Supplementary Table 1. Differentially regulated proteins identified in stromal vascular fraction (SVF) cells compared to mature adipocytes isolated from both arm and abdomen adipose tissue.

Spot Number	Accession Number/ Charge	Proteins/Peptide Sequence	Number of Peptides[a]	Molecular Mass[b]	pI[b]	Sequence Coverage (%)	Protein Score (Mascot)	Protein Score (PLGS)
Up Regulated in SVF cells								
507	P06753	Tropomyosin alpha-3 chain	3	32798	4.5	10.2	145	10.0
	2	MELQEIQLK						
	2	LVIIEGDLER						
	2	IQLVEEELDR						
507	P67936	Tropomyosin alpha-4 chain	2	28504	4.5	9.7	132	10.0
	2	IQLVEEELDR						
	2	IQALQQQADEAEDR						
614	P08670	Vimentin	7	53619	4.9	15.2	420	12.3
	2	DNLAEDIMR						
	2	FADLSEAANR						
	2	VELQELNDR						
	2	ILLAELEQLK						
	2	LGDLYEEEMR						
	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
614	P67936	Tropomyosin alpha-4 chain	1	28504	4.5	4.0	53	8.8
	2	IQLVEEELDR						
1606	P08107	Heat shock 70 kDa protein 1A/1B	2	70009	5.3	3.1	91	10.6
	2	LLQDFFNGR						
	2	NALESYAFNMK						
4402	P60174	Triosephosphate isomerase	2	26652	6.5	12.4	74	10.0
	2	VVLAYEPMWAIGTGK						
	2	VTNGAFTGEISPGMIK						
7505	P00915	Carbonic anhydrase 1	4	28852	6.7	19.5	189	10.0
	2	VLDALQAIK						
	2	ADGLAVIGVLMK						
	2	ESISVSSEQLAQFR						
	2	LYPIANGNNQSPVDIK						
7511	P00915	Carbonic anhydrase 1	6	28852	6.7	29.9	310	12.3
	2	VLDALQAIK						
	2	GGPFSDSYR						
	2	ADGLAVIGVLMK						
	3	KHDTSLKPISVSYNPATAK						

	2	ESISVSSEQLAQFR						
	2	LYPIANGNNQSPVDIK						
7522	P00915	Carbonic anhydrase 1	3	28852	6.7	13.4	164	12.3
	2	VLDALQAIK						
	2	ADGLAVIGVLMK						
	2	ESISVSSEQLAQFR						
7524	P00915	Carbonic anhydrase 1	1	28852	6.7	5.4	43	9.7
	2	ESISVSSEQLAQFR						
7541	P00915	Carbonic anhydrase 1	2	28852	6.7	10.0	63	10.0
	2	ADGLAVIGVLMK						
	2	ESISVSSEQLAQFR						
7541	P23396	40S ribosomal protein S3	1	26671	10	5.3	53	4.0
	2	ELAEDGYSGVEVR						
8231	P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	1	11943	7.9	12.0	53	N/A
	2	GVQVETISPGDGR						
8403	P00918	Carbonic anhydrase 2	5	29227	7.0	28.5	336	10.0
	2	VVDVLDSIK						
	2	EPISVSSEQVLK						
	3	ILNNGHAFNVEFDDSQDK						
	3	YDPSLKPLSVSYDQATSLR						
	2	AVQQPDGLAVLGIFLK						
8412	P30043	Flavin reductase	2	22105	7.9	14.1	145	13.0
	2	NDLSPTTVMSEGAR						
	2	TVAGQDAVIVLLGTR						

Up Regulated in Adipocytes

204	P08670	Vimentin	2	53619	4.9	4.9	149	10.0
	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
304	P23396	40S ribosomal protein S3	5	26671	10	25.9	253	11.2
	2	AELNEFLTR						
	2	GLCAIAQAESLR						
	2	ELAEDGYSGVEVR						
	2	DEILPTTPISEQK						
	2	GGKPEPPAMPQPVPTA						
304	P08670	Vimentin	2	53619	4.9	4.5	109	11.7
	2	ILLAELEQLK						
	2	EEAENTLQSFR						
402	P08758	Annexin A5	3	35914	4.7	16.6	238	10.0
	2	GTVTDFPGFDER						
	2	GLGTDEESILTLLTSR						
	3	DPDAGIDEAQVEQDAQALFQAGELK						

1319	P32119	Peroxiredoxin-2	2	21878	5.6	14.1	86	9.3
	2	QITVNDLPVGR						
	2	EGGLGPLNIPLLADVTR						
1402	P04083	Annexin A1	3	38689	6.6	11.0	148	10.0
	2	TPAQFDADELR						
	2	GVDEATIIDILTK						
	2	GTDVNVFNTILTTR						
5506	P42126	3,2-trans-enoyl-CoA isomerase, mitochondrial	1	32795	8.7	5.0	68	10.0
	2	VLVEPDAGAGVAVMK						
7601	P16930	Fumarylacetoacetase	5	46344	6.5	14.3	275	13.0
	2	LGEPIPISK						
	2	HLFTGPVLSK						
	2	ASSVVVSGTPIR						
	2	VFLQNLLSVSQAR						
	2	IGVAIGDQILDLSIIK						
7603	P40925	Malate dehydrogenase, cytoplasmic	1	36403	7.2	5.1	84	10.0
	2	VIVVGNPANTNCLTASK						
7603	P04406	Glyceraldehyde-3-phosphate dehydrogenase	1	36030	8.7	4.2	48	N/A
	2	LVINGNPITIFQER						

[a] The number of unique peptides that matched with the identified protein in mass analyses.

[b] Molecular mass and isoelectric point (pI) are theoretical values.

Supplementary Table 2. Differentially regulated proteins identified in stromal vascular fraction (SVF) cells compared to mature adipocytes isolated from arm adipose tissue.

Spot Number	Accession Number/ Charge	Proteins/Peptide Sequence	Number of Peptides[a]	Molecular Mass[b]	pI[b]	Sequence Coverage (%)	Protein Score (Mascot)	Protein Score (PLGS)
Up Regulated in SVF cells								
205	P60660	Myosin light polypeptide 6	3	16919	4.4	27.8	142	10.0
	3	VLDFEHFLPMLQTVAK						
	2	ALGQNPTNAEVLK						
	2	DQGTYEDYVEGLR						
205	P08670	Vimentin	2	53619	4.9	4.9	168	10.0
	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
205	P30049	ATP synthase subunit delta, mitochondrial	1	17479	5.2	8.3	72	10.0
	2	AQAELVGTADEATR						
214	P08670	Vimentin	4	53619	4.9	9.2	293	10.0
	2	ILLAELEQLK						
	2	LGDLYEEEMR						
	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
305	P08670	Vimentin	7	53619	4.9	15.0	456	10.0
	2	LQEEMLQR						
	2	QDVDNASLAR						
	2	VELQELNDR						
	2	ILLAELEQLK						
	2	LGDLYEEEMR						
	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
306	P08670	Vimentin	4	53619	4.9	9.0	204	12.3
	2	VELQELNDR						
	2	ILLAELEQLK						
	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
309	P08670	Vimentin	6	53619	4.9	12.9	376	12.3
	2	LQEEMLQR						
	2	DNLAEDIMR						
	2	ILLAELEQLK						
	2	LGDLYEEEMR						
	2	EEAENTLQSFR						

	2	VESLQEEIAFLK						
504	P23396	40S ribosomal protein S3	3	26671	10	14.4	161	11.1
	2	AELNEFLTR						
	2	ELAEDGYSGVEVR						
	2	DEILPTTPISEQK						
504	Q6NZI2	Polymerase I and transcript release factor	3	43449	5.3	10.8	192	12.0
	2	LEVNEAELLR						
	2	SDQVNGVLVLSLLDK						
	2	QAEMEGAVQSIQGELSK						
507	P06753	Tropomyosin alpha-3 chain	3	32798	4.5	10.2	145	10.0
	2	MELQEIQLK						
	2	LVIIEGDLER						
	2	IQLVEEELDR						
507	P67936	Tropomyosin alpha-4 chain	2	28504	4.5	9.7	132	10.0
	2	IQLVEEELDR						
	2	IQALQQQADEAEDR						
509	P08670	Vimentin	5	53619	4.9	11.2	315	10.0
	2	LQEEMLQR						
	2	LGDLYEEEMR						
	2	MALDIEIATYR						
	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
509	P06753	Tropomyosin alpha-3 chain	4	32798	4.5	14.1	178	10.0
	2	MELQEIQLK						
	2	LVIIEGDLER						
	2	IQLVEEELDR						
	2	QLEDELVSLQK						
520	Q6NZI2	Polymerase I and transcript release factor	2	43449	5.3	8.2	214	12.0
	2	SDQVNGVLVLSLLDK						
	2	QAEMEGAVQSIQGELSK						
531	P61981	14-3-3 protein gamma	3	28284	4.6	13.8	198	10.0
	2	YLAEVATGEK						
	2	DSTLIMQLLR						
	2	NVTELNEPLSNEER						
531	P00918	Carbonic anhydrase 2	2	29227	7.0	8.1	131	N/A
	2	VLDALDSIK						
	2	EPISVSSQQMLK						
614	P08670	Vimentin	7	53619	4.9	15.2	420	12.3
	2	DNLAEDIMR						
	2	FADLSEAANR						
	2	VELQELNDR						
	2	ILLAELEQLK						
	2	LGDLYEEEMR						

	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
614	P67936	Tropomyosin alpha-4 chain	1	28504	4.5	4.0	53	8.8
	2	IQLVEEELDR						
1605	P63267	Actin, gamma-enteric smooth muscle	4	41849	5.2	14.6	196	8.6
	2	GYSFVTTAER						
	2	EITALAPSTMK						
	3	VAPEEHPTLLTEAPLNPK						
	2	SYELPDGQVITIGNER						
1606	P08107	Heat shock 70 kDa protein 1A/1B	2	70009	5.3	3.1	91	10.6
	2	LLQDFFNGR						
	2	NALESYAFNMK						
1617	P08758	Annexin A5	5	35914	4.7	24.7	393	10.0
	2	NFATSLYSMIK						
	2	GTVTDFPGFDER						
	2	ETSGNLEQLLLAVVK						
	2	GLGTDEESILTLLTSR						
	3	DPDAGIDEAQVEQDAQALFQAGELK						
1709	P06576	ATP synthase subunit beta, mitochondrial	14	56524	5.1	38.2	842	12.3
	2	IGLFGGAGVGK						
	2	IPVGPETLGR						
	2	VVDLLAPYAK						
	2	TIAMDGTEGLVR						
	3	AIAELGIYPAVDPLDSTSR						
	3	FLSQPFQVAEVFTGHMGK						
	2	IMNVIGEPIDER						
	2	FTQAGSEVSALLGR						
	2	VALTGLTVAEYFR						
	2	TVLIMELINNVAK						
	3	IPSAVGYQPTLATDMGTMQER						
	2	VALVYGQMNEPPGAR						
	2	LVLEVAQHLGESTVR						
	2	AIAELGIYPAVDPLDSTSR						
1709	Q15084	Protein disulfide-isomerase A6	1	48091	4.8	3.2	70	10.0
	2	TGEAIVDAALSALR						
2306	P02545	Lamin-A/C	6	74094	6.6	8.6	315	10.0
	2	LQLELSK						
	2	EGDLIAAQAR						
	2	SLETENAGLR						
	2	EAALSTALSEK						
	2	EDLQELNDR						
	2	ITESEEVVSR						

	2	EGGLGPLNIPLLADVTR						
2705	P60709	Actin, cytoplasmic 1	4	41709	5.1	17.6	265	5.1
	2	EITALAPSTMK						
	3	VAPEEHPVLLTEAPLNPK						
	2	SYELPDGQVITIGNER						
	2	DLYANTVLSGGTTMYPGIADR						
2705	Q6NZI2	Polymerase I and transcript release factor	1	43449	5.3	3.8	74	10.0
	2	SDQVNGVLVLSLLDK						
3203	P15090	Fatty acid-binding protein, adipocyte	3	14709	7.0	36.4	242	10.0
	2	LVSSENFDDYMK						
	2	STITLDGGVLVHVQK						
	3	NTEISFILGQEFDEVTADDRK						
3409	P02545	Lamin-A/C	3	74094	6.6	4.8	166	10.0
	2	SLETENAGLR						
	2	EAALSTALSEK						
	2	ITESEEVVSR						
3409	P12111	Collagen alpha-3(VI) chain	1	343453	6.3	0.4	51	N/A
	2	SLDEISQPAQELK						
4402	P60174	Triosephosphate isomerase	2	26652	6.5	12.4	74	10.0
	2	VVLAYEPMWAIGTGK						
	2	VTNGAFTGEISPGMIK						
5202	P15090	Fatty acid-binding protein, adipocyte	4	14709	7.0	37.9	318	10.0
	2	EVGVGFATR						
	2	LVVECVMK						
	2	LVSSENFDDYMK						
	3	NTEISFILGQEFDEVTADDRK						
5207	P15090	Fatty acid-binding protein, adipocyte	2	14709	7.0	15.2	111	10.0
	2	LVVECVMK						
	2	LVSSENFDDYMK						
5207	P46108	Proto-oncogene C-crk	1	33810	5.4	3.6	52	N/A
	2	QEAVALLQGQR						
5217	Q01469	Fatty acid-binding protein, epidermal	2	15154	6.8	14.8	59	2.7
	2	ELGVGIALR						
	2	TTQFSCTLGEK						
5406	Q99497	Protein DJ-1	3	19878	6.4	29.1	180	10.0
	2	DVVICPDASLEDAK						
	2	GAEEMETVIPVDVMR						
	3	EGPYDVVVLPGGNLGAQNLSESAAVK						
7416	P60174	Triosephosphate isomerase	2	26652	6.5	12.0	156	11.7
	2	QSLGELIGTLNAAK						
	2	VTNGAFTGEISPGMIK						
7418	Q06830	Peroxiredoxin-1	4	22096	8.2	23.6	182	10.0
	2	TIAQDYGVLK						

	2	LVQAFQFTDK						
	2	QITVNDLPVGR						
	2	QGGLGPMNIPLVSDPK						
7418	P04179	Superoxide dismutase [Mn], mitochondrial	1	24706	8.4	6.3	83	10.0
	2	GDVTAQIALQPALK						
7505	P00915	Carbonic anhydrase 1	4	28852	6.7	19.5	189	10.0
	2	VLDALQAIK						
	2	ADGLAVIGVLMK						
	2	ESISVSSEQLAQFR						
	2	LYPIANGNNQSPVDIK						
7507	P04406	Glyceraldehyde-3-phosphate dehydrogenase	2	36030	8.7	8.7	114	12.3
	2	GALQNIIPASTGAAK						
	2	LVINGNPITIFQER						
7511	P00915	Carbonic anhydrase 1	6	28852	6.7	29.9	310	12.3
	2	VLDALQAIK						
	2	GGPFSDSYR						
	2	ADGLAVIGVLMK						
	3	HDTSLKPISVSYNPATAK						
	2	ESISVSSEQLAQFR						
	2	LYPIANGNNQSPVDIK						
7512	P04406	Glyceraldehyde-3-phosphate dehydrogenase	2	36030	8.7	8.7	99	12.3
	2	GALQNIIPASTGAAK						
	2	LVINGNPITIFQER						
7522	P00915	Carbonic anhydrase 1	3	28852	6.7	13.4	164	12.3
	2	VLDALQAIK						
	2	ADGLAVIGVLMK						
	2	ESISVSSEQLAQFR						
7524	P00915	Carbonic anhydrase 1	1	28852	6.7	5.4	43	9.7
	2	ESISVSSEQLAQFR						
7541	P00915	Carbonic anhydrase 1	2	28852	6.7	10.0	63	10.0
	2	ADGLAVIGVLMK						
	2	ESISVSSEQLAQFR						
7541	P23396	40S ribosomal protein S3	1	26671	10	5.3	53	4.0
	2	ELAEDGYSGVEVR						
7706	P04040	Catalase	3	59718	7.0	7.0	214	13.0
	2	LNVITVGPR						
	2	FSTVAGESGSADTVR						
	2	FNTANDDNVTQVR						
7712	P04040	Catalase	3	59718	7.0	8.2	207	10.0
	2	ADVLTTGAGNPVGDK						
	2	FSTVAGESGSADTVR						
	2	FNTANDDNVTQVR						
7713	P04040	Catalase	3	59718	7.0	7.0	181	13.0

	2	LNVITVGPR						
	2	FSTVAGESGSADTVR						
	2	FNTANDDNVTQVR						
7715	P04040	Catalase	4	59718	7.0	9.3	191	13.0
	2	LNVITVGPR						
	2	LVNANGEAVYCK						
	2	FSTVAGESGSADTVR						
	2	FNTANDDNVTQVR						
7716	P06733	Alpha-enolase	3	47139	7.2	9.7	193	10.0
	2	GNPTVEVDLFTSK						
	2	VVIGMDVAASEFFR						
	2	VNQIGSVTESLQACK						
8212	P62937	Peptidyl-prolyl cis-trans isomerase A	2	17887	8.5	12.2	104	10.2
	2	VSFELFADK						
	2	EGMNIVEAMER						
8231	P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	1	11943	7.9	12.0	53	N/A
	2	GVQVETISPGDGR						
8403	P00918	Carbonic anhydrase 2	5	29227	7.0	28.5	336	10.0
	2	VVDVLDSIK						
	2	EPISVSSEQVLK						
	3	ILNNGHAFNVEFDDSQDK						
	3	YDPSLKPLSVSYDQATSLR						
	2	AVQQPDGLAVLGIFLK						
8412	P30043	Flavin reductase	2	22105	7.9	14.1	145	13.0
	2	NDLSPTTVMSEGAR						
	2	TVAGQDAVIVLLGTR						
8422	Q06830	Peroxiredoxin-1	4	22096	8.2	21.1	177	10.0
	2	TIAQDYGVLK						
	2	LVQAFQFTDK						
	2	QITVNDLPVGR						
	2	ATAVMPDGQFK						
8608	P04406	Glyceraldehyde-3-phosphate dehydrogenase	3	36030	8.7	12.8	194	10.0
	2	GALQNIIPASTGAAK						
	2	VPTANVSVVDLTCR						
	2	LVINGNPITIFQER						
8609	P00558	Phosphoglycerate kinase 1	5	44586	10	18.9	320	10.0
	2	IQLINNMLDK						
	3	ITLPVDFVTADKFDENAK						
	2	VNEMIIGGGMAFTFLK						
	2	ACANPAAGSVILLENLR						
	2	VLNNMEIGTSLFDEEGAK						
8609	P00918	Carbonic anhydrase 2	1	29227	7.0	6.2	41	5.7
	2	AVQQPDGLAVLGIFLK						

8615	P23396	40S ribosomal protein S3	1	26671	10	5.8	55	10.0
	2	FGFPEGSVELYAEK						

Up Regulated in Adipocytes

204	P08670	Vimentin	2	53619	4.9	4.9	149	10.0
	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
219	P08670	Vimentin	2	53619	4.9	5.2	109	10.0
	2	MALDIEIATYR						
	2	QVQSLTCEVDALK						
304	P23396	40S ribosomal protein S3	5	26671	10	25.9	253	11.2
	2	AELNEFLTR						
	2	GLCAIAQAESLR						
	2	ELAEDGYSGVEVR						
	2	DEILPTTPISEQK						
	2	GGKPEPPAMPQPVPTA						
304	P08670	Vimentin	2	53619	4.9	4.5	109	11.7
	2	ILLAELEQLK						
	2	EEAENTLQSFR						
402	P08758	Annexin A5	3	35914	4.7	16.6	238	10.0
	2	GTVTDFPGFDER						
	2	GLGTDEESILTLLTSR						
	3	DPDAGIDEAQVEQDAQALFQAGELK						
405	P08758	Annexin A5	1	35914	4.7	5.0	67	0.0
	2	GLGTDEESILTLLTSR						
1307	P12111	Collagen alpha-3(VI) chain	2	343453	6.3	0.9	108	N/A
	2	SLDEISQPAQELK						
	2	AAPLQGMLPGLLAPLR						
1314	P04083	Annexin A1	5	38689	6.6	20.2	350	10.0
	2	DITSDTSGDFR						
	2	GVDEATIIDILTK						
	2	GTDVNVFNTILTTR						
	2	GLGTDEDTLIEILASR						
	2	SEDFGVNEDLADSDAR						
1319	P32119	Peroxiredoxin-2	2	21878	5.6	14.1	86	9.3
	2	QITVNDLPVGR						
	2	EGGLGPLNIPLLADVTR						
1402	P04083	Annexin A1	3	38689	6.6	11.0	148	10.0
	2	TPAQFDADELR						
	2	GVDEATIIDILTK						
	2	GTDVNVFNTILTTR						
1507	P60709	Actin, cytoplasmic 1	3	41709	5.1	12.0	204	9.3

	2	ELTALAPSTMK						
	3	VAPEEHPVLLTEAPLNPK						
	2	SYELPDGQVITIGNER						
1507	P08758	Annexin A5	2	35914	4.7	9.7	198	10.0
	2	ETSGNLEQLLLAVVK						
	2	GLGTDEESILTLLTSR						
1508	P00918	Carbonic anhydrase 2	2	29227	7.0	8.1	62	N/A
	2	VLDALDSIK						
	2	EPISVSSQQMLK						
2303	P06576	ATP synthase subunit beta, mitochondrial	2	56524	5.1	4.9	39	1.7
	2	VALTGLTVAEYFR						
	2	TVLIMELINNVAK						
2405	P23396	40S ribosomal protein S3	1	26671	10	5.3	66	N/A
	2	ELAEDGYSGVEVR						
3201	P07355	Annexin A2	2	38579	7.8	7.4	150	10.0
	2	TPAQYDASELK						
	2	GVDEVTIVNILTNR						
3506	P35232	Prohibitin	2	24393	6.9	8.1	73	11.4
	2	FDAGELITQR						
	2	AAELIANSLATAGDGLIELR						
3506	P07355	Annexin A2	1	38579	7.8	4.1	43	10.0
	2	GVDEVTIVNILTNR						
3706	P63267	Actin, gamma-enteric smooth muscle	2	41849	5.2	7.7	92	8.6
	2	EITALAPSTMK						
	3	VAPEEHPTLLTEAPLNPK						
4404	P63104	14-3-3 protein zeta/delta	2	27727	4.5	9.0	104	3.7
	2	DSTLIMQLLR						
	2	DICNDVLSLLEK						
4622	P23396	40S ribosomal protein S3	3	26671	10	14.4	157	10.6
	2	AELNEFLTR						
	2	ELAEDGYSGVEVR						
	2	DEILPTTPISEQK						
5506	P42126	3,2-trans-enoyl-CoA isomerase, mitochondrial	1	32795	8.7	5.0	68	10.0
	2	VLVEPDAGAGVAVMK						
6310	P02511	Alpha-crystallin B chain	2	20159	6.4	10.9	24	13.0
	2	HFSPEELK						
	2	VLGDMVEIHGK						
7601	P16930	Fumarylacetoacetase	5	46344	6.5	14.3	275	13.0
	2	LGEPIPISK						
	2	HLFTGPVLSK						
	2	ASSVVVSGTPIR						
	2	VFLQNLLSVSQAR						
	2	IGVAIGDQILDLSIIK						

7603	P40925	Malate dehydrogenase, cytoplasmic	1	36403	7.2	5.1	84	10.0
	2	VIVVGNPANTNCLTASK						
7603	P04406	Glyceraldehyde-3-phosphate dehydrogenase	1	36030	8.7	4.2	48	N/A
	2	LVINGNPITIFQER						

[a] The number of unique peptides that matched with the identified protein in mass analyses.
[b] Molecular mass and isoelectric point (pI) are theoretical values.

Supplementary Table 3. Differentially regulated proteins identified in stromal vascular fraction (SVF) cells compared to mature adipocytes isolated from abdomen adipose tissue.

Spot Number	Accession Number/ Charge	Proteins/Peptide Sequence	Number of Peptides[a]	Molecular Mass[b]	pI[b]	Sequence Coverage (%)	Protein Score (Mascot)	Protein Score (PLGS)
Up Regulated in SVF cells								
4402	P60174	Triosephposphate isomerase	2	26652	6.5	12.4	74	10.0
	2	VVLAYEPMWAIGTGK						
	2	VTNGAFTGEISPGMIK						
7505	P00915	Carbonic anhydrase 1	4	28852	6.7	19.5	189	10.0
	2	VLDALQAIK						
	2	ADGLAVIGVLMK						
	2	ESISVSSEQLAQFR						
	2	LYPIANGNNQSPVDIK						
7511	P00915	Carbonic anhydrase 1	6	28852	6.7	29.9	310	12.3
	2	VLDALQAIK						
	2	GGPFSDSYR						
	2	ADGLAVIGVLMK						
	3	HDTSLKPISVSYNPATAK						
	2	ESISVSSEQLAQFR						
	2	LYPIANGNNQSPVDIK						
7524	P00915	Carbonic anhydrase 1	1	28852	6.7	5.4	43	9.7
	2	ESISVSSEQLAQFR						
7541	P00915	Carbonic anhydrase 1	2	28852	6.7	10.0	63	10.0
	2	ADGLAVIGVLMK						
	2	ESISVSSEQLAQFR						
7541	P23396	40S ribosomal protein S3	1	26671	10	5.3	53	4.0
	2	ELAEDGYSGVEVR						
8231	P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	1	11943	7.9	12.0	53	N/A
	2	GVQVETISPGDGR						
8403	P00918	Carbonic anhydrase 2	5	29227	7.0	28.5	336	10.0
	2	VVDVLDSIK						
	2	EPISVSSEQVLK						
	3	ILNNGHAFNVEFDDSQDK						
	3	YDPSLKPLSVSYDQATSLR						
	2	AVQQPDGLAVLGIFLK						

Up Regulated in Adipocytes

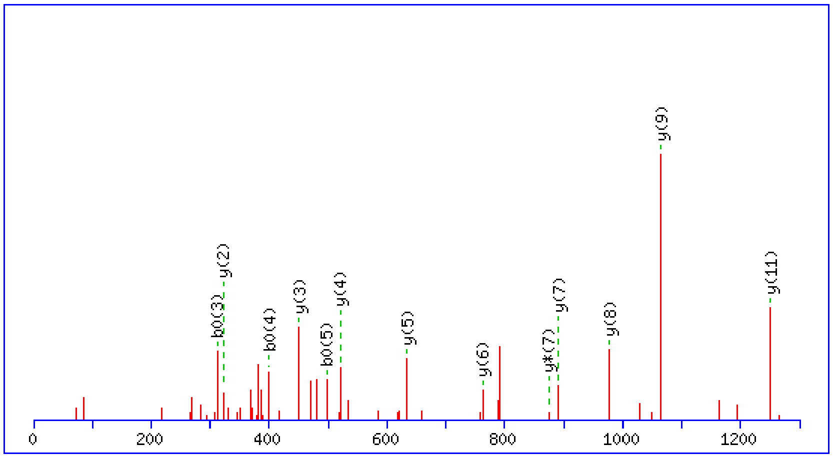
204	P08670	Vimentin	2	53619	4.9	4.9	149	10.0
	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
309	P08670	Vimentin	6	53619	4.9	12.9	376	12.3
	2	LQEEMLQR						
	2	DNLAEDIMR						
	2	ILLAELEQLK						
	2	LGDLYEEEMR						
	2	EEAENTLQSFR						
	2	VESLQEEIAFLK						
1319	P32119	Peroxiredoxin-2	2	21878	5.6	14.1	86	9.3
	2	QITVNDLPVGR						
	2	EGGLGPLNIPLLADVTR						
1402	P04083	Annexin A1	3	38689	6.6	11.0	148	10.0
	2	TPAQFDADELR						
	2	GVDEATIIDILTK						
	2	GTDVNVFNTILTTR						
1617	P08758	Annexin A5	5	35914	4.7	24.7	393	10.0
	2	NFATSLYSMIK						
	2	GTVTDFPGFDER						
	2	ETSGNLEQLLLAVVK						
	2	GLGTDEESILTLLTSR						
	3	DPDAGIDEAQVEQDAQALFQAGELK						
1709	P06576	ATP synthase subunit beta, mitochondrial	14	56524	5.1	38.2	842	12.3
	2	IGLFGGAGVGK						
	2	IPVGPETLGR						
	2	VVDLLAPYAK						
	2	TIAMDGTEGLVR						
	3	AIAELGIYPAVDPLDSTSR						
	3	FLSQPFQVAEVFTGHMGK						
	2	IMNVIGEPIDER						
	2	FTQAGSEVSALLGR						
	2	VALTGLTVAEYFR						
	2	TVLIMELINNVAK						
	3	IPSAVGYQPTLATDMGTMQER						
	2	VALVYGQMNEPPGAR						
	2	LVLEVAQHLGESTVR						
	2	AIAELGIYPAVDPLDSTSR						
1709	Q15084	Protein disulfide-isomerase A6	1	48091	4.8	3.2	70	10.0
	2	TGEAIVDAALSALR						
5202	P15090	Fatty acid-binding protein, adipocyte	4	14709	7.0	37.9	318	10.0

	2	EVGVGFATR						
	2	LVVECVMK						
	2	LVSSENFDDYMK						
	3	NTEISFILGQEFDEVTADDRK						
5506	P42126	3,2-trans-enoyl-CoA isomerase, mitochondrial	1	32795	8.7	5.0	68	10.0
	2	VLVEPDAGAGVAVMK						
7416	P60174	Triosephosphate isomerase	2	26652	6.5	12.0	156	11.7
	2	QSLGELIGTLNAAK						
	2	VTNGAFTGEISPGMIK						
7601	P16930	Fumarylacetoacetase	5	46344	6.5	14.3	275	13.0
	2	LGEPIPISK						
	2	HLFTGPVLSK						
	2	ASSVVVSGTPIR						
	2	VFLQNLLSVSQAR						
	2	IGVAIGDQILDLSIIK						
7713	P04040	Catalase	3	59718	7.0	7.0	181	13.0
	2	LNVITVGPR						
	2	FSTVAGESGSADTVR						
	2	FNTANDDNVTQVR						
7716	P06733	Alpha-enolase	3	47139	7.2	9.7	193	10.0
	2	GNPTVEVDLFTSK						
	2	VVIGMDVAASEFFR						
	2	VNQIGSVTESLQACK						
8608	P04406	Glyceraldehyde-3-phosphate dehydrogenase	3	36030	8.7	12.8	194	10.0
	2	GALQNIIPASTGAAK						
	2	VPTANVSVVDLTCR						
	2	LVINGNPITIFQER						
8615	P23396	40S ribosomal protein S3	1	26671	10	5.8	55	10.0
	2	FGFPEGSVELYAEK						

[a] The number of unique peptides that matched with the identified protein in mass analyses.
[b] Molecular mass and isoelectric point (pI) are theoretical values.

Supplementary Table 4. Tandem mass spectra and peptide sequences of proteins identified using single peptides.

Spot 7524
P00915 Carbonic anhydrase 1
790.8600 m/z (z = +2), Mass error (ppm) = -49.84, Mascot score = 43



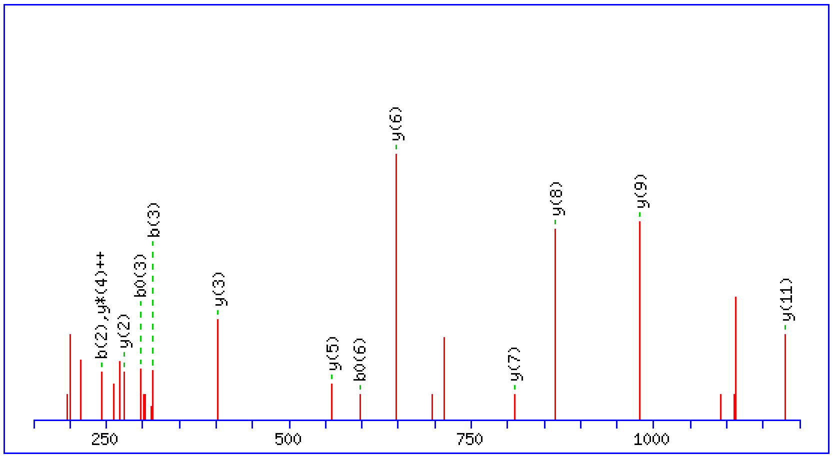
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							14
2	217.0819	109.0446			199.0713	100.0393	S	1451.7489	726.3781	1434.7223	717.8648	1433.7383	717.3728	13
3	330.1660	165.5866			312.1554	156.5813	I	1364.7169	682.8621	1347.6903	674.3488	1346.7063	673.8568	12
4	417.1980	209.1026			399.1874	200.0973	S	**1251.6328**	626.3200	1234.6062	617.8068	1233.6222	617.3148	11
5	516.2664	258.6368			498.2558	249.6316	V	1164.6008	582.8040	1147.5742	574.2907	1146.5902	573.7987	10
6	603.2984	302.1529			585.2879	293.1476	S	**1065.5323**	533.2698	1048.5058	524.7565	1047.5218	524.2645	9
7	690.3305	345.6689			672.3199	336.6636	S	**978.5003**	489.7538	961.4738	481.2405	960.4898	480.7485	8
8	819.3731	410.1902			801.3625	401.1849	E	**891.4683**	446.2378	874.4417	437.7245	873.4577	437.2325	7
9	947.4316	474.2195	930.4051	465.7062	929.4211	465.2142	Q	**762.4257**	381.7165	745.3992	373.2032			6
10	1060.5157	530.7615	1043.4891	522.2482	1042.5051	521.7562	L	**634.3671**	317.6872	617.3406	309.1739			5
11	1131.5528	566.2800	1114.5263	557.7668	1113.5422	557.2748	A	**521.2831**	261.1452	504.2565	252.6319			4
12	1259.6114	630.3093	1242.5848	621.7961	1241.6008	621.3040	Q	**450.2459**	225.6266	433.2194	217.1133			3
13	1406.6798	703.8435	1389.6533	695.3303	1388.6692	694.8383	F	**322.1874**	161.5973	305.1608	153.0840			2
14							R	175.1190	88.0631	158.0924	79.5498			1

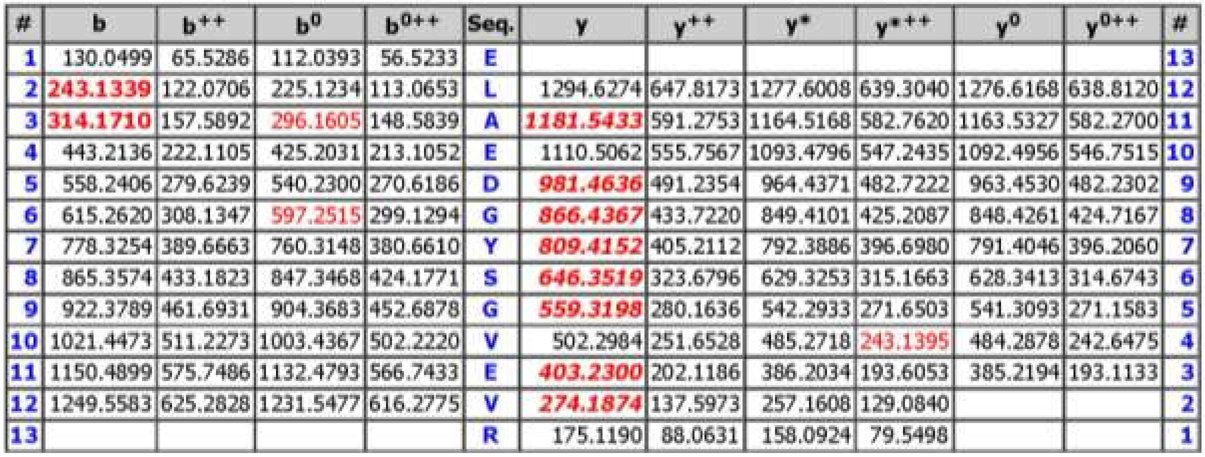
Monoisotopic mass of neutral peptide Mr(calc): 1579.7842
Ions Score: 43 **Expect:** 0.031
Matches : 13/128 fragment ions using 31 most intense peaks

Matched peptides shown in **Bold Red**

1 MASPDWGYDD KNGPEQWSKL YPIANGNNQS PVDIKTSETK HDTSLKPISV
51 SYNPATAKEI INVGHSFHVN FEDNDNRSVL KGGPFSDSYR LFQFHFHWGS
101 TNEHGSEHTV DGVKYSAELH VAHWNSAKYS SLAEAASKAD GLAVIGVLMK
151 VGEANPKLQK VLDALQAIKT KGKRAPFTNF DPSTLLPSSL DFWTYPGSLT
201 HPPLYESVTW IICK**ESISVS SEQLAQFR**SL LSNVEGDNAV PMQHNNRPTQ
251 PLKGRTVRAS F

Spot 7541
P23396 40s ribosomal protein S3
712.3198 m/z (z = +2), Mass error (ppm) = -26.45, Mascot score = 53





#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							13
2	**243.1339**	122.0706	225.1234	113.0653	L	1294.6274	647.8173	1277.6008	639.3040	1276.6168	638.8120	12
3	**314.1710**	157.5892	296.1605	148.5839	A	***1181.5433***	591.2753	1164.5168	582.7620	1163.5327	582.2700	11
4	443.2136	222.1105	425.2031	213.1052	E	1110.5062	555.7567	1093.4796	547.2435	1092.4956	546.7515	10
5	558.2406	279.6239	540.2300	270.6186	D	***981.4636***	491.2354	964.4371	482.7222	963.4530	482.2302	9
6	615.2620	308.1347	597.2515	299.1294	G	***866.4367***	433.7220	849.4101	425.2087	848.4261	424.7167	8
7	778.3254	389.6663	760.3148	380.6610	Y	***809.4152***	405.2112	792.3886	396.6980	791.4046	396.2060	7
8	865.3574	433.1823	847.3468	424.1771	S	***646.3519***	323.6796	629.3253	315.1663	628.3413	314.6743	6
9	922.3789	461.6931	904.3683	452.6878	G	***559.3198***	280.1636	542.2933	271.6503	541.3093	271.1583	5
10	1021.4473	511.2273	1003.4367	502.2220	V	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
11	1150.4899	575.7486	1132.4793	566.7433	E	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
12	1249.5583	625.2828	1231.5477	616.2775	V	***274.1874***	137.5973	257.1608	129.0840			2
13					R	175.1190	88.0631	158.0924	79.5498			1

Monoisotopic mass of neutral peptide Mr(calc): 1422.6627
Ions Score: 53 **Expect:** 0.0026
Matches : 13/116 fragment ions using 23 most intense peaks

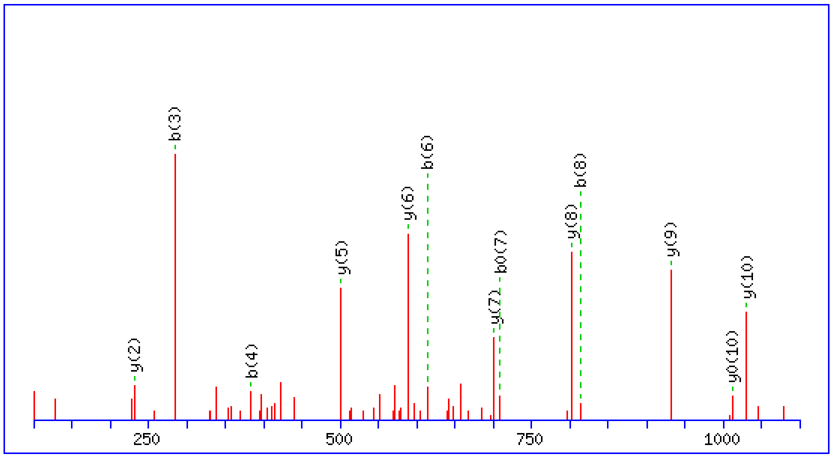
Matched peptides shown in **Bold Red**

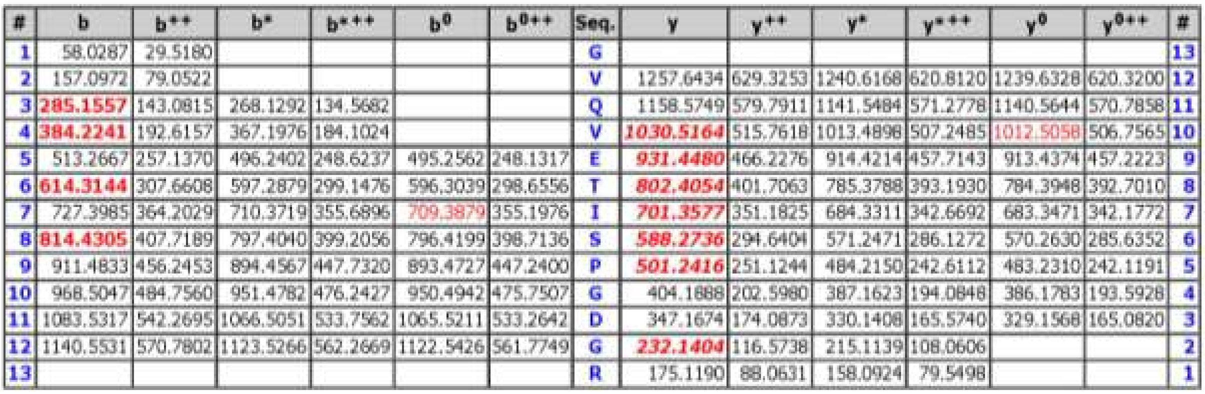
1 MAVQISKKRK FVADGIFKAE LNEFLTR**ELA EDGYSGVEVR** VTPTRTEIII
51 LATRTQNVLG EKGRRIRELT AVVQKRFGFP EGSVELYAEK VATRGLCAIA
101 QAESLRYKLL GGLAVRRACY GVLRFIMESG AKGCEVVVSG KLRGQRAKSM
151 KFVDGLMIHS GDPVNYYVDT AVRHVLLRQG VLGIKVKIML PWDPTGKIGP
201 KKPLPDHVSI VEPKDEILPT TPISEQKGGK PEPPAMPQPV PTA

Spot 8231

P62942 Peptidyl-prolyl cis-trans isomerase

657.8242 m/z (z = +2), Mass error (ppm) = -18.05, Mascot score = 53





#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							13
2	157.0972	79.0522					V	1257.6434	629.3253	1240.6168	620.8120	1239.6328	620.3200	12
3	**285.1557**	143.0815	268.1292	134.5682			Q	1158.5749	579.7911	1141.5484	571.2778	1140.5644	570.7858	11
4	**384.2241**	192.6157	367.1976	184.1024			V	***1030.5164***	515.7618	1013.4898	507.2485	1012.5058	506.7565	10
5	513.2667	257.1370	496.2402	248.6237	495.2562	248.1317	E	***931.4480***	466.2276	914.4214	457.7143	913.4374	457.2223	9
6	**614.3144**	307.6608	597.2879	299.1476	596.3039	298.6556	T	***802.4054***	401.7063	785.3788	393.1930	784.3948	392.7010	8
7	727.3985	364.2029	710.3719	355.6896	709.3879	355.1976	I	***701.3577***	351.1825	684.3311	342.6692	683.3471	342.1772	7
8	**814.4305**	407.7189	797.4040	399.2056	796.4199	398.7136	S	***588.2736***	294.6404	571.2471	286.1272	570.2630	285.6352	6
9	911.4833	456.2453	894.4567	447.7320	893.4727	447.2400	P	***501.2416***	251.1244	484.2150	242.6112	483.2310	242.1191	5
10	968.5047	484.7560	951.4782	476.2427	950.4942	475.7507	G	404.1888	202.5980	387.1623	194.0848	386.1783	193.5928	4
11	1083.5317	542.2695	1066.5051	533.7562	1065.5211	533.2642	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
12	1140.5531	570.7802	1123.5266	562.2669	1122.5426	561.7749	G	***232.1404***	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1

Monoisotopic mass of neutral peptide Mr(calc): 1313.6576

Ions Score: 53 **Expect:** 0.0041

Matches : 13/128 fragment ions using 19 most intense peaks

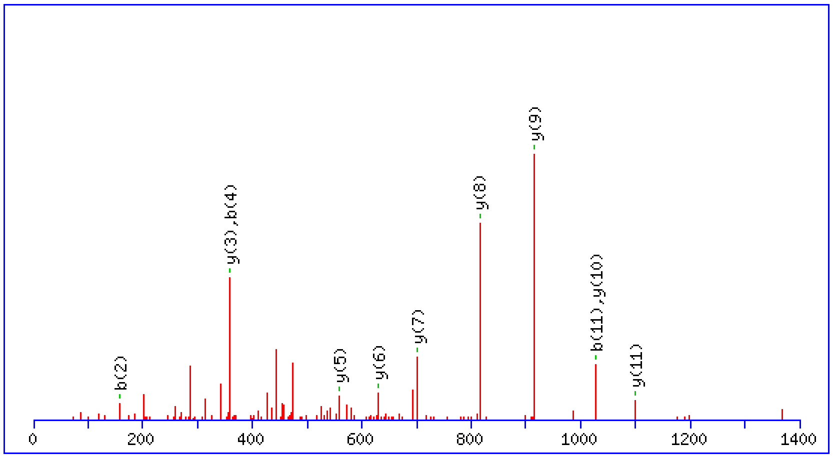
Matched peptides shown in **Bold Red**

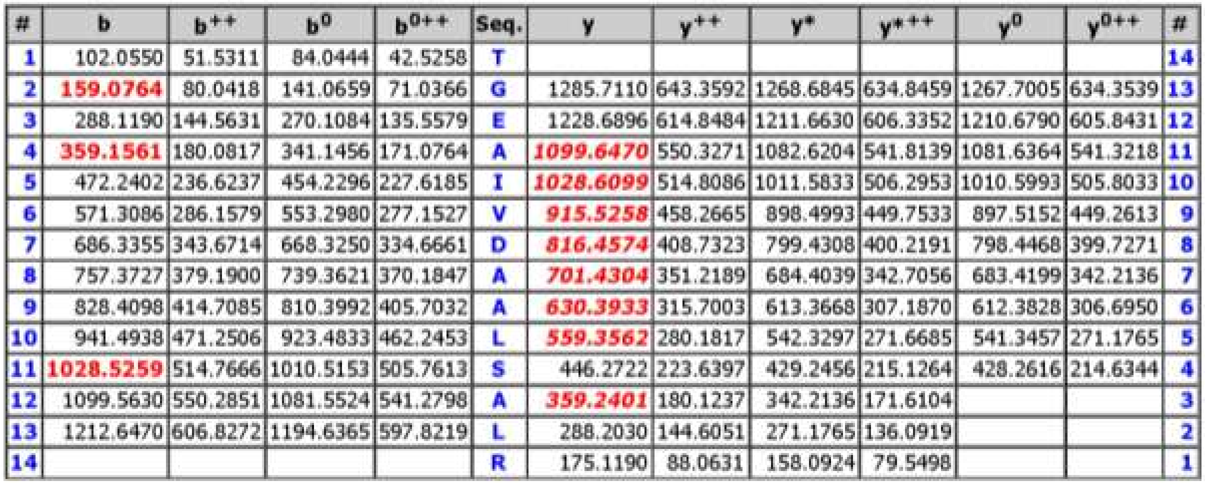
1 M**GVQVETISP GDGR**TFPKRG QTCVVHYTGM LEDGKKFDSS RDRNKPFKFM
51 LGKQEVIRGW EEGVAQMSVG QRAKLTISPD YAYGATGHPG IIPPHATLVF
101 DVELLKLE

Spot 1709

Q15084 Protein disulfide-isomerase A6

693.8756 m/z (z = +2), Mass error (ppm) = -10.66, Mascot score = 70





#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							14
2	**159.0764**	80.0418	141.0659	71.0366	G	1285.7110	643.3592	1268.6845	634.8459	1267.7005	634.3539	13
3	288.1190	144.5631	270.1084	135.5579	E	1228.6896	614.8484	1211.6630	606.3352	1210.6790	605.8431	12
4	**359.1561**	180.0817	341.1456	171.0764	A	***1099.6470***	550.3271	1082.6204	541.8139	1081.6364	541.3218	11
5	472.2402	236.6237	454.2296	227.6185	I	***1028.6099***	514.8086	1011.5833	506.2953	1010.5993	505.8033	10
6	571.3086	286.1579	553.2980	277.1527	V	***915.5258***	458.2665	898.4993	449.7533	897.5152	449.2613	9
7	686.3355	343.6714	668.3250	334.6661	D	***816.4574***	408.7323	799.4308	400.2191	798.4468	399.7271	8
8	757.3727	379.1900	739.3621	370.1847	A	***701.4304***	351.2189	684.4039	342.7056	683.4199	342.2136	7
9	828.4098	414.7085	810.3992	405.7032	A	***630.3933***	315.7003	613.3668	307.1870	612.3828	306.6950	6
10	941.4938	471.2506	923.4833	462.2453	L	***559.3562***	280.1817	542.3297	271.6685	541.3457	271.1765	5
11	**1028.5259**	514.7666	1010.5153	505.7613	S	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
12	1099.5630	550.2851	1081.5524	541.2798	A	***359.2401***	180.1237	342.2136	171.6104			3
13	1212.6470	606.8272	1194.6365	597.8219	L	288.2030	144.6051	271.1765	136.0919			2
14					R	175.1190	88.0631	158.0924	79.5498			1

Monoisotopic mass of neutral peptide Mr(calc): 1385.7514

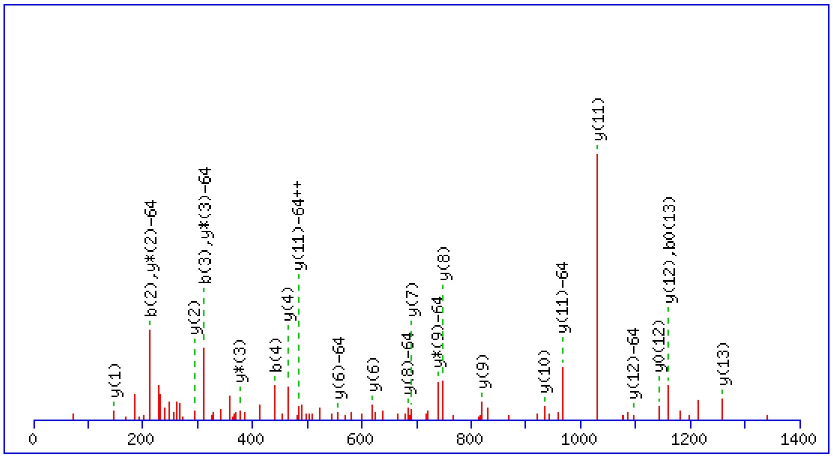
Ions Score: 70 **Expect:** 7.9e-05

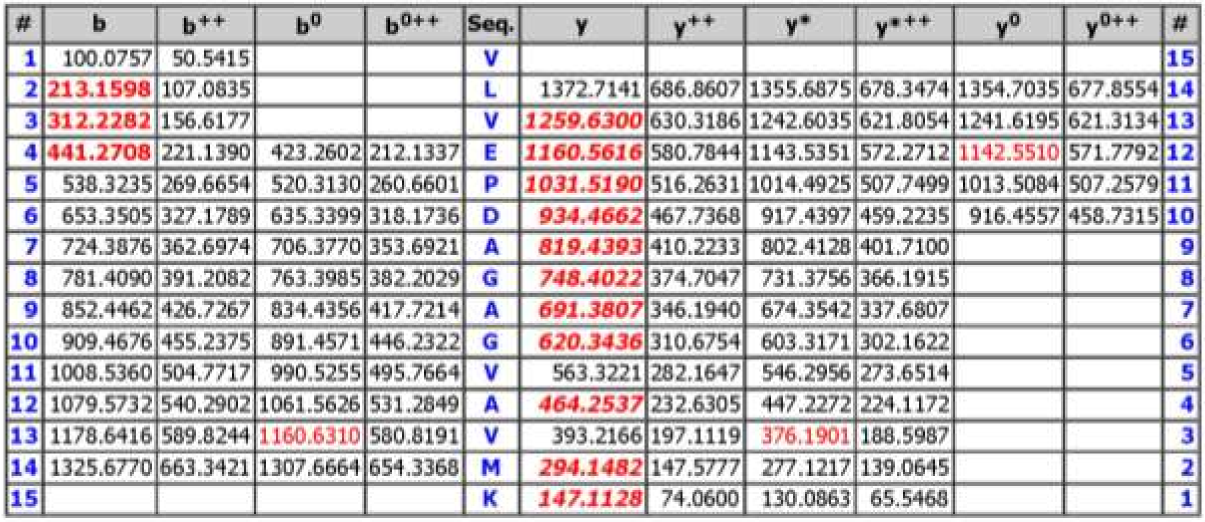
Matches : 11/124 fragment ions using 13 most intense peaks

Matched peptides shown in **Bold Red**

1 MALLVLGLVS CTFFLAVNGL YSSSDDVIEL TPSNFNREVI QSDSLWLVEF
51 YAPWCGHCQR LTPEWKKAAT ALKDVVKVGA VDADKHHSLG GQYGVQGFPT
101 IKIFGSNKNR PEDYQGGR**TG EAIVDAALSA LR**QLVKDRLG GRSGGYSSGK
151 QGRSDSSSKK DVIELTDDSF DKNVLDSEDV WMVEFYAPWC GHCKNLEPEW
201 AAAASEVKEQ TKGKVKLAAV DATVNQVLAS RYGIRGFPTI KIFQKGESPV
251 DYDGGRTRSD IVSRALDLFS DNAPPPELLE IINEDIAKRT CEEHQLCVVA
301 VLPHILDTGA AGRNSYLEVL LKLADKYKKK MWGWLWTEAG AQSELETALG
351 IGGFGYPAMA AINARKMKFA LLKGSFSEQG INEFLRELSF GRGSTAPVGG
401 GAFPTIVERE PWDGRDGELP VEDDIDLSDV ELDDLGKDEL

Spot 5506
P42126 3,2-trans-enoyl-CoA isomerase, mitochondrial
736.3927 m/z (z = +2), Mass error (ppm) = -2.97, Mascot score = 68





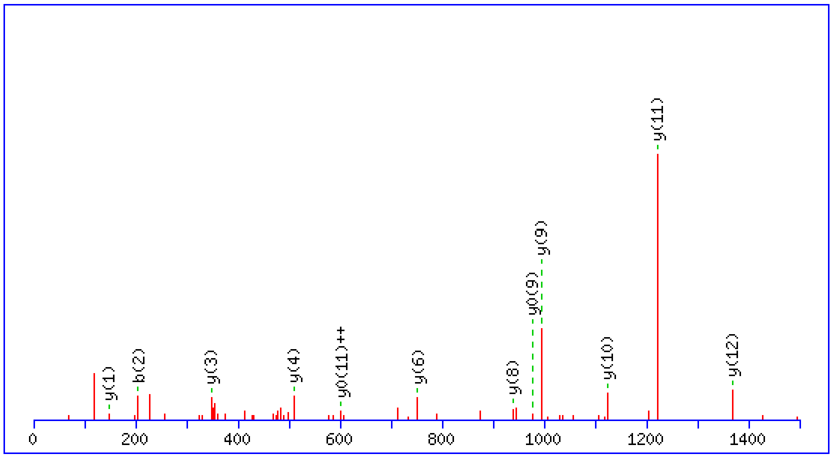
#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415			V							15
2	**213.1598**	107.0835			L	1372.7141	686.8607	1355.6875	678.3474	1354.7035	677.8554	14
3	**312.2282**	156.6177			V	**1259.6300**	630.3186	1242.6035	621.8054	1241.6195	621.3134	13
4	**441.2708**	221.1390	423.2602	212.1337	E	**1160.5616**	580.7844	1143.5351	572.2712	1142.5510	571.7792	12
5	538.3235	269.6654	520.3130	260.6601	P	**1031.5190**	516.2631	1014.4925	507.7499	1013.5084	507.2579	11
6	653.3505	327.1789	635.3399	318.1736	D	**934.4662**	467.7368	917.4397	459.2235	916.4557	458.7315	10
7	724.3876	362.6974	706.3770	353.6921	A	**819.4393**	410.2233	802.4128	401.7100			9
8	781.4090	391.2082	763.3985	382.2029	G	**748.4022**	374.7047	731.3756	366.1915			8
9	852.4462	426.7267	834.4356	417.7214	A	**691.3807**	346.1940	674.3542	337.6807			7
10	909.4676	455.2375	891.4571	446.2322	G	**620.3436**	310.6754	603.3171	302.1622			6
11	1008.5360	504.7717	990.5255	495.7664	V	563.3221	282.1647	546.2956	273.6514			5
12	1079.5732	540.2902	1061.5626	531.2849	A	**464.2537**	232.6305	447.2272	224.1172			4
13	1178.6416	589.8244	1160.6310	580.8191	V	393.2166	197.1119	376.1901	188.5987			3
14	1325.6770	663.3421	1307.6664	654.3368	M	**294.1482**	147.5777	277.1217	139.0645			2
15					K	**147.1128**	74.0600	130.0863	65.5468			1

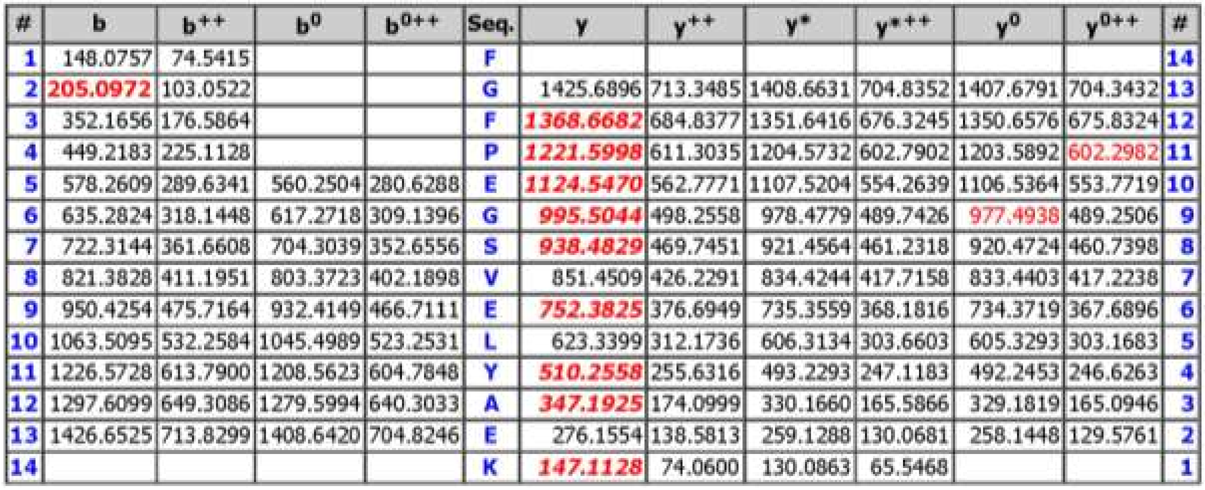
Monoisotopic mass of neutral peptide Mr(calc): 1470.7752
Ions Score: 68 **Expect:** 0.00012
Matches : 25/182 fragment ions using 45 most intense peaks

Matched peptides shown in **Bold Red**

1 MALVASVRVP ARVLLRAGAR LPGAALGRTE RAAGGGDGAR RFGSQR**VLVE**
51 **PDAGAGVAVM K**FKNPPVNSL SLEFLTELVI SLEKLENDKS FRGVILTSDR
101 PGVFSAGLDL TEMCGRSPAH YAGYWKAVQE LWLRLYQSNL VLVSAINGAC
151 PAGGCLVALT CDYRILADNP RYCIGLNETQ LGIIAPFWLK DTLENTIGHR
201 AAERALQLGL LFPPAEALQV GIVDQVVPEE QVQSTALSAI AQWMAIPDHA
251 RQLTKAMMRK ATASRLVTQR DADVQNFVSF ISKDSIQKSL QMYLERLKEE
301 KG

Spot 8615
P23396 40S ribosomal protein s3
786.8586 m/z (z = +2), Mass error (ppm) = -30.61, Mascot score = 55





#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							14
2	**205.0972**	103.0522			G	1425.6896	713.3485	1408.6631	704.8352	1407.6791	704.3432	13
3	352.1656	176.5864			F	***1368.6682***	684.8377	1351.6416	676.3245	1350.6576	675.8324	12
4	449.2183	225.1128			P	***1221.5998***	611.3035	1204.5732	602.7902	1203.5892	602.2982	11
5	578.2609	289.6341	560.2504	280.6288	E	***1124.5470***	562.7771	1107.5204	554.2639	1106.5364	553.7719	10
6	635.2824	318.1448	617.2718	309.1396	G	***995.5044***	498.2558	978.4779	489.7426	977.4938	489.2506	9
7	722.3144	361.6608	704.3039	352.6556	S	***938.4829***	469.7451	921.4564	461.2318	920.4724	460.7398	8
8	821.3828	411.1951	803.3723	402.1898	V	851.4509	426.2291	834.4244	417.7158	833.4403	417.2238	7
9	950.4254	475.7164	932.4149	466.7111	E	***752.3825***	376.6949	735.3559	368.1816	734.3719	367.6896	6
10	1063.5095	532.2584	1045.4989	523.2531	L	623.3399	312.1736	606.3134	303.6603	605.3293	303.1683	5
11	1226.5728	613.7900	1208.5623	604.7848	Y	***510.2558***	255.6316	493.2293	247.1183	492.2453	246.6263	4
12	1297.6099	649.3086	1279.5994	640.3033	A	***347.1925***	174.0999	330.1660	165.5866	329.1819	165.0946	3
13	1426.6525	713.8299	1408.6420	704.8246	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
14					K	***147.1128***	74.0600	130.0863	65.5468			1

Monoisotopic mass of neutral peptide Mr(calc): 1571.7508
Ions Score: 55 **Expect:** 0.0021
Matches : 12/120 fragment ions using 26 most intense peaks

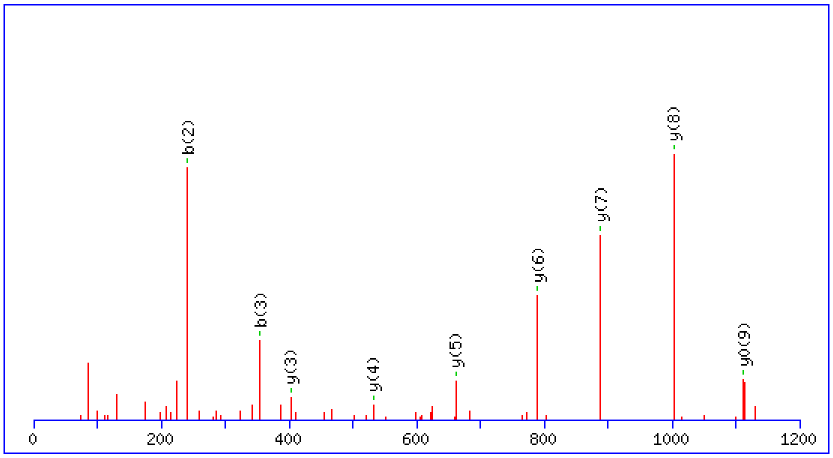
Matched peptides shown in **Bold Red**

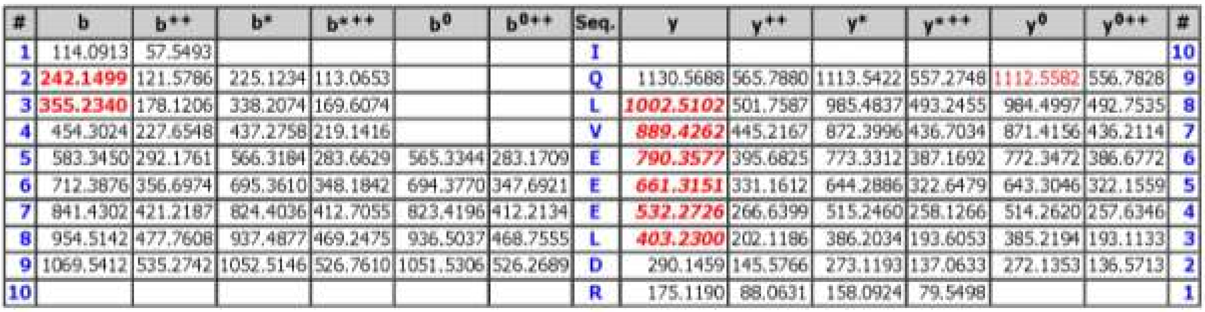
1 MAVQISKKRK FVADGIFKAE LNEFLTRELA EDGYSGVEVR VTPTRTEIII
51 LATRTQNVLG EKGRRIRELT AVVQKR**FGFP EGSVELYAEK** VATRGLCAIA
101 QAESLRYKLL GGLAVRRACY GVLRFIMESG AKGCEVVVSG KLRGQRAKSM
151 KFVDGLMIHS GDPVNYYVDT AVRHVLLRQG VLGIKVKIML PWDPTGKIGP
201 KKPLPDHVSI VEPKDEILPT TPISEQKGGK PEPPAMPQPV PTA

Spot 0614

P67936 Tropomyosin alpha-4 chain

622.2897 m/z (z = +2), Mass error (ppm) = -64.95, Mascot score = 53





#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							10
2	**242.1499**	121.5786	225.1234	113.0653			Q	1130.5688	565.7880	1113.5422	557.2748	1112.5582	556.7828	9
3	**355.2340**	178.1206	338.2074	169.6074			L	***1002.5102***	501.7587	985.4837	493.2455	984.4997	492.7535	8
4	454.3024	227.6548	437.2758	219.1416			V	***889.4262***	445.2167	872.3996	436.7034	871.4156	436.2114	7
5	583.3450	292.1761	566.3184	283.6629	565.3344	283.1709	E	***790.3577***	395.6825	773.3312	387.1692	772.3472	386.6772	6
6	712.3876	356.6974	695.3610	348.1842	694.3770	347.6921	E	***661.3151***	331.1612	644.2886	322.6479	643.3046	322.1559	5
7	841.4302	421.2187	824.4036	412.7055	823.4196	412.2134	E	***532.2726***	266.6399	515.2460	258.1266	514.2620	257.6346	4
8	954.5142	477.7608	937.4877	469.2475	936.5037	468.7555	L	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
9	1069.5412	535.2742	1052.5146	526.7610	1051.5306	526.2689	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
10							R	175.1190	88.0631	158.0924	79.5498			1

Monoisotopic mass of neutral peptide Mr(calc): 1242.6456

Ions Score: 53 **Expect:** 0.004

Matches : 9/96 fragment ions using 11 most intense peaks

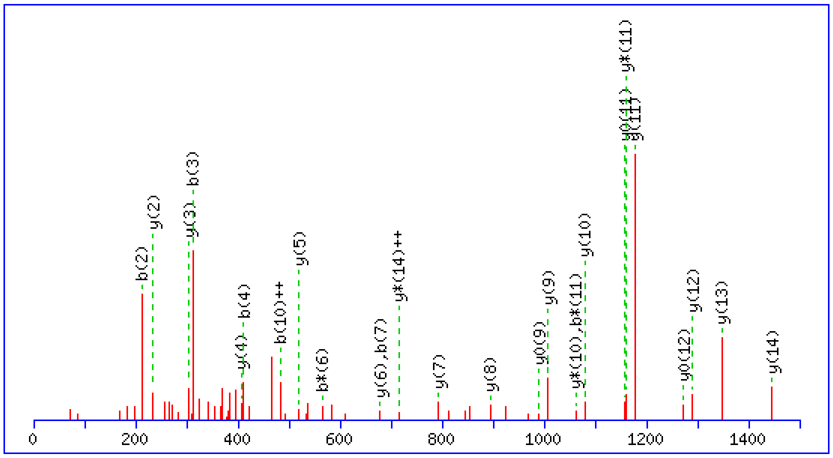
Matched peptides shown in **Bold Red**

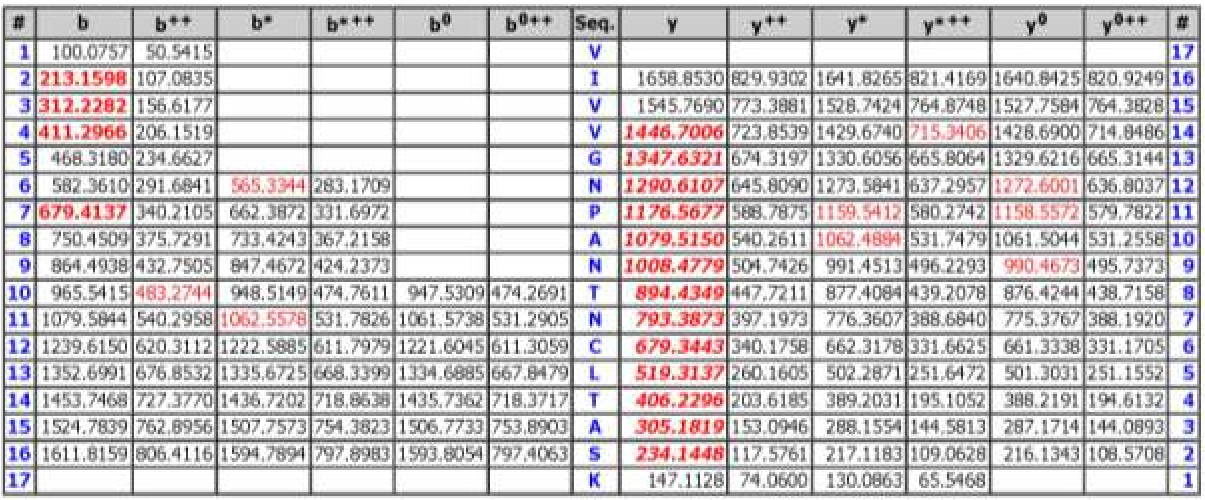
1 MDAIKKKMQM LKLDKENALD RAEQAEADKK AAEDRSKQLE DELVSLQKKL
51 KGTEDELDKY SEALKDAQEK LELAEKKATD AEADVASLNR R**IQLVEEELD**
101 **R**AQERLATAL QKLEEAEKAA DESERGMKVI ESRAQKDEEK MEIQEIQLKE
151 AKHIAEDADR KYEEVARKLV IIESDLERAE ERAELSEGKC AELEEELKTV
201 TNNLKSLEAQ AEKYSQKEDR YEEEIKVLSD KLKEAETRAE FAERSVTKLE
251 KSIDDLEDEL YAQKLKYKAI SEELDHALND MTSI

Spot 7603

P40925 Malate dehydrogenase, cytoplasmic

879.4485 m/z (z = +2), Mass error (ppm) = -18.05, Mascot score = 84





#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							17
2	**213.1598**	107.0835					I	1658.8530	829.9302	1641.8265	821.4169	1640.8425	820.9249	16
3	**312.2282**	156.6177					V	1545.7690	773.3881	1528.7424	764.8748	1527.7584	764.3828	15
4	**411.2966**	206.1519					V	**1446.7006**	723.8539	1429.6740	715.3406	1428.6900	714.8486	14
5	468.3180	234.6627					G	**1347.6321**	674.3197	1330.6056	665.8064	1329.6216	665.3144	13
6	582.3610	291.6841	565.3344	283.1709			N	**1290.6107**	645.8090	1273.5841	637.2957	1272.6001	636.8037	12
7	**679.4137**	340.2105	662.3872	331.6972			P	**1176.5677**	588.7875	1159.5412	580.2742	1158.5572	579.7822	11
8	750.4509	375.7291	733.4243	367.2158			A	**1079.5150**	540.2611	1062.4884	531.7479	1061.5044	531.2558	10
9	864.4938	432.7505	847.4672	424.2373			N	**1008.4779**	504.7426	991.4513	496.2293	990.4673	495.7373	9
10	965.5415	483.2744	948.5149	474.7611	947.5309	474.2691	T	**894.4349**	447.7211	877.4084	439.2078	876.4244	438.7158	8
11	1079.5844	540.2958	1062.5578	531.7826	1061.5738	531.2905	N	**793.3873**	397.1973	776.3607	388.6840	775.3767	388.1920	7
12	1239.6150	620.3112	1222.5885	611.7979	1221.6045	611.3059	C	**679.3443**	340.1758	662.3178	331.6625	661.3338	331.1705	6
13	1352.6991	676.8532	1335.6725	668.3399	1334.6885	667.8479	L	**519.3137**	260.1605	502.2871	251.6472	501.3031	251.1552	5
14	1453.7468	727.3770	1436.7202	718.8638	1435.7362	718.3717	T	**406.2296**	203.6185	389.2031	195.1052	388.2191	194.6132	4
15	1524.7839	762.8956	1507.7573	754.3823	1506.7733	753.8903	A	**305.1819**	153.0946	288.1554	144.5813	287.1714	144.0893	3
16	1611.8159	806.4116	1594.7894	797.8983	1593.8054	797.4063	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2
17							K	147.1128	74.0600	130.0863	65.5468			1

Monoisotopic mass of neutral peptide Mr(calc): 1756.9142

Ions Score: 84 **Expect:** 2.6e-06

Matches : 26/162 fragment ions using 49 most intense peaks

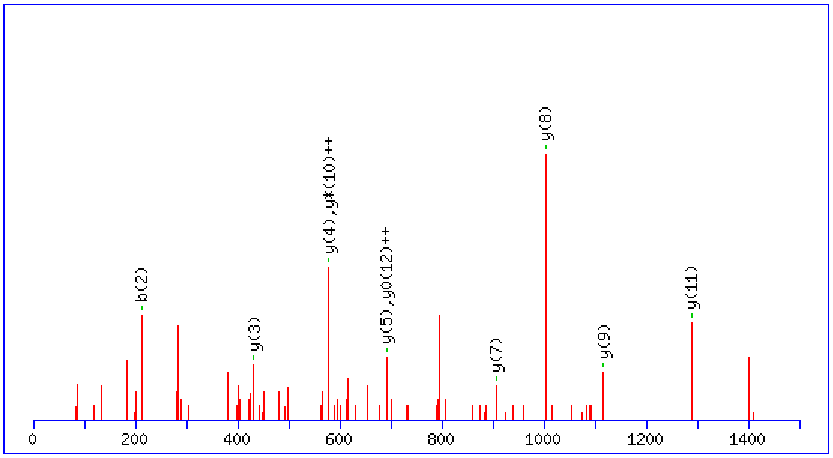
Matched peptides shown in **Bold Red**

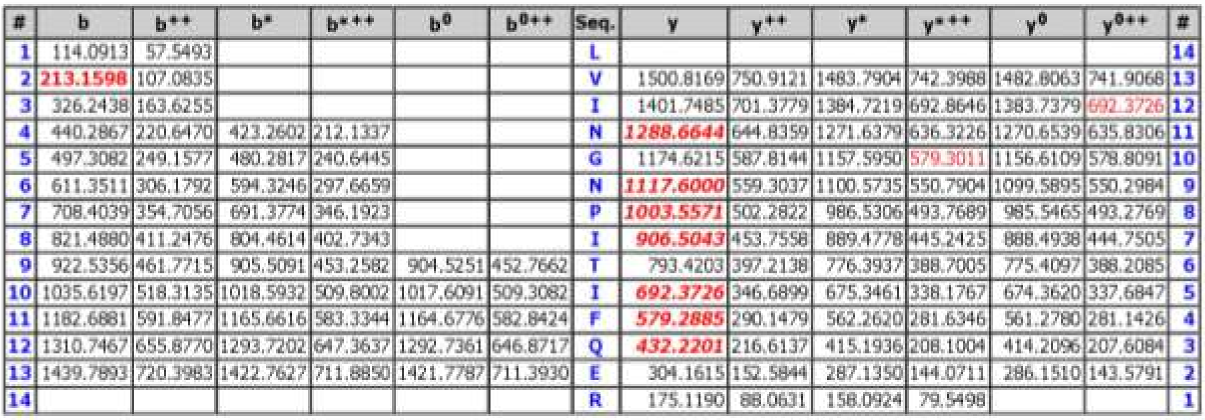
1 MSEPIRVLVT GAAGQIAYSL LYSIGNGSVF GKDQPIILVL LDITPMMGVL
51 DGVLMELQDC ALPLLKDVIA TDKEDVAFKD LDVAILVGSM PRREGMERKD
101 LLKANVKIFK SQGAALDKYA KKSVK**VIVVG NPANTNCLTA SK**SAPSIPKE
151 NFSCLTRLDH NRAKAQIALK LGVTANDVKN VIIWGNHSST QYPDVNHAKV
201 KLQGKEVGVY EALKDDSWLK GEFVTTVQQR GAAVIKARKL SSAMSAAKAI
251 CDHVRDIWFG TPEGEFVSMG VISDGNSYGV PDDLLYSFPV VIKNKTWKFV
301 EGLPINDFSR EKMDLTAKEL TEEKESAFEF LSSA

Spot 7603

P04406 Glyceraldehyde-3-phosphate dehydrogenase

807.4574 m/z (z = +2), Mass error (ppm) = 4.07, Mascot score = 48





#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							14
2	**213.1598**	107.0835					V	1500.8169	750.9121	1483.7904	742.3988	1482.8063	741.9068	13
3	326.2438	163.6255					I	1401.7485	701.3779	1384.7219	692.8646	1383.7379	692.3726	12
4	440.2867	220.6470	423.2602	212.1337			N	***1288.6644***	644.8359	1271.6379	636.3226	1270.6539	635.8306	11
5	497.3082	249.1577	480.2817	240.6445			G	1174.6215	587.8144	1157.5950	579.3011	1156.6109	578.8091	10
6	611.3511	306.1792	594.3246	297.6659			N	***1117.6000***	559.3037	1100.5735	550.7904	1099.5895	550.2984	9
7	708.4039	354.7056	691.3774	346.1923			P	***1003.5571***	502.2822	986.5306	493.7689	985.5465	493.2769	8
8	821.4880	411.2476	804.4614	402.7343			I	***906.5043***	453.7558	889.4778	445.2425	888.4938	444.7505	7
9	922.5356	461.7715	905.5091	453.2582	904.5251	452.7662	T	793.4203	397.2138	776.3937	388.7005	775.4097	388.2085	6
10	1035.6197	518.3135	1018.5932	509.8002	1017.6091	509.3082	I	***692.3726***	346.6899	675.3461	338.1767	674.3620	337.6847	5
11	1182.6881	591.8477	1165.6616	583.3344	1164.6776	582.8424	F	***579.2885***	290.1479	562.2620	281.6346	561.2780	281.1426	4
12	1310.7467	655.8770	1293.7202	647.3637	1292.7361	646.8717	Q	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	3
13	1439.7893	720.3983	1422.7627	711.8850	1421.7787	711.3930	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498			1

Monoisotopic mass of neutral peptide Mr(calc): 1612.8937

Ions Score: 48 **Expect:** 0.01

Matches : 10/132 fragment ions using 13 most intense peaks

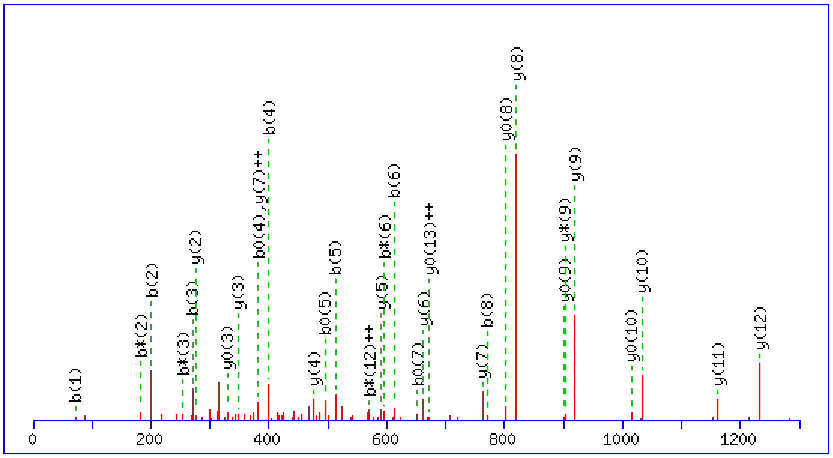
Matched peptides shown in **Bold Red**

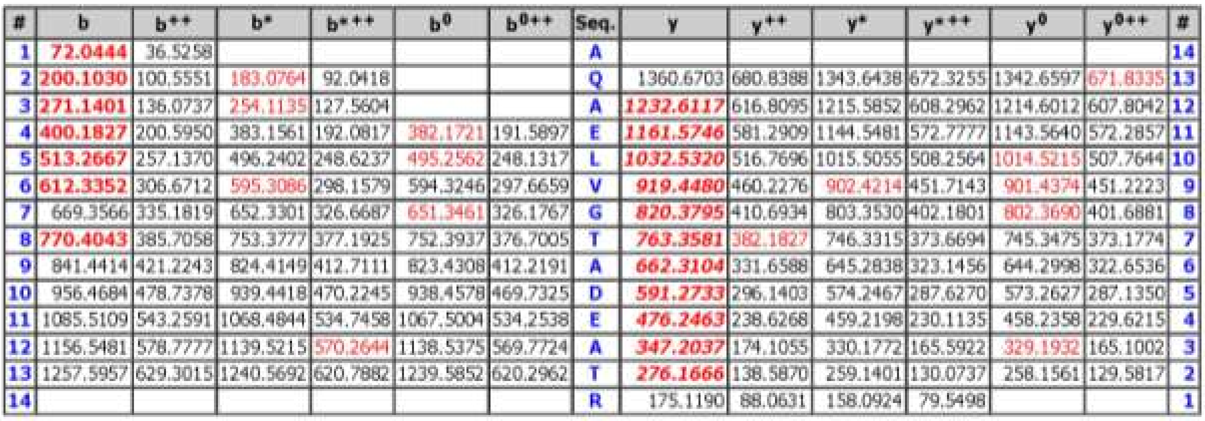
1 MGKVKVGVNG FGRIGRLVTR AAFNSGKVDI VAINDPFIDL NYMVYMFQYD
51 STHGKFHGTV KAENGK**LVIN GNPITIFQER** DPSKIKWGDA GAEYVVESTG
101 VFTTMEKAGA HLQGGAKRVI ISAPSADAPM FVMGVNHEKY DNSLKIISNA
151 SCTTNCLAPL AKVIHDNFGI VEGLMTTVHA ITATQKTVDG PSGKLWRDGR
201 GALQNIIPAS TGAAKAVGKV IPELNGKLTG MAFRVPTANV SVVDLTCRLE
251 KPAKYDDIKK VVKQASEGPL KGILGYTEHQ VVSSDFNSDT HSSTFDAGAG
301 IALNDHFVKL ISWYDNEFGY SNRVVDLMAH MASKE

Spot 0205

ATP synthase subunit delta, mitochondrial

716.3362 m/z (z = +2), Mass error (ppm) = -29.55, Mascot score = 72





#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**72.0444**	36.5258					A							14
2	**200.1030**	100.5551	183.0764	92.0418			Q	1360.6703	680.8388	1343.6438	672.3255	1342.6597	671.8335	13
3	**271.1401**	136.0737	254.1135	127.5604			A	***1232.6117***	616.8095	1215.5852	608.2962	1214.6012	607.8042	12
4	**400.1827**	200.5950	383.1561	192.0817	382.1721	191.5897	E	***1161.5746***	581.2909	1144.5481	572.7777	1143.5640	572.2857	11
5	**513.2667**	257.1370	496.2402	248.6237	495.2562	248.1317	L	***1032.5320***	516.7696	1015.5055	508.2564	1014.5215	507.7644	10
6	**612.3352**	306.6712	595.3086	298.1579	594.3246	297.6659	V	***919.4480***	460.2276	902.4214	451.7143	901.4374	451.2223	9
7	669.3566	335.1819	652.3301	326.6687	651.3461	326.1767	G	***820.3795***	410.6934	803.3530	402.1801	802.3690	401.6881	8
8	**770.4043**	385.7058	753.3777	377.1925	752.3937	376.7005	T	***763.3581***	382.1827	746.3315	373.6694	745.3475	373.1774	7
9	841.4414	421.2243	824.4149	412.7111	823.4308	412.2191	A	***662.3104***	331.6588	645.2838	323.1456	644.2998	322.6536	6
10	956.4684	478.7378	939.4418	470.2245	938.4578	469.7325	D	***591.2733***	296.1403	574.2467	287.6270	573.2627	287.1350	5
11	1085.5109	543.2591	1068.4844	534.7458	1067.5004	534.2538	E	***476.2463***	238.6268	459.2198	230.1135	458.2358	229.6215	4
12	1156.5481	578.7777	1139.5215	570.2644	1138.5375	569.7724	A	***347.2037***	174.1055	330.1772	165.5922	329.1932	165.1002	3
13	1257.5957	629.3015	1240.5692	620.7882	1239.5852	620.2962	T	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	2
14							R	175.1190	88.0631	158.0924	79.5498			1

Monoisotopic mass of neutral peptide Mr(calc): 1430.7001

Ions Score: 72 **Expect:** 0.00014

Matches : 32/146 fragment ions using 60 most intense peaks

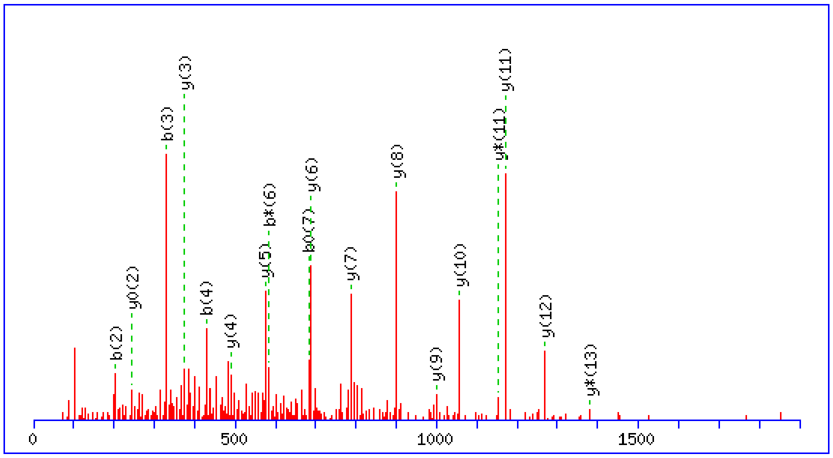
Matched peptides shown in **Bold Red**

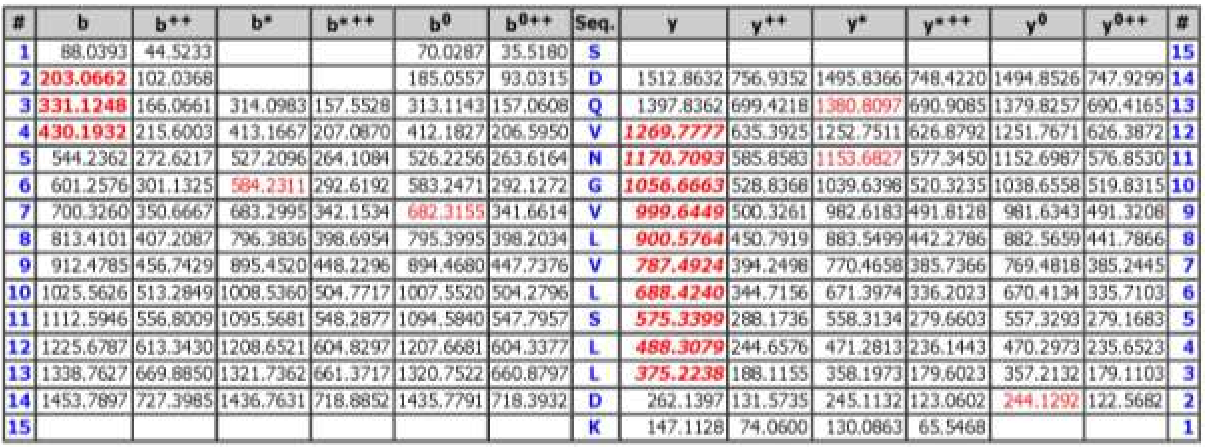
1 MLPAALLRRP GLGRLVRHAR AYAEAAAAPA AASGPNQMSF TFASPTQVFF
51 NGANVRQVDV PTLTGAFGIL AAHVPTLQVL RPGLVVVHAE DGTTSKYFVS
101 SGSIAVNADS SVQLLAEEAV TLDMLDLGAA KANLEK**AQAE LVGTADEATR**
151 AEIQIRIEAN EALVKALE

Spot 2705

Q6NZI2 Polymerase I and transcript release factor

800.4467 m/z (z = +2), Mass error (ppm) = -9.44, Mascot score = 74





#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							15
2	**203.0662**	102.0368			185.0557	93.0315	D	1512.8632	756.9352	1495.8366	748.4220	1494.8526	747.9299	14
3	**331.1248**	166.0661	314.0983	157.5528	313.1143	157.0608	Q	1397.8362	699.4218	1380.8097	690.9085	1379.8257	690.4165	13
4	**430.1932**	215.6003	413.1667	207.0870	412.1827	206.5950	V	***1269.7777***	635.3925	1252.7511	626.8792	1251.7671	626.3872	12
5	544.2362	272.6217	527.2096	264.1084	526.2256	263.6164	N	***1170.7093***	585.8583	1153.6827	577.3450	1152.6987	576.8530	11
6	601.2576	301.1325	584.2311	292.6192	583.2471	292.1272	G	***1056.6663***	528.8368	1039.6398	520.3235	1038.6558	519.8315	10
7	700.3260	350.6667	683.2995	342.1534	682.3155	341.6614	V	***999.6449***	500.3261	982.6183	491.8128	981.6343	491.3208	9
8	813.4101	407.2087	796.3836	398.6954	795.3995	398.2034	L	***900.5764***	450.7919	883.5499	442.2786	882.5659	441.7866	8
9	912.4785	456.7429	895.4520	448.2296	894.4680	447.7376	V	***787.4924***	394.2498	770.4658	385.7366	769.4818	385.2445	7
10	1025.5626	513.2849	1008.5360	504.7717	1007.5520	504.2796	L	***688.4240***	344.7156	671.3974	336.2023	670.4134	335.7103	6
11	1112.5946	556.8009	1095.5681	548.2877	1094.5840	547.7957	S	***575.3399***	288.1736	558.3134	279.6603	557.3293	279.1683	5
12	1225.6787	613.3430	1208.6521	604.8297	1207.6681	604.3377	L	***488.3079***	244.6576	471.2813	236.1443	470.2973	235.6523	4
13	1338.7627	669.8850	1321.7362	661.3717	1320.7522	660.8797	L	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	3
14	1453.7897	727.3985	1436.7631	718.8852	1435.7791	718.3932	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
15							K	147.1128	74.0600	130.0863	65.5468			1

Monoisotopic mass of neutral peptide Mr(calc): 1598.8879

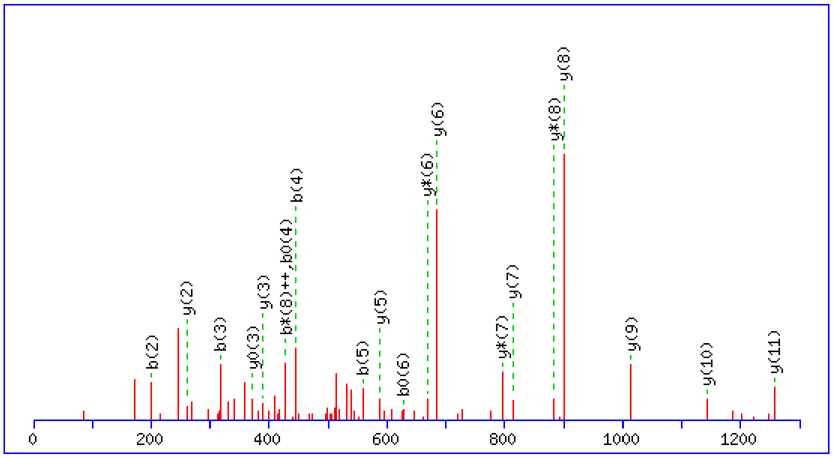
Ions Score: 74 **Expect:** 2.6e-05

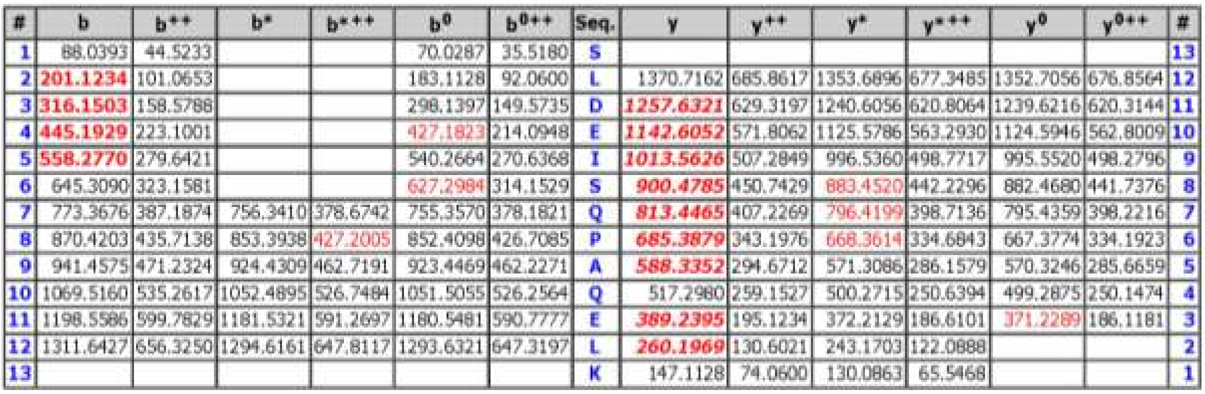
Matches : 18/162 fragment ions using 29 most intense peaks

Matched peptides shown in **Bold Red**

1 MEDPTLYIVE RPLPGYPDAE APEPSSAGAQ AAEEPSGAGS EELIK**SDQVN**
51 **GVLVLSLLDK** IIGAVDQIQL TQAQLEERQA EMEGAVQSIQ GELSKLGKAH
101 ATTSNTVSKL LEKVRKVSVN VKTVRGSLER QAGQIKKLEV NEAELLRRRN
151 FKVMIYQDEV KLPAKLSISK SLKESEALPE KEGEELGEGE RPEEDAAALE
201 LSSDEAVEVE EVIEESRAER IKRSGLRRVD DFKKAFSKEK MEKTKVRTRE
251 NLEKTRLKTK ENLEKTRHTL EKRMNKLGTR LVPAERREKL KTSRDKLRKS
301 FTPDHVVYAR SKTAVYKVPP FTFHVKKIRE GQVEVLKATE MVEVGADDDE
351 GGAERGEAGD LRRGSSPDVH ALLEITEESD AVLVDKSDSD

Spot 3409
P12111 Collagen alpha-3(VI)chain
729.3748 m/z (z = +2), Mass error (ppm) = -4.02, Mascot score = 51





#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	**201.1234**	101.0653			183.1128	92.0600	L	1370.7162	685.8617	1353.6896	677.3485	1352.7056	676.8564	12
3	**316.1503**	158.5788			298.1397	149.5735	D	***1257.6321***	629.3197	1240.6056	620.8064	1239.6216	620.3144	11
4	**445.1929**	223.1001			427.1823	214.0948	E	***1142.6052***	571.8062	1125.5786	563.2930	1124.5946	562.8009	10
5	**558.2770**	279.6421			540.2664	270.6368	I	***1013.5626***	507.2849	996.5360	498.7717	995.5520	498.2796	9
6	645.3090	323.1581			627.2984	314.1529	S	***900.4785***	450.7429	883.4520	442.2296	882.4680	441.7376	8
7	773.3676	387.1874	756.3410	378.6742	755.3570	378.1821	Q	***813.4465***	407.2269	796.4199	398.7136	795.4359	398.2216	7
8	870.4203	435.7138	853.3938	427.2005	852.4098	426.7085	P	***685.3879***	343.1976	668.3614	334.6843	667.3774	334.1923	6
9	941.4575	471.2324	924.4309	462.7191	923.4469	462.2271	A	***588.3352***	294.6712	571.3086	286.1579	570.3246	285.6659	5
10	1069.5160	535.2617	1052.4895	526.7484	1051.5055	526.2564	Q	517.2980	259.1527	500.2715	250.6394	499.2875	250.1474	4
11	1198.5586	599.7829	1181.5321	591.2697	1180.5481	590.7777	E	***389.2395***	195.1234	372.2129	186.6101	371.2289	186.1181	3
12	1311.6427	656.3250	1294.6161	647.8117	1293.6321	647.3197	L	***260.1969***	130.6021	243.1703	122.0888			2
13							K	147.1128	74.0600	130.0863	65.5468			1

Monoisotopic mass of neutral peptide Mr(calc): 1456.7409
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.0054
Matches : 20/128 fragment ions using 42 most intense peaks

Matched peptides shown in **Bold Red**

1 MRKHRHLPLV AVFCLFLSGF PTTHAQQQQA DVKNGAAADI IFLVDSSWTI
51 GEEHFQLVRE FLYDVVKSLA VGENDFHFAL VQFNGNPHTE FLLNTYRTKQ
101 EVLSHISNMS YIGGTNQTGK GLEYIMQSHL TKAAGSRAGD GVPQVIVVLT
151 DGHSKDGLAL PSAELKSADV NVFAIGVEDA DEGALKEIAS EPLNMHMFNL
201 ENFTSLHDIV GNLVSCVHSS VSPERAGDTE TLKDITAQDS ADIIFLIDGS
251 NNTGSVNFAV ILDFLVNLLE KLPIGTQQIR VGVVQFSDEP RTMFSLDTYS
301 TKAQVLGAVK ALGFAGGELA NIGLALDFVV ENHFTRAGGS RVEEGVPQVL
351 VLISAGPSSD EIRYGVVALK QASVFSFGLG AQAASRAELQ HIATDDNLVF
401 TVPEFRSFGD LQEKLLPYIV GVAQRHIVLK PPTIVTQVIE VNKRDIVFLV
451 DGSSALGLAN FNAIRDFIAK VIQRLEIGQD LIQVAVAQYA DTVRPEFYFN
501 THPTKREVIT AVRKMKPLDG SALYTGSALD FVRNNLFTSS AGYRAAEGIP

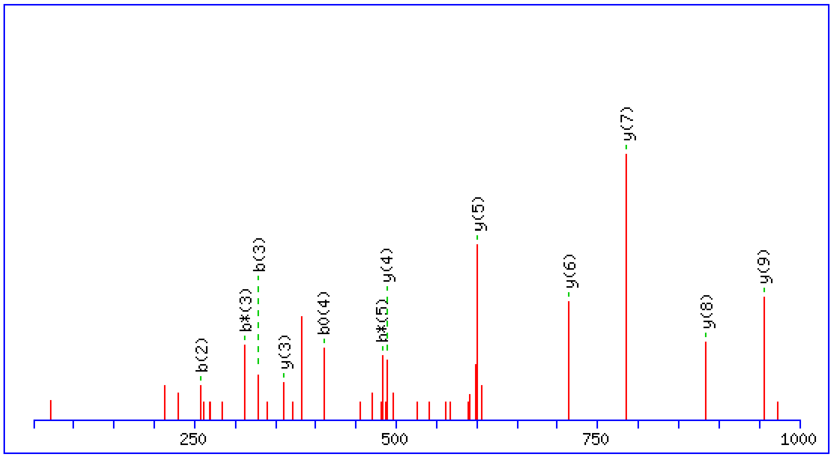
551 KLLVLITGGK **SLDEISQPAQ ELK**RSSIMAF AIGNKGADQA ELEEIAFDSS
601 LVFIPAEFRA APLQGMLPGL LAPLRTLSGT PEVHSNKRDI IFLLDGSANV
651 GKTNFPYVRD FVMNLVNSLD IGNDNIRVGL VQFSDTPVTE FSLNTYQTKS
701 DILGHLRQLQ LQGGSGLNTG SALSYVYANH FTEAGGSRIR EHVPQLLLLL
751 TAGQSEDSYL QAANALTRAG ILTFCVGASQ ANKAELEQIA FNPSLVYLMD
801 DFSSLPALPQ QLIQPLTTYV SGGVEEVPLA QPESKRDILF LFDGSANLVG
851 QFPVVRDFLY KIIDELNVKP EGTRIAVAQY SDDVKVESRF DEHQSKPEIL
901 NLVKRMKIKT GKALNLGYAL DYAQRYIFVK SAGSRIEDGV LQFLVLLVAG
951 RSSDRVDGPA SNLKQSGVVP FIFQAKNADP AELEQIVLSP AFILAAESLP
1001 KIGDLHPQIV NLLKSVHNGA PAPVSGEKDV VFLLDGSEGV RSGFPLLKEF
1051 VQRVVESLDV GQDRVRVAVV QYSDRTRPEF YLNSYMNKQD VVNAVRQLTL
1101 LGGPTPNTGA ALEFVLRNIL VSSAGSRITE GVPQLLIVLT ADRSGDDVRN
1151 PSVVVKRGGA VPIGIGIGNA DITEMQTISF IPDFAVAIPT FRQLGTVQQV
1201 ISERVTQLTR EELSRLQPVL QPLPSPGVGG KRDVVFLIDG SQSAGPEFQY
1251 VRTLIERLVD YLDVGFDTTR VAVIQFSDDP KVEFLLNAHS SKDEVQNAVQ
1301 RLRPKGGRQI NVGNALEYVS RNIFKRPLGS RIEEGVPQFL VLISSGKSDD
1351 EVDDPAVELK QFGVAPFTIA RNADQEELVK ISLSPEYVFS VSTFRELPSL
1401 EQKLLTPITT LTSEQIQKLL ASTRYPPPAV ESDAADIVFL IDSSEGVRPD
1451 GFAHIRDFVS RIVRRLNIGP SKVRVGVVQF SNDVFPEFYL KTYRSQAPVL
1501 DAIRRLRLRG GSPLNTGKAL EFVARNLFVK SAGSRIEDGV PQHLVLVLGG
1551 KSQDDVSRFA QVIRSSGIVS LGVGDRNIDR TELQTITNDP RLVFTVREFR
1601 ELPNIEERIM NSFGPSAATP APPGVDTPPP SRPEKKKADI VFLLDGSINF
1651 RRDSFQEVLR FVSEIVDTVY EDGDSIQVGL VQYNSDPTDE FFLKDFSTKR
1701 QIIDAINKVV YKGGRHANTK VGLEHLRVNH FVPEAGSRLD QRVPQIAFVI
1751 TGGKSVEDAQ DVSLALTQRG VKVFAVGVRN IDSEEVGKIA SNSATAFRVG
1801 NVQELSELSE QVLETLHDAM HETLCPGVTD AAKACNLDVI LGFDGSRDQN
1851 VFVAQKGFES KVDAILNRIS QMHRVSCSGG RSPTVRVSVV ANTPSGPVEA
1901 FDFDEYQPEM LEKFRNMRSQ HPYVLTEDTL KVYLNKFRQS SPDSVKVVIH
1951 FTDGADGDLA DLHRASENLR QEGVRALILV GLERVVNLER LMHLEFGRGF
2001 MYDRPLRLNL LDLDYELAEQ LDNIAEKACC GVPCKCSGQR GDRGPIGSIG
2051 PKGIPGEDGY RGYPGDEGGP GERGPPGVNG TQGFQGCPGQ RGVKGSRGFP
2101 GEKGEVGEIG LDGLDGEDGD KGLPGSSGEK GNPGRRGDKG PRGEKGERGD
2151 VGIRGDPGNP GQDSQERGPK GETGDLGPMG VPGRDGVPGG PGETGKNGGF
2201 GRRGPPGAKG NKGGPGQPGF EGEQGTRGAQ GPAGPAGPPG LIGEQGISGP
2251 RGSGGAAGAP GERGRTGPLG RKGEPGEPGP KGGIGNRGPR GETGDDGRDG
2301 VGSEGRRGKK GERGFPGYPG PKGNPGEPGL NGTTGPKGIR GRRGNSGPPG
2351 IVGQKGDPGY PGPAGPKGNR GDSIDQCALI QSIKDKCPCC YGPLECPVFP
2401 TELAFALDTS EGVNQDTFGR MRDVVLSIVN DLTIAESNCP RGARVAVVTY
2451 NNEVTTEIRF ADSKRKSVLL DKIKNLQVAL TSKQQSLETA MSFVARNTFK
2501 RVRNGFLMRK VAVFFSNTPT RASPQLREAV LKLSDAGITP LFLTRQEDRQ
2551 LINALQINNT AVGHALVLPA GRDLTDFLEN VLTCHVCLDI CNIDPSCGFG
2601 SWRPSFRDRR AAGSDVDIDM AFILDSAETT TLFQFNEMKK YIAYLVRQLD
2651 MSPDPKASQH FARVAVVQHA PSESVDNASM PPVKVEFSLT DYGSKEKLVD
2701 FLSRGMTQLQ GTRALGSAIE YTIENVFESA PNPRDLKIVV LMLTGEVPEQ
2751 QLEEAQRVIL QAKCKGYFFV VLGIGRKVNI KEVYTFASEP NDVFFKLVDK
2801 STELNEEPLM RFGRLLPSFV SSENAFYLSP DIRKQCDWFQ GDQPTKNLVK
2851 FGHKQVNVPN NVTSSPTSNP VTTTKPVTTT KPVTTTTKPV TTTTKPVTII
2901 NQPSVKPAAA KPAPAKPVAA KPVATKTATV RPPVAVKPAT AAKPVAAKPA
2951 AVRPPAAAAA KPVATKPEVP RPQAAKPAAT KPATTKPMVK MSREVQVFEI

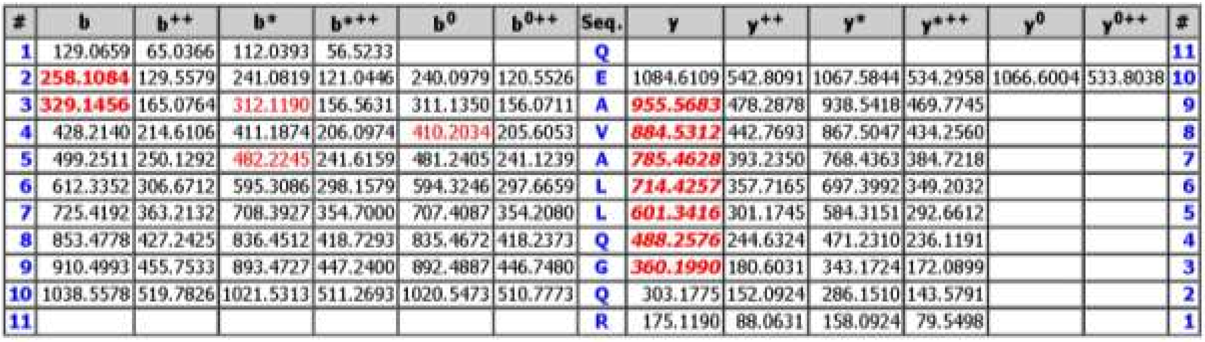
3001 TENSAKLHWE RPEPPGPYFY DLTVTSAHDQ SLVLKQNLTV TDRVIGGLLA
3051 GQTYHVAVVC YLRSQVRATY HGSFSTKKSQ PPPPQPARSA SSSTINLMVS
3101 TEPLALTETD ICKLPKDEGT CRDFILKWYY DPNTKSCARF WYGGCGGNEN
3151 KFGSQKECEK VCAPVLAKPG VISVMGT

Spot 5207

P46108 Proto-oncogene C-crk

606.8183 m/z (z = +2), Mass error (ppm) = -33.15, Mascot score = 52





#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							11
2	**258.1084**	129.5579	241.0819	121.0446	240.0979	120.5526	E	1084.6109	542.8091	1067.5844	534.2958	1066.6004	533.8038	10
3	**329.1456**	165.0764	312.1190	156.5631	311.1350	156.0711	A	**955.5683**	478.2878	938.5418	469.7745			9
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	V	**884.5312**	442.7693	867.5047	434.2560			8
5	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	A	**785.4628**	393.2350	768.4363	384.7218			7
6	612.3352	306.6712	595.3086	298.1579	594.3246	297.6659	L	**714.4257**	357.7165	697.3992	349.2032			6
7	725.4192	363.2132	708.3927	354.7000	707.4087	354.2080	L	**601.3416**	301.1745	584.3151	292.6612			5
8	853.4778	427.2425	836.4512	418.7293	835.4672	418.2373	Q	**488.2576**	244.6324	471.2310	236.1191			4
9	910.4993	455.7533	893.4727	447.2400	892.4887	446.7480	G	**360.1990**	180.6031	343.1724	172.0899			3
10	1038.5578	519.7826	1021.5313	511.2693	1020.5473	510.7773	Q	303.1775	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1

Monoisotopic mass of neutral peptide Mr(calc): 1211.6622
Ions Score: 52 **Expect:** 0.0045
Matches : 12/100 fragment ions using 21 most intense peaks

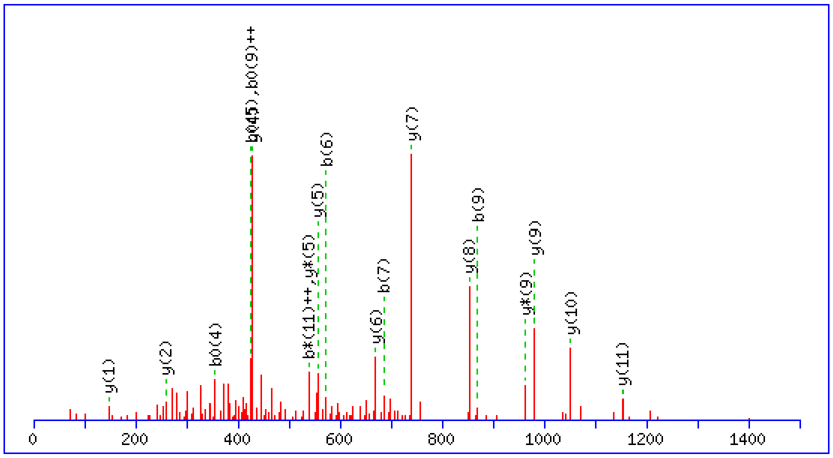
Matched peptides shown in **Bold Red**

1 MAGNFDSEER SSWYWGRLSR **QEAVALLQGQ R**HGVFLVRDS STSPGDYVLS
51 VSENSRVSHY IINSSGPRPP VPPSPAQPPP GVSPSRLRIG DQEFDSLPAL
101 LEFYKIHYLD TTTLIEPVSR SRQGSGVILR QEEAEYVRAL FDFNGNDEED
151 LPFKKGDILR IRDKPEEQWW NAEDSEGKRG MIPVPYVEKY RPASASVSAL
201 IGGNQEGSHP QPLGGPEPGP YAQPSVNTPL PNLQNGPIYA RVIQKRVPNA
251 YDKTALALEV GELVKVTKIN VSGQWEGECN GKRGHFPFTH VRLLDQQNPD
301 EDFS

Spot 7418

P04179 Superoxide dismutase [Mn], mitochondrial

712.8985 m/z (z = +2), Mass error (ppm) = -14.76, Mascot score = 83



#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							14
2	173.0557	87.0315			155.0451	78.0262	D	1367.7893	684.3983	1350.7627	675.8850	1349.7787	675.3930	13
3	272.1241	136.5657			254.1135	127.5604	V	1252.7624	626.8848	1235.7358	618.3715	1234.7518	617.8795	12
4	373.1718	187.0895			355.1612	178.0842	T	***1153.6939***	577.3506	1136.6674	568.8373	1135.6834	568.3453	11
5	444.2089	222.6081			426.1983	213.6028	A	***1052.6463***	526.8268	1035.6197	518.3135			10
6	**572.2675**	286.6374	555.2409	278.1241	554.2569	277.6321	Q	***981.6091***	491.3082	964.5826	482.7949			9
7	**685.3515**	343.1794	668.3250	334.6661	667.3410	334.1741	I	***853.5506***	427.2789	836.5240	418.7656			8
8	756.3886	378.6980	739.3621	370.1847	738.3781	369.6927	A	***740.4665***	370.7369	723.4400	362.2236			7
9	**869.4727**	435.2400	852.4462	426.7267	851.4621	426.2347	L	***669.4294***	335.2183	652.4028	326.7051			6
10	997.5313	499.2693	980.5047	490.7560	979.5207	490.2640	Q	***556.3453***	278.6763	539.3188	270.1630			5
11	1094.5841	547.7957	1077.5575	539.2824	1076.5735	538.7904	P	***428.2867***	214.6470	411.2602	206.1337			4
12	1165.6212	583.3142	1148.5946	574.8009	1147.6106	574.3089	A	331.2340	166.1206	314.2074	157.6074			3
13	1278.7052	639.8563	1261.6787	631.3430	1260.6947	630.8510	L	***260.1969***	130.6021	243.1703	122.0888			2
14							K	***147.1128***	74.0600	130.0863	65.5468			1

Monoisotopic mass of neutral peptide Mr(calc): 1423.8035
Ions Score: 83 **Expect:** 3.7e-06
Matches : 19/124 fragment ions using 25 most intense peaks

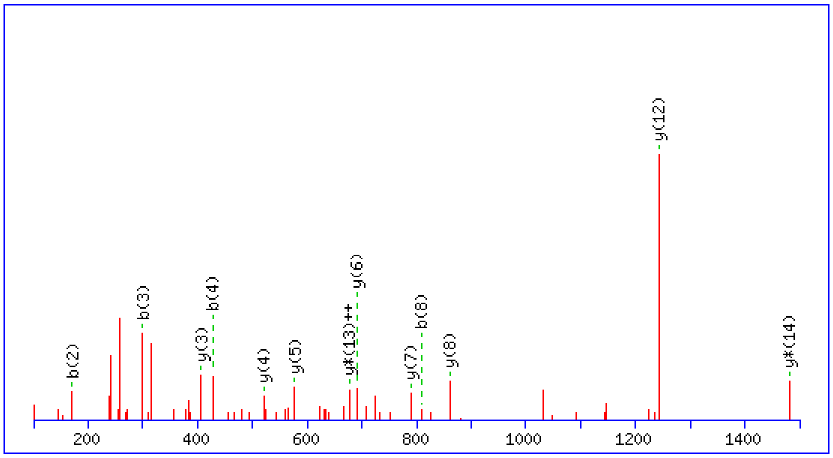
Matched peptides shown in **Bold Red**

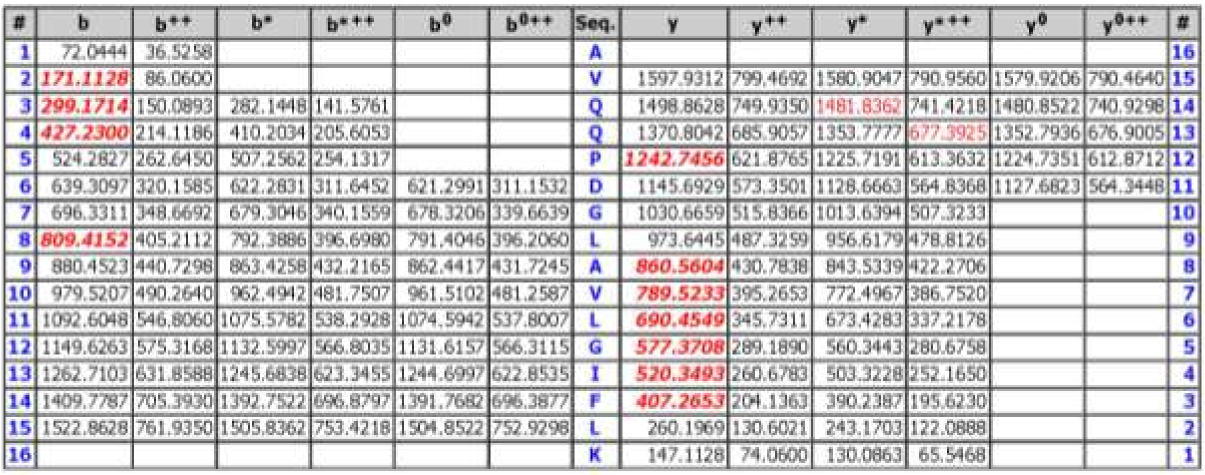
1 MLSRAVCGTS RQLAPALGYL GSRQKHSLPD LPYDYGALEP HINAQIMQLH
51 HSKHHAAYVN NLNVTEEKYQ EALAK**GDVTA QIALQPALK**F NGGGHINHSI
101 FWTNLSPNGG GEPKGELLEA IKRDFGSFDK FKEKLTAASV GVQGSGWGWL
151 GFNKERGHLQ IAACPNQDPL QGTTGLIPLL GIDVWEHAYY LQYKNVRPDY
201 LKAIWNVINW ENVTERYMAC KK

Spot 8609

P00918 Carbonic anhydrase 2

834.9622 m/z (z = +2), Mass error (ppm) = -30.69, Mascot score = 41





#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							16
2	**171.1128**	86.0600					V	1597.9312	799.4692	1580.9047	790.9560	1579.9206	790.4640	15
3	**299.1714**	150.0893	282.1448	141.5761			Q	1498.8628	749.9350	1481.8362	741.4218	1480.8522	740.9298	14
4	**427.2300**	214.1186	410.2034	205.6053			Q	1370.8042	685.9057	1353.7777	677.3925	1352.7936	676.9005	13
5	524.2827	262.6450	507.2562	254.1317			P	**1242.7456**	621.8765	1225.7191	613.3632	1224.7351	612.8712	12
6	639.3097	320.1585	622.2831	311.6452	621.2991	311.1532	D	1145.6929	573.3501	1128.6663	564.8368	1127.6823	564.3448	11
7	696.3311	348.6692	679.3046	340.1559	678.3206	339.6639	G	1030.6659	515.8366	1013.6394	507.3233			10
8	**809.4152**	405.2112	792.3886	396.6980	791.4046	396.2060	L	973.6445	487.3259	956.6179	478.8126			9
9	880.4523	440.7298	863.4258	432.2165	862.4417	431.7245	A	**860.5604**	430.7838	843.5339	422.2706			8
10	979.5207	490.2640	962.4942	481.7507	961.5102	481.2587	V	**789.5233**	395.2653	772.4967	386.7520			7
11	1092.6048	546.8060	1075.5782	538.2928	1074.5942	537.8007	L	**690.4549**	345.7311	673.4283	337.2178			6
12	1149.6263	575.3168	1132.5997	566.8035	1131.6157	566.3115	G	**577.3708**	289.1890	560.3443	280.6758			5
13	1262.7103	631.8588	1245.6838	623.3455	1244.6997	622.8535	I	**520.3493**	260.6783	503.3228	252.1650			4
14	1409.7787	705.3930	1392.7522	696.8797	1391.7682	696.3877	F	**407.2653**	204.1363	390.2387	195.6230			3
15	1522.8628	761.9350	1505.8362	753.4218	1504.8522	752.9298	L	260.1969	130.6021	243.1703	122.0888			2
16							K	147.1128	74.0600	130.0863	65.5468			1

Monoisotopic mass of neutral peptide Mr(calc): 1667.9610

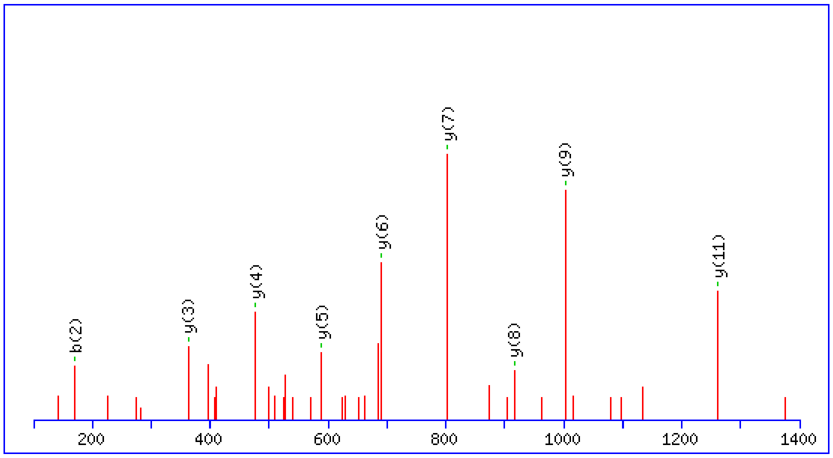
Ions Score: 41 **Expect:** 0.05

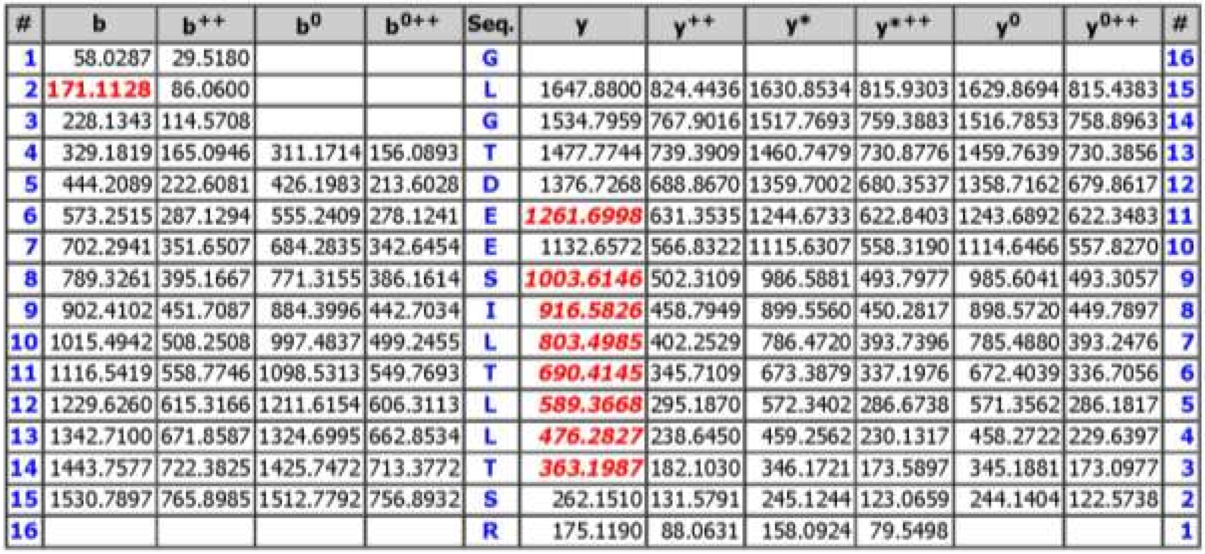
Matches : 13/146 fragment ions using 23 most intense peaks

Matched peptides shown in **Bold Red**

1 MSHHWGYGKH NGPEHWHKDF PIAKGERQSP VDIDTHTAKY DPSLKPLSVS
51 YDQATSLRIL NNGHAFNVEF DDSQDKAVLK GGPLDGTYRL IQFHFHWGSL
101 DGQGSEHTVD KKKYAAELHL VHWNTKYGDF GK**AVQQPDGL AVLGIFLK**VG
151 SAKPGLQKVV DVLDSIKTKG KSADFTNFDP RGLLPESLDY WTYPGSLTTP
201 PLLECVTWIV LKEPISVSSE QVLKFRKLNF NGEGEPEELM VDNWRPAQPL
251 KNRQIKASFK

Spot 0405
P08758 Annexin A5
852.9268 m/z (z = +2), Mass error (ppm) = -32.33, Mascot score = 67





#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							16
2	**171.1128**	86.0600			L	1647.8800	824.4436	1630.8534	815.9303	1629.8694	815.4383	15
3	228.1343	114.5708			G	1534.7959	767.9016	1517.7693	759.3883	1516.7853	758.8963	14
4	329.1819	165.0946	311.1714	156.0893	T	1477.7744	739.3909	1460.7479	730.8776	1459.7639	730.3856	13
5	444.2089	222.6081	426.1983	213.6028	D	1376.7268	688.8670	1359.7002	680.3537	1358.7162	679.8617	12
6	573.2515	287.1294	555.2409	278.1241	E	***1261.6998***	631.3535	1244.6733	622.8403	1243.6892	622.3483	11
7	702.2941	351.6507	684.2835	342.6454	E	1132.6572	566.8322	1115.6307	558.3190	1114.6466	557.8270	10
8	789.3261	395.1667	771.3155	386.1614	S	***1003.6146***	502.3109	986.5881	493.7977	985.6041	493.3057	9
9	902.4102	451.7087	884.3996	442.7034	I	***916.5826***	458.7949	899.5560	450.2817	898.5720	449.7897	8
10	1015.4942	508.2508	997.4837	499.2455	L	***803.4985***	402.2529	786.4720	393.7396	785.4880	393.2476	7
11	1116.5419	558.7746	1098.5313	549.7693	T	***690.4145***	345.7109	673.3879	337.1976	672.4039	336.7056	6
12	1229.6260	615.3166	1211.6154	606.3113	L	***589.3668***	295.1870	572.3402	286.6738	571.3562	286.1817	5
13	1342.7100	671.8587	1324.6995	662.8534	L	***476.2827***	238.6450	459.2562	230.1317	458.2722	229.6397	4
14	1443.7577	722.3825	1425.7472	713.3772	T	***363.1987***	182.1030	346.1721	173.5897	345.1881	173.0977	3
15	1530.7897	765.8985	1512.7792	756.8932	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
16					R	175.1190	88.0631	158.0924	79.5498			1

Monoisotopic mass of neutral peptide Mr(calc): 1703.8941
Ions Score: 67 **Expect:** 0.00013
Matches : 9/142 fragment ions using 12 most intense peaks

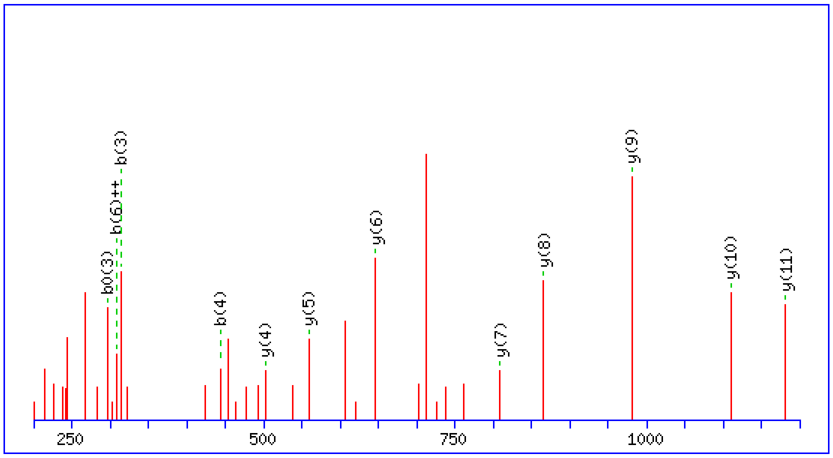
Matched peptides shown in **Bold Red**

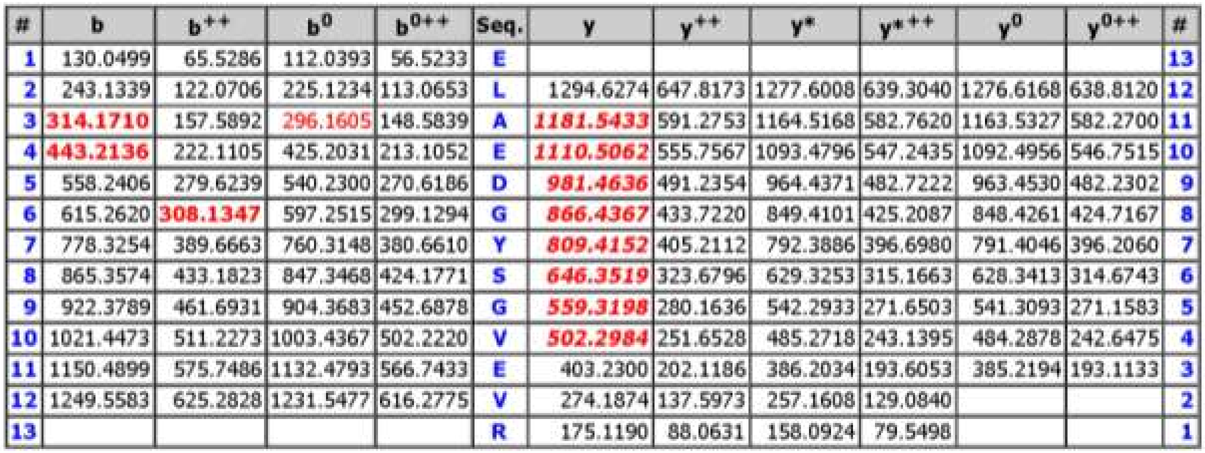
1 MAQVLRGTVT DFPGFDERAD AETLRKAMK**G LGTDEESILT LLTSR**SNAQR
51 QEISAAFKTL FGRDLLDDLK SELTGKFEKL IVALMKPSRL YDAYELKHAL
101 KGAGTNEKVL TEIIASRTPE ELRAIKQVYE EEYGSSLEDD VVGDTSGYYQ
151 RMLVVLLQAN RDPDAGIDEA QVEQDAQALF QAGELKWGTD EEKFITIFGT
201 RSVSHLRKVF DKYMTISGFQ IEETIDRETS GNLEQLLLAV VKSIRSIPAY
251 LAETLYYAMK GAGTDDHTLI RVMVSRSEID LFNIRKEFRK NFATSLYSMI
301 KGDTSGDYKK ALLLLCGEDD

Spot 2405

P23396 40S ribosomal protein S3

712.3304 m/z (z = +2), Mass error (ppm) = -11.55, Mascot score = 66





#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							13
2	243.1339	122.0706	225.1234	113.0653	L	1294.6274	647.8173	1277.6008	639.3040	1276.6168	638.8120	12
3	**314.1710**	157.5892	296.1605	148.5839	A	***1181.5433***	591.2753	1164.5168	582.7620	1163.5327	582.2700	11
4	**443.2136**	222.1105	425.2031	213.1052	E	***1110.5062***	555.7567	1093.4796	547.2435	1092.4956	546.7515	10
5	558.2406	279.6239	540.2300	270.6186	D	***981.4636***	491.2354	964.4371	482.7222	963.4530	482.2302	9
6	615.2620	**308.1347**	597.2515	299.1294	G	***866.4367***	433.7220	849.4101	425.2087	848.4261	424.7167	8
7	778.3254	389.6663	760.3148	380.6610	Y	***809.4152***	405.2112	792.3886	396.6980	791.4046	396.2060	7
8	865.3574	433.1823	847.3468	424.1771	S	***646.3519***	323.6796	629.3253	315.1663	628.3413	314.6743	6
9	922.3789	461.6931	904.3683	452.6878	G	***559.3198***	280.1636	542.2933	271.6503	541.3093	271.1583	5
10	1021.4473	511.2273	1003.4367	502.2220	V	***502.2984***	251.6528	485.2718	243.1395	484.2878	242.6475	4
11	1150.4899	575.7486	1132.4793	566.7433	E	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
12	1249.5583	625.2828	1231.5477	616.2775	V	274.1874	137.5973	257.1608	129.0840			2
13					R	175.1190	88.0631	158.0924	79.5498			1

Monoisotopic mass of neutral peptide Mr(calc): 1422.6627

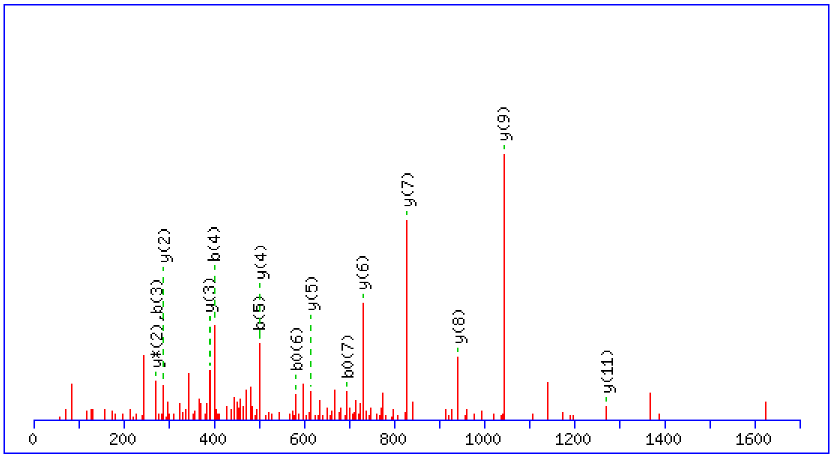
Ions Score: 66 **Expect:** 0.0002

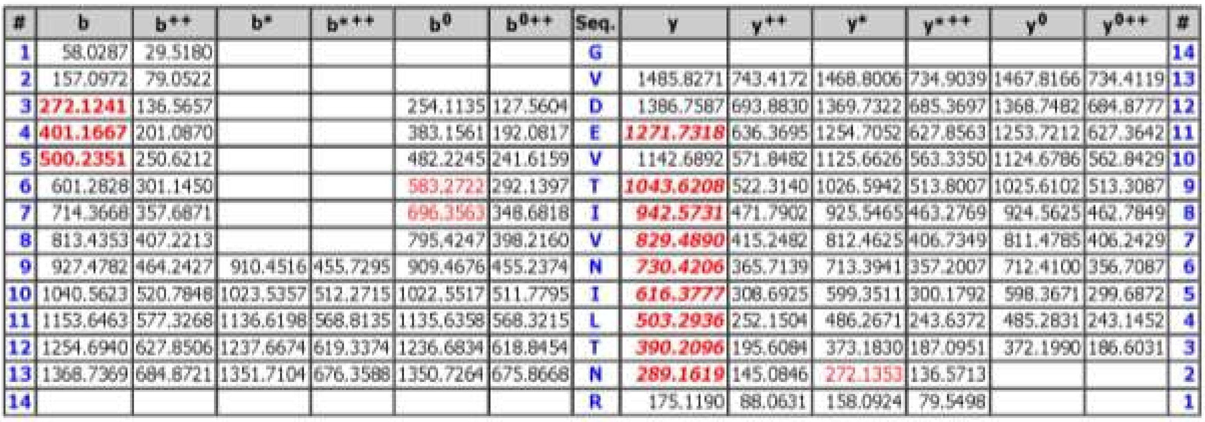
Matches : 12/116 fragment ions using 17 most intense peaks

Matched peptides shown in **Bold Red**

1 MAVQISKKRK FVADGIFKAE LNEFLTR**ELA** **EDGYSGVEVR** VTPTRTEIII
51 LATRTQNVLG EKGRRIRELT AVVQKRFGFP EGSVELYAEK VATRGLCAIA
101 QAESLRYKLL GGLAVRRACY GVLRFIMESG AKGCEVVVSG KLRGQRAKSM
151 KFVDGLMIHS GDPVNYYVDT AVRHVLLRQG VLGIKVKIML PWDPTGKIGP
201 KKPLPDHVSI VEPKDEILPT TPISEQKGGK PEPPAMPQPV PTA

Spot 3506
P07355 Annexin A2
771.9196 m/z (z = +2), Mass error (ppm) = -10.82, Mascot score = 43





#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							14
2	157.0972	79.0522					V	1485.8271	743.4172	1468.8006	734.9039	1467.8166	734.4119	13
3	**272.1241**	136.5657			254.1135	127.5604	D	1386.7587	693.8830	1369.7322	685.3697	1368.7482	684.8777	12
4	**401.1667**	201.0870			383.1561	192.0817	E	***1271.7318***	636.3695	1254.7052	627.8563	1253.7212	627.3642	11
5	**500.2351**	250.6212			482.2245	241.6159	V	1142.6892	571.8482	1125.6626	563.3350	1124.6786	562.8429	10
6	601.2828	301.1450			583.2722	292.1397	T	***1043.6208***	522.3140	1026.5942	513.8007	1025.6102	513.3087	9
7	714.3668	357.6871			696.3563	348.6818	I	***942.5731***	471.7902	925.5465	463.2769	924.5625	462.7849	8
8	813.4353	407.2213			795.4247	398.2160	V	***829.4890***	415.2482	812.4625	406.7349	811.4785	406.2429	7
9	927.4782	464.2427	910.4516	455.7295	909.4676	455.2374	N	***730.4206***	365.7139	713.3941	357.2007	712.4100	356.7087	6
10	1040.5623	520.7848	1023.5357	512.2715	1022.5517	511.7795	I	***616.3777***	308.6925	599.3511	300.1792	598.3671	299.6872	5
11	1153.6463	577.3268	1136.6198	568.8135	1135.6358	568.3215	L	***503.2936***	252.1504	486.2671	243.6372	485.2831	243.1452	4
12	1254.6940	627.8506	1237.6674	619.3374	1236.6834	618.8454	T	***390.2096***	195.6084	373.1830	187.0951	372.1990	186.6031	3
13	1368.7369	684.8721	1351.7104	676.3588	1350.7264	675.8668	N	***289.1619***	145.0846	272.1353	136.5713			2
14							R	175.1190	88.0631	158.0924	79.5498			1

Monoisotopic mass of neutral peptide Mr(calc): 1541.8413
Ions Score: 43 **Expect:** 0.03
Matches : 15/132 fragment ions using 39 most intense peaks

Matched peptides shown in **Bold Red**

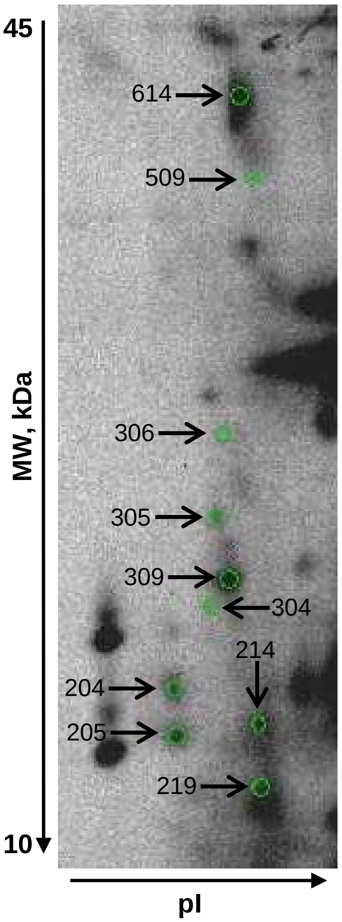
1 MSTVHEILCK LSLEGDHSTP PSAYGSVKAY TNFDAERDAL NIETAIKTK**G**
51 **VDEVTIVNIL TNR**SNAQRQD IAFAYQRRTK KELASALKSA LSGHLETVIL
101 GLLKTPAQYD ASELKASMKG LGTDEDSLIE IICSRTNQEL QEINRVYKEM
151 YKTDLEKDII SDTSGDFRKL MVALAKGRRA EDGSVIDYEL IDQDARDLYD
201 AGVKRKGTDV PKWISIMTER SVPHLQKVFD RYKSYSPYDM LESIRKEVKG
251 DLENAFLNLV QCIQNKPLYF ADRLYDSMKG KGTRDKVLIR IMVSRSEVDM
301 LKIRSEFKRK YGKSLYYYIQ QDTKGDYQKA LLYLCGGDD

Supplementary Table 5. Results of the proteome pathway analysis. The table shows 8 most statistically significant interconnected groups of proteins (pathways) according to GeneGo Metacore analysis. The function of such groups can be estimated by associated GO Process terms.

No	Network	GO Processes	p-Value
1	G3P2, PGK1, TPI1, FAAA, G3P1	pyruvate metabolic process (27.8%; 2.520e-09), gluconeogenesis (22.2%; 2.256e-08), hexose biosynthetic process (22.2%; 6.045e-08), monosaccharide biosynthetic process (22.2%; 1.871e-07), glycolysis (22.2%; 2.375e-07)	5.93E-27
2	HSPA1A, Cyclophilin A, PRDX1, HSP70, Lamin A/C	cellular response to stress (41.0%; 2.130e-12), cellular response to stimulus (41.0%; 1.826e-09), response to DNA damage stimulus (28.2%; 5.033e-09), response to stress (53.8%; 5.165e-09), cellular response to hydrogen peroxide (12.8%; 5.225e-09)	8.93E-34
3	DJ-1, FKBP12, A-FABP, Annexin V, PRDX1	positive regulation of biological process (68.2%; 2.144e-14), positive regulation of cellular process (63.6%; 1.832e-13), response to stimulus (77.3%; 9.068e-12), response to stress (56.8%; 3.680e-11), regulation of biological quality (52.3%; 1.320e-10)	1.06E-27
4	ENO1, Annexin II, Lamin A/C, Vimentin, HSPA1A	regulation of apoptosis (53.2%; 1.826e-17), positive regulation of biological process (72.3%; 2.094e-17), regulation of programmed cell death (53.2%; 2.420e-17), regulation of cell death (53.2%; 2.727e-17), regulation of binding (31.9%; 1.334e-16)	7.23E-25
5	Vimentin, DJ-1, PRDX1, A-FABP, G3P2	regulation of biological quality (57.5%; 9.503e-12), homeostatic process (42.5%; 7.719e-11), positive regulation of cellular process (57.5%; 5.035e-10), response to stress (55.0%; 1.296e-09), positive regulation of biological process (57.5%; 3.546e-09)	1.29E-22
6	Carbonic anhydrase II, CRK, DJ-1, Cyclophilin A, Annexin V	protein kinase cascade (36.1%; 1.446e-11), intracellular signaling cascade (47.2%; 8.781e-09), regulation of immune system process (30.6%; 4.584e-08), stress-activated protein kinase signaling pathway (16.7%; 5.265e-08), regulation of cellular component movement (22.2%; 1.789e-07)	1.12E-17
7	ENO1, CRK, PRDX1, PGK1, Catalase	protein kinase cascade (46.7%; 1.049e-20), intracellular signaling cascade (62.2%; 9.012e-18), regulation of phosphorylation (44.4%; 1.318e-16), regulation of phosphorus metabolic process (44.4%; 2.598e-16), regulation of phosphate metabolic process (44.4%; 2.598e-16)	3.48E-17
8	Annexin II, Annexin V, 14-3-3 gamma, PKC-alpha, Rac1	regulation of receptor-mediated endocytosis (23.1%; 9.745e-07), regulation of phosphorylation (46.2%; 5.805e-06), regulation of phosphorus metabolic process (46.2%; 7.113e-06), regulation of phosphate metabolic process (46.2%; 7.113e-06), regulation of vesicle-mediated transport (30.8%; 8.384e-06)	1.68E-07

Supplementary Figure 1

Vimentin

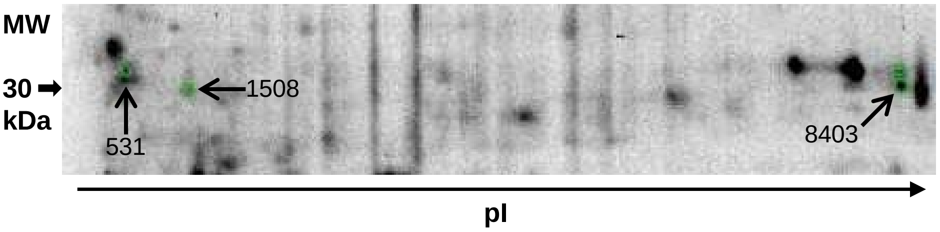


Spot #	Start - End
614	105 – 304
509	146 – 401
309	130 – 235
306	105 – 235
305	105 – 235
304	130 – 207
219	322 – 401
214	130 – 235
205	197 – 235
204	197 – 235

Vimentin was identified in spots ranging in 10 kDa – 40 kDa. Based on the peptides identified in mass spectrometry data, a table including start and end positions of protein sequences is presented. These data suggest that these spots represent various fragments of vimentin.

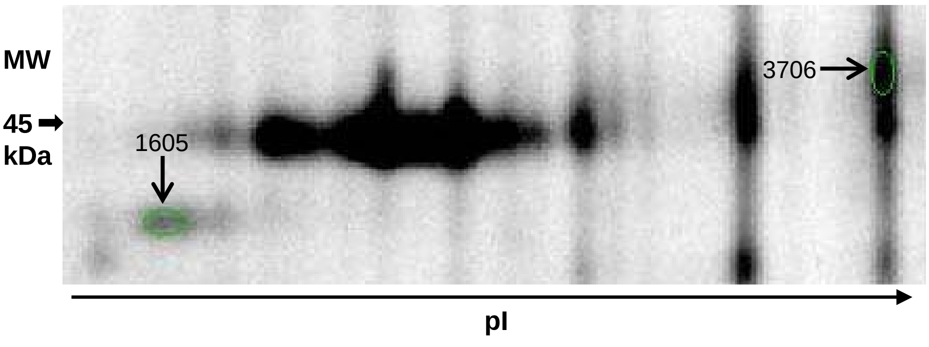
Supplementary Figure 2

Carbonic anhydrase 2



Carbonic anhydrase 2 was identified in protein spots 531, 1508, 7541 and 8403. These spots are present at similar MW but different pI, representing various isoforms of carbonic anhydrase 2.

Supplementary Figure 3



Actin, gamma-enteric smooth muscle

Two isoforms of actin were identified in spots 1605 and 3706.

Supplementary Figure 4

Total protein stained on nitrocellulose using MemCode reversible stain