

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **DSTLMQLLR**

Found in **Locus_175_Transcript_1/1_Confidence_1.000**, Locus_175_Transcript_1/1_Confidence_1.000

Translated in frame 4 ([nucleic acid sequence](#))

Match to Query 679: 1188.648208 from(595.331380,2+) intensity(51373.5200) scans(4433) rtinseconds(3792.8761) rawscans(sn4433) index(2161)

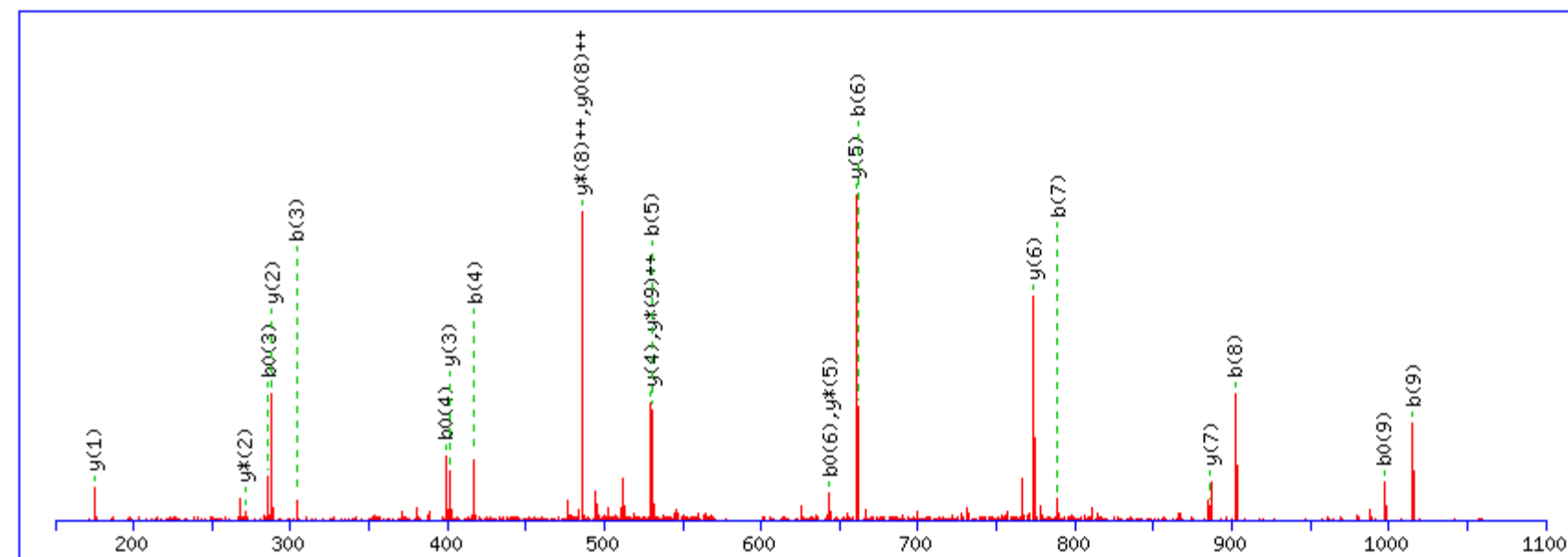
Title: 2162: Scan 4433 (rt=3792.88)

Data file Distiller_dionaeaA-3

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



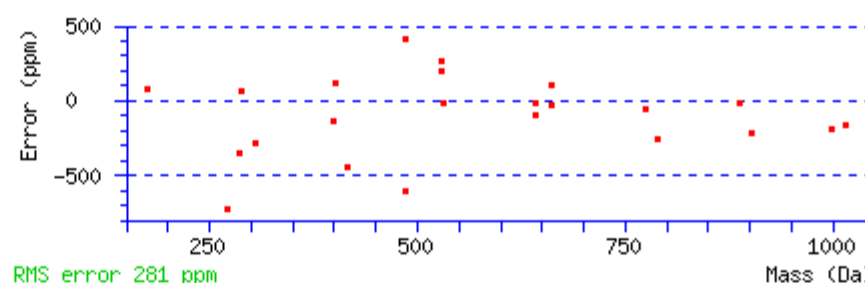
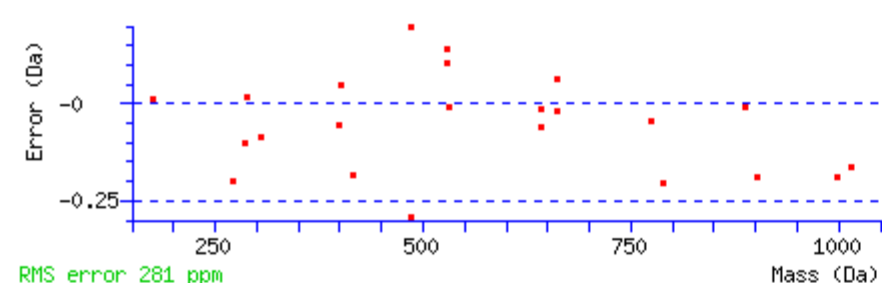
Monoisotopic mass of neutral peptide Mr(calc): 1188.653625

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 56 Expect: 3.9e-005

Matches: 23/82 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.034219	58.520748			98.023654	49.515465	D							10
2	203.066247	102.036761			185.055682	93.031479	S	1074.633978	537.820627	1057.607429	529.307353	1056.623413	528.815345	9
3	304.113926	152.560601			286.103361	143.555319	T	987.601950	494.304613	970.575401	485.791339	969.591385	485.299331	8
4	417.197990	209.102633			399.187425	200.097351	L	886.554271	443.780774	869.527722	435.267499			7
5	530.282054	265.644665			512.271489	256.639383	I	773.470207	387.238742	756.443658	378.725467			6
6	661.322539	331.164908			643.311974	322.159625	M	660.386143	330.696710	643.359594	322.183435			5
7	789.381117	395.194197	772.354568	386.680922	771.370552	386.188914	Q	529.345658	265.176467	512.319109	256.663193			4
8	902.465181	451.736229	885.438632	443.222954	884.454616	442.730946	L	401.287080	201.147178	384.260531	192.633904			3
9	1015.549245	508.278261	998.522696	499.764986	997.538680	499.272978	L	288.203016	144.605146	271.176467	136.091872			2
10							R	175.118952	88.063114	158.092403	79.549840			1



NCBI BLAST search of **DSTLMQLLR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.7	1188.653625	-0.005417	DSTLMQLLR
28.0	1188.650238	-0.002030	YAIQSQLEIR
20.9	1188.657440	-0.009232	SSLSSRAAAAIR
14.5	1188.636337	0.011871	HPDSSHLKLR
11.8	1188.650238	-0.002030	FEAIAEQLLR
8.5	1188.651611	-0.003403	RIFWGGLGQR
8.1	1188.643723	0.004485	MSGWKPKSLR
7.2	1188.650269	-0.002061	DFVGEILLQR
5.7	1188.657669	-0.009461	VMKVWLLVGE
5.7	1188.647095	0.001113	RMPMALSLVR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **ESTLHLVLR**

Found in **Locus_1790_Transcript_1/2_Confidence_1.000**, Locus_1790_Transcript_1/2_Confidence_1.000

Translated in frame 6 ([nucleic acid sequence](#))

Match to Query 318: 1066.610408 from(534.312480,2+) intensity(22522.0350) scans(1524) rtinseconds(1558.3844) rawscans(sn1524) index(532)

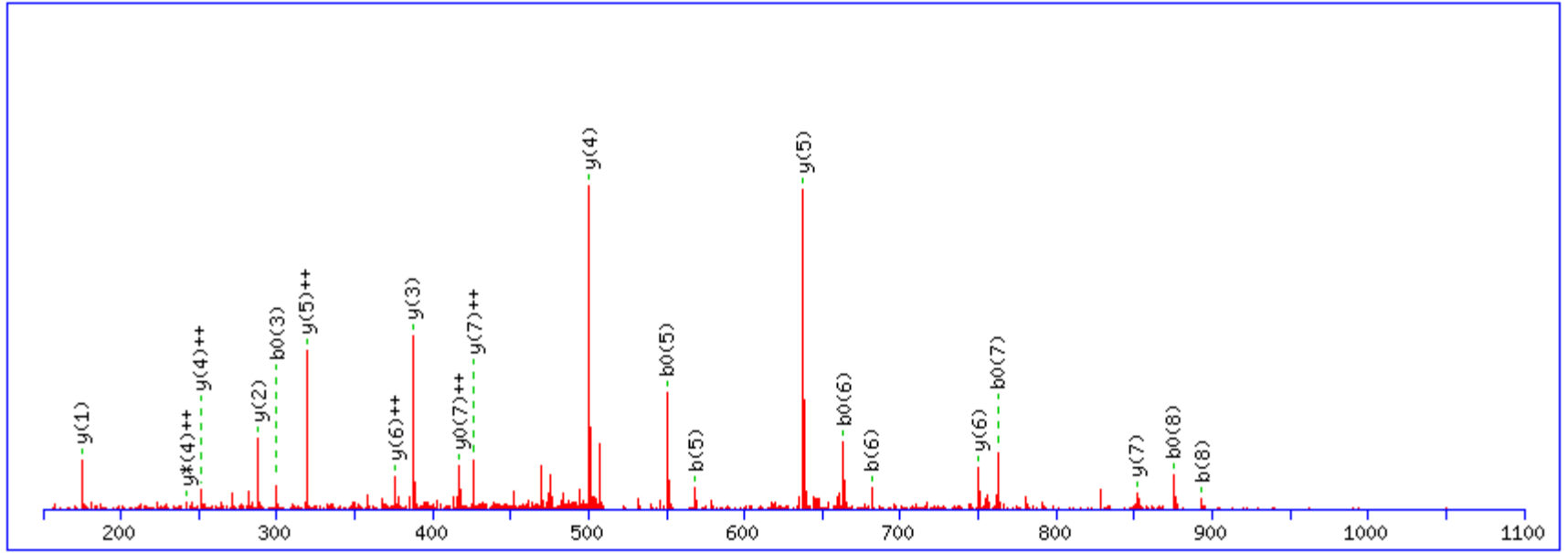
Title: 533: Scan 1524 (rt=25.9731)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



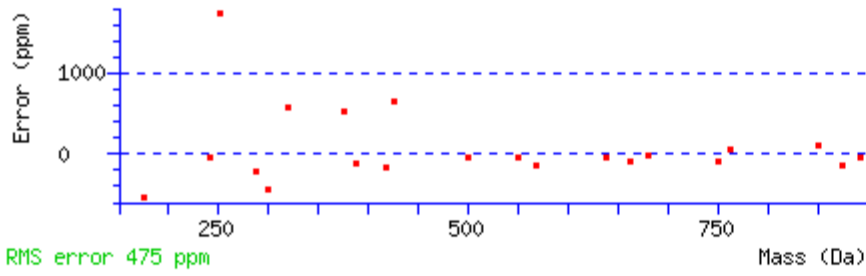
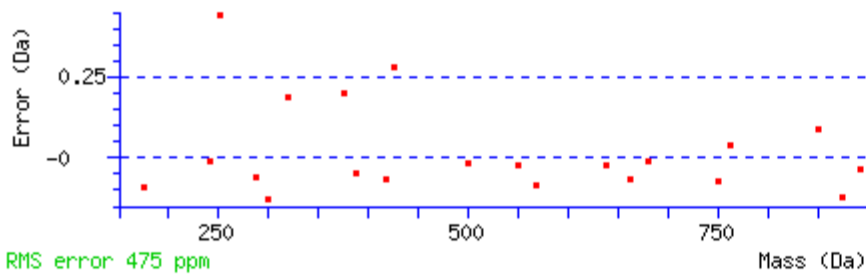
Monoisotopic mass of neutral peptide Mr(calc): 1066.613480

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.00016

Matches : 21/68 fragment ions using 36 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572	112.039304	56.523290	E							9
2	217.081897	109.044586	199.071332	100.039304	S	938.578177	469.792727	921.551628	461.279452	920.567612	460.787444	8
3	318.129576	159.568426	300.119011	150.563144	T	851.546149	426.276713	834.519600	417.763438	833.535584	417.271430	7
4	431.213640	216.110458	413.203075	207.105176	L	750.498470	375.752873	733.471921	367.239599			6
5	568.272552	284.639914	550.261987	275.634632	H	637.414406	319.210841	620.387857	310.697566			5
6	681.356616	341.181946	663.346051	332.176664	L	500.355494	250.681385	483.328945	242.168110			4
7	780.425030	390.716153	762.414465	381.710871	V	387.271430	194.139353	370.244881	185.626078			3
8	893.509094	447.258185	875.498529	438.252903	L	288.203016	144.605146	271.176467	136.091871			2
9					R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [ESTLHLVLR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.6	1066.613480	-0.003072	ESTLHLVLR
15.1	1066.606949	0.003459	NMKGHVLLR
8.3	1066.617508	-0.007100	LPFLPLDPR
0.5	1066.613495	-0.003087	ETVTVLHLR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VTVISTSPSK**

Found in **Locus_187_Transcript_30/39_Confidence_0.191**, Locus_187_Transcript_30/39_Confidence_0.191

Translated in frame 2 ([nucleic acid sequence](#))

Match to Query 697: 1017.572448 from(509.793500,2+) intensity(19286.0470) scans(3564) rtinseconds(3153.0653) rawscans(sn3564) index (1318)

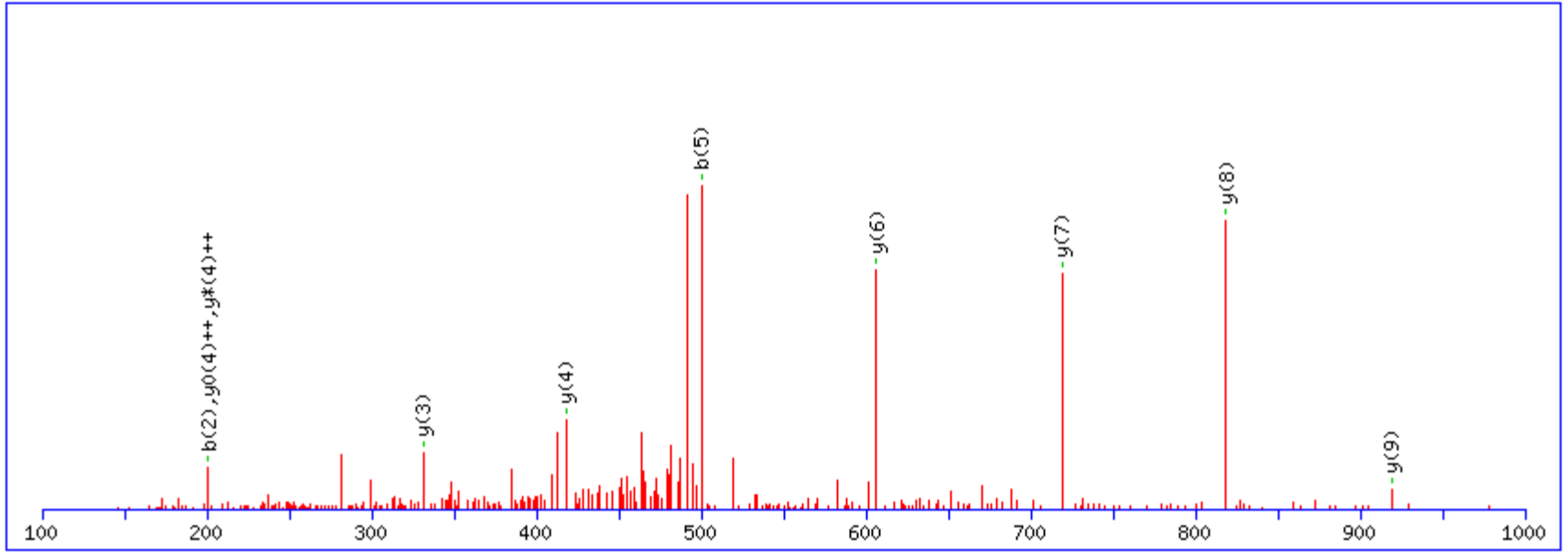
Title: 1319: Scan 3564 (rt=3153.07)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



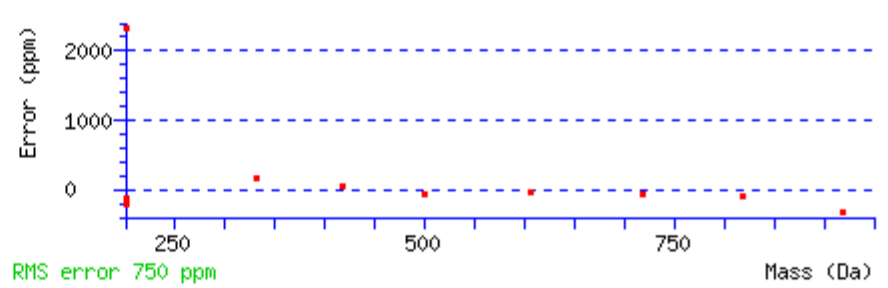
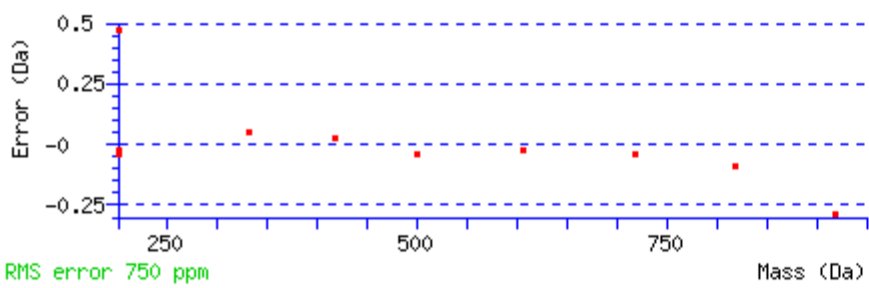
Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1017.570633

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 57 Expect: 2.9e-005

Matches : 10/86 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483			V							10
2	201.123369	101.065322	183.112804	92.060040	T	919.509488	460.258382	902.482939	451.745108	901.498923	451.253100	9
3	300.191783	150.599529	282.181218	141.594247	V	818.461809	409.734543	801.435260	401.221268	800.451244	400.729260	8
4	413.275847	207.141561	395.265282	198.136279	I	719.393395	360.200336	702.366846	351.687061	701.382830	351.195053	7
5	500.307875	250.657576	482.297310	241.652293	S	606.309331	303.658304	589.282782	295.145029	588.298766	294.653021	6
6	601.355554	301.181415	583.344989	292.176133	T	519.277303	260.142290	502.250754	251.629015	501.266738	251.137007	5
7	688.387582	344.697429	670.377017	335.692147	S	418.229624	209.618450	401.203075	201.105175	400.219059	200.613167	4
8	785.440346	393.223811	767.429781	384.218529	P	331.197596	166.102436	314.171047	157.589161	313.187031	157.097153	3
9	872.472374	436.739825	854.461809	427.734543	S	234.144832	117.576054	217.118283	109.062779	216.134267	108.570771	2
10					K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **VTVISTSPSK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
57.3	1017.570633	0.001815	VTVISTSPSK
19.4	1017.575317	-0.002869	SLVIQMRR
8.2	1017.571945	0.000503	LWLSSRTR
5.2	1017.570618	0.001830	EAVVSIVSSK
4.6	1017.568100	0.004348	WIIQLMAK
3.9	1017.579346	-0.006898	LSVKVWMR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TPLTNEAVDTVIK**

Found in **Locus_1944_Transcript_1/1_Confidence_1.000**, Locus_1944_Transcript_1/1_Confidence_1.000

Translated in frame 4 ([nucleic acid sequence](#))

Match to Query 815: 1399.752908 from(700.883730,2+) intensity(52712.7300) scans(1879) rtinseconds(1856.5356) rawscans(sn1879) index(766)

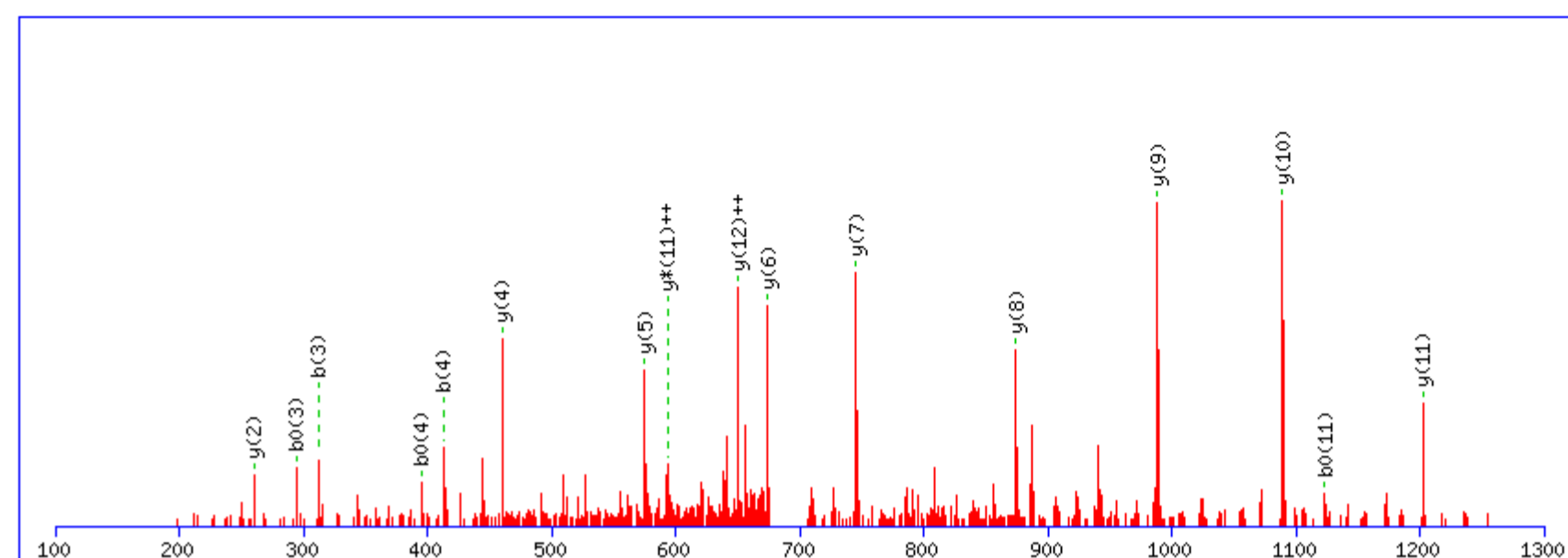
Title: 767: Scan 1879 (rt=1856.54)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



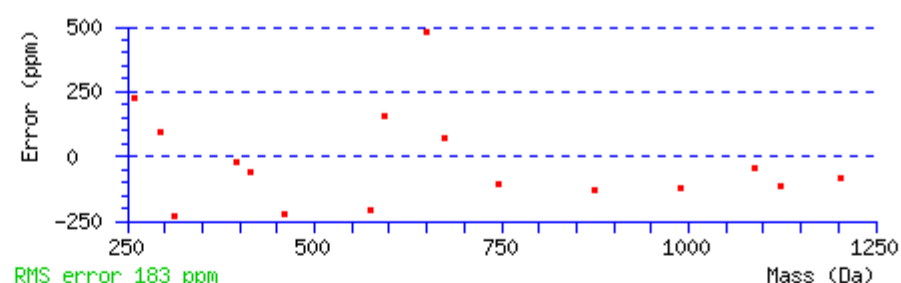
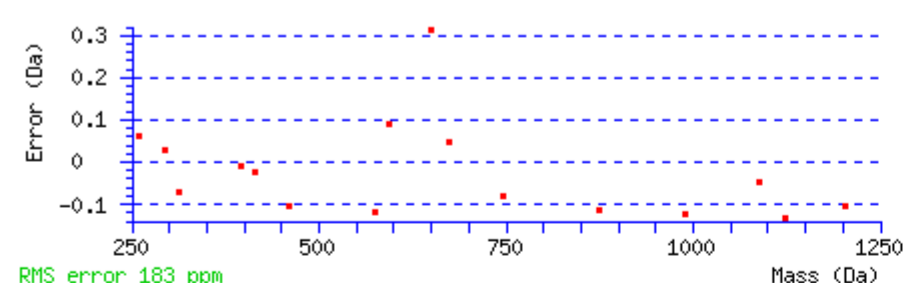
Monoisotopic mass of neutral peptide Mr(calc): 1399.755859

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 72 Expect: 7.6e-007

Matches: 16/130 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	199.107719	100.057497			181.097154	91.052215	P	1299.715459	650.361368	1282.688910	641.848093	1281.704894	641.356085	12
3	312.191783	156.599529			294.181218	147.594247	L	1202.662695	601.834986	1185.636146	593.321711	1184.652130	592.829703	11
4	413.239462	207.123369			395.228897	198.118087	T	1089.578631	545.292954	1072.552082	536.779679	1071.568066	536.287671	10
5	527.282389	264.144833	510.255840	255.631558	509.271824	255.139550	N	988.530952	494.769114	971.504403	486.255840	970.520387	485.763832	9
6	656.324982	328.666129	639.298433	320.152855	638.314417	319.660847	E	874.488025	437.747651	857.461476	429.234376	856.477460	428.742368	8
7	727.362096	364.184686	710.335547	355.671412	709.351531	355.179404	A	745.445432	373.226354	728.418883	364.713079	727.434867	364.221071	7
8	826.430510	413.718893	809.403961	405.205619	808.419945	404.713611	V	674.408318	337.707797	657.381769	329.194523	656.397753	328.702515	6
9	941.457453	471.232365	924.430904	462.719090	923.446888	462.227082	D	575.339904	288.173590	558.313355	279.660316	557.329339	279.168308	5
10	1042.505132	521.756204	1025.478583	513.242930	1024.494567	512.750922	T	460.312961	230.660118	443.286412	222.146844	442.302396	221.654836	4
11	1141.573546	571.290411	1124.546997	562.777137	1123.562981	562.285129	V	359.265282	180.136279	342.238733	171.623004			3
12	1254.657610	627.832443	1237.631061	619.319169	1236.647045	618.827160	I	260.196868	130.602072	243.170319	122.088797			2
13							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **TPLTNEAVDTVIK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.0	1399.755859	-0.002951	TPLTNEAVDTVIK

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TAGAVTPVK**

Found in **Locus_21_Transcript_3/6_Confidence_0.562**, Locus_21_Transcript_3/6_Confidence_0.562

Translated in frame 1 ([nucleic acid sequence](#))

Match to Query 260: 842.489848 from(422.252200,2+) intensity(216952.1800) scans(2595-2613) rtinseconds(2533.3873-2542.7754)

rawscans(sn2595:sn2613) index(729)

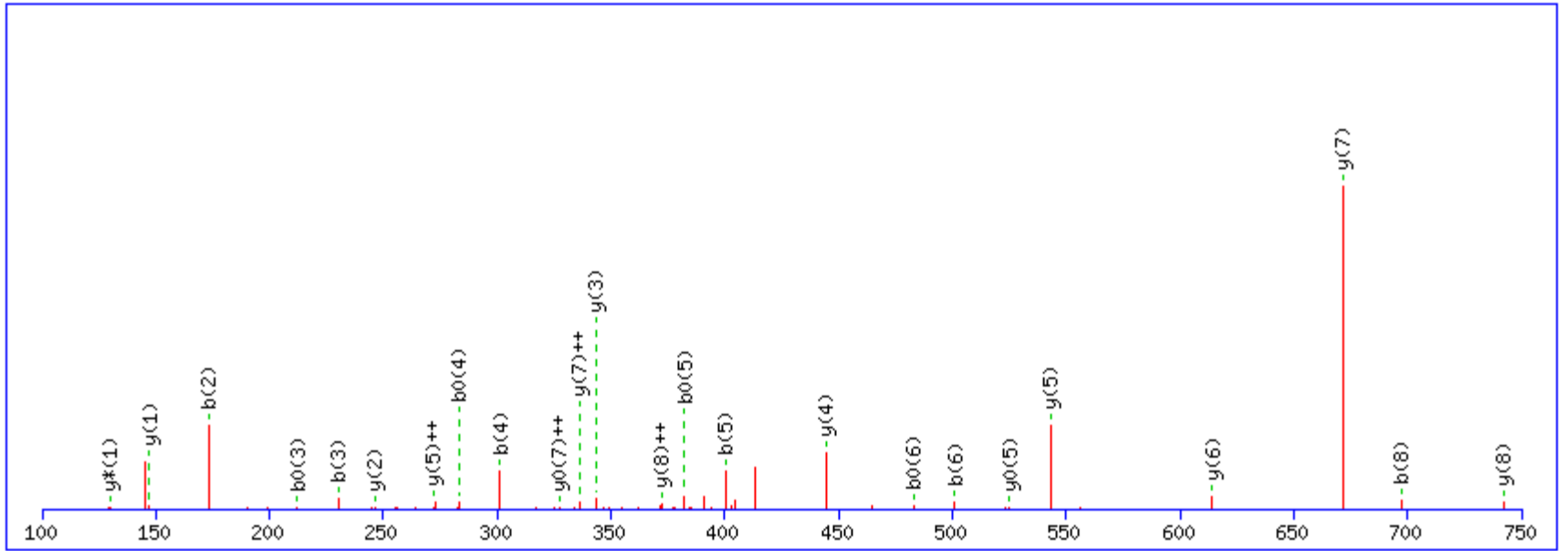
Title: 730: Sum of 2 scans in range 2595 (rt=2533.39) to 2613 (rt=2542.78)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



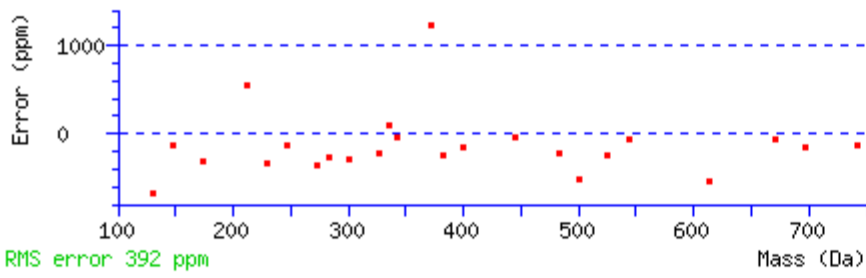
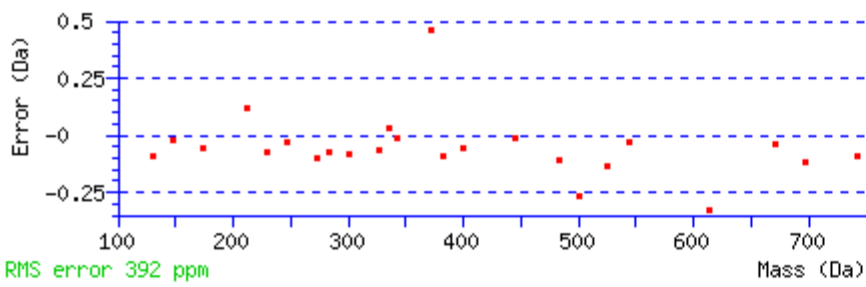
Monoisotopic mass of neutral peptide Mr(calc): 842.486176

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 68 Expect: 2.7e-006

Matches : 24/74 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	173.092069	87.049672	155.081504	78.044390	A	742.445767	371.726522	725.419218	363.213247	724.435202	362.721239	8
3	230.113533	115.560404	212.102968	106.555122	G	671.408653	336.207965	654.382104	327.694690	653.398088	327.202682	7
4	301.150647	151.078961	283.140082	142.073679	A	614.387189	307.697233	597.360640	299.183958	596.376624	298.691950	6
5	400.219061	200.613169	382.208496	191.607886	V	543.350075	272.178676	526.323526	263.665401	525.339510	263.173393	5
6	501.266740	251.137008	483.256175	242.131726	T	444.281661	222.644468	427.255112	214.131194	426.271096	213.639186	4
7	598.319504	299.663390	580.308939	290.658108	P	343.233982	172.120629	326.207433	163.607354			3
8	697.387918	349.197597	679.377353	340.192315	V	246.181218	123.594247	229.154669	115.080972			2
9					K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [TAGAVTPVK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.3	842.486176	0.003672	TAGAVTPVK
9.4	842.486160	0.003688	SGKIDPVK
8.8	842.486145	0.003703	TAAINQII
8.5	842.497391	-0.007543	TARVNVLA
5.8	842.487488	0.002360	YHVRIR
5.5	842.486176	0.003672	QVVSSPVK
5.2	842.497391	-0.007543	TQIVLRN
3.8	842.486160	0.003688	DGIPSVKK
3.3	842.486145	0.003703	LAAGSLSPK
2.5	842.486145	0.003703	GENAIVLK

Mascot Search Results

Peptide View

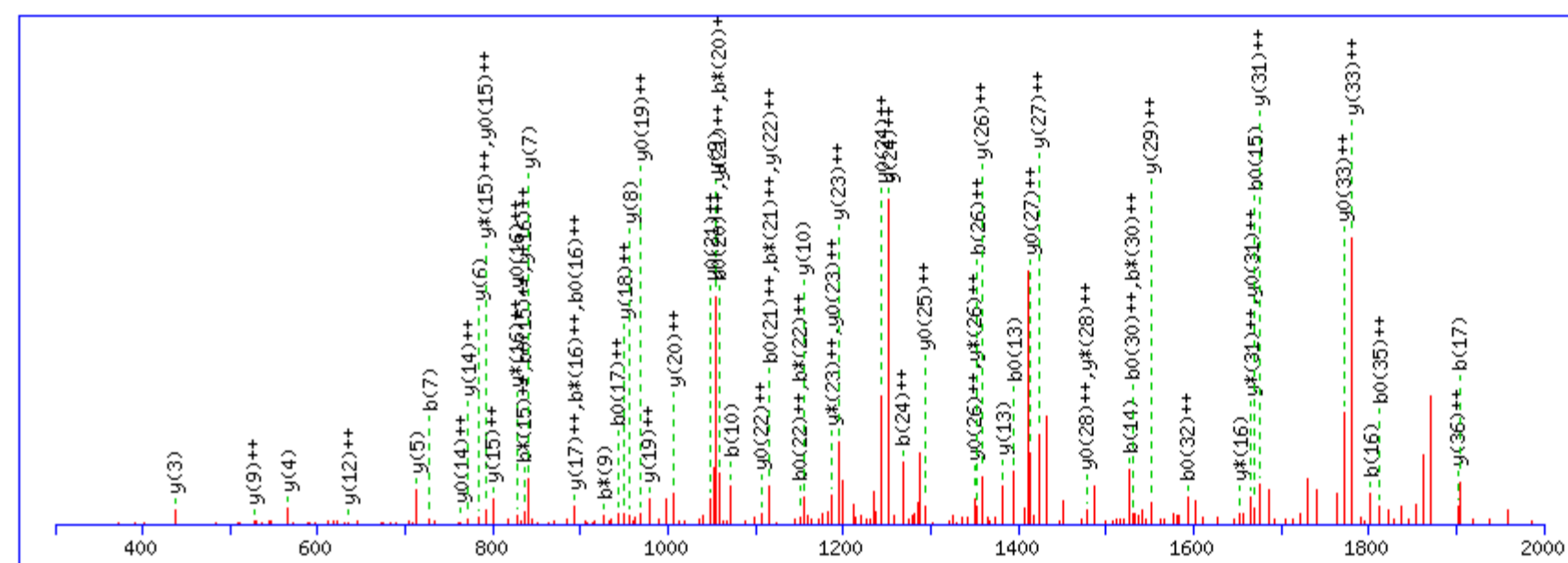
MS/MS Fragmentation of **NGALPDCSEQIVDCDTGGNDAGCNGGTPDGAFFEYVR**
 Found in **Locus_21_Transcript_5/6_Confidence_0.188**, Locus_21_Transcript_5/6_Confidence_0.188
 Translated in frame 1 ([nucleic acid sequence](#))

Match to Query 7272: 3915.604872 from(1306.208900,3+) intensity(843775.8100) scans(7584) rtinseconds(4773.9623) rawscans(sn7584) index(4225)
 Title: 4226: Scan 7584 (rt=4773.96)
 Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

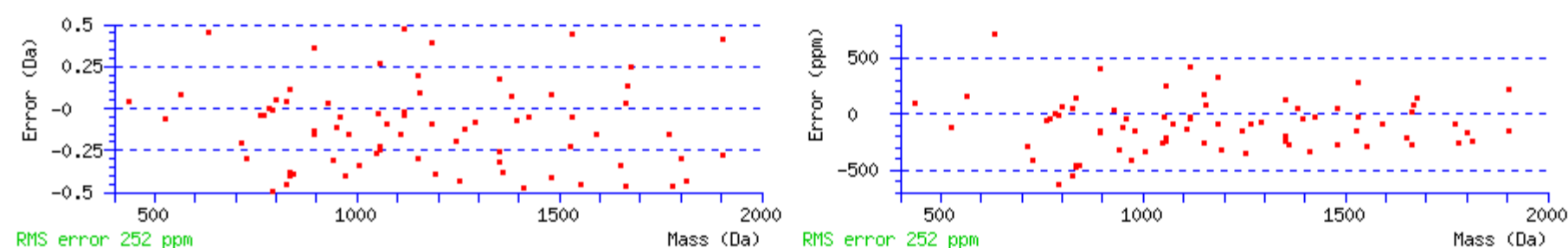
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3915.600708
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Ions Score: 101 Expect: 7.4e-011
 Matches : 74/416 fragment ions using 109 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.050203	58.028740	98.023654	49.515465			N							37
2	172.071667	86.539471	155.045118	78.026197			G	3802.565013	1901.786144	3785.538464	1893.272870	3784.554448	1892.780862	36
3	243.108781	122.058028	226.082232	113.544754			A	3745.543549	1873.275412	3728.517000	1864.762138	3727.532984	1864.270130	35
4	356.192845	178.600060	339.166296	170.086786			L	3674.506435	1837.756855	3657.479886	1829.243581	3656.495870	1828.751573	34
5	453.245609	227.126443	436.219060	218.613168			P	3561.422371	1781.214823	3544.395822	1772.701549	3543.411806	1772.209541	33
6	568.272552	284.639914	551.246003	276.126640	550.261987	275.634632	D	3464.369607	1732.688441	3447.343058	1724.175167	3446.359042	1723.683159	32
7	728.303201	364.655239	711.276652	356.141964	710.292636	355.649956	C	3349.342664	1675.174970	3332.316115	1666.661695	3331.332099	1666.169687	31
8	815.335229	408.171253	798.308680	399.657978	797.324664	399.165970	S	3189.312015	1595.159645	3172.285466	1586.646371	3171.301450	1586.154363	30
9	944.377822	472.692549	927.351273	464.179275	926.367257	463.687267	E	3102.279987	1551.643631	3085.253438	1543.130357	3084.269422	1542.638349	29
10	1072.436400	536.721838	1055.409851	528.208564	1054.425835	527.716556	Q	2973.237394	1487.122335	2956.210845	1478.609060	2955.226829	1478.117052	28
11	1200.494978	600.751127	1183.468429	592.237853	1182.484413	591.745844	Q	2845.178816	1423.093046	2828.152267	1414.579771	2827.168251	1414.087763	27
12	1313.579042	657.293159	1296.552493	648.779884	1295.568477	648.287876	I	2717.120238	1359.063757	2700.093689	1350.550482	2699.109673	1350.058474	26
13	1412.647456	706.827366	1395.620907	698.314092	1394.636891	697.822083	V	2604.036174	1302.521725	2587.009625	1294.008450	2586.025609	1293.516442	25
14	1527.674399	764.340838	1510.647850	755.827563	1509.663834	755.335555	D	2504.967760	1252.987518	2487.941211	1244.474243	2486.957195	1243.982235	24
15	1687.705048	844.356162	1670.678499	835.842888	1669.694483	835.350880	C	2389.940817	1195.474046	2372.914268	1186.960772	2371.930252	1186.468764	23
16	1802.731991	901.869634	1785.705442	893.356359	1784.721426	892.864351	D	2229.910168	1115.458722	2212.883619	1106.945447	2211.899603	1106.453439	22
17	1903.779670	952.393473	1886.753121	943.880199	1885.769105	943.388191	T	2114.883225	1057.945250	2097.856676	1049.431976	2096.872660	1048.939968	21
18	1960.801134	980.904205	1943.774585	972.390931	1942.790569	971.898923	G	2013.835546	1007.421411	1996.808997	998.908136	1995.824981	998.416128	20
19	2017.822598	1009.414937	2000.796049	1000.901663	1999.812033	1000.409655	G	1956.814082	978.910679	1939.787533	970.397404	1938.803517	969.905396	19
20	2131.865525	1066.436400	2114.838976	1057.923126	2113.854960	1057.431118	N	1899.792618	950.399947	1882.766069	941.886672	1881.782053	941.394664	18
21	2246.892468	1123.949872	2229.865919	1115.436597	2228.881903	1114.944589	D	1785.749691	893.378483	1768.723142	884.865209	1767.739126	884.373201	17
22	2317.929582	1159.468429	2300.903033	1150.955154	2299.919017	1150.463146	A	1670.722748	835.865012	1653.696199	827.351737	1652.712183	826.859729	16
23	2374.951046	1187.979161	2357.924497	1179.465886	2356.940481	1178.973878	G	1599.685634	800.346455	1582.659085	791.833180	1581.675069	791.341172	15
24	2534.981695	1267.994485	2517.955146	1259.481211	2516.971130	1258.989203	C	1542.664170	771.835723	1525.637621	763.322448	1524.653605	762.830440	14
25	2649.024622	1325.015949	2631.998073	1316.502674	2631.014057	1316.010666	N	1382.633521	691.820398	1365.606972	683.307124	1364.622956	682.815116	13
26	2706.046086	1353.526681	2689.019537	1345.013406	2688.035521	1344.521398	G	1268.590594	634.798935	1251.564045	626.285660	1250.580029	625.793652	12
27	2763.067550	1382.037413	2746.041001	1373.524138	2745.056985	1373.032130	G	1211.569130	606.288203	1194.542581	597.774928	1193.558565	597.282920	11
28	2864.115229	1432.561252	2847.088680	1424.047978	2846.104664	1423.555970	T	1154.547666	577.777471	1137.521117	569.264196	1136.537101	568.772188	10
29	2961.167993	1481.087634	2944.141444	1472.574360	2943.157428	1472.082352	P	1053.499987	527.253631	1036.473438	518.740357	1035.489422	518.248349	9
30	3076.194936	1538.601106	3059.168387	1530.087831	3058.184371	1529.595823	D	956.447223	478.727249	939.420674	470.213975	938.436658	469.721967	8
31	3133.216400	1567.111838	3116.189851	1558.598563	3115.205835	1558.106555	G	841.420280	421.213778	824.393731	412.700504	823.409715	412.208496	7
32	3204.253514	1602.630395	3187.226965	1594.117120	3186.242949	1593.625112	A	784.398816	392.703046	767.372267	384.189772	766.388251	383.697764	6
33	3351.321928	1676.164602	3334.295379	1667.651327	3333.311363	1667.159319	F	713.361702	357.184489	696.335153	348.671214	695.351137	348.179206	5
34	3480.364521	1740.685898	3463.337972	1732.172624	3462.353956	1731.680616	E	566.293288	283.650282	549.266739	275.137008	548.282723	274.645000	4
35	3643.427850	1822.217563	3626.401301	1813.704288	3625.417285	1813.212280	Y	437.250695	219.128985	420.224146	210.615711			3
36	3742.496264	1871.751770	3725.469715	1863.238495	3724.485699	1862.746487	V	274.187366	137.597321	257.160817	129.084046			2
37							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **NGALPDCSEQIVDCDTGGNDAGCNGGTPDGAFFEYVR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
101.3	3915.600708	0.004164	NGALPDCSEQIVDCDTGGNDAGCNGGTPDGAFFEYVR

Mascot: <http://www.matrixscience.com/>

Peptide View

MS/MS Fragmentation of **IIVYDLAHQR**

Found in **Locus_3385_Transcript_1/2_Confidence_1.000**, Locus_3385_Transcript_1/2_Confidence_1.000

Translated in frame 2 ([nucleic acid sequence](#))

Match to Query 497: 1226.673828 from(614.344190,2+) intensity(11763.6930) scans(1348) rtinseconds(1379.601) rawscans(sn1348) index(425)

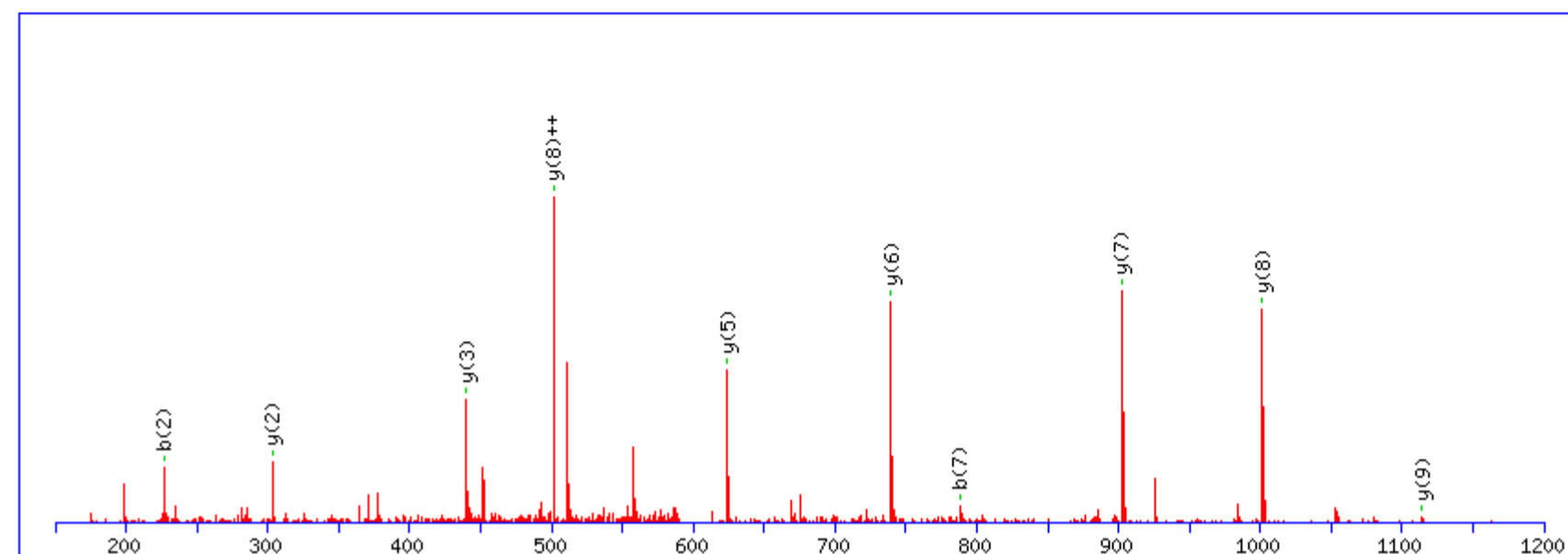
Title: 426: Scan 1348 (rt=22.9934)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



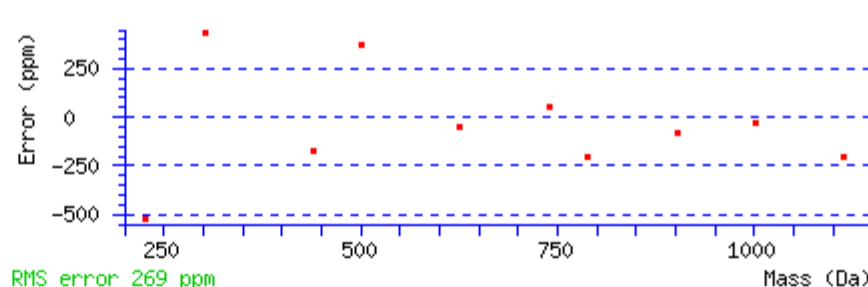
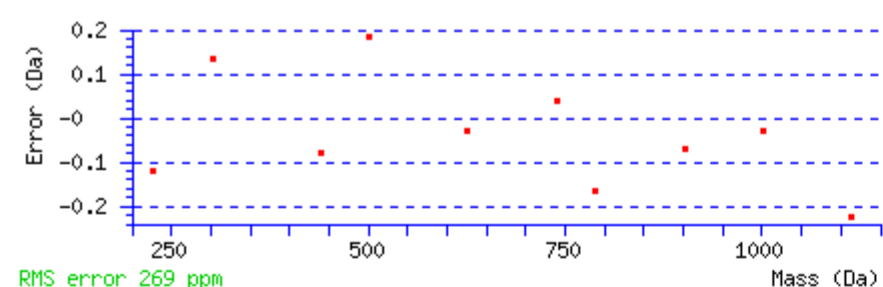
Monoisotopic mass of neutral peptide Mr(calc): 1226.677139

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 68 Expect: 2.3e-006

Matches : 10/74 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							10
2	227.175404	114.091340					I	1114.600370	557.803823	1097.573821	549.290549	1096.589805	548.798541	9
3	326.243818	163.625547					V	1001.516306	501.261791	984.489757	492.748516	983.505741	492.256509	8
4	489.307147	245.157211					Y	902.447892	451.727584	885.421343	443.214310	884.437327	442.722302	7
5	604.334090	302.670683			586.323525	293.665401	D	739.384563	370.195920	722.358014	361.682645	721.373998	361.190637	6
6	717.418154	359.212715			699.407589	350.207433	L	624.357620	312.682448	607.331071	304.169174			5
7	788.455268	394.731272			770.444703	385.725990	A	511.273556	256.140416	494.247007	247.627141			4
8	925.514180	463.260728			907.503615	454.255446	H	440.236442	220.621859	423.209893	212.108584			3
9	1053.572758	527.290017	1036.546209	518.776743	1035.562193	518.284735	Q	303.177530	152.092403	286.150981	143.579128			2
10							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **IIVYDLAHQR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.5	1226.677139	-0.003311	IIVYDLAHQR
14.2	1226.673126	0.000702	LLPDTRTQQR
5.3	1226.680511	-0.006683	LIVMVSHKER
4.9	1226.677124	-0.003296	ILNNAPAPVYR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **HGTCSESVLNEHAYFQAALSLK**

Found in **Locus_3837_Transcript_1/1_Confidence_1.000**, Locus_3837_Transcript_1/1_Confidence_1.000

Translated in frame 5 ([nucleic acid sequence](#))

Match to Query 5658: 2461.178892 from(821.400240,3+) intensity(206077.1600) scans(7951) rtinseconds(4933.523) rawscans(sn7951) index(4481)

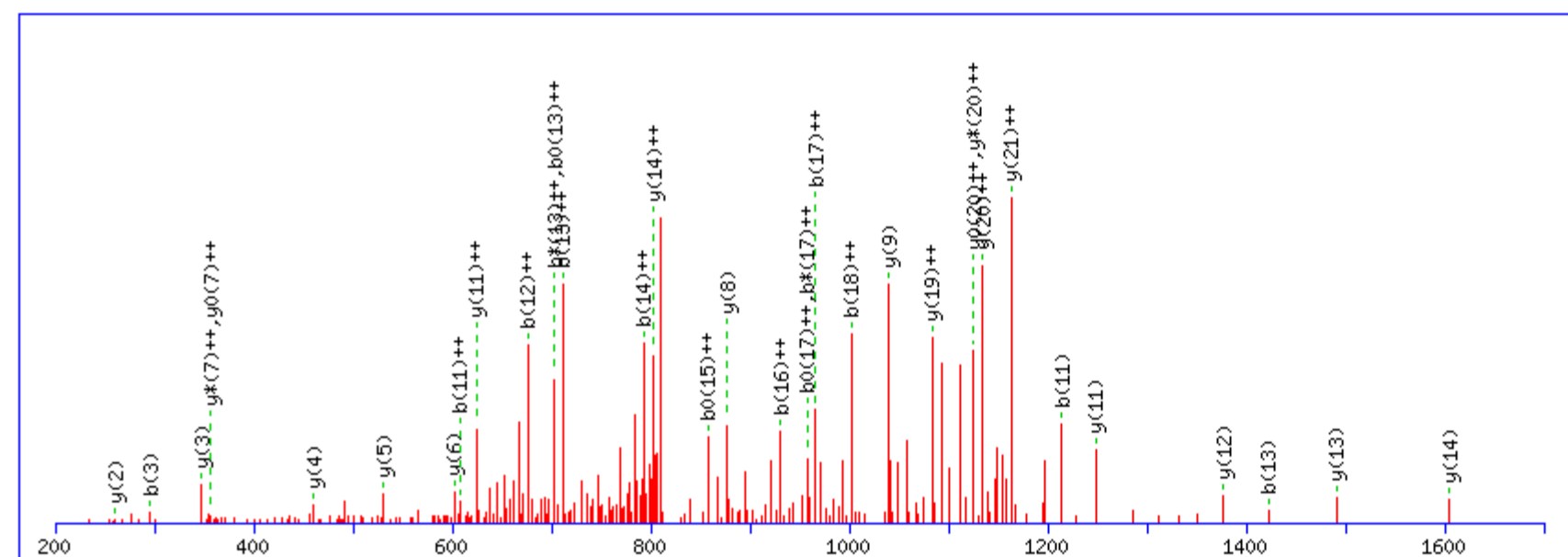
Title: 4482: Scan 7951 (rt=4933.52)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches Label matches used for scoring



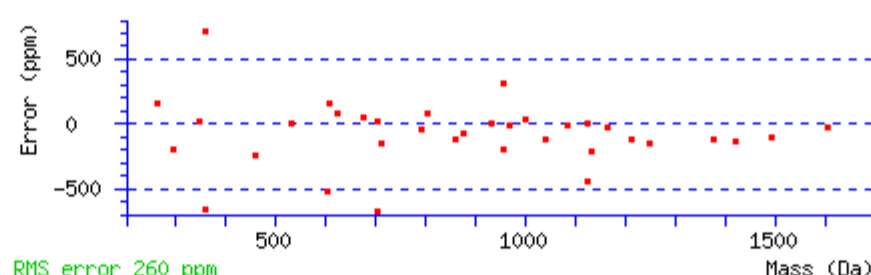
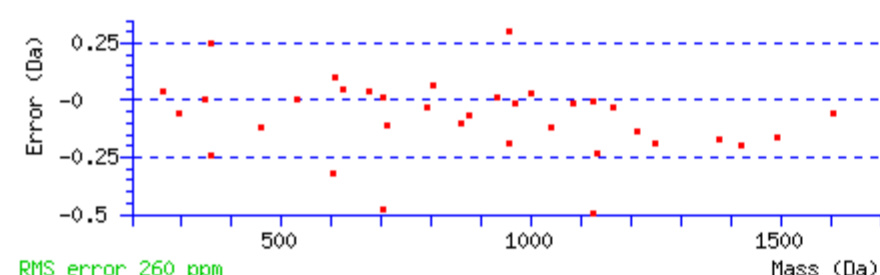
Monoisotopic mass of neutral peptide Mr(calc): 2461.169586

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 84 Expect: 2.3e-008

Matches : 35/226 fragment ions using 38 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	138.066188	69.536732					H							22
2	195.087652	98.047464					G	2325.117974	1163.062625	2308.091425	1154.549350	2307.107409	1154.057342	21
3	296.135331	148.571304			278.124766	139.566021	T	2268.096510	1134.551893	2251.069961	1126.038618	2250.085945	1125.546610	20
4	456.165980	228.586628			438.155415	219.581346	C	2167.048831	1084.028053	2150.022282	1075.514779	2149.038266	1075.022771	19
5	543.198008	272.102642			525.187443	263.097360	S	2007.018182	1004.012729	1989.991633	995.499455	1989.007617	995.007447	18
6	672.240601	336.623939			654.230036	327.618656	E	1919.986154	960.496715	1902.959605	951.983441	1901.975589	951.491433	17
7	759.272629	380.139953			741.262064	371.134670	S	1790.943561	895.975419	1773.917012	887.462144	1772.932996	886.970136	16
8	858.341043	429.674160			840.330478	420.668877	V	1703.911533	852.459405	1686.884984	843.946130	1685.900968	843.454122	15
9	971.425107	486.216192			953.414542	477.210909	L	1604.843119	802.925198	1587.816570	794.411923	1586.832554	793.919915	14
10	1085.468034	543.237655	1068.441485	534.724381	1067.457469	534.232373	N	1491.759055	746.383166	1474.732506	737.869891	1473.748490	737.377883	13
11	1214.510627	607.758951	1197.484078	599.245677	1196.500062	598.753669	E	1377.716128	689.361702	1360.689579	680.848428	1359.705563	680.356420	12
12	1351.569539	676.288407	1334.542990	667.775133	1333.558974	667.283125	H	1248.673535	624.840406	1231.646986	616.327131	1230.662970	615.835123	11
13	1422.606653	711.806964	1405.580104	703.293690	1404.596088	702.801682	A	1111.614623	556.310950	1094.588074	547.797675	1093.604058	547.305667	10
14	1585.669982	793.338629	1568.643433	784.825355	1567.659417	784.333346	Y	1040.577509	520.792393	1023.550960	512.279118	1022.566944	511.787110	9
15	1732.738396	866.872836	1715.711847	858.359562	1714.727831	857.867553	F	877.514180	439.260728	860.487631	430.747454	859.503615	430.255446	8
16	1860.796974	930.902125	1843.770425	922.388851	1842.786409	921.896843	Q	730.445766	365.726521	713.419217	357.213247	712.435201	356.721239	7
17	1931.834088	966.420682	1914.807539	957.907408	1913.823523	957.415400	A	602.387188	301.697232	585.360639	293.183958	584.376623	292.691950	6
18	2002.871202	1001.939239	1985.844653	993.425965	1984.860637	992.933957	A	531.350074	266.178675	514.323525	257.665401	513.339509	257.173393	5
19	2115.955266	1058.481271	2098.928717	1049.967996	2097.944701	1049.475988	L	460.312960	230.660118	443.286411	222.146844	442.302395	221.654836	4
20	2202.987294	1101.997285	2185.960745	1093.484010	2184.976729	1092.992002	S	347.228896	174.118086	330.202347	165.604812	329.218331	165.112804	3
21	2316.071358	1158.539317	2299.044809	1150.026042	2298.060793	1149.534035	L	260.196868	130.602072	243.170319	122.088798			2
22							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [HGTCSESVLNEHAYFQAALSLK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.1	2461.169586	0.009306	HGTCSESVLNEHAYFQAALSLK

Mascot: <http://www.matrixscience.com/>

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VCYVDCDSPICK**

Found in **Locus_448_Transcript_1/1_Confidence_1.000**, Locus_448_Transcript_1/1_Confidence_1.000

Translated in frame 3 ([nucleic acid sequence](#))

Match to Query 2528: 1514.622848 from(758.318700,2+) intensity(41221.7730) scans(5069) rtinseconds(3792.7253) rawscans(sn5069) index(2491)

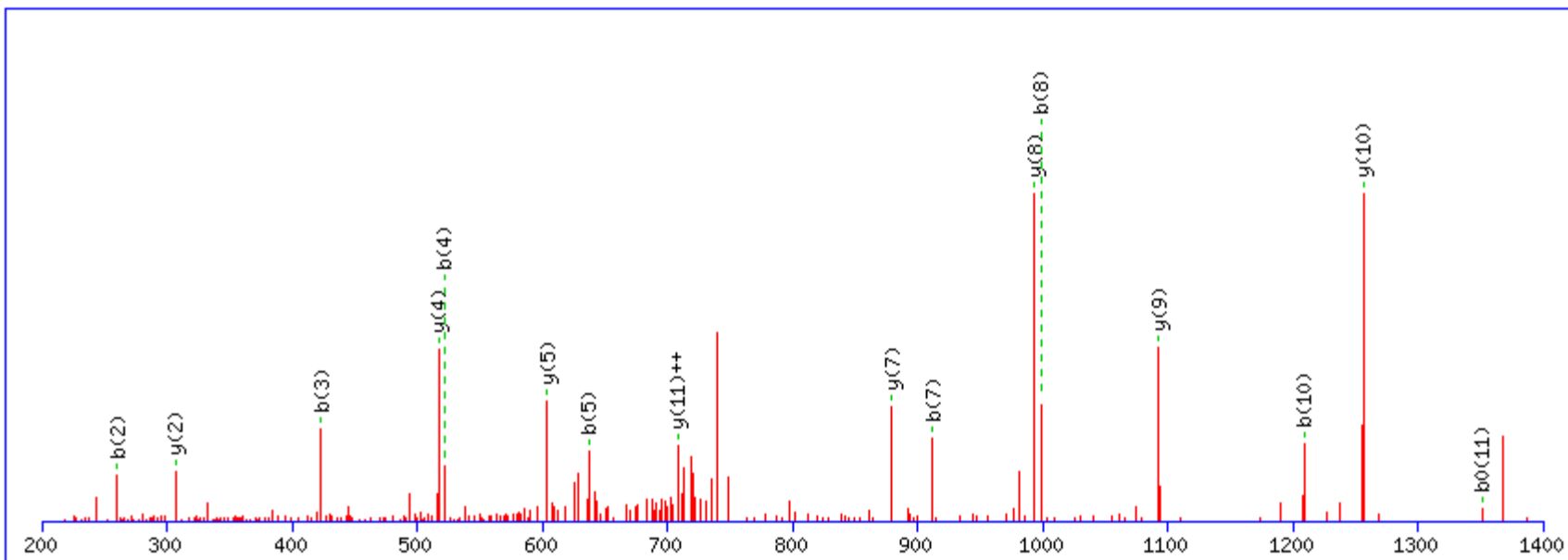
Title: 2492: Scan 5069 (rt=3792.73)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



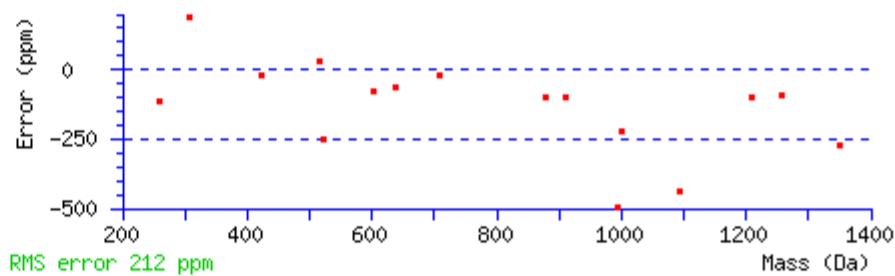
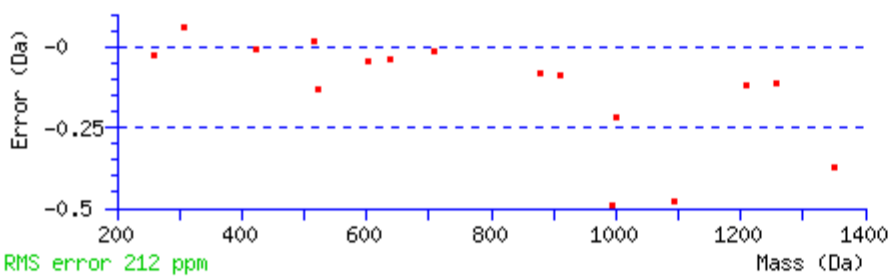
Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1514.620392

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 2.7e-005

Matches : 16/94 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483			V							12
2	260.106339	130.556807			C	1416.559236	708.783256	1399.532687	700.269981	1398.548671	699.777973	11
3	423.169668	212.088472			Y	1256.528587	628.767932	1239.502038	620.254657	1238.518022	619.762649	10
4	522.238082	261.622679			V	1093.465258	547.236267	1076.438709	538.722993	1075.454693	538.230984	9
5	637.265025	319.136151	619.254460	310.130868	D	994.396844	497.702060	977.370295	489.188785	976.386279	488.696777	8
6	797.295674	399.151475	779.285109	390.146193	C	879.369901	440.188588	862.343352	431.675314	861.359336	431.183306	7
7	912.322617	456.664947	894.312052	447.659664	D	719.339252	360.173264	702.312703	351.659989	701.328687	351.167981	6
8	999.354645	500.180961	981.344080	491.175678	S	604.312309	302.659792	587.285760	294.146518	586.301744	293.654510	5
9	1096.407409	548.707342	1078.396844	539.702060	P	517.280281	259.143779	500.253732	250.630504			4
10	1209.491473	605.249374	1191.480908	596.244092	I	420.227517	210.617396	403.200968	202.104122			3
11	1369.522122	685.264699	1351.511557	676.259416	C	307.143453	154.075365	290.116904	145.562090			2
12					K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [VCYVDCDSPICK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
51.1	1514.620392	0.002456	VCYVDCDSPICK

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SPLNTVLR**

Found in **Locus_5180_Transcript_1/1_Confidence_1.000**, Locus_5180_Transcript_1/1_Confidence_1.000

Translated in frame 4 ([nucleic acid sequence](#))

Match to Query 355: 898.525328 from(450.269940,2+) intensity(122257.3900) scans(5573-5604) rtinseconds(4218.6691-4234.9702) rawscans(sn5573:sn5604) index (2757)

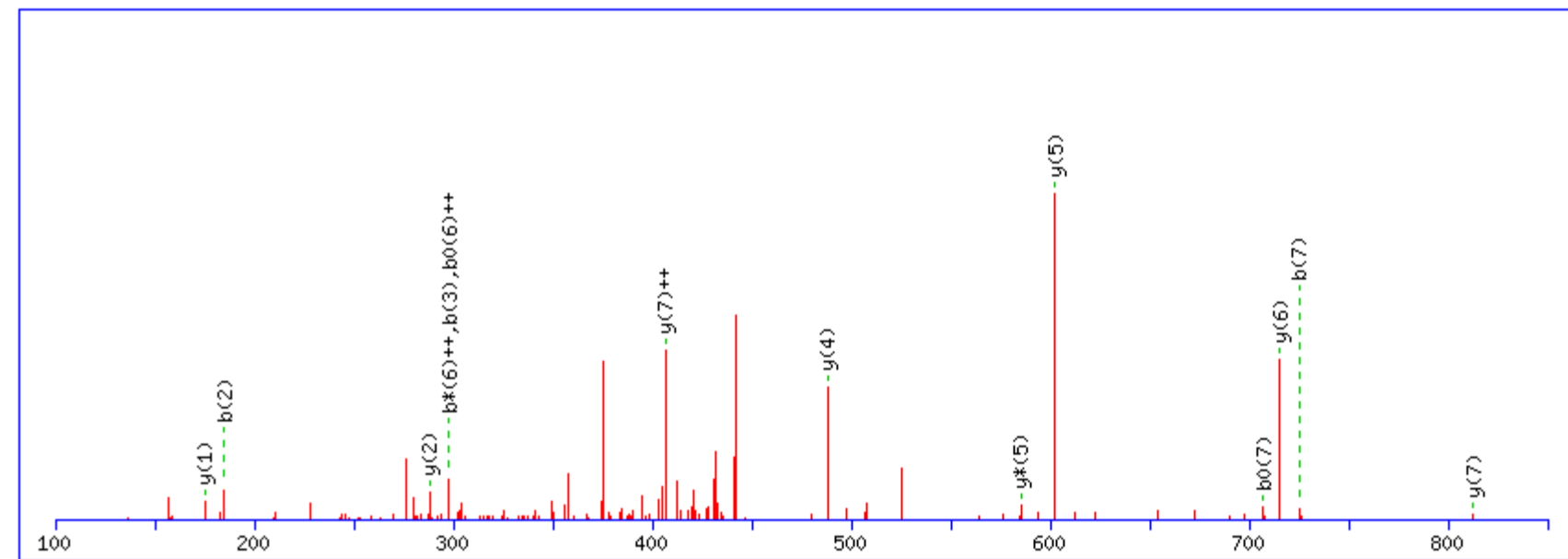
Title: 2758: Sum of 2 scans in range 5573 (rt=4218.67) to 5604 (rt=4234.97)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



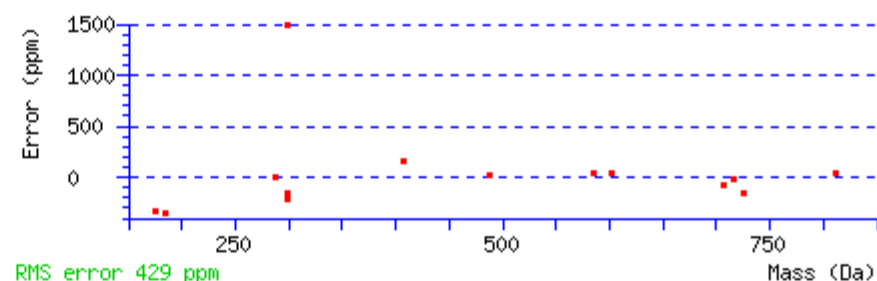
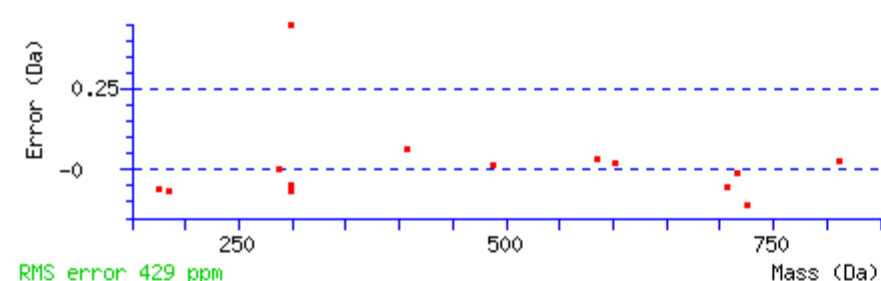
Monoisotopic mass of neutral peptide Mr(calc): 898.523605

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 52 Expect: 4.9e-005

Matches : 14/72 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							8
2	185.092068	93.049672			167.081503	84.044389	P	812.498864	406.753070	795.472315	398.239796	794.488299	397.747788	7
3	298.176132	149.591704			280.165567	140.586422	L	715.446100	358.226688	698.419551	349.713414	697.435535	349.221406	6
4	412.219059	206.613168	395.192510	198.099893	394.208494	197.607885	N	602.362036	301.684656	585.335487	293.171382	584.351471	292.679374	5
5	513.266738	257.137007	496.240189	248.623733	495.256173	248.131725	T	488.319109	244.663192	471.292560	236.149918	470.308544	235.657910	4
6	612.335152	306.671214	595.308603	298.157940	594.324587	297.665932	V	387.271430	194.139353	370.244881	185.626078			3
7	725.419216	363.213246	708.392667	354.699972	707.408651	354.207964	L	288.203016	144.605146	271.176467	136.091871			2
8							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [SPLNTVLR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.3	898.523605	0.001723	SPLNTVLR
33.2	898.523590	0.001738	SNILPSLR
23.4	898.523590	0.001738	LPSNSLLR
21.0	898.523590	0.001738	SPKGIEIR
18.5	898.523590	0.001738	SSPLINLR
17.9	898.523590	0.001738	GKPELSLR
17.0	898.530991	-0.005663	SPIVMPKK
16.7	898.523590	0.001738	LPSSLNLR
15.2	898.523605	0.001723	PSIVSLQR
14.6	898.523605	0.001723	SSLLVGPAR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AGLQFPVGR**

Found in **Locus_522_Transcript_1/2_Confidence_1.000**, Locus_522_Transcript_1/2_Confidence_1.000

Translated in frame 6 ([nucleic acid sequence](#))

Match to Query 490: 943.525868 from(472.770210,2+) intensity(33369.2340) scans(5754) rtinseconds(4315.7374) rawscans(sn5754) index(2896)

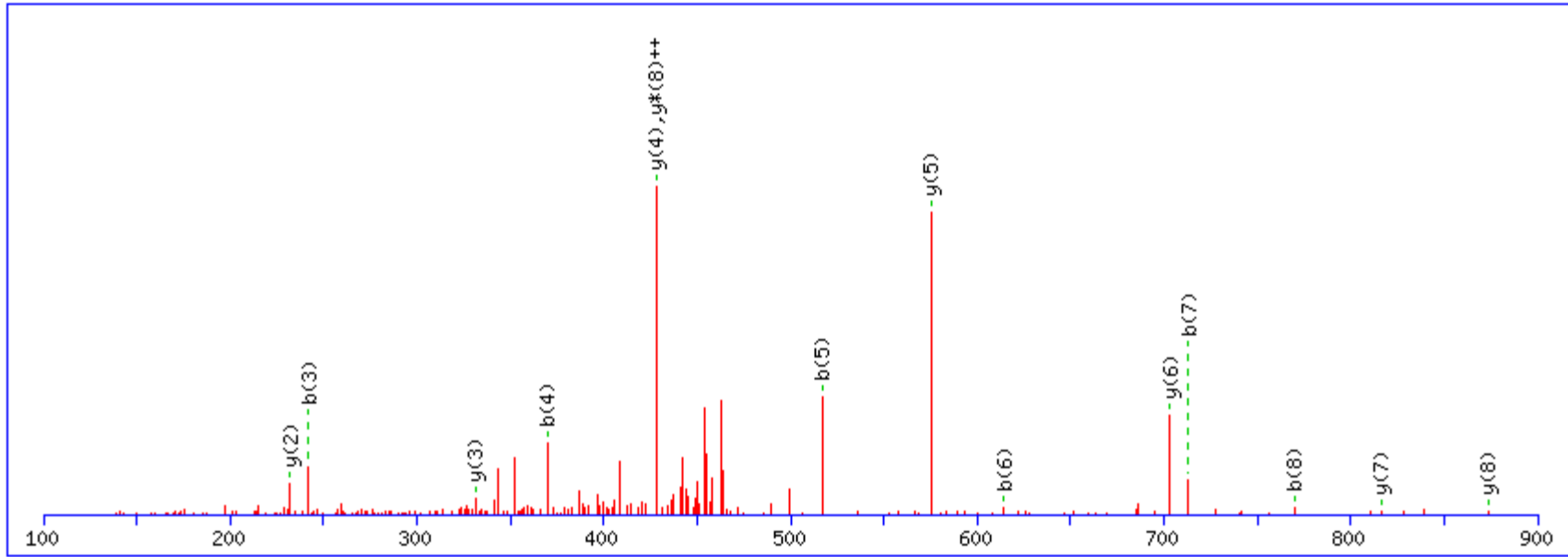
Title: 2897: Scan 5754 (rt=4315.74)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



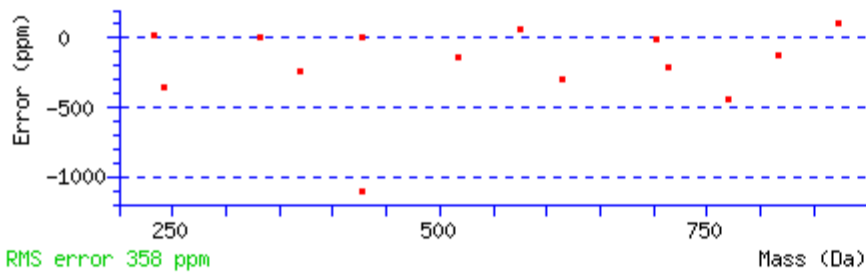
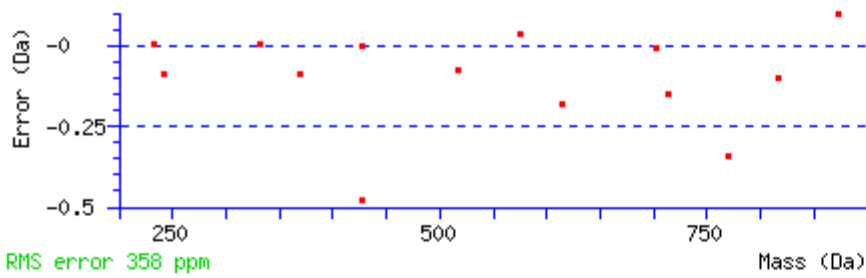
Monoisotopic mass of neutral peptide Mr(calc): 943.523956

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 70 Expect: 2.2e-006

Matches : 14/58 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	72.044390	36.525833			A					9
2	129.065854	65.036565			G	873.494114	437.250695	856.467565	428.737421	8
3	242.149918	121.578597			L	816.472650	408.739963	799.446101	400.226689	7
4	370.208496	185.607886	353.181947	177.094612	Q	703.388586	352.197931	686.362037	343.684657	6
5	517.276910	259.142093	500.250361	250.628819	F	575.330008	288.168642	558.303459	279.655368	5
6	614.329674	307.668475	597.303125	299.155201	P	428.261594	214.634435	411.235045	206.121160	4
7	713.398088	357.202682	696.371539	348.689408	V	331.208830	166.108053	314.182281	157.594778	3
8	770.419552	385.713414	753.393003	377.200140	G	232.140416	116.573846	215.113867	108.060571	2
9					R	175.118952	88.063114	158.092403	79.549839	1



NCBI BLAST search of [AGLQFPVGR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.5	943.523956	0.001912	AGLQFPVGR
15.9	943.535172	-0.009304	LQFQRPR
15.3	943.519913	0.005955	AIKGNQTGR
13.8	943.531143	-0.005275	ASTTRPRR
12.2	943.533813	-0.007945	QIGEKIEK
10.4	943.519928	0.005940	GSSSVVRPR
10.0	943.527313	-0.001445	QMLLQVGR
8.7	943.519913	0.005955	AGLGSQQKR
8.0	943.519913	0.005955	LQDLRSGR
7.4	943.519913	0.005955	SGILGGERR

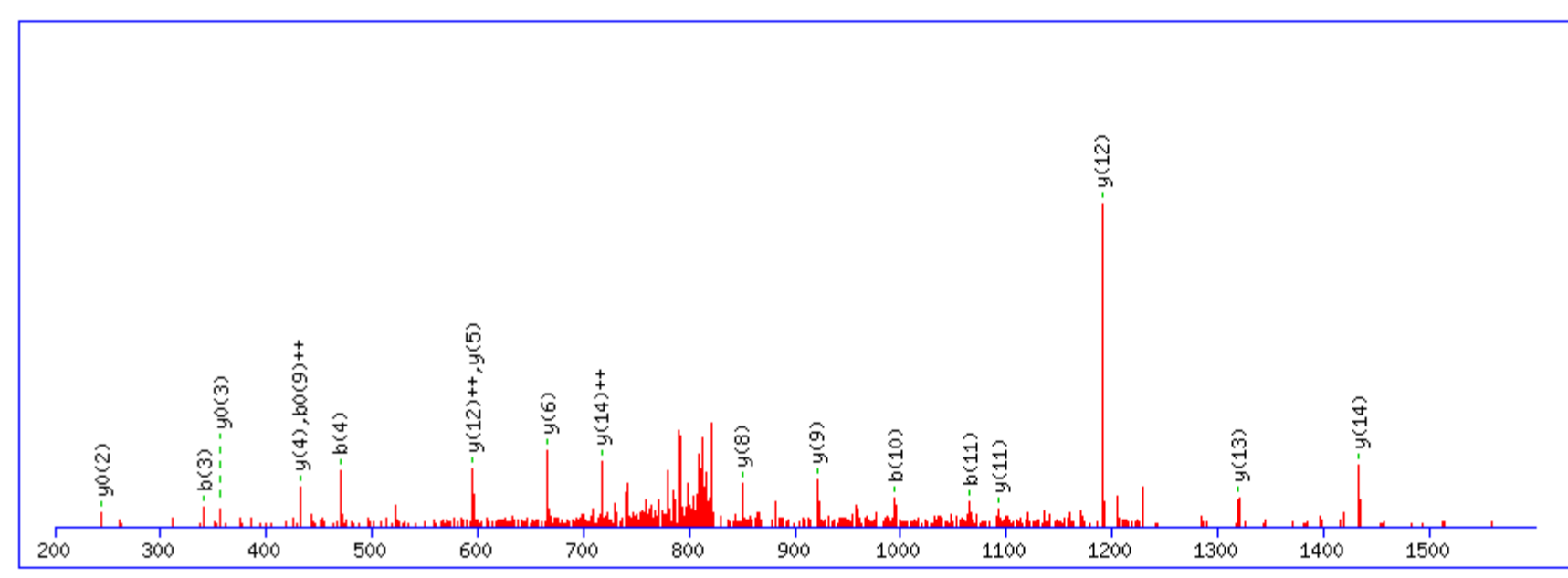
MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **IINEPTAAAIAYGLDK**
 Found in **Locus_5247_Transcript_1/1_Confidence_1.000**, Locus_5247_Transcript_1/1_Confidence_1.000
 Translated in frame 3 ([nucleic acid sequence](#))

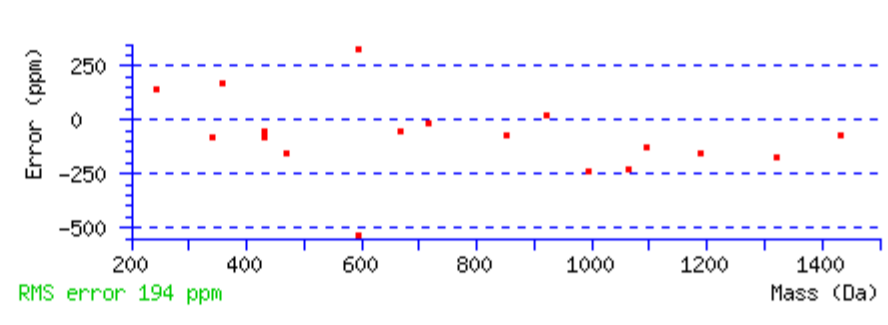
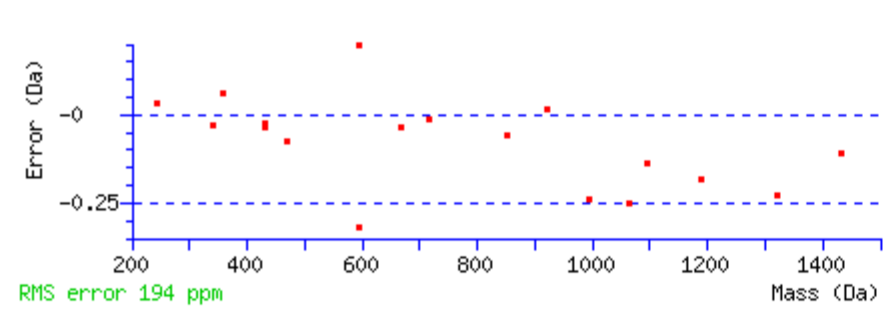
Match to Query 961: 1658.886828 from(830.450690,2+) intensity(12390.5150) scans(2569) rtinseconds(2653.443) rawscans(sn2569) index(1149)
 Title: 1150: Scan 2569 (rt=44.224)
 Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1658.887894
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Ions Score: 57 Expect: 6.3e-006
 Matches : 18/168 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							16
2	227.175404	114.091340					I	1546.811151	773.909214	1529.784602	765.395939	1528.800586	764.903931	15
3	341.218331	171.112803	324.191782	162.599529			N	1433.727087	717.367182	1416.700538	708.853907	1415.716522	708.361899	14
4	470.260924	235.634100	453.234375	227.120826	452.250359	226.628818	E	1319.684160	660.345718	1302.657611	651.832444	1301.673595	651.340436	13
5	567.313688	284.160482	550.287139	275.647208	549.303123	275.155200	P	1190.641567	595.824421	1173.615018	587.311147	1172.631002	586.819139	12
6	668.361367	334.684322	651.334818	326.171047	650.350802	325.679039	T	1093.588803	547.298039	1076.562254	538.784765	1075.578238	538.292757	11
7	739.398481	370.202879	722.371932	361.689604	721.387916	361.197596	A	992.541124	496.774200	975.514575	488.260925	974.530559	487.768917	10
8	810.435595	405.721436	793.409046	397.208161	792.425030	396.716153	A	921.504010	461.255643	904.477461	452.742369	903.493445	452.250361	9
9	881.472709	441.239993	864.446160	432.726718	863.462144	432.234710	A	850.466896	425.737086	833.440347	417.223812	832.456331	416.731804	8
10	994.556773	497.782025	977.530224	489.268750	976.546208	488.776742	I	779.429782	390.218529	762.403233	381.705255	761.419217	381.213247	7
11	1065.593887	533.300582	1048.567338	524.787307	1047.583322	524.295299	A	666.345718	333.676497	649.319169	325.163223	648.335153	324.671215	6
12	1228.657216	614.832246	1211.630667	606.318972	1210.646651	605.826964	Y	595.308604	298.157940	578.282055	289.644666	577.298039	289.152658	5
13	1285.678680	643.342978	1268.652131	634.829704	1267.668115	634.337696	G	432.245275	216.626275	415.218726	208.113001	414.234710	207.620993	4
14	1398.762744	699.885010	1381.736195	691.371736	1380.752179	690.879727	L	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
15	1513.789687	757.398482	1496.763138	748.885207	1495.779122	748.393199	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
16							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **IINEPTAAAIAYGLDK**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.3	1658.887894	-0.001066	IINEPTAAAIAYGLDK
1.9	1658.882065	0.004763	KDIPVQSIYFFFR

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLAGQILDVPIK**

Found in **Locus_5734_Transcript_1/1_Confidence_1.000**, Locus_5734_Transcript_1/1_Confidence_1.000

Translated in frame 6 ([nucleic acid sequence](#))

Match to Query 562: 1278.788748 from(640.401650,2+) intensity(23807.5450) scans(2795) rtinseconds(2875.8321) rawscans(sn2795) index(1270)

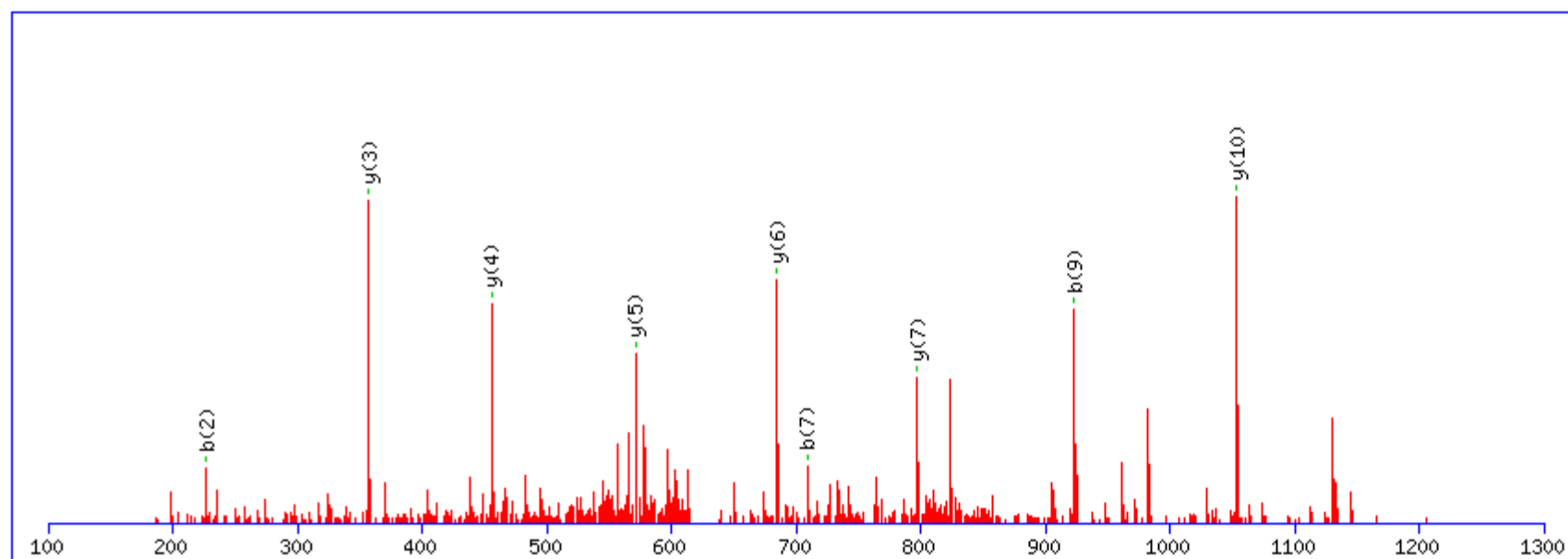
Title: 1271: Scan 2795 (rt=47.9305)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



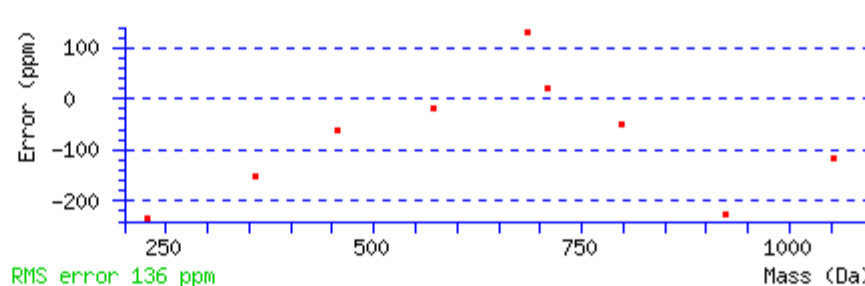
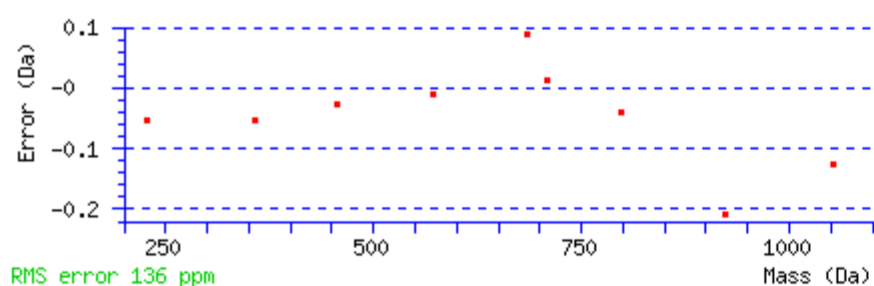
Monoisotopic mass of neutral peptide Mr(calc): 1278.791107

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 49 Expect: 1.7e-005

Matches : 9/102 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							12
2	227.175404	114.091340					L	1166.714337	583.860807	1149.687788	575.347532	1148.703772	574.855524	11
3	298.212518	149.609897					A	1053.630273	527.318775	1036.603724	518.805500	1035.619708	518.313492	10
4	355.233982	178.120629					G	982.593159	491.800218	965.566610	483.286943	964.582594	482.794935	9
5	483.292560	242.149918	466.266011	233.636643			Q	925.571695	463.289486	908.545146	454.776211	907.561130	454.284203	8
6	596.376624	298.691950	579.350075	290.178676			I	797.513117	399.260197	780.486568	390.746922	779.502552	390.254914	7
7	709.460688	355.233982	692.434139	346.720708			L	684.429053	342.718165	667.402504	334.204890	666.418488	333.712882	6
8	824.487631	412.747454	807.461082	404.234179	806.477066	403.742171	D	571.344989	286.176133	554.318440	277.662858	553.334424	277.170850	5
9	923.556045	462.281660	906.529496	453.768386	905.545480	453.276378	V	456.318046	228.662661	439.291497	220.149386			4
10	1020.608809	510.808043	1003.582260	502.294768	1002.598244	501.802760	P	357.249632	179.128454	340.223083	170.615180			3
11	1133.692873	567.350075	1116.666324	558.836800	1115.682308	558.344792	I	260.196868	130.602072	243.170319	122.088798			2
12							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **LLAGQILDVPIK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.4	1278.791107	-0.002359	LLAGQILDVPIK

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **EGLATDYMDPQPSISLFR**

Found in **Locus_5819_Transcript_1/1_Confidence_1.000**, Locus_5819_Transcript_1/1_Confidence_1.000

Translated in frame 6 ([nucleic acid sequence](#))

Match to Query 1428: 2054.957648 from(1028.486100,2+) intensity(21217.5680) scans(2960) rtinseconds(3027.5302) rawscans(sn2960) index(1350)

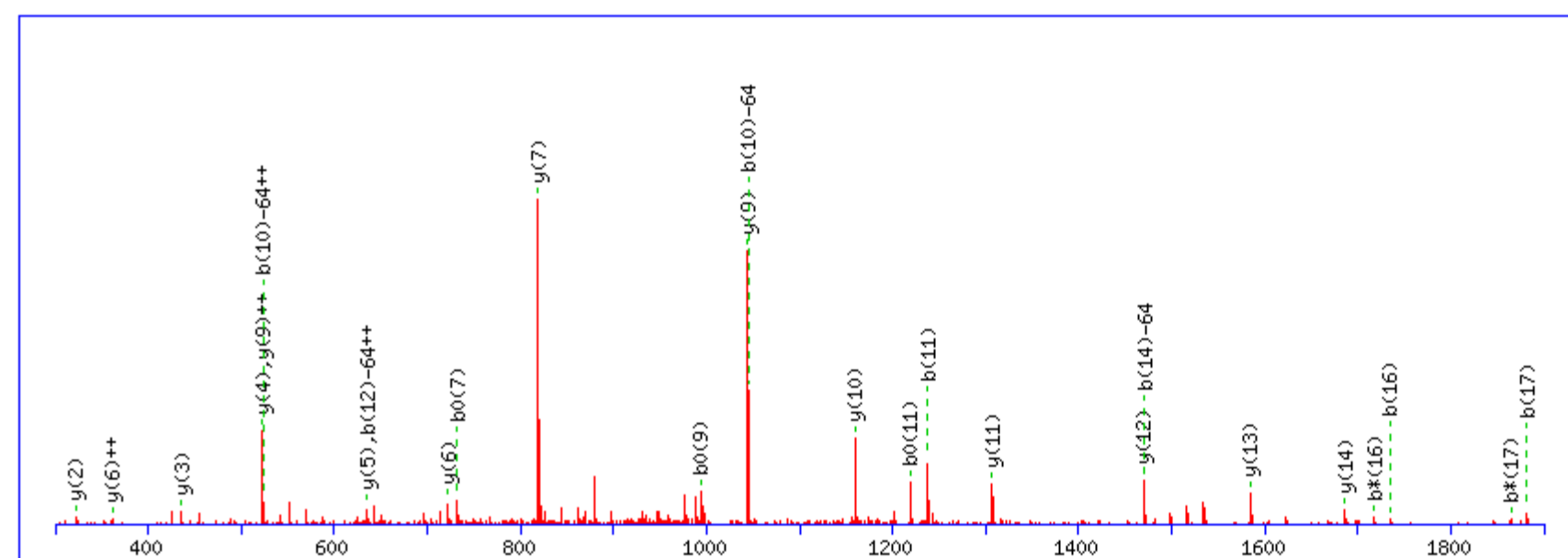
Title: 1351: Scan 2960 (rt=50.4588)

Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2054.961899

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

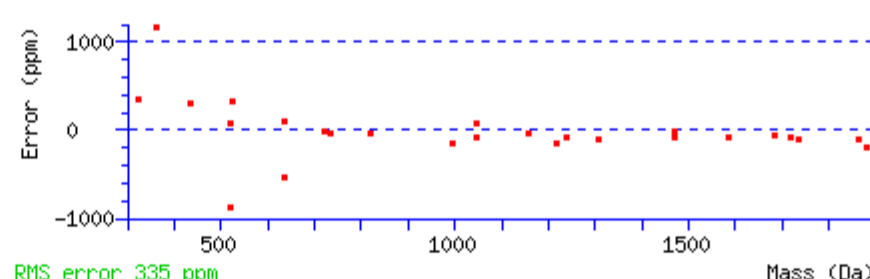
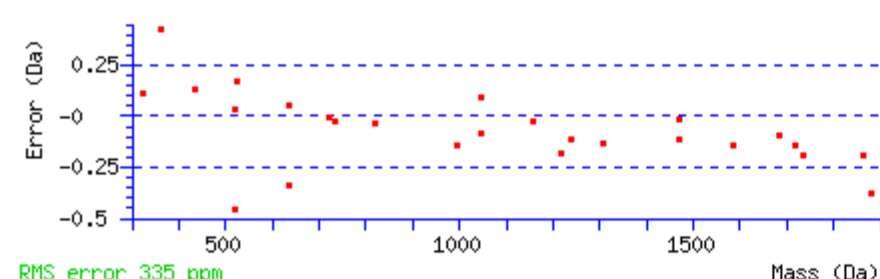
Variable modifications:

M8 : Oxidation (M), with neutral losses 0.000000 (shown in table), 63.998285

Ions Score: 98 Expect: 1.1e-009

Matches : 26/274 fragment ions using 32 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							18
2	187.071333	94.039305			169.060768	85.034022	G	1926.926592	963.966934	1909.900043	955.453660	1908.916027	954.961652	17
3	300.155397	150.581336			282.144832	141.576054	L	1869.905128	935.456202	1852.878579	926.942928	1851.894563	926.450919	16
4	371.192511	186.099894			353.181946	177.094611	A	1756.821064	878.914170	1739.794515	870.400896	1738.810499	869.908887	15
5	472.240190	236.623733			454.229625	227.618451	T	1685.783950	843.395613	1668.757401	834.882338	1667.773385	834.390330	14
6	587.267133	294.137205			569.256568	285.131922	D	1584.736271	792.871774	1567.709722	784.358499	1566.725706	783.866491	13
7	750.330462	375.668869			732.319897	366.663587	Y	1469.709328	735.358302	1452.682779	726.845028	1451.698763	726.353019	12
8	897.365862	449.186569			879.355297	440.181287	M	1306.645999	653.826637	1289.619450	645.313363	1288.635434	644.821355	11
9	1012.392805	506.700041			994.382240	497.694758	D	1159.610599	580.308937	1142.584050	571.795663	1141.600034	571.303655	10
10	1109.445569	555.226423			1091.435004	546.221140	P	1044.583656	522.795466	1027.557107	514.282192	1026.573091	513.790184	9
11	1237.504147	619.255711	1220.477598	610.742437	1219.493582	610.250429	Q	947.530892	474.269084	930.504343	465.755810	929.520327	465.263802	8
12	1334.556911	667.782093	1317.530362	659.268819	1316.546346	658.776811	P	819.472314	410.239795	802.445765	401.726521	801.461749	401.234513	7
13	1421.588939	711.298108	1404.562390	702.784833	1403.578374	702.292825	S	722.419550	361.713413	705.393001	353.200139	704.408985	352.708131	6
14	1534.673003	767.840139	1517.646454	759.326865	1516.662438	758.834857	I	635.387522	318.197399	618.360973	309.684125	617.376957	309.192117	5
15	1621.705031	811.356154	1604.678482	802.842879	1603.694466	802.350871	S	522.303458	261.655367	505.276909	253.142093	504.292893	252.650085	4
16	1734.789095	867.898185	1717.762546	859.384911	1716.778530	858.892903	L	435.271430	218.139353	418.244881	209.626078			3
17	1881.857509	941.432392	1864.830960	932.919118	1863.846944	932.427110	F	322.187366	161.597321	305.160817	153.084047			2
18							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [EGLATDYMDPQPSISLFR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
98.1	2054.961899	-0.004251	EGLATDYMDPQPSISLFR

Mascot: <http://www.matrixscience.com/>