Supplementary Figure 1.

Protein band 4 (-Mn): PilC2

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Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 22%

Matched peptides shown in Bold Red

   1 MFSHTGGGGQ AQAQTYKYAI VMNERKQPEV KWESQYNQSA LKDKGRERTF
  51 SHTSQKNRFG ITSNFISFNN NDELVSQQSG TAVFGTATYL PPYGKVSGFD
 101 TAELNKRGNA VNWIHTTRPG LAGYGYDGIR CGSAQDCPKL TYKTRFSFDN
 151 PDLVKTRGGL DRHTEPSREN SPIYKLKDHP WLGVSFNLGG EGTAKDGRSS
 201 SKLVSSFDEN NSNSNQNLVY TTEGHRISLG NWQRETTAMA YYLNAKLHLL
 251 DKKQIKDIAQ GKTVRLGVLK PSIDVKTQNT GLSGLLNFWS KWDIKDNGQI
 301 PVKLGLPQVK AVRCTNTAHP NKTAQAPSPA LTAPALWFGP VQNGKVQMYS
 351 ASVSTYPGSS SSRIFLQELK TQTDPARPGR HSLAALDTQN IKSREPNFNS
 401 RQTVIRLPGG VYKINPGKNG GRVAGINGND GKNDTFGIFK DRYVTPETDE
 451 WSEMLLPWTA RYYGNDDIFK TFNQPNSKTQ NGKKQYSQKY RIRTKEDDND
 501 KPRDLGDIVN SPIVAVGGYL ATSANDGMVH IFKKTGTDER SYNLKLSYIP
 551 GTMERKDIEG NDSDLAKELR TFAEKGYVGD RYGVDGGFVL RRITDDQDKQ
 601 KHFFMFGAMG LGGRGAYALD LSKIDSSNLT GVSMFDVQND KNNNNNKNDN
 651 NRVKLGYTVG TPQIGKTQNG KYAAFLASGY AAKNIGSGDN TTALYVYDLG
 701 NTLGTPIAKI EVKDGKGGLS SPTLVDKDLD GTVDIAYAGD RGGNMYRFDL
 751 SSDKPSEWTV RTIFEGGKPI TSAPAVSRLA DKRVVIFGTG SDLSEEDVTS
 801 QDIQHVYGIF DNDTDMGAAQ DGQGKGLLEQ NLMQENKTLF LNKRSDGSGS
 851 KGWVVKLREG ERVTVKPTVV LRTAFVTIRS YTGNDKCGAQ TAILGINTAD
 901 GGALTPRSAR PIVPDHNSVA QYSGHKKTSK GKSIPIGCME KGGKTVCPNG
 951 YVYDKPVNVR YLDEKKTDDF PVTADGDAGG SGTFKEGKKP ARNNRCFSGK
1001 GVRTLLMNDL DSLDITGPMC GIKRLSWREV FF
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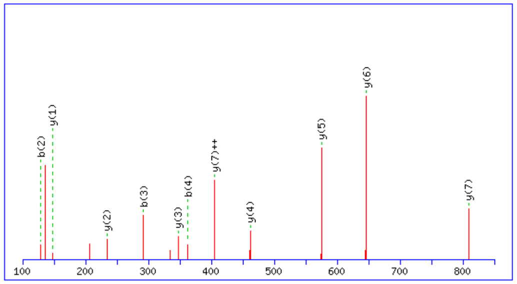
Score: 868 M$_r$: 115036



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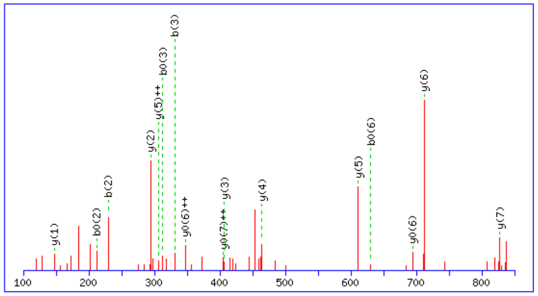
Monoisotopic mass of neutral peptide Mr(calc): 936.4916
Ions Score: 58  Expect: 0.029
Matches (Bold Red): 11/68 fragment ions using 18 most intense peaks
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							9
2	**129.0659**	65.0366			A	880.4775	440.7424	863.4509	432.2291	862.4669	431.7371	8
3	**292.1292**	146.5682			Y	**809.4403**	**405.2238**	792.4138	396.7105	791.4298	396.2185	7
4	**363.1663**	182.0868			A	**646.3770**	323.6921	629.3505	315.1789	628.3665	314.6869	6
5	476.2504	238.6288			L	**575.3399**	288.1736	558.3134	279.6603	557.3293	279.1683	5
6	591.2773	296.1423	573.2667	287.1370	D	**462.2558**	231.6316	445.2293	223.1183	444.2453	222.6263	4
7	704.3614	352.6843	686.3508	343.6790	L	**347.2289**	174.1181	330.2023	165.6048	329.2183	165.1128	3
8	791.3934	396.2003	773.3828	387.1951	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2
9					K	**147.1128**	74.0600	130.0863	65.5468			1



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Monoisotopic mass of neutral peptide Mr(calc): 940.4654
Ions Score: 40  Expect: 1.8
Matches (Bold Red): 16/72 fragment ions using 42 most intense peaks
```
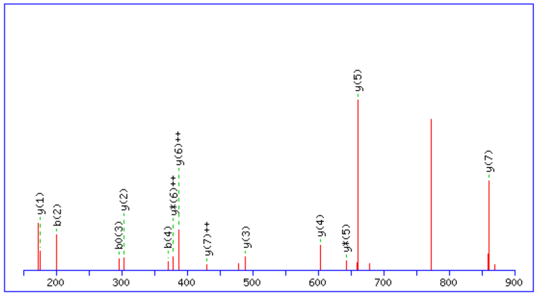

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							8
2	**230.0771**	115.5422	213.0506	107.0289	**212.0666**	106.5369	D	**827.4298**	414.2185	810.4032	405.7053	809.4192	**405.2132**	7
3	**331.1248**	166.0661	314.0983	157.5528	**313.1143**	157.0608	T	**712.4028**	356.7051	695.3763	348.1918	**694.3923**	**347.6998**	6
4	478.1932	239.6003	461.1667	231.0870	460.1827	230.5950	F	**611.3552**	**306.1812**	594.3286	297.6679			5
5	535.2147	268.1110	518.1882	259.5977	517.2041	259.1057	G	**464.2867**	232.6470	447.2602	224.1337			4
6	648.2988	324.6530	631.2722	316.1397	**630.2882**	315.6477	I	**407.2653**	204.1363	390.2387	195.6230			3
7	795.3672	398.1872	778.3406	389.6740	777.3566	389.1819	F	**294.1812**	147.5942	277.1547	139.0810			2
8							K	**147.1128**	74.0600	130.0863	65.5468			1



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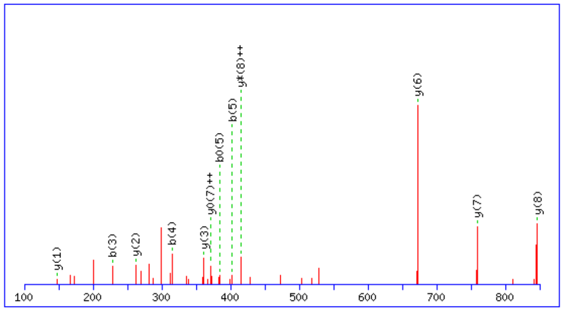
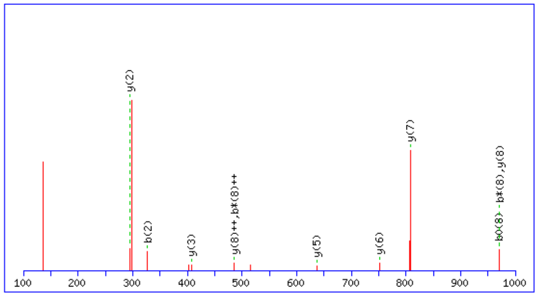
Monoisotopic mass of neutral peptide Mr(calc): 972.5141
Ions Score: 50  Expect: 0.19
Matches (Bold Red): 13/62 fragment ions using 19 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							8
2	**201.1234**	101.0653			183.1128	92.0600	S	**860.4373**	**430.7223**	843.4108	422.2090	842.4268	421.7170	7
3	314.2074	157.6074			**296.1969**	148.6021	L	773.4053	**387.2063**	756.3787	**378.6930**			6
4	**371.2289**	186.1181			353.2183	177.1128	G	**660.3212**	330.6643	**643.2947**	322.1510			5
5	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	N	**603.2998**	302.1535	586.2732	293.6402			4
6	671.3511	336.1792	654.3246	327.6659	653.3406	327.1739	W	**489.2568**	245.1321	472.2303	236.6188			3
7	799.4097	400.2085	782.3832	391.6952	781.3991	391.2032	Q	**303.1775**	152.0924	286.1510	143.5791			2
8							R	**175.1190**	88.0631	158.0924	79.5498			1



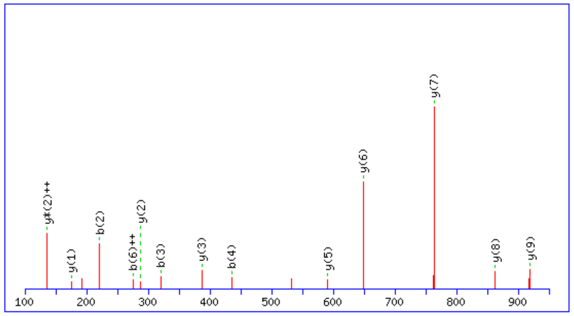
Monoisotopic mass of neutral peptide Mr(calc): 1072.5764
Ions Score: 34 Expect: 7.1
Matches (Bold Red): 12/92 fragment ions using 27 most intense peaks

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180			G							11
2	115.0502	58.0287			G	1016.5623	508.7848	999.5357	500.2715	998.5517	499.7795	10
3	**228.1343**	114.5708			L	959.5408	480.2740	942.5142	471.7608	941.5302	471.2687	9
4	**315.1663**	158.0868	297.1557	149.0815	S	**846.4567**	423.7320	829.4302	**415.2187**	828.4462	414.7267	8
5	**402.1983**	201.6028	**384.1878**	192.5975	S	**759.4247**	380.2160	742.3981	371.7027	741.4141	**371.2107**	7
6	499.2511	250.1292	481.2405	241.1239	P	**672.3927**	336.7000	655.3661	328.1867	654.3821	327.6947	6
7	600.2988	300.6530	582.2882	291.6477	T	575.3399	288.1736	558.3134	279.6603	557.3293	279.1683	5
8	713.3828	357.1951	695.3723	348.1898	L	474.2922	237.6498	457.2657	229.1365	456.2817	228.6445	4
9	812.4512	406.7293	794.4407	397.7240	V	**361.2082**	181.1077	344.1816	172.5944	343.1976	172.1024	3
10	927.4782	464.2427	909.4676	455.2374	D	**262.1397**	131.5735	245.1132	123.0602	244.1292	122.5682	2
11					K	**147.1128**	74.0600	130.0863	65.5468			1



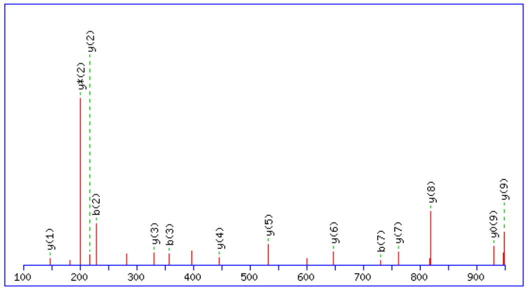
Monoisotopic mass of neutral peptide Mr(calc): 1133.5029
Ions Score: 34 Expect: 6.7
Matches (Bold Red): 11/76 fragment ions using 14 most intense peaks

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							9
2	**327.1339**	164.0706					Y	**971.4469**	**486.2271**	954.4203	477.7138	953.4363	477.2218	8
3	384.1554	192.5813					G	**808.3836**	404.6954	791.3570	396.1821	790.3730	395.6901	7
4	498.1983	249.6028	481.1718	241.0895			N	**751.3621**	376.1847	734.3355	367.6714	733.3515	367.1794	6
5	613.2253	307.1163	596.1987	298.6030	595.2147	298.1110	D	**637.3192**	319.1632	620.2926	310.6499	619.3086	310.1579	5
6	728.2522	364.6297	711.2257	356.1165	710.2416	355.6245	D	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
7	841.3363	421.1718	824.3097	412.6585	823.3257	412.1665	I	**407.2653**	204.1363	390.2387	195.6230			3
8	988.4047	494.7060	**971.3781**	**486.1927**	**970.3941**	485.7007	F	**294.1812**	147.5942	277.1547	139.0810			2
9							K	147.1128	74.0600	130.0863	65.5468			1



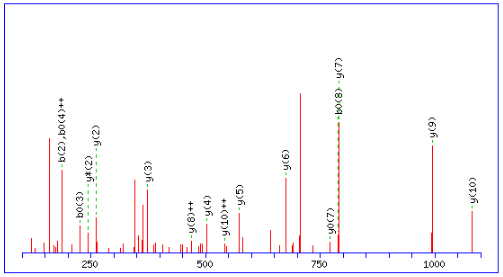
Monoisotopic mass of neutral peptide Mr(calc): 1081.5557
Ions Score: 78 Expect: 0.00025
Matches (Bold Red): 13/72 fragment ions using 17 most intense peaks

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389			Y							10
2	**221.0921**	111.0497			G	**919.4996**	460.2534	902.4730	451.7402	901.4890	451.2482	9
3	**320.1605**	160.5839			V	**862.4781**	431.7427	845.4516	423.2294	844.4676	422.7374	8
4	**435.1874**	218.0974	417.1769	209.0921	D	**763.4097**	382.2085	746.3832	373.6952	745.3991	373.2032	7
5	492.2089	246.6081	474.1983	237.6028	G	**648.3828**	324.6950	631.3562	316.1817			6
6	549.2304	**275.1188**	531.2198	266.1135	G	**591.3613**	296.1843	574.3348	287.6710			5
7	696.2988	348.6530	678.2882	339.6477	F	534.3398	267.6736	517.3133	259.1603			4
8	795.3672	398.1872	777.3566	389.1819	V	**387.2714**	194.1394	370.2449	185.6261			3
9	908.4512	454.7293	890.4407	445.7240	L	**288.2030**	144.6051	271.1765	**136.0919**			2
10					R	**175.1190**	88.0631	158.0924	79.5498			1



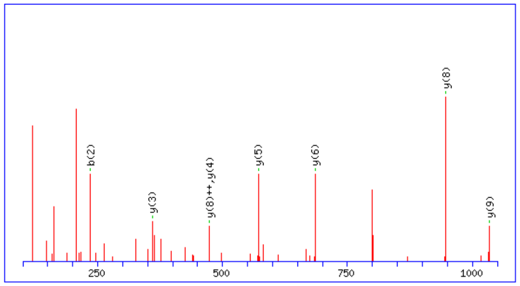
Monoisotopic mass of neutral peptide Mr(calc): 1175.5306
Ions Score: 80 Expect: 0.00017
Matches (Bold Red): 14/106 fragment ions using 21 most intense peaks

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							11
2	**229.1183**	115.0628			211.1077	106.0575	I	1061.5109	531.2591	1044.4844	522.7458	1043.5004	522.2538	10
3	**358.1609**	179.5841			340.1503	170.5788	E	**948.4269**	474.7171	931.4003	466.2038	**930.4163**	465.7118	9
4	415.1823	208.0948			397.1718	199.0895	G	**819.3843**	410.1958	802.3577	401.6825	801.3737	401.1905	8
5	529.2253	265.1163	512.1987	256.6030	511.2147	256.1110	N	**762.3628**	381.6850	745.3363	373.1718	744.3523	372.6798	7
6	644.2522	322.6297	627.2257	314.1165	626.2416	313.6245	D	**648.3199**	324.6636	631.2933	316.1503	630.3093	315.6583	6
7	**731.2842**	366.1458	714.2577	357.6325	713.2737	357.1405	S	**533.2930**	267.1501	516.2664	258.6368	515.2824	258.1448	5
8	846.3112	423.6592	829.2846	415.1460	828.3006	414.6539	D	**446.2609**	223.6341	429.2344	215.1208	428.2504	214.6288	4
9	959.3952	480.2013	942.3687	471.6880	941.3847	471.1960	L	**331.2340**	166.1206	314.2074	157.6074			3
10	1030.4324	515.7198	1013.4058	507.2065	1012.4218	506.7145	A	**218.1499**	109.5786	**201.1234**	101.0653			2
11							K	**147.1128**	74.0600	130.0863	65.5468			1



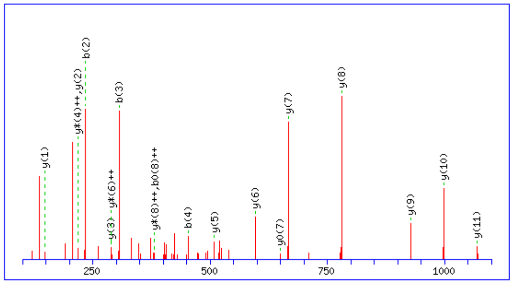
Monoisotopic mass of neutral peptide Mr(calc): 1179.5772
Ions Score: 64 Expect: 0.0067
Matches (Bold Red): 17/94 fragment ions using 24 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							11
2	**187.1077**	94.0575			169.0972	85.0522	S	**1081.5160**	**541.2617**	1064.4895	532.7484	1063.5055	532.2564	10
3	**244.1292**	122.5682			**226.1186**	113.5629	G	**994.4840**	497.7456	977.4575	489.2324	976.4734	488.7404	9
4	391.1976	196.1024			373.1870	**187.0972**	F	937.4625	**469.2349**	920.4360	460.7216	919.4520	460.2296	8
5	506.2245	253.6159			488.2140	244.6106	D	**790.3941**	395.7007	773.3676	387.1874	**772.3836**	386.6954	7
6	607.2722	304.1397			589.2617	295.1345	T	**675.3672**	338.1872	658.3406	329.6740	657.3566	329.1819	6
7	678.3093	339.6583			660.2988	330.6530	A	**574.3195**	287.6634	557.2930	279.1501	556.3089	278.6581	5
8	807.3519	404.1796			**789.3414**	395.1743	E	**503.2824**	252.1448	486.2558	243.6316	485.2718	243.1395	4
9	920.4360	460.7216			902.4254	451.7164	L	**374.2398**	187.6235	357.2132	179.1103			3
10	1034.4789	517.7431	1017.4524	509.2298	1016.4684	508.7378	N	**261.1557**	131.0815	**244.1292**	122.5682			2
11							K	147.1128	74.0600	130.0863	65.5468			1



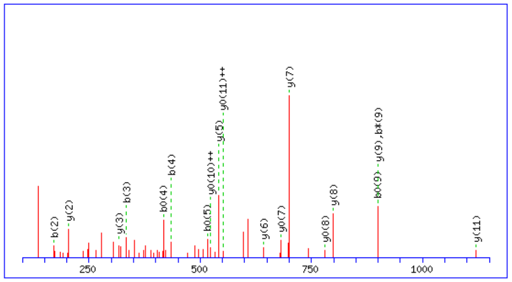
Monoisotopic mass of neutral peptide Mr(calc): 1180.5764
Ions Score: 48 Expect: 0.28
Matches (Bold Red): 8/92 fragment ions using 13 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							10
2	**235.1077**	118.0575			217.0972	109.0522	S	**1034.5153**	517.7613	1017.4888	509.2480	1016.5047	508.7560	9
3	382.1761	191.5917			364.1656	182.5864	F	**947.4833**	**474.2453**	930.4567	465.7320	929.4727	465.2400	8
4	497.2031	249.1052			479.1925	240.0999	D	800.4149	400.7111	783.3883	392.1978	782.4043	391.7058	7
5	611.2460	306.1266	594.2195	297.6134	593.2354	297.1214	N	**685.3879**	343.1976	668.3614	334.6843	667.3774	334.1923	6
6	708.2988	354.6530	691.2722	346.1397	690.2882	345.6477	P	**571.3450**	286.1761	554.3184	277.6629	553.3344	277.1709	5
7	823.3257	412.1665	806.2992	403.6532	805.3151	403.1612	D	**474.2922**	237.6498	457.2657	229.1365	456.2817	228.6445	4
8	936.4098	468.7085	919.3832	460.1953	918.3992	459.7032	L	**359.2653**	180.1363	342.2387	171.6230			3
9	1035.4782	518.2427	1018.4516	509.7295	1017.4676	509.2374	V	246.1812	123.5942	229.1547	115.0810			2
10							K	147.1128	74.0600	130.0863	65.5468			1



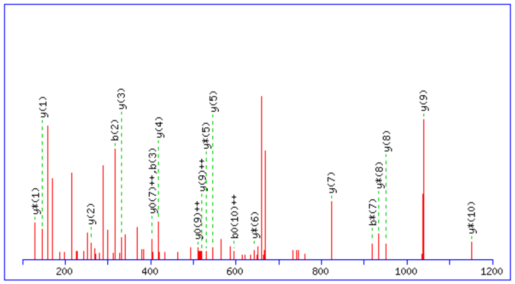
Monoisotopic mass of neutral peptide Mr(calc): 1231.6237
Ions Score: 53 Expect: 0.084
Matches (Bold Red): 18/88 fragment ions using 48 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			Y							12
2	**235.1077**	118.0575			A	**1069.5677**	535.2875	1052.5411	526.7742	1051.5571	526.2822	11
3	**306.1448**	153.5761			A	**998.5306**	499.7689	981.5040	491.2556	980.5200	490.7636	10
4	**453.2132**	227.1103			F	**927.4934**	464.2504	910.4669	455.7371	909.4829	455.2451	9
5	566.2973	283.6523			L	**780.4250**	390.7162	763.3985	**382.2029**	762.4145	381.7109	8
6	637.3344	319.1709			A	**667.3410**	334.1741	650.3144	325.6608	**649.3304**	325.1688	7
7	724.3665	362.6869	706.3559	353.6816	S	**596.3039**	298.6556	579.2773	**290.1423**	578.2933	289.6503	6
8	781.3879	391.1976	763.3774	**382.1923**	G	**509.2718**	255.1396	492.2453	246.6263			5
9	944.4512	472.7293	926.4407	463.7240	Y	452.2504	226.6288	435.2238	**218.1155**			4
10	1015.4884	508.2478	997.4778	499.2425	A	**289.1870**	145.0972	272.1605	136.5839			3
11	1086.5255	543.7664	1068.5149	534.7611	A	**218.1499**	109.5786	201.1234	101.0653			2
12					K	**147.1128**	74.0600	130.0863	65.5468			1



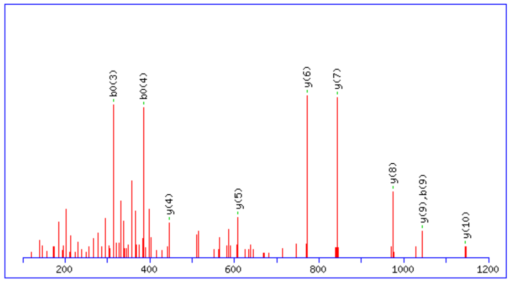
Monoisotopic mass of neutral peptide Mr(calc): 1232.6765
Ions Score: 49 Expect: 0.24
Matches (Bold Red): 19/100 fragment ions using 37 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							12
2	**171.1128**	86.0600					G	**1120.5997**	560.8035	1103.5732	552.2902	1102.5891	**551.7982**	11
3	**334.1761**	167.5917					Y	1063.5782	532.2928	1046.5517	523.7795	1045.5677	**523.2875**	10
4	**435.2238**	218.1155			**417.2132**	209.1103	T	**900.5149**	450.7611	883.4884	442.2478	882.5043	441.7558	9
5	534.2922	267.6498			**516.2817**	258.6445	V	**799.4672**	400.2373	782.4407	391.7240	**781.4567**	391.2320	8
6	591.3137	296.1605			573.3031	287.1552	G	**700.3988**	350.7030	683.3723	342.1898	**682.3883**	341.6978	7
7	692.3614	346.6843			674.3508	337.6790	T	**643.3774**	322.1923	626.3508	313.6790	625.3668	313.1870	6
8	789.4141	395.2107			771.4036	386.2054	P	**542.3297**	271.6685	525.3031	263.1552			5
9	917.4727	459.2400	**900.4462**	450.7267	**899.4621**	450.2347	Q	445.2769	223.1421	428.2504	214.6288			4
10	1030.5568	515.7820	1013.5302	507.2688	1012.5462	506.7767	I	**317.2183**	159.1128	300.1918	150.5995			3
11	1087.5782	544.2928	1070.5517	535.7795	1069.5677	535.2875	G	**204.1343**	102.5708	187.1077	94.0575			2
12							K	147.1128	74.0600	130.0863	65.5468			1



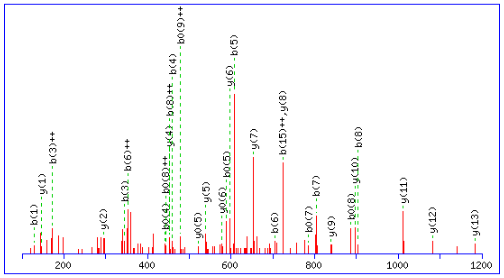
Monoisotopic mass of neutral peptide Mr(calc): 1352.6360
Ions Score: 43 Expect: 0.84
Matches (Bold Red): 20/106 fragment ions using 47 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.0866	94.0469					W							11
2	**316.1292**	158.5682			298.1186	149.5629	E	1167.5640	584.2857	**1150.5375**	575.7724	1149.5535	575.2804	10
3	**403.1612**	202.0842			385.1506	193.0790	S	**1038.5214**	**519.7644**	1021.4949	511.2511	1020.5109	**510.7591**	9
4	531.2198	266.1135	514.1932	257.6003	513.2092	257.1082	Q	**951.4894**	476.2483	**934.4629**	467.7351	933.4789	467.2431	8
5	694.2831	347.6452	677.2566	339.1319	676.2726	338.6399	Y	**823.4308**	412.2191	806.4043	403.7058	805.4203	**403.2138**	7
6	808.3260	404.6667	791.2995	396.1534	790.3155	395.6614	N	660.3675	330.6874	**643.3410**	322.1741	642.3569	321.6821	6
7	936.3846	468.6959	**919.3581**	460.1827	918.3741	459.6907	Q	**546.3246**	273.6659	**529.2980**	265.1527	528.3140	264.6606	5
8	1023.4167	512.2120	1006.3901	503.6987	1005.4061	503.2067	S	**418.2660**	209.6366	401.2395	201.1234	400.2554	200.6314	4
9	1094.4538	547.7305	1077.4272	539.2172	1076.4432	538.7252	A	**331.2340**	166.1206	314.2074	157.6074			3
10	1207.5378	604.2726	1190.5113	595.7593	1189.5273	**595.2673**	L	**260.1969**	130.6021	243.1703	122.0888			2
11							K	**147.1128**	74.0600	**130.0863**	65.5468			1



Monoisotopic mass of neutral peptide Mr(calc): 1374.6489
Ions Score: 61 Expect: 0.012
Matches (Bold Red): 10/96 fragment ions using 15 most intense peaks

#	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							12
2	231.0975	116.0524			213.0870	107.0471	T	1246.6136	623.8105	1229.5871	615.2972	1228.6031	614.8052	11
3	332.1452	166.5763			**314.1347**	157.5710	T	**1145.5660**	573.2866	1128.5394	564.7733	1127.5554	564.2813	10
4	403.1823	202.0948			**385.1718**	193.0895	A	**1044.5183**	522.7628	1027.4917	514.2495			9
5	534.2228	267.6151			516.2123	258.6098	M	**973.4812**	487.2442	956.4546	478.7309			8
6	605.2599	303.1336			587.2494	294.1283	A	**842.4407**	421.7240	825.4141	413.2107			7
7	768.3233	384.6653			750.3127	375.6600	Y	**771.4036**	386.2054	754.3770	377.6921			6
8	931.3866	466.1969			913.3760	457.1917	Y	**608.3402**	304.6738	591.3137	296.1605			5
9	**1044.4707**	522.7390			1026.4601	513.7337	L	**445.2769**	223.1421	428.2504	214.6288			4
10	1158.5136	579.7604	1141.4870	571.2472	1140.5030	570.7551	N	332.1928	166.6001	315.1663	158.0868			3
11	1229.5507	615.2790	1212.5242	606.7657	1211.5401	606.2737	A	218.1499	109.5786	201.1234	101.0653			2
12							K	147.1128	74.0600	130.0863	65.5468			1



Monoisotopic mass of neutral peptide Mr(calc): 1984.9015
Ions Score: 62 Expect: 0.0084
Matches (Bold Red): 31/222 fragment ions using 68 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.1022**	65.0548	112.0757	56.5415			K							20
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	T	1857.8137	929.4105	1840.7872	920.8972	1839.8032	920.4052	19
3	**345.1769**	**173.0921**	328.1503	164.5788	327.1663	164.0868	D	1756.7661	878.8867	1739.7395	870.3734	1738.7555	869.8814	18
4	**460.2038**	230.6055	443.1773	222.0923	**442.1932**	221.6003	D	1641.7391	821.3732	1624.7126	812.8599	1623.7285	812.3679	17
5	**607.2722**	304.1397	590.2457	295.6265	**589.2617**	295.1345	F	1526.7122	763.8597	1509.6856	755.3464	1508.7016	754.8544	16
6	**704.3250**	**352.6661**	687.2984	344.1529	686.3144	343.6608	P	1379.6438	690.3255	1362.6172	681.8122	1361.6332	681.3202	15
7	**803.3934**	402.2003	786.3668	393.6871	**785.3828**	393.1951	V	1282.5910	641.7991	1265.5644	633.2859	1264.5804	632.7938	14
8	**904.4411**	**452.7242**	887.4145	444.2109	**886.4305**	**443.7189**	T	**1183.5226**	592.2649	1166.4960	583.7517	1165.5120	583.2596	13
9	975.4782	488.2427	958.4516	479.7295	957.4676	**479.2375**	A	**1082.4749**	541.7411	1065.4483	533.2278	1064.4643	532.7358	12
10	1090.5051	545.7562	1073.4786	537.2429	1072.4946	536.7509	D	**1011.4378**	506.2225	994.4112	497.7093	993.4272	497.2172	11
11	1147.5266	574.2669	1130.5000	565.7537	1129.5160	565.2617	G	**896.4108**	448.7091	879.3843	440.1958	878.4003	439.7038	10
12	1262.5535	631.7804	1245.5270	623.2671	1244.5430	622.7751	D	**839.3894**	420.1983	822.3628	411.6851	821.3788	411.1930	9
13	1333.5907	667.2990	1316.5641	658.7857	1315.5801	658.2937	A	**724.3624**	362.6849	707.3359	354.1716	706.3519	353.6796	8
14	1390.6121	695.8097	1373.5856	687.2964	1372.6016	686.8044	G	**653.3253**	327.1663	636.2988	318.6530	635.3148	318.1610	7
15	1447.6336	**724.3204**	1430.6070	715.8072	1429.6230	715.3151	G	**596.3039**	298.6556	579.2773	290.1423	**578.2933**	289.6503	6
16	1534.6656	767.8364	1517.6391	759.3232	1516.6550	758.8312	S	**539.2824**	270.1448	522.2558	261.6316	**521.2718**	261.1396	5
17	1591.6871	796.3472	1574.6605	787.8339	1573.6765	787.3419	G	**452.2504**	226.6288	435.2238	218.1155	434.2398	217.6235	4
18	1692.7348	846.8710	1675.7082	838.3577	1674.7242	837.8657	T	395.2289	198.1181	378.2023	189.6048	377.2183	189.1128	3
19	1839.8032	920.4052	1822.7766	911.8919	1821.7926	911.3999	F	**294.1812**	147.5942	277.1547	139.0810			2
20							K	**147.1128**	74.0600	130.0863	65.5468			1

Protein band 6 (-Mn): Elongation Factor Tu

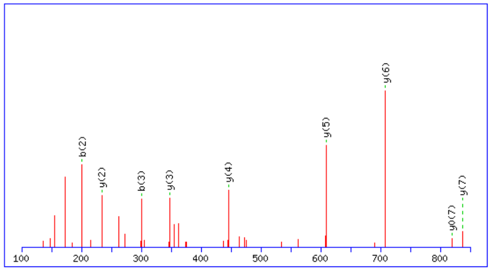
Score: 1327

M_r: 42926

Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 60%

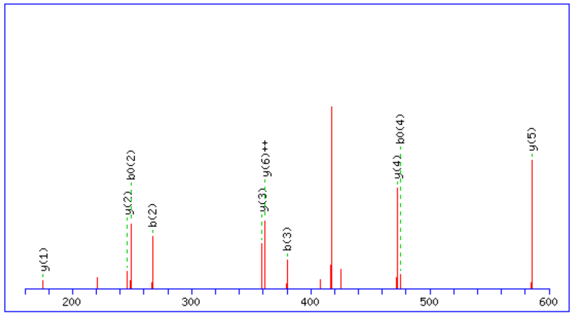
Matched peptides shown in **Bold Red**

1 MAKEKFERSK PHVNVGTIGH VDHGK**TTLTA ALTTILAK**KF GGAAK**AYDQI**
51 **DNAPEEK**ARG **ITINTSHVEY ETETR**HYAHV DCPGHADYVK **NMITGAAQMD**
101 **GAILVCSAAD GPMPQTREHI LLARQVGVPY IIVFMNKCDM VDDAELLELV**
151 **EMEIRDLLSS YDFPGDDCPI VQGSALKALE GDAAYEEKIF ELATALDSYI**
201 **PTPERAVDKP FLLPIEDVFS ISGR**GTVVTG RVER**GIIHVG DEIEIVGLK**E
251 TQK**TTCTGVE MFR**K**LLDEGQ AGDNVGVLLR** GTKREDVERG QVLAKPGTIT
301 PHTK**FKAEVY VLSK**EEGGRH TPFFANYRPQ FYFR**TTDVTG AVTLEK**GVEM
351 VMPGENVTIT VELIAPIAME EGLRFAIREG GRTVGAGVVS SVIA



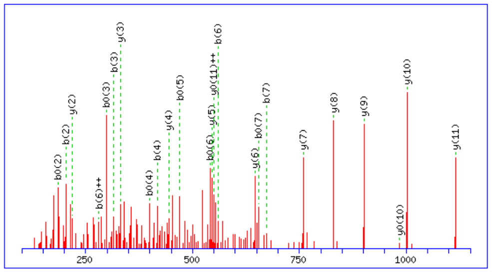
Monoisotopic mass of neutral peptide Mr(calc): 907.5015
Ions Score: 52 Expect: 0.11
Matches (**Bold Red**): 9/66 fragment ions using 9 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							8
2	**201.0870**	101.0471	183.0764	92.0418	E	**837.4716**	419.2395	820.4451	410.7262	**819.4611**	410.2342	7
3	**300.1554**	150.5813	282.1448	141.5761	V	**708.4291**	354.7182	691.4025	346.2049	690.4185	345.7129	6
4	463.2187	232.1130	445.2082	223.1077	Y	**609.3606**	305.1840	592.3341	296.6707	591.3501	296.1787	5
5	562.2871	281.6472	544.2766	272.6419	V	**446.2973**	223.6523	429.2708	215.1390	428.2867	214.6470	4
6	675.3712	338.1892	657.3606	329.1840	L	**347.2289**	174.1181	330.2023	165.6048	329.2183	165.1128	3
7	762.4032	381.7053	744.3927	372.7000	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2
8					K	147.1128	74.0600	130.0863	65.5468			1



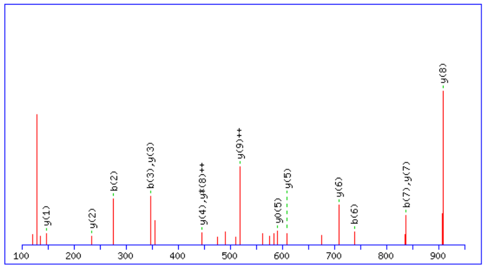
Monoisotopic mass of neutral peptide Mr(calc): 850.5025
Ions Score: 40 Expect: 1.6
Matches (**Bold Red**): 10/48 fragment ions using 15 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.0499	65.5286	112.0393	56.5233	E					7
2	**267.1088**	134.0580	**249.0982**	125.0527	H	722.4672	**361.7372**	705.4406	353.2239	6
3	**380.1928**	190.6001	362.1823	181.5948	I	**585.4083**	293.2078	568.3817	284.6945	5
4	493.2769	247.1421	**475.2663**	238.1368	L	**472.3242**	236.6657	455.2976	228.1525	4
5	606.3610	303.6841	588.3504	294.6788	L	**359.2401**	180.1237	342.2136	171.6104	3
6	677.3981	339.2027	659.3875	330.1974	A	**246.1561**	123.5817	229.1295	115.0684	2
7					R	**175.1190**	88.0631	158.0924	79.5498	1



Monoisotopic mass of neutral peptide Mr(calc): 1316.7915
Ions Score: 59 Expect: 0.022
Matches (**Bold Red**): 24/112 fragment ions using 53 most intense peaks

#	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							13
2	**203.1026**	102.0550	**185.0921**	93.0497	T	1216.7511	608.8792	1199.7246	600.3659	1198.7406	599.8739	12
3	**316.1867**	158.5970	**298.1761**	149.5917	L	**1115.7034**	558.3554	1098.6769	549.8421	1097.6929	**549.3501**	11
4	**417.2344**	209.1208	**399.2238**	200.1155	T	**1002.6194**	501.8133	985.5928	493.3001	**984.6088**	492.8080	10
5	488.2715	244.6394	**470.2609**	235.6341	A	**901.5717**	451.2895	884.5451	442.7762	883.5611	442.2842	9
6	**559.3086**	**280.1579**	**541.2980**	271.1527	A	**830.5346**	415.7709	813.5080	407.2577	812.5240	406.7656	8
7	**672.3927**	336.7000	**654.3821**	327.6947	L	**759.4975**	380.2524	742.4709	371.7391	741.4869	371.2471	7
8	773.4403	387.2238	755.4298	378.2185	T	**646.4134**	323.7103	629.3869	315.1971	628.4028	314.7051	6
9	874.4880	437.7477	856.4775	428.7424	T	**545.3657**	273.1865	528.3392	264.6732	527.3552	264.1812	5
10	987.5721	494.2897	969.5615	485.2844	I	**444.3180**	222.6627	427.2915	214.1494			4
11	1100.6562	550.8317	1082.6456	541.8264	L	**331.2340**	166.1206	314.2074	157.6074			3
12	1171.6933	586.3503	1153.6827	577.3450	A	**218.1499**	109.5786	201.1234	101.0653			2
13					K	147.1128	74.0600	130.0863	65.5468			1



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Monoisotopic mass of neutral peptide Mr(calc): 1182.6648
Ions Score: 65  Expect: 0.005
Matches (Bold Red): 15/98 fragment ions using 19 most intense peaks
```
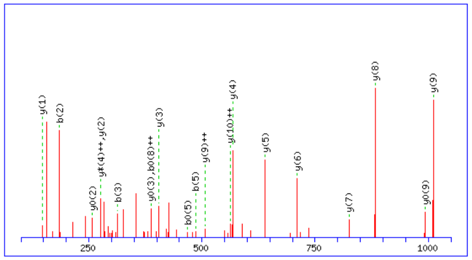
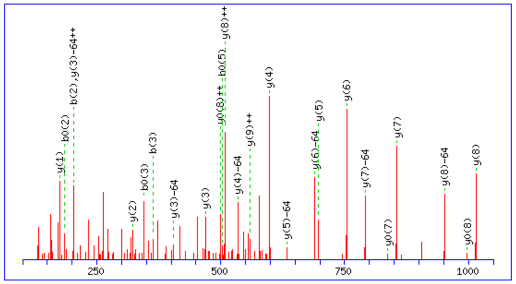

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							10
2	**276.1707**	138.5890	259.1441	130.0757			K	1036.6037	**518.8055**	1019.5772	510.2922	1018.5932	509.8002	9
3	**347.2078**	174.1075	330.1812	165.5942			A	**908.5088**	454.7580	891.4822	**446.2447**	890.4982	445.7527	8
4	476.2504	238.6288	459.2238	230.1155	458.2398	229.6235	E	**837.4716**	419.2395	820.4451	410.7262	819.4611	410.2342	7
5	575.3188	288.1630	558.2922	279.6498	557.3082	279.1577	V	**708.4291**	354.7182	691.4025	346.2049	690.4185	345.7129	6
6	**738.3821**	369.6947	721.3556	361.1814	720.3715	360.6894	Y	**609.3606**	305.1840	592.3341	296.6707	**591.3501**	296.1787	5
7	**837.4505**	419.2289	820.4240	410.7156	819.4400	410.2236	V	**446.2973**	223.6523	429.2708	215.1390	428.2867	214.6470	4
8	950.5346	475.7709	933.5080	467.2577	932.5240	466.7656	L	**347.2289**	174.1181	330.2023	165.6048	329.2183	165.1128	3
9	1037.5666	519.2869	1020.5401	510.7737	1019.5560	510.2817	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2
10							K	**147.1128**	74.0600	130.0863	65.5468			1



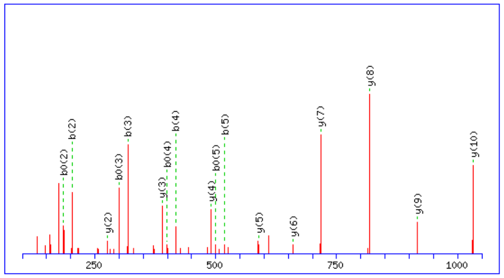
```
Monoisotopic mass of neutral peptide Mr(calc): 1194.5404
Ions Score: 65  Expect: 0.005
Matches (Bold Red): 20/94 fragment ions using 36 most intense peaks
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							11
2	**185.1285**	93.0679			L	1124.5106	**562.7589**	1107.4841	554.2457	1106.5000	553.7537	10
3	**314.1710**	157.5892	296.1605	148.5839	E	**1011.4265**	**506.2169**	994.4000	497.7036	**993.4160**	497.2116	9
4	371.1925	186.0999	353.1819	177.0946	G	**882.3840**	441.6956	865.3574	433.1823	864.3734	432.6903	8
5	**486.2195**	243.6134	**468.2089**	234.6081	D	**825.3625**	413.1849	808.3359	404.6716	807.3519	404.1796	7
6	557.2566	279.1319	539.2460	270.1266	A	**710.3355**	355.6714	693.3090	347.1581	692.3250	346.6661	6
7	628.2937	314.6505	610.2831	305.6452	A	**639.2984**	320.1529	622.2719	311.6396	621.2879	311.1476	5
8	791.3570	396.1821	773.3464	**387.1769**	Y	**568.2613**	284.6343	551.2348	**276.1210**	550.2508	275.6290	4
9	920.3996	460.7034	902.3890	451.6982	E	**405.1980**	203.1026	388.1714	194.5894	**387.1874**	194.0974	3
10	1049.4422	525.2247	1031.4316	516.2195	E	**276.1554**	138.5813	259.1288	130.0681	**258.1448**	129.5761	2
11					K	**147.1128**	74.0600	130.0863	65.5468			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1216.5217
Variable modifications:
C3      : Carbamidomethyl (C)
M8      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 46  Expect: 0.45
Matches (Bold Red): 25/132 fragment ions using 49 most intense peaks
```

#	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							10
2	**203.1026**	102.0550	**185.0921**	93.0497	T	1116.4813	**558.7443**	1099.4547	550.2310	1098.4707	549.7390	9
3	**363.1333**	182.0703	**345.1227**	173.0650	C	**1015.4336**	**508.2204**	998.4070	499.7072	**997.4230**	**499.2151**	8
4	464.1810	232.5941	446.1704	223.5888	T	**855.4029**	428.2051	838.3764	419.6918	**837.3924**	419.1998	7
5	521.2024	261.1049	**503.1919**	252.0996	G	**754.3552**	377.6813	737.3287	369.1680	736.3447	368.6760	6
6	620.2708	310.6391	602.2603	301.6338	V	**697.3338**	349.1705	680.3072	340.6573	679.3232	340.1652	5
7	749.3134	375.1604	731.3029	366.1551	E	**598.2654**	299.6363	581.2388	291.1230	580.2548	290.6310	4
8	896.3488	448.6781	878.3383	439.6728	M	**469.2228**	235.1150	452.1962	226.6017			3
9	1043.4173	522.2123	1025.4067	513.2070	F	**322.1874**	161.5973	305.1608	153.0840			2
10					R	**175.1190**	88.0631	158.0924	79.5498			1



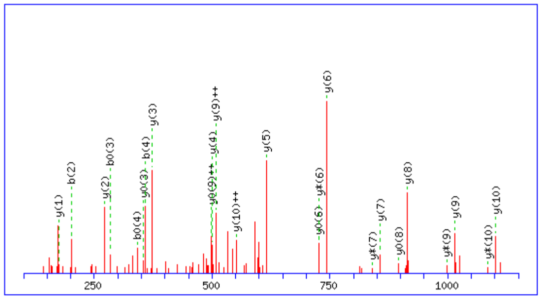
```
Monoisotopic mass of neutral peptide Mr(calc): 1233.6453
Ions Score: 81  Expect: 0.00014
Matches (Bold Red): 17/108 fragment ions using 24 most intense peaks
```

#	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							12
2	**203.1026**	102.0550	**185.0921**	93.0497	T	1133.6048	567.3061	1116.5783	558.7928	1115.5943	558.3008	11
3	**318.1296**	159.5684	**300.1190**	150.5631	D	**1032.5572**	516.7822	1015.5306	508.2689	1014.5466	507.7769	10
4	**417.1980**	209.1026	**399.1874**	200.0974	V	**917.5302**	459.2688	900.5037	450.7555	899.5197	450.2635	9
5	**518.2457**	259.6265	**500.2351**	250.6212	T	**818.4618**	409.7345	801.4353	401.2213	800.4512	400.7293	8
6	575.2671	288.1372	557.2566	279.1319	G	**717.4141**	359.2107	700.3876	350.6974	699.4036	350.2054	7
7	646.3042	323.6558	628.2937	314.6505	A	**660.3927**	330.7000	643.3661	322.1867	642.3821	321.6947	6
8	745.3727	373.1900	727.3621	364.1847	V	**589.3556**	295.1814	572.3290	286.6681	571.3450	286.1761	5
9	846.4203	423.7138	828.4098	414.7085	T	**490.2871**	245.6472	473.2606	237.1339	472.2766	236.6419	4
10	959.5044	480.2558	941.4938	471.2506	L	**389.2395**	195.1234	372.2129	186.6101	371.2289	186.1181	3
11	1088.5470	544.7771	1070.5364	535.7719	E	**276.1554**	138.5813	259.1288	130.0681	258.1448	129.5761	2
12					K	147.1128	74.0600	130.0863	65.5468			1

Protein band 6 (-Mn): DnaJ

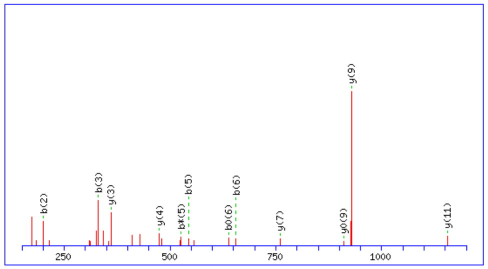
Score: 127 M$_r$: 40590

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%

Matched peptides shown in Bold Red

  1 MSNQDFYATL GVARTATDDE IKKAYRKLAM KYHPDRNPDN KEAEEKFKEV
 51 QKAYETLSDK EKRAMYDQYG HAAFEGGGQG GFGGFGGFGG AQGFDFGDIF
101 SQMFGGGSGR AQPDYQGEDV QVGIEITLEE AAKGVKKRIN IPTYEACDVC
151 NGSGAKPGTS PETCPTCKGS GTVHIQQAIF RMQQTCPTCH GAGKHIKEPC
201 VKCRGAGRNK AVKTVEVNIP AGIDDGQRIR LSGEGGPGMH GAPAGDLYVT
251 VRIRAHKIFQ RDGLDLHCEL PISFATAALG GELEVPTLDG KVKLTVPKET
301 QTGRRMRVKG KGVKSLRSSA TGDLYCHIVV ETPVNLTDRQ KELLEEFERI
351 STGLENQTPR KKSFLDKLRD LFD
```



```
Monoisotopic mass of neutral peptide Mr(calc): 1214.6255
Ions Score: 87  Expect: 3.4e-05
Matches (Bold Red): 24/102 fragment ions using 42 most intense peaks
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.0913	57.5493					I							11
2	**201.1234**	101.0653			183.1128	92.0600	S	**1102.5487**	**551.7780**	**1085.5222**	543.2647	1084.5382	542.7727	10
3	302.1710	151.5892			**284.1605**	142.5839	T	**1015.5167**	**508.2620**	**998.4902**	499.7487	997.5061	**499.2567**	9
4	**359.1925**	180.0999			**341.1819**	171.0946	G	**914.4690**	457.7381	897.4425	449.2249	**896.4585**	448.7329	8
5	472.2766	236.6419			454.2660	227.6366	L	**857.4476**	429.2274	**840.4210**	420.7141	839.4370	420.2221	7
6	601.3192	301.1632			583.3086	292.1579	E	**744.3635**	372.6854	**727.3369**	364.1721	**726.3529**	363.6801	6
7	715.3621	358.1847	698.3355	349.6714	697.3515	349.1794	N	**615.3209**	308.1641	598.2944	299.6508	597.3103	299.1588	5
8	843.4207	422.2140	826.3941	413.7007	825.4101	413.2087	Q	**501.2780**	251.1426	484.2514	242.6293	483.2674	242.1373	4
9	944.4684	472.7378	927.4418	464.2245	926.4578	463.7325	T	**373.2194**	187.1133	356.1928	178.6001	**355.2088**	178.1081	3
10	1041.5211	521.2642	1024.4946	512.7509	1023.5106	512.2589	P	**272.1717**	136.5895	255.1452	128.0762			2
11							R	**175.1190**	88.0631	158.0924	79.5498			1



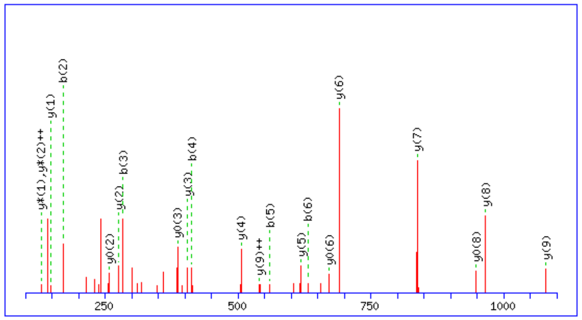
```
Monoisotopic mass of neutral peptide Mr(calc): 1582.7951
Ions Score: 40  Expect: 1.6
Matches (Bold Red): 12/154 fragment ions using 18 most intense peaks
```

#	b	b^{++}	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							15
2	**201.1234**	101.0653			183.1128	92.0600	V	1482.7547	741.8810	1465.7281	733.3677	1464.7441	732.8757	14
3	**330.1660**	165.5866			312.1554	156.5813	E	1383.6863	692.3468	1366.6597	683.8335	1365.6757	683.3415	13
4	429.2344	215.1208			411.2238	206.1155	V	1254.6437	627.8255	1237.6171	619.3122	1236.6331	618.8202	12
5	**543.2773**	272.1423	**526.2508**	263.6290	525.2667	263.1370	N	**1155.5753**	578.2913	1138.5487	569.7780	1137.5647	569.2860	11
6	**656.3614**	328.6843	639.3348	320.1710	**638.3508**	319.6790	I	1041.5324	521.2698	1024.5058	512.7565	1023.5218	512.2645	10
7	753.4141	377.2107	736.3876	368.6974	735.4036	368.2054	P	**928.4483**	464.7278	911.4217	456.2145	**910.4377**	455.7225	9
8	824.4512	412.7293	807.4247	404.2160	806.4407	403.7240	A	831.3955	416.2014	814.3690	407.6881	813.3850	407.1961	8
9	881.4727	441.2400	864.4462	432.7267	863.4621	432.2347	G	**760.3584**	380.6828	743.3319	372.1696	742.3478	371.6776	7
10	994.5568	497.7820	977.5302	489.2688	976.5462	488.7767	I	703.3369	352.1721	686.3104	343.6588	685.3264	343.1668	6
11	1109.5837	555.2955	1092.5572	546.7822	1091.5732	546.2902	D	590.2529	295.6301	573.2263	287.1168	572.2423	286.6248	5
12	1224.6107	612.8090	1207.5841	604.2957	1206.6001	603.8037	D	**475.2259**	238.1166	458.1994	229.6033	457.2154	229.1113	4
13	1281.6321	641.3197	1264.6056	632.8064	1263.6216	632.3144	G	**360.1990**	180.6031	343.1724	172.0899			3
14	1409.6907	705.3490	1392.6642	696.8357	1391.6801	696.3437	Q	303.1775	152.0924	286.1510	143.5791			2
15							R	175.1190	88.0631	158.0924	79.5498			1

Protein band 15 (+Mn): 50S ribosomal protein L3

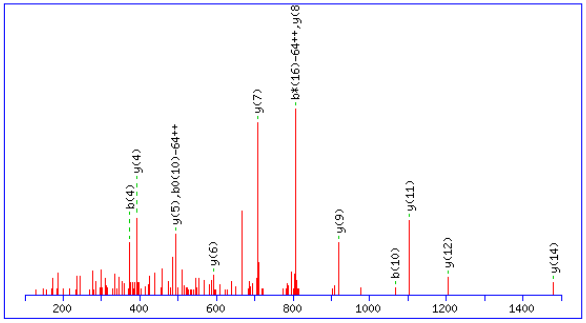
Score: 164 M$_r$: 22663

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%

Matched peptides shown in Bold Red

      1 MTLGLVGRKV GMTRVFDEQG VSVPVTVLDM SANRVTQVKS KDTDGYTAVQ
     51 VTFGQKKANR VNKAEAGHFA KAGVEAGRGL IEFALTEEKL AELKAGDEIT
    101 VSMFEVGQLV DVTGTSKGKG FSGTIKRHNF GAQRTSHGNS RSHRVPGSIG
    151 MAQDPGRVFP GKRMAGQYGN TKATVQKLEV VRVDAERQLL LVKGAVPGAV
    201 NSDVVVRPSV KVGA
```



```
Monoisotopic mass of neutral peptide Mr(calc): 1248.6601
Ions Score: 64  Expect: 0.0067
Matches (Bold Red): 21/92 fragment ions using 37 most intense peaks
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							11
2	**171.1128**	86.0600			L	1192.6460	596.8266	1175.6194	588.3134	1174.6354	587.8213	10
3	**284.1969**	142.6021			I	**1079.5619**	**540.2846**	1062.5354	531.7713	1061.5514	531.2793	9
4	**413.2395**	207.1234	395.2289	198.1181	E	**966.4779**	483.7426	949.4513	475.2293	**948.4673**	474.7373	8
5	**560.3079**	280.6576	542.2973	271.6523	F	**837.4353**	419.2213	820.4087	410.7080	819.4247	410.2160	7
6	**631.3450**	316.1761	613.3344	307.1709	A	**690.3668**	345.6871	673.3403	337.1738	**672.3563**	336.6818	6
7	744.4291	372.7182	726.4185	363.7129	L	**619.3297**	310.1685	602.3032	301.6552	601.3192	301.1632	5
8	845.4767	423.2420	827.4662	414.2367	T	**506.2457**	253.6265	489.2191	245.1132	488.2351	244.6212	4
9	974.5193	487.7633	956.5088	478.7580	E	**405.1980**	203.1026	388.1714	194.5894	**387.1874**	194.0974	3
10	1103.5619	552.2846	1085.5514	543.2793	E	**276.1554**	138.5813	259.1288	**130.0681**	**258.1448**	129.5761	2
11					K	**147.1128**	74.0600	**130.0863**	65.5468			1

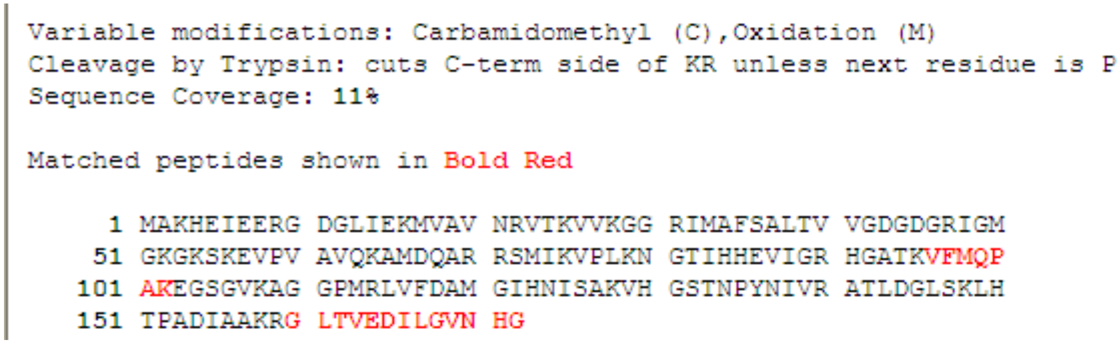


```
Monoisotopic mass of neutral peptide Mr(calc): 2398.1574
Variable modifications:
M9     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 69  Expect: 0.0014
Matches (Bold Red): 13/354 fragment ions using 17 most intense peaks
```

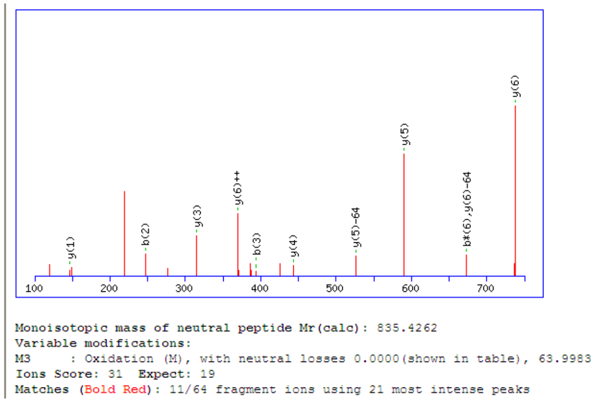
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							23
2	129.0659	65.0366					G	2328.1275	1164.5674	2311.1010	1156.0541	2310.1170	1155.5621	22
3	244.0928	122.5500			226.0822	113.5448	D	2271.1061	1136.0567	2254.0795	1127.5434	2253.0955	1127.0514	21
4	**373.1354**	187.0713			355.1248	178.0661	E	2156.0791	1078.5432	2139.0526	1070.0299	2138.0686	1069.5379	20
5	486.2195	243.6134			468.2089	234.6081	I	2027.0365	1014.0219	2010.0100	1005.5086	2009.0260	1005.0166	19
6	587.2671	294.1372			569.2566	285.1319	T	1913.9525	957.4799	1896.9259	948.9666	1895.9419	948.4746	18
7	686.3355	343.6714			668.3250	334.6661	V	1812.9048	906.9560	1795.8782	898.4428	1794.8942	897.9508	17
8	773.3676	387.1874			755.3570	378.1821	S	1713.8364	857.4218	1696.8098	848.9086	1695.8258	848.4165	16
9	920.4030	460.7051			902.3924	451.6998	M	1626.8044	813.9058	1609.7778	805.3925	1608.7938	804.9005	15
10	**1067.4714**	534.2393			1049.4608	525.2341	F	**1479.7690**	740.3881	1462.7424	731.8748	1461.7584	731.3828	14
11	1196.5140	598.7606			1178.5034	589.7553	E	1332.7005	666.8539	1315.6740	658.3406	1314.6900	657.8486	13
12	1295.5824	648.2948			1277.5718	639.2896	V	**1203.6579**	602.3326	1186.6314	593.8193	1185.6474	593.3273	12
13	1352.6039	676.8056			1334.5933	667.8003	G	**1104.5895**	552.7984	1087.5630	544.2851	1086.5790	543.7931	11
14	1480.6624	740.8349	1463.6359	732.3216	1462.6519	731.8296	Q	1047.5681	524.2877	1030.5415	515.7744	1029.5575	515.2824	10
15	1593.7465	797.3769	1576.7200	788.8636	1575.7359	788.3716	L	**919.5095**	460.2584	902.4829	451.7451	901.4989	451.2531	9
16	1692.8149	846.9111	1675.7884	838.3978	1674.8044	837.9058	V	**806.4254**	403.7164	789.3989	395.2031	788.4149	394.7111	8
17	1807.8419	904.4246	1790.8153	895.9113	1789.8313	895.4193	D	**707.3570**	354.1821	690.3305	345.6689	689.3464	345.1769	7
18	1906.9103	953.9588	1889.8837	945.4455	1888.8997	944.9535	V	**592.3301**	296.6687	575.3035	288.1554	574.3195	287.6634	6
19	2007.9580	1004.4826	1990.9314	995.9693	1989.9474	995.4773	T	**493.2617**	247.1345	476.2351	238.6212	475.2511	238.1292	5
20	2064.9794	1032.9933	2047.9529	1024.4801	2046.9689	1023.9881	G	**392.2140**	196.6106	375.1874	188.0974	374.2034	187.6053	4
21	2166.0271	1083.5172	2149.0005	1075.0039	2148.0165	1074.5119	T	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
22	2253.0591	1127.0332	2236.0326	1118.5199	2235.0486	1118.0279	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
23							K	147.1128	74.0600	130.0863	65.5468			1

Protein band 15 (+Mn): 50S ribosomal protein S5

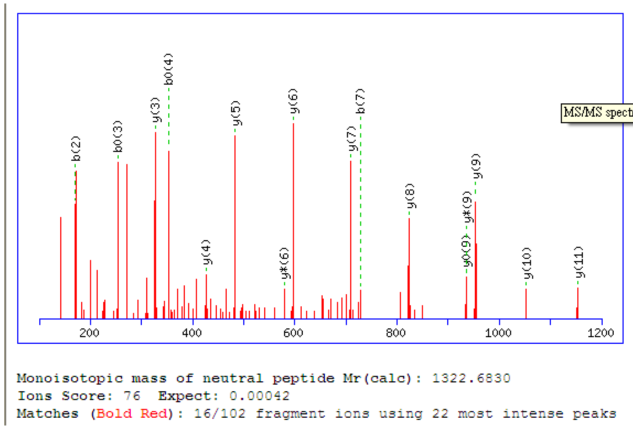
Score: 106 M_r: 18231



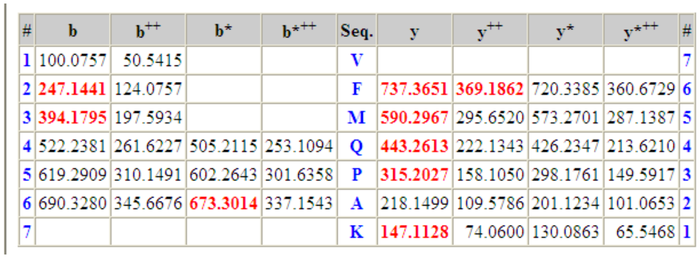
```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 11%

Matched peptides shown in Bold Red

      1 MAKHEIEERG DGLIEKMVAV NRVTKVVKGG RIMAFSALTV VGDGDGRIGM
     51 GKGKSKEVPV AVQKAMDQAR RSMIKVPLKN GTIHHEVIGR HGATKVFMQP
    101 AKEGSGVKAG GPMRLVFDAM GIHNISAKVH GSTNPYNIVR ATLDGLSKLH
    151 TPADIAAKRG LTVEDILGVN HG
```



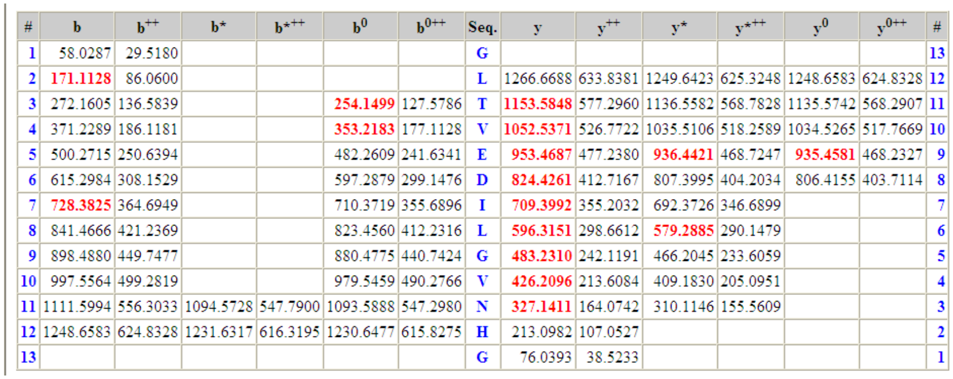
```
Monoisotopic mass of neutral peptide Mr(calc): 835.4262
Variable modifications:
M3     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 31  Expect: 19
Matches (Bold Red): 11/64 fragment ions using 21 most intense peaks
```



```
Monoisotopic mass of neutral peptide Mr(calc): 1322.6830
Ions Score: 76  Expect: 0.00042
Matches (Bold Red): 16/102 fragment ions using 22 most intense peaks
```



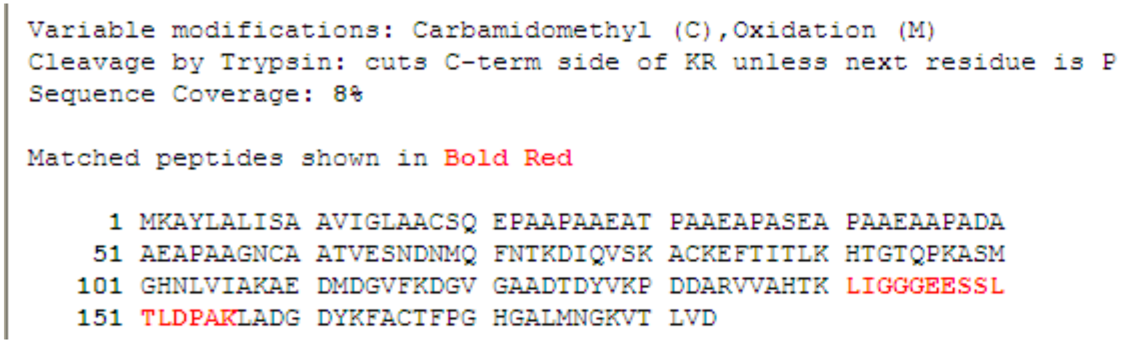
#	b	b^{++}	b^*	b^{*++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	100.0757	50.5415			V					7
2	**247.1441**	124.0757			F	**737.3651**	**369.1862**	720.3385	360.6729	6
3	**394.1795**	197.5934			M	**590.2967**	295.6520	573.2701	287.1387	5
4	522.2381	261.6227	505.2115	253.1094	Q	**443.2613**	222.1343	426.2347	213.6210	4
5	619.2909	310.1491	602.2643	301.6358	P	**315.2027**	158.1050	298.1761	149.5917	3
6	690.3280	345.6676	**673.3014**	337.1543	A	218.1499	109.5786	201.1234	101.0653	2
7					K	**147.1128**	74.0600	130.0863	65.5468	1



#	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	**171.1128**	86.0600					L	1266.6688	633.8381	1249.6423	625.3248	1248.6583	624.8328	12
3	272.1605	136.5839			**254.1499**	127.5786	T	**1153.5848**	577.2960	1136.5582	568.7828	1135.5742	568.2907	11
4	371.2289	186.1181			**353.2183**	177.1128	V	**1052.5371**	526.7722	1035.5106	518.2589	1034.5265	517.7669	10
5	500.2715	250.6394			482.2609	241.6341	E	**953.4687**	477.2380	**936.4421**	468.7247	**935.4581**	468.2327	9
6	615.2984	308.1529			597.2879	299.1476	D	**824.4261**	412.7167	807.3995	404.2034	806.4155	403.7114	8
7	**728.3825**	364.6949			710.3719	355.6896	I	**709.3992**	355.2032	692.3726	346.6899			7
8	841.4666	421.2369			823.4560	412.2316	L	**596.3151**	298.6612	**579.2885**	290.1479			6
9	898.4880	449.7477			880.4775	440.7424	G	**483.2310**	242.1191	466.2045	233.6059			5
10	997.5564	499.2819			979.5459	490.2766	V	**426.2096**	213.6084	409.1830	205.0951			4
11	1111.5994	556.3033	1094.5728	547.7900	1093.5888	547.2980	N	**327.1411**	164.0742	310.1146	155.5609			3
12	1248.6583	624.8328	1231.6317	616.3195	1230.6477	615.8275	H	213.0982	107.0527					2
13							G	76.0393	38.5233					1

Protein band 15 (+Mn): H.8 OMP (azurin-like protein, Laz)

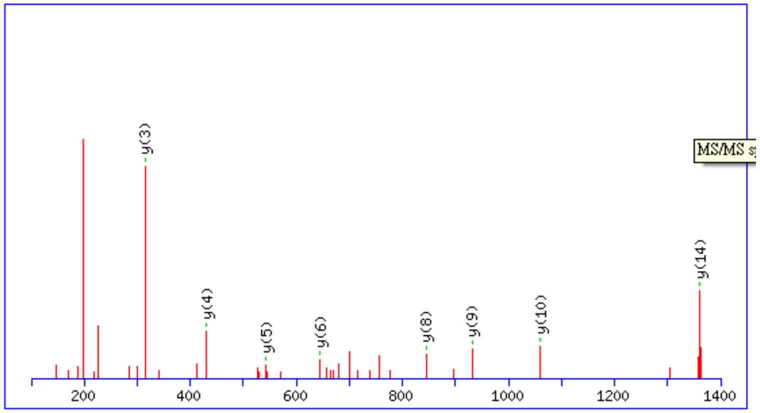
Score: 65 M_r: 18516



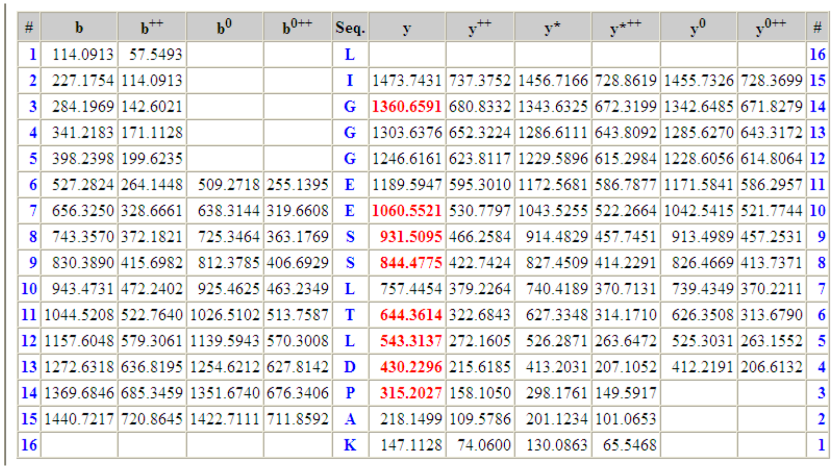
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

Matched peptides shown in **Bold Red**

1 MKAYLALISA AVIGLAACSQ EPAAPAAEAT PAAEAPASEA PAAEAAPADA
51 AEAPAAGNCA ATVESNDNMQ FNTKDIQVSK ACKEFTITLK HTGTQPKASM
101 GHNLVIAKAE DMDGVFKDGV GAADTDYVKP DDARVVAHTK **LIGGGEESSL**
151 **TLDPAK**LADG DYKFACTFPG HGALMNGKVT LVD



Monoisotopic mass of neutral peptide Mr(calc): 1585.8199
Ions Score: 65 Expect: 0.0056
Matches (**Bold Red**): 8/134 fragment ions using 12 most intense peaks

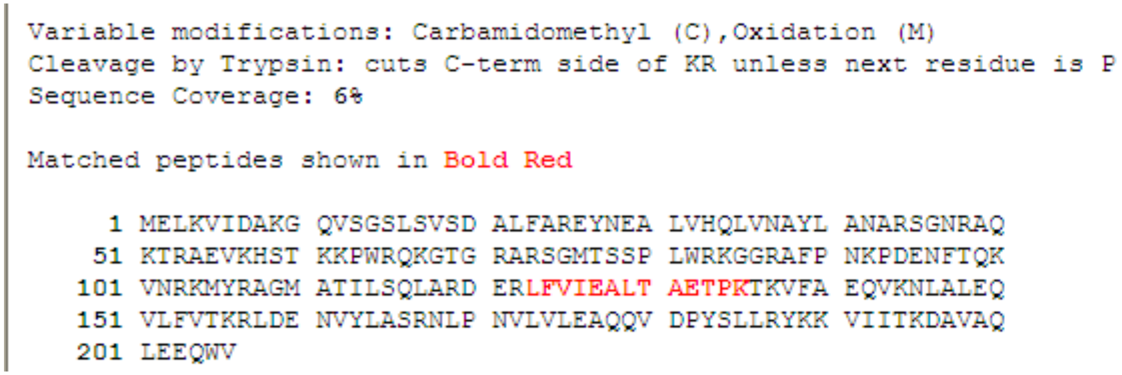


#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			L							16
2	227.1754	114.0913			I	1473.7431	737.3752	1456.7166	728.8619	1455.7326	728.3699	15
3	284.1969	142.6021			G	**1360.6591**	680.8332	1343.6325	672.3199	1342.6485	671.8279	14
4	341.2183	171.1128			G	1303.6376	652.3224	1286.6111	643.8092	1285.6270	643.3172	13
5	398.2398	199.6235			G	1246.6161	623.8117	1229.5896	615.2984	1228.6056	614.8064	12
6	527.2824	264.1448	509.2718	255.1395	E	1189.5947	595.3010	1172.5681	586.7877	1171.5841	586.2957	11
7	656.3250	328.6661	638.3144	319.6608	E	**1060.5521**	530.7797	1043.5255	522.2664	1042.5415	521.7744	10
8	743.3570	372.1821	725.3464	363.1769	S	**931.5095**	466.2584	914.4829	457.7451	913.4989	457.2531	9
9	830.3890	415.6982	812.3785	406.6929	S	**844.4775**	422.7424	827.4509	414.2291	826.4669	413.7371	8
10	943.4731	472.2402	925.4625	463.2349	L	757.4454	379.2264	740.4189	370.7131	739.4349	370.2211	7
11	1044.5208	522.7640	1026.5102	513.7587	T	**644.3614**	322.6843	627.3348	314.1710	626.3508	313.6790	6
12	1157.6048	579.3061	1139.5943	570.3008	L	**543.3137**	272.1605	526.2871	263.6472	525.3031	263.1552	5
13	1272.6318	636.8195	1254.6212	627.8142	D	**430.2296**	215.6185	413.2031	207.1052	412.2191	206.6132	4
14	1369.6846	685.3459	1351.6740	676.3406	P	**315.2027**	158.1050	298.1761	149.5917			3
15	1440.7217	720.8645	1422.7111	711.8592	A	218.1499	109.5786	201.1234	101.0653			2
16					K	147.1128	74.0600	130.0863	65.5468			1

Protein band 15 (+Mn): 50S ribosomal protein L4

Score: 64

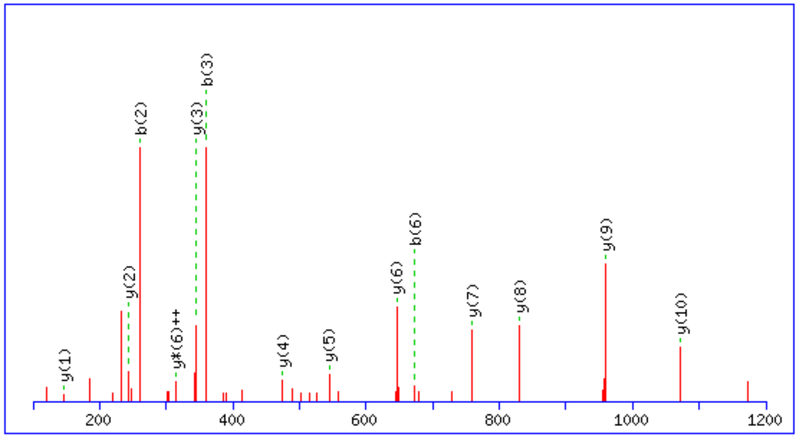
M_r: 23288



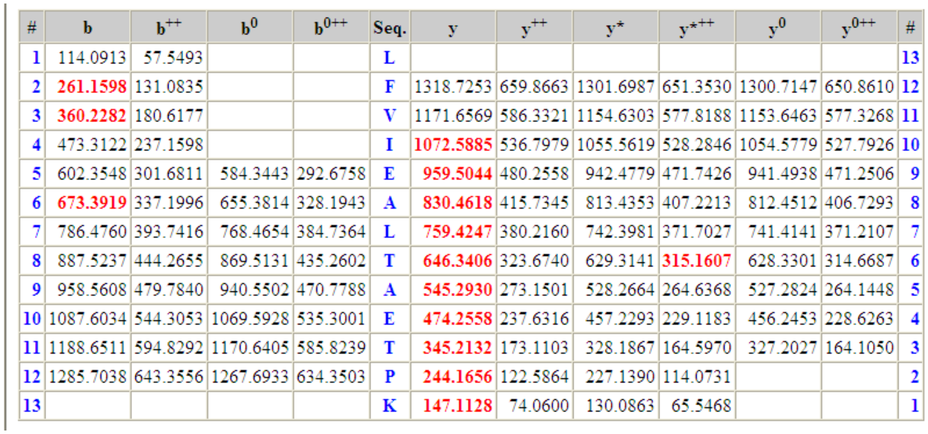
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%

Matched peptides shown in **Bold Red**

1 MELKVIDAKG QVSGSLSVSD ALFAREYNEA LVHQLVNAYL ANARSGNRAQ
51 KTRAEVKHST KKPWRQKGTG RARSGMTSSP LWRKGGRAFP NKPDENFTQK
101 VNRKMYRAGM ATILSQLARD ER**LFVIEALT AETPK**TKVFA EQVKNLALEQ
151 VLFVTKRLDE NVYLASRNLP NVLVLEAQQV DPYSLLRYKK VIITKDAVAQ
201 LEEQWV



Monoisotopic mass of neutral peptide Mr(calc): 1430.8021
Ions Score: 64 Expect: 0.0062
Matches (**Bold Red**): 14/108 fragment ions using 34 most intense peaks

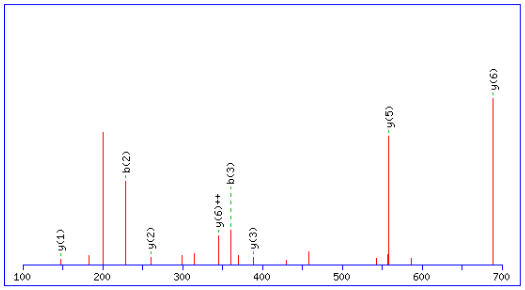


#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							13
2	**261.1598**	131.0835			F	1318.7253	659.8663	1301.6987	651.3530	1300.7147	650.8610	12
3	**360.2282**	180.6177			V	1171.6569	586.3321	1154.6303	577.8188	1153.6463	577.3268	11
4	473.3122	237.1598			I	**1072.5885**	536.7979	1055.5619	528.2846	1054.5779	527.7926	10
5	602.3548	301.6811	584.3443	292.6758	E	**959.5044**	480.2558	942.4779	471.7426	941.4938	471.2506	9
6	**673.3919**	337.1996	655.3814	328.1943	A	**830.4618**	415.7345	813.4353	407.2213	812.4512	406.7293	8
7	786.4760	393.7416	768.4654	384.7364	L	**759.4247**	380.2160	742.3981	371.7027	741.4141	371.2107	7
8	887.5237	444.2655	869.5131	435.2602	T	**646.3406**	323.6740	629.3141	**315.1607**	628.3301	314.6687	6
9	958.5608	479.7840	940.5502	470.7788	A	**545.2930**	273.1501	528.2664	264.6368	527.2824	264.1448	5
10	1087.6034	544.3053	1069.5928	535.3001	E	**474.2558**	237.6316	457.2293	229.1183	456.2453	228.6263	4
11	1188.6511	594.8292	1170.6405	585.8239	T	**345.2132**	173.1103	328.1867	164.5970	327.2027	164.1050	3
12	1285.7038	643.3556	1267.6933	634.3503	P	**244.1656**	122.5864	227.1390	114.0731			2
13					K	**147.1128**	74.0600	130.0863	65.5468			1

Protein band 17 (+Mn): Bacterioferritin A

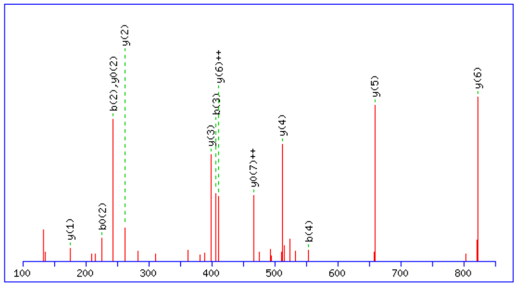
Score: 583 M_r: 17962

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 79%

Matched peptides shown in Bold Red

     1 MQGNQAVVDY MNELLSGELA ARDQYFIHSR LYSEWGYTKL FERLNHEMEE
    51 ETTHAEDFIR RILMLGGTPK MARSELNIGT DVVSCLKADL QTEYEVRDAL
   101 KKGIKLCEEA QDYVTRDLMV AQLKDTEEDH AHWLEQQLRL IELIGEGNYY
   151 QSQL
```



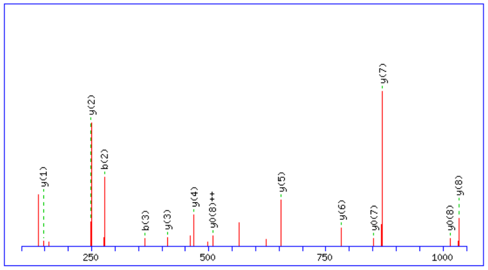
```
Monoisotopic mass of neutral peptide Mr(calc): 916.5052
Ions Score: 23  Expect: 1e+02
Matches (Bold Red): 8/60 fragment ions using 21 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	116.0342	58.5207			98.0237	49.5155	D					8
2	**229.1183**	115.0628			211.1077	106.0575	L	802.4855	401.7464	785.4590	393.2331	7
3	**360.1588**	180.5830			342.1482	171.5777	M	**689.4015**	**345.2044**	672.3749	336.6911	6
4	459.2272	230.1172			441.2166	221.1119	V	**558.3610**	279.6841	541.3344	271.1709	5
5	530.2643	265.6358			512.2537	256.6305	A	459.2926	230.1499	442.2660	221.6366	4
6	658.3229	329.6651	641.2963	321.1518	640.3123	320.6598	Q	**388.2554**	194.6314	371.2289	186.1181	3
7	771.4069	386.2071	754.3804	377.6938	753.3964	377.2018	L	**260.1969**	130.6021	243.1703	122.0888	2
8							K	**147.1128**	74.0600	130.0863	65.5468	1



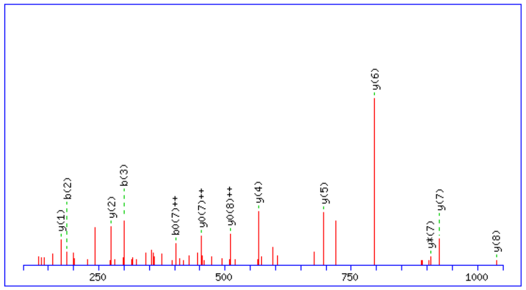
```
Monoisotopic mass of neutral peptide Mr(calc): 1064.5039
Ions Score: 47  Expect: 0.36
Matches (Bold Red): 13/80 fragment ions using 18 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							8
2	**244.0928**	122.5500	227.0662	114.0368	**226.0822**	113.5448	Q	950.4843	475.7458	933.4577	467.2325	932.4737	**466.7405**	7
3	**407.1561**	204.0817	390.1296	195.5684	389.1456	195.0764	Y	**822.4257**	**411.7165**	805.3992	403.2032	804.4151	402.7112	6
4	**554.2245**	277.6159	537.1980	269.1026	536.2140	268.6106	F	**659.3624**	330.1848	642.3358	321.6715	641.3518	321.1795	5
5	667.3086	334.1579	650.2821	325.6447	649.2980	325.1527	I	**512.2940**	256.6506	495.2674	248.1373	494.2834	247.6453	4
6	804.3675	402.6874	787.3410	394.1741	786.3570	393.6821	H	**399.2099**	200.1086	382.1833	191.5953	381.1993	191.1033	3
7	891.3995	446.2034	874.3730	437.6901	873.3890	437.1981	S	**262.1510**	131.5791	245.1244	123.0659	**244.1404**	122.5738	2
8							R	**175.1190**	88.0631	158.0924	79.5498			1



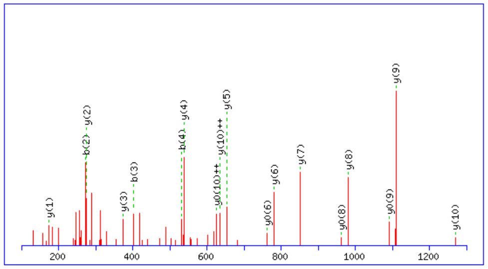
```
Monoisotopic mass of neutral peptide Mr(calc): 1145.5393
Ions Score: 62  Expect: 0.012
Matches (Bold Red): 13/74 fragment ions using 23 most intense peaks
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							9
2	**277.1547**	139.0810			Y	**1033.4625**	517.2349	1016.4360	508.7216	**1015.4520**	**508.2296**	8
3	**364.1867**	182.5970	346.1761	173.5917	S	**870.3992**	435.7032	853.3727	427.1900	**852.3886**	426.6980	7
4	493.2293	247.1183	475.2187	238.1130	E	**783.3672**	392.1872	766.3406	383.6740	765.3566	383.1819	6
5	679.3086	340.1579	661.2980	331.1527	W	**654.3246**	327.6659	637.2980	319.1527	636.3140	318.6607	5
6	736.3301	368.6687	718.3195	359.6634	G	**468.2453**	234.6263	451.2187	226.1130	450.2347	225.6210	4
7	899.3934	450.2003	881.3828	441.1951	Y	**411.2238**	206.1155	394.1973	197.6023	393.2132	197.1103	3
8	1000.4411	500.7242	982.4305	491.7189	T	**248.1605**	124.5839	231.1339	116.0706	230.1499	115.5786	2
9					K	**147.1128**	74.0600	130.0863	65.5468			1



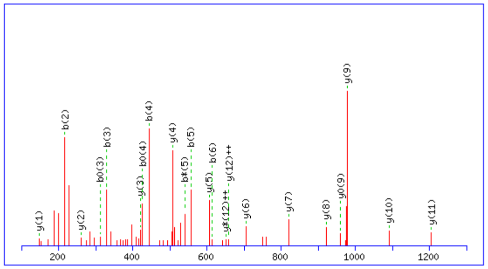
Monoisotopic mass of neutral peptide Mr(calc): 1222.5830
Ions Score: 62 Expect: 0.012
Matches (Bold Red): 13/96 fragment ions using 18 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							10
2	**187.0713**	94.0393			169.0608	85.0340	D	1152.5531	576.7802	1135.5266	568.2669	1134.5426	567.7749	9
3	**300.1554**	150.5813			282.1448	141.5761	L	**1037.5262**	519.2667	1020.4997	510.7535	1019.5156	**510.2615**	8
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	Q	**924.4421**	462.7247	**907.4156**	454.2114	906.4316	**453.7194**	7
5	529.2617	265.1345	512.2351	256.6212	511.2511	256.1292	T	**796.3836**	398.6954	779.3570	390.1821	778.3730	389.6901	6
6	658.3042	329.6558	641.2777	321.1425	640.2937	320.6505	E	**695.3359**	348.1716	678.3093	339.6583	677.3253	339.1663	5
7	821.3676	411.1874	804.3410	402.6742	803.3570	**402.1821**	Y	**566.2933**	283.6503	549.2667	275.1370	548.2827	274.6450	4
8	950.4102	475.7087	933.3836	467.1954	932.3996	466.7034	E	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
9	1049.4786	525.2429	1032.4520	516.7297	1031.4680	516.2376	V	**274.1874**	137.5973	257.1608	129.0840			2
10							R	**175.1190**	88.0631	158.0924	79.5498			1



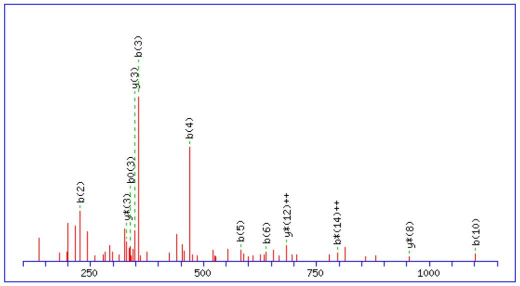
Monoisotopic mass of neutral peptide Mr(calc): 1382.6136
Variable modifications:
C2 : Carbamidomethyl (C)
Ions Score: 77 Expect: 0.00026
Matches (Bold Red): 18/104 fragment ions using 33 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	**274.1220**	137.5646					C	**1270.5368**	**635.7721**	1253.5103	627.2588	1252.5263	**626.7668**	10
3	**403.1646**	202.0859			385.1540	193.0806	E	**1110.5062**	555.7567	1093.4796	547.2435	**1092.4956**	546.7515	9
4	**532.2072**	266.6072			514.1966	257.6019	E	**981.4636**	491.2354	964.4371	482.7222	**963.4530**	482.2302	8
5	603.2443	302.1258			585.2337	293.1205	A	**852.4210**	426.7141	835.3945	418.2009	834.4104	417.7089	7
6	731.3029	366.1551	714.2763	357.6418	713.2923	357.1498	Q	**781.3839**	391.1956	764.3573	382.6823	**763.3733**	382.1903	6
7	846.3298	423.6685	829.3033	415.1553	828.3193	414.6633	D	**653.3253**	327.1663	636.2988	318.6530	635.3148	318.1610	5
8	1009.3931	505.2002	992.3666	496.6869	991.3826	496.1949	Y	**538.2984**	269.6528	521.2718	261.1396	520.2878	260.6475	4
9	1108.4616	554.7344	1091.4350	546.2211	1090.4510	545.7291	V	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	1209.5092	605.2583	1192.4827	596.7450	1191.4987	596.2530	T	**276.1666**	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	**175.1190**	88.0631	158.0924	79.5498			1



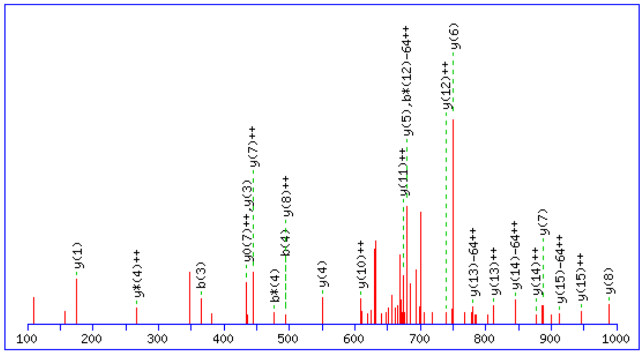
Monoisotopic mass of neutral peptide Mr(calc): 1533.7709
Variable modifications:
C12 : Carbamidomethyl (C)
Ions Score: 72 Expect: 0.0011
Matches (Bold Red): 22/144 fragment ions using 47 most intense peaks

#	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							14
2	**217.0819**	109.0446			199.0713	100.0393	E	1447.7461	724.3767	1430.7196	715.8634	1429.7355	715.3714	13
3	**330.1660**	165.5866			**312.1554**	156.5813	L	1318.7035	**659.8554**	1301.6770	**651.3421**	1300.6930	650.8501	12
4	**444.2089**	222.6081	427.1823	214.0948	**426.1983**	213.6028	N	**1205.6195**	603.3134	1188.5929	594.8001	1187.6089	594.3081	11
5	**557.2930**	279.1501	**540.2664**	270.6368	539.2824	270.1448	I	**1091.5765**	546.2919	1074.5500	537.7786	1073.5660	537.2866	10
6	**614.3144**	307.6608	597.2879	299.1476	596.3039	298.6556	G	**978.4925**	489.7499	961.4659	481.2366	**960.4819**	480.7446	9
7	715.3621	358.1847	698.3355	349.6714	697.3515	349.1794	T	**921.4710**	461.2391	904.4445	452.7259	903.4604	452.2339	8
8	830.3890	415.6982	813.3625	407.1849	812.3785	406.6929	D	**820.4233**	410.7153	803.3968	402.2020	802.4128	401.7100	7
9	929.4575	465.2324	912.4309	456.7191	911.4469	456.2271	V	**705.3964**	353.2018	688.3698	344.6886	687.3858	344.1965	6
10	1028.5259	514.7666	1011.4993	506.2533	1010.5153	505.7613	V	**606.3280**	303.6676	589.3014	295.1543	588.3174	294.6623	5
11	1115.5579	558.2826	1098.5313	549.7693	1097.5473	549.2773	S	**507.2596**	254.1334	490.2330	245.6201	489.2490	245.1281	4
12	1275.5885	638.2979	1258.5620	629.7846	1257.5780	629.2926	C	**420.2275**	210.6174	403.2010	202.1041			3
13	1388.6726	694.8399	1371.6461	686.3267	1370.6620	685.8347	L	**260.1969**	130.6021	243.1703	122.0888			2
14							K	**147.1128**	74.0600	130.0863	65.5468			1



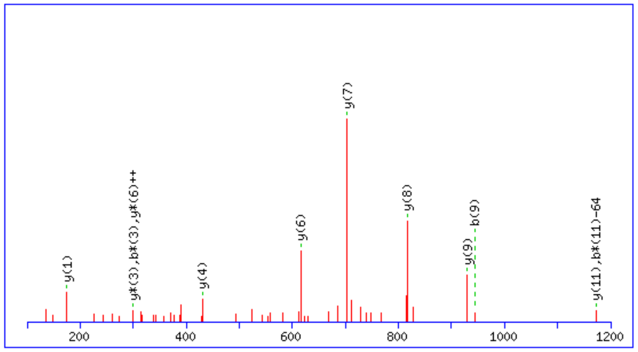
Monoisotopic mass of neutral peptide Mr(calc): 1738.8777
Ions Score: 21 Expect: 1.1e+02
Matches (Bold Red): 12/142 fragment ions using 25 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							15
2	**227.1754**	114.0913					I	1626.8010	813.9041	1609.7744	805.3909	1608.7904	804.8988	14
3	**356.2180**	178.6126			**338.2074**	169.6074	E	1513.7169	757.3621	1496.6904	748.8488	1495.7064	748.3568	13
4	**469.3021**	235.1547			451.2915	226.1494	L	1384.6743	692.8408	1367.6478	**684.3275**	1366.6638	683.8355	12
5	**582.3861**	291.6967			564.3756	282.6914	I	1271.5903	636.2988	1254.5637	627.7855	1253.5797	627.2935	11
6	**639.4076**	320.2074			621.3970	311.2022	G	1158.5062	579.7567	1141.4796	571.2435	1140.4956	570.7515	10
7	768.4502	384.7287			750.4396	375.7234	E	1101.4847	551.2460	1084.4582	542.7327	1083.4742	542.2407	9
8	825.4716	413.2395			807.4611	404.2342	G	972.4421	486.7247	**955.4156**	478.2114	954.4316	477.7194	8
9	939.5146	470.2609	922.4880	461.7477	921.5040	461.2556	N	915.4207	458.2140	898.3941	449.7007	897.4101	449.2087	7
10	**1102.5779**	551.7926	1085.5514	543.2793	1084.5673	542.7873	Y	801.3777	401.1925	784.3512	392.6792	783.3672	392.1872	6
11	1265.6412	633.3243	1248.6147	624.8110	1247.6307	624.3190	Y	638.3144	319.6608	621.2879	311.1476	620.3039	310.6556	5
12	1393.6998	697.3535	1376.6733	688.8403	1375.6892	688.3483	Q	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	4
13	1480.7318	740.8696	1463.7053	732.3563	1462.7213	731.8643	S	**347.1925**	174.0999	**330.1660**	165.5866	329.1819	165.0946	3
14	1608.7904	804.8988	1591.7639	**796.3856**	1590.7799	795.8936	Q	260.1605	130.5839	243.1339	122.0706			2
15							L	132.1019	66.5546					1



```
Monoisotopic mass of neutral peptide Mr(calc): 2115.9167
Variable modifications:
M5     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 52  Expect: 0.054
Matches (Bold Red): 24/274 fragment ions using 44 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							17
2	228.1343	114.5708	211.1077	106.0575			N	2003.8400	1002.4236	1986.8134	993.9103	1985.8294	993.4183	16
3	**365.1932**	183.1002	348.1666	174.5870			H	1889.7970	**945.4022**	1872.7705	936.8889	1871.7865	936.3969	15
4	**494.2358**	247.6215	**477.2092**	239.1082	476.2252	238.6162	E	1752.7381	**876.8727**	1735.7116	868.3594	1734.7276	867.8674	14
5	641.2712	321.1392	624.2446	312.6260	623.2606	312.1339	M	1623.6955	**812.3514**	1606.6690	803.8381	1605.6850	803.3461	13
6	770.3138	385.6605	753.2872	377.1472	752.3032	376.6552	E	1476.6601	**738.8337**	1459.6336	730.3204	1458.6496	729.8284	12
7	899.3564	450.1818	882.3298	441.6685	881.3458	441.1765	E	1347.6175	**674.3124**	1330.5910	665.7991	1329.6070	665.3071	11
8	1028.3990	514.7031	1011.3724	506.1898	1010.3884	505.6978	E	1218.5749	**609.7911**	1201.5484	601.2778	1200.5644	600.7858	10
9	1129.4466	565.2270	1112.4201	556.7137	1111.4361	556.2217	T	1089.5324	545.2698	1072.5058	536.7565	1071.5218	536.2645	9
10	1230.4943	615.7508	1213.4678	607.2375	1212.4837	606.7455	T	**988.4847**	**494.7460**	971.4581	486.2327	970.4741	485.7407	8
11	1367.5532	684.2803	1350.5267	675.7670	1349.5427	675.2750	H	**887.4370**	**444.2221**	870.4104	435.7089	869.4264	**435.2169**	7
12	1438.5903	719.7988	1421.5638	711.2855	1420.5798	710.7935	A	**750.3781**	375.6927	733.3515	367.1794	732.3675	366.6874	6
13	1567.6329	784.3201	1550.6064	775.8068	1549.6224	775.3148	E	**679.3410**	340.1741	662.3144	331.6608	661.3304	331.1688	5
14	1682.6599	841.8336	1665.6333	833.3203	1664.6493	832.8283	D	**550.2984**	275.6528	533.2718	**267.1396**	532.2878	266.6475	4
15	1829.7283	915.3678	1812.7017	906.8545	1811.7177	906.3625	F	**435.2714**	218.1394	418.2449	209.6261			3
16	1942.8124	971.9098	1925.7858	963.3965	1924.8018	962.9045	I	288.2030	144.6051	271.1765	136.0919			2
17							R	**175.1190**	88.0631	158.0924	79.5498			1



```
Monoisotopic mass of neutral peptide Mr(calc): 2424.1413
Variable modifications:
M11    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 58  Expect: 0.014
Matches (Bold Red): 12/352 fragment ions using 11 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.0478	66.5275					M							22
2	260.1063	130.5568	243.0798	122.0435			Q	2294.1081	1147.5577	2277.0816	1139.0444	2276.0976	1138.5524	21
3	317.1278	159.0675	**300.1013**	150.5543			G	2166.0496	1083.5284	2149.0230	1075.0151	2148.0390	1074.5231	20
4	431.1707	216.0890	414.1442	207.5757			N	2109.0281	1055.0177	2092.0016	1046.5044	2091.0175	1046.0124	19
5	559.2293	280.1183	542.2028	271.6050			Q	1994.9852	997.9962	1977.9586	989.4830	1976.9746	988.9909	18
6	630.2664	315.6368	613.2399	307.1236			A	1866.9266	933.9669	1849.9000	925.4537	1848.9160	924.9617	17
7	729.3348	365.1711	712.3083	356.6578			V	1795.8895	898.4484	1778.8629	889.9351	1777.8789	889.4431	16
8	828.4032	414.7053	811.3767	406.1920			V	1696.8211	848.9142	1679.7945	840.4009	1678.8105	839.9089	15
9	**943.4302**	472.2187	926.4036	463.7055	925.4196	463.2135	D	1597.7527	799.3800	1580.7261	790.8667	1579.7421	790.3747	14
10	1106.4935	553.7504	1089.4670	545.2371	1088.4830	544.7451	Y	1482.7257	741.8665	1465.6992	733.3532	1464.7151	732.8612	13
11	1253.5289	627.2681	1236.5024	618.7548	1235.5184	618.2628	M	1319.6624	660.3348	1302.6358	651.8216	1301.6518	651.3295	12
12	1367.5719	684.2896	1350.5453	675.7763	1349.5613	675.2843	N	**1172.6270**	586.8171	1155.6004	578.3039	1154.6164	577.8118	11
13	1496.6144	748.8109	1479.5879	740.2976	1478.6039	739.8056	E	1058.5841	529.7957	1041.5575	521.2824	1040.5735	520.7904	10
14	1609.6985	805.3529	1592.6720	796.8396	1591.6879	796.3476	L	**929.5415**	465.2744	912.5149	456.7611	911.5309	456.2691	9
15	1722.7826	861.8949	1705.7560	853.3817	1704.7720	852.8896	L	**816.4574**	408.7323	799.4308	400.2191	798.4468	399.7271	8
16	1809.8146	905.4109	1792.7881	896.8977	1791.8040	896.4057	S	**703.3733**	352.1903	686.3468	343.6770	685.3628	343.1850	7
17	1866.8361	933.9217	1849.8095	925.4084	1848.8255	924.9164	G	**616.3413**	308.6743	599.3148	**300.1610**	598.3307	299.6690	6
18	1995.8787	998.4430	1978.8521	989.9297	1977.8681	989.4377	E	559.3198	280.1636	542.2933	271.6503	541.3093	271.1583	5
19	2108.9627	1054.9850	2091.9362	1046.4717	2090.9522	1045.9797	L	**430.2772**	215.6423	413.2507	207.1290			4
20	2179.9998	1090.5036	2162.9733	1081.9903	2161.9893	1081.4983	A	317.1932	159.1002	**300.1666**	150.5870			3
21	2251.0370	1126.0221	2234.0104	1117.5088	2233.0264	1117.0168	A	246.1561	123.5817	229.1295	115.0684			2
22							R	**175.1190**	88.0631	158.0924	79.5498			1

Protein band 17 (+Mn): 50S ribosomal protein L9

Score: 572 M_r: 15687

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 75%

Matched peptides shown in Bold Red

    1 MQIILLEKIG GLGNLGDIVT VKNGYARNFL IPAGKAKRAT EANMKEFEAR
   51 RAELEAKQAE ILADARARQE KLDGQTVTVA QKAGVDGRLF GSVTNADIAA
  101 AIVAAGIEAV KANVRLPNGP LKAVGEYEVE VALHTDAVAK ITVAVIAAAE
  151
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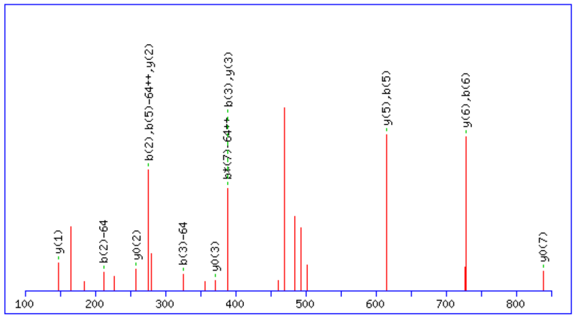
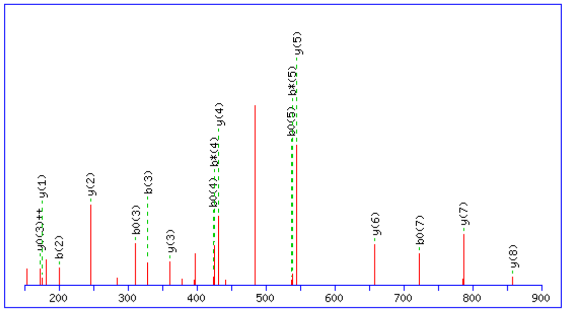


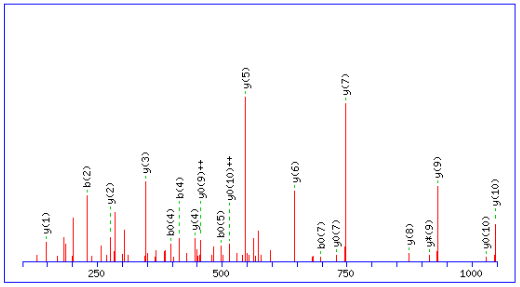
```
Monoisotopic mass of neutral peptide Mr(calc): 1002.5783
Variable modifications:
M1     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40  Expect: 2.2
Matches (Bold Red): 16/96 fragment ions using 17 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0427	74.5250					M							8
2	**276.1013**	138.5543	259.0747	130.0410			Q	856.5502	428.7788	839.5237	420.2655	**838.5397**	419.7735	7
3	**389.1853**	195.0963	372.1588	186.5830			I	**728.4917**	364.7495	711.4651	356.2362	710.4811	355.7442	6
4	502.2694	251.6383	485.2428	243.1251			I	**615.4076**	308.2074	598.3810	299.6942	597.3970	299.2022	5
5	**615.3535**	308.1804	598.3269	299.6671			L	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
6	**728.4375**	364.7224	711.4110	356.2091			L	**389.2395**	195.1234	372.2129	186.6101	**371.2289**	186.1181	3
7	857.4801	429.2437	840.4536	420.7304	839.4695	420.2384	E	**276.1554**	138.5813	259.1288	130.0681	**258.1448**	129.5761	2
8							K	**147.1128**	74.0600	130.0863	65.5468			1



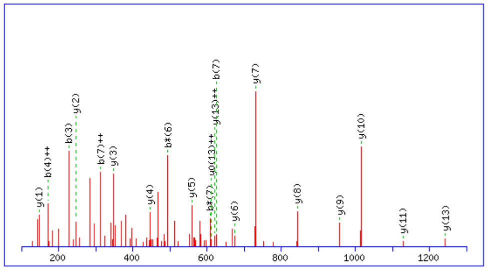
```
Monoisotopic mass of neutral peptide Mr(calc): 985.5192
Ions Score: 69  Expect: 0.0026
Matches (Bold Red): 17/88 fragment ions using 28 most intense peaks
```

#	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							9
2	**200.1030**	100.5551	183.0764	92.0418			A	**858.4680**	429.7376	841.4414	421.2243	840.4574	420.7323	8
3	**329.1456**	165.0764	312.1190	156.5631	**311.1350**	156.0711	E	**787.4308**	394.2191	770.4043	385.7058	769.4203	385.2138	7
4	442.2296	221.6185	**425.2031**	213.1052	**424.2191**	212.6132	I	**658.3883**	329.6978	641.3617	321.1845	640.3777	320.6925	6
5	555.3137	278.1605	**538.2871**	269.6472	**537.3031**	269.1552	L	**545.3042**	273.1557	528.2776	264.6425	527.2936	264.1504	5
6	626.3508	313.6790	609.3243	305.1658	608.3402	304.6738	A	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	4
7	741.3777	371.1925	724.3512	362.6792	**723.3672**	362.1872	D	**361.1830**	181.0951	344.1565	172.5819	343.1724	**172.0899**	3
8	812.4149	406.7111	795.3883	398.1978	794.4043	397.7058	A	**246.1561**	123.5817	229.1295	115.0684			2
9							R	**175.1190**	88.0631	158.0924	79.5498			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1158.6245
Ions Score: 88  Expect: 3.1e-05
Matches (Bold Red): 20/104 fragment ions using 33 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	**229.1183**	115.0628			211.1077	106.0575	D	**1046.5477**	523.7775	1029.5211	515.2642	**1028.5371**	**514.7722**	10
3	286.1397	143.5735			268.1292	134.5682	G	**931.5207**	466.2640	**914.4942**	457.7507	913.5102	**457.2587**	9
4	**414.1983**	207.6028	397.1718	199.0895	**396.1878**	198.5975	Q	**874.4993**	437.7533	857.4727	429.2400	856.4887	428.7480	8
5	515.2460	258.1266	498.2195	249.6134	**497.2354**	249.1214	T	**746.4407**	373.7240	729.4141	365.2107	**728.4301**	364.7187	7
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	V	**645.3930**	323.2001	628.3665	314.6869	627.3824	314.1949	6
7	715.3621	358.1847	698.3355	349.6714	**697.3515**	349.1794	T	**546.3246**	273.6659	529.2980	265.1527	528.3140	264.6607	5
8	814.4305	407.7189	797.4040	399.2056	796.4199	398.7136	V	**445.2769**	223.1421	428.2504	214.6288			4
9	885.4676	443.2375	868.4411	434.7242	867.4571	434.2322	A	**346.2085**	173.6079	329.1819	165.0946			3
10	1013.5262	507.2667	996.4997	498.7535	995.5156	498.2615	Q	**275.1714**	138.0893	258.1448	129.5761			2
11							K	**147.1128**	74.0600	130.0863	65.5468			1



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Monoisotopic mass of neutral peptide Mr(calc): 1354.7820
Ions Score: 105  Expect: 5.4e-07
Matches (Bold Red): 21/126 fragment ions using 31 most intense peaks
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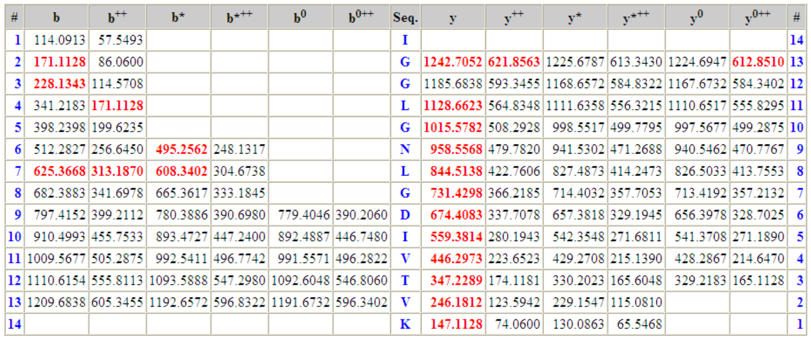
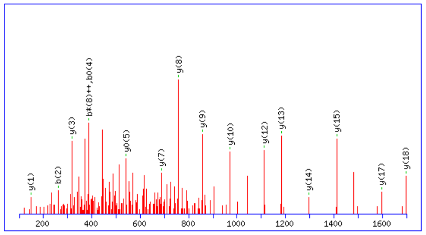
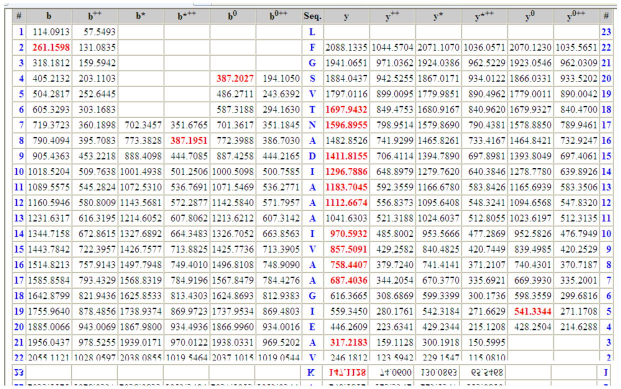


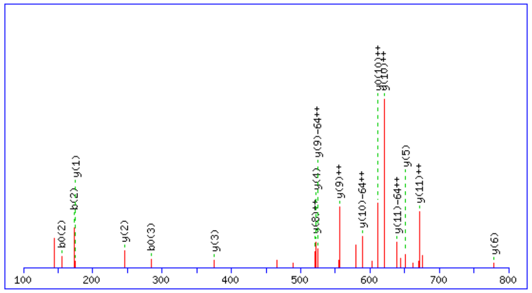
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							14
2	**171.1128**	86.0600					G	**1242.7052**	**621.8563**	1225.6787	613.3430	1224.6947	**612.8510**	13
3	**228.1343**	114.5708					G	1185.6838	593.3455	1168.6572	584.8322	1167.6732	584.3402	12
4	341.2183	**171.1128**					L	**1128.6623**	564.8348	1111.6358	556.3215	1110.6517	555.8295	11
5	398.2398	199.6235					G	**1015.5782**	508.2928	998.5517	499.7795	997.5677	499.2875	10
6	512.2827	256.6450	**495.2562**	248.1317			N	**958.5568**	479.7820	941.5302	471.2688	940.5462	470.7767	9
7	**625.3668**	**313.1870**	**608.3402**	304.6738			L	**844.5138**	422.7606	827.4873	414.2473	826.5033	413.7553	8
8	682.3883	341.6978	665.3617	333.1845			G	**731.4298**	366.2185	714.4032	357.7053	713.4192	357.2132	7
9	797.4152	399.2112	780.3886	390.6980	779.4046	390.2060	D	**674.4083**	337.7078	657.3818	329.1945	656.3978	328.7025	6
10	910.4993	455.7533	893.4727	447.2400	892.4887	446.7480	I	**559.3814**	280.1943	542.3548	271.6811	541.3708	271.1890	5
11	1009.5677	505.2875	992.5411	496.7742	991.5571	496.2822	V	**446.2973**	223.6523	429.2708	215.1390	428.2867	214.6470	4
12	1110.6154	555.8113	1093.5888	547.2980	1092.6048	546.8060	T	**347.2289**	174.1181	330.2023	165.6048	329.2183	165.1128	3
13	1209.6838	605.3455	1192.6572	596.8322	1191.6732	596.3402	V	**246.1812**	123.5942	229.1547	115.0810			2
14							K	**147.1128**	74.0600	130.0863	65.5468			1



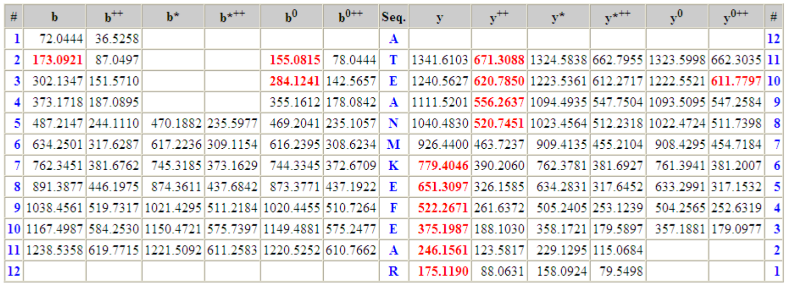
```
Monoisotopic mass of neutral peptide Mr(calc): 2200.2103
Ions Score: 104  Expect: 4.7e-07
Matches (Bold Red): 16/240 fragment ions using 21 most intense peaks
```



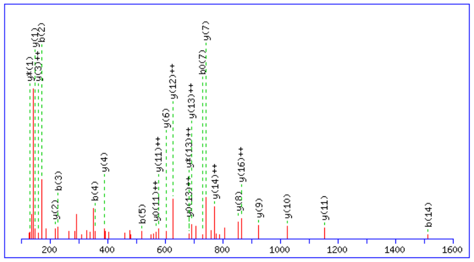
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							23
2	**261.1598**	131.0835					F	2088.1335	1044.5704	2071.1070	1036.0571	2070.1230	1035.5651	22
3	318.1812	159.5942					G	1941.0651	971.0362	1924.0386	962.5229	1923.0546	962.0309	21
4	405.2132	203.1103			**387.2027**	194.1050	S	1884.0437	942.5255	1867.0171	934.0122	1866.0331	933.5202	20
5	504.2817	252.6445			486.2711	243.6392	V	1797.0116	899.0095	1779.9851	890.4962	1779.0011	890.0042	19
6	605.3293	303.1683			587.3188	294.1630	T	**1697.9432**	849.4753	1680.9167	840.9620	1679.9327	840.4700	18
7	719.3723	360.1898	702.3457	351.6765	701.3617	351.1845	N	**1596.8955**	798.9514	1579.8690	790.4381	1578.8850	789.9461	17
8	790.4094	395.7083	773.3828	**387.1951**	772.3988	386.7030	A	1482.8526	741.9299	1465.8261	733.4167	1464.8421	732.9247	16
9	905.4363	453.2218	888.4098	444.7085	887.4258	444.2165	D	**1411.8155**	706.4114	1394.7890	697.8981	1393.8049	697.4061	15
10	1018.5204	509.7638	1001.4938	501.2506	1000.5098	500.7585	I	**1296.7886**	648.8979	1279.7620	640.3846	1278.7780	639.8926	14
11	1089.5575	545.2824	1072.5310	536.7691	1071.5469	536.2771	A	**1183.7045**	592.3559	1166.6780	583.8426	1165.6939	583.3506	13
12	1160.5946	580.8009	1143.5681	572.2877	1142.5840	571.7957	A	**1112.6674**	556.8373	1095.6408	548.3241	1094.6568	547.8320	12
13	1231.6317	616.3195	1214.6052	607.8062	1213.6212	607.3142	A	1041.6303	521.3188	1024.6037	512.8055	1023.6197	512.3135	11
14	1344.7158	672.8615	1327.6892	664.3483	1326.7052	663.8563	I	**970.5932**	485.8002	953.5666	477.2869	952.5826	476.7949	10
15	1443.7842	722.3957	1426.7577	713.8825	1425.7736	713.3905	V	**857.5091**	429.2582	840.4825	420.7449	839.4985	420.2529	9
16	1514.8213	757.9143	1497.7948	749.4010	1496.8108	748.9090	A	**758.4407**	379.7240	741.4141	371.2107	740.4301	370.7187	8
17	1585.8584	793.4329	1568.8319	784.9196	1567.8479	784.4276	A	**687.4036**	344.2054	670.3770	335.6921	669.3930	335.2001	7
18	1642.8799	821.9436	1625.8533	813.4303	1624.8693	812.9383	G	616.3665	308.6869	599.3399	300.1736	598.3559	299.6816	6
19	1755.9640	878.4856	1738.9374	869.9723	1737.9534	869.4803	I	559.3450	280.1761	542.3184	271.6629	**541.3344**	271.1708	5
20	1885.0066	943.0069	1867.9800	934.4936	1866.9960	934.0016	E	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
21	1956.0437	978.5255	1939.0171	970.0122	1938.0331	969.5202	A	**317.2183**	159.1128	300.1918	150.5995			3
22	2055.1121	1028.0597	2038.0855	1019.5464	2037.1015	1019.0544	V	246.1812	123.5942	229.1547	115.0810			2
23							K	**147.1128**	74.0600	130.0863	65.5468			1



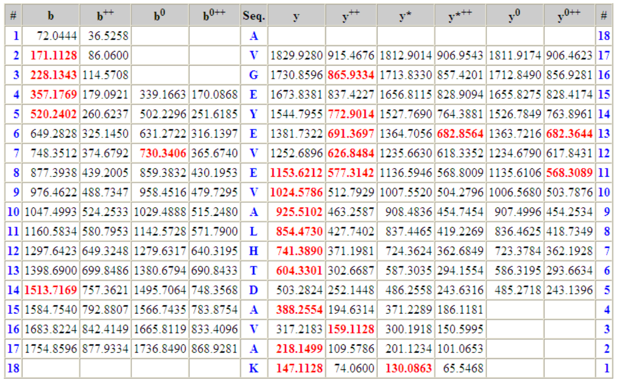
```
Monoisotopic mass of neutral peptide Mr(calc): 1411.6401
Variable modifications:
M6      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 51  Expect: 0.11
Matches (Bold Red): 17/184 fragment ions using 23 most intense peaks
```



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							12
2	**173.0921**	87.0497			**155.0815**	78.0444	T	1341.6103	**671.3088**	1324.5838	662.7955	1323.5998	662.3035	11
3	302.1347	151.5710			**284.1241**	142.5657	E	1240.5627	**620.7850**	1223.5361	612.2717	1222.5521	**611.7797**	10
4	373.1718	187.0895			355.1612	178.0842	A	1111.5201	**556.2637**	1094.4935	547.7504	1093.5095	547.2584	9
5	487.2147	244.1110	470.1882	235.5977	469.2041	235.1057	N	1040.4830	**520.7451**	1023.4564	512.2318	1022.4724	511.7398	8
6	634.2501	317.6287	617.2236	309.1154	616.2395	308.6234	M	926.4400	463.7237	909.4135	455.2104	908.4295	454.7184	7
7	762.3451	381.6762	745.3185	373.1629	744.3345	372.6709	K	**779.4046**	390.2060	762.3781	381.6927	761.3941	381.2007	6
8	891.3877	446.1975	874.3611	437.6842	873.3771	437.1922	E	**651.3097**	326.1585	634.2831	317.6452	633.2991	317.1532	5
9	1038.4561	519.7317	1021.4295	511.2184	1020.4455	510.7264	F	**522.2671**	261.6372	505.2405	253.1239	504.2565	252.6319	4
10	1167.4987	584.2530	1150.4721	575.7397	1149.4881	575.2477	E	**375.1987**	188.1030	358.1721	179.5897	357.1881	179.0977	3
11	1238.5358	619.7715	1221.5092	611.2583	1220.5252	610.7662	A	**246.1561**	123.5817	229.1295	115.0684			2
12							R	**175.1190**	88.0631	158.0924	79.5498			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1899.9578
Ions Score: 55  Expect: 0.041
Matches (Bold Red): 25/156 fragment ions using 51 most intense peaks
```



#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							18
2	**171.1128**	86.0600			V	1829.9280	915.4676	1812.9014	906.9543	1811.9174	906.4623	17
3	**228.1343**	114.5708			G	1730.8596	**865.9334**	1713.8330	857.4201	1712.8490	856.9281	16
4	**357.1769**	179.0921	339.1663	170.0868	E	1673.8381	837.4227	1656.8115	828.9094	1655.8275	828.4174	15
5	**520.2402**	260.6237	502.2296	251.6185	Y	1544.7955	**772.9014**	1527.7690	764.3881	1526.7849	763.8961	14
6	649.2828	325.1450	631.2722	316.1397	E	1381.7322	**691.3697**	1364.7056	**682.8564**	1363.7216	**682.3644**	13
7	748.3512	374.6792	**730.3406**	365.6740	V	1252.6896	**626.8484**	1235.6630	618.3352	1234.6790	617.8431	12
8	877.3938	439.2005	859.3832	430.1953	E	**1153.6212**	**577.3142**	1136.5946	568.8009	1135.6106	**568.3089**	11
9	976.4622	488.7347	958.4516	479.7295	V	**1024.5786**	512.7929	1007.5520	504.2796	1006.5680	503.7876	10
10	1047.4993	524.2533	1029.4888	515.2480	A	**925.5102**	463.2587	908.4836	454.7454	907.4996	454.2534	9
11	1160.5834	580.7953	1142.5728	571.7900	L	**854.4730**	427.7402	837.4465	419.2269	836.4625	418.7349	8
12	1297.6423	649.3248	1279.6317	640.3195	H	**741.3890**	371.1981	724.3624	362.6849	723.3784	362.1928	7
13	1398.6900	699.8486	1380.6794	690.8433	T	**604.3301**	302.6687	587.3035	294.1554	586.3195	293.6634	6
14	**1513.7169**	757.3621	1495.7064	748.3568	D	503.2824	252.1448	486.2558	243.6316	485.2718	243.1396	5
15	1584.7540	792.8807	1566.7435	783.8754	A	**388.2554**	194.6314	371.2289	186.1181			4
16	1683.8224	842.4149	1665.8119	833.4096	V	317.2183	**159.1128**	300.1918	150.5995			3
17	1754.8596	877.9334	1736.8490	868.9281	A	**218.1499**	109.5786	201.1234	101.0653			2
18					K	**147.1128**	74.0600	**130.0863**	65.5468			1

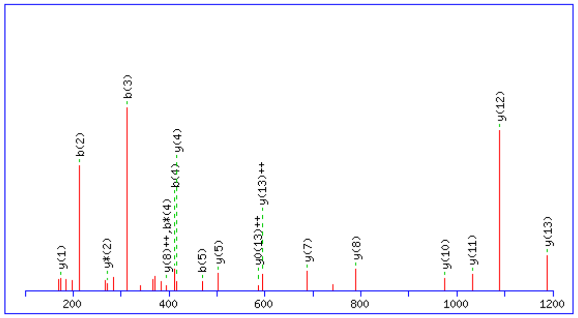
Protein band 17 (+Mn): 30S ribosomal protein S9

Score: 200 M_r: 14363

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 40%

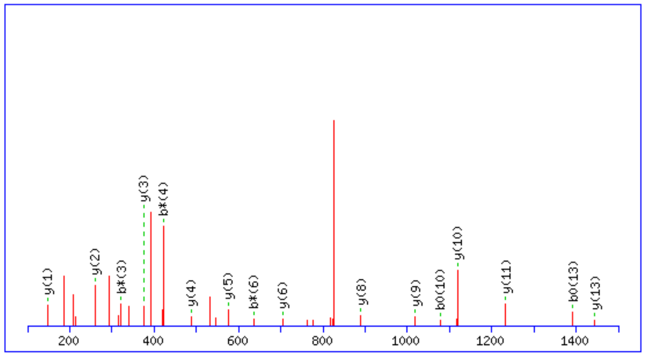
Matched peptides shown in Bold Red

  1 MNGKYYYGTG RRKSSVARVF LTKGTGQIIV NGRPVDEFFA RETSRMVVRQ
 51 PLVLTENAES LDIKVNVVGG GETGQSGAIR HGITRALIDF DAALKPALSQ
101 AGFVTRDARE VERKKPGLRK ARRAKQFSKR
```



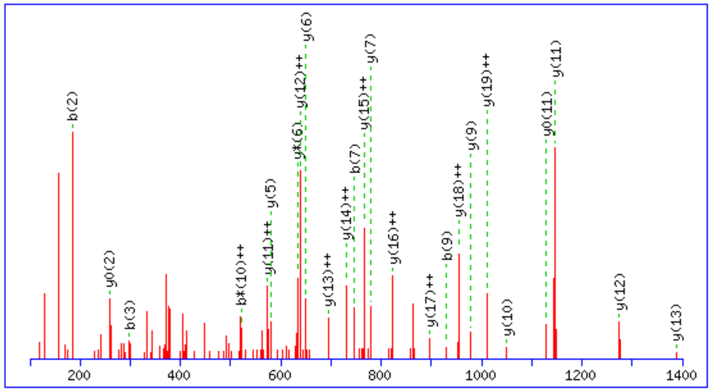
```
Monoisotopic mass of neutral peptide Mr(calc): 1499.7692
Ions Score: 67  Expect: 0.0034
Matches (Bold Red): 18/156 fragment ions using 28 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							16
2	**214.1186**	107.5629	197.0921	99.0497			N	1401.7081	701.3577	1384.6815	692.8444	1383.6975	692.3524	15
3	**313.1870**	157.0972	296.1605	148.5839			V	1287.6652	644.3362	1270.6386	635.8229	1269.6546	635.3309	14
4	**412.2554**	206.6314	**395.2289**	198.1181			V	**1188.5967**	**594.8020**	1171.5702	586.2887	1170.5862	**585.7967**	13
5	**469.2769**	235.1421	452.2504	226.6288			G	**1089.5283**	545.2678	1072.5018	536.7545	1071.5178	536.2625	12
6	526.2984	263.6528	509.2718	255.1396			G	**1032.5069**	516.7571	1015.4803	508.2438	1014.4963	507.7518	11
7	583.3198	292.1636	566.2933	283.6503			G	**975.4854**	488.2463	958.4589	479.7331	957.4748	479.2411	10
8	712.3624	356.6849	695.3359	348.1716	694.3519	347.6796	E	918.4639	459.7356	901.4374	451.2223	900.4534	450.7303	9
9	813.4101	407.2087	796.3836	398.6954	795.3995	398.2034	T	**789.4213**	**395.2143**	772.3948	386.7010	771.4108	386.2090	8
10	870.4316	435.7194	853.4050	427.2062	852.4210	426.7141	G	**688.3737**	344.6905	671.3471	336.1772	670.3631	335.6852	7
11	998.4902	499.7487	981.4636	491.2354	980.4796	490.7434	Q	631.3522	316.1797	614.3257	307.6665	613.3416	307.1745	6
12	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	S	**503.2936**	252.1504	486.2671	243.6372	485.2831	243.1452	5
13	1142.5436	571.7755	1125.5171	563.2622	1124.5331	562.7702	G	**416.2616**	208.6344	399.2350	200.1212			4
14	1213.5808	607.2940	1196.5542	598.7807	1195.5702	598.2887	A	359.2401	180.1237	342.2136	171.6104			3
15	1326.6648	663.8360	1309.6383	655.3228	1308.6543	654.8308	I	288.2030	144.6051	**271.1765**	136.0919			2
16							R	**175.1190**	88.0631	158.0924	79.5498			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1668.8934
Ions Score: 72  Expect: 0.00087
Matches (Bold Red): 16/154 fragment ions using 28 most intense peaks
```

#	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							15
2	226.1186	113.5629	209.0921	105.0497			P	1541.8421	771.4247	1524.8156	762.9114	1523.8316	762.4194	14
3	339.2027	170.1050	**322.1761**	161.5917			L	**1444.7894**	722.8983	1427.7628	714.3850	1426.7788	713.8930	13
4	438.2711	219.6392	**421.2445**	211.1259			V	1331.7053	666.3563	1314.6787	657.8430	1313.6947	657.3510	12
5	551.3552	276.1812	534.3286	267.6679			L	**1232.6369**	616.8221	1215.6103	608.3088	1214.6263	607.8168	11
6	652.4028	326.7051	**635.3763**	318.1918	634.3923	317.6998	T	**1119.5528**	560.2800	1102.5263	551.7668	1101.5422	551.2748	10
7	781.4454	391.2264	764.4189	382.7131	763.4349	382.2211	E	**1018.5051**	509.7562	1001.4786	501.2429	1000.4946	500.7509	9
8	895.4884	448.2478	878.4618	439.7345	877.4778	439.2425	N	**889.4625**	445.2349	872.4360	436.7216	871.4520	436.2296	8
9	966.5255	483.7664	949.4989	475.2531	948.5149	474.7611	A	775.4196	388.2134	758.3931	379.7002	757.4090	379.2082	7
10	1095.5681	548.2877	1078.5415	539.7744	**1077.5575**	539.2824	E	**704.3825**	352.6949	687.3559	344.1816	686.3719	343.6896	6
11	1182.6001	591.8037	1165.5735	583.2904	1164.5895	582.7984	S	**575.3399**	288.1736	558.3134	279.6603	557.3293	279.1683	5
12	1295.6842	648.3457	1278.6576	639.8324	1277.6736	639.3404	L	**488.3079**	244.6576	471.2813	236.1443	470.2973	235.6523	4
13	1410.7111	705.8592	1393.6846	697.3459	**1392.7005**	696.8539	D	**375.2238**	188.1155	358.1973	179.6023	357.2132	179.1103	3
14	1523.7952	762.4012	1506.7686	753.8879	1505.7846	753.3959	I	**260.1969**	130.6021	243.1703	122.0888			2
15							K	**147.1128**	74.0600	130.0863	65.5468			1

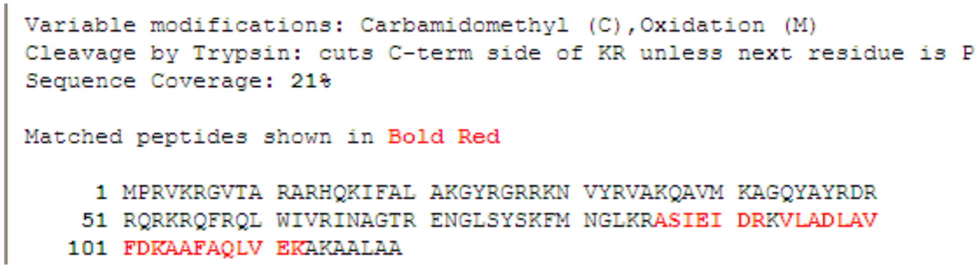


```
Monoisotopic mass of neutral peptide Mr(calc): 2203.2001
Ions Score: 61  Expect: 0.0087
Matches (Bold Red): 25/214 fragment ions using 47 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							21
2	**185.1285**	93.0679					L	2133.1703	1067.0888	2116.1437	1058.5755	2115.1597	1058.0835	20
3	**298.2125**	149.6099					I	2020.0862	**1010.5467**	2003.0597	1002.0335	2002.0756	1001.5415	19
4	413.2395	207.1234			395.2289	198.1181	D	1907.0021	**954.0047**	1889.9756	945.4914	1888.9916	944.9994	18
5	560.3079	280.6576			542.2973	271.6523	F	1791.9752	**896.4912**	1774.9486	887.9780	1773.9646	887.4860	17
6	675.3348	338.1710			657.3243	329.1658	D	1644.9068	**822.9570**	1627.8802	814.4438	1626.8962	813.9517	16
7	**746.3719**	373.6896			728.3614	364.6843	A	1529.8798	**765.4436**	1512.8533	756.9303	1511.8693	756.4383	15
8	817.4090	409.2082			799.3985	400.2029	A	1458.8427	**729.9250**	1441.8162	721.4117	1440.8322	720.9197	14
9	**930.4931**	465.7502			912.4825	456.7449	L	**1387.8056**	**694.4064**	1370.7791	685.8932	1369.7950	685.4012	13
10	1058.5881	529.7977	1041.5615	**521.2844**	1040.5775	520.7924	K	**1274.7215**	**637.8644**	1257.6950	629.3511	1256.7110	628.8591	12
11	1155.6408	578.3241	1138.6143	569.8108	1137.6303	569.3188	P	**1146.6266**	**573.8169**	1129.6000	565.3037	**1128.6160**	564.8116	11
12	1226.6780	613.8426	1209.6514	605.3293	1208.6674	604.8373	A	**1049.5738**	525.2905	1032.5473	516.7773	1031.5633	516.2853	10
13	1339.7620	670.3846	1322.7355	661.8714	1321.7514	661.3794	L	**978.5367**	489.7720	961.5102	481.2587	960.5261	480.7667	9
14	1426.7940	713.9007	1409.7675	705.3874	1408.7835	704.8954	S	865.4526	433.2300	848.4261	424.7167	847.4421	424.2247	8
15	1554.8526	777.9299	1537.8261	769.4167	1536.8421	768.9247	Q	**778.4206**	389.7139	761.3941	381.2007	760.4101	380.7087	7
16	1625.8897	813.4485	1608.8632	804.9352	1607.8792	804.4432	A	**650.3620**	325.6847	**633.3355**	317.1714	632.3515	316.6794	6
17	1682.9112	841.9592	1665.8847	833.4460	1664.9006	832.9540	G	**579.3249**	290.1661	562.2984	281.6528	561.3144	281.1608	5
18	1829.9796	915.4934	1812.9531	906.9802	1811.9690	906.4882	F	522.3035	261.6554	505.2769	253.1421	504.2929	252.6501	4
19	1929.0480	965.0277	1912.0215	956.5144	1911.0375	956.0224	V	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
20	2030.0957	1015.5515	2013.0692	1007.0382	2012.0851	1006.5462	T	276.1666	138.5870	259.1401	130.0737	**258.1561**	129.5817	2
21							R	175.1190	88.0631	158.0924	79.5498			1

Protein band 17 (+Mn): 50S ribosomal protein L20

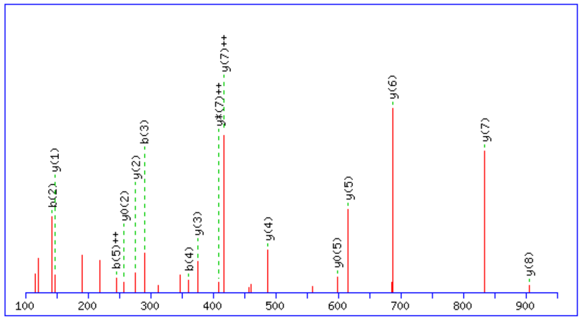
Score: 178 M_r: 13664



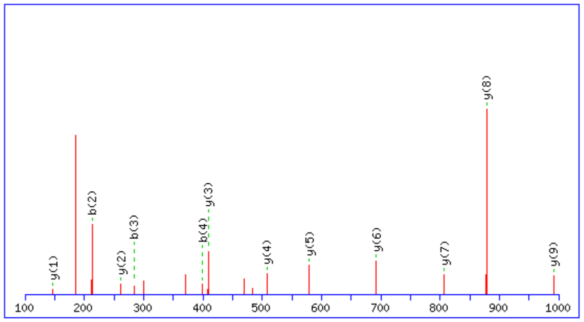
```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 21%

Matched peptides shown in Bold Red

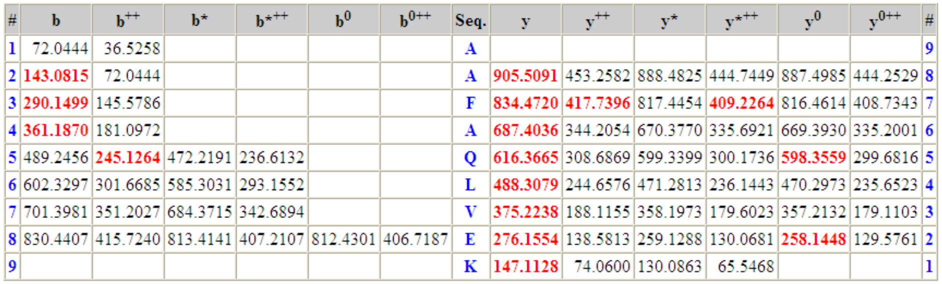
      1 MPRVKRGVTA RARHQKIFAL AKGYRGRRKN VYRVAKQAVM KAGQYAYRDR
     51 RQRKRQFRQL WIVRINAGTR ENGLSYSKFM NGLKRASIEI DRKVLADLAV
    101 FDKAAFAQLV EKAKAALAA
```



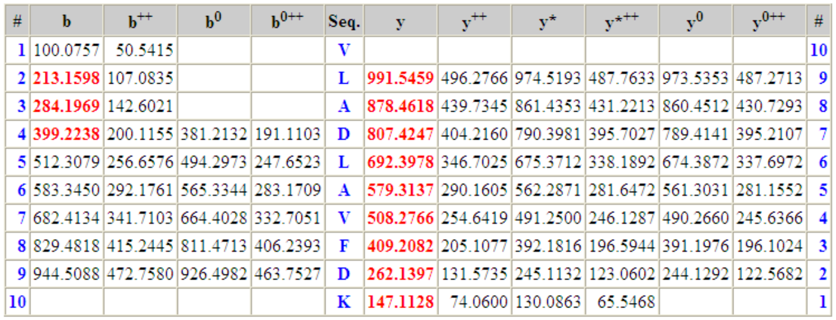
Monoisotopic mass of neutral peptide Mr(calc): 975.5389
Ions Score: 62 Expect: 0.013
Matches (Bold Red): 16/72 fragment ions using 27 most intense peaks



Monoisotopic mass of neutral peptide Mr(calc): 1089.6070
Ions Score: 77 Expect: 0.0004
Matches (Bold Red): 12/82 fragment ions using 21 most intense peaks



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							9
2	**143.0815**	72.0444					A	**905.5091**	453.2582	888.4825	444.7449	887.4985	444.2529	8
3	**290.1499**	145.5786					F	**834.4720**	**417.7396**	817.4454	**409.2264**	816.4614	408.7343	7
4	**361.1870**	181.0972					A	**687.4036**	344.2054	670.3770	335.6921	669.3930	335.2001	6
5	489.2456	**245.1264**	472.2191	236.6132			Q	**616.3665**	308.6869	599.3399	300.1736	**598.3559**	299.6816	5
6	602.3297	301.6685	585.3031	293.1552			L	**488.3079**	244.6576	471.2813	236.1443	470.2973	235.6523	4
7	701.3981	351.2027	684.3715	342.6894			V	**375.2238**	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	830.4407	415.7240	813.4141	407.2107	812.4301	406.7187	E	**276.1554**	138.5813	259.1288	130.0681	**258.1448**	129.5761	2
9							K	**147.1128**	74.0600	130.0863	65.5468			1



#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							10
2	**213.1598**	107.0835			L	**991.5459**	496.2766	974.5193	487.7633	973.5353	487.2713	9
3	**284.1969**	142.6021			A	**878.4618**	439.7345	861.4353	431.2213	860.4512	430.7293	8
4	**399.2238**	200.1155	381.2132	191.1103	D	**807.4247**	404.2160	790.3981	395.7027	789.4141	395.2107	7
5	512.3079	256.6576	494.2973	247.6523	L	**692.3978**	346.7025	675.3712	338.1892	674.3872	337.6972	6
6	583.3450	292.1761	565.3344	283.1709	A	**579.3137**	290.1605	562.2871	281.6472	561.3031	281.1552	5
7	682.4134	341.7103	664.4028	332.7051	V	**508.2766**	254.6419	491.2500	246.1287	490.2660	245.6366	4
8	829.4818	415.2445	811.4713	406.2393	F	**409.2082**	205.1077	392.1816	196.5944	391.1976	196.1024	3
9	944.5088	472.7580	926.4982	463.7527	D	**262.1397**	131.5735	245.1132	123.0602	244.1292	122.5682	2
10					K	**147.1128**	74.0600	130.0863	65.5468			1

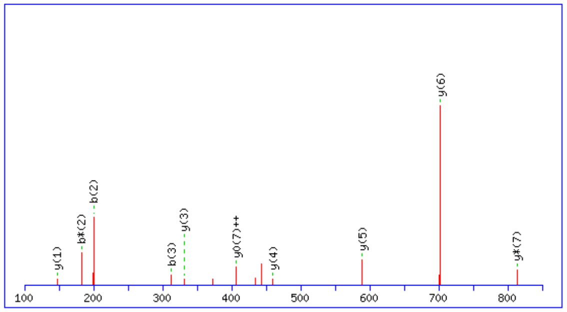
Protein band 17 (+Mn): 50S ribosomal protein L11

Score: 143 M$_r$: 14942

Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 21%

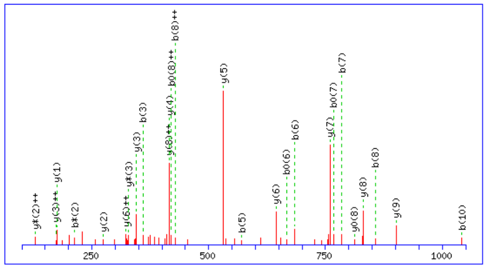
Matched peptides shown in **Bold Red**

1 MAKKIIGYIK LQIPAGKANP SPPVGPALGQ RGLNIMEFCK AFNAATQGME
51 SGLPIPVVIT AFADK**SFTFV** **MK**TPPASILL KKAAGLQKGS SNPLTNKVGK
101 LTR**AQLEEIA** **KTKEPDLTAA** **DLDAAVR**TIA GSARSMGLDV EGVV



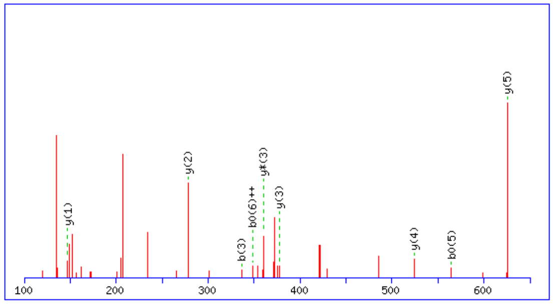
Monoisotopic mass of neutral peptide Mr(calc): 900.4916
Ions Score: 41 Expect: 1.7
Matches (**Bold Red**): 10/70 fragment ions using 15 most intense peaks

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	72.0444	36.5258					A							8
2	**200.1030**	100.5551	**183.0764**	92.0418			Q	830.4618	415.7345	**813.4353**	407.2213	812.4512	**406.7293**	7
3	**313.1870**	157.0972	296.1605	148.5839			L	**702.4032**	351.7053	685.3767	343.1920	684.3927	342.7000	6
4	442.2296	221.6185	425.2031	213.1052	424.2191	212.6132	E	**589.3192**	295.1632	572.2926	286.6499	571.3086	286.1579	5
5	571.2722	286.1397	554.2457	277.6265	553.2617	277.1345	E	**460.2766**	230.6419	443.2500	222.1287	442.2660	221.6366	4
6	684.3563	342.6818	667.3297	334.1685	666.3457	333.6765	I	**331.2340**	166.1206	314.2074	157.6074			3
7	755.3934	378.2003	738.3668	369.6871	737.3828	369.1951	A	218.1499	109.5786	201.1234	101.0653			2
8							K	**147.1128**	74.0600	130.0863	65.5468			1



Monoisotopic mass of neutral peptide Mr(calc): 1684.8632
Ions Score: 62 Expect: 0.0086
Matches (**Bold Red**): 26/170 fragment ions using 42 most intense peaks

#	b	b^{++}	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							16
2	230.1499	115.5786	**213.1234**	107.0653	212.1394	106.5733	K	1584.8228	792.9150	1567.7962	784.4018	1566.8122	783.9097	15
3	**359.1925**	180.0999	342.1660	171.5866	341.1819	171.0946	E	1456.7278	728.8675	1439.7013	720.3543	1438.7172	719.8623	14
4	456.2453	228.6263	439.2187	220.1130	438.2347	219.6210	P	1327.6852	664.3462	1310.6587	655.8330	1309.6747	655.3410	13
5	**571.2722**	286.1397	554.2457	277.6265	553.2617	277.1345	D	1230.6325	615.8199	1213.6059	607.3066	1212.6219	606.8146	12
6	**684.3563**	342.6818	667.3297	334.1685	**666.3457**	333.6765	L	1115.6055	558.3064	1098.5790	549.7931	1097.5949	549.3011	11
7	**785.4040**	393.2056	768.3774	384.6923	**767.3934**	384.2003	T	1002.5215	501.7644	985.4949	493.2511	984.5109	492.7591	10
8	**856.4411**	**428.7242**	839.4145	420.2109	838.4305	**419.7189**	A	**901.4738**	451.2405	884.4472	442.7272	883.4632	442.2352	9
9	927.4782	464.2427	910.4516	455.7295	909.4676	455.2375	A	**830.4367**	**415.7220**	813.4101	407.2087	**812.4261**	406.7167	8
10	**1042.5051**	521.7562	1025.4786	513.2429	1024.4946	512.7509	D	**759.3995**	380.2034	742.3730	371.6901	741.3890	371.1981	7
11	1155.5892	578.2982	1138.5626	569.7850	1137.5786	569.2930	L	**644.3726**	**322.6899**	627.3461	314.1767	626.3620	313.6847	6
12	1270.6161	635.8117	1253.5896	627.2984	1252.6056	626.8064	D	**531.2885**	266.1479	514.2620	257.6346	513.2780	257.1426	5
13	1341.6533	671.3303	1324.6267	662.8170	1323.6427	662.3250	A	**416.2616**	208.6344	399.2350	200.1212			4
14	1412.6904	706.8488	1395.6638	698.3355	1394.6798	697.8435	A	**345.2245**	**173.1159**	**328.1979**	164.6026			3
15	1511.7588	756.3830	1494.7322	747.8698	1493.7482	747.3777	V	**274.1874**	137.5973	257.1608	**129.0840**			2
16							R	**175.1190**	88.0631	158.0924	79.5498			1



Monoisotopic mass of neutral peptide Mr(calc): 858.4310
Ions Score: 21 Expect: 2e+02
Matches (**Bold Red**): 9/52 fragment ions using 27 most intense peaks

#	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							7
2	235.1077	118.0575	217.0972	109.0522	F	772.4062	386.7067	755.3797	378.1935	754.3956	377.7015	6
3	**336.1554**	168.5813	318.1448	159.5761	T	**625.3378**	313.1725	608.3112	304.6593	607.3272	304.1673	5
4	483.2238	242.1155	465.2132	233.1103	F	**524.2901**	262.6487	507.2636	254.1354			4
5	582.2922	291.6498	**564.2817**	282.6445	V	**377.2217**	189.1145	**360.1952**	180.6012			3
6	713.3327	357.1700	695.3221	**348.1647**	M	**278.1533**	139.5803	261.1267	131.0670			2
7					K	**147.1128**	74.0600	130.0863	65.5468			1

Protein band 31 (+Mn): Porin IB

Score: 438 M_r: 37174

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 35%

Matched peptides shown in Bold Red

     1 DVTLYGAIKA GVQTYRSVEH TDGKVSKVET GSEIADFGSK IGFKGQEDLG
    51 NGLKAVWQLE QGASVAGTNT GWGNKQSFVG LKGGFGTIRA GSLNSPLKNT
   101 KDNVNAWESG KFTGNVLEIS GMAKREHRYL SVRYDSPEFA GFSGSVQYAP
   151 KDNSGSNGES YHVGLNYQNS GFFAQYAGLF QRYGEGTKKI EYEHQVYSIP
   201 SPSLFVEKLQ VHRLVGGYDN NALYVSVAAQ QQDAKLYGAR RANSHNSQTE
   251 VAATAAYRFG NVTPRVSYAH GFKGTVDSAD HDNTYDQVVV GAEYDFSKRT
   301 SALVSAGWLQ EGKGADKTVS TASAVVLRHK F
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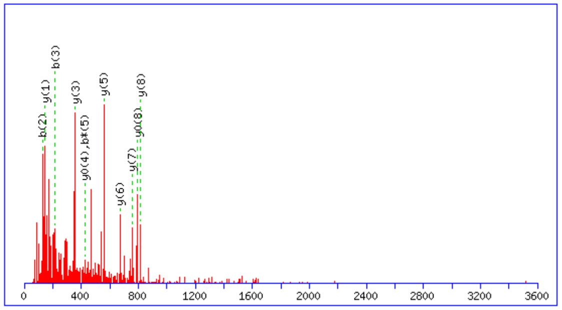
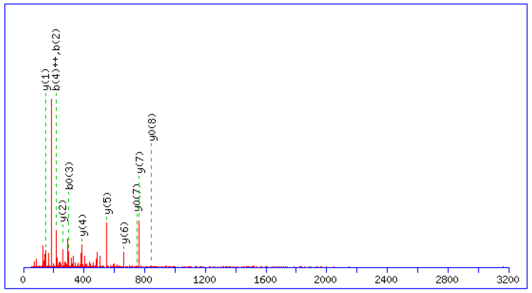


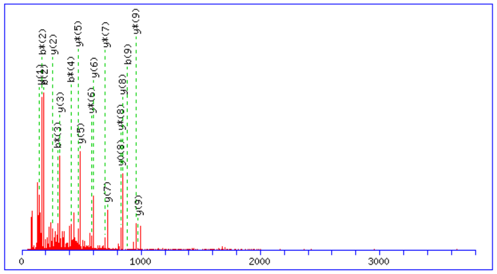
```
Monoisotopic mass of neutral peptide Mr(calc): 885.4920
Ions Score: 43  Expect: 1.1
Matches (Bold Red): 11/78 fragment ions using 69 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							9
2	**129.0659**	65.0366					G	**815.4621**	408.2347	798.4356	399.7214	**797.4516**	399.2294	8
3	**216.0979**	108.5526			198.0873	99.5473	S	**758.4407**	379.7240	741.4141	371.2107	740.4301	370.7187	7
4	329.1819	165.0946			311.1714	156.0893	L	**671.4087**	336.2080	654.3821	327.6947	653.3981	327.2027	6
5	443.2249	222.1161	**426.1983**	213.6028	425.2143	213.1108	N	**558.3246**	279.6659	541.2980	271.1527	540.3140	270.6606	5
6	530.2569	265.6321	513.2304	257.1188	512.2463	256.6268	S	444.2817	222.6445	427.2551	214.1312	**426.2711**	213.6392	4
7	627.3097	314.1585	610.2831	305.6452	609.2991	305.1532	P	**357.2496**	179.1285	340.2231	170.6152			3
8	740.3937	370.7005	723.3672	362.1872	722.3832	361.6952	L	260.1969	130.6021	243.1703	122.0888			2
9							K	**147.1128**	74.0600	130.0863	65.5468			1



```
Monoisotopic mass of neutral peptide Mr(calc): 978.5386
Ions Score: 32  Expect: 12
Matches (Bold Red): 11/68 fragment ions using 26 most intense peaks
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207	98.0237	49.5155	D							9
2	**215.1026**	108.0550	197.0921	99.0497	V	864.5189	432.7631	847.4924	424.2498	**846.5084**	423.7578	8
3	316.1503	158.5788	**298.1397**	149.5735	T	**765.4505**	383.2289	748.4240	374.7156	**747.4400**	374.2236	7
4	429.2344	**215.1208**	411.2238	206.1155	L	**664.4028**	332.7051	647.3763	324.1918			6
5	592.2977	296.6525	574.2871	287.6472	Y	**551.3188**	276.1630	534.2922	267.6498			5
6	649.3192	325.1632	631.3086	316.1579	G	**388.2554**	194.6314	371.2289	186.1181			4
7	720.3563	360.6818	702.3457	351.6765	A	331.2340	166.1206	314.2074	157.6074			3
8	833.4403	417.2238	815.4298	408.2185	I	**260.1969**	130.6021	243.1703	122.0888			2
9					K	**147.1128**	74.0600	130.0863	65.5468			1



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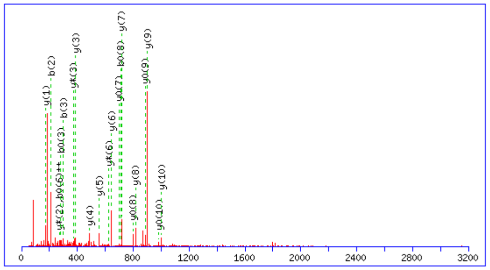
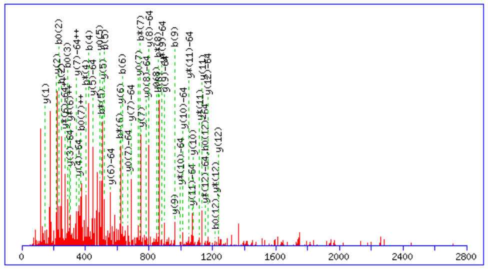
Monoisotopic mass of neutral peptide Mr(calc): 1029.5091
Ions Score: 51  Expect: 0.2
Matches (Bold Red): 19/90 fragment ions using 40 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							10
2	**186.0873**	93.5473	**169.0608**	85.0340			Q	**973.4949**	487.2511	**956.4684**	478.7378	955.4843	478.2458	9
3	315.1299	158.0686	**298.1034**	149.5553	297.1193	149.0633	E	**845.4363**	423.2218	**828.4098**	414.7085	**827.4258**	414.2165	8
4	430.1569	215.5821	**413.1303**	207.0688	412.1463	206.5768	D	**716.3937**	358.7005	**699.3672**	350.1872	698.3832	349.6952	7
5	543.2409	272.1241	526.2144	263.6108	525.2304	263.1188	L	**601.3668**	301.1870	**584.3402**	292.6738			6
6	600.2624	300.6348	583.2358	292.1216	582.2518	291.6295	G	**488.2827**	244.6450	**471.2562**	236.1317			5
7	714.3053	357.6563	697.2788	349.1430	696.2947	348.6510	N	431.2613	216.1343	414.2347	207.6210			4
8	771.3268	386.1670	754.3002	377.6538	753.3162	377.1617	G	**317.2183**	159.1128	300.1918	150.5995			3
9	**884.4108**	442.7091	867.3843	434.1958	866.4003	433.7038	L	**260.1969**	130.6021	243.1703	122.0888			2
10							K	**147.1128**	74.0600	130.0863	65.5468			1



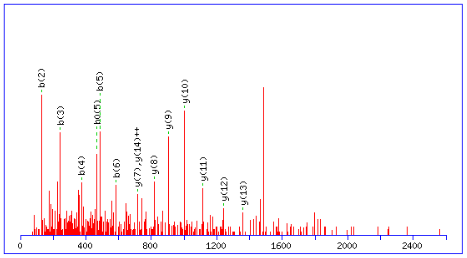
Monoisotopic mass of neutral peptide Mr(calc): 1114.6710
Ions Score: 73 Expect: 0.00089
Matches (Bold Red): 21/86 fragment ions using 49 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							11
2	**213.1598**	107.0835			V	**1002.5942**	501.8007	985.5677	493.2875	**984.5837**	492.7955	10
3	**300.1918**	150.5995	**282.1812**	141.5942	S	**903.5258**	452.2665	886.4993	443.7533	**885.5152**	443.2613	9
4	401.2395	201.1234	383.2289	192.1181	T	**816.4938**	408.7505	799.4672	400.2373	**798.4832**	399.7452	8
5	472.2766	236.6419	454.2660	227.6366	A	**715.4461**	358.2267	698.4196	349.7134	**697.4355**	349.2214	7
6	559.3086	280.1579	541.2980	**271.1527**	S	**644.4090**	322.7081	**627.3824**	314.1949	626.3984	313.7028	6
7	630.3457	315.6765	612.3352	306.6712	A	**557.3770**	279.1921	540.3504	270.6788			5
8	729.4141	365.2107	**711.4036**	356.2054	V	**486.3398**	243.6736	469.3133	235.1603			4
9	828.4825	414.7449	810.4720	405.7396	V	**387.2714**	194.1394	**370.2449**	185.6261			3
10	941.5666	471.2869	923.5560	462.2817	L	288.2030	144.6051	**271.1765**	136.0919			2
11					R	**175.1190**	88.0631	158.0924	79.5498			1



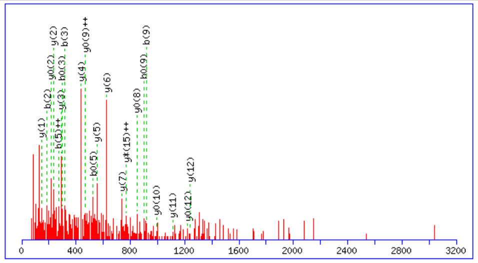
Monoisotopic mass of neutral peptide Mr(calc): 1381.6911
Variable modifications:
M11 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 62 Expect: 0.01
Matches (Bold Red): 49/196 fragment ions using 93 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							13
2	**249.1234**	125.0653			**231.1128**	116.0600	T	**1171.6317**	586.3195	**1154.6052**	577.8062	1153.6212	577.3142	12
3	306.1448	153.5761			**288.1343**	144.5708	G	**1070.5840**	535.7957	**1053.5575**	527.2824	1052.5735	526.7904	11
4	**420.1878**	210.5975	**403.1612**	202.0842	402.1772	201.5922	N	**1013.5626**	507.2849	**996.5360**	498.7717	995.5520	498.2796	10
5	**519.2562**	260.1317	**502.2296**	251.6185	501.2456	251.1264	V	**899.5197**	450.2635	**882.4931**	441.7502	881.5091	441.2582	9
6	**632.3402**	316.6738	**615.3137**	308.1605	614.3297	307.6685	L	**800.4512**	400.7293	783.4247	392.2160	**782.4407**	391.7240	8
7	761.3828	381.1951	**744.3563**	372.6818	743.3723	**372.1898**	E	**687.3672**	**344.1872**	670.3406	335.6740	**669.3566**	335.1819	7
8	874.4669	437.7371	**857.4403**	429.2238	856.4563	428.7318	I	**558.3246**	279.6659	541.2980	**271.1527**	540.3140	270.6606	6
9	**961.4989**	481.2531	944.4724	472.7398	943.4884	472.2478	S	**445.2405**	223.1239	428.2140	214.6106	427.2300	214.1186	5
10	1018.5204	509.7638	1001.4938	501.2506	1000.5098	500.7585	G	**358.2085**	179.6079	341.1819	171.0946			4
11	1101.5575	551.2824	1084.5310	542.7691	1083.5469	542.2771	M	**301.1870**	151.0972	284.1605	142.5839			3
12	1172.5946	586.8009	1155.5681	578.2877	**1154.5840**	577.7957	A	**218.1499**	109.5786	201.1234	101.0653			2
13							K	**147.1128**	74.0600	130.0863	65.5468			1



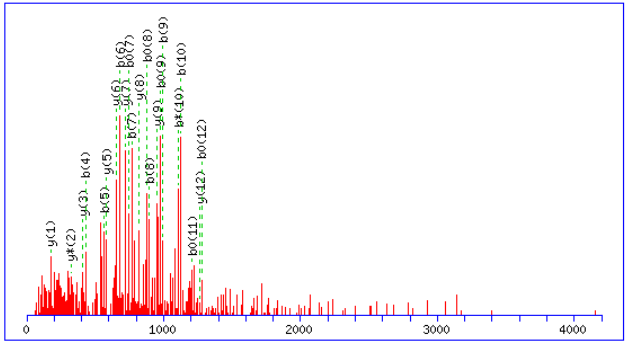
Monoisotopic mass of neutral peptide Mr(calc): 1485.8515
Ions Score: 59 Expect: 0.021
Matches (Bold Red): 14/148 fragment ions using 53 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							15
2	**129.0659**	65.0366					A	1429.8373	**715.4223**	1412.8108	706.9090	1411.8267	706.4170	14
3	**244.0928**	122.5500			226.0822	113.5448	D	**1358.8002**	679.9037	1341.7736	671.3905	1340.7896	670.8985	13
4	**372.1878**	186.5975	355.1612	178.0842	354.1772	177.5922	K	**1243.7732**	622.3903	1226.7467	613.8770	1225.7627	613.3850	12
5	**485.2718**	243.1396	468.2453	234.6263	**467.2613**	234.1343	I	**1115.6783**	558.3428	1098.6517	549.8295	1097.6677	549.3375	11
6	**584.3402**	292.6738	567.3137	284.1605	566.3297	283.6685	V	**1002.5942**	501.8007	985.5677	493.2875	984.5837	492.7955	10
7	671.3723	336.1898	654.3457	327.6765	653.3617	327.1845	S	**903.5258**	452.2665	886.4993	443.7533	885.5152	443.2613	9
8	772.4199	386.7136	755.3934	378.2003	754.4094	377.7083	T	**816.4938**	408.7505	799.4672	400.2373	798.4832	399.7452	8
9	843.4571	422.2322	826.4305	413.7189	825.4465	413.2269	A	**715.4461**	358.2267	698.4196	349.7134	697.4355	349.2214	7
10	930.4891	465.7482	913.4625	457.2349	912.4785	456.7429	S	644.4090	322.7081	627.3824	314.1949	626.3984	313.7028	6
11	1001.5262	501.2667	984.4997	492.7535	983.5156	492.2615	A	557.3770	279.1921	540.3504	270.6788			5
12	1100.5946	550.8009	1083.5681	542.2877	1082.5840	541.7957	V	486.3398	243.6736	469.3133	235.1603			4
13	1199.6630	600.3352	1182.6365	591.8219	1181.6525	591.3299	V	387.2714	194.1394	370.2449	185.6261			3
14	1312.7471	656.8772	1295.7205	648.3639	1294.7365	647.8719	L	288.2030	144.6051	271.1765	136.0919			2
15							R	175.1190	88.0631	158.0924	79.5498			1



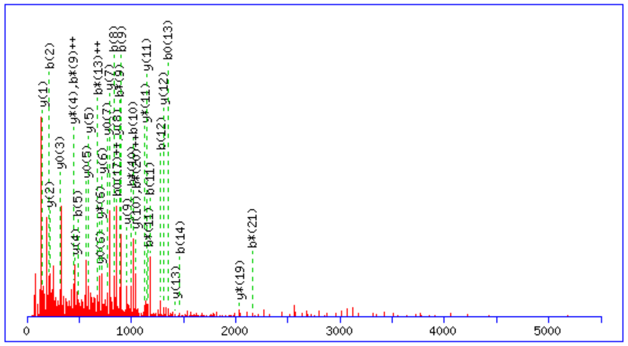
Monoisotopic mass of neutral peptide Mr(calc): 1652.8257
Ions Score: 25 Expect: 42
Matches (Bold Red): 22/172 fragment ions using 84 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							16
2	**187.1077**	94.0575			169.0972	85.0522	S	1554.7646	777.8859	1537.7380	**769.3727**	1536.7540	768.8807	15
3	**315.2027**	158.1050	298.1761	149.5917	**297.1921**	149.0997	K	1467.7326	734.3699	1450.7060	725.8566	1449.7220	725.3646	14
4	414.2711	207.6392	397.2445	199.1259	396.2605	198.6339	V	1339.6376	670.3224	1322.6111	661.8092	1321.6270	661.3172	13
5	543.3137	**272.1605**	526.2871	263.6472	**525.3031**	263.1552	E	**1240.5692**	620.7882	1223.5426	612.2750	**1222.5586**	611.7829	12
6	644.3614	322.6843	627.3348	314.1710	626.3508	313.6790	T	**1111.5266**	556.2669	1094.5000	547.7537	1093.5160	547.2617	11
7	701.3828	351.1951	684.3563	342.6818	683.3723	342.1898	G	1010.4789	505.7431	993.4524	497.2298	**992.4684**	496.7378	10
8	788.4149	394.7111	771.3883	386.1978	770.4043	385.7058	S	953.4575	477.2324	936.4309	468.7191	935.4469	**468.2271**	9
9	**917.4575**	459.2324	900.4309	450.7191	**899.4469**	450.2271	E	866.4254	433.7164	849.3989	425.2031	**848.4149**	424.7111	8
10	1030.5415	515.7744	1013.5150	507.2611	1012.5310	506.7691	I	**737.3828**	369.1951	720.3563	360.6818	719.3723	360.1898	7
11	1101.5786	551.2930	1084.5521	542.7797	1083.5681	542.2877	A	**624.2988**	312.6530	607.2722	304.1397	606.2882	303.6477	6
12	1216.6056	608.8064	1199.5790	600.2932	1198.5950	599.8011	D	**553.2617**	277.1345	536.2351	268.6212	535.2511	268.1292	5
13	1363.6740	682.3406	1346.6474	673.8274	1345.6634	673.3353	F	**438.2347**	219.6210	421.2082	211.1077	420.2241	210.6157	4
14	1420.6955	710.8514	1403.6689	702.3381	1402.6849	701.8461	G	**291.1663**	146.0868	274.1397	137.5735	273.1557	137.0815	3
15	1507.7275	754.3674	1490.7009	745.8541	1489.7169	745.3621	S	**234.1448**	117.5761	217.1183	109.0628	**216.1343**	108.5708	2
16							K	**147.1128**	74.0600	130.0863	65.5468			1



Monoisotopic mass of neutral peptide Mr(calc): 1945.9354
Ions Score: 37 Expect: 2.6
Matches (Bold Red): 22/190 fragment ions using 81 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							18
2	228.1455	114.5764	211.1190	106.0631			A	1790.8416	895.9244	1773.8151	887.4112	1772.8311	886.9192	17
3	342.1884	171.5979	325.1619	163.0846			N	1719.8045	860.4059	1702.7780	851.8926	1701.7939	851.4006	16
4	**429.2205**	215.1139	412.1939	206.6006	411.2099	206.1086	S	1605.7616	803.3844	1588.7350	794.8712	1587.7510	794.3791	15
5	**566.2794**	283.6433	549.2528	275.1300	548.2688	274.6380	H	1518.7295	759.8684	1501.7030	751.3551	1500.7190	750.8631	14
6	**680.3223**	340.6648	663.2957	332.1515	662.3117	331.6595	N	1381.6706	691.3390	1364.6441	682.8257	1363.6601	682.3337	13
7	**767.3543**	384.1808	750.3278	375.6675	**749.3438**	375.1755	S	**1267.6277**	634.3175	1250.6012	625.8042	1249.6171	625.3122	12
8	**895.4129**	448.2101	878.3864	439.6968	**877.4023**	439.2048	Q	1180.5957	590.8015	1163.5691	582.2882	1162.5851	581.7962	11
9	**996.4606**	498.7339	979.4340	490.2207	**978.4500**	489.7286	T	1052.5371	526.7722	1035.5106	518.2589	1034.5265	517.7669	10
10	**1125.5032**	563.2552	**1108.4766**	554.7419	1107.4926	554.2499	E	**951.4894**	476.2483	934.4629	467.7351	933.4789	467.2431	9
11	1224.5716	612.7894	1207.5450	604.2762	**1206.5610**	603.7841	V	**822.4468**	411.7271	805.4203	403.2138	804.4363	402.7218	8
12	1295.6087	648.3080	1278.5822	639.7947	**1277.5981**	639.3027	A	**723.3784**	362.1928	706.3519	353.6796	705.3679	353.1876	7
13	1366.6458	683.8265	1349.6193	675.3133	1348.6352	674.8213	A	**652.3413**	326.6743	635.3148	318.1610	634.3307	317.6690	6
14	1467.6935	734.3504	1450.6669	725.8371	1449.6829	725.3451	T	**581.3042**	291.1557	564.2776	282.6425	563.2936	282.1504	5
15	1538.7306	769.8689	1521.7041	761.3557	1520.7200	760.8637	A	480.2565	240.6319	463.2300	232.1186			4
16	1609.7677	805.3875	1592.7412	796.8742	1591.7572	796.3822	A	**409.2194**	205.1133	392.1928	196.6001			3
17	1772.8311	886.9192	1755.8045	878.4059	1754.8205	877.9139	Y	338.1823	169.5948	**321.1557**	161.0815			2
18							R	**175.1190**	88.0631	158.0924	79.5498			1



Monoisotopic mass of neutral peptide Mr(calc): 2323.1444
Ions Score: 45 Expect: 0.36
Matches (Bold Red): 37/226 fragment ions using 115 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							22
2	**213.1598**	107.0835					V	2211.0677	1106.0375	2194.0411	1097.5242	2193.0571	1097.0322	21
3	270.1812	135.5942					G	2111.9992	1056.5033	2094.9727	1047.9900	2093.9887	1047.4980	20
4	327.2027	164.1050					G	2054.9778	1027.9925	**2037.9512**	1019.4793	2036.9672	1018.9872	19
5	**490.2660**	245.6366					Y	1997.9563	999.4818	1980.9298	990.9685	1979.9457	990.4765	18
6	605.2930	303.1501			587.2824	294.1448	D	1834.8930	917.9501	1817.8664	909.4369	1816.8824	908.9448	17
7	719.3359	360.1716	702.3093	351.6583	701.3253	351.1663	N	1719.8660	860.4367	1702.8395	851.9234	1701.8555	851.4314	16
8	**833.3788**	417.1930	816.3523	408.6798	815.3682	408.1878	N	1605.8231	803.4152	1588.7966	794.9019	1587.8125	794.4099	15
9	**904.4159**	452.7116	**887.3894**	**444.1983**	886.4054	443.7063	A	1491.7802	746.3937	1474.7536	737.8805	1473.7696	737.3884	14
10	**1017.5000**	509.2536	**1000.4734**	500.7404	999.4894	500.2483	L	**1420.7431**	710.8752	1403.7165	702.3619	1402.7325	701.8699	13
11	**1180.5633**	590.7853	**1163.5368**	582.2720	1162.5527	581.7800	Y	**1307.6590**	654.3331	1290.6325	645.8199	1289.6484	645.3279	12
12	**1279.6317**	640.3195	1262.6052	631.8062	1261.6212	631.3142	V	**1144.5957**	572.8015	**1127.5691**	564.2882	1126.5851	563.7962	11
13	1366.6638	683.8355	1349.6372	**675.3222**	**1348.6532**	674.8302	S	**1045.5273**	523.2673	1028.5007	514.7540	1027.5167	514.2620	10
14	**1465.7322**	733.3697	1448.7056	724.8564	1447.7216	724.3644	V	**958.4952**	479.7513	941.4687	471.2380	940.4847	470.7460	9
15	1536.7693	768.8883	1519.7427	760.3750	1518.7587	759.8830	A	**859.4268**	430.2170	842.4003	421.7038	841.4163	421.2118	8
16	1607.8064	804.4068	1590.7799	795.8936	1589.7958	795.4016	A	**788.3897**	394.6985	771.3632	386.1852	**770.3791**	385.6932	7
17	1735.8650	868.4361	1718.8384	859.9229	1717.8544	**859.4308**	Q	**717.3526**	359.1799	**700.3260**	350.6667	**699.3420**	350.1747	6
18	1863.9236	932.4654	1846.8970	923.9521	1845.9130	923.4601	Q	**589.2940**	295.1506	572.2675	286.6374	**571.2835**	286.1454	5
19	1991.9821	996.4947	1974.9556	987.9814	1973.9716	987.4894	Q	**461.2354**	231.1214	**444.2089**	222.6081	443.2249	222.1161	4
20	2107.0091	1054.0082	2089.9825	**1045.4949**	2088.9985	1045.0029	D	333.1769	167.0921	316.1503	158.5788	**315.1663**	158.0868	3
21	2178.0462	1089.5267	**2161.0196**	1081.0135	2160.0356	1080.5215	A	**218.1499**	109.5786	201.1234	101.0653			2
22							K	**147.1128**	74.0600	130.0863	65.5468			1

Protein band 39 (+Mn): Iron-superoxide dismutase

Score: 72 M_r: 17395

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Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 22%

Matched peptides shown in Bold Red

      1 YHHGKHHQTY ITNLNNQIKG TEFENLPLEE IVKKSSGGVF NNAAQTWNHT
     51 FYWLGFTPKG QGKPAGELAA AIDAKWGSFE KFQEAFNACA AGTFGSGWAW
    101 LVKTPVGGLD LISTSNAATP LTTENTPLLT CDVWEHAYY
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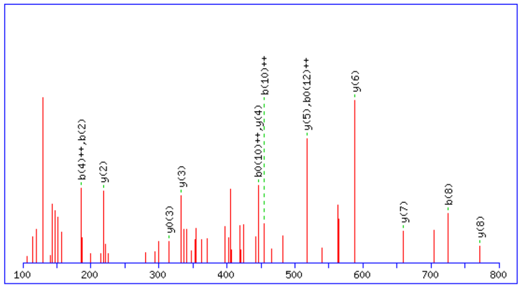

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Monoisotopic mass of neutral peptide Mr(calc): 1495.7994
Ions Score: 51  Expect: 0.12
Matches (Bold Red): 14/160 fragment ions using 16 most intense peaks
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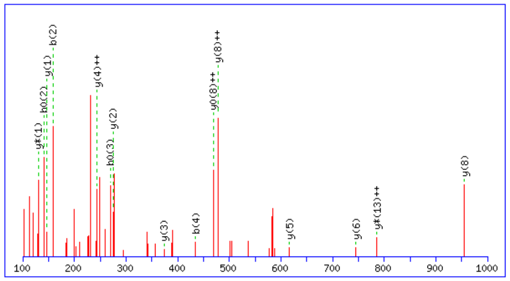
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							16
2	**186.0873**	93.5473	169.0608	85.0340			Q	1439.7853	720.3963	1422.7587	711.8830	1421.7747	711.3910	15
3	243.1088	122.0580	226.0822	113.5448			G	1311.7267	656.3670	1294.7001	647.8537	1293.7161	647.3617	14
4	371.2037	**186.1055**	354.1772	177.5922			K	1254.7052	627.8563	1237.6787	619.3430	1236.6947	618.8510	13
5	468.2565	234.6319	451.2300	226.1186			P	1126.6103	563.8088	1109.5837	555.2955	1108.5997	554.8035	12
6	539.2936	270.1504	522.2671	261.6372			A	1029.5575	515.2824	1012.5310	506.7691	1011.5469	506.2771	11
7	596.3151	298.6612	579.2885	290.1479			G	958.5204	479.7638	941.4938	471.2506	940.5098	470.7585	10
8	**725.3577**	363.1825	708.3311	354.6692	707.3471	354.1772	E	901.4989	451.2531	884.4724	442.7398	883.4884	442.2478	9
9	838.4417	419.7245	821.4152	411.2112	820.4312	410.7192	L	**772.4563**	386.7318	755.4298	378.2185	754.4458	377.7265	8
10	909.4789	**455.2431**	892.4523	446.7298	891.4683	**446.2378**	A	**659.3723**	330.1898	642.3457	321.6765	641.3617	321.1845	7
11	980.5160	490.7616	963.4894	482.2483	962.5054	481.7563	A	**588.3352**	294.6712	571.3086	286.1579	570.3246	285.6659	6
12	1051.5531	526.2802	1034.5265	517.7669	1033.5425	**517.2749**	A	**517.2980**	259.1527	500.2715	250.6394	499.2875	250.1474	5
13	1164.6372	582.8222	1147.6106	574.3089	1146.6266	573.8169	I	**446.2609**	223.6341	429.2344	215.1208	428.2504	214.6288	4
14	1279.6641	640.3357	1262.6375	631.8224	1261.6535	631.3304	D	**333.1769**	167.0921	316.1503	158.5788	**315.1663**	158.0868	3
15	1350.7012	675.8542	1333.6747	667.3410	1332.6906	666.8490	A	**218.1499**	109.5786	201.1234	101.0653			2
16							K	147.1128	74.0600	130.0863	65.5468			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1744.9247
Ions Score: 22  Expect: 90
Matches (Bold Red): 15/148 fragment ions using 36 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							15
2	**159.0764**	80.0418			**141.0659**	71.0366	T	1688.9105	844.9589	1671.8840	836.4456	1670.9000	835.9536	14
3	288.1190	144.5631			**270.1084**	135.5579	E	1587.8629	794.4351	1570.8363	**785.9218**	1569.8523	785.4298	13
4	**435.1874**	218.0974			417.1769	209.0921	F	1458.8203	729.9138	1441.7937	721.4005	1440.8097	720.9085	12
5	564.2300	282.6186			546.2195	273.6134	E	1311.7518	656.3796	1294.7253	647.8663	1293.7413	647.3743	11
6	678.2729	339.6401	661.2464	331.1268	660.2624	330.6348	N	1182.7093	591.8583	1165.6827	583.3450	1164.6987	582.8530	10
7	791.3570	396.1821	774.3305	387.6689	773.3464	387.1769	L	1068.6663	534.8368	1051.6398	526.3235	1050.6558	525.8315	9
8	888.4098	444.7085	871.3832	436.1953	870.3992	435.7032	P	**955.5823**	**478.2948**	938.5557	469.7815	937.5717	**469.2895**	8
9	1001.4938	501.2506	984.4673	492.7373	983.4833	492.2453	L	858.5295	429.7684	841.5029	421.2551	840.5189	420.7631	7
10	1130.5364	565.7719	1113.5099	557.2586	1112.5259	556.7666	E	**745.4454**	373.2264	728.4189	364.7131	727.4349	364.2211	6
11	1259.5790	630.2932	1242.5525	621.7799	1241.5685	621.2879	E	**616.4028**	308.7051	599.3763	300.1918	598.3923	299.6998	5
12	1372.6631	686.8352	1355.6365	678.3219	1354.6525	677.8299	I	487.3602	**244.1838**	470.3337	235.6705			4
13	1471.7315	736.3694	1454.7050	727.8561	1453.7209	727.3641	V	**374.2762**	187.6417	357.2496	179.1285			3
14	1599.8265	800.4169	1582.7999	791.9036	1581.8159	791.4116	K	**275.2078**	138.1075	258.1812	129.5942			2
15							K	**147.1128**	74.0600	**130.0863**	65.5468			1

Protein band 42 (-Mn): Pilin

Score: 62 M_r: 18087

Variable modifications: Carbamidomethyl (C),Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 8%

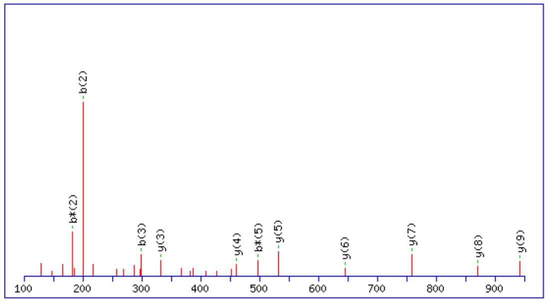
Matched peptides shown in **Bold Red**

1 MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTAR**AQV** **SEAILLAEGQ**

51 **K**SAVTEYYLN HGIWPENNGA AGVASPASDI KGKYVQSVTV ANGVVTAQMK

101 SDGVNKEIKN KKLSLWARRE AGSVKWFCGQ PVTRDKAVTD DAVKDVTGND

151 KIETKHLPST CRDNFDAS



Monoisotopic mass of neutral peptide Mr(calc): 1455.7933
Ions Score: 63 Expect: 0.0073
Matches (**Bold Red**): 11/142 fragment ions using 14 most intense peaks

#	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	1385.7635	693.3854	1368.7369	684.8721	1367.7529	684.3801	13
3	**299.1714**	150.0893	282.1448	141.5761			V	1257.7049	629.3561	1240.6783	620.8428	1239.6943	620.3508	12
4	386.2034	193.6053	369.1769	185.0921	368.1928	184.6001	S	1158.6365	579.8219	1141.6099	571.3086	1140.6259	570.8166	11
5	515.2460	258.1266	**498.2195**	249.6134	497.2354	249.1214	E	1071.6045	536.3059	1054.5779	527.7926	1053.5939	527.3006	10
6	586.2831	293.6452	569.2566	285.1319	568.2726	284.6399	A	**942.5619**	471.7846	925.5353	463.2713	924.5513	462.7793	9
7	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	I	**871.5247**	436.2660	854.4982	427.7527	853.5142	427.2607	8
8	812.4512	406.7293	795.4247	398.2160	794.4407	397.7240	L	**758.4407**	379.7240	741.4141	371.2107	740.4301	370.7187	7
9	925.5353	463.2713	908.5088	454.7580	907.5247	454.2660	L	**645.3566**	323.1819	628.3301	314.6687	627.3461	314.1767	6
10	996.5724	498.7898	979.5459	490.2766	978.5619	489.7846	A	**532.2726**	266.6399	515.2460	258.1266	514.2620	257.6346	5
11	1125.6150	563.3111	1108.5885	554.7979	1107.6045	554.3059	E	**461.2354**	231.1214	444.2089	222.6081	443.2249	222.1161	4
12	1182.6365	591.8219	1165.6099	583.3086	1164.6259	582.8166	G	**332.1928**	166.6001	315.1663	158.0868			3
13	1310.6951	655.8512	1293.6685	647.3379	1292.6845	646.8459	Q	275.1714	138.0893	258.1448	129.5761			2
14							K	147.1128	74.0600	130.0863	65.5468			1

Protein band 61 (+Mn): pilO protein

Score: 73 M_r: 23301

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%

Matched peptides shown in Bold Red

  1 MASKSSKTNL DLNNLHLLNL PARLFIALLA VAAVLGLGYA GLFKSQMESL
 51 EEYEAKETEL KNTYKQKSID AASLNNLRDE LASIRSAFDI MLKQLPTDAE
101 IPNLVQELHQ AGSSNGLRLD SVMPQPPVDD GPIKRLPYSI SITGNYEQIS
151 QFTRDVGSLS RIITLESLKI AQSPENGGNP DGKSSILNLS AIATTYQAKS
201 VEELAAEAAQ NAEQK
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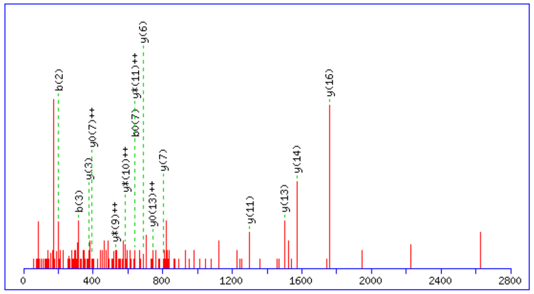
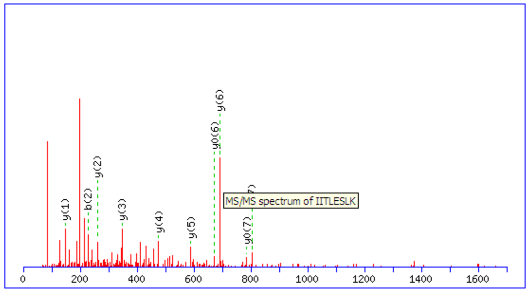


```
Monoisotopic mass of neutral peptide Mr(calc): 1957.0228
Ions Score: 6   Expect: 2.9e+03
Matches (Bold Red): 15/186 fragment ions using 84 most intense peaks
```

#	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							18
2	**201.1234**	101.0653			183.1128	92.0600	I	1870.9981	936.0027	1853.9716	927.4894	1852.9875	926.9974	17
3	**316.1503**	158.5788			298.1397	149.5735	D	**1757.9141**	879.4607	1740.8875	870.9474	1739.9035	870.4554	16
4	387.1874	194.0974			369.1769	185.0921	A	1642.8871	821.9472	1625.8606	813.4339	1624.8765	812.9419	15
5	458.2245	229.6159			440.2140	220.6106	A	**1571.8500**	786.4286	1554.8234	777.9154	1553.8394	777.4234	14
6	545.2566	273.1319			527.2460	264.1266	S	**1500.8129**	750.9101	1483.7863	742.3968	1482.8023	**741.9048**	13
7	658.3406	329.6740			**640.3301**	320.6687	L	1413.7809	707.3941	1396.7543	698.8808	1395.7703	698.3888	12
8	772.3836	386.6954	755.3570	378.1821	754.3730	377.6901	N	**1300.6968**	650.8520	1283.6702	**642.3388**	1282.6862	641.8467	11
9	886.4265	443.7169	869.3999	435.2036	868.4159	434.7116	N	1186.6539	593.8306	1169.6273	**585.3173**	1168.6433	584.8253	10
10	999.5105	500.2589	982.4840	491.7456	981.5000	491.2536	L	1072.6109	536.8091	1055.5844	**528.2958**	1054.6004	527.8038	9
11	1155.6117	578.3095	1138.5851	569.7962	1137.6011	569.3042	R	959.5269	480.2671	942.5003	471.7538	941.5163	471.2618	8
12	1270.6386	635.8229	1253.6121	627.3097	1252.6280	626.8177	D	**803.4258**	402.2165	786.3992	393.7032	785.4152	**393.2112**	7
13	1399.6812	700.3442	1382.6546	691.8310	1381.6706	691.3390	E	**688.3988**	344.7030	671.3723	336.1898	670.3882	335.6978	6
14	1512.7653	756.8863	1495.7387	748.3730	1494.7547	747.8810	L	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	5
15	1583.8024	792.4048	1566.7758	783.8916	1565.7918	783.3995	A	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
16	1670.8344	835.9208	1653.8079	827.4076	1652.8238	826.9156	S	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	3
17	1783.9185	892.4629	1766.8919	883.9496	1765.9079	883.4576	I	288.2030	144.6051	271.1765	136.0919			2
18							R	175.1190	88.0631	158.0924	79.5498			1



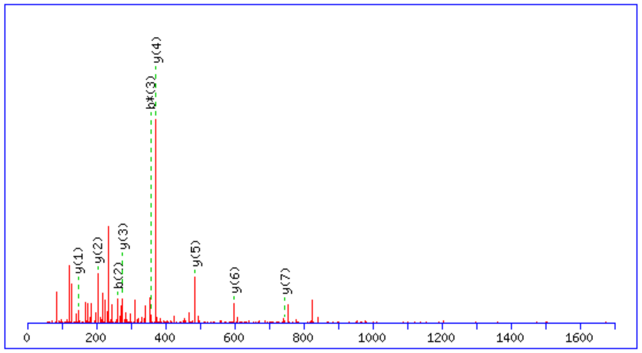
```
Monoisotopic mass of neutral peptide Mr(calc): 915.5641
Ions Score: 36   Expect: 5.2
Matches (Bold Red): 10/62 fragment ions using 23 most intense peaks
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							8
2	**227.1754**	114.0913			I	**803.4873**	402.2473	786.4607	393.7340	**785.4767**	393.2420	7
3	328.2231	164.6152	310.2125	155.6099	T	**690.4032**	345.7053	673.3767	337.1920	**672.3927**	336.7000	6
4	441.3071	221.1572	423.2966	212.1519	L	**589.3556**	295.1814	572.3290	286.6681	571.3450	286.1761	5
5	570.3497	285.6785	552.3392	276.6732	E	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	4
6	657.3818	329.1945	639.3712	320.1892	S	**347.2289**	174.1181	330.2023	165.6048	329.2183	165.1128	3
7	770.4658	385.7366	752.4553	376.7313	L	**260.1969**	130.6021	243.1703	122.0888			2
8					K	**147.1128**	74.0600	130.0863	65.5468			1

Protein band 73 (+Mn): 50S ribosomal protein L9

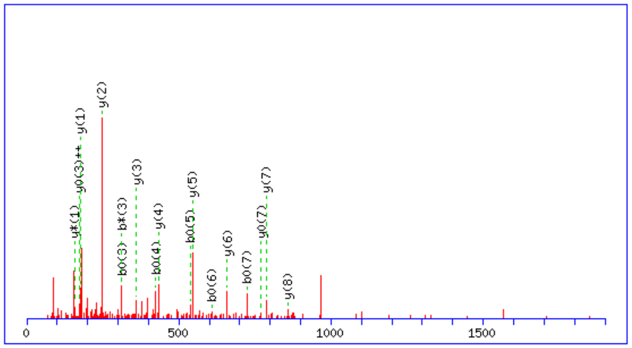
Score: 237 M_r: 15687

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 28%

Matched peptides shown in Bold Red

     1 MQIILLEKIG GLGNLGDIVT VKNGYARNFL IPAGKAKRAT EANMKEFEAR
    51 RAELEAKQAE ILADARARQE KLDGQTVTVA QKAGVDGRHN GSVTNADIAA
   101 AIVAAGIEAV KANVRLPNGP LKAVGEYEVE VALHTDAVAK ITVAVIAAAE
   151
```



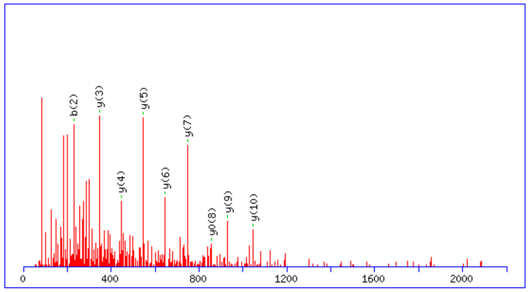
```
Monoisotopic mass of neutral peptide Mr(calc): 858.4963
Ions Score: 32  Expect: 14
Matches (Bold Red): 9/56 fragment ions using 36 most intense peaks
```

#	b	b^{++}	b^*	b^{*++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	115.0502	58.0287	98.0237	49.5155	N					8
2	**262.1186**	131.5629	245.0921	123.0497	F	**745.4607**	373.2340	728.4341	364.7207	7
3	375.2027	188.1050	**358.1761**	179.5917	L	**598.3923**	299.6998	581.3657	291.1865	6
4	488.2867	244.6470	471.2602	236.1337	I	**485.3082**	243.1577	468.2817	234.6445	5
5	585.3395	293.1734	568.3130	284.6601	P	**372.2241**	186.6157	355.1976	178.1024	4
6	656.3766	328.6919	639.3501	320.1787	A	**275.1714**	138.0893	258.1448	129.5761	3
7	713.3981	357.2027	696.3715	348.6894	G	**204.1343**	102.5708	187.1077	94.0575	2
8					K	**147.1128**	74.0600	130.0863	65.5468	1



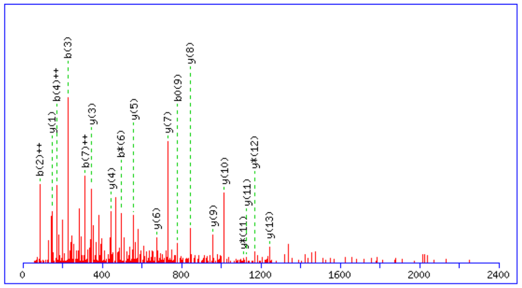
```
Monoisotopic mass of neutral peptide Mr(calc): 985.5192
Ions Score: 53  Expect: 0.11
Matches (Bold Red): 17/88 fragment ions using 29 most intense peaks
```

#	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							9
2	200.1030	100.5551	183.0764	92.0418			A	**858.4680**	429.7376	841.4414	421.2243	840.4574	420.7323	8
3	329.1456	165.0764	**312.1190**	156.5631	**311.1350**	156.0711	E	**787.4308**	394.2191	770.4043	385.7058	**769.4203**	385.2138	7
4	442.2296	221.6185	425.2031	213.1052	**424.2191**	212.6132	I	**658.3883**	329.6978	641.3617	321.1845	640.3777	320.6925	6
5	555.3137	278.1605	538.2871	269.6472	**537.3031**	269.1552	L	**545.3042**	273.1557	528.2776	264.6425	527.2936	264.1504	5
6	626.3508	313.6790	609.3243	305.1658	**608.3402**	304.6738	A	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	4
7	741.3777	371.1925	724.3512	362.6792	**723.3672**	362.1872	D	**361.1830**	181.0951	344.1565	172.5819	343.1724	**172.0899**	3
8	812.4149	406.7111	795.3883	398.1978	794.4043	397.7058	A	**246.1561**	123.5817	229.1295	115.0684			2
9							R	**175.1190**	88.0631	**158.0924**	79.5498			1



Monoisotopic mass of neutral peptide Mr(calc): 1158.6245
Ions Score: 51 Expect: 0.14
Matches (Bold Red): 9/104 fragment ions using 17 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	**229.1183**	115.0628			211.1077	106.0575	D	**1046.5477**	523.7775	1029.5211	515.2642	1028.5371	514.7722	10
3	286.1397	143.5735			268.1292	134.5682	G	**931.5207**	466.2640	914.4942	457.7507	913.5102	457.2587	9
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	Q	874.4993	437.7533	857.4727	429.2400	**856.4887**	428.7480	8
5	515.2460	258.1266	498.2195	249.6134	497.2354	249.1214	T	**746.4407**	373.7240	729.4141	365.2107	728.4301	364.7187	7
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	V	**645.3930**	323.2001	628.3665	314.6869	627.3824	314.1949	6
7	715.3621	358.1847	698.3355	349.6714	697.3515	349.1794	T	**546.3246**	273.6659	529.2980	265.1527	528.3140	264.6607	5
8	814.4305	407.7189	797.4040	399.2056	796.4199	398.7136	V	**445.2769**	223.1421	428.2504	214.6288			4
9	885.4676	443.2375	868.4411	434.7242	867.4571	434.2322	A	**346.2085**	173.6079	329.1819	165.0946			3
10	1013.5262	507.2667	996.4997	498.7535	995.5156	498.2615	Q	275.1714	138.0893	258.1448	129.5761			2
11							K	147.1128	74.0600	130.0863	65.5468			1



Monoisotopic mass of neutral peptide Mr(calc): 1354.7820
Ions Score: 101 Expect: 1.2e-06
Matches (Bold Red): 20/126 fragment ions using 28 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							14
2	**171.1128**	**86.0600**					G	**1242.7052**	621.8563	1225.6787	613.3430	1224.6947	612.8510	13
3	**228.1343**	114.5708					G	1185.6838	593.3455	**1168.6572**	584.8322	1167.6732	584.3402	12
4	341.2183	**171.1128**					L	**1128.6623**	564.8348	**1111.6358**	556.3215	1110.6517	555.8295	11
5	398.2398	199.6235					G	**1015.5782**	508.2928	998.5517	499.7795	997.5677	499.2875	10
6	512.2827	256.6450	**495.2562**	248.1317			N	**958.5568**	479.7820	941.5302	471.2688	940.5462	470.7767	9
7	625.3668	**313.1870**	608.3402	304.6738			L	**844.5138**	422.7606	827.4873	414.2473	826.5033	413.7553	8
8	682.3883	341.6978	665.3617	333.1845			G	**731.4298**	366.2185	714.4032	357.7053	713.4192	357.2132	7
9	797.4152	399.2112	780.3886	390.6980	**779.4046**	390.2060	D	**674.4083**	337.7078	657.3818	329.1945	656.3978	328.7025	6
10	910.4993	455.7533	893.4727	447.2400	892.4887	446.7480	I	**559.3814**	280.1943	542.3548	271.6811	541.3708	271.1890	5
11	1009.5677	505.2875	992.5411	496.7742	991.5571	496.2822	V	**446.2973**	223.6523	429.2708	215.1390	428.2867	214.6470	4
12	1110.6154	555.8113	1093.5888	547.2980	1092.6048	546.8060	T	**347.2289**	174.1181	330.2023	165.6048	329.2183	165.1128	3
13	1209.6838	605.3455	1192.6572	596.8322	1191.6732	596.3402	V	246.1812	123.5942	229.1547	115.0810			2
14							K	**147.1128**	74.0600	130.0863	65.5468			1

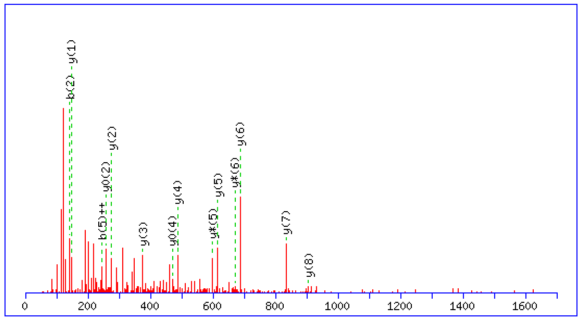
Protein band 73 (+Mn): 50S ribosomal protein L20

Score: 112 M_r: 13664

Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%

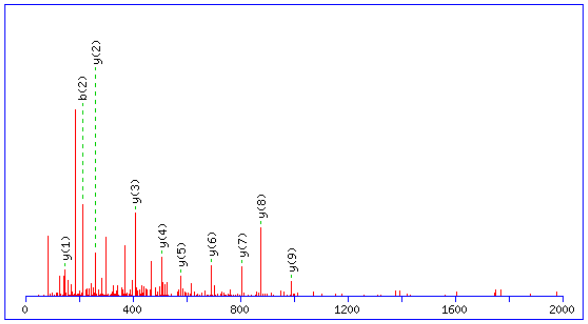
Matched peptides shown in **Bold Red**

1 MPRVKRGVTA RARHQKIFAL AKGYRGRRKN VYRVAKQAVM KAGQYAYRDR
51 RQRKRQFRQL WIVRINAGTR ENGLSYSKFM NGLKRASIEI DRK**VLADLAV**
101 **FDKAAFAQLV EK**AKAALAA



Monoisotopic mass of neutral peptide Mr(calc): 975.5389
Ions Score: 44 Expect: 0.77
Matches (**Bold Red**): 14/72 fragment ions using 51 most intense peaks

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							9
2	**143.0815**	72.0444					A	**905.5091**	453.2582	888.4825	444.7449	887.4985	444.2529	8
3	290.1499	145.5786					F	**834.4720**	417.7396	817.4454	409.2264	816.4614	408.7343	7
4	361.1870	181.0972					A	**687.4036**	344.2054	**670.3770**	335.6921	669.3930	335.2001	6
5	489.2456	**245.1264**	472.2191	236.6132			Q	**616.3665**	308.6869	**599.3399**	300.1736	598.3559	299.6816	5
6	602.3297	301.6685	585.3031	293.1552			L	**488.3079**	244.6576	471.2813	236.1443	**470.2973**	235.6523	4
7	701.3981	351.2027	684.3715	342.6894			V	**375.2238**	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	830.4407	415.7240	813.4141	407.2107	812.4301	406.7187	E	**276.1554**	138.5813	259.1288	130.0681	**258.1448**	129.5761	2
9							K	**147.1128**	74.0600	130.0863	65.5468			1



Monoisotopic mass of neutral peptide Mr(calc): 1089.6070
Ions Score: 68 Expect: 0.003
Matches (**Bold Red**): 10/82 fragment ions using 25 most intense peaks

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415			V							10
2	**213.1598**	107.0835			L	**991.5459**	496.2766	974.5193	487.7633	973.5353	487.2713	9
3	284.1969	142.6021			A	**878.4618**	439.7345	861.4353	431.2213	860.4512	430.7293	8
4	399.2238	200.1155	381.2132	191.1103	D	**807.4247**	404.2160	790.3981	395.7027	789.4141	395.2107	7
5	512.3079	256.6576	494.2973	247.6523	L	**692.3978**	346.7025	675.3712	338.1892	674.3872	337.6972	6
6	583.3450	292.1761	565.3344	283.1709	A	**579.3137**	290.1605	562.2871	281.6472	561.3031	281.1552	5
7	682.4134	341.7103	664.4028	332.7051	V	**508.2766**	254.6419	491.2500	246.1287	490.2660	245.6366	4
8	829.4818	415.2445	811.4713	406.2393	F	**409.2082**	205.1077	392.1816	196.5944	391.1976	196.1024	3
9	944.5088	472.7580	926.4982	463.7527	D	**262.1397**	131.5735	245.1132	123.0602	244.1292	122.5682	2
10					K	**147.1128**	74.0600	130.0863	65.5468			1

Protein band 73 (+Mn): 30S ribosomal protein S9

Score: 63 M_r: 14363

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 12%

Matched peptides shown in Bold Red

     1 MNGKYYYGTG RRKSSVARVF LIKGTGQIIV NGRPVDEFFA RETSRMVVRQ
    51 PLVLTENAES FDIKVNVVGG GETGQSGAIR HGITRALIDF DAALKPALSQ
   101 AGFVTRDARE VERKKPGLRK ARRAKQFSKR
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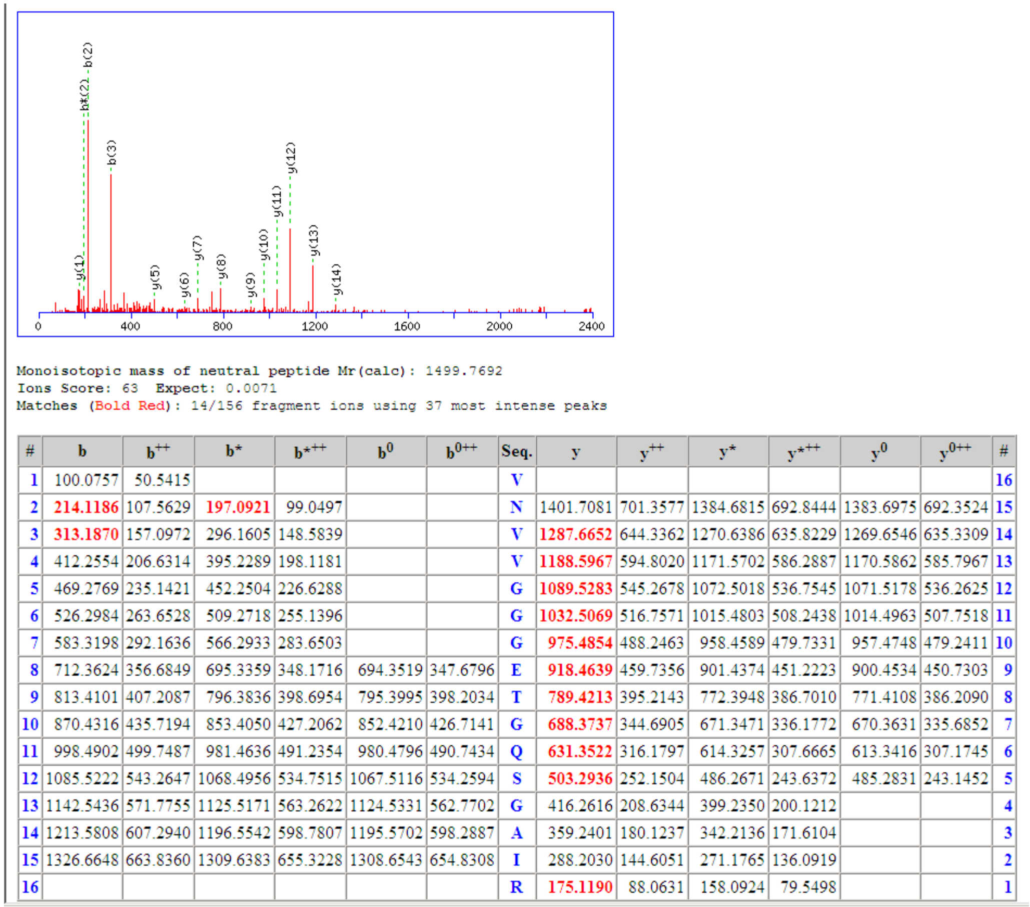

```
Monoisotopic mass of neutral peptide Mr(calc): 1499.7692
Ions Score: 63  Expect: 0.0071
Matches (Bold Red): 14/156 fragment ions using 37 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							16
2	**214.1186**	107.5629	**197.0921**	99.0497			N	1401.7081	701.3577	1384.6815	692.8444	1383.6975	692.3524	15
3	**313.1870**	157.0972	296.1605	148.5839			V	**1287.6652**	644.3362	1270.6386	635.8229	1269.6546	635.3309	14
4	412.2554	206.6314	395.2289	198.1181			V	**1188.5967**	594.8020	1171.5702	586.2887	1170.5862	585.7967	13
5	469.2769	235.1421	452.2504	226.6288			G	**1089.5283**	545.2678	1072.5018	536.7545	1071.5178	536.2625	12
6	526.2984	263.6528	509.2718	255.1396			G	**1032.5069**	516.7571	1015.4803	508.2438	1014.4963	507.7518	11
7	583.3198	292.1636	566.2933	283.6503			G	**975.4854**	488.2463	958.4589	479.7331	957.4748	479.2411	10
8	712.3624	356.6849	695.3359	348.1716	694.3519	347.6796	E	**918.4639**	459.7356	901.4374	451.2223	900.4534	450.7303	9
9	813.4101	407.2087	796.3836	398.6954	795.3995	398.2034	T	**789.4213**	395.2143	772.3948	386.7010	771.4108	386.2090	8
10	870.4316	435.7194	853.4050	427.2062	852.4210	426.7141	G	**688.3737**	344.6905	671.3471	336.1772	670.3631	335.6852	7
11	998.4902	499.7487	981.4636	491.2354	980.4796	490.7434	Q	**631.3522**	316.1797	614.3257	307.6665	613.3416	307.1745	6
12	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	S	**503.2936**	252.1504	486.2671	243.6372	485.2831	243.1452	5
13	1142.5436	571.7755	1125.5171	563.2622	1124.5331	562.7702	G	416.2616	208.6344	399.2350	200.1212			4
14	1213.5808	607.2940	1196.5542	598.7807	1195.5702	598.2887	A	359.2401	180.1237	342.2136	171.6104			3
15	1326.6648	663.8360	1309.6383	655.3228	1308.6543	654.8308	I	288.2030	144.6051	271.1765	136.0919			2
16							R	**175.1190**	88.0631	158.0924	79.5498			1

Protein band 78 (-Mn): Transferrin-binding protein A

Score: 140 M$_r$: 101940

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

Matched peptides shown in Bold Red

  1 MQQQHLFRFN ILCLSLMTAL PAYAENVQAG QAQEKQLDTI QVKAKKQKTR
 51 RDNEVTGLGK LVKTADTLSK EQVLDIRDLT RYDPGIAVVE QGRGASSGYS
101 IRGMDKNRVA LTVDGLAQIQ SYTAQAALGG TRTAGSSGAI NEIEYENVKA
151 VEISKGSNSV EQGSGALAGS VAFQTKTADD VIGEGRQWGI QSKTAYSGKN
201 RGLTQSIALA GRIGGAEALL IRTGRHAGEI RAHEAAGRGV QSFNRLAPVD
251 DASTWAYFIV EEECKNRDYE TCKAKPKKDV DGKDERQTVS TRDYTGPNRF
301 LADPLSYESR SWLFRPGFRF ENKRHYIGGI LERTQQTFDT RDMTVPAFLT
351 KAVFDENKKY GSIRGYGKYA GDHRYGGLIT NSENGAQVGA EYGTGVFYDE
401 THTKSRYGLE YVYTNADKDT WADYARLSYD RQGIGLDNHF QQTHCSADGS
451 DKYCRPSADK PSSYYKSDRV IYGESHRLLQ AAFKKSFDTA KIRHNLSVNL
501 GYDRFGSDLR HQDYYYQHAN RAYSLKTPPQ NGDKKTIPPN GGKDKPYWVS
551 IGGGNVVTGQ ICFFGNNTYT DCTPRSINGK SYYAAVRDNV RLGRWADVGA
601 GLRYDYRSTH SDDGSVSTGT HRTLSWNTGI VLKPADWLDL TYRTSTGFRL
651 PSFAEMYGWR SGDKIKAVKI DPEKSFNKEA GIVFKGDFGN LEASWFNNAY
701 RDLIVRGYEV EITDGKEQAK GDPAYLNAQS ARITGINILG KIDWNGVWDK
751 LPEGWYSTFA YNRVRVRDIK KRADRTDIQS HLFDAIQPSR YVVGSGYDQP
801 EGKWGVNGML TYSKAKEITE LLGSRALLNG NSRNTKATAR RTRPWYIVDV
851 SGYYTVKKHF TLRAGVYNLL NHRYVTWENV RQTAAGAVNQ HKNVGVYNRY
901 AAPGRNYTFS LEMKF
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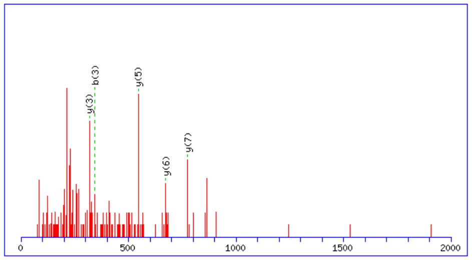
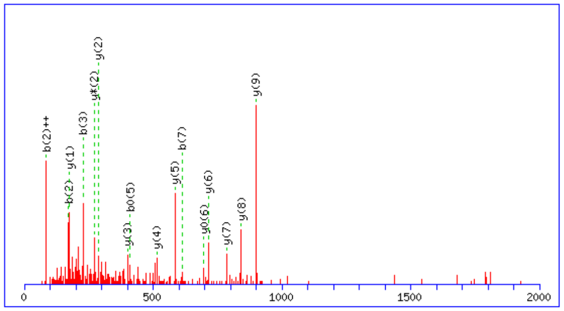


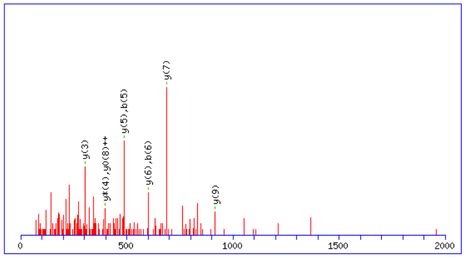
```
Monoisotopic mass of neutral peptide Mr(calc): 1016.5502
Ions Score: 18  Expect: 3.5e+02
Matches (Bold Red): 5/78 fragment ions using 10 most intense peaks
```

#	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							9
2	243.1339	122.0706	225.1234	113.0653	I	888.5149	444.7611	871.4884	436.2478	870.5043	435.7558	8
3	**344.1816**	172.5944	326.1710	163.5892	T	**775.4308**	388.2191	758.4043	379.7058	757.4203	379.2138	7
4	473.2242	237.1157	455.2136	228.1105	E	**674.3832**	337.6952	657.3566	329.1819	656.3726	328.6899	6
5	586.3083	293.6578	568.2977	284.6525	L	**545.3406**	273.1739	528.3140	264.6606	527.3300	264.1686	5
6	699.3923	350.1998	681.3818	341.1945	L	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
7	756.4138	378.7105	738.4032	369.7053	G	**319.1724**	160.0899	302.1459	151.5766	301.1619	151.0846	3
8	843.4458	422.2266	825.4353	413.2213	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9					R	175.1190	88.0631	158.0924	79.5498			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1011.6077
Ions Score: 88  Expect: 2.8e-05
Matches (Bold Red): 16/72 fragment ions using 27 most intense peaks
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			I							10
2	**171.1128**	**86.0600**			G	**899.5309**	450.2691	882.5043	441.7558	881.5203	441.2638	9
3	**228.1343**	114.5708			G	**842.5094**	421.7584	825.4829	413.2451	824.4989	412.7531	8
4	299.1714	150.0893			A	**785.4880**	393.2476	768.4614	384.7343	767.4774	384.2423	7
5	428.2140	214.6106	**410.2034**	205.6053	E	**714.4509**	357.7291	697.4243	349.2158	**696.4403**	348.7238	6
6	499.2511	250.1292	481.2405	241.1239	A	**585.4083**	293.2078	568.3817	284.6945			5
7	**612.3352**	306.6712	594.3246	297.6659	L	**514.3711**	257.6892	497.3446	249.1759			4
8	725.4192	363.2132	707.4087	354.2080	L	**401.2871**	201.1472	384.2605	192.6339			3
9	838.5033	419.7553	820.4927	410.7500	I	**288.2030**	144.6051	**271.1765**	136.0919			2
10					R	**175.1190**	88.0631	158.0924	79.5498			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1085.6193
Ions Score: 35  Expect: 5.9
Matches (Bold Red): 9/98 fragment ions using 13 most intense peaks
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							11
2	171.1128	86.0600					L	1029.6051	515.3062	1012.5786	506.7929	1011.5946	506.3009	10
3	272.1605	136.5839			254.1499	127.5786	T	**916.5211**	458.7642	899.4945	450.2509	898.5105	449.7589	9
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	Q	815.4734	408.2403	798.4468	399.7271	797.4628	**399.2350**	8
5	**487.2511**	244.1292	470.2245	235.6159	469.2405	235.1239	S	**687.4148**	344.2110	670.3883	335.6978	669.4042	335.2058	7
6	**600.3352**	300.6712	583.3086	292.1579	582.3246	291.6659	I	**600.3828**	300.6950	583.3562	292.1817			6
7	671.3723	336.1898	654.3457	327.6765	653.3617	327.1845	A	**487.2987**	244.1530	470.2722	235.6397			5
8	784.4563	392.7318	767.4298	384.2185	766.4458	383.7265	L	416.2616	208.6344	**399.2350**	200.1212			4
9	855.4934	428.2504	838.4669	419.7371	837.4829	419.2451	A	**303.1775**	152.0924	286.1510	143.5791			3
10	912.5149	456.7611	895.4884	448.2478	894.5043	447.7558	G	232.1404	116.5738	215.1139	108.0606			2
11							R	175.1190	88.0631	158.0924	79.5498			1

Protein band 82 (-Mn): PilQ

Score: 467 M_r: 77943

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 19%

Matched peptides shown in Bold Red

    1 MNTKLTKIIS GLFVATAAFQ TASAGNITDI KVSSLPNKQK IVKVSFDKEI
   51 VNPTGFVTSS PARIALDFEQ TGISMDQQVL EYADPLLSKI SAAQNSSRAR
  101 LVLNLNKPGQ YNTEVRGNKV WIFINESDDT VSAPARPAVK AAPAAPAKQQ
  151 AAAPFTESVV SVSAPFSPAK QQAAASAKQT NIDFRKDGKN AGIIELAALG
  201 FAGQPDISQQ HDHIIVTLKN HTLPTALQRS LDVADFKTPV QKVTLKRLNN
  251 DTQLIITTTG NWELVNKSAA PGYFTFQVLP KKQNLESGGV NNAPKTFTGR
  301 KISLDFQDVE IRTILQILAK ESGMNIVASD SVSGKMTLSL KDVPWDQALD
  351 LVMQARNLDM RQQGNIVNIA PRDELLAKDK AFLQAEKDIA DLGALYSQNF
  401 QLKYKNVEEF RSILRLDNAD TTGNRNTLVS GRGSVLIDPA TNTLIVTDTR
  451 SVIEKFRKLI DELDVPAQQV MIEARIVEAA DGFSRDLGVK FGATGRKKLK
  501 NETSAFGWGV NSGFGGGDKW EAQTKINLPV AAAANSISLV RAISSGALNL
  551 ELSASESLSK TKTLANPRVL TQNRKEAKIE SGYEIPFTVT TASGGGNSTN
  601 TELKKAVLGL TVTPNITPDG QIIMTVKINK DSPAQCASGN NTILCISTKS
  651 LNTQAMVENG GTLIVGGIYE ENNGNTLTKV PLLGDIPVIG NLFKTRGKKT
  701 DRRELLIFIT PRIIDTAGNS LRY
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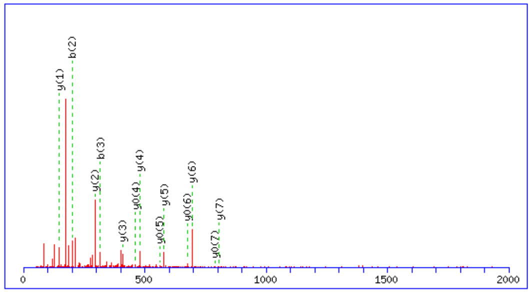
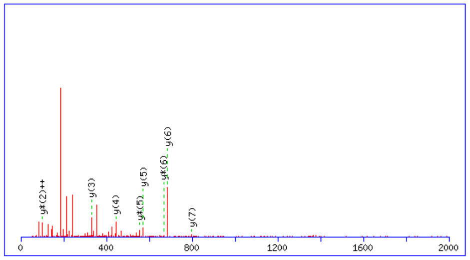


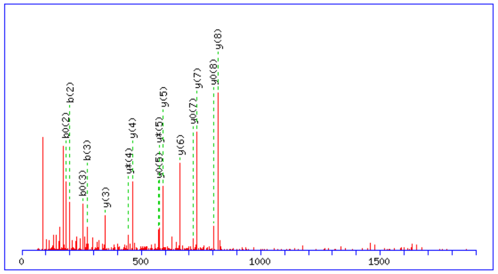
```
Monoisotopic mass of neutral peptide Mr(calc): 893.4494
Ions Score: 46  Expect: 0.46
Matches (Bold Red): 13/66 fragment ions using 38 most intense peaks
```

#	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							8
2	201.1234	101.0653	183.1128	92.0600	L	807.4247	404.2160	790.3981	395.7027	789.4141	395.2107	7
3	316.1503	158.5788	298.1397	149.5735	D	694.3406	347.6740	677.3141	339.1607	676.3301	338.6687	6
4	415.2187	208.1130	397.2082	199.1077	V	579.3137	290.1605	562.2871	281.6472	561.3031	281.1552	5
5	486.2558	243.6316	468.2453	234.6263	A	480.2453	240.6263	463.2187	232.1130	462.2347	231.6210	4
6	601.2828	301.1450	583.2722	292.1397	D	409.2082	205.1077	392.1816	196.5944	391.1976	196.1024	3
7	748.3512	374.6792	730.3406	365.6740	F	294.1812	147.5942	277.1547	139.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1



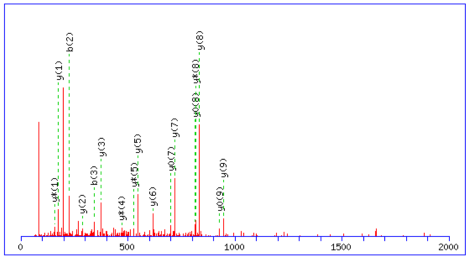
```
Monoisotopic mass of neutral peptide Mr(calc): 898.5851
Ions Score: 24  Expect: 71
Matches (Bold Red): 8/64 fragment ions using 21 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.0550	51.5311			84.0444	42.5258	T					8
2	215.1390	108.0731			197.1285	99.0679	I	798.5448	399.7760	781.5182	391.2627	7
3	328.2231	164.6152			310.2125	155.6099	L	685.4607	343.2340	668.4341	334.7207	6
4	456.2817	228.6445	439.2551	220.1312	438.2711	219.6392	Q	572.3766	286.6920	555.3501	278.1787	5
5	569.3657	285.1865	552.3392	276.6732	551.3552	276.1812	I	444.3180	222.6627	427.2915	214.1494	4
6	682.4498	341.7285	665.4232	333.2153	664.4392	332.7233	L	331.2340	166.1206	314.2074	157.6074	3
7	753.4869	377.2471	736.4604	368.7338	735.4763	368.2418	A	218.1499	109.5786	201.1234	101.0653	2
8							K	147.1128	74.0600	130.0863	65.5468	1



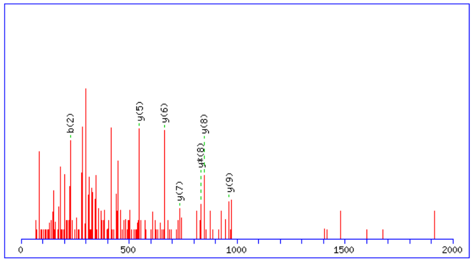
```
Monoisotopic mass of neutral peptide Mr(calc): 932.4675
Ions Score: 39  Expect: 2.6
Matches (Bold Red): 15/84 fragment ions using 30 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							9
2	201.1234	101.0653			183.1128	92.0600	S	820.3908	410.6990	803.3642	402.1857	802.3802	401.6937	8
3	272.1605	136.5839			254.1499	127.5786	A	733.3587	367.1830	716.3322	358.6697	715.3482	358.1777	7
4	343.1976	172.1024			325.1870	163.0972	A	662.3216	331.6645	645.2951	323.1512	644.3111	322.6592	6
5	471.2562	236.1317	454.2296	227.6185	453.2456	227.1264	Q	591.2845	296.1459	574.2580	287.6326	573.2739	287.1406	5
6	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	N	463.2259	232.1166	446.1994	223.6033	445.2154	223.1113	4
7	672.3311	336.6692	655.3046	328.1559	654.3206	327.6639	S	349.1830	175.0951	332.1565	166.5819	331.1724	166.0899	3
8	759.3632	380.1852	742.3366	371.6719	741.3526	371.1799	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9							R	175.1190	88.0631	158.0924	79.5498			1



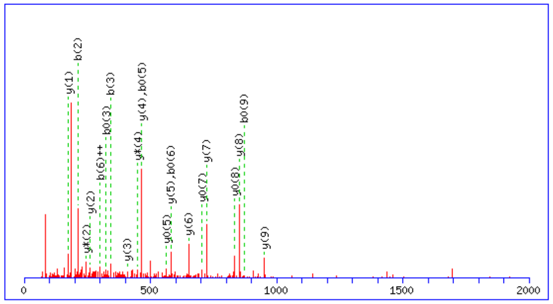
Monoisotopic mass of neutral peptide Mr(calc): 1058.5720
Ions Score: 60 Expect: 0.022
Matches (Bold Red): 17/88 fragment ions using 36 most intense peaks

#	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	**227.1754**	114.0913					I	**946.4952**	473.7513	929.4687	465.2380	**928.4847**	464.7460	9
3	**342.2023**	171.6048			324.1918	162.5995	D	**833.4112**	417.2092	**816.3846**	408.6959	**815.4006**	408.2039	8
4	443.2500	222.1287			425.2395	213.1234	T	**718.3842**	359.6958	701.3577	351.1825	**700.3737**	350.6905	7
5	514.2871	257.6472			496.2766	248.6419	A	**617.3365**	309.1719	600.3100	300.6586	599.3260	300.1666	6
6	571.3086	286.1579			553.2980	277.1527	G	**546.2994**	273.6534	**529.2729**	265.1401	528.2889	264.6481	5
7	685.3515	343.1794	668.3250	334.6661	667.3410	334.1741	N	489.2780	245.1426	**472.2514**	236.6293	471.2674	236.1373	4
8	772.3836	386.6954	755.3570	378.1821	754.3730	377.6901	S	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	3
9	885.4676	443.2374	868.4411	434.7242	867.4571	434.2322	L	**288.2030**	144.6051	271.1765	136.0919			2
10							R	**175.1190**	88.0631	**158.0924**	79.5498			1



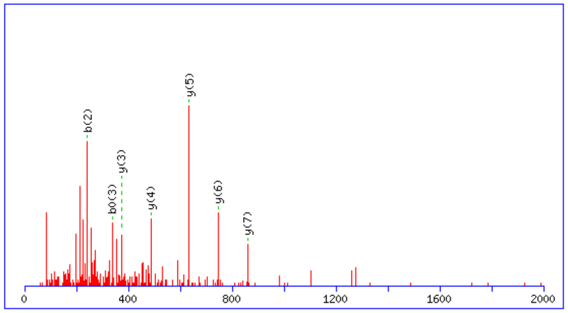
Monoisotopic mass of neutral peptide Mr(calc): 1075.4894
Ions Score: 30 Expect: 18
Matches (Bold Red): 7/96 fragment ions using 13 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							10
2	**229.1183**	115.0628			211.1077	106.0575	D	**963.4126**	482.2100	946.3861	473.6967	945.4021	473.2047	9
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	N	**848.3857**	424.6965	**831.3591**	416.1832	830.3751	415.6912	8
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	A	**734.3428**	367.6750	717.3162	359.1617	716.3322	358.6697	7
5	529.2253	265.1163	512.1987	256.6030	511.2147	256.1110	D	**663.3056**	332.1565	646.2791	323.6432	645.2951	323.1512	6
6	630.2729	315.6401	613.2464	307.1268	612.2624	306.6348	T	**548.2787**	274.6430	531.2522	266.1297	530.2681	265.6377	5
7	731.3206	366.1640	714.2941	357.6507	713.3101	357.1587	T	447.2310	224.1191	430.2045	215.6059	429.2205	215.1139	4
8	788.3421	394.6747	771.3155	386.1614	770.3315	385.6694	G	346.1833	173.5953	329.1568	165.0820			3
9	902.3850	451.6961	885.3585	443.1829	884.3745	442.6909	N	289.1619	145.0846	272.1353	136.5713			2
10							R	175.1190	88.0631	158.0924	79.5498			1



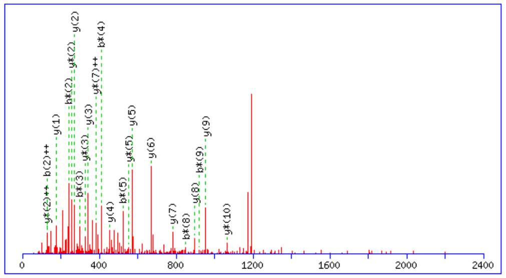
Monoisotopic mass of neutral peptide Mr(calc): 1063.5298
Ions Score: 45 Expect: 0.61
Matches (Bold Red): 21/84 fragment ions using 62 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							10
2	**213.1598**	107.0835			V	**951.4530**	476.2302	934.4265	467.7169	933.4425	467.2249	9
3	**342.2023**	171.6048	**324.1918**	162.5995	E	**852.3846**	426.6959	835.3581	418.1827	**834.3741**	417.6907	8
4	413.2395	207.1234	395.2289	198.1181	A	**723.3420**	362.1747	706.3155	353.6614	**705.3315**	353.1694	7
5	484.2766	242.6419	**466.2660**	233.6366	A	**652.3049**	326.6561	635.2784	318.1428	634.2944	317.6508	6
6	599.3035	**300.1554**	**581.2930**	291.1501	D	**581.2678**	291.1375	564.2413	282.6243	**563.2572**	282.1323	5
7	656.3250	328.6661	638.3144	319.6608	G	**466.2409**	233.6241	**449.2143**	225.1108	448.2303	224.6188	4
8	803.3934	402.2003	785.3828	393.1951	F	**409.2194**	205.1133	392.1928	196.6001	391.2088	196.1081	3
9	890.4254	445.7163	**872.4149**	436.7111	S	**262.1510**	131.5791	**245.1244**	123.0659	244.1404	122.5738	2
10					R	**175.1190**	88.0631	158.0924	79.5498			1



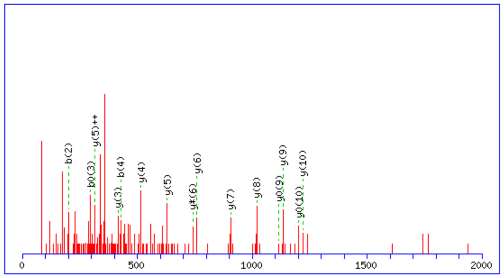
Monoisotopic mass of neutral peptide Mr(calc): 1100.6594
Ions Score: 37 Expect: 3.6
Matches (Bold Red): 7/76 fragment ions using 14 most intense peaks

#	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							9
2	**243.1339**	122.0706	225.1234	113.0653	L	972.6241	486.8157	955.5975	478.3024	954.6135	477.8104	8
3	356.2180	178.6126	**338.2074**	169.6074	L	**859.5400**	430.2736	842.5135	421.7604	841.5294	421.2684	7
4	469.3021	235.1547	451.2915	226.1494	I	**746.4559**	373.7316	729.4294	365.2183	728.4454	364.7263	6
5	616.3705	308.6889	598.3599	299.6836	F	**633.3719**	317.1896	616.3453	308.6763	615.3613	308.1843	5
6	729.4545	365.2309	711.4440	356.2256	I	**486.3035**	243.6554	469.2769	235.1421	468.2929	234.6501	4
7	830.5022	415.7547	812.4917	406.7495	T	**373.2194**	187.1133	356.1928	178.6001	355.2088	178.1081	3
8	927.5550	464.2811	909.5444	455.2758	P	272.1717	136.5895	255.1452	128.0762			2
9					R	175.1190	88.0631	158.0924	79.5498			1



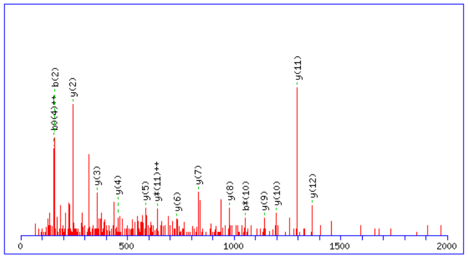
```
Monoisotopic mass of neutral peptide Mr(calc): 1208.6626
Ions Score: 42  Expect: 1.1
Matches (Bold Red): 23/80 fragment ions using 51 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	**129.0659**	65.0366	112.0393	56.5233	Q					11
2	257.1244	**129.0659**	**240.0979**	120.5526	Q	1081.6113	541.3093	**1064.5847**	532.7960	10
3	314.1459	157.5766	**297.1193**	149.0633	G	**953.5527**	477.2800	936.5261	468.7667	9
4	428.1888	214.5980	**411.1623**	206.0848	N	**896.5312**	448.7693	879.5047	440.2560	8
5	541.2729	271.1401	**524.2463**	262.6268	I	**782.4883**	391.7478	765.4617	**383.2345**	7
6	640.3413	320.6743	623.3148	312.1610	V	**669.4042**	335.2058	652.3777	326.6925	6
7	754.3842	377.6958	737.3577	369.1825	N	**570.3358**	285.6715	**553.3093**	277.1583	5
8	867.4683	434.2378	**850.4417**	425.7245	I	**456.2929**	228.6501	439.2663	220.1368	4
9	938.5054	469.7563	**921.4789**	461.2431	A	**343.2088**	172.1081	**326.1823**	163.5948	3
10	1035.5582	518.2827	1018.5316	509.7694	P	**272.1717**	136.5895	**255.1452**	**128.0762**	2
11					R	**175.1190**	88.0631	158.0924	79.5498	1



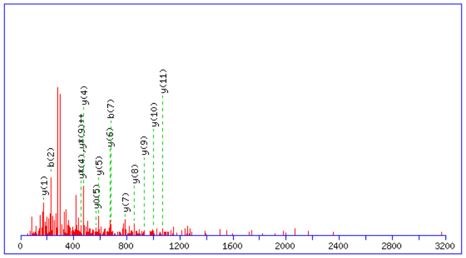
```
Monoisotopic mass of neutral peptide Mr(calc): 1333.6878
Ions Score: 51  Expect: 0.14
Matches (Bold Red): 15/104 fragment ions using 25 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							11
2	**201.1234**	101.0653			183.1128	92.0600	S	**1221.6110**	611.3091	1204.5844	602.7959	**1203.6004**	602.3039	10
3	314.2074	157.6074			**296.1969**	148.6021	L	**1134.5790**	567.7931	1117.5524	559.2798	**1116.5684**	558.7878	9
4	**429.2344**	215.1208			411.2238	206.1155	D	**1021.4949**	511.2511	1004.4684	502.7378	1003.4843	502.2458	8
5	576.3028	288.6550			558.2922	279.6498	F	**906.4680**	453.7376	889.4414	445.2243	888.4574	444.7323	7
6	704.3614	352.6843	687.3348	344.1710	686.3508	343.6790	Q	**759.3995**	380.2034	**742.3730**	371.6901	741.3890	371.1981	6
7	819.3883	410.1978	802.3618	401.6845	801.3777	401.1925	D	**631.3410**	**316.1741**	614.3144	307.6608	613.3304	307.1688	5
8	918.4567	459.7320	901.4302	451.2187	900.4462	450.7267	V	**516.3140**	258.6606	499.2875	250.1474	498.3035	249.6554	4
9	1047.4993	524.2533	1030.4728	515.7400	1029.4888	515.2480	E	**417.2456**	209.1264	400.2191	200.6132	399.2350	200.1212	3
10	1160.5834	580.7953	1143.5568	572.2821	1142.5728	571.7900	I	288.2030	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1



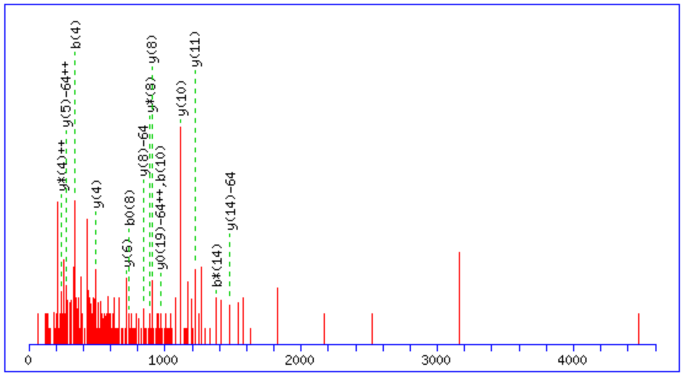
```
Monoisotopic mass of neutral peptide Mr(calc): 1524.7977
Ions Score: 59  Expect: 0.021
Matches (Bold Red): 15/126 fragment ions using 31 most intense peaks
```

#	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							14
2	**159.0764**	80.0418			141.0659	71.0366	A	1438.7729	719.8901	1421.7464	711.3768	1420.7624	710.8848	13
3	230.1135	115.5604			212.1030	106.5551	A	**1367.7358**	684.3715	1350.7093	675.8583	1349.7252	675.3663	12
4	327.1663	164.0868			309.1557	**155.0815**	P	**1296.6987**	648.8530	1279.6721	**640.3397**	1278.6881	639.8477	11
5	384.1878	192.5975			366.1772	183.5922	G	**1199.6459**	600.3266	1182.6194	591.8133	1181.6354	591.3213	10
6	547.2511	274.1292			529.2405	265.1239	Y	**1142.6245**	571.8159	1125.5979	563.3026	1124.6139	562.8106	9
7	694.3195	347.6634			676.3089	338.6581	F	**979.5611**	490.2842	962.5346	481.7709	961.5506	481.2789	8
8	795.3672	398.1872			777.3566	389.1819	T	**832.4927**	416.7500	815.4662	408.2367	814.4822	407.7447	7
9	942.4356	471.7214			924.4250	462.7162	F	**731.4450**	366.2262	714.4185	357.7129			6
10	1070.4942	535.7507	**1053.4676**	527.2375	1052.4836	526.7454	Q	**584.3766**	292.6920	567.3501	284.1787			5
11	1169.5626	585.2849	1152.5360	576.7717	1151.5520	576.2796	V	**456.3180**	228.6627	439.2915	220.1494			4
12	1282.6467	641.8270	1265.6201	633.3137	1264.6361	632.8217	L	**357.2496**	179.1285	340.2231	170.6152			3
13	1379.6994	690.3533	1362.6729	681.8401	1361.6889	681.3481	P	**244.1656**	122.5864	227.1390	114.0731			2
14							K	147.1128	74.0600	130.0863	65.5468			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1607.9359
Ions Score: 30  Expect: 16
Matches (Bold Red): 14/152 fragment ions using 52 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							16
2	**228.1343**	114.5708	211.1077	106.0575			N	1495.8591	748.4332	1478.8326	739.9199	1477.8485	739.4279	15
3	341.2183	171.1128	324.1918	162.5995			L	1381.8162	691.4117	1364.7896	682.8985	1363.8056	682.4064	14
4	438.2711	219.6392	421.2445	211.1259			P	1268.7321	634.8697	1251.7056	626.3564	1250.7215	625.8644	13
5	537.3395	269.1734	520.3130	260.6601			V	1171.6793	586.3433	1154.6528	577.8300	1153.6688	577.3380	12
6	608.3766	304.6919	591.3501	296.1787			A	**1072.6109**	536.8091	1055.5844	528.2958	1054.6004	527.8038	11
7	**679.4137**	340.2105	662.3872	331.6972			A	**1001.5738**	501.2905	984.5473	492.7773	983.5633	492.2853	10
8	750.4509	375.7291	733.4243	367.2158			A	**930.5367**	465.7720	913.5102	**457.2587**	912.5261	456.7667	9
9	821.4880	411.2476	804.4614	402.7343			A	**859.4996**	430.2534	842.4730	421.7402	841.4890	421.2482	8
10	935.5309	468.2691	918.5043	459.7558			N	**788.4625**	394.7349	771.4359	386.2216	770.4519	385.7296	7
11	1022.5629	511.7851	1005.5364	503.2718	1004.5524	502.7798	S	**674.4195**	337.7134	657.3930	329.2001	656.4090	328.7081	6
12	1135.6470	568.3271	1118.6204	559.8139	1117.6364	559.3218	I	**587.3875**	294.1974	570.3610	285.6841	**569.3770**	285.1921	5
13	1222.6790	611.8431	1205.6525	603.3299	1204.6684	602.8379	S	**474.3035**	237.6554	**457.2769**	229.1421	456.2929	228.6501	4
14	1335.7631	668.3852	1318.7365	659.8719	1317.7525	659.3799	L	387.2714	194.1394	370.2449	185.6261			3
15	1434.8315	717.9194	1417.8049	709.4061	1416.8209	708.9141	V	274.1874	137.5973	257.1608	129.0840			2
16							R	**175.1190**	88.0631	158.0924	79.5498			1



```
Monoisotopic mass of neutral peptide Mr(calc): 2296.2712
Variable modifications:
M19    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
 Ions Score: 5  Expect: 3.8e+03
Matches (Bold Red): 15/346 fragment ions using 51 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							22
2	171.1128	86.0600					V	2226.2414	1113.6243	2209.2148	1105.1111	2208.2308	1104.6191	21
3	284.1969	142.6021					L	2127.1730	1064.0901	2110.1464	1055.5769	2109.1624	1055.0848	20
4	**341.2183**	171.1128					G	2014.0889	1007.5481	1997.0624	999.0348	1996.0783	998.5428	19
5	454.3024	227.6548					L	1957.0674	979.0374	1940.0409	970.5241	1939.0569	970.0321	18
6	555.3501	278.1787			537.3395	269.1734	T	1843.9834	922.4953	1826.9568	913.9821	1825.9728	913.4900	17
7	654.4185	327.7129			636.4079	318.7076	V	1742.9357	871.9715	1725.9092	863.4582	1724.9251	862.9662	16
8	755.4662	378.2367			**737.4556**	369.2314	T	1643.8673	822.4373	1626.8407	813.9240	1625.8567	813.4320	15
9	852.5189	426.7631			834.5084	417.7578	P	1542.8196	771.9134	1525.7931	763.4002	1524.8090	762.9082	14
10	**966.5619**	483.7846	949.5353	475.2713	948.5513	474.7793	N	1445.7668	723.3871	1428.7403	714.8738	1427.7563	714.3818	13
11	1079.6459	540.3266	1062.6194	531.8133	1061.6354	531.3213	I	1331.7239	666.3656	1314.6974	657.8523	1313.7134	657.3603	12
12	1180.6936	590.8504	1163.6671	582.3372	1162.6830	581.8452	T	**1218.6399**	609.8236	1201.6133	601.3103	1200.6293	600.8183	11
13	1277.7464	639.3768	1260.7198	630.8635	1259.7358	630.3715	P	**1117.5922**	559.2997	1100.5656	550.7865	1099.5816	550.2944	10
14	1392.7733	696.8903	**1375.7468**	688.3770	1374.7627	687.8850	D	1020.5394	510.7733	1003.5129	502.2601	1002.5288	501.7681	9
15	1449.7948	725.4010	1432.7682	716.8878	1431.7842	716.3957	G	**905.5125**	453.2599	**888.4859**	444.7466	887.5019	444.2546	8
16	1577.8534	789.4303	1560.8268	780.9170	1559.8428	780.4250	Q	848.4910	424.7491	831.4645	416.2359	830.4804	415.7439	7
17	1690.9374	845.9723	1673.9109	837.4591	1672.9268	836.9671	I	**720.4324**	360.7199	703.4059	352.2066	702.4219	351.7146	6
18	1804.0215	902.5144	1786.9949	894.0011	1786.0109	893.5091	I	607.3484	304.1778	590.3218	295.6645	589.3378	295.1725	5
19	1951.0569	976.0321	1934.0303	967.5188	1933.0463	967.0268	M	**494.2643**	247.6358	477.2378	**239.1225**	476.2537	238.6305	4
20	2052.1046	1026.5559	2035.0780	1018.0426	2034.0940	1017.5506	T	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
21	2151.1730	1076.0901	2134.1464	1067.5769	2133.1624	1067.0848	V	246.1812	123.5942	229.1547	115.0810			2
22							K	147.1128	74.0600	130.0863	65.5468			1

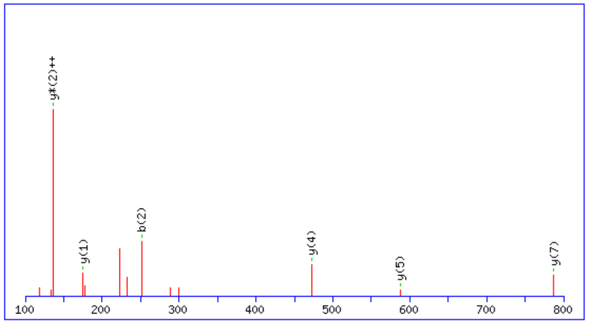
Protein band 89 (+Mn): MafA adhesin

Score: 202 M_r: 34738

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%

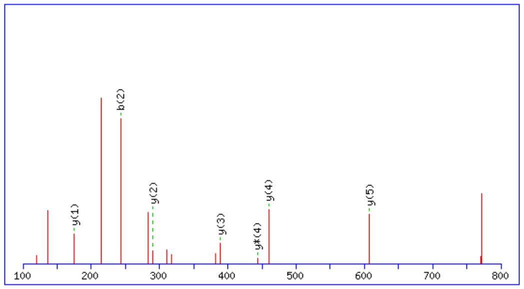
Matched peptides shown in Bold Red

     1 MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
    51 DMDLQALHGR KVALYIATMG DQGSGSLTGG RYSIDALIRG EYINSPAVRT
   101 DYTYPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSRSSLGLN
   151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
   201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
   251 AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIQPYGNHTG NSAPSVEADN
   301 SHEGYGYSDE AVRQHRQGQP
```



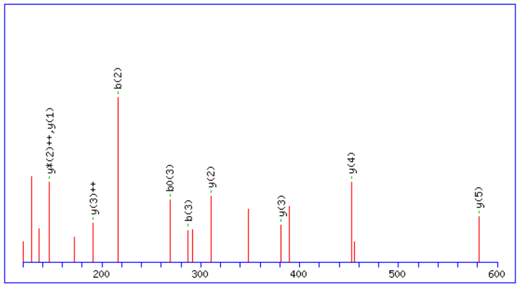
```
Monoisotopic mass of neutral peptide Mr(calc): 949.5233
Ions Score: 36  Expect: 4.4
Matches (Bold Red): 6/60 fragment ions using 7 most intense peaks
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389			Y							8
2	**251.1026**	126.0550	233.0921	117.0497	S	**787.4672**	394.2373	770.4407	385.7240	769.4567	385.2320	7
3	364.1867	182.5970	346.1761	173.5917	I	700.4352	350.7212	683.4087	342.2080	682.4246	341.7160	6
4	479.2136	240.1105	461.2031	231.1052	D	**587.3511**	294.1792	570.3246	285.6659	569.3406	285.1739	5
5	550.2508	275.6290	532.2402	266.6237	A	**472.3242**	236.6657	455.2976	228.1525			4
6	663.3348	332.1710	645.3243	323.1658	L	401.2871	201.1472	384.2605	192.6339			3
7	776.4189	388.7131	758.4083	379.7078	I	288.2030	144.6051	271.1765	**136.0919**			2
8					R	**175.1190**	88.0631	158.0924	79.5498			1



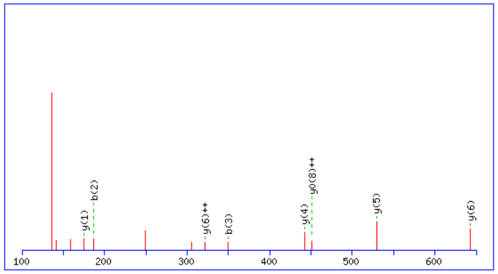
```
Monoisotopic mass of neutral peptide Mr(calc): 1011.5025
Ions Score: 25  Expect: 45
Matches (Bold Red): 7/66 fragment ions using 15 most intense peaks
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			L							8
2	**243.1339**	122.0706	225.1234	113.0653	E	899.4258	450.2165	882.3992	441.7032	881.4152	441.2112	7
3	406.1973	203.6023	388.1867	194.5970	Y	770.3832	385.6952	753.3566	377.1819	752.3726	376.6899	6
4	553.2657	277.1365	535.2551	268.1312	F	**607.3198**	304.1636	590.2933	295.6503	589.3093	295.1583	5
5	624.3028	312.6550	606.2922	303.6498	A	**460.2514**	230.6293	**443.2249**	222.1161	442.2409	221.6241	4
6	723.3712	362.1892	705.3606	353.1840	V	**389.2143**	195.1108	372.1878	186.5975	371.2037	186.1055	3
7	838.3981	419.7027	820.3876	410.6974	D	**290.1459**	145.5766	273.1193	137.0633	272.1353	136.5713	2
8					R	**175.1190**	88.0631	158.0924	79.5498			1



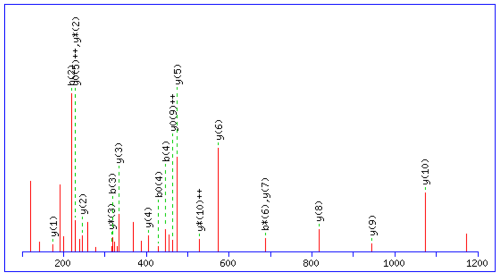
```
Monoisotopic mass of neutral peptide Mr(calc): 1013.4818
Ions Score: 34  Expect: 7.6
Matches (Bold Red): 10/86 fragment ions using 14 most intense peaks
```

#	b	b^{++}	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							9
2	**216.0979**	108.5526	199.0713	100.0393	198.0873	99.5473	N	913.4414	457.2243	896.4149	448.7111	895.4308	448.2191	8
3	**287.1350**	144.0711	270.1084	135.5579	**269.1244**	135.0659	A	799.3985	400.2029	782.3719	391.6896	781.3879	391.1976	7
4	434.2034	217.6053	417.1769	209.0921	416.1928	208.6001	F	728.3614	364.6843	711.3348	356.1710	710.3508	355.6790	6
5	563.2460	282.1266	546.2195	273.6134	545.2354	273.1214	E	**581.2930**	291.1501	564.2664	282.6368	563.2824	282.1448	5
6	634.2831	317.6452	617.2566	309.1319	616.2726	308.6399	A	**452.2504**	226.6288	435.2238	218.1155			4
7	705.3202	353.1638	688.2937	344.6505	687.3097	344.1585	A	**381.2132**	**191.1103**	364.1867	182.5970			3
8	868.3836	434.6954	851.3570	426.1821	850.3730	425.6901	Y	**310.1761**	155.5917	293.1496	**147.0784**			2
9							K	**147.1128**	74.0600	130.0863	65.5468			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1104.5564
Ions Score: 29  Expect: 22
Matches (Bold Red): 8/90 fragment ions using 11 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							10
2	**187.0713**	94.0393			169.0608	85.0340	E	1048.5422	524.7747	1031.5156	516.2615	1030.5316	515.7694	9
3	**350.1347**	175.5710			332.1241	166.5657	Y	919.4996	460.2534	902.4730	451.7402	901.4890	**451.2482**	8
4	463.2187	232.1130			445.2082	223.1077	I	756.4363	378.7218	739.4097	370.2085	738.4257	369.7165	7
5	577.2617	289.1345	560.2351	280.6212	559.2511	280.1292	N	**643.3522**	**322.1797**	626.3256	313.6665	625.3416	313.1745	6
6	664.2937	332.6505	647.2671	324.1372	646.2831	323.6452	S	**529.3093**	265.1583	512.2827	256.6450	511.2987	256.1530	5
7	761.3464	381.1769	744.3199	372.6636	743.3359	372.1716	P	**442.2772**	221.6423	425.2507	213.1290			4
8	832.3836	416.6954	815.3570	408.1821	814.3730	407.6901	A	345.2245	173.1159	328.1979	164.6026			3
9	931.4520	466.2296	914.4254	457.7163	913.4414	457.2243	V	274.1874	137.5973	257.1608	129.0840			2
10							R	**175.1190**	88.0631	158.0924	79.5498			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1389.7252
Ions Score: 78  Expect: 0.00029
Matches (Bold Red): 20/126 fragment ions using 30 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							13
2	**219.1128**	110.0600					A	1243.6641	622.3357	1226.6375	613.8224	1225.6535	613.3304	12
3	**318.1812**	159.5942					V	1172.6270	586.8171	1155.6004	578.3039	1154.6164	577.8118	11
4	**447.2238**	224.1155			**429.2132**	215.1103	E	**1073.5586**	537.2829	1056.5320	**528.7696**	1055.5480	528.2776	10
5	575.2824	288.1448	558.2558	279.6316	557.2718	279.1396	Q	**944.5160**	472.7616	927.4894	464.2483	926.5054	**463.7563**	9
6	704.3250	352.6661	**687.2984**	344.1529	686.3144	343.6608	E	**816.4574**	408.7323	799.4308	400.2191	798.4468	399.7271	8
7	817.4090	409.2082	800.3825	400.6949	799.3985	400.2029	L	**687.4148**	344.2110	670.3883	335.6978	669.4042	335.2058	7
8	916.4775	458.7424	899.4509	450.2291	898.4669	449.7371	V	**574.3307**	287.6690	557.3042	279.1557	556.3202	278.6637	6
9	987.5146	494.2609	970.4880	485.7477	969.5040	485.2556	A	**475.2623**	238.1348	458.2358	229.6215	457.2518	**229.1295**	5
10	1058.5517	529.7795	1041.5251	521.2662	1040.5411	520.7742	A	**404.2252**	202.6162	387.1987	194.1030	386.2146	193.6110	4
11	1145.5837	573.2955	1128.5572	564.7822	1127.5732	564.2902	S	**333.1881**	167.0977	**316.1615**	158.5844	315.1775	158.0924	3
12	1216.6208	608.8141	1199.5943	600.3008	1198.6103	599.8088	A	**246.1561**	123.5817	**229.1295**	115.0684			2
13							R	**175.1190**	88.0631	158.0924	79.5498			1

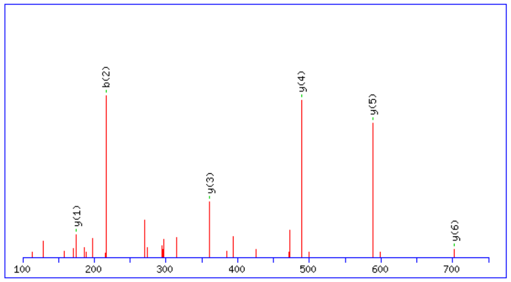
Protein band 93 (+Mn): Outer membrane protein PIII

Score: 249 M$_r$: 25525

```
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 36%

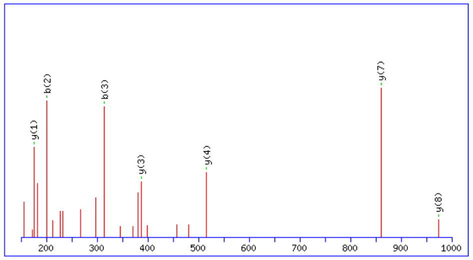
Matched peptides shown in Bold Red

     1 MTKQLKLSAL FVALLASGTA VAGEASVQGY TVSGQSNEIV RNNYGECWKN
    51 AYFDKASQGR VECGDAVAVP EPEPAPVAVV EQAPQYVDET ISLSAKTLFG
   101 FDKDSLRAEA QDNLKVLAQR LSRTNVQSVR VEGHTDFMGS EKYNQALSER
   151 RAYVVANNLV SNGVPASRIS AVGLGESQAQ MTQVCQAEVA KLGAKASKAK
   201 KREALIACIE PDRRVDVKIR SIVTRQVVPA RNHHQH
```



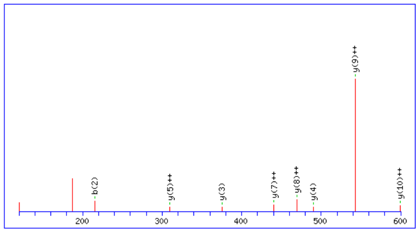
```
Monoisotopic mass of neutral peptide Mr(calc): 802.4297
Ions Score: 55  Expect: 0.075
Matches (Bold Red): 6/66 fragment ions using 6 most intense peaks
```

#	b	b^{++}	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							7
2	**216.0979**	108.5526	199.0713	100.0393	198.0873	99.5473	N	**702.3893**	351.6983	685.3628	343.1850	684.3787	342.6930	6
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	V	**588.3464**	294.6768	571.3198	286.1636	570.3358	285.6715	5
4	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	Q	**489.2780**	245.1426	472.2514	236.6293	471.2674	236.1373	4
5	530.2569	265.6321	513.2304	257.1188	512.2463	256.6268	S	**361.2194**	181.1133	344.1928	172.6001	343.2088	172.1081	3
6	629.3253	315.1663	612.2988	306.6530	611.3148	306.1610	V	274.1874	137.5973	257.1608	129.0840			2
7							R	**175.1190**	88.0631	158.0924	79.5498			1



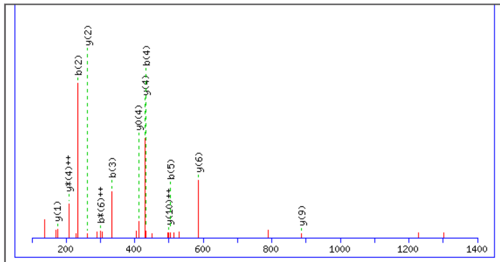
```
Monoisotopic mass of neutral peptide Mr(calc): 1285.6336
Variable modifications:
C6     : Carbamidomethyl (C)
Ions Score: 38  Expect: 3
Matches (Bold Red): 7/98 fragment ions using 10 most intense peaks
```

#	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							11
2	**201.0870**	101.0471	183.0764	92.0418	A	1157.5983	579.3028	1140.5718	570.7895	1139.5878	570.2975	10
3	**314.1710**	157.5892	296.1605	148.5839	L	1086.5612	543.7842	1069.5347	535.2710	1068.5506	534.7790	9
4	427.2551	214.1312	409.2445	205.1259	I	**973.4771**	487.2422	956.4506	478.7289	955.4666	478.2369	8
5	498.2922	249.6498	480.2817	240.6445	A	**860.3931**	430.7002	843.3665	422.1869	842.3825	421.6949	7
6	658.3229	329.6651	640.3123	320.6598	C	789.3560	395.1816	772.3294	386.6683	771.3454	386.1763	6
7	771.4069	386.2071	753.3964	377.2018	I	629.3253	315.1663	612.2988	306.6530	611.3148	306.1610	5
8	900.4495	450.7284	882.4390	441.7231	E	**516.2413**	258.6243	499.2147	250.1110	498.2307	249.6190	4
9	997.5023	499.2548	979.4917	490.2495	P	**387.1987**	194.1030	370.1721	185.5897	369.1881	185.0977	3
10	1112.5292	556.7683	1094.5187	547.7630	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
11					R	**175.1190**	88.0631	158.0924	79.5498			1



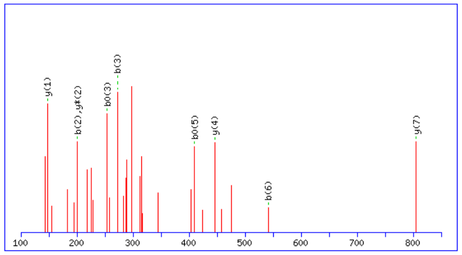
```
Monoisotopic mass of neutral peptide Mr(calc): 1297.6667
Ions Score: 39  Expect: 2.3
Matches (Bold Red): 8/104 fragment ions using 11 most intense peaks
```

#	b	b^{++}	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							11
2	**215.1390**	108.0731			197.1285	99.0679	L	1197.6262	**599.3168**	1180.5997	590.8035	1179.6157	590.3115	10
3	362.2074	181.6074			344.1969	172.6021	F	1084.5422	**542.7747**	1067.5156	534.2615	1066.5316	533.7694	9
4	419.2289	210.1181			401.2183	201.1128	G	937.4738	**469.2405**	920.4472	460.7272	919.4632	460.2352	8
5	566.2973	283.6523			548.2867	274.6470	F	880.4523	**440.7298**	863.4258	432.2165	862.4417	431.7245	7
6	681.3243	341.1658			663.3137	332.1605	D	733.3839	367.1956	716.3573	358.6823	715.3733	358.1903	6
7	809.4192	405.2132	792.3927	396.7000	791.4087	396.2080	K	618.3569	**309.6821**	601.3304	301.1688	600.3464	300.6768	5
8	924.4462	462.7267	907.4196	454.2134	906.4356	453.7214	D	**490.2620**	245.6346	473.2354	237.1214	472.2514	236.6293	4
9	1011.4782	506.2427	994.4516	497.7295	993.4676	497.2374	S	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	1124.5623	562.7848	1107.5357	554.2715	1106.5517	553.7795	L	288.2030	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1



```
Monoisotopic mass of neutral peptide Mr(calc): 1729.9111
Ions Score: 33  Expect: 7
Matches (Bold Red): 13/162 fragment ions using 25 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							17
2	**235.1077**	118.0575					Y	1659.8813	830.4443	1642.8547	821.9310	1641.8707	821.4390	16
3	**334.1761**	167.5917					V	1496.8180	748.9126	1479.7914	740.3993	1478.8074	739.9073	15
4	**433.2445**	217.1259					V	1397.7496	699.3784	1380.7230	690.8651	1379.7390	690.3731	14
5	**504.2817**	252.6445					A	1298.6811	649.8442	1281.6546	641.3309	1280.6706	640.8389	13
6	618.3246	309.6659	601.2980	**301.1527**			N	1227.6440	614.3256	1210.6175	605.8124	1209.6335	605.3204	12
7	732.3675	366.6874	715.3410	358.1741			N	1113.6011	557.3042	1096.5745	548.7909	1095.5905	548.2989	11
8	845.4516	423.2294	828.4250	414.7162			L	999.5582	**500.2827**	982.5316	491.7694	981.5476	491.2774	10
9	944.5200	472.7636	927.4934	464.2504			V	**886.4741**	443.7407	869.4476	435.2274	868.4635	434.7354	9
10	1031.5520	516.2796	1014.5255	507.7664	1013.5415	507.2744	S	787.4057	394.2065	770.3791	385.6932	769.3951	385.2012	8
11	1145.5949	573.3011	1128.5684	564.7878	1127.5844	564.2958	N	700.3737	350.6905	683.3471	342.1772	682.3631	341.6852	7
12	1202.6164	601.8118	1185.5899	593.2986	1184.6058	592.8066	G	**586.3307**	293.6690	569.3042	285.1557	568.3202	284.6637	6
13	1301.6848	651.3461	1284.6583	642.8328	1283.6743	642.3408	V	529.3093	265.1583	512.2827	256.6450	511.2987	256.1530	5
14	1398.7376	699.8724	1381.7110	691.3592	1380.7270	690.8672	P	**430.2409**	215.6241	413.2143	**207.1108**	**412.2303**	206.6188	4
15	1469.7747	735.3910	1452.7482	726.8777	1451.7641	726.3857	A	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
16	1556.8067	778.9070	1539.7802	770.3937	1538.7962	769.9017	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
17							R	**175.1190**	88.0631	158.0924	79.5498			1



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Monoisotopic mass of neutral peptide Mr(calc): 2420.1676
Variable modifications:
M13    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
C17    : Carbamidomethyl (C)
Ions Score: 19  Expect: 1.5e+02
Matches (Bold Red): 9/370 fragment ions using 15 most intense peaks
```
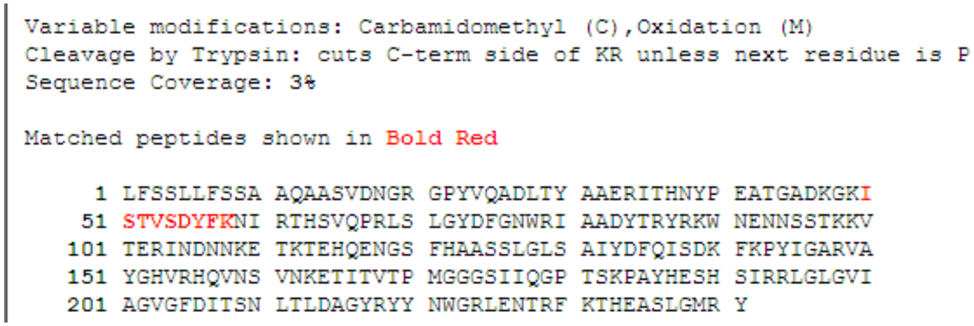

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							23
2	**201.1234**	101.0653			183.1128	92.0600	S	2308.0908	1154.5490	2291.0642	1146.0358	2290.0802	1145.5437	22
3	**272.1605**	136.5839			**254.1499**	127.5786	A	2221.0588	1111.0330	2204.0322	1102.5197	2203.0482	1102.0277	21
4	371.2289	186.1181			353.2183	177.1128	V	2150.0216	1075.5145	2132.9951	1067.0012	2132.0111	1066.5092	20
5	428.2504	214.6288			**410.2398**	205.6235	G	2050.9532	1025.9803	2033.9267	1017.4670	2032.9427	1016.9750	19
6	**541.3344**	271.1709			523.3239	262.1656	L	1993.9318	997.4695	1976.9052	988.9562	1975.9212	988.4642	18
7	598.3559	299.6816			580.3453	290.6763	G	1880.8477	940.9275	1863.8212	932.4142	1862.8371	931.9222	17
8	727.3985	364.2029			709.3879	355.1976	E	1823.8262	912.4168	1806.7997	903.9035	1805.8157	903.4115	16
9	814.4305	407.7189			796.4199	398.7136	S	1694.7836	847.8955	1677.7571	839.3822	1676.7731	838.8902	15
10	942.4891	471.7482	925.4625	463.2349	924.4785	462.7429	Q	1607.7516	804.3794	1590.7251	795.8662	1589.7411	795.3742	14
11	1013.5262	507.2667	996.4997	498.7535	995.5156	498.2615	A	1479.6930	740.3502	1462.6665	731.8369	1461.6825	731.3449	13
12	1141.5848	571.2960	1124.5582	562.7828	1123.5742	562.2907	Q	1408.6559	704.8316	1391.6294	696.3183	1390.6454	695.8263	12
13	1288.6202	644.8137	1271.5936	636.3005	1270.6096	635.8084	M	1280.5973	640.8023	1263.5708	632.2890	1262.5868	631.7970	11
14	1389.6679	695.3376	1372.6413	686.8243	1371.6573	686.3323	T	1133.5619	567.2846	1116.5354	558.7713	1115.5514	558.2793	10
15	1517.7264	759.3669	1500.6999	750.8536	1499.7159	750.3616	Q	1032.5143	516.7608	1015.4877	508.2475	1014.5037	507.7555	9
16	1616.7949	808.9011	1599.7683	800.3878	1598.7843	799.8958	V	904.4557	452.7315	887.4291	444.2182	886.4451	443.7262	8
17	1776.8255	888.9164	1759.7990	880.4031	1758.8149	879.9111	C	**805.3873**	403.1973	788.3607	394.6840	787.3767	394.1920	7
18	1904.8841	952.9457	1887.8575	944.4324	1886.8735	943.9404	Q	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	6
19	1975.9212	988.4642	1958.8947	979.9510	1957.9106	979.4590	A	517.2980	259.1527	500.2715	250.6394	499.2875	250.1474	5
20	2104.9638	1052.9855	2087.9372	1044.4723	2086.9532	1043.9803	E	**446.2609**	223.6341	429.2344	215.1208	428.2504	214.6288	4
21	2204.0322	1102.5197	2187.0057	1094.0065	2186.0216	1093.5145	V	317.2183	159.1128	300.1918	150.5995			3
22	2275.0693	1138.0383	2258.0428	1129.5250	2257.0588	1129.0330	A	218.1499	109.5786	**201.1234**	101.0653			2
23							K	**147.1128**	74.0600	130.0863	65.5468			1

Protein band 146 (-Mn): Opa protein

Score: 70 M_r: 28339



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Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

Matched peptides shown in Bold Red

     1 LFSSLLFSSA AQAASVDNGR GPYVQADLTY AAERITHNYP EATGADKGKI
    51 STVSDYFKNI RTHSVQPRLS LGYDFGNWRI AADYTRYRKW NENNSSTKKV
   101 TERINDNNKE TKTEHQENGS FHAASSLGLS AIYDFQISDK FKPYIGARVA
   151 YGHVRHQVNS VNKETITVTP MGGGSIIQGP TSKPAYHESH SIRRLGLGVI
   201 AGVGFDITSN LTLDAGYRYY NWGRLENTRF KTHEASLGMR Y
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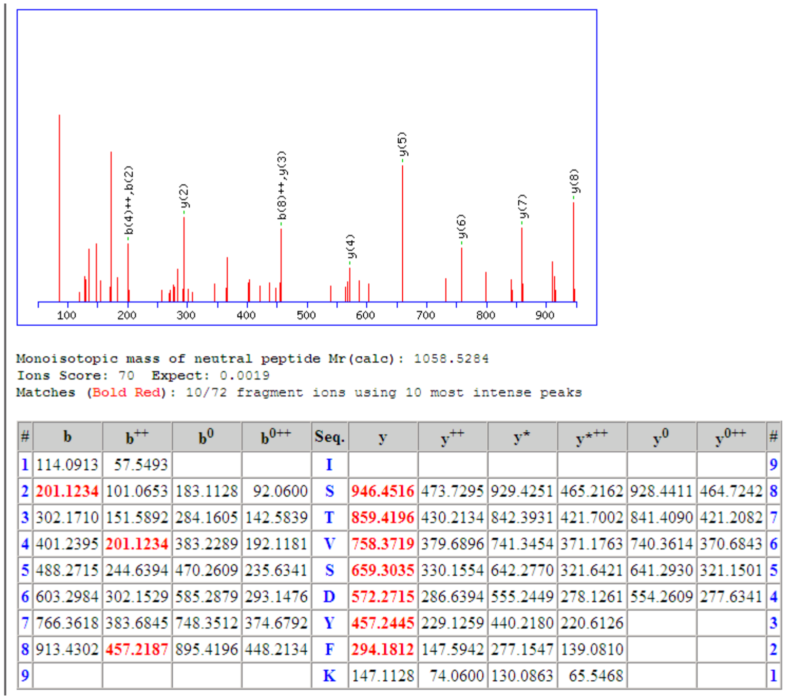

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Monoisotopic mass of neutral peptide Mr(calc): 1058.5284
Ions Score: 70  Expect: 0.0019
Matches (Bold Red): 10/72 fragment ions using 10 most intense peaks
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#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							9
2	**201.1234**	101.0653	183.1128	92.0600	S	**946.4516**	473.7295	929.4251	465.2162	928.4411	464.7242	8
3	302.1710	151.5892	284.1605	142.5839	T	**859.4196**	430.2134	842.3931	421.7002	841.4090	421.2082	7
4	401.2395	**201.1234**	383.2289	192.1181	V	**758.3719**	379.6896	741.3454	371.1763	740.3614	370.6843	6
5	488.2715	244.6394	470.2609	235.6341	S	**659.3035**	330.1554	642.2770	321.6421	641.2930	321.1501	5
6	603.2984	302.1529	585.2879	293.1476	D	**572.2715**	286.6394	555.2449	278.1261	554.2609	277.6341	4
7	766.3618	383.6845	748.3512	374.6792	Y	**457.2445**	229.1259	440.2180	220.6126			3
8	913.4302	**457.2187**	895.4196	448.2134	F	**294.1812**	147.5942	277.1547	139.0810			2
9					K	147.1128	74.0600	130.0863	65.5468			1