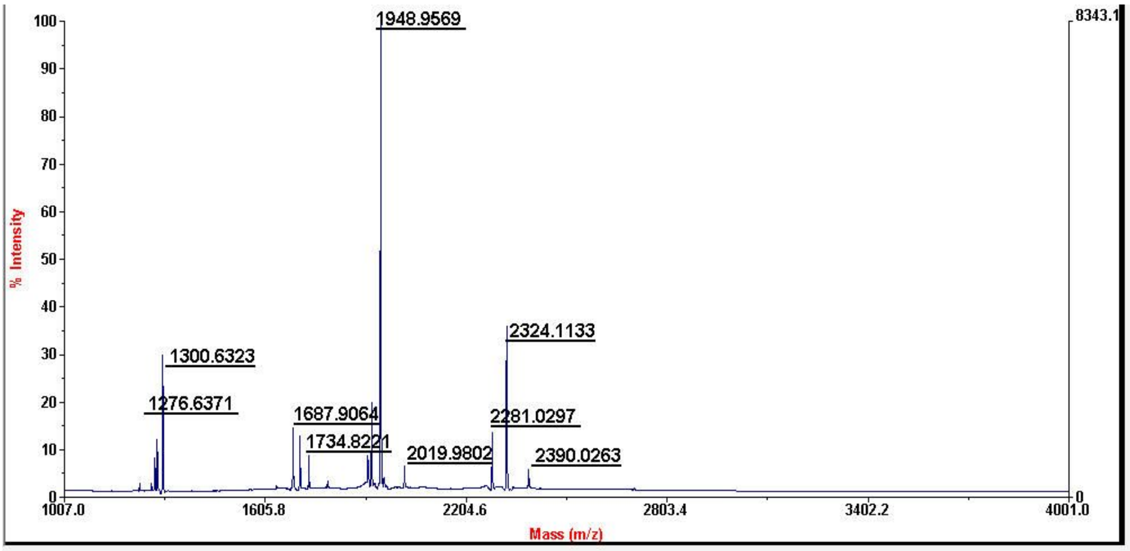
473 Inosine-5'-monophosphate dehydrogenase 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
109 - 124	1820.9035	1819.8962	1819.9720	-0.0758	1	K.KYEQGFITDPVVLSPK.D
137 - 149	1430.6396	1429.6323	1429.6773	-0.0449	0	R.HGFCGIPITDTGR.M
182 - 195	1481.8050	1480.7977	1480.8613	-0.0636	1	K.REDLVVAPAGITLK.E
207 - 224	1965.0531	1964.0458	1964.0942	-0.0484	1	K.GKLPIVNEDDELVAIIAR.T
209 - 224	1779.9378	1778.9305	1778.9778	-0.0473	0	K.LPIVNEDDELVAIIAR.T
243 - 259	1946.9345	1945.9272	1945.9316	-0.0044	1	K.QLLCGAAIGTHEDDKYR.L
356 - 375	2048.0988	2047.0915	2047.1327	-0.0412	1	R.RFGVPVIADGGIQNVGHIAK.A
494 - 511	1915.8573	1914.8500	1914.9072	-0.0571	0	R.TSSAQVEGGVHSLHSYEK.R

No match to: 1339.6408, 1428.6835, 1701.8598

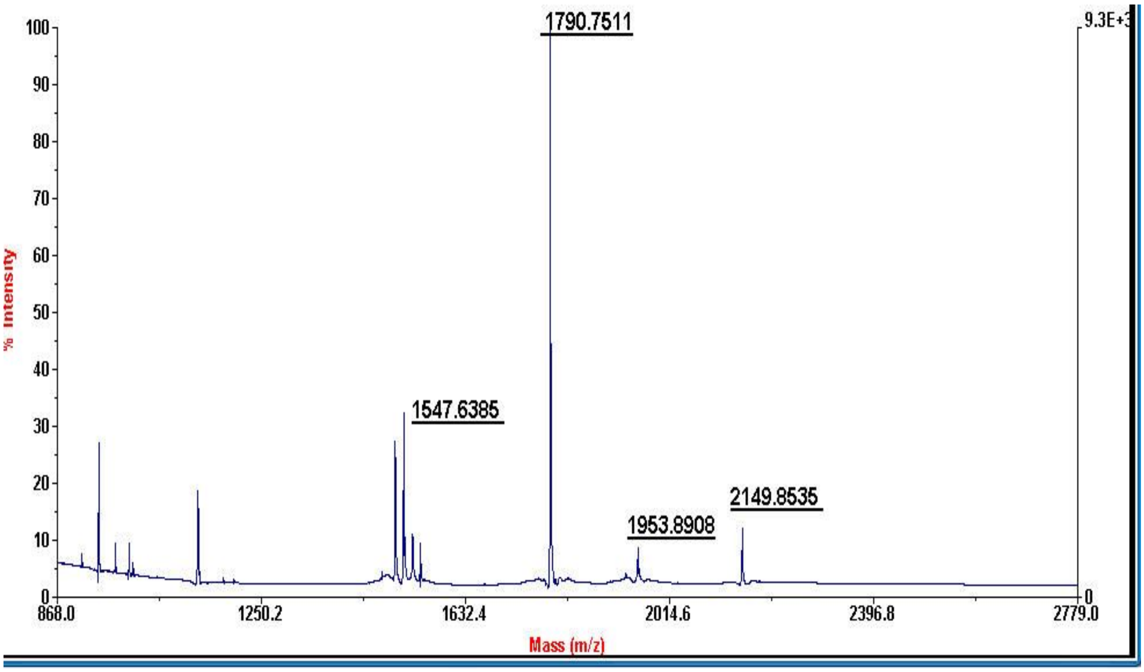
474 RuvB-like 1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
34 - 46	1300.6323	1299.6250	1299.6531	-0.0281	0	K.QAASGLVGQENAR.E
172 - 182	1276.6371	1275.6298	1275.6711	-0.0412	0	K.LDPSIFESLQK.E
183 - 201	2019.9802	2018.9729	2019.0273	-0.0543	1	K.ERVEAGDVIYIEANSGAVK.R
185 - 201	1734.8221	1733.8148	1733.8836	-0.0688	0	R.VEAGDVIYIEANSGAVK.R
206 - 225	2390.0263	2389.0190	2389.0671	-0.0481	0	R.CDTYATEFDLEAEEYVPLPK.G
318 - 333	1687.9064	1686.8992	1686.9304	-0.0313	0	R.ALESSIAPIVIFASNR.G
340 - 357	1948.9569	1947.9496	1947.9902	-0.0406	0	R.GTEDITSPHGIPLDLLDR.V
379 - 400	2324.1133	2323.1061	2323.1655	-0.0595	0	R.AQTEGINISEEALNHLGEIGTK.T
423 - 441	2281.0297	2280.0224	2280.0797	-0.0573	1	K.DSIEKEHVEEISELFYDAK.S
428 - 441	1708.7524	1707.7451	1707.7991	-0.0540	0	K.EHVEEISELFYDAK.S

No match to: 1910.8881, 1921.9467

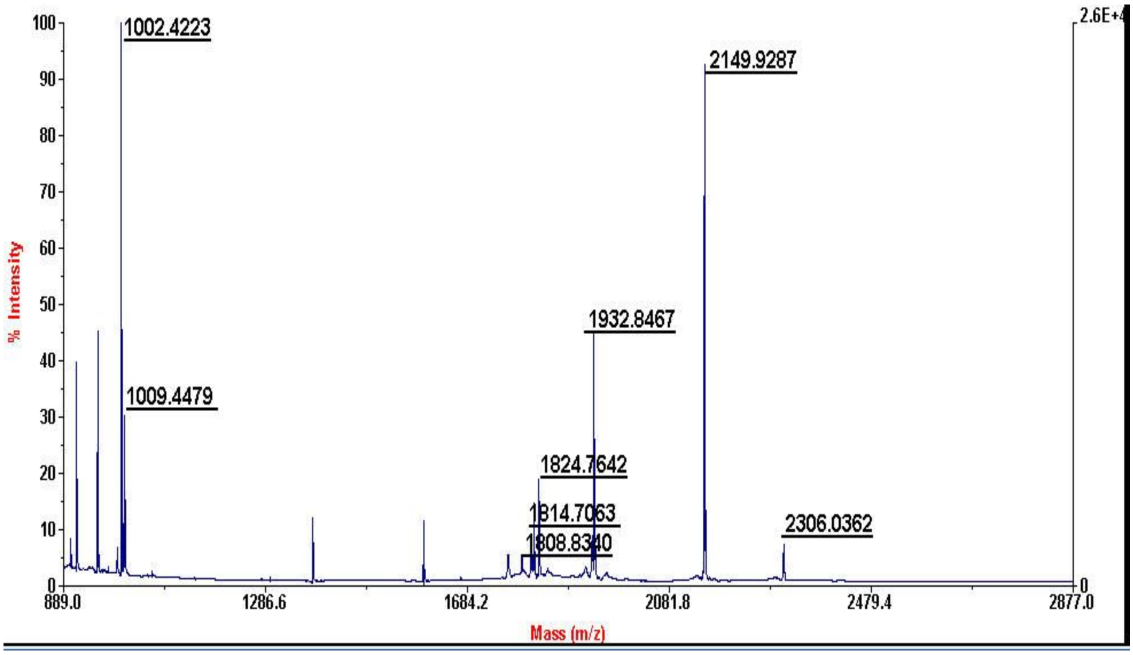
475 60S acidic ribosomal protein P2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 17	1953.8908	1952.8835	1952.9409	-0.0574	1	-.MMKYLAAYLLSTMSGNK.S 2 Oxidation (M)
2 - 17	1790.7511	1789.7438	1789.9106	-0.1668	1	M.MKYLAAYLLSTMSGNK.S
4 - 17	1547.6385	1546.6312	1546.7701	-0.1389	0	K.YLAAYLLSTMSGNK.S Oxidation (M)
23 - 42	2149.8535	2148.8462	2148.9733	-0.1271	0	K.DIEDVLGSVGLDVDMEDANK.V Oxidation (M)

No match to:1500.5941, 1516.6088, 1533.6389

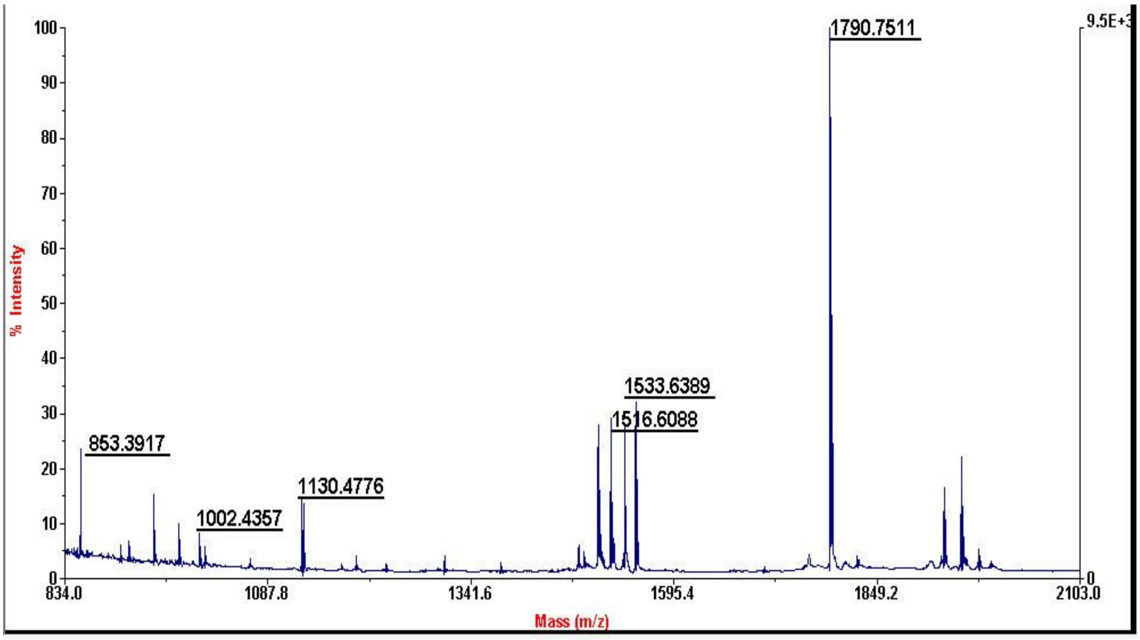
476 Glutamine synthetase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
26 - 41	1808.8340	1807.8268	1807.8927	-0.0659	0	K.VQAMYIWIDGTGEGLR.C
26 - 41	1824.7642	1823.7569	1823.8876	-0.1307	0	K.VQAMYIWIDGTGEGLR.C Oxidation (M)
107 - 114	956.4437	955.4364	955.5199	-0.0835	0	R.RPAETNLR.H
174 - 181	1002.4223	1001.4150	1001.4930	-0.0780	0	R.DIVEAHYR.A
280 - 286	1009.4479	1008.4406	1008.5366	-0.0960	1	K.RHQYHIR.A
281 - 286	853.3805	852.3732	852.4355	-0.0622	0	R.HQYHIR.A
299 - 319	2306.0362	2305.0289	2305.1199	-0.0910	1	R.RLTGFHETSNINDFSAGVANR.S
300 - 319	2149.9287	2148.9215	2149.0188	-0.0974	0	R.LTGFHETSNINDFSAGVANR.S
334 - 340	914.3578	913.3505	913.4294	-0.0788	1	K.KGYFEDR.R
341 - 357	1932.8467	1931.8394	1931.9523	-0.1129	0	R.RPSANCDPFSVTEALIR.T
358 - 372	1814.7063	1813.6990	1813.8193	-0.1202	0	R.TCLLNETGDEPFQYK.N

No match to:865.3779, 1379.5995, 1597.6643

477 Ankyrin repeat domain-containing protein 13B

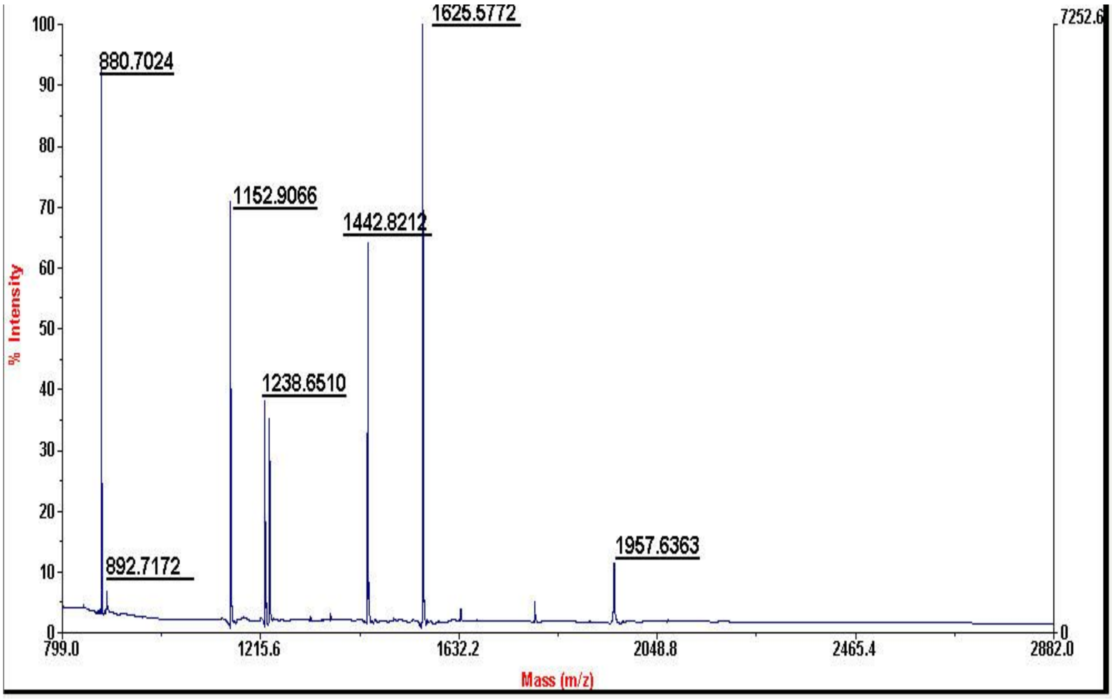


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
16 - 28	1790.7511	1789.7438	1789.9277	-0.1839	1	K.YPLHYLVWHNRHR.E
93 - 104	1516.6088	1515.6015	1515.8773	-0.2758	1	R.DLELVQLVLRYR.D
126 - 134	1130.4776	1129.4704	1129.5114	-0.0410	0	K.AQDFYVEMK.W
488 - 496	1002.4357	1001.4284	1001.4059	0.0225	0	R.GYSMMGGQR.E Oxidation (M)

552 - 559	853.3917	852.3844	852.4454	-0.0609	0	R.SAPPTPQR.Q
592 - 604	1533.6389	1532.6316	1532.7140	-0.0824	0	R.LAMELSAQEQEER.R

No match to:1500.5941, 1547.6385, 1953.8908

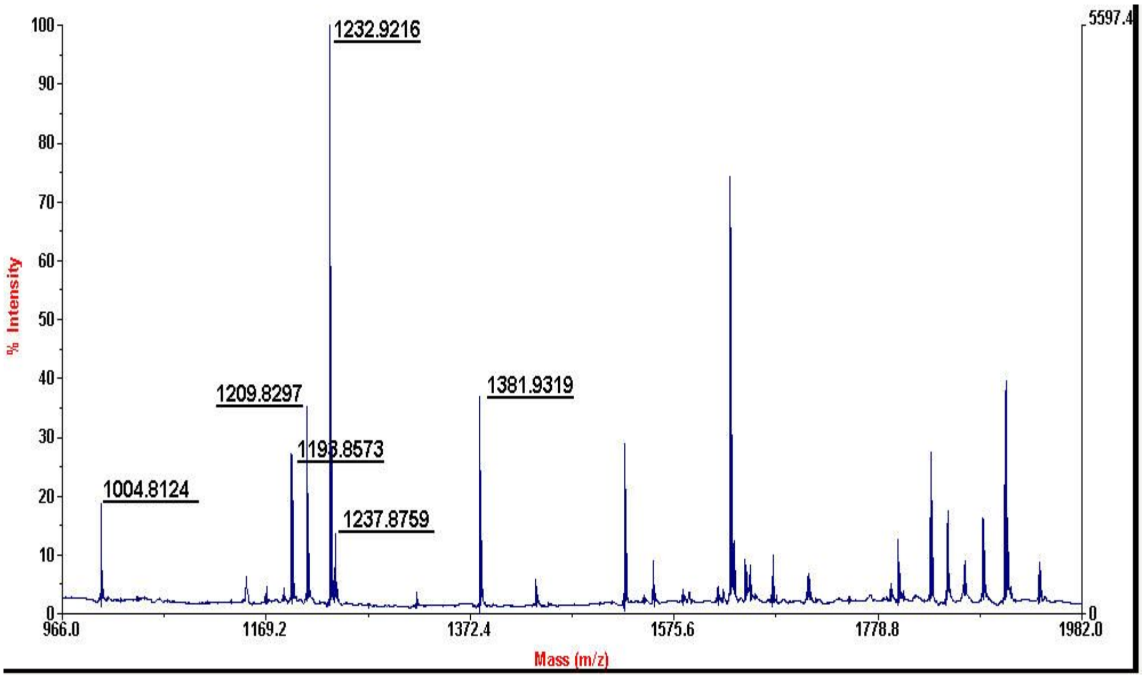
478 Tudor domain-containing protein 7



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
125 - 136	1238.6510	1237.6438	1237.6091	0.0346	0	R.QPGFASNFSVGK.K	
137 - 144	892.7172	891.7099	891.5290	0.1809	0	K.KPNPAPLR.D	
406 - 415	1152.9066	1151.8993	1151.6914	0.2079	1	K.LPLPTDKIQK.D	
658 - 674	1957.6363	1956.6290	1956.8744	-0.2454	0	K.VTNICSDGTLYCQVPCK.G	2
864 - 878	1625.5772	1624.5699	1624.6722	-0.1023	0	K.NGNMPMSGNTGENFR.K	
997 - 1003	880.7024	879.6951	879.4926	0.2025	0	K.HELVNIR.K	
1015 - 1028	1442.8212	1441.8139	1441.8293	-0.0154	0	K.LPFQAVTAQLAGVK.C	

No match to: 1224.9746, 1556.2144

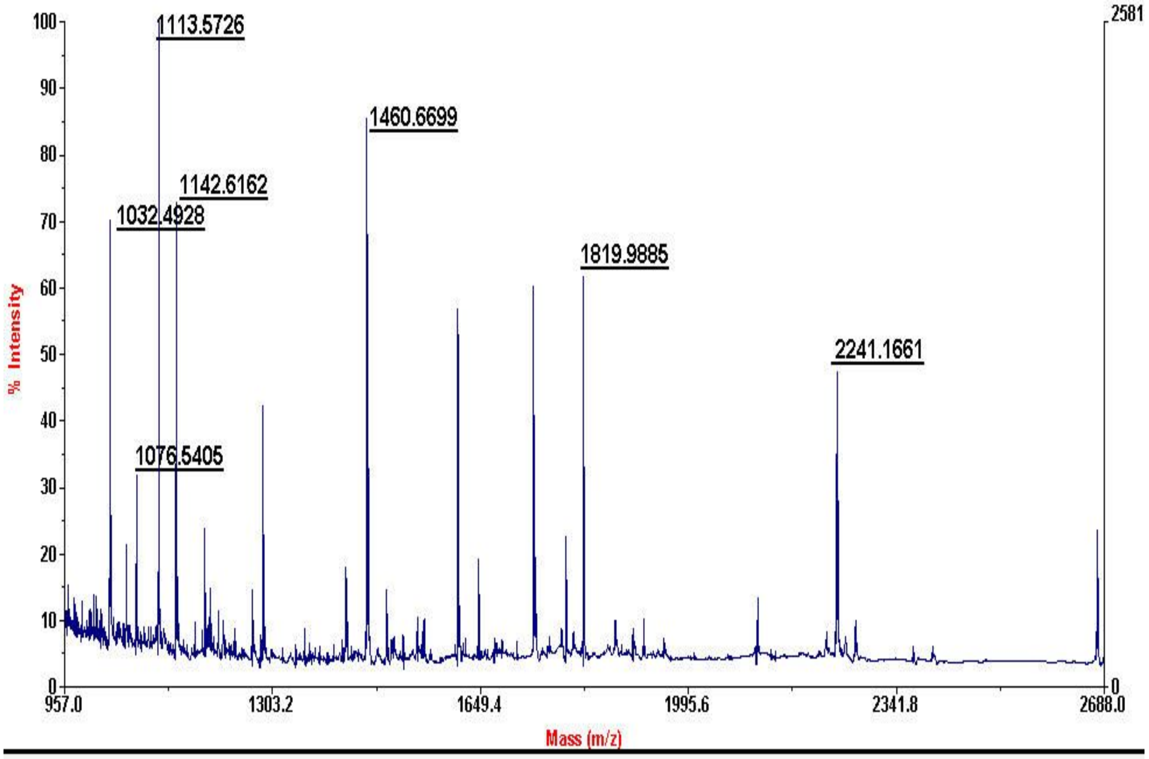
479 aminopeptidase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
177 - 188	1381.9319	1380.9246	1380.6310	0.2936	0	K.LYGSGDQEAWQK.G	
189 - 200	1232.9216	1231.9144	1231.6673	0.2471	0	K.GVLFASGQNLAR.Q	
215 - 221	849.6457	848.6384	848.4643	0.1741	0	R.FAEIIEK.N	
268 - 282	1526.0918	1525.0845	1524.7936	0.2909	0	K.GSPNANEPPLVFVGK.G	
418 - 428	1237.8759	1236.8687	1236.5986	0.2700	0	K.LFEASIETGDR.V	
432 - 440	1193.8573	1192.8501	1192.5699	0.2802	0	R.MPLFEHYTR.Q	
432 - 440	1209.8297	1208.8224	1208.5648	0.2576	0	R.MPLFEHYTR.Q	Oxidation (M)
506 - 513	1004.8124	1003.8052	1003.6066	0.1986	0	R.TLIEFLLR.F	

No match to: 1631.1433, 1831.2621, 1847.3574, 1883.3356, 1905.3339, 2056.3686, 2096.4867, 2224.6262, 3792.6709

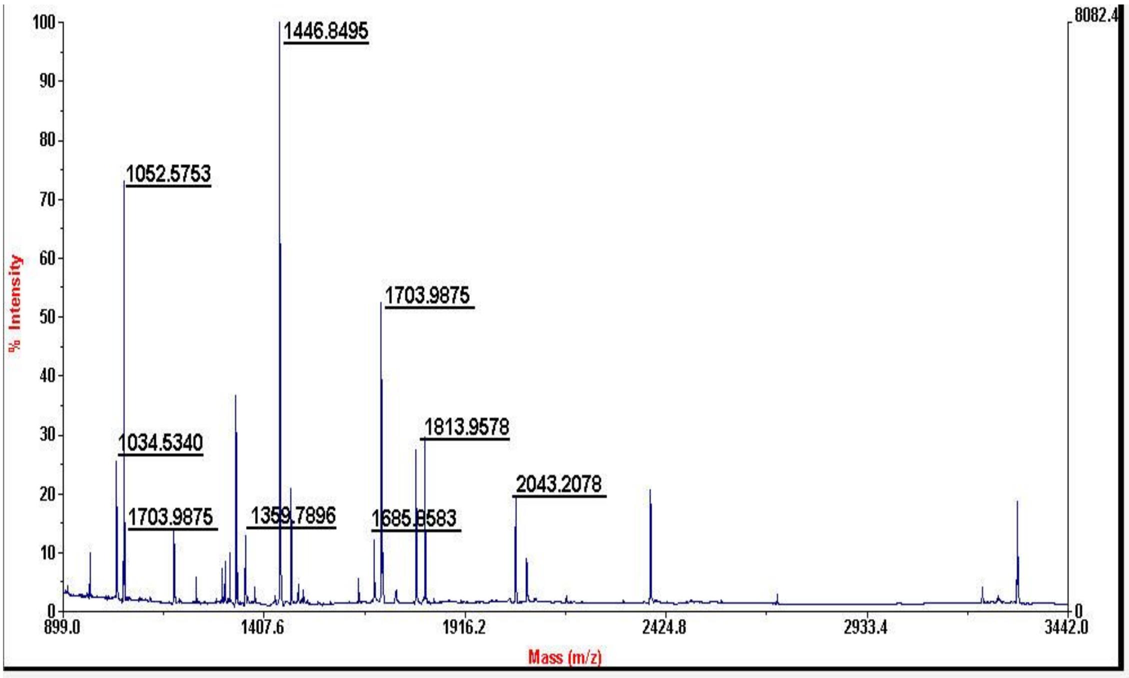
480 Fascin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 63	2241.1661	2240.1588	2240.0896	0.0692	0	K.QIWTLEQPPDEAGSAAVCLR.S
69 - 82	1611.8094	1610.8021	1610.7359	0.0663	1	R.YLAADKDGNVTCER.E
91 - 100	1142.6162	1141.6089	1141.5880	0.0209	0	R.FLIVAHDDGR.W
101 - 109	1113.5726	1112.5654	1112.5363	0.0291	0	R.WSLQSEAHR.R
111 - 118	944.4434	943.4361	943.4036	0.0326	0	R.YFGGTEDR.L
186 - 194	1076.5405	1075.5332	1075.5047	0.0286	0	R.YSVQTADHR.F
202 - 217	1819.9885	1818.9813	1818.9628	0.0184	0	R.LVARPEPATGYTLEFR.S
331 - 341	1460.6699	1459.6626	1459.6190	0.0436	0	K.NASCYFDIEWR.D
390 - 398	1032.4928	1031.4856	1031.4607	0.0249	0	R.GEHGFIGCR.K

No match to: 817.4428, 1287.6955, 1737.9261

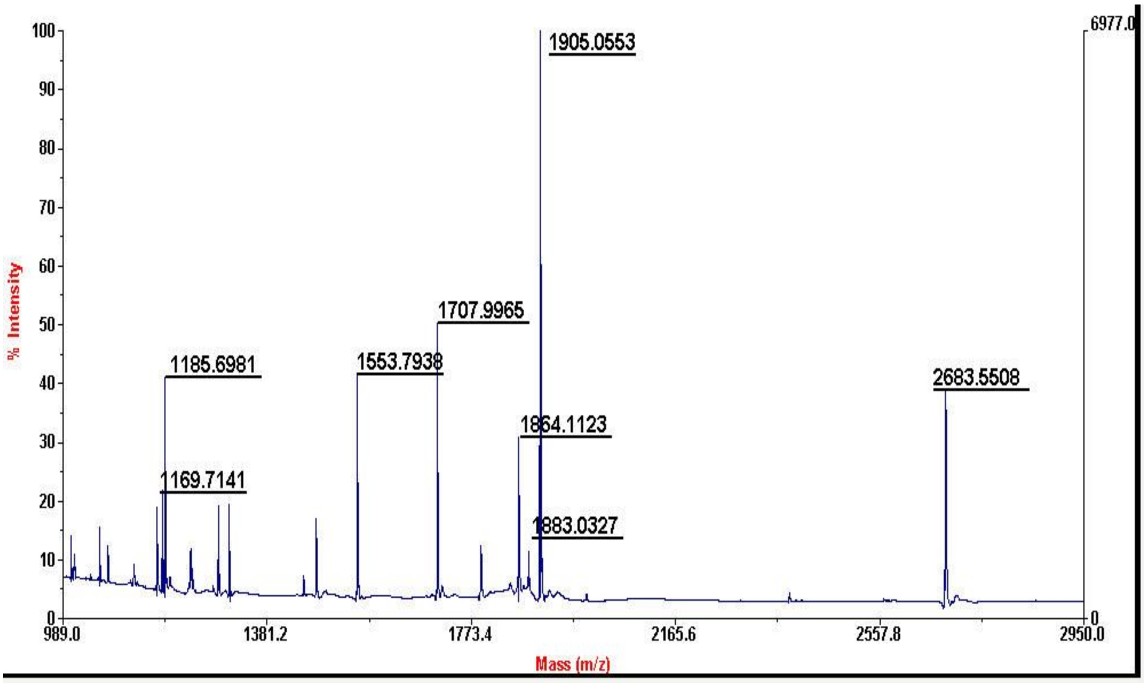
481 Annexin A11



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
192 - 204	1359.7896	1358.7823	1358.6830	0.0993	0	R.GTITDAPGFDPLR.D
192 - 210	2043.2078	2042.2005	2042.0433	0.1572	1	R.GTITDAPGFDPLRDAEVLR.K
287 - 302	1703.9875	1702.9802	1702.8560	0.1242	0	K.GVGTDEACLIEILASR.S
328 - 336	1034.5340	1033.5267	1033.4577	0.0690	0	R.SDTSGHFQR.L
360 - 371	1336.7073	1335.7001	1335.6055	0.0946	0	R.DAQELYAAGENR.L
389 - 400	1446.8495	1445.8422	1445.7415	0.1007	0	R.AHLVAVFNEYQR.M
431 - 439	1052.5753	1051.5680	1051.5087	0.0594	0	K.NTPAFFAER.L
480 - 494	1685.8583	1684.8510	1684.7329	0.1181	0	K.SLYHDISGDTSGDYR.K
480 - 495	1813.9578	1812.9505	1812.8278	0.1227	1	K.SLYHDISGDTSGDYRK.I

No match to: 1475.8669, 2072.0410, 2384.1736, 3312.6326

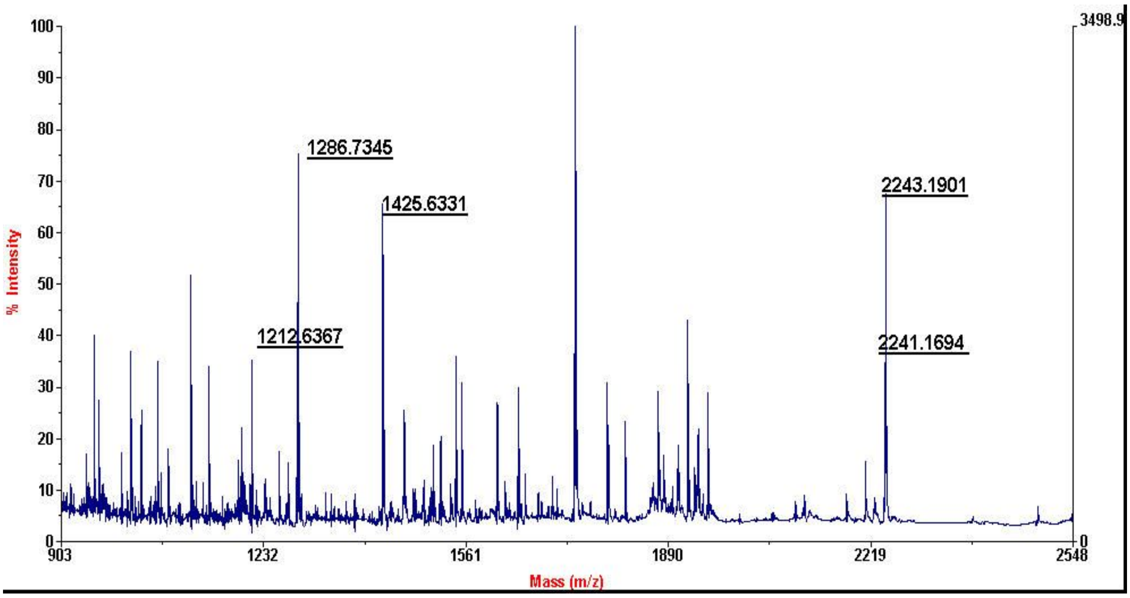
482 Alpha-aminoadipic semialdehyde dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 17	1185.6981	1184.6908	1184.6336	0.0572	1	R.ALCVHAAKTSK.L
49 - 62	1553.7938	1552.7865	1552.6542	0.1323	0	R.EENEGVYNGSWGGR.G
63 - 79	1905.0553	1904.0480	1903.9098	0.1382	0	R.GEVITTYCPANNEPIAR.V
139 - 162	2683.5508	2682.5435	2682.3211	0.2225	0	K.ILVEGVGEVQEYVDICDYAVGLSR.M
163 - 173	1169.7141	1168.7068	1168.6274	0.0794	0	R.MIGGPILPSER.S
335 - 349	1864.1123	1863.1050	1862.9751	0.1299	1	R.RLFIHESIHDEVVNR.L
336 - 349	1707.9965	1706.9893	1706.8740	0.1152	0	R.LFIHESIHDEVVNR.L
352 - 358	849.5574	848.5501	848.4868	0.0633	1	K.KAYAQIR.V
438 - 452	1883.0327	1882.0254	1881.8897	0.1357	1	K.FKNEEEVFAWNNEVK.Q

No match to: 1287.7586, 1307.8220, 1475.8734

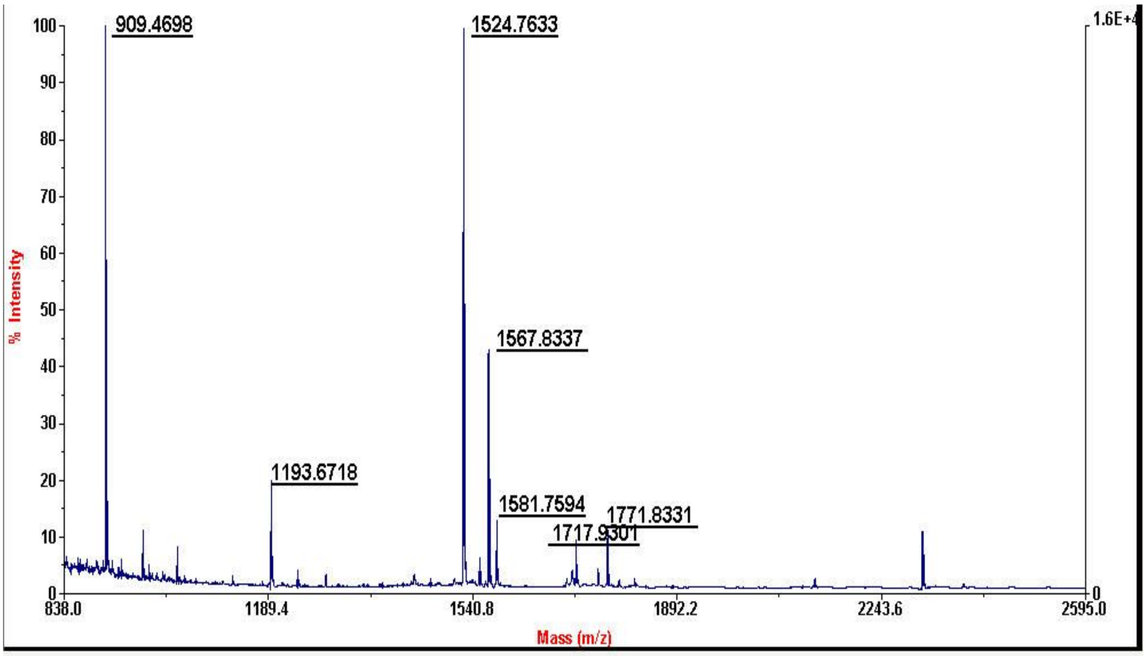
483 Y-box-binding protein 2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
117 - 127	1286.7345	1285.7272	1285.6667	0.0605	0	K.EDVFVHQTAIK.R
223 - 231	1212.6367	1211.6295	1211.5586	0.0708	0	R.WCPPPFFYR.R
223 - 232	1425.6331	1424.6259	1424.6812	-0.0553	1	R.WCPPPFFYRR.R
237 - 256	2243.1901	2242.1829	2242.1454	0.0374	1	R.GPRPPNQQQPIEGTDRVEPK.E
257 - 276	2241.1694	2240.1621	2240.0934	0.0687	1	K.ETAPLEGHQQQGDERVPPPR.F

No match to: 1059.5374, 1113.5494, 1460.6711, 1553.7533, 1645.8205, 1737.8977, 1920.9431

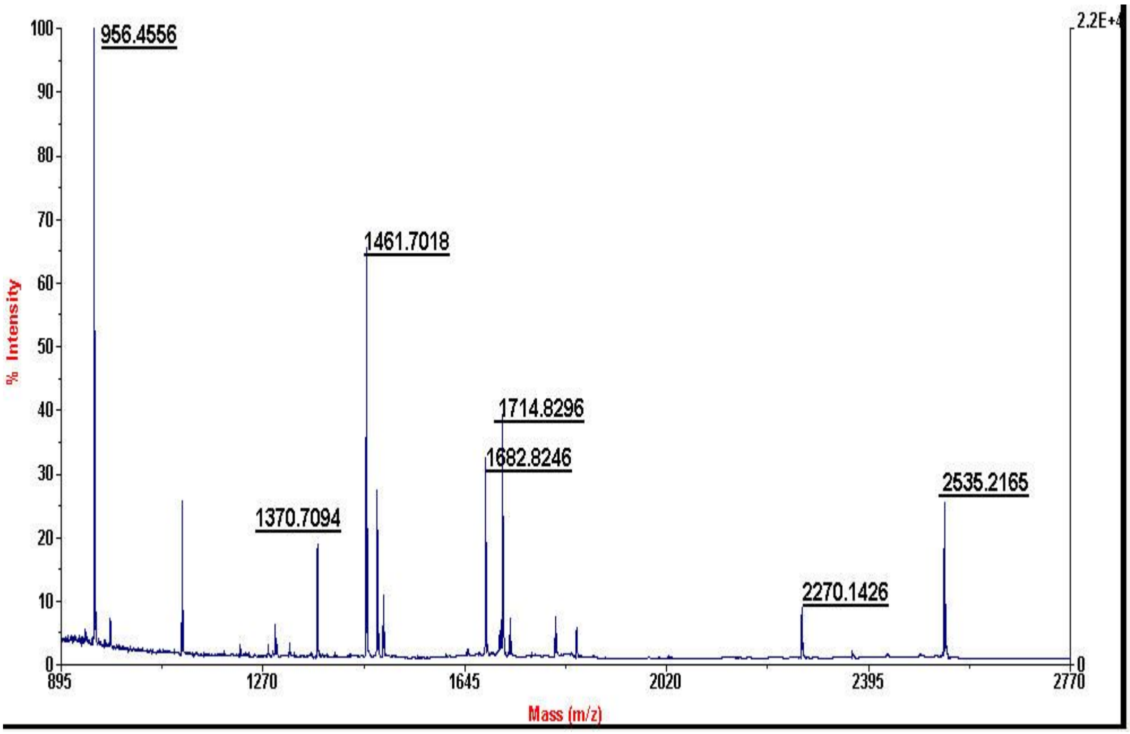
484 Dihydrolipoyl dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
90 - 104	1771.8331	1770.8258	1770.8260	-0.0002	0	K.ALLNNSHYYHMAHGK.D	Oxidation (M)
301 - 315	1717.9301	1716.9229	1716.8903	0.0326	0	K.AEVITCDVLLVCIGR.R	2
321 - 334	1567.8337	1566.8264	1566.8253	0.0011	0	K.NLGLEELGIELDPR.G	
405 - 417	1581.7594	1580.7521	1580.7569	-0.0048	1	K.SEEQLKEEGIEYK.V	
418 - 428	1193.6718	1192.6646	1192.6353	0.0293	1	K.VGKFPFAANSR.A	
421 - 428	909.4698	908.4625	908.4504	0.0121	0	K.FPFAANSR.A	
483 - 495	1524.7633	1523.7560	1523.7303	0.0257	0	R.VCHAHPTLSEAFR.E	

No match to: 973.5048, 2314.1941

485 Delta-1-pyrroline-5-carboxylate dehydrogenase

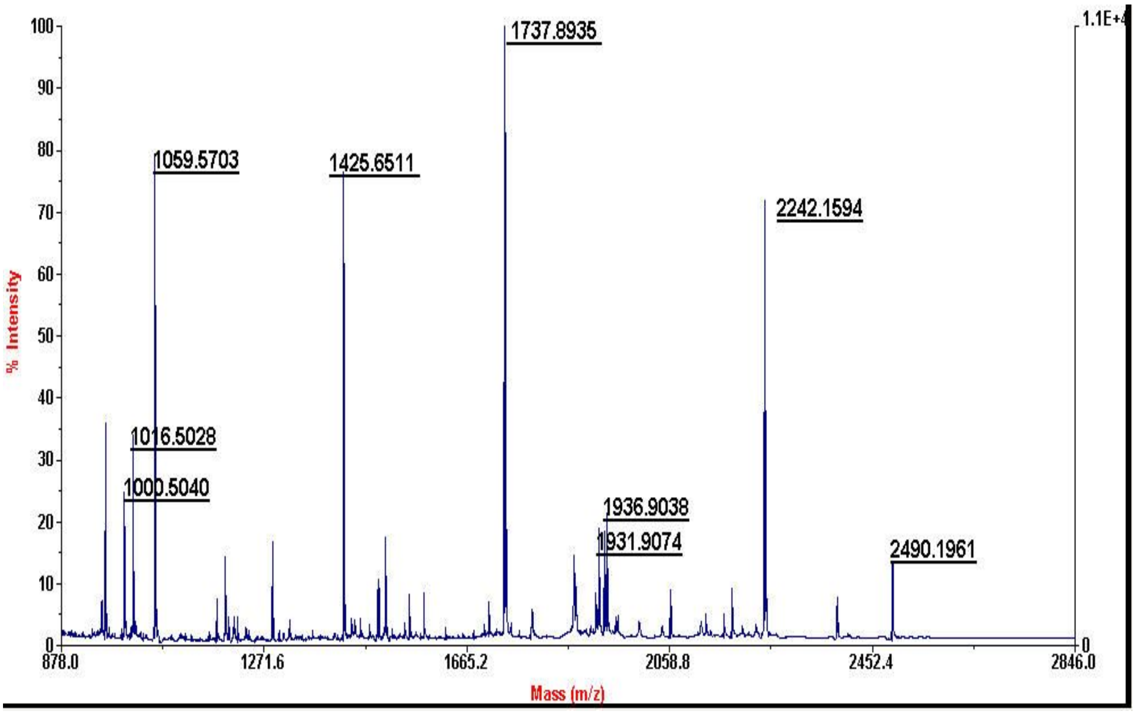


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
32 - 47	1714.8296	1713.8223	1713.8686	-0.0463	0	K.VANEPVLAFTQGSPER.D
32 - 52	2270.1426	2269.1353	2269.1702	-0.0349	1	K.VANEPVLAFTQGSPERDALQK.A
114 - 124	1370.7094	1369.7021	1369.7354	-0.0333	1	R.KEWDLKPIADR.A
176 - 198	2535.2165	2534.2093	2534.2653	-0.0560	0	K.YAVELEGQQPISVPPSTNSTVYR.G
305 - 310	804.3882	803.3809	803.4079	-0.0269	0	R.FHTFPR.L

319 - 325	956.4556	955.4484	955.4777	-0.0293	0	K.NFHFVHR.S
403 - 408	811.3959	810.3886	810.4137	-0.0251	0	K.WLEHAR.S
510 - 524	1461.7018	1460.6945	1460.7372	-0.0427	0	K.STGSIVGQQPFGGAR.A
525 - 540	1682.8246	1681.8173	1681.8536	-0.0363	0	R.ASGTNDKPGGPHYILR.W

No match to: 1119.5353, 1481.7066, 1493.6728

486 Glutamate dehydrogenase 1

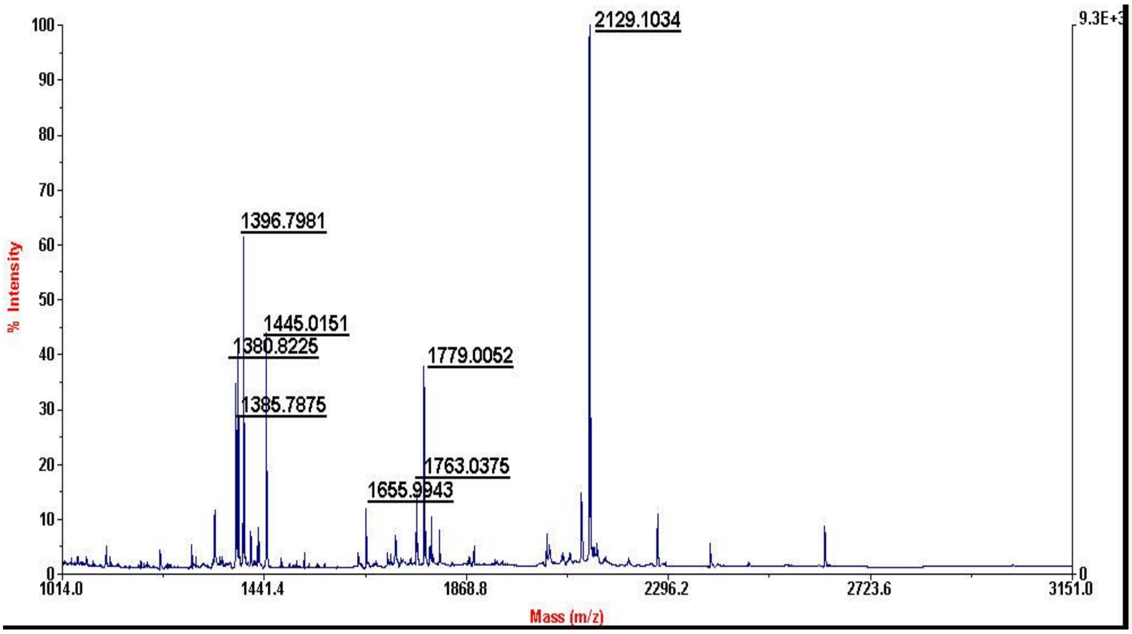


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
69 - 76	1000.5040	999.4968	999.4484	0.0483	0	K.MVEGFFDR.G	
69 - 76	1016.5028	1015.4955	1015.4433	0.0522	0	K.MVEGFFDR.G	Oxidation (M)
125 - 136	1425.6511	1424.6439	1424.6208	0.0230	0	R.DDGSWEVIEGYR.A	
137 - 143	863.4567	862.4494	862.4158	0.0336	0	R.AQHSQHR.T	
213 - 231	1931.9074	1930.9001	1930.9095	-0.0094	0	K.GFIGPGIDVPAPDMSTGER.E	Oxidation (M)
364 - 386	2490.1961	2489.1889	2489.2359	-0.0470	0	K.AKPYEGSILEADCDILIPAASEK.Q	
400 - 420	2242.1594	2241.1521	2241.1641	-0.0120	1	K.IIAEGANGPTTPEADKIFLER.N	
445 - 453	1059.5703	1058.5630	1058.5257	0.0373	0	K.NLNHVSYGR.L	
461 - 476	1920.9126	1919.9053	1919.9047	0.0007	0	R.DSNYHLLMSVQESLER.K	

461 - 476	1936.9038	1935.8965	1935.8996	-0.0031	0	R.DSNYHLLMSVQESLER.K	Oxidation (M)
481 - 496	1737.8935	1736.8862	1736.8846	0.0016	0	K.HGGTIPIVPTAEFQDR.I	
528 - 535	963.5728	962.5655	962.5185	0.0470	0	K.YNLGLDLR.T	

No match to: 1286.7326, 1739.8467

487 UPF0027 protein C22orf28

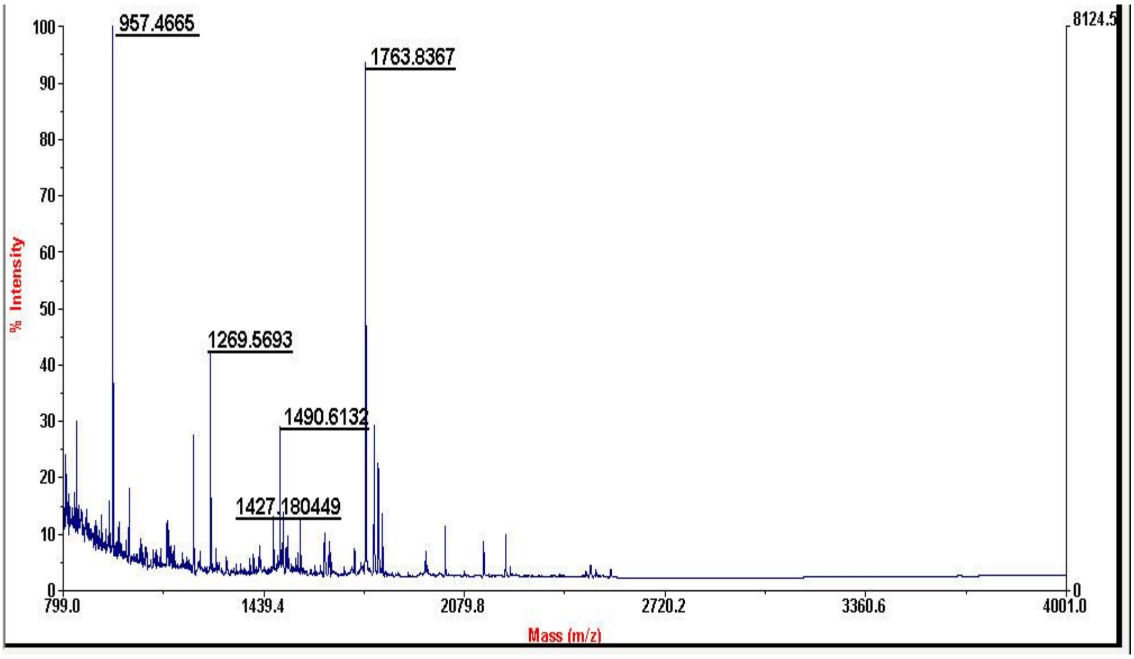


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
4 - 14	1385.7875	1384.7802	1384.6510	0.1292	0	R.SYNDELQFLEK.I	
45 - 51	953.5766	952.5693	952.4688	0.1005	0	K.LMFEELR.N	Oxidation (M)
68 - 81	1445.0151	1444.0079	1443.8310	0.1768	0	K.QIGNVAALPGIVHR.S	
167 - 181	1763.0375	1762.0302	1761.8243	0.2059	0	K.DLEEALEMGVDWSLR.E	
167 - 181	1779.0052	1777.9979	1777.8192	0.1787	0	K.DLEEALEMGVDWSLR.E	Oxidation (M)
182 - 198	2129.1034	2128.0961	2127.8592	0.2369	1	R.EGYAWAEDKEHCEEYGR.M	
264 - 279	1655.9943	1654.9870	1654.8349	0.1521	0	R.GLGHQVATDALVAMEK.A	Oxidation (M)
309 - 321	1380.8225	1379.8152	1379.6404	0.1748	0	K.GMAAAGNYAWVNR.S	

309 - 321	1396.7981	1395.7909	1395.6353	0.1555	0	K.GMAAAGNYAWVNR.S	Oxidation (M)

No match to: 1336.3818, 2111.1168

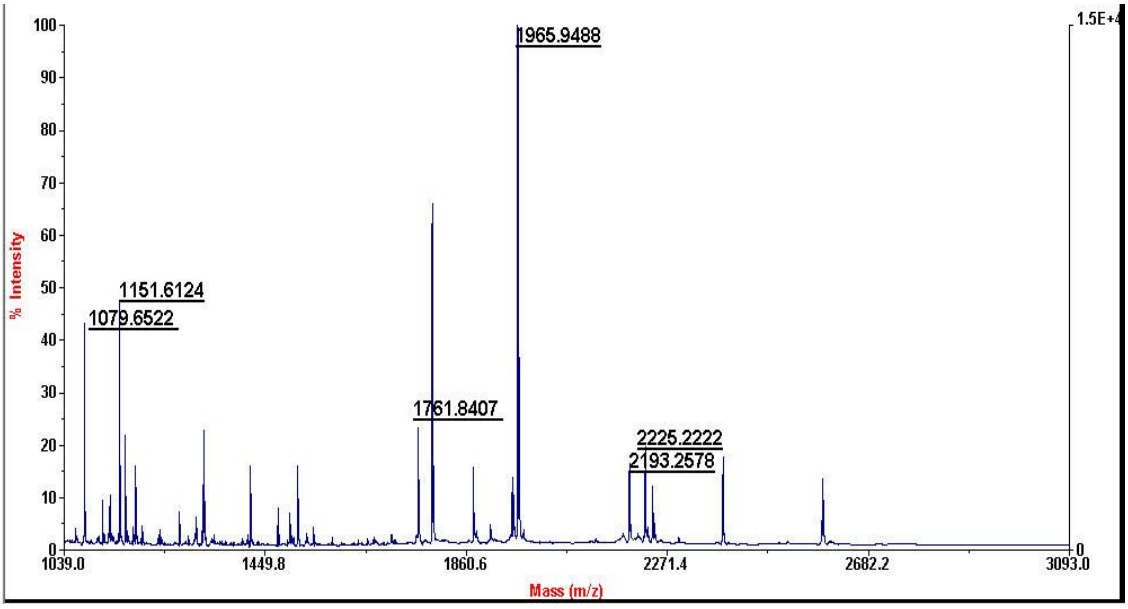
488 Fumarate hydratase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
52 - 61	1214.5462	1213.5389	1213.5867	-0.0477	0	R.IEYDTFGELK.V
67 - 74	957.4665	956.4592	956.4716	-0.0124	0	K.YYGAQTVR.S
102 - 115	1490.6132	1489.6059	1489.7049	-0.0989	0	R.AAAEVNQDYGLDPK.I
173 - 183	1269.5693	1268.5620	1268.6626	-0.1005	0	K.IPVHPNDHVNK.S
269 - 286	1763.8367	1762.8294	1762.9214	-0.0919	0	R.IYELAAGGTAVGTGLNTR.I

No match to: 1469.7050, 1804.8531, 1816.7826

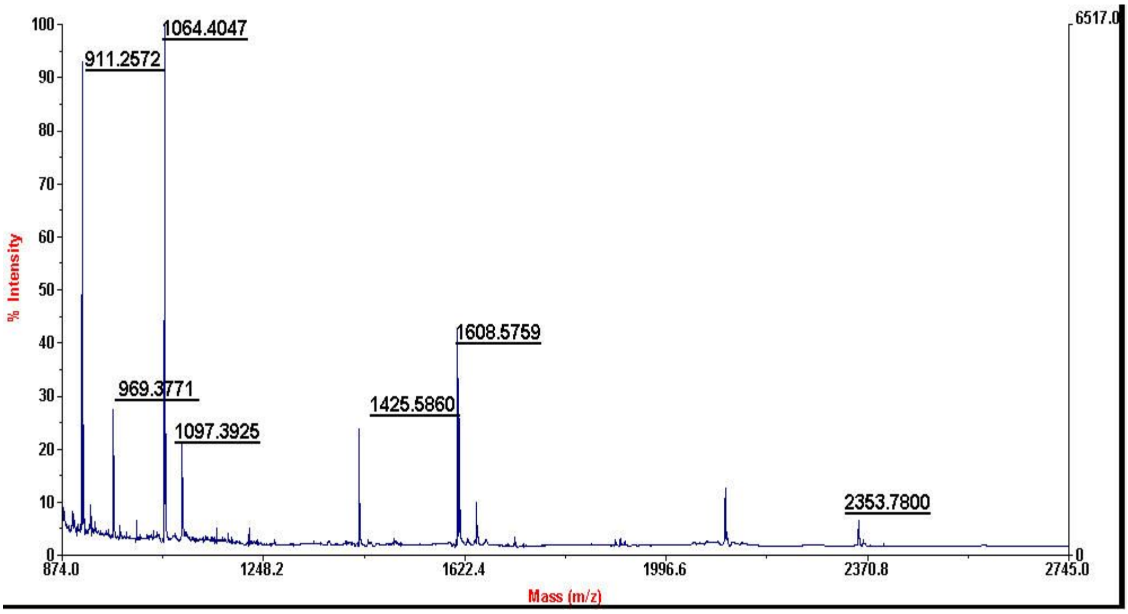
489 Thioredoxin domain-containing protein 5



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
95 - 113	2225.2222	2224.2149	2224.0106	0.2043	1	R.LQPTWNDLGDKYNSMEDAK.V	
119 - 134	1761.8407	1760.8334	1760.7570	0.0764	0	K.VDCTAHSDVCSAQGVR.G	2
222 - 241	2193.2578	2192.2505	2192.1477	0.1028	0	K.ALAPTWEQLALGLEHSETVK.I	
245 - 260	1965.9488	1964.9415	1964.8469	0.0946	0	K.VDCTQHYELCSGNQVR.G	2
288 - 296	1151.6124	1150.6052	1150.5618	0.0433	0	R.EYVESQLQR.T	
376 - 385	1163.5874	1162.5801	1162.5288	0.0513	0	K.IAEVDCTAER.N	
395 - 403	1079.6522	1078.6449	1078.6175	0.0274	0	R.GYPTLLLFR.G	

No match to: 1184.6773, 1323.5758, 1419.8079, 1790.9696, 1874.9409, 2384.0851, 2587.3215

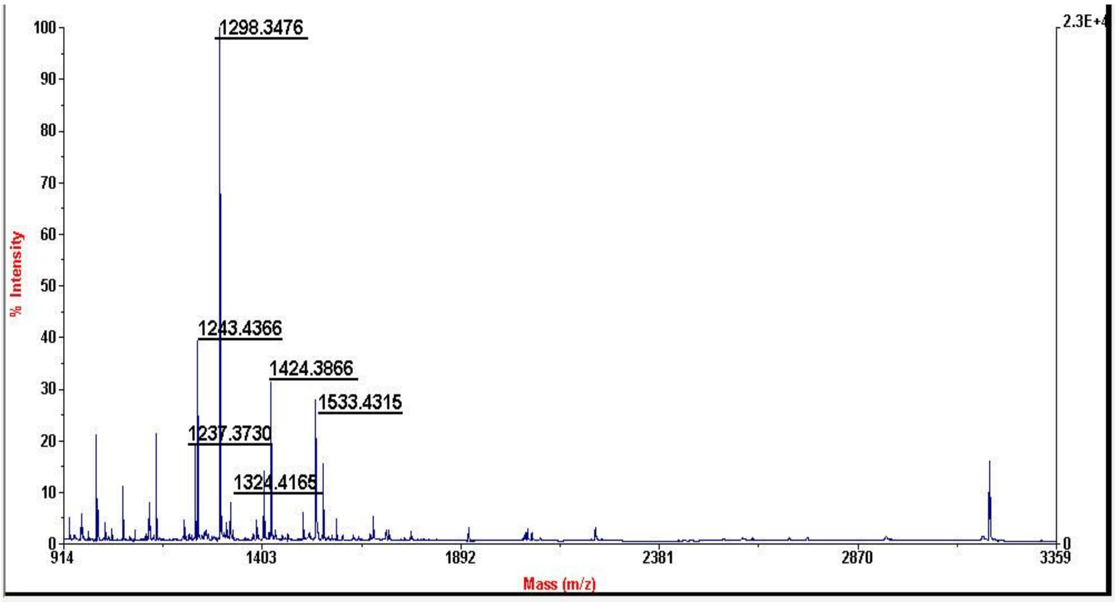
490 NADH-ubiquinone oxidoreductase 75 kDa



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
63 - 68	911.2572	910.2499	910.3756	-0.1256	0	R.FCYHER.L	
185 - 200	1608.5759	1607.5687	1607.7791	-0.2105	0	R.FASEIAGVDDLGTTGR.G	
292 - 299	969.3771	968.3698	968.5080	-0.1381	1	R.FAYDGLKR.Q	
361 - 382	2353.7800	2352.7727	2353.0744	-0.3017	0	R.VDSDTLCTEEVFPTAGAGTDLR.S	
409 - 417	1064.4047	1063.3974	1063.5451	-0.1477	0	R.FEAPLFNAR.I	
502 - 511	1097.3925	1096.3852	1096.4859	-0.1007	0	R.MTSGVTGDWK.V	Oxidation (M)
644 - 655	1425.5860	1424.5787	1424.7735	-0.1948	1	R.NRLEEVSPNLVR.Y	

No match to: 2105.6000

491 Lamin-B2

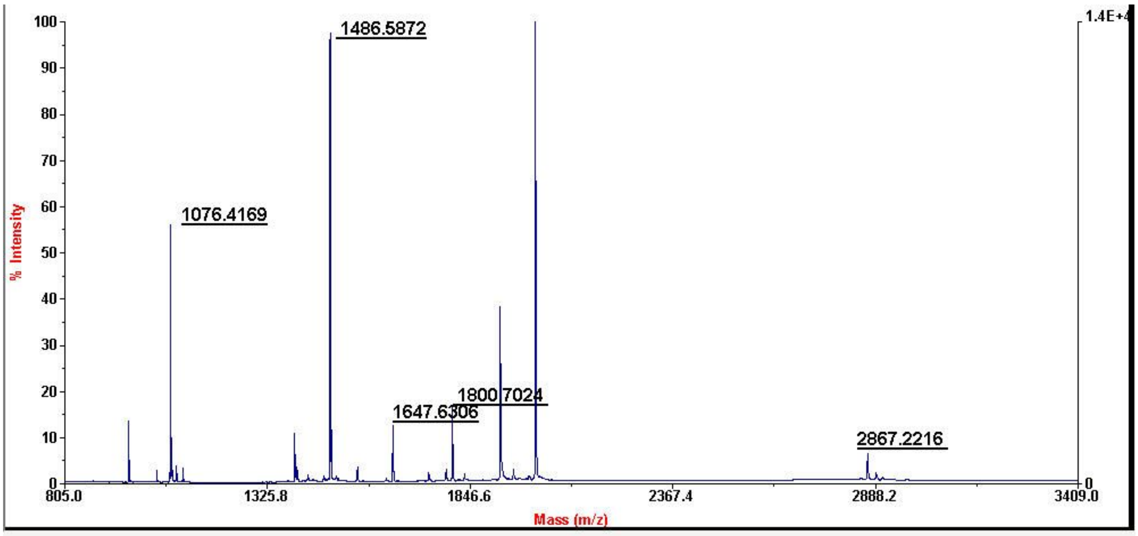


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

74 - 84	1237.3730	1236.3658	1236.5986	-0.2328	0	K.ALYESELADAR.R	
129 - 138	1243.4366	1242.4293	1242.6721	-0.2428	1	R.VKDLESLFHR.S	
192 - 202	1424.3866	1423.3793	1423.6402	-0.2608	0	R.CQSLQEELDFR.K	
204 - 211	994.3283	993.3210	993.4767	-0.1557	0	K.SVFEEEVR.E	
362 - 372	1324.4165	1323.4092	1323.6492	-0.2400	0	K.LALDMEINAYR.K	Oxidation (M)
470 - 482	1533.4315	1532.4243	1532.6968	-0.2725	1	K.NNSDKDQSLGNWR.I	
530 - 541	1298.3476	1297.3403	1297.5687	-0.2284	0	K.GQSSWGTGESFR.T	

No match to: 1117.3881, 1675.5382, 3192.6775

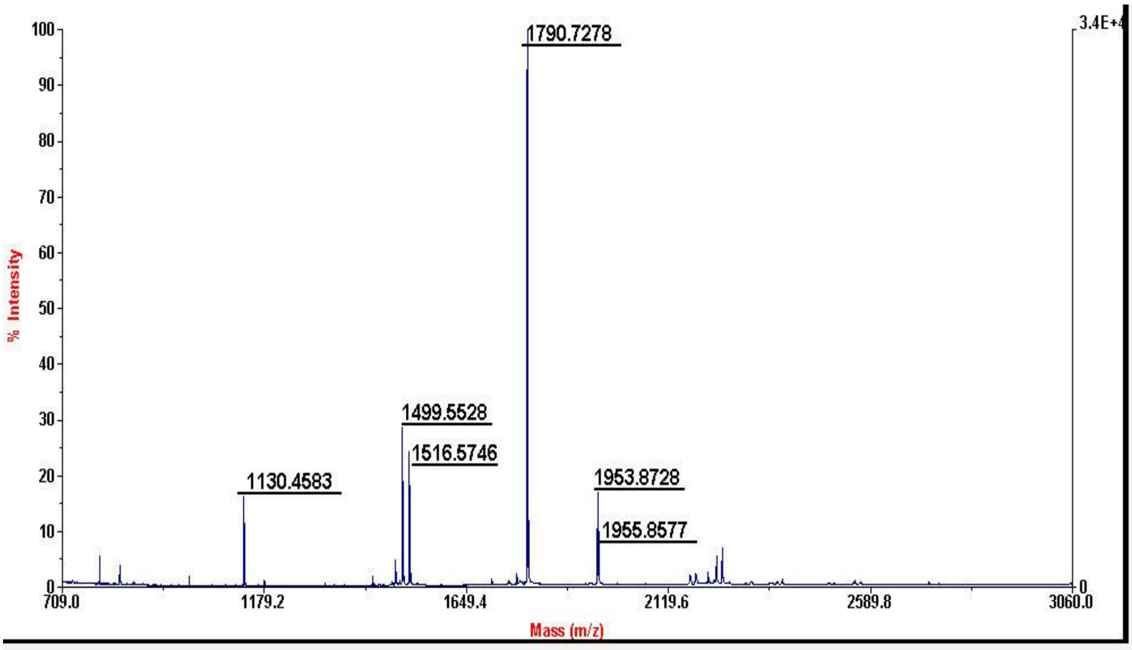
492 Galectin-1



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
38 - 49	1486.5872	1485.5800	1485.6783	-0.0983	0	K.DSNNLCLHFNPR.F	
50 - 64	1647.6306	1646.6234	1646.7471	-0.1237	0	R.FNAHGDANTIVCNSK.D	
65 - 74	1076.4169	1075.4096	1075.4683	-0.0587	0	K.DGGAWGTEQR.E	
75 - 100	2867.2216	2866.2144	2866.4212	-0.2068	0	R.EAVFPFQPGSVAEVCITFDQANLTVK.L	
113 - 128	1800.7024	1799.6951	1799.8400	-0.1449	0	R.LNLEAINYMAADGDFK.I	Oxidation (M)

No match to: 1395.6050, 1922.8754, 2013.9011

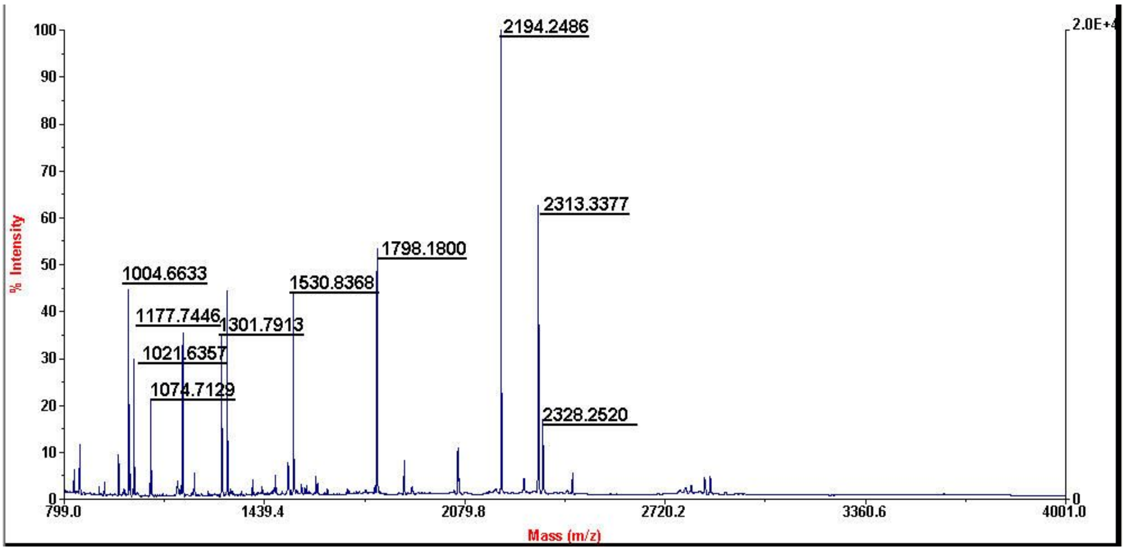
493 Chloride transport protein 6



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
2 - 13	1516.5746	1515.5674	1515.5622	0.0052	1	M.AGCRGSLCCCCR.W	5
6 - 21	1955.8577	1954.8504	1954.6316	0.2188	1	R.GSLCCCCRWCCCCGER.E	3
14 - 21	1130.4583	1129.4511	1129.3562	0.0949	0	R.WCCCCGER.E	3
56 - 71	1953.8728	1952.8655	1952.8859	-0.0204	0	R.CINDPYLEVLETMDNK.K	
584 - 598	1790.7278	1789.7205	1789.8444	-0.1239	0	R.GVPLLEWETEVEMDK.L	Oxidation (M)
675 - 687	1499.5528	1498.5456	1498.7086	-0.1630	1	R.SQSMKSYPSSELR.N	

No match to: 1500.5726

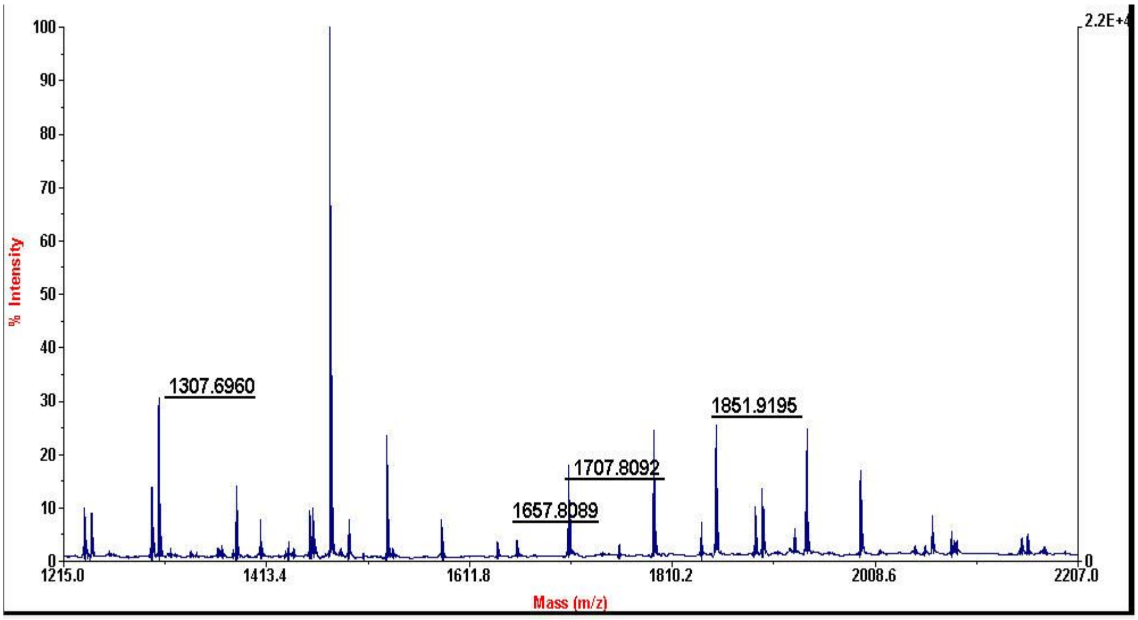
494 Collagen alpha-2



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
96 - 115	2194.2486	2193.2413	2193.0127	0.2286	0	R.YGGLHFSDQVEVFSPPGSDR.A
121 - 129	1021.6357	1020.6284	1020.5352	0.0932	0	K.NLQGISSFR.R
121 - 130	1177.7446	1176.7374	1176.6363	0.1010	1	K.NLQGISSFRR.G
187 - 202	1798.1800	1797.1727	1796.9897	0.1830	1	R.LFAVAPNQNLKEQGLR.D
203 - 213	1301.7913	1300.7841	1300.6411	0.1429	0	R.DIASTPHELYR.N
214 - 233	2328.2520	2327.2447	2327.0223	0.2224	0	R.NDYATMLPDSTEIDQDTINR.I
Oxidation (M)						
636 - 644	1074.7129	1073.7057	1073.5982	0.1075	0	K.NFVINVVNR.L
855 - 862	1004.6633	1003.6561	1003.5563	0.0998	1	R.FVEQVARR.L
994 - 1013	2313.3377	2312.3304	2312.0862	0.2442	1	R.AAVFHEKDYDSLAQPGFFDR.F
1001 - 1013	1530.8368	1529.8295	1529.6787	0.1508	0	K.DYDSLAQPGFFDR.F

No match to: 1319.7812

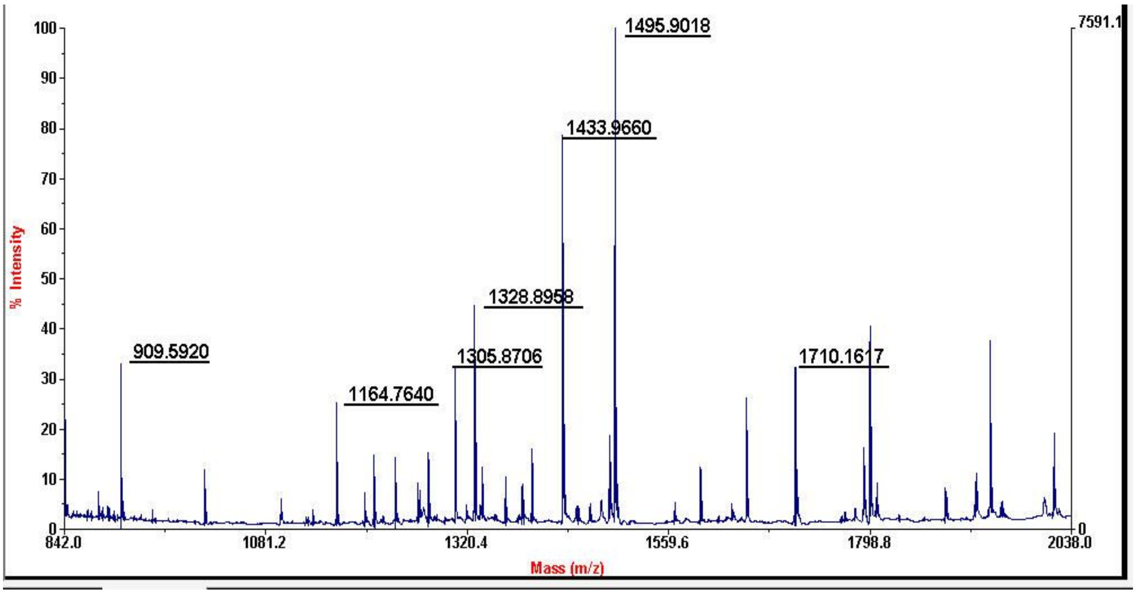
495 Ras-related protein Rab-3D



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
25 - 41	1851.9195	1850.9122	1851.0618	-0.1496	1	K.LLLIGNSSVGKTSFLFR.Y	
84 - 93	1307.6960	1306.6887	1306.6670	0.0218	1	R.YRTITTAYYR.G	
122 - 136	1707.8092	1706.8020	1706.8628	-0.0608	0	K.TYSWDNAQVILVGNK.C	
203 - 219	1657.8089	1656.8016	1656.6872	0.1144	0	K.GPAVGDAPAPQPSSCSC.-	2

No match to: 1638.8456, 1791.7115, 1897.8929

496 26S protease regulatory subunit S10B

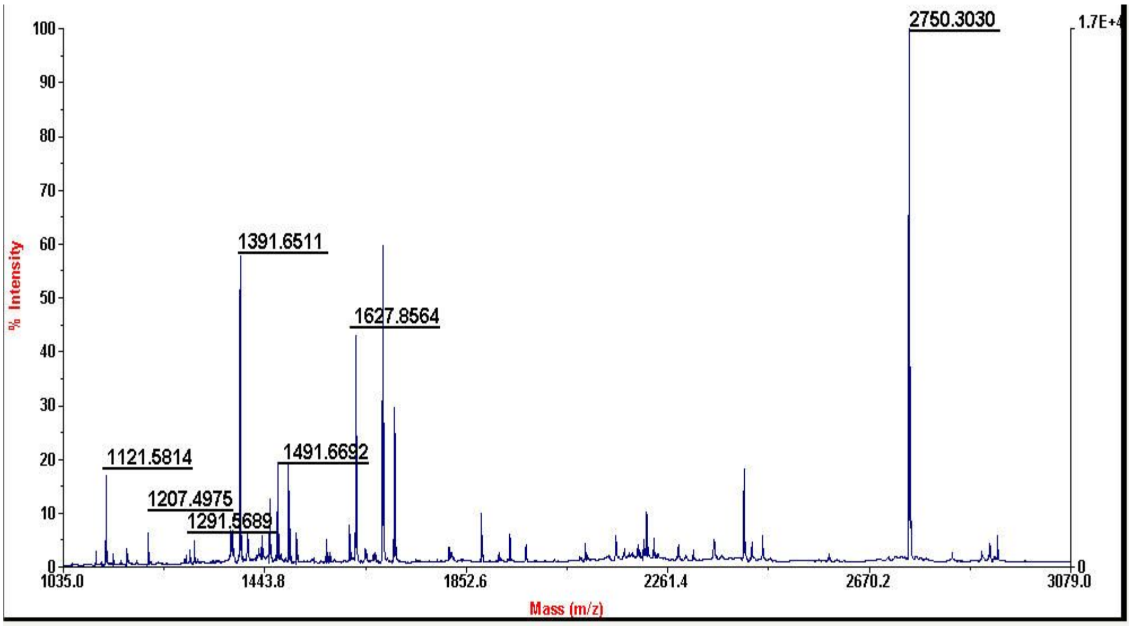


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

79 - 85	909.5920	908.5847	908.4651	0.1197	1	R.YVVGCRR.Q	
198 - 213	1710.1617	1709.1544	1708.8996	0.2549	1	K.VVSSSIVDKYIGESAR.L	
214 - 223	1328.8958	1327.8885	1327.6707	0.2179	1	R.LIREMFNYAR.D	Oxidation (M)
243 - 255	1495.9018	1494.8946	1494.7063	0.1883	1	R.FSEGTSADREIQR.T	
298 - 309	1433.9660	1432.9587	1432.7786	0.1801	1	R.KIHIDLPNEQAR.L	
299 - 309	1305.8706	1304.8633	1304.6837	0.1796	0	K.IHIDLPNEQAR.L	
334 - 344	1164.7640	1163.7568	1163.5571	0.1997	0	K.LSDGFNGADLR.N	

No match to: 1489.0929, 1798.2945, 1941.2550, 2066.3008, 2196.5953

497 Aflatoxin B1 aldehyde reductase member 3

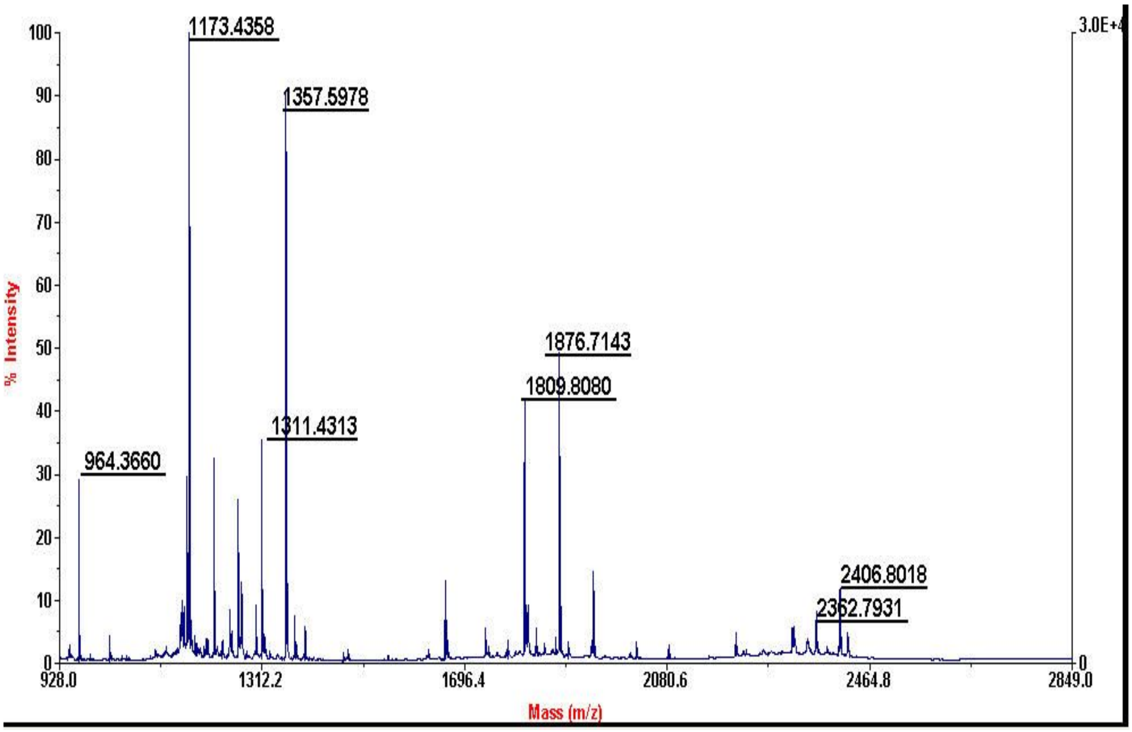


Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
8 - 21	1491.6692	1490.6620	1490.7334	-0.0714	0	R.ARPATVLGAMEMGR.R	2 Oxidation (M)
22 - 33	1291.5689	1290.5616	1290.6350	-0.0734	1	R.RMDAPTSAAVTR.A	Oxidation (M)
39 - 64	2750.3030	2749.2958	2749.3559	-0.0601	0	R.GHTEIDTAFVYSEGQSETILGGLGLR.L	
78 - 92	1627.8564	1626.8491	1626.9093	-0.0602	0	K.AIPLFGNSLKPDSLR.F	
93 - 101	1121.5814	1120.5742	1120.6240	-0.0499	1	R.FQLETSLKR.L	
101 - 106	829.4280	828.4207	828.4388	-0.0181	1	K.RLQCPR.V	

127 - 136	1207.4975	1206.4902	1206.5564	-0.0661	0	R.ACHQLHQEGK.F
178 - 188	1391.6511	1390.6439	1390.6915	-0.0476	0	R.QVETELFPCLR.H

No match to: 892.4615, 944.5231, 1374.6338, 1507.6752, 1682.8009, 1706.8011

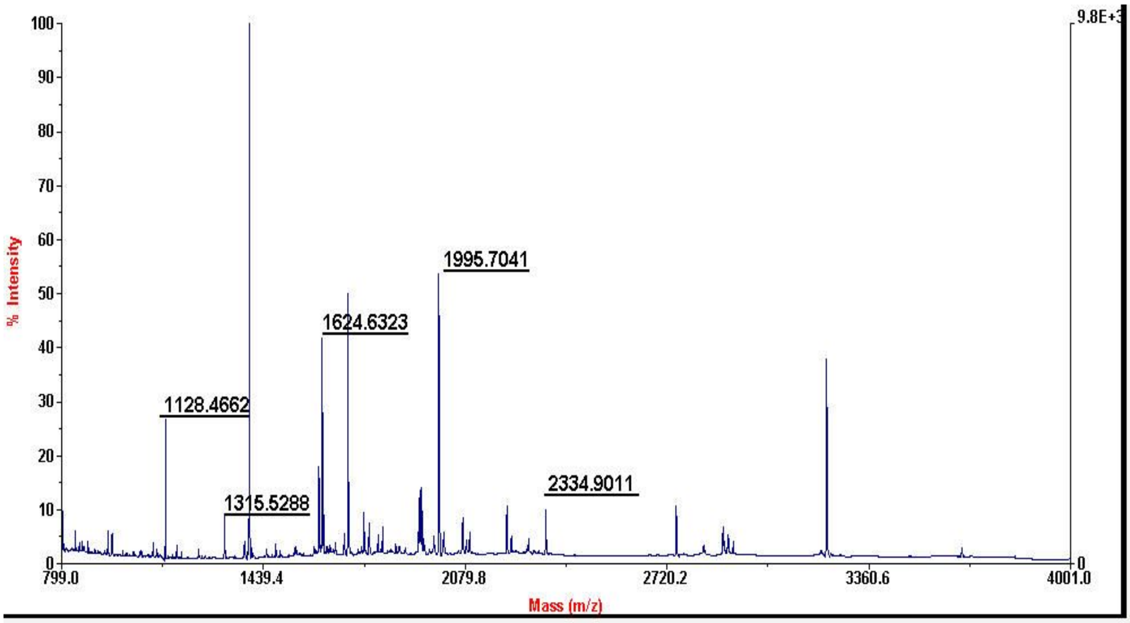
498 Ester hydrolase C11orf54



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 51	964.3660	963.3587	963.5066	-0.1478	0	K.EPFTFPVK.G
59 - 75	1809.8080	1808.8007	1809.0400	-0.2393	0	R.IAEVGGVPYLLPLVNQK.K
149 - 169	2362.7931	2361.7858	2362.0834	-0.2976	0	K.CHDFQCALLANLFASEGQPGK.V 2
179 - 189	1311.4313	1310.4241	1310.6111	-0.1871	0	R.TGPLNFVTCMR.E ; Oxidation (M)
195 - 211	1876.7143	1875.7070	1875.9665	-0.2595	0	K.HYGNKPIGMGGTFIIQK.G Oxidation (M)
216 - 236	2406.8018	2405.7946	2406.0468	-0.2522	0	K.SHIMPAEFSSCPLNSDEEVNK.W ; Oxidation (M)
245 - 256	1357.5978	1356.5906	1356.7588	-0.1682	0	K.APLVCLPVFVSR.D
257 - 263	819.2908	818.2835	818.3923	-0.1088	0	R.DPGFDLR.L
264 - 272	1173.4358	1172.4286	1172.5727	-0.1441	0	R.LEHTHFFSR.H

No match to: 1220.4209, 1266.5961, 1659.6312, 1939.7709, 2263.5245

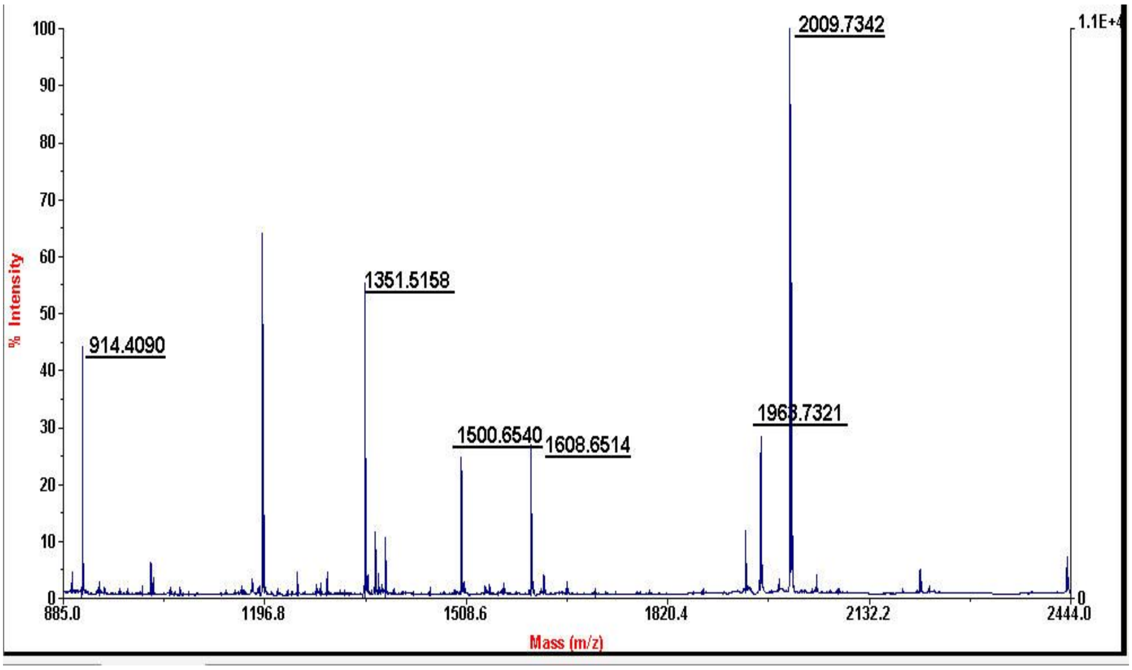
499 UDP-glucose 4-epimerase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
41 - 51	1128.4662	1127.4590	1127.6047	-0.1458	1	R.GGGSLPESLRR.V	
59 - 75	1995.7041	1994.6968	1994.9255	-0.2287	0	R.SVEFEEMDILDQGALQR.L	Oxidation (M)
93 - 106	1624.6323	1623.6251	1623.8257	-0.2006	0	K.AVGESVQKPLDYYR.V	
160 - 169	1315.5288	1314.5215	1314.6642	-0.1427	1	K.SKFFIEEMIR.D	Oxidation (M)
266 - 286	2334.9011	2333.8939	2334.1236	-0.2297	0	R.IYNLGTGTGYSVLQMVQAMEK.A	2 Oxidation (M)

No match to: 1393.5314, 1615.6615, 1706.6511, 1757.6643, 2010.1068, 2210.8630

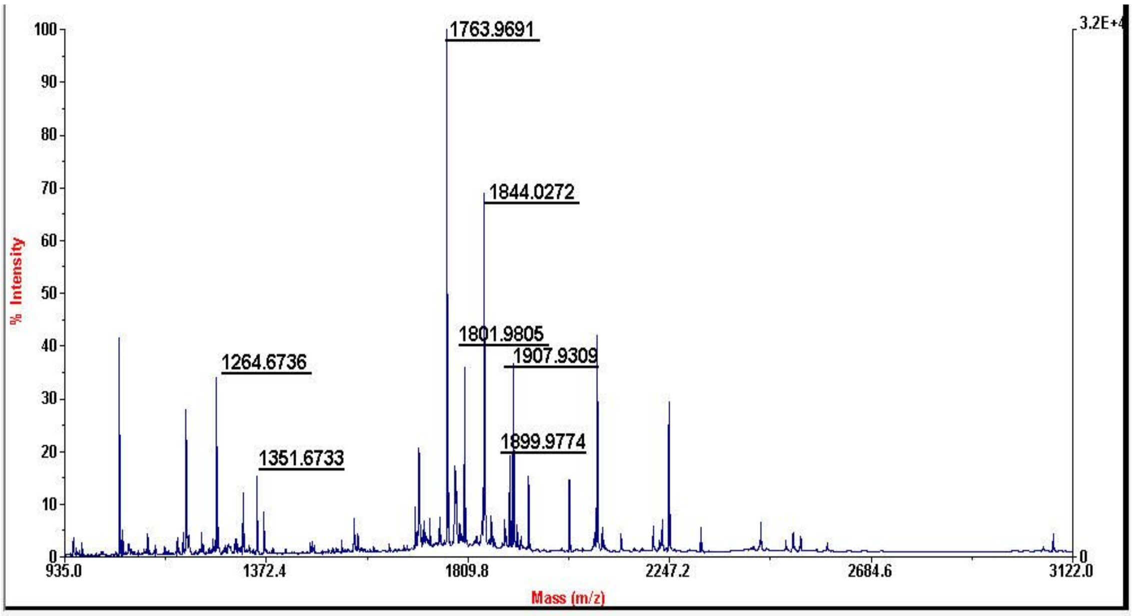
500 Thiosulfate sulfurtransferase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 8	914.4090	913.4017	913.5134	-0.1117	0	M.VHQVLYR.A
31 - 42	1351.5158	1350.5085	1350.6568	-0.1483	0	R.VLDASWYSPGTR.E
137 - 154	1963.7321	1962.7248	1962.9799	-0.2551	0	K.EGHPVTSEPSRPEPAVFK.A
164 - 176	1608.6514	1607.6441	1607.8155	-0.1714	1	K.TYEQVLENLESKR.F
177 - 183	864.3590	863.3517	863.4501	-0.0984	0	R.FQLVDSR.S
188 - 206	2009.7342	2008.7269	2008.9854	-0.2585	0	R.FLGTEPEPDAVGLDSGHIR.G
238 - 250	1500.6540	1499.6467	1499.8130	-0.1662	1	K.VDLSQPLIATCRK.G

No match to: 1193.4908, 1940.6342, 2210.8071, 2437.8706, 2760.8740

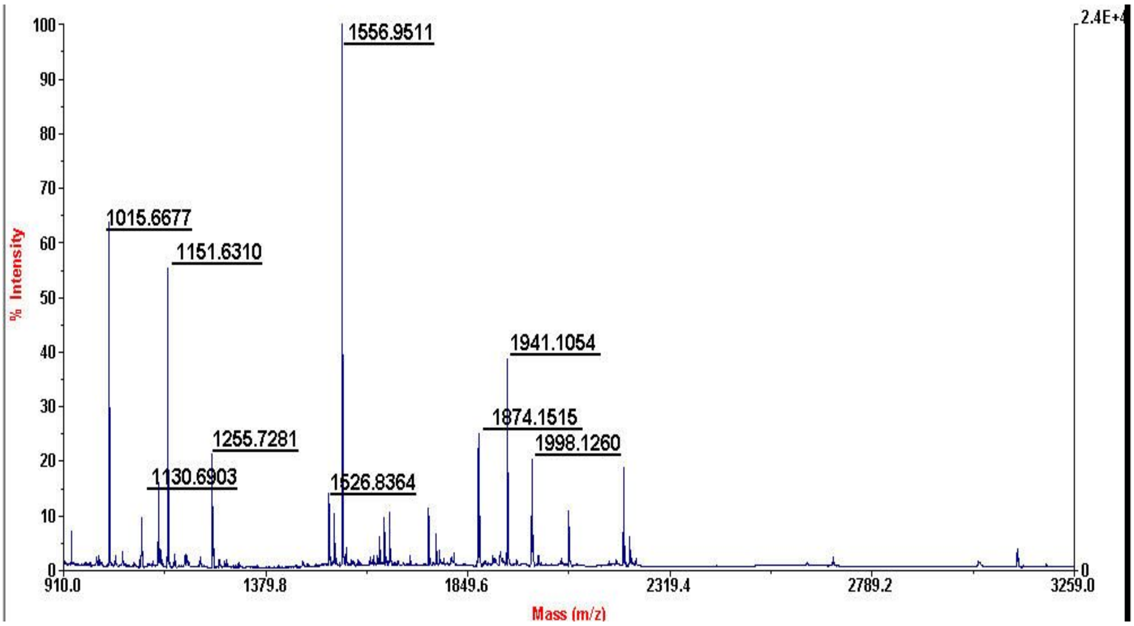
501 Pyruvate dehydrogenase E1 component subunit beta



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
37 - 52	1907.9309	1906.9236	1906.8214	0.1022	1	R.DAINQGMDEELERDEK.V	Oxidation (M)
53 - 68	1801.9805	1800.9733	1800.8934	0.0798	0	K.VFLLGEEVAQYDGAYK.V	
130 - 145	1844.0272	1843.0200	1842.9339	0.0861	0	K.TYYMSGGLQPVPIVFR.G	Oxidation (M)
259 - 269	1351.6733	1350.6660	1350.5908	0.0753	0	K.EGVECEVINMR.T	; Oxidation (M)
270 - 285	1899.9774	1898.9702	1898.8788	0.0914	0	R.TIRPMDMETIEASVMK.T	3 Oxidation (M)
309 - 324	1763.9691	1762.9618	1762.8712	0.0906	0	R.IMEGPAFNFLDAPAVR.V	Oxidation (M)
325 - 336	1264.6736	1263.6663	1263.6169	0.0494	0	R.VTGADVPMPYAK.I	Oxidation (M)

No match to: 1053.6247, 1197.7769, 1779.9986, 2089.1646, 2101.2001, 2245.2190

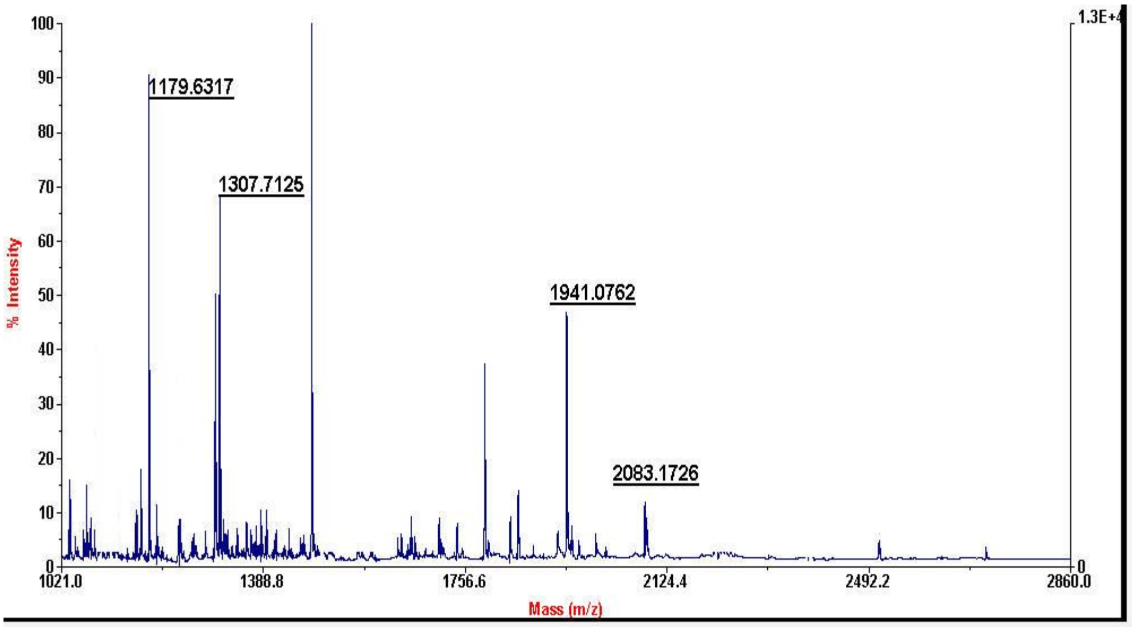
502 Glycerol-3-phosphate dehydrogenase



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
21 - 35	1556.9511	1555.9439	1555.8107	0.1332	0	K.IVGGNAAQLAQFDPR.V	
36 - 48	1526.8364	1525.8292	1525.7123	0.1169	0	R.VTMWVFEEDIGGK.K	Oxidation (M)
131 - 139	1015.6677	1014.6605	1014.5709	0.0895	0	K.LISEVIGER.L	
179 - 187	1151.6310	1150.6238	1150.5441	0.0797	0	K.ELMQTPNFR.I	Oxidation (M)
188 - 204	1874.1515	1873.1442	1872.9867	0.1575	0	R.ITVVQEVDTVEICGALK.N	
205 - 224	1941.1054	1940.0981	1939.9099	0.1883	0	K.NVVAVGAGFCDGLGFGDNTK.A	
205 - 224	1998.1260	1997.1187	1996.9313	0.1874	0	K.NVVAVGAGFCDGLGFGDNTK.A	
230 - 240	1255.7281	1254.7209	1254.6352	0.0857	0	R.LGLMEMIAFAK.L	2 Oxidation (M)
272 - 279	891.5854	890.5781	890.4974	0.0807	1	R.KVAEAFAR.T	
305 - 313	1130.6903	1129.6830	1129.6131	0.0699	0	R.ELYSILQHK.G	

No match to: 1091.1449, 2083.2092, 2211.3017

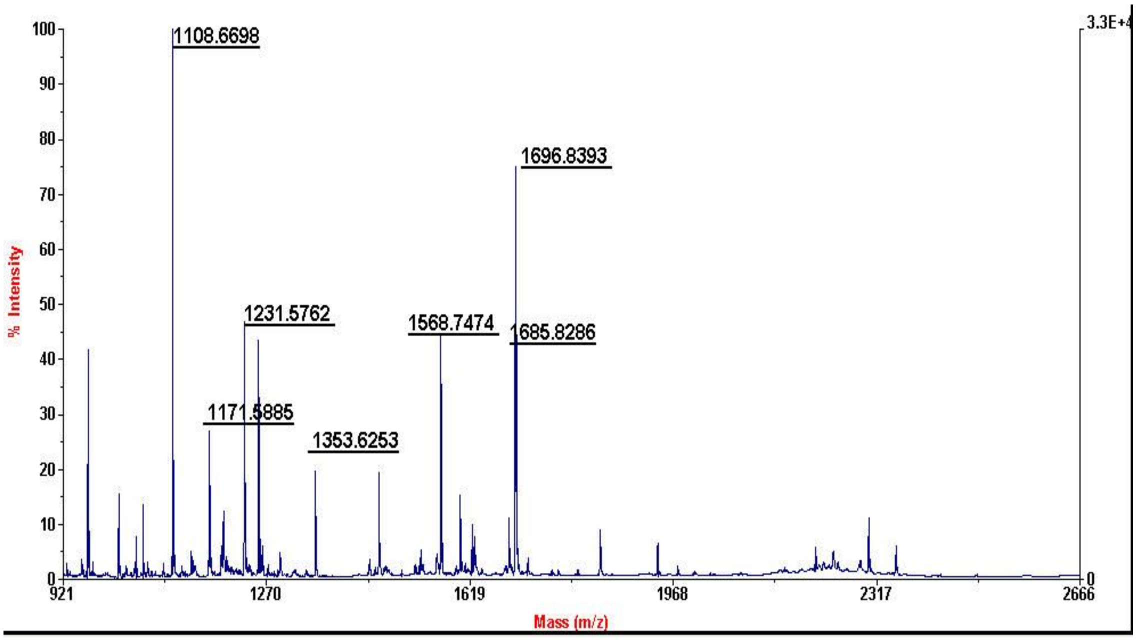
503 Hepatoma-derived growth factor



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
22 - 39	2083.1726	2082.1653	2081.9993	0.1660	1	K.GYPHWPARIDEMPEAAVK.S
Oxidation (M)						
126 - 138	1307.7125	1306.7053	1306.5637	0.1416	1	K.KGNAEGSSDEEGK.L
127 - 138	1179.6317	1178.6245	1178.4687	0.1557	0	K.GNAEGSSDEEGK.L
181 - 197	1941.0762	1940.0690	1939.9924	0.0765	0	K.EAATLEVERPLPMEVEK.N

No match to: 1300.6647, 1494.9468, 1852.1132

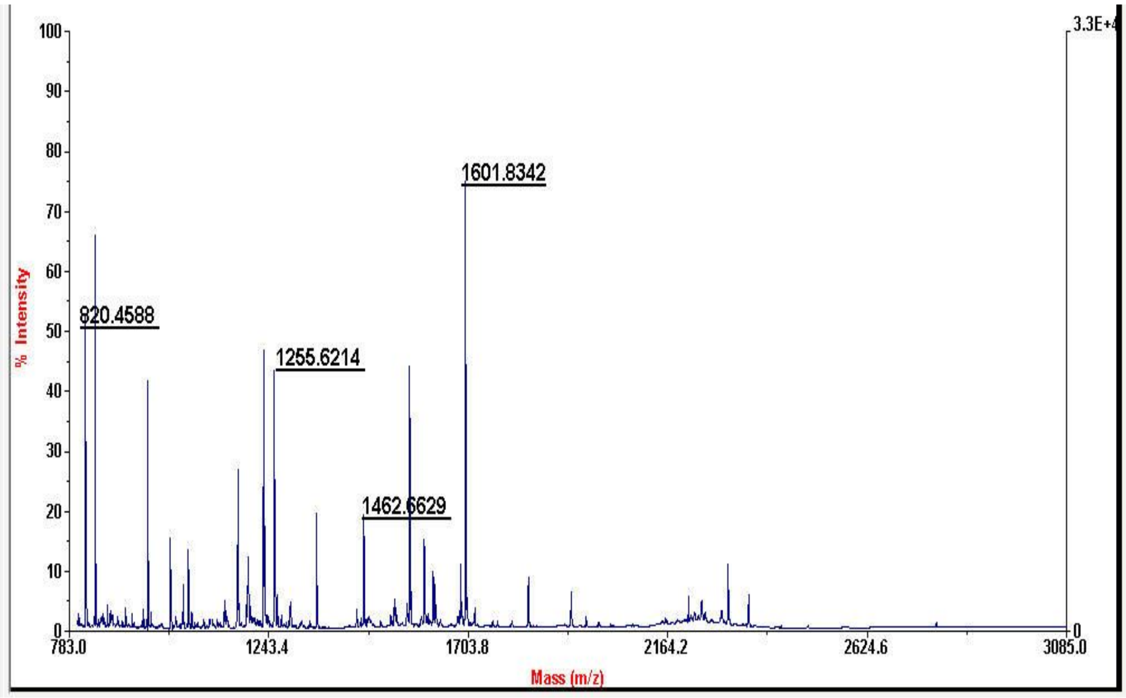
504 F-actin-capping protein



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
15 - 23	1108.6698	1107.6625	1107.6400	0.0225	1	R.RLPPQQIEK.N	
58 - 66	1231.5762	1230.5689	1230.5339	0.0350	0	K.DYLLCDYNR.D	
95 - 108	1696.8393	1695.8321	1695.8216	0.0104	1	R.KLEVEANNAFDQYR.D	
96 - 108	1568.7474	1567.7401	1567.7267	0.0134	0	K.LEVEANNAFDQYR.D	
146 - 159	1685.8286	1684.8213	1684.7879	0.0334	0	K.GCWDSIHVVEVQEK.S	
182 - 195	1353.6253	1352.6180	1352.6354	-0.0174	0	K.SGSGTMNLGGSLTR.Q	Oxidation (M)
226 - 235	1171.5885	1170.5812	1170.5921	-0.0108	0	R.STLNEIYFGK.T	

No match to: 820.4588, 963.4790, 1057.6218, 1255.6214, 1462.6629, 1601.8342

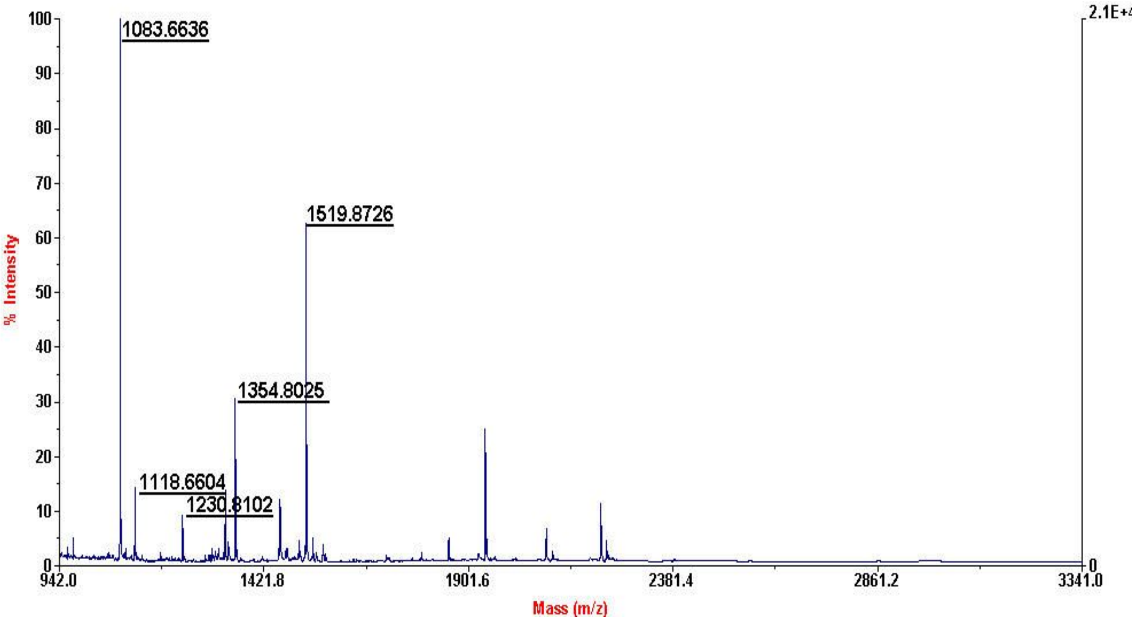
505 Cathepsin D



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
195 - 205	1255.6214	1254.6141	1254.6067	0.0074	0	K.FDGILGMAYPR.I	Oxidation (M)
223 - 235	1601.8342	1600.8269	1600.8249	0.0020	0	K.LVDQNIFSFYLSR.D	
393 - 399	963.4790	962.4717	962.4498	0.0219	0	R.YYTVFDR.D	
393 - 403	1462.6629	1461.6556	1461.6637	-0.0081	1	R.YYTVFDRDNNR.V	
404 - 411	820.4588	819.4515	819.4239	0.0277	0	R.VGFAEAAR.L	

No match to: 1171.5885, 1353.6253, 1568.7474, 1685.8286

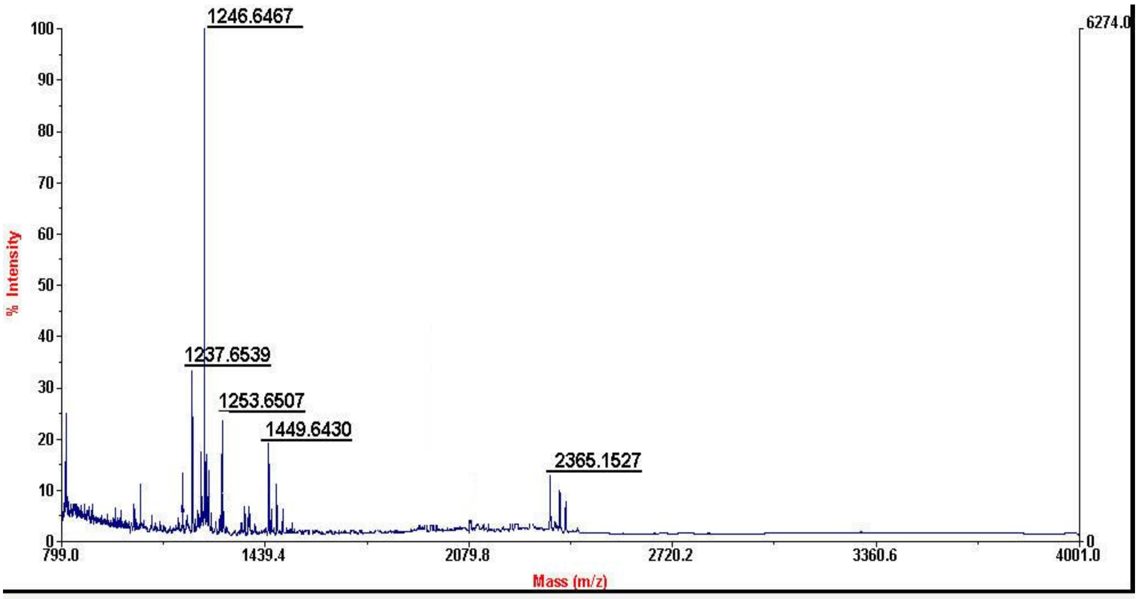
506 Peflin



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
182 - 187	849.5609	848.5536	848.4545	0.0991	0	K.FIQQWK.N	
188 - 195	1083.6636	1082.6563	1082.5145	0.1418	0	K.NLFQQYDR.D	
188 - 197	1354.8025	1353.7952	1353.6425	0.1527	1	K.NLFQQYDRDR.S	
233 - 242	1118.6604	1117.6531	1117.5186	0.1346	0	R.SANPAMQLDR.F	Oxidation (M)
259 - 269	1230.8102	1229.8030	1229.6364	0.1666	1	R.EKDTAVQGNIR.L	
270 - 282	1519.8726	1518.8653	1518.7025	0.1629	0	R.LSFEDFVTMTASR.M	Oxidation (M)

No match to: 1330.8182, 1459.1242, 1855.2211, 1941.1449, 2083.2198, 2211.3716

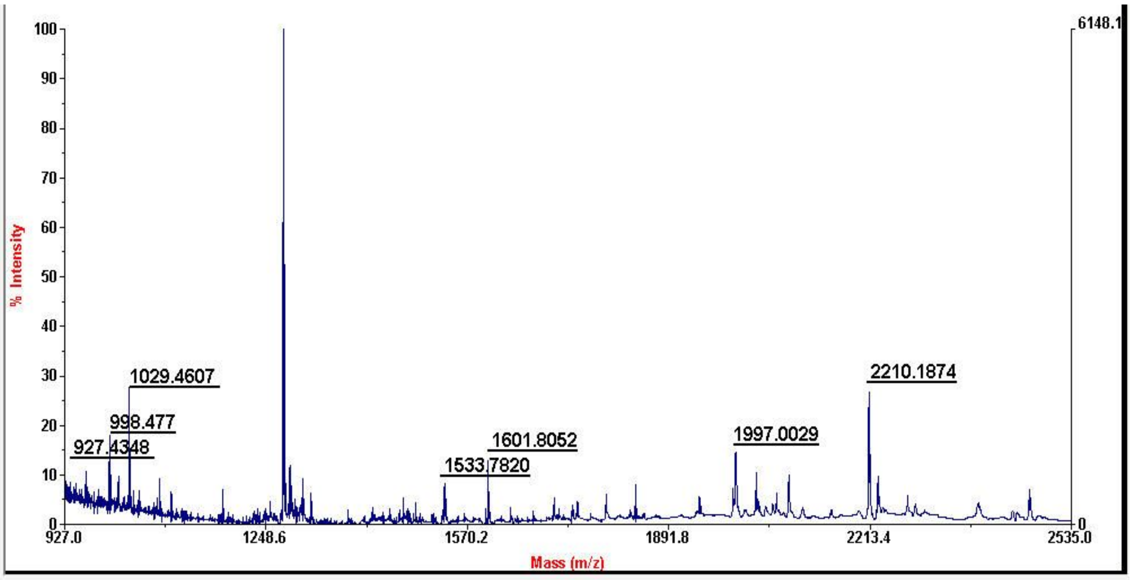
507 Myosin regulatory light polypeptide 9



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
36 - 45	1237.6539	1236.6467	1236.5557	0.0910	0	K.EAFNMIDQNR.D	
36 - 45	1253.6507	1252.6434	1252.5506	0.0928	0	K.EAFNMIDQNR.D	Oxidation (M)
105 - 124	2365.1527	2364.1454	2364.0229	0.1225	0	R.NAFACFDEEASGFIHEDHLR.E	
134 - 144	1449.6430	1448.6357	1448.5766	0.0591	0	R.FTDEEVDEMYR.E	Oxidation (M)
152 - 161	1246.6467	1245.6395	1245.5778	0.0616	0	K.GNFNYVEFTR.I	

No match to: 1210.6176

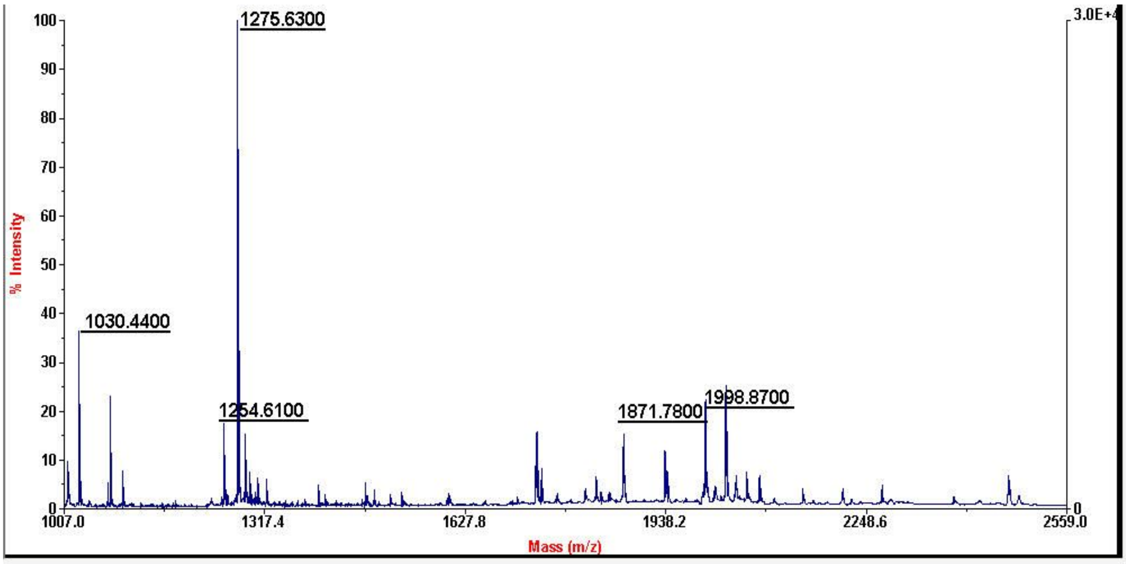
508 Oral-facial-digital syndrome 1 protein



Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
22 - 28	927.4348	926.4275	926.5225	-0.0950	1	K.KLYQTFK.D	
29 - 37	1030.4679	1029.4607	1029.5818	-0.1212	1	K.DRGILDTLK.T	
42 - 60	2211.1947	2210.1874	2210.1630	0.0244	0	R.NQLIHELMHPVLSGELQPR.S	
733 - 741	998.4776	997.4703	997.5920	-0.1217	1	R.RLSSTPLPK.A	
780 - 794	1602.8125	1601.8052	1601.8413	-0.0361	0	R.HSLSIPPVSSPPEQK.V	
933 - 948	1998.0102	1997.0029	1996.8605	0.1424	0	K.ELEMENELEMSNQEIK.D	2 Oxidation (M)
951 - 963	1533.7820	1532.7747	1532.7293	0.0454	1	K.SAHSENPLEKYMK.I	

No match to: 1275.6968, 1276.6791, 1286.6521

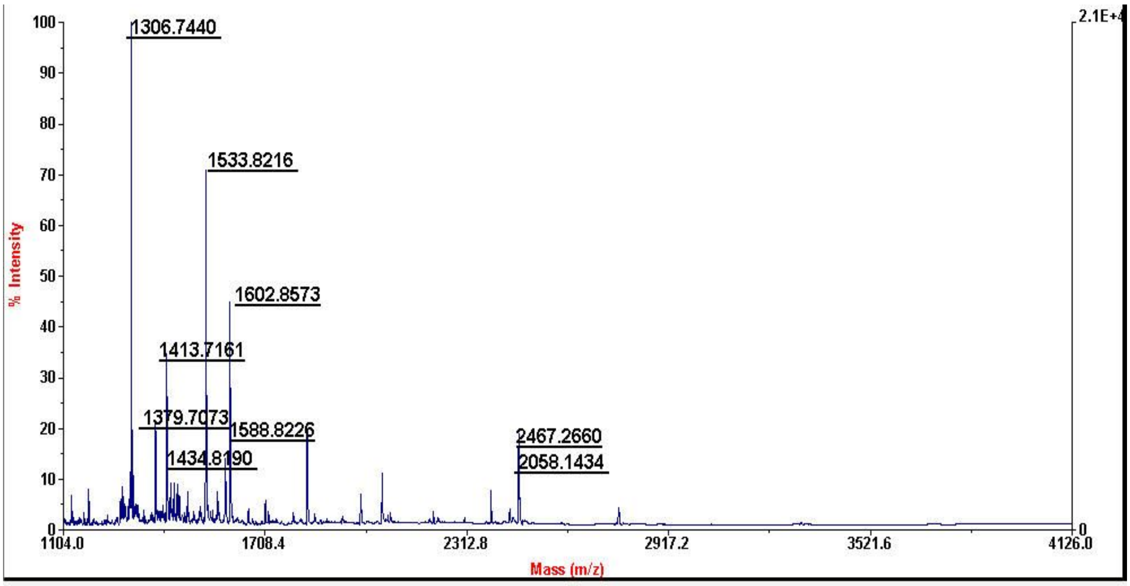
509 BTB/POZ domain-containing protein 10



```
 Start - End      Observed    Mr(expt)    Mr(calc)      Delta   Miss Sequence
     49 - 60      1254.6100   1253.6027   1253.5571     0.0456     0  K.MSLHGASGGHER.S
Oxidation (M)
    145 - 161     1871.7800   1870.7727   1870.8883    -0.1156     1
 K.TAGEMVFVYENAKEGAR.N
    169 - 177      1030.4400   1029.4327   1029.5819    -0.1491     0  R.VTLIVDNTR.F
    250 - 265     1998.8700   1997.8627   1997.8750    -0.0123     0
 R.EACDYLCISFEYSTIK.C   2
    412 - 421      1275.6300   1274.6227   1274.6190     0.0037     1  K.SRHVDFQCVK.S

 No match to: 1078.4300, 1286.6200, 1738.6700
```

510 Filamin-A



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Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss Sequence
   761 - 773     1306.7440   1305.7368   1305.7153     0.0214     1   R.VNVGAGSHPNKVK.V
   959 - 973     1533.8216   1532.8143   1532.8086     0.0057     0   K.SPFSVAVSPSLDLSK.I
  1810 - 1824    1602.8573   1601.8500   1601.8083     0.0417     1   R.MPSGKVAQPTITDNK.D
Oxidation (M)
  1832 - 1845    1588.8226   1587.8154   1587.7351     0.0803     0   R.YAPSEAGLHEMDIR.Y
  2311 - 2333    2467.2660   2466.2587   2466.1816     0.0771     0
K.FNEEHIPDSPFVVPVASPSGDAR.R
  2347 - 2367    2058.1434   2057.1361   2057.0905     0.0456     1
K.VNQPASFAVSLNGAKGAIDAK.V
  2501 - 2513    1379.7073   1378.7001   1378.6670     0.0331     0   K.YGGPYHIGGSPFK.A
  2585 - 2598    1434.8190   1433.8118   1433.7561     0.0556     0   K.AGNNMLLVGVHGPR.T
  2632 - 2643    1413.7161   1412.7088   1412.6473     0.0615     0   K.WGDEHIPGSPYR.V

No match to: 1126.5514, 1529.7966, 1834.0086
```