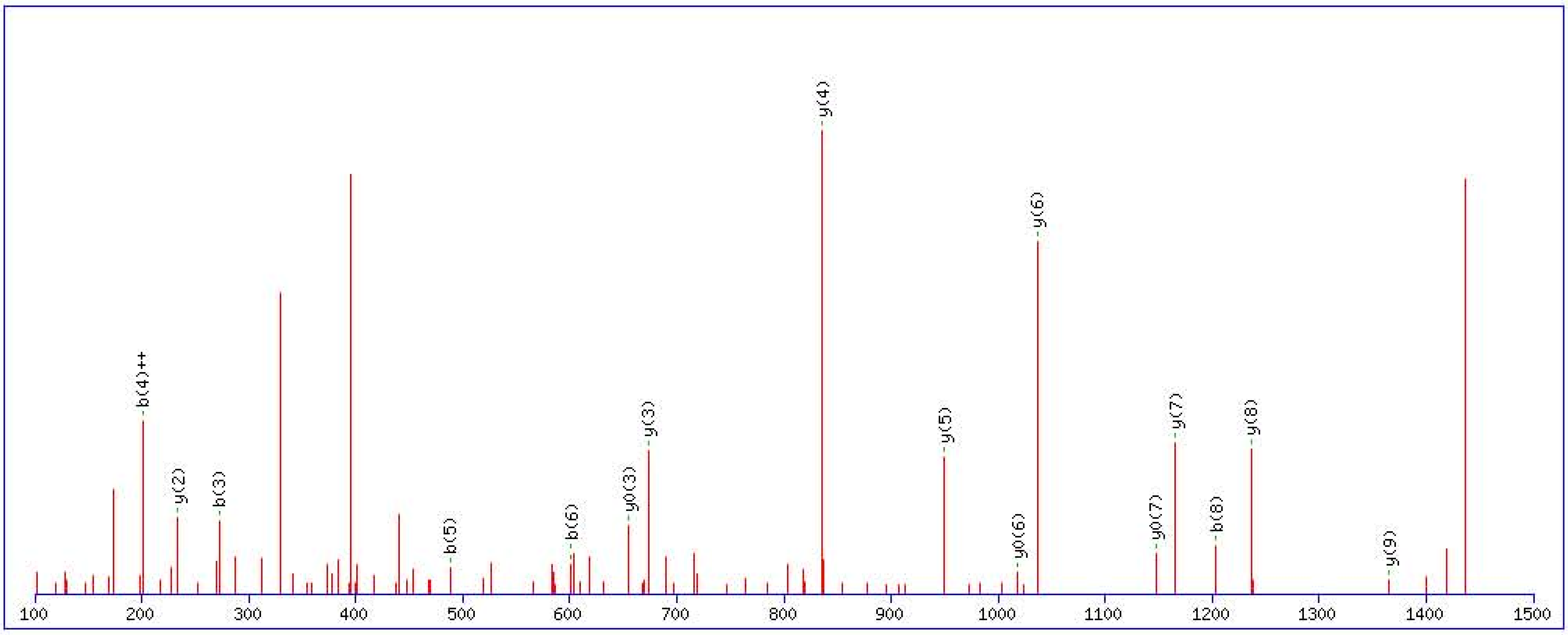
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEAESLYQSK**
Found in **K2C1_HUMAN**, Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6

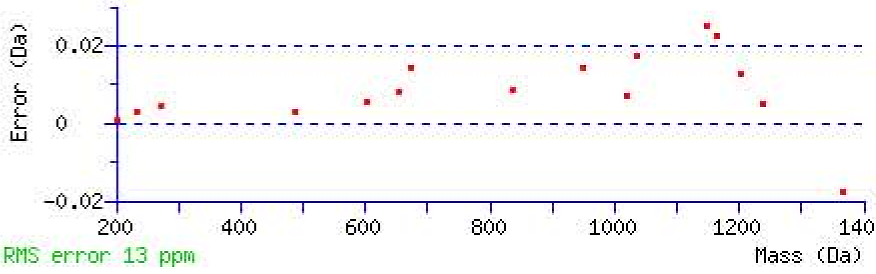
Match to Query 36581: 1435.717728 from(718.866140,2+) rtinseconds(1653) index(22238)
Title: Locus:1.1.1.2530.11 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

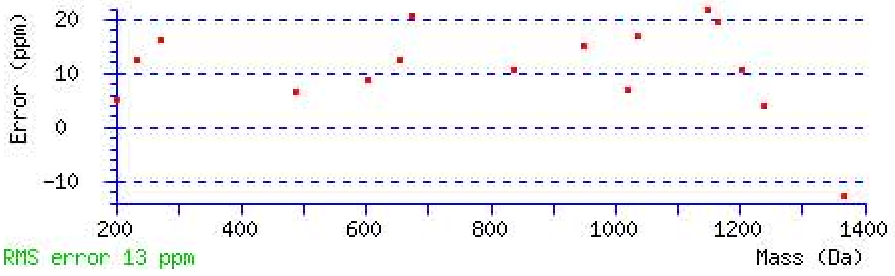
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1435.701675
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 58 **Expect:** 4.8e-006
Matches : 17/90 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	72.044390	36.525833					A							10
2	**201.086983**	101.047130			183.076418	92.041847	E	***1365.671879***	683.339578	1348.645330	674.826303	1347.661314	674.334295	9
3	**272.124097**	136.565687			254.113532	127.560404	A	***1236.629286***	618.818281	1219.602737	610.305007	1218.618721	609.812999	8
4	401.166690	201.086983			383.156125	192.081701	E	***1165.592172***	583.299724	1148.565623	574.786450	1147.581607	574.294442	7
5	**488.198718**	244.602997			470.188153	235.597715	S	***1036.549579***	518.778428	1019.523030	510.265153	1018.539014	509.773145	6
6	**601.282782**	301.145029			583.272217	292.139747	L	***949.517551***	475.262414	932.491002	466.749139	931.506986	466.257131	5
7	764.346111	382.676694			746.335546	373.671411	Y	***836.433487***	418.720382	819.406938	410.207107	818.422922	409.715099	4
8	**1203.571437**	602.289357	1186.544888	593.776082	1185.560872	593.284074	Q	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
9	1290.603465	645.805371	1273.576916	637.292096	1272.592900	636.800088	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.3	1435.701675	0.016053	AEAESLYQSK
1.6	1435.735397	-0.017669	LSARDGHNQK

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

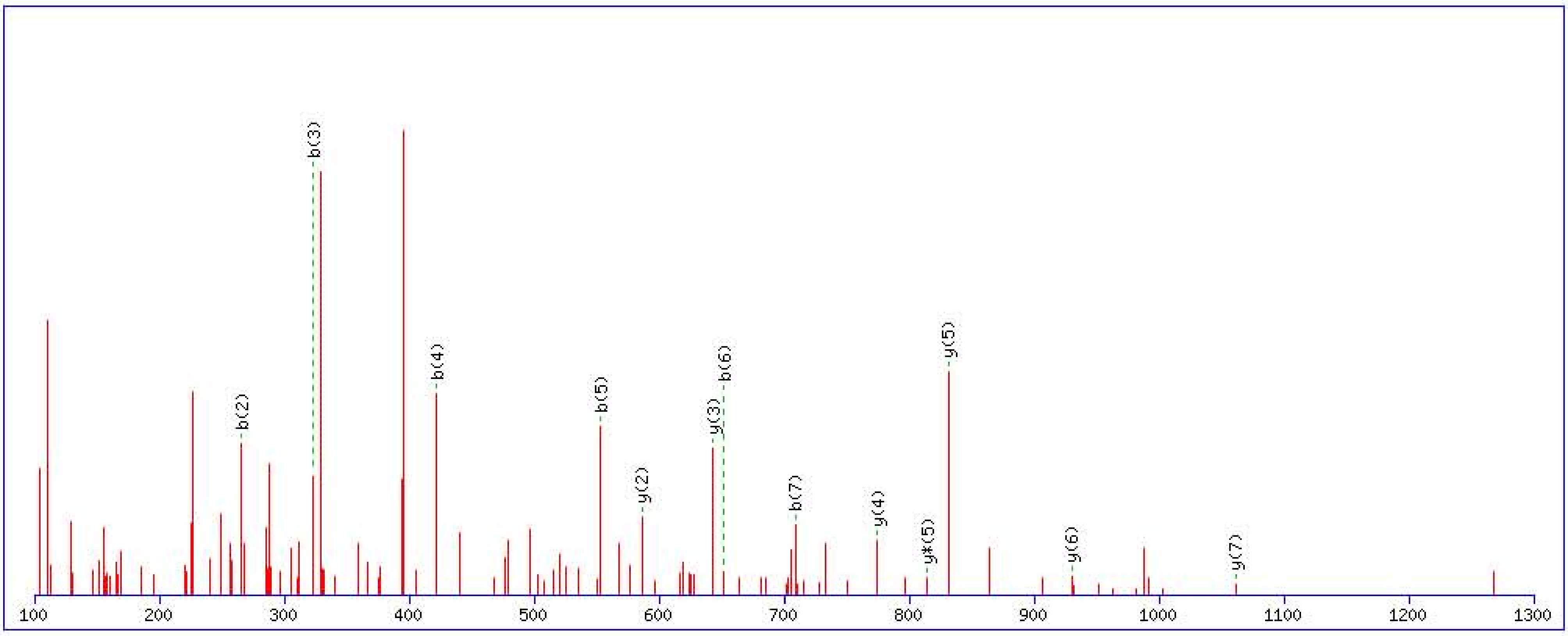
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQGVMVGMGQK**
Found in **ACTA_HUMAN**, Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

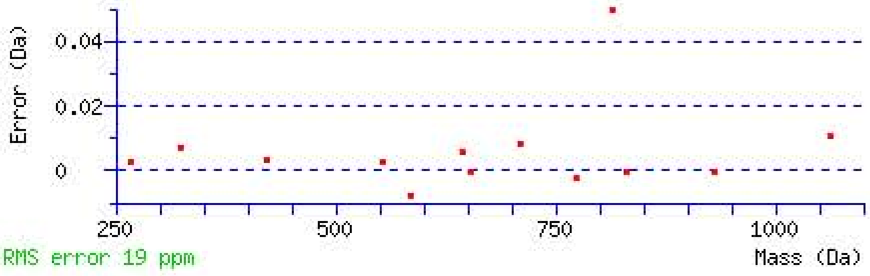
Match to Query 38144: 1481.728392 from(494.916740,3+) rtinseconds(1526) index(39057)
Title: Locus:1.1.1.2815.12 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

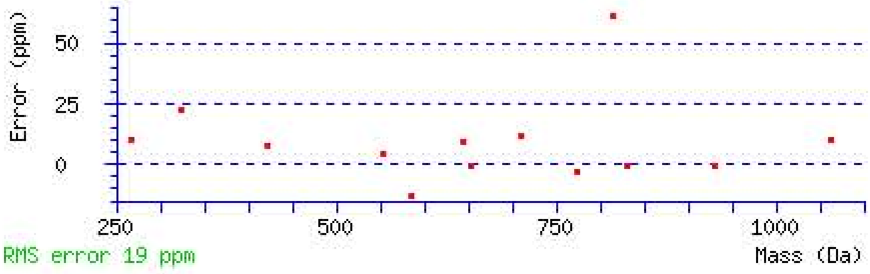
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1481.730545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0098
Matches : 13/78 fragment ions using 29 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	138.066188	69.536732			H					11
2	*266.124766*	133.566021	249.098217	125.052746	Q	1345.678898	673.343087	1328.652349	664.829813	10
3	*323.146230*	162.076753	306.119681	153.563478	G	1217.620320	609.313798	1200.593771	600.800524	9
4	*422.214644*	211.610960	405.188095	203.097685	V	1160.598856	580.803066	1143.572307	572.289792	8
5	*553.255129*	277.131203	536.228580	268.617928	M	*1061.530442*	531.268859	1044.503893	522.755585	7
6	*652.323543*	326.665410	635.296994	318.152135	V	*930.489957*	465.748617	913.463408	457.235342	6
7	*709.345007*	355.176142	692.318458	346.662867	G	*831.421543*	416.214410	814.394994	407.701135	5
8	840.385492	420.696384	823.358943	412.183110	M	*774.400079*	387.703678	757.373530	379.190403	4
9	897.406956	449.207116	880.380407	440.693842	G	*643.359594*	322.183435	626.333045	313.670161	3
10	1336.632282	668.819779	1319.605733	660.306505	Q	*586.338130*	293.672703	569.311581	285.159429	2
11					K	147.112804	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.5	1481.730545	-0.002153	HQGVMVGMGQK

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

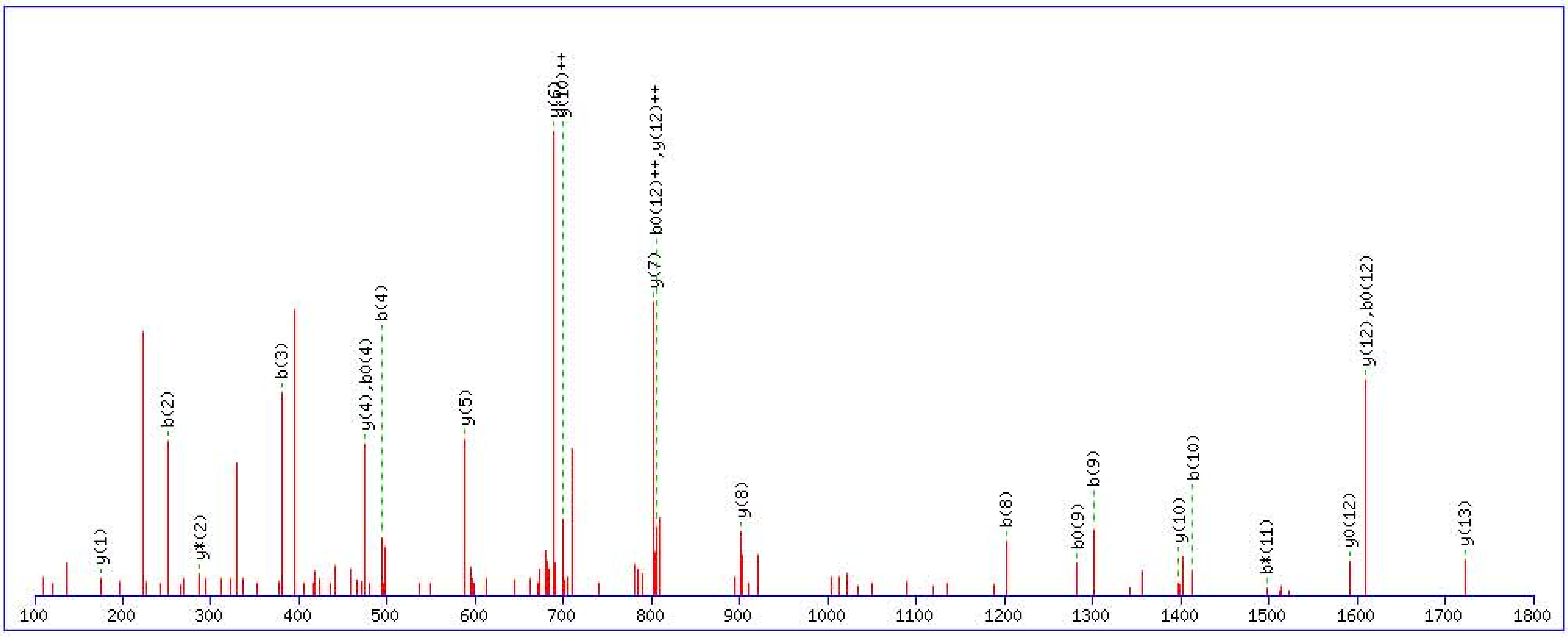
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYELPDGQVITIGNER**
Found in **ACTA_HUMAN**, Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

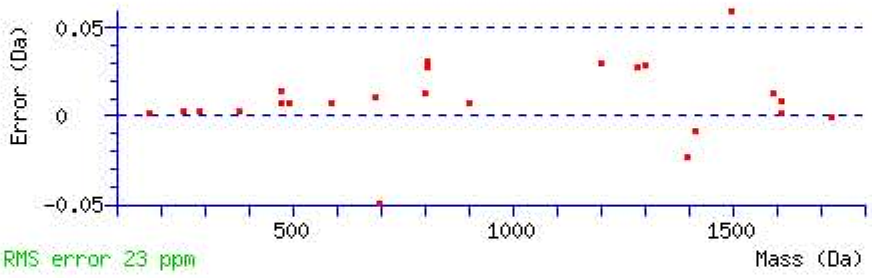
Match to Query 56086: 2101.073172 from(701.365000,3+) rtinseconds(2604) index(64643)
Title: Locus:1.1.1.3211.10 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

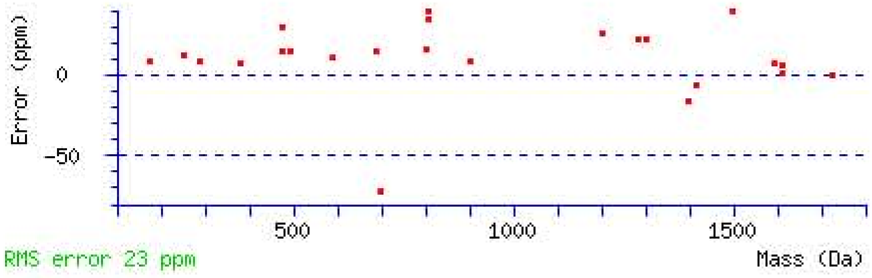
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2101.051376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00023
Matches : 24/164 fragment ions using 44 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							16
2	**251.102633**	126.054954			233.092068	117.049672	Y	2015.026640	1008.016958	1998.000091	999.503683	1997.016075	999.011675	15
3	**380.145226**	190.576251			362.134661	181.570969	E	1851.963311	926.485294	1834.936762	917.972019	1833.952746	917.480011	14
4	**493.229290**	247.118283			475.218725	238.113001	L	***1722.920718***	861.963997	1705.894169	853.450722	1704.910153	852.958714	13
5	590.282054	295.644665			572.271489	286.639383	P	***1609.836654***	805.421965	1592.810105	796.908691	1591.826089	796.416682	12
6	705.308997	353.158137			687.298432	344.152854	D	1512.783890	756.895583	1495.757341	748.382309	1494.773325	747.890300	11
7	762.330461	381.668869			744.319896	372.663586	G	***1397.756947***	699.382111	1380.730398	690.868837	1379.746382	690.376829	10
8	**1201.555787**	601.281532	1184.529238	592.768257	1183.545222	592.276249	Q	1340.735483	670.871379	1323.708934	662.358105	1322.724918	661.866097	9
9	**1300.624201**	650.815739	1283.597652	642.302464	1282.613636	641.810456	V	***901.510157***	451.258716	884.483608	442.745442	883.499592	442.253434	8
10	**1413.708265**	707.357771	1396.681716	698.844496	1395.697700	698.352488	I	***802.441743***	401.724509	785.415194	393.211235	784.431178	392.719227	7
11	1514.755944	757.881610	1497.729395	749.368336	1496.745379	748.876328	T	***689.357679***	345.182478	672.331130	336.669203	671.347114	336.177195	6
12	1627.840008	814.423642	1610.813459	805.910368	1609.829443	805.418359	I	***588.310000***	294.658638	571.283451	286.145363	570.299435	285.653355	5
13	1684.861472	842.934374	1667.834923	834.421099	1666.850907	833.929091	G	***475.225936***	238.116606	458.199387	229.603331	457.215371	229.111323	4
14	1798.904399	899.955837	1781.877850	891.442563	1780.893834	890.950555	N	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
15	1927.946992	964.477134	1910.920443	955.963860	1909.936427	955.471851	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.5	2101.051376	0.021796	SYELPDGQVITIGNER
3.7	2101.047363	0.025809	IMGGNSILHSAADSVTSAVQK

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

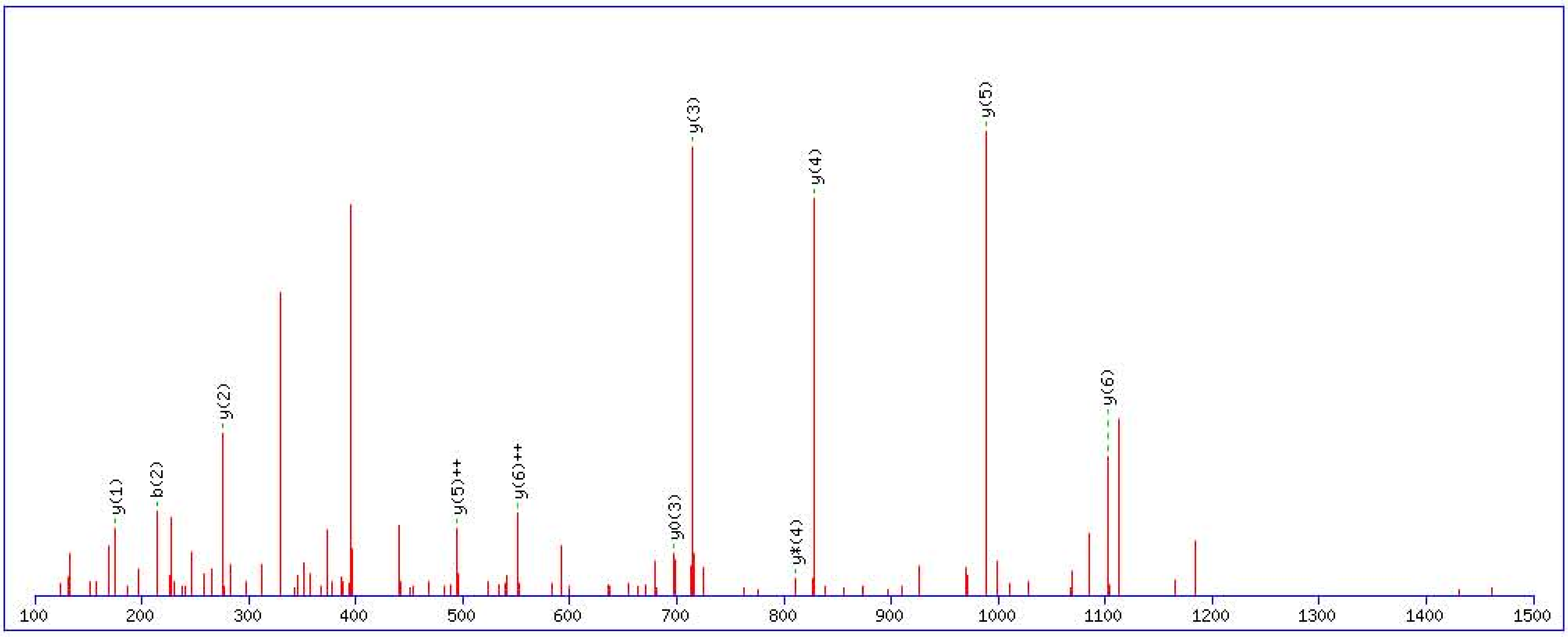
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNCLQTR**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

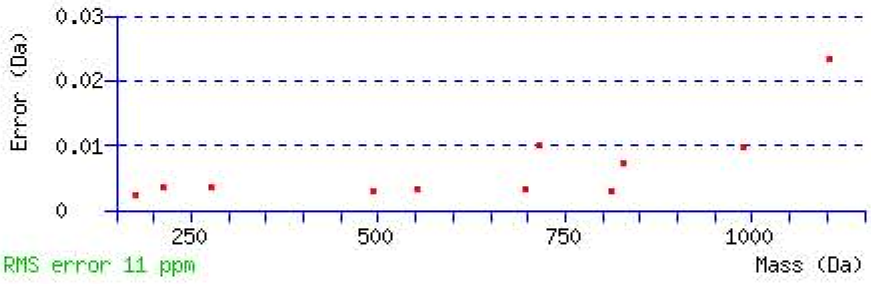
Match to Query 27699: 1200.619288 from(601.316920,2+) rtinseconds(1469) index(3534)
Title: Locus:1.1.1.2643.20 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

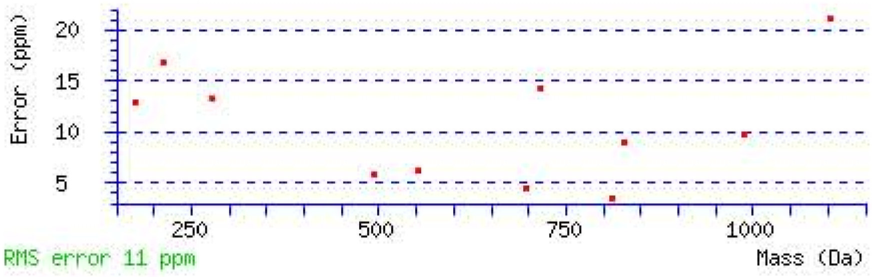
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1200.610733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0013
Matches : 11/58 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	100.075690	50.541483					V							7
2	214.118617	107.562947	197.092068	99.049672			N	***1102.549597***	551.778437	1085.523048	543.265162	1084.539032	542.773154	6
3	374.149266	187.578271	357.122717	179.064997			C	***988.506670***	494.756973	971.480121	486.243698	970.496105	485.751691	5
4	487.233330	244.120303	470.206781	235.607029			L	***828.476021***	414.741649	811.449472	406.228374	810.465456	405.736366	4
5	926.458656	463.732966	909.432107	455.219692			Q	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
6	1027.506335	514.256806	1010.479786	505.743531	1009.495770	505.251523	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.1	1200.610733	0.008555	VNCLQTR
5.1	1200.628479	-0.009191	MVAALLGGGEAR
3.7	1200.635010	-0.015722	ELDLQVLDTR
3.5	1200.628464	-0.009176	LLQLQEMGNR
3.5	1200.611191	0.008097	HDSHLAKHTR
3.5	1200.603333	0.015955	GRIAEPSVCGR
2.4	1200.632462	-0.013174	YKMYLEKAR
1.0	1200.609848	0.009440	ERAPVSGTQEK
0.6	1200.634964	-0.015676	NVAAEIEAKEK
0.3	1200.621948	-0.002660	VNMLKHCKR

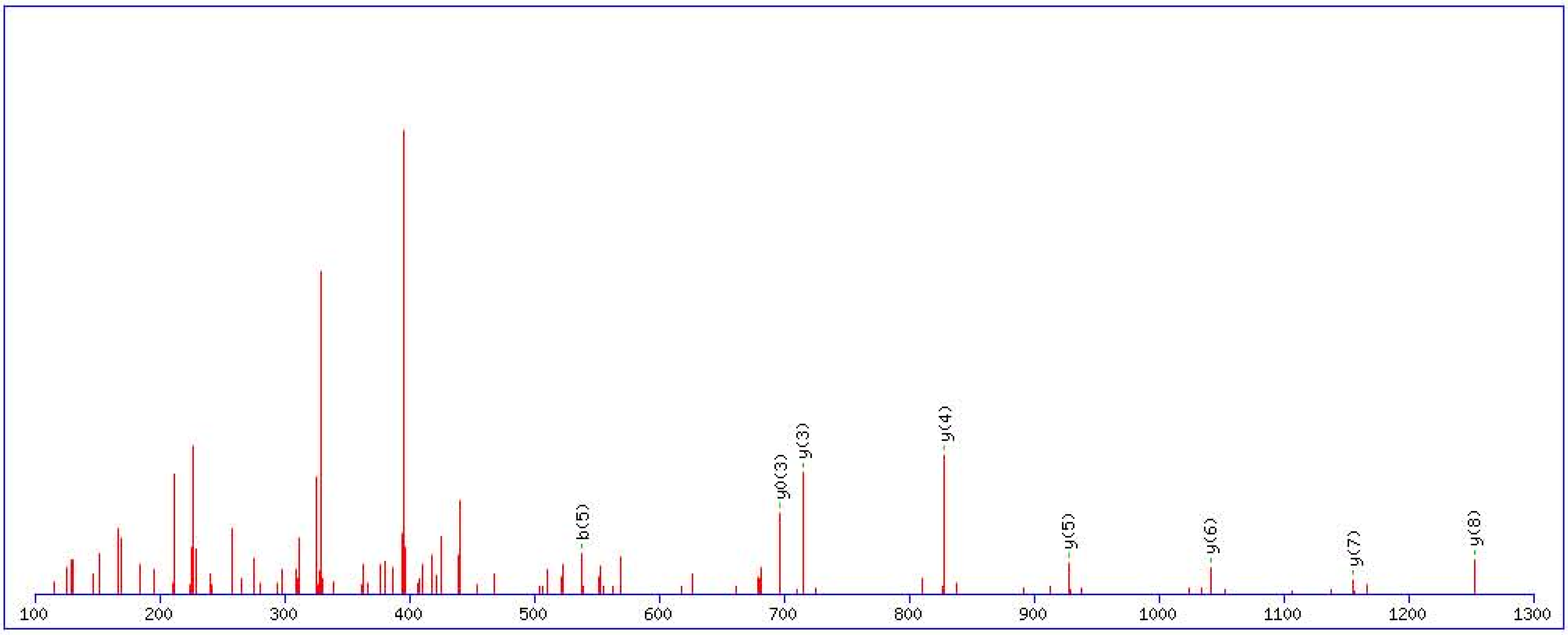
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPNNVLQEK**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

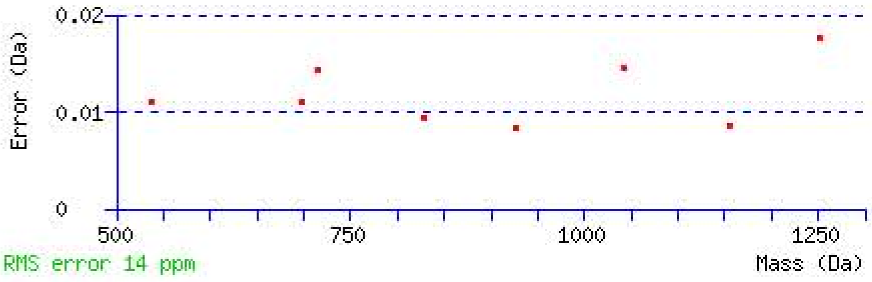
Match to Query 33380: 1364.756832 from(455.926220,3+) rtinseconds(1828) index(5818)
Title: Locus:1.1.1.2769.5 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

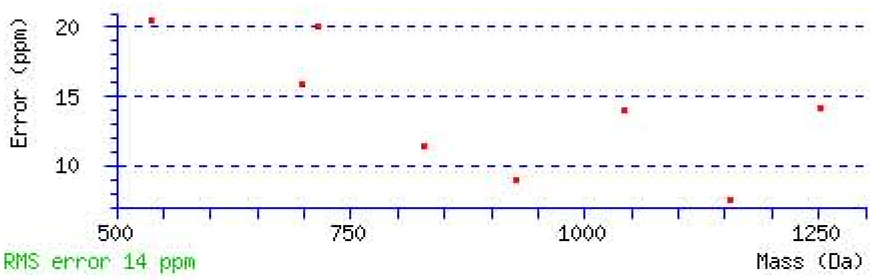
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1364.748581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0017
Matches : 8/76 fragment ions using 12 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							9
2	211.144104	106.075690					P	***1252.671819***	626.839548	1235.645270	618.326273	1234.661254	617.834265	8
3	325.187031	163.097153	308.160482	154.583879			N	***1155.619055***	578.313166	1138.592506	569.799891	1137.608490	569.307883	7
4	439.229958	220.118617	422.203409	211.605343			N	***1041.576128***	521.291702	1024.549579	512.778428	1023.565563	512.286420	6
5	**538.298372**	269.652824	521.271823	261.139550			V	***927.533201***	464.270239	910.506652	455.756964	909.522636	455.264956	5
6	651.382436	326.194856	634.355887	317.681582			L	***828.464787***	414.736032	811.438238	406.222757	810.454222	405.730749	4
7	1090.607762	545.807519	1073.581213	537.294245			Q	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
8	1219.650355	610.328816	1202.623806	601.815541	1201.639790	601.323533	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.3	1364.748581	0.008251	LPNNVLQEK
8.2	1364.759827	-0.002995	QTSSLIIHR
1.7	1364.766342	-0.009510	QPVEPKKPVESK
0.9	1364.745239	0.011593	KVVSWIDVYTR
0.4	1364.752609	0.004223	ILPIMFPSLYR

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

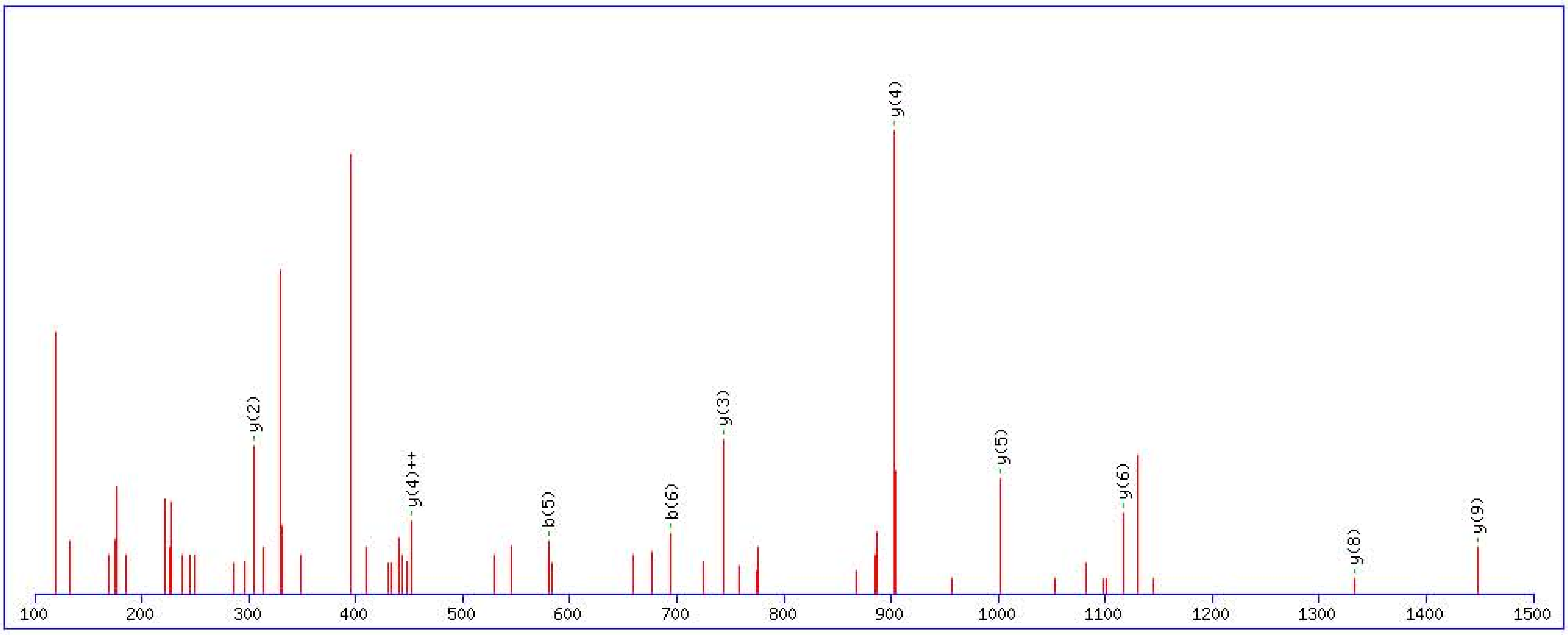
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FTDSENVCQER**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

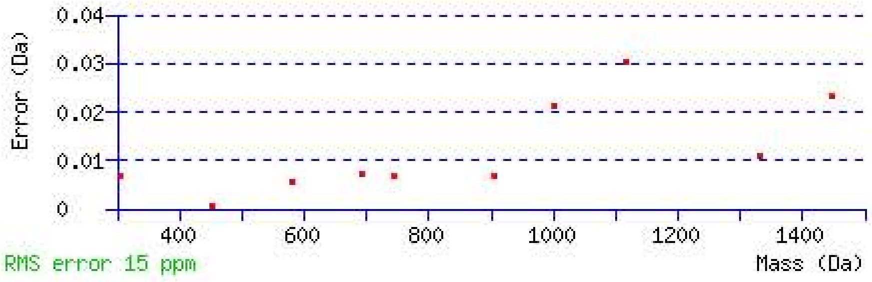
Match to Query 45648: 1694.745132 from(565.922320,3+) rtinseconds(1529) index(3942)
Title: Locus:1.1.1.2664.21 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

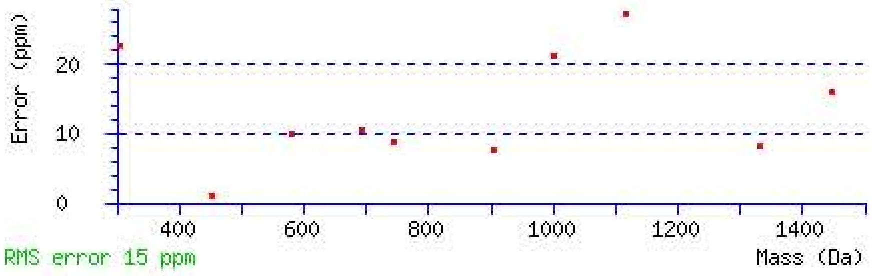
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1694.739243
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 3e-005
Matches : 10/106 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							11
2	249.123369	125.065322			231.112804	116.060040	T	1548.678104	774.842690	1531.651555	766.329416	1530.667539	765.837408	10
3	364.150312	182.578794			346.139747	173.573512	D	***1447.630425***	724.318851	1430.603876	715.805576	1429.619860	715.313568	9
4	451.182340	226.094808			433.171775	217.089526	S	***1332.603482***	666.805379	1315.576933	658.292105	1314.592917	657.800097	8
5	**580.224933**	290.616105			562.214368	281.610822	E	1245.571454	623.289365	1228.544905	614.776091	1227.560889	614.284083	7
6	**694.267860**	347.637568	677.241311	339.124294	676.257295	338.632286	N	***1116.528861***	558.768069	1099.502312	550.254794	1098.518296	549.762786	6
7	793.336274	397.171775	776.309725	388.658501	775.325709	388.166493	V	***1002.485934***	501.746605	985.459385	493.233331	984.475369	492.741323	5
8	953.366923	477.187100	936.340374	468.673825	935.356358	468.181817	C	***903.417520***	452.212398	886.390971	443.699124	885.406955	443.207116	4
9	1392.592249	696.799763	1375.565700	688.286488	1374.581684	687.794480	Q	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
10	1521.634842	761.321059	1504.608293	752.807785	1503.624277	752.315777	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.6	1694.739243	0.005889	FTDSENVCQER

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

{MATRIX SCIENCE}

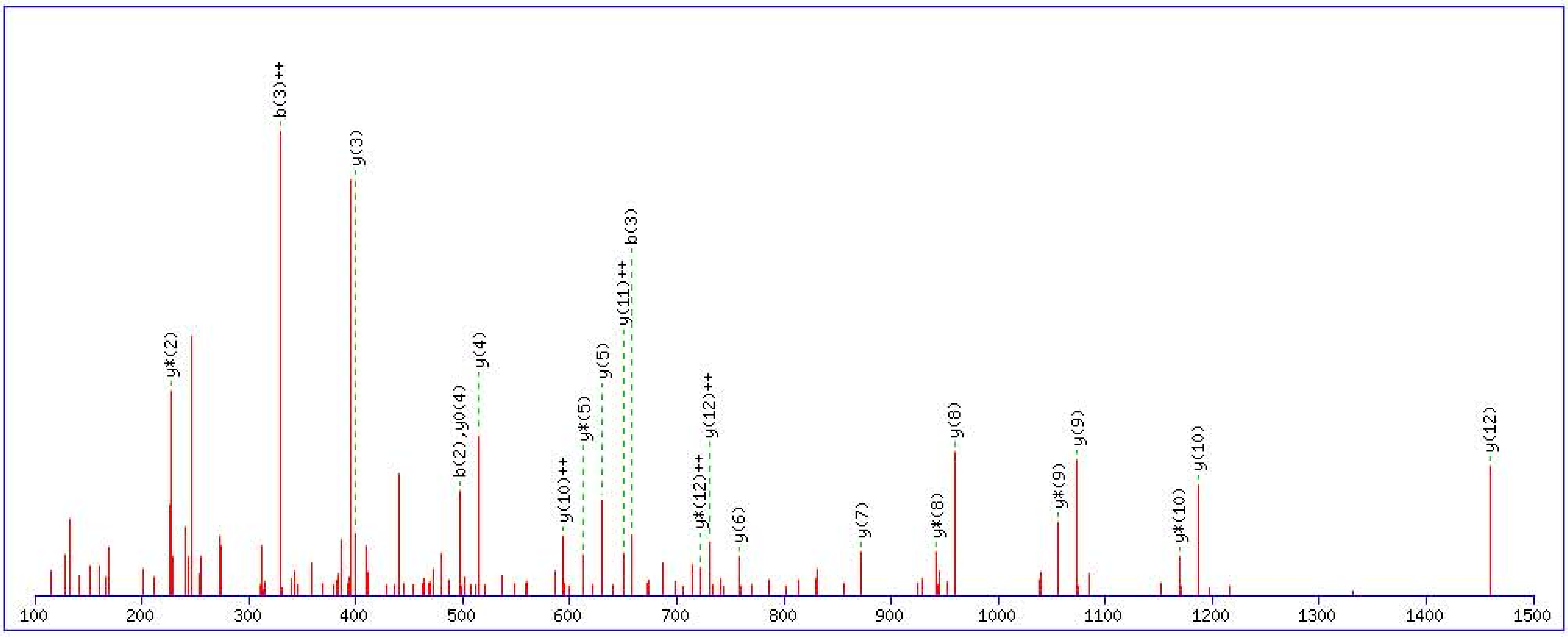
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQCIINSNKDDRPK**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

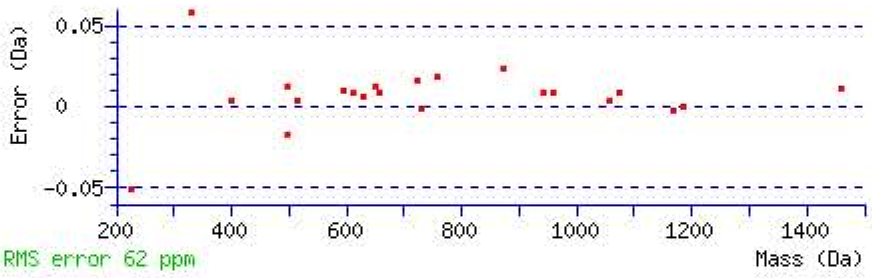
Match to Query 51831: 1954.982816 from(489.752980,4+) rtinseconds(1318) index(2428)
Title: Locus:1.1.1.2591.4 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

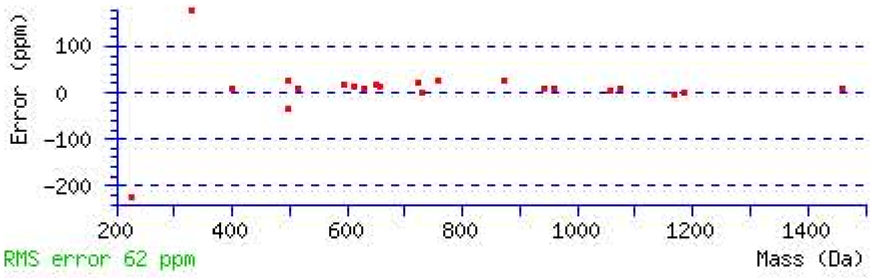
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1954.971680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 0.00023
Matches : 22/136 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							14
2	**497.254066**	249.130671	480.227517	240.617397			Q	1898.957513	949.982395	1881.930964	941.469120	1880.946948	940.977112	13
3	**657.284715**	329.145996	640.258166	320.632721			C	***1459.732187***	730.369732	1442.705638	721.856457	1441.721622	721.364449	12
4	770.368779	385.688028	753.342230	377.174753			I	1299.701538	650.354407	1282.674989	641.841133	1281.690973	641.349125	11
5	883.452843	442.230060	866.426294	433.716785			I	***1186.617474***	593.812375	1169.590925	585.299101	1168.606909	584.807093	10
6	997.495770	499.251523	980.469221	490.738249			N	***1073.533410***	537.270343	1056.506861	528.757069	1055.522845	528.265061	9
7	1084.527798	542.767537	1067.501249	534.254263	1066.517233	533.762255	S	***959.490483***	480.248880	942.463934	471.735605	941.479918	471.243597	8
8	1198.570725	599.789001	1181.544176	591.275726	1180.560160	590.783718	N	***872.458455***	436.732866	855.431906	428.219591	854.447890	427.727583	7
9	1326.665688	663.836482	1309.639139	655.323208	1308.655123	654.831200	K	***758.415528***	379.711402	741.388979	371.198128	740.404963	370.706120	6
10	1441.692631	721.349954	1424.666082	712.836679	1423.682066	712.344671	D	***630.320565***	315.663921	613.294016	307.150646	612.310000	306.658638	5
11	1556.719574	778.863425	1539.693025	770.350151	1538.709009	769.858143	D	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	4
12	1712.820685	856.913981	1695.794136	848.400706	1694.810120	847.908698	R	***400.266679***	200.636977	383.240130	192.123703			3
13	1809.873449	905.440363	1792.846900	896.927088	1791.862884	896.435080	P	244.165568	122.586422	227.139019	114.073148			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.8	1954.971680	0.011136	GQCIINSNKDDRPK

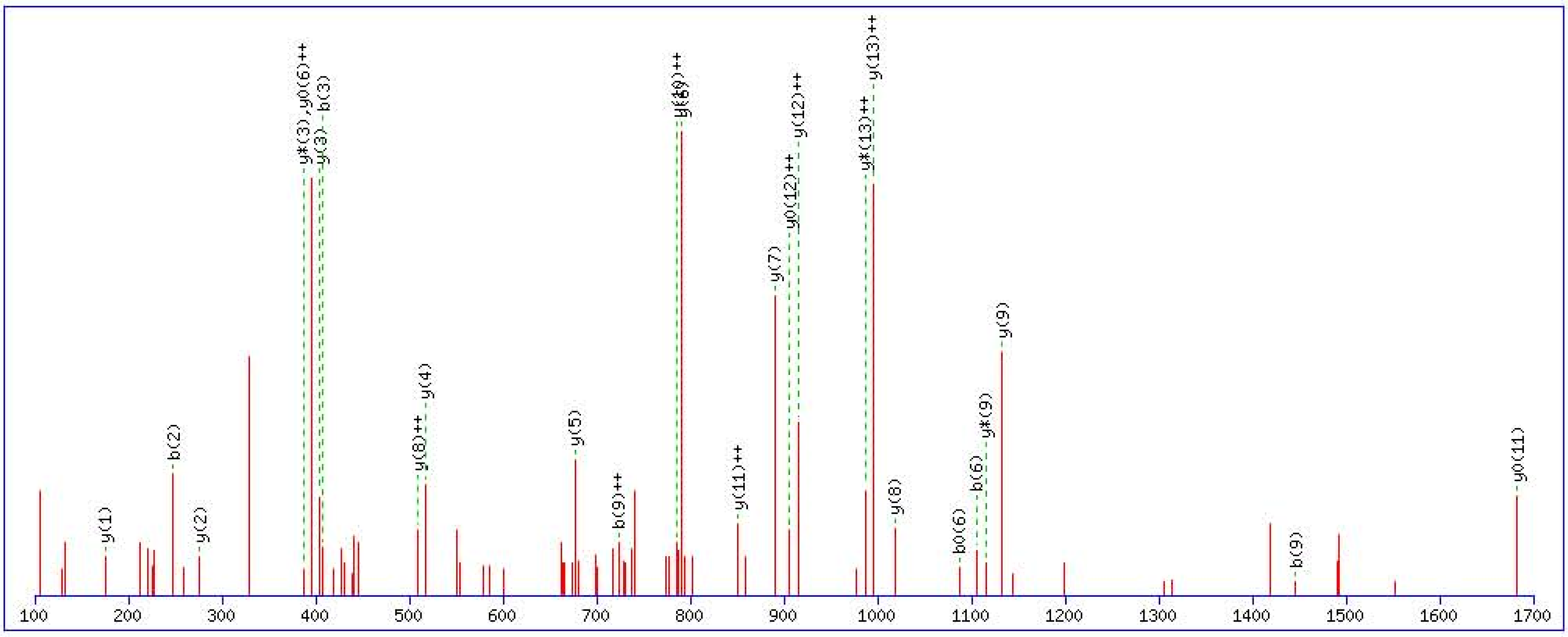
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SCCEEQNKVNCLQTR**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

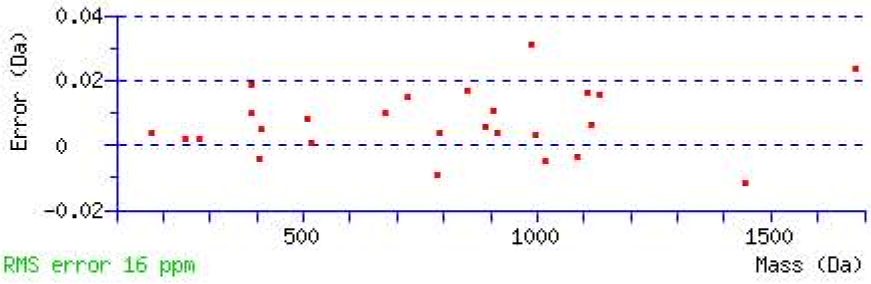
Match to Query 59039: 2235.994932 from(746.338920,3+) rtinseconds(1403) index(3005)
Title: Locus:1.1.1.2620.23 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

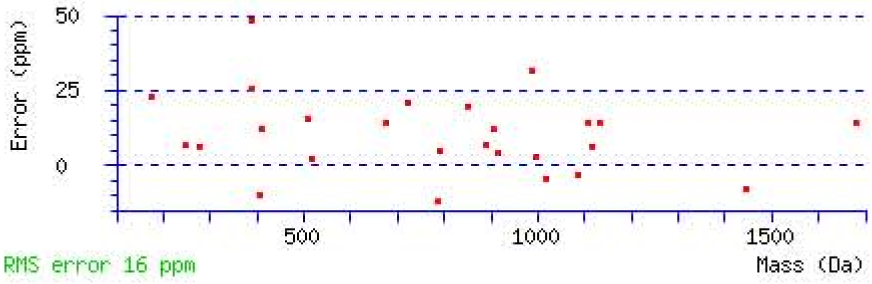
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2235.985703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0012
Matches : 26/156 fragment ions using 58 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							15
2	**248.069953**	124.538614			230.059388	115.533332	C	2149.960963	1075.484119	2132.934414	1066.970845	2131.950398	1066.478837	14
3	**408.100602**	204.553939			390.090037	195.548657	C	1989.930314	995.468795	1972.903765	986.955521	1971.919749	986.463512	13
4	537.143195	269.075236			519.132630	260.069953	E	1829.899665	915.453470	1812.873116	906.940196	1811.889100	906.448188	12
5	666.185788	333.596532			648.175223	324.591250	E	1700.857072	850.932174	1683.830523	842.418899	1682.846507	841.926891	11
6	**1105.411114**	553.209195	1088.384565	544.695921	1087.400549	544.203913	Q	1571.814479	786.410877	1554.787930	777.897603	1553.803914	777.405595	10
7	1219.454041	610.230659	1202.427492	601.717384	1201.443476	601.225376	N	***1132.589153***	566.798214	1115.562604	558.284940	1114.578588	557.792932	9
8	1347.549004	674.278140	1330.522455	665.764866	1329.538439	665.272858	K	***1018.546226***	509.776751	1001.519677	501.263476	1000.535661	500.771468	8
9	**1446.617418**	723.812347	1429.590869	715.299073	1428.606853	714.807065	V	***890.451263***	445.729269	873.424714	437.215995	872.440698	436.723987	7
10	1560.660345	780.833811	1543.633796	772.320536	1542.649780	771.828528	N	***791.382849***	396.195062	774.356300	387.681788	773.372284	387.189780	6
11	1720.690994	860.849135	1703.664445	852.335861	1702.680429	851.843853	C	***677.339922***	339.173599	660.313373	330.660324	659.329357	330.168316	5
12	1833.775058	917.391167	1816.748509	908.877893	1815.764493	908.385885	L	***517.309273***	259.158274	500.282724	250.645000	499.298708	250.152992	4
13	1961.833636	981.420456	1944.807087	972.907182	1943.823071	972.415174	Q	***404.225209***	202.616242	387.198660	194.102968	386.214644	193.610960	3
14	2062.881315	1031.944295	2045.854766	1023.431021	2044.870750	1022.939013	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.9	2235.985703	0.009229	SCCEEQNKVNCLQTR

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQDSPGNK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

Match to Query 31196: 1312.619308 from(657.316930,2+) rtinseconds(1119) index(1102)
Title: Locus:1.1.1.2521.9 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1312.608139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0028
Matches : 30/86 fragment ions using 63 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							9
2	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1184.572834	592.790055	1167.546285	584.276780	1166.562269	583.784772	8
3	697.333773	349.170525	680.307224	340.657250	679.323208	340.165242	Q	***745.347508***	373.177392	728.320959	364.664117	727.336943	364.172109	7
4	**812.360716**	406.683996	795.334167	398.170722	794.350151	397.678714	D	***617.288930***	309.148103	600.262381	300.634828	599.278365	300.142820	6
5	**899.392744**	450.200010	882.366195	441.686736	881.382179	441.194728	S	***502.261987***	251.634631	485.235438	243.121357	484.251422	242.629349	5
6	996.445508	498.726392	979.418959	490.213118	978.434943	489.721110	P	***415.229959***	208.118617	398.203410	199.605343			4
7	1053.466972	527.237124	1036.440423	518.723850	1035.456407	518.231841	G	***318.177195***	159.592235	301.150646	151.078961			3
8	**1167.509899**	584.258587	1150.483350	575.745313	1149.499334	575.253305	N	***261.155731***	131.081503	244.129182	122.568229			2
9							K	***147.112804***	74.060040	130.086255	65.546765			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.0	1312.608139	0.011169	EQQDSPGNK
19.8	1312.608139	0.011169	EQQDSPGNK
4.8	1312.637115	-0.017807	KTNHSSPEAQSK
4.1	1312.626770	-0.007462	QQASPSCPK
4.0	1312.626770	-0.007462	QQASPSCPK

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

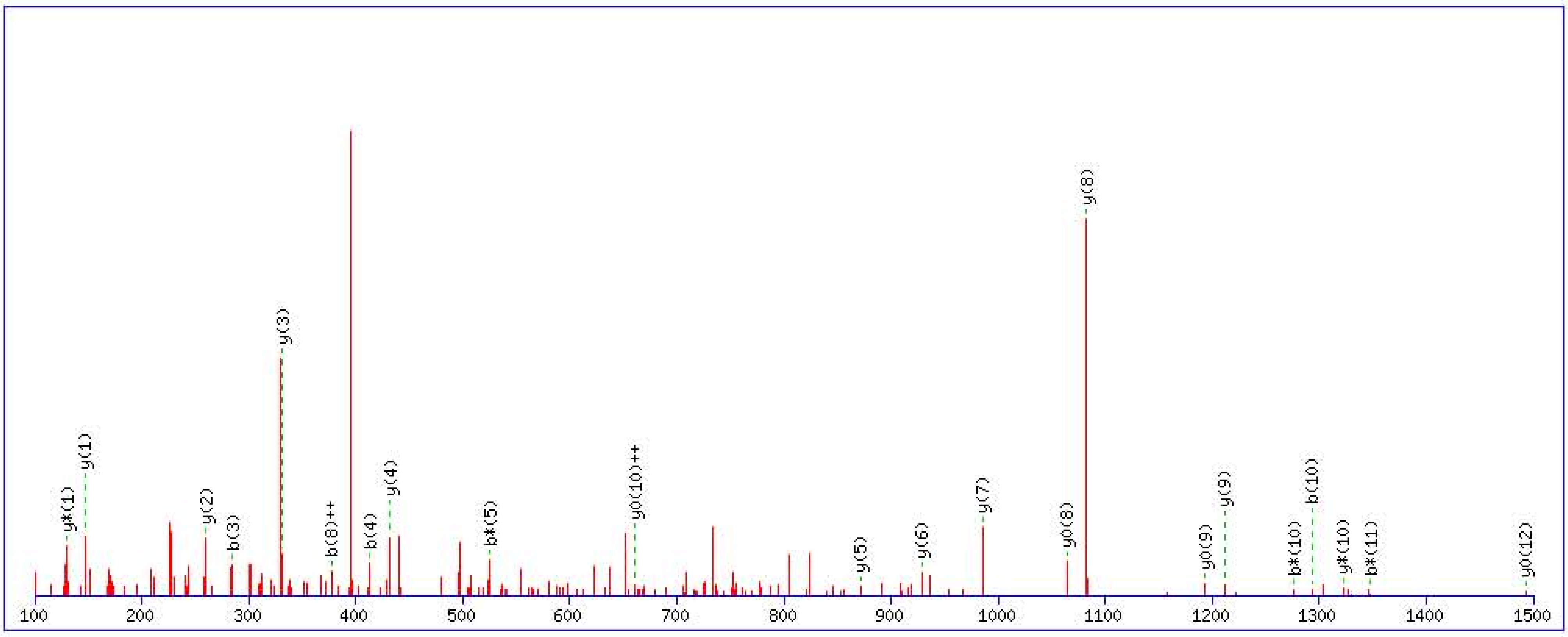
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGNQEPGGQTALK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

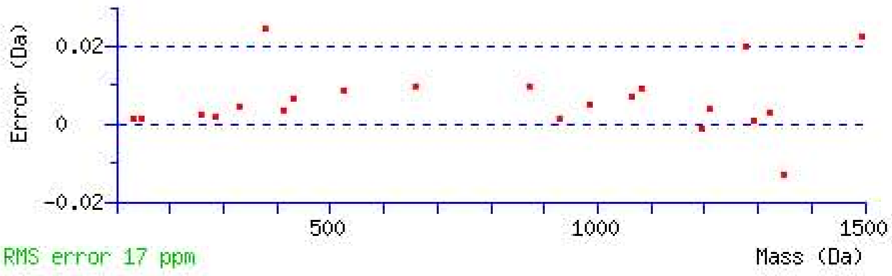
Match to Query 43219: 1622.853582 from(541.958470,3+) rtinseconds(1589) index(4342)
Title: Locus:1.1.1.2685.14 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

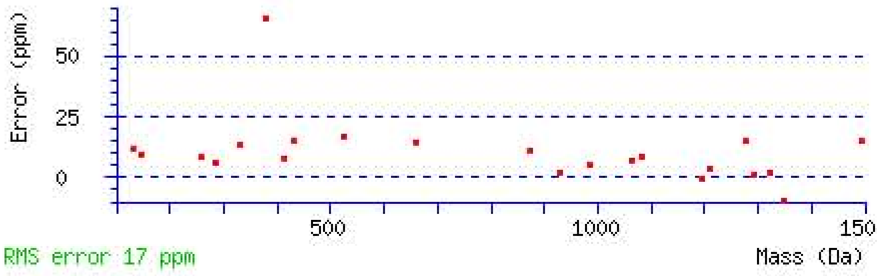
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1622.845016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0019
Matches : 22/126 fragment ions using 60 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							13
2	171.112804	86.060040					G	1510.768241	755.887759	1493.741692	747.374484	1492.757676	746.882476	12
3	**285.155731**	143.081504	268.129182	134.568229			N	1453.746777	727.377027	1436.720228	718.863752	1435.736212	718.371744	11
4	**413.214309**	207.110793	396.187760	198.597518			Q	1339.703850	670.355563	1322.677301	661.842289	1321.693285	661.350281	10
5	542.256902	271.632089	525.230353	263.118815	524.246337	262.626807	E	***1211.645272***	606.326274	1194.618723	597.813000	1193.634707	597.320991	9
6	639.309666	320.158471	622.283117	311.645197	621.299101	311.153189	P	***1082.602679***	541.804978	1065.576130	533.291703	1064.592114	532.799695	8
7	696.331130	348.669203	679.304581	340.155929	678.320565	339.663921	G	***985.549915***	493.278596	968.523366	484.765321	967.539350	484.273313	7
8	753.352594	377.179935	736.326045	368.666661	735.342029	368.174653	G	***928.528451***	464.767864	911.501902	456.254589	910.517886	455.762581	6
9	1192.577920	596.792598	1175.551371	588.279324	1174.567355	587.787316	Q	***871.506987***	436.257132	854.480438	427.743857	853.496422	427.251849	5
10	**1293.625599**	647.316438	1276.599050	638.803163	1275.615034	638.311155	T	***432.281661***	216.644468	415.255112	208.131194	414.271096	207.639186	4
11	1364.662713	682.834995	1347.636164	674.321720	1346.652148	673.829712	A	***331.233982***	166.120629	314.207433	157.607354			3
12	1477.746777	739.377027	1460.720228	730.863752	1459.736212	730.371744	L	***260.196868***	130.602072	243.170319	122.088797			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	1622.845016	0.008566	LGNQEPGGQTALK
5.8	1622.845016	0.008566	LGNQEPGGQTALK
4.0	1622.858917	-0.005335	SVLLMELEVNYGLK

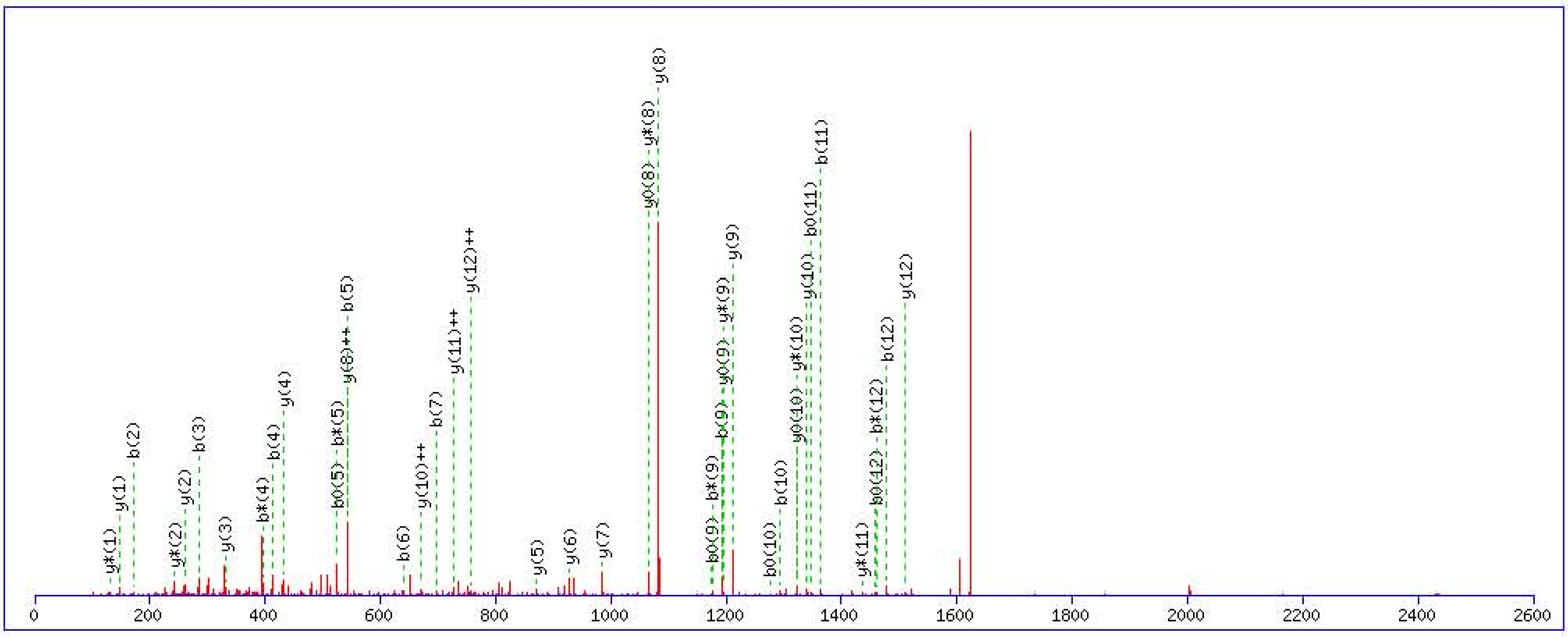
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGNQEPGGQTALK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

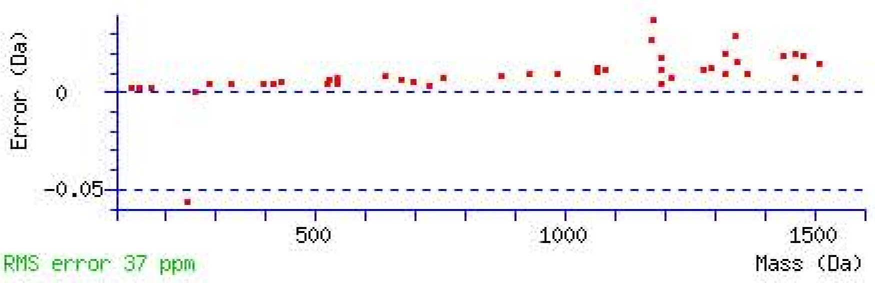
Match to Query 43222: 1622.856528 from(812.435540,2+) rtinseconds(1581) index(4300)
Title: Locus:1.1.1.2682.16 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

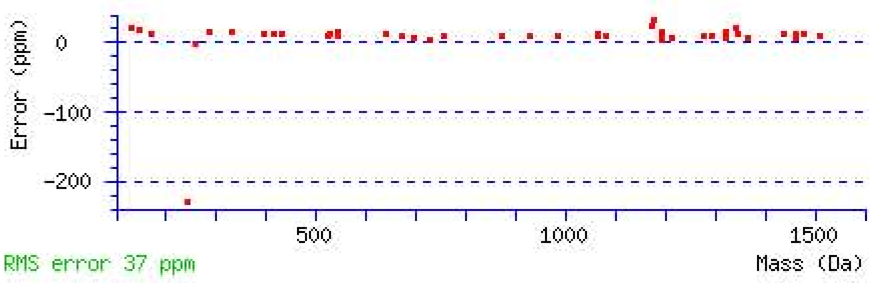
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1622.845016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 2.4e-005
Matches : 43/126 fragment ions using 93 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							13
2	**171.112804**	86.060040					G	***1510.768241***	755.887759	1493.741692	747.374484	1492.757676	746.882476	12
3	**285.155731**	143.081504	268.129182	134.568229			N	1453.746777	727.377027	1436.720228	718.863752	1435.736212	718.371744	11
4	**413.214309**	207.110793	396.187760	198.597518			Q	***1339.703850***	670.355563	1322.677301	661.842289	1321.693285	661.350281	10
5	**542.256902**	271.632089	525.230353	263.118815	524.246337	262.626807	E	***1211.645272***	606.326274	1194.618723	597.813000	1193.634707	597.320991	9
6	**639.309666**	320.158471	622.283117	311.645197	621.299101	311.153189	P	***1082.602679***	541.804978	1065.576130	533.291703	1064.592114	532.799695	8
7	**696.331130**	348.669203	679.304581	340.155929	678.320565	339.663921	G	***985.549915***	493.278596	968.523366	484.765321	967.539350	484.273313	7
8	753.352594	377.179935	736.326045	368.666661	735.342029	368.174653	G	***928.528451***	464.767864	911.501902	456.254589	910.517886	455.762581	6
9	**1192.577920**	596.792598	1175.551371	588.279324	1174.567355	587.787316	Q	***871.506987***	436.257132	854.480438	427.743857	853.496422	427.251849	5
10	**1293.625599**	647.316438	1276.599050	638.803163	1275.615034	638.311155	T	***432.281661***	216.644468	415.255112	208.131194	414.271096	207.639186	4
11	**1364.662713**	682.834995	1347.636164	674.321720	1346.652148	673.829712	A	***331.233982***	166.120629	314.207433	157.607354			3
12	**1477.746777**	739.377027	1460.720228	730.863752	1459.736212	730.371744	L	***260.196868***	130.602072	243.170319	122.088797			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.9	1622.845016	0.011512	LGNQEPGGQTALK
25.5	1622.845016	0.011512	LGNQEPGGQTALK
7.2	1622.858917	-0.002389	SVLLMELEVNYGLK
5.8	1622.837601	0.018927	SQSEKQTYLEVRR
1.9	1622.878021	-0.021493	RLQPPDFIDPLANK
1.8	1622.860260	-0.003732	EHSAFQAPAVKK
1.8	1622.864288	-0.007760	FPLPSMYRALVWK
1.8	1622.849045	0.007483	IPMPDFDLHLKGPK
0.2	1622.870132	-0.013604	QAKPAEELLEGK

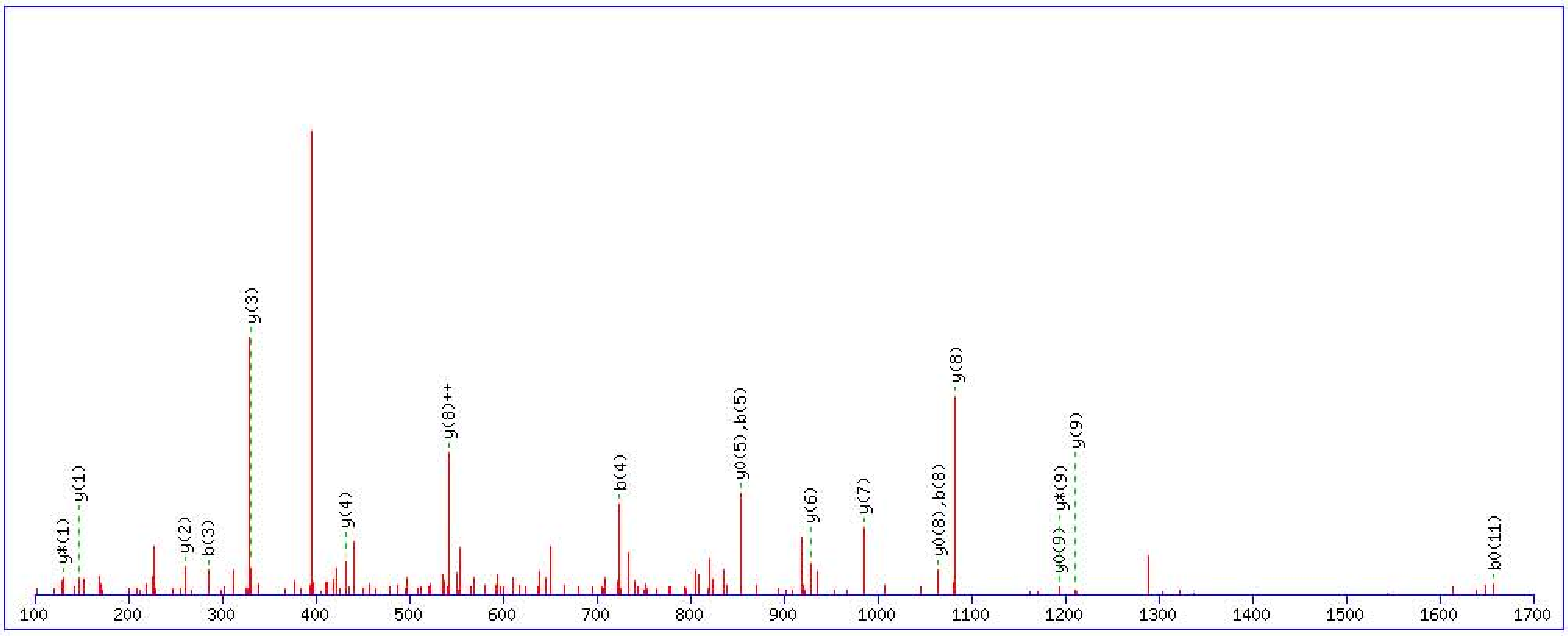
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGNQEPGGQTALK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

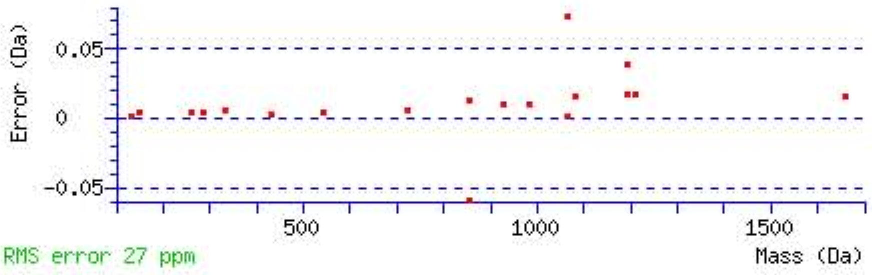
Match to Query 51388: 1934.028342 from(645.683390,3+) rtinseconds(1942) index(6683)
Title: Locus:1.1.1.2808.10 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

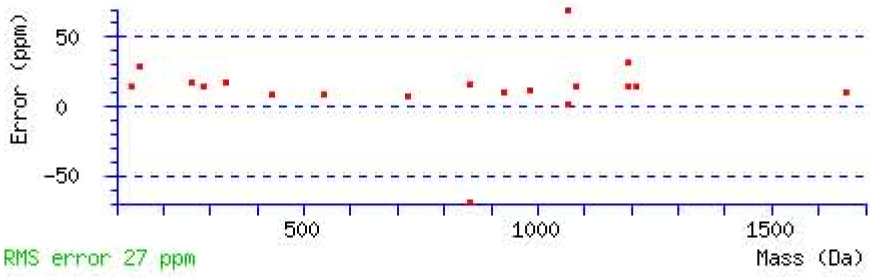
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1934.011765
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.018
Matches : 19/126 fragment ions using 43 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							13
2	171.112804	86.060040					G	1821.934989	911.471133	1804.908440	902.957858	1803.924424	902.465850	12
3	**285.155731**	143.081504	268.129182	134.568229			N	1764.913525	882.960400	1747.886976	874.447126	1746.902960	873.955118	11
4	**724.381057**	362.694167	707.354508	354.180892			Q	1650.870598	825.938937	1633.844049	817.425663	1632.860033	816.933654	10
5	**853.423650**	427.215463	836.397101	418.702189	835.413085	418.210181	E	***1211.645272***	606.326274	1194.618723	597.813000	1193.634707	597.320991	9
6	950.476414	475.741845	933.449865	467.228571	932.465849	466.736563	P	***1082.602679***	541.804977	1065.576130	533.291703	1064.592114	532.799695	8
7	1007.497878	504.252577	990.471329	495.739303	989.487313	495.247295	G	***985.549915***	493.278595	968.523366	484.765321	967.539350	484.273313	7
8	**1064.519342**	532.763309	1047.492793	524.250035	1046.508777	523.758027	G	***928.528451***	464.767863	911.501902	456.254589	910.517886	455.762581	6
9	1503.744668	752.375972	1486.718119	743.862698	1485.734103	743.370690	Q	871.506987	436.257132	854.480438	427.743857	853.496422	427.251849	5
10	1604.792347	802.899812	1587.765798	794.386537	1586.781782	793.894529	T	***432.281661***	216.644468	415.255112	208.131194	414.271096	207.639186	4
11	1675.829461	838.418369	1658.802912	829.905094	1657.818896	829.413086	A	***331.233982***	166.120629	314.207433	157.607354			3
12	1788.913525	894.960400	1771.886976	886.447126	1770.902960	885.955118	L	***260.196868***	130.602072	243.170319	122.088797			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.5	1934.011765	0.016577	LGNQEPGGQTALK
9.0	1934.032867	-0.004525	KSRPLTGLMDLAKEMTK

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

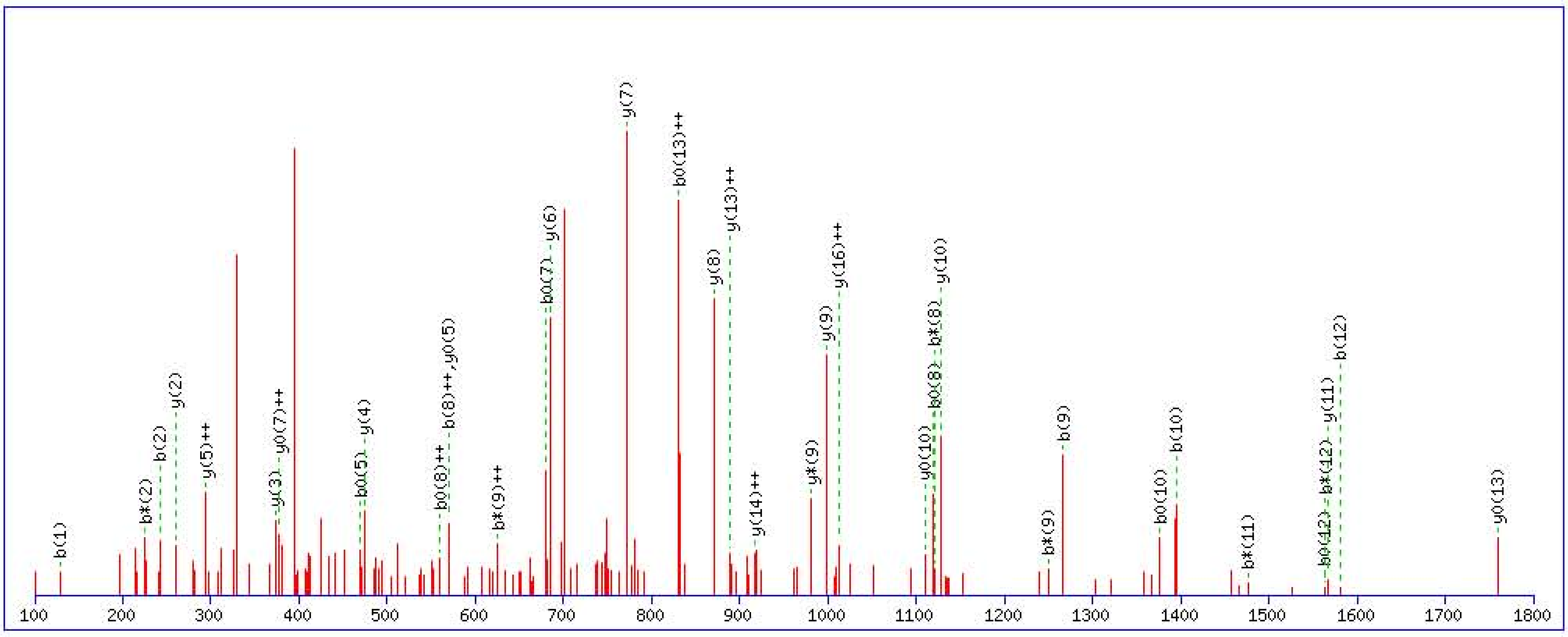
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLTSGPNQEQVSPLTLLK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

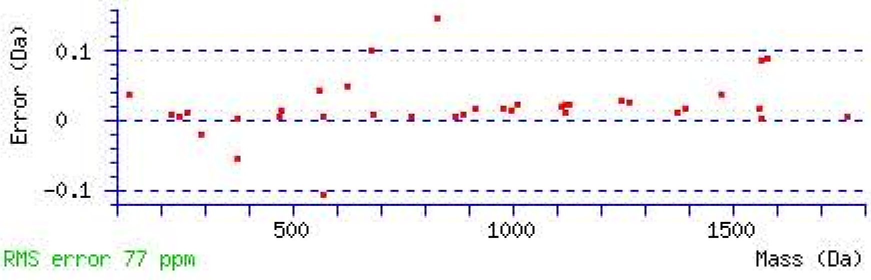
Match to Query 59736: 2263.251942 from(755.424590,3+) rtinseconds(2502) index(10243)
Title: Locus:1.1.1.3003.22 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

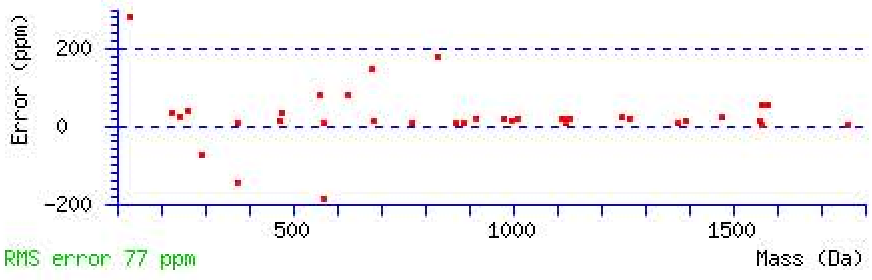
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2263.224594
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 8.2e-005
Matches : 37/194 fragment ions using 59 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.065854**	65.036565	112.039305	56.523291			Q							18
2	**242.149918**	121.578597	225.123369	113.065323			L	2136.173304	1068.590290	2119.146755	1060.077015	2118.162739	1059.585007	17
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	2023.089240	1012.048258	2006.062691	1003.534984	2005.078675	1003.042976	16
4	430.229625	215.618450	413.203076	207.105176	412.219060	206.613168	S	1922.041561	961.524419	1905.015012	953.011144	1904.030996	952.519136	15
5	487.251089	244.129182	470.224540	235.615908	469.240524	235.123900	G	1835.009533	918.008405	1817.982984	909.495130	1816.998968	909.003122	14
6	584.303853	292.655565	567.277304	284.142290	566.293288	283.650282	P	1777.988069	889.497673	1760.961520	880.984398	1759.977504	880.492390	13
7	698.346780	349.677028	681.320231	341.163753	680.336215	340.671745	N	1680.935305	840.971291	1663.908756	832.458016	1662.924740	831.966008	12
8	1137.572106	569.289691	1120.545557	560.776416	1119.561541	560.284408	Q	***1566.892378***	783.949827	1549.865829	775.436553	1548.881813	774.944545	11
9	**1266.614699**	633.810988	1249.588150	625.297713	1248.604134	624.805705	E	***1127.667052***	564.337164	1110.640503	555.823890	1109.656487	555.331882	10
10	**1394.673277**	697.840277	1377.646728	689.327002	1376.662712	688.834994	Q	***998.624459***	499.815868	981.597910	491.302593	980.613894	490.810585	9
11	1493.741691	747.374484	1476.715142	738.861209	1475.731126	738.369201	V	***870.565881***	435.786579	853.539332	427.273304	852.555316	426.781296	8
12	**1580.773719**	790.890498	1563.747170	782.377223	1562.763154	781.885215	S	***771.497467***	386.252372	754.470918	377.739097	753.486902	377.247089	7
13	1677.826483	839.416880	1660.799934	830.903605	1659.815918	830.411597	P	***684.465439***	342.736358	667.438890	334.223083	666.454874	333.731075	6
14	1790.910547	895.958912	1773.883998	887.445637	1772.899982	886.953629	L	587.412675	294.209976	570.386126	285.696701	569.402110	285.204693	5
15	1891.958226	946.482751	1874.931677	937.969477	1873.947661	937.477469	T	***474.328611***	237.667944	457.302062	229.154669	456.318046	228.662661	4
16	2005.042290	1003.024783	1988.015741	994.511509	1987.031725	994.019501	L	***373.280932***	187.144104	356.254383	178.630830			3
17	2118.126354	1059.566815	2101.099805	1051.053540	2100.115789	1050.561532	L	***260.196868***	130.602072	243.170319	122.088798			2
18							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.9	2263.224594	0.027348	QLTSGPNQEQVSPLTLLK
35.5	2263.224594	0.027348	QLTSGPNQEQVSPLTLLK
25.6	2263.224594	0.027348	QLTSGPNQEQVSPLTLLK
4.3	2263.224594	0.027348	GLALSSNKVKSVVMVVFDNEK

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

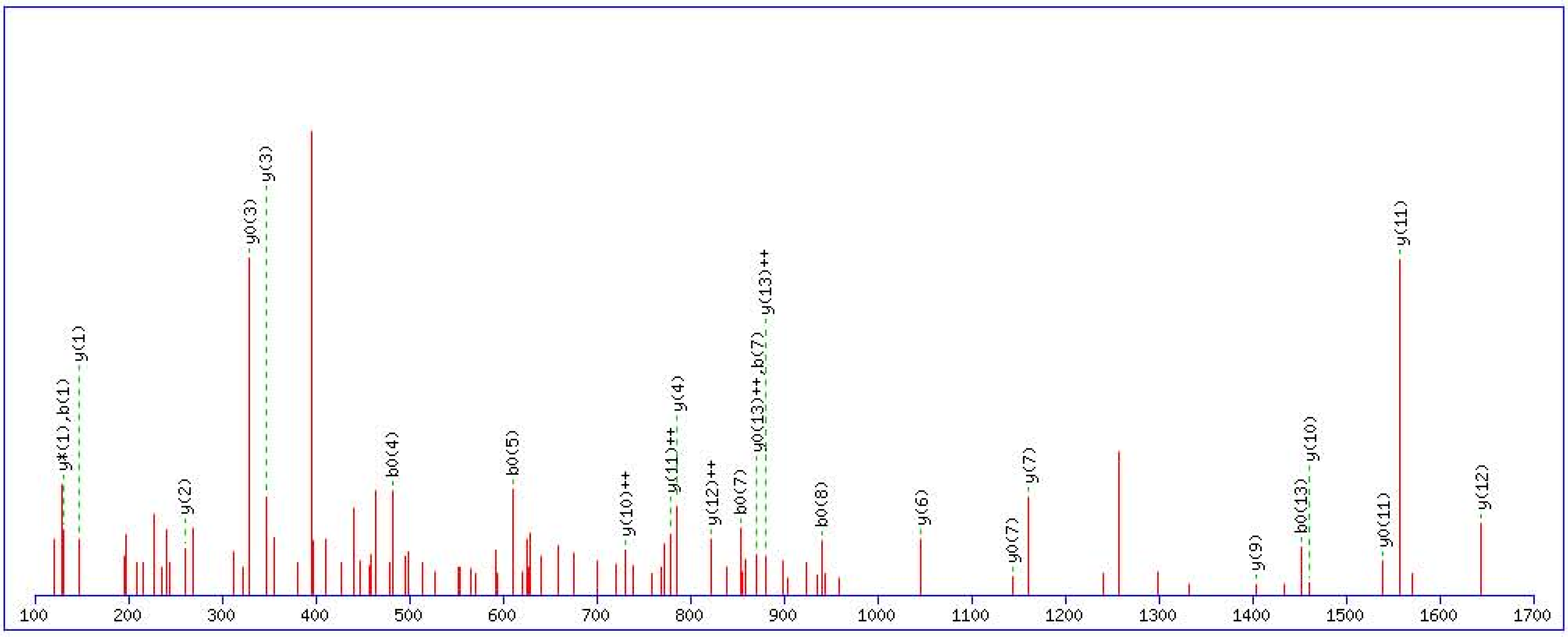
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELKEQQDSPGNKDFLQSLK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

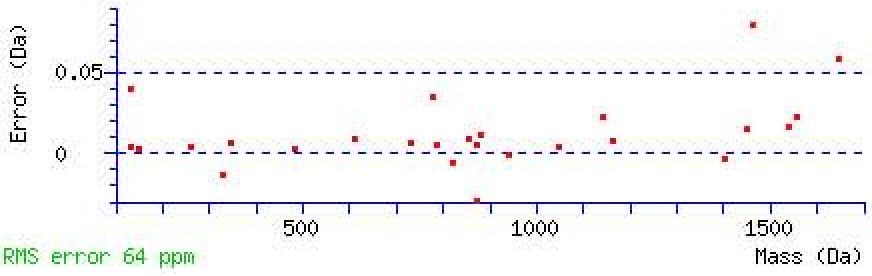
Match to Query 65702: 2514.300896 from(629.582500,4+) rtinseconds(1882) index(6243)
Title: Locus:1.1.1.2787.19 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

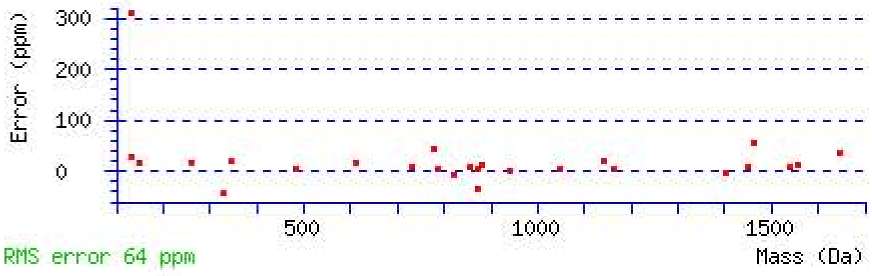
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2514.278793
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00014
Matches : 26/208 fragment ions using 52 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							19
2	243.133933	122.070605			225.123368	113.065322	L	2386.243508	1193.625392	2369.216959	1185.112117	2368.232943	1184.620109	18
3	371.228896	186.118086	354.202347	177.604812	353.218331	177.112804	K	2273.159444	1137.083360	2256.132895	1128.570085	2255.148879	1128.078077	17
4	500.271489	250.639383	483.244940	242.126108	482.260924	241.634100	E	2145.064481	1073.035878	2128.037932	1064.522604	2127.053916	1064.030596	16
5	628.330067	314.668672	611.303518	306.155397	610.319502	305.663389	Q	2016.021888	1008.514582	1998.995339	1000.001308	1998.011323	999.509300	15
6	756.388645	378.697961	739.362096	370.184686	738.378080	369.692678	Q	1887.963310	944.485293	1870.936761	935.972019	1869.952745	935.480011	14
7	**871.415588**	436.211432	854.389039	427.698158	853.405023	427.206150	D	1759.904732	880.456004	1742.878183	871.942730	1741.894167	871.450722	13
8	958.447616	479.727446	941.421067	471.214172	940.437051	470.722164	S	***1644.877789***	822.942533	1627.851240	814.429258	1626.867224	813.937250	12
9	1055.500380	528.253828	1038.473831	519.740554	1037.489815	519.248545	P	***1557.845761***	779.426519	1540.819212	770.913244	1539.835196	770.421236	11
10	1112.521844	556.764560	1095.495295	548.251285	1094.511279	547.759277	G	***1460.792997***	730.900137	1443.766448	722.386862	1442.782432	721.894854	10
11	1226.564771	613.786023	1209.538222	605.272749	1208.554206	604.780741	N	***1403.771533***	702.389405	1386.744984	693.876130	1385.760968	693.384122	9
12	1354.659734	677.833505	1337.633185	669.320230	1336.649169	668.828222	K	1289.728606	645.367941	1272.702057	636.854667	1271.718041	636.362659	8
13	1469.686677	735.346976	1452.660128	726.833702	1451.676112	726.341694	D	***1161.633643***	581.320460	1144.607094	572.807185	1143.623078	572.315177	7
14	1616.755091	808.881184	1599.728542	800.367909	1598.744526	799.875901	F	***1046.606700***	523.806988	1029.580151	515.293714	1028.596135	514.801706	6
15	1729.839155	865.423215	1712.812606	856.909941	1711.828590	856.417933	L	899.538286	450.272781	882.511737	441.759507	881.527721	441.267499	5
16	2169.064481	1085.035878	2152.037932	1076.522604	2151.053916	1076.030596	Q	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
17	2256.096509	1128.551892	2239.069960	1120.038618	2238.085944	1119.546610	S	***347.228896***	174.118086	330.202347	165.604812	329.218331	165.112804	3
18	2369.180573	1185.093925	2352.154024	1176.580650	2351.170008	1176.088642	L	***260.196868***	130.602072	243.170319	122.088798			2
19							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.5	2514.278793	0.022103	ELKEQQDSPGNKDFLQSLK
3.4	2514.268951	0.031945	GNSGPPGIVGQKGDPGYPGPAGPK

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

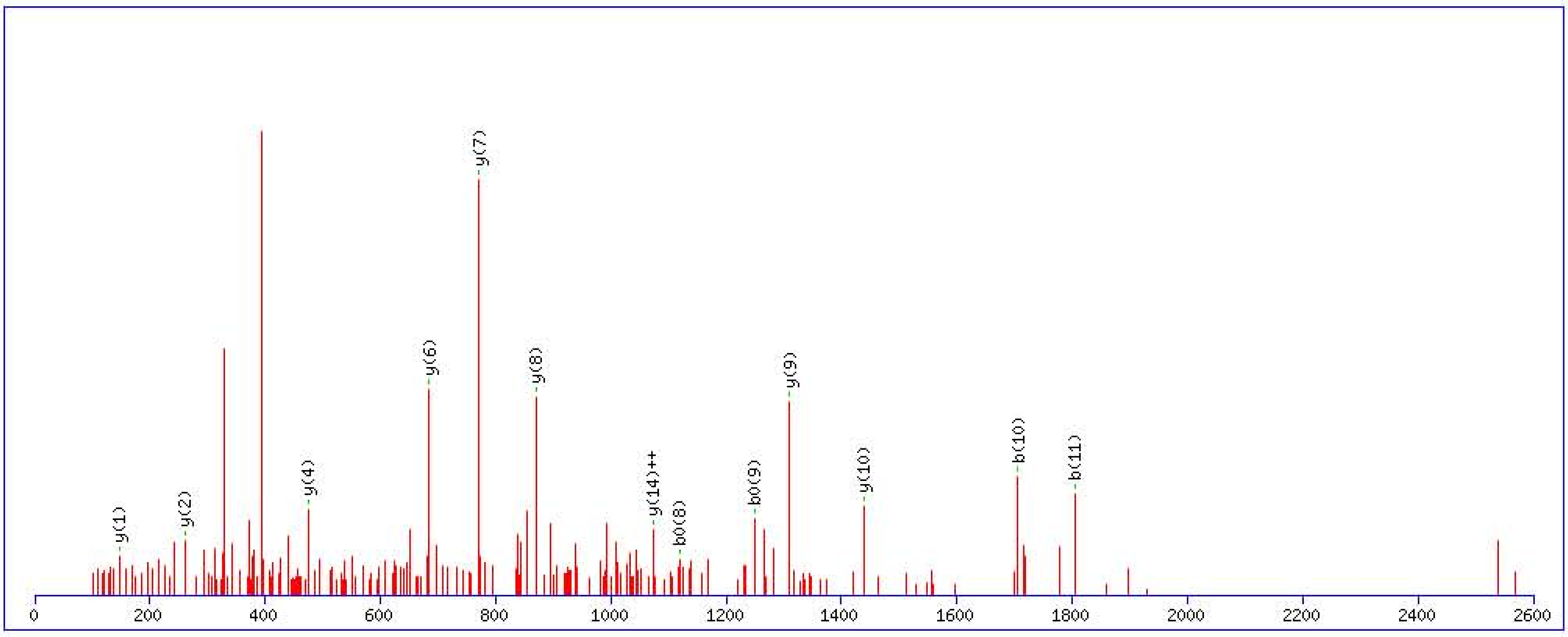
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLTSGPNQEQVSPLTLLK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

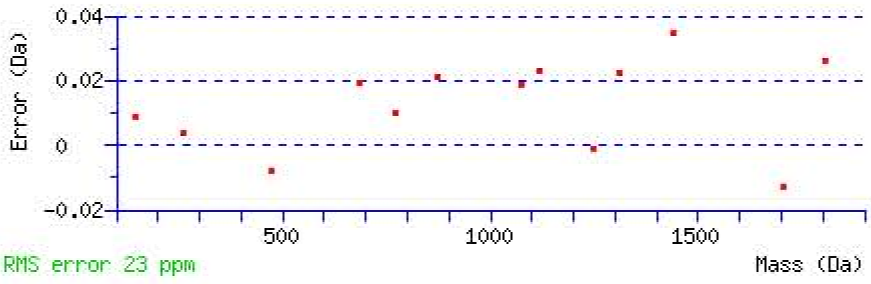
Match to Query 66306: 2574.423582 from(859.148470,3+) rtinseconds(2681) index(11246)
Title: Locus:1.1.1.3065.14 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

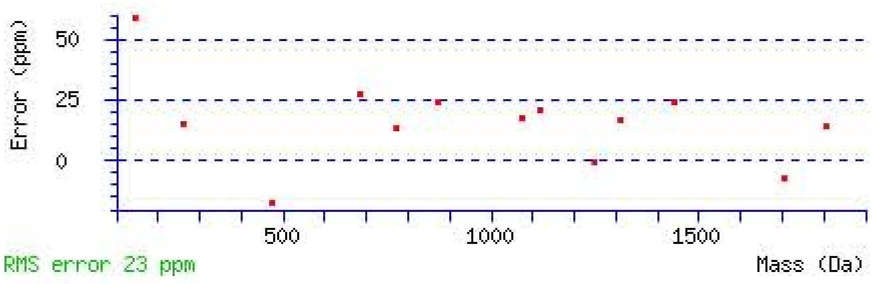
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2574.391342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00028
Matches : 13/194 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							18
2	242.149918	121.578597	225.123369	113.065323			L	2447.340052	1224.173664	2430.313503	1215.660389	2429.329487	1215.168381	17
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	2334.255988	1167.631632	2317.229439	1159.118357	2316.245423	1158.626349	16
4	430.229625	215.618450	413.203076	207.105176	412.219060	206.613168	S	2233.208309	1117.107792	2216.181760	1108.594518	2215.197744	1108.102510	15
5	487.251089	244.129182	470.224540	235.615908	469.240524	235.123900	G	2146.176281	1073.591778	2129.149732	1065.078504	2128.165716	1064.586496	14
6	584.303853	292.655565	567.277304	284.142290	566.293288	283.650282	P	2089.154817	1045.081046	2072.128268	1036.567772	2071.144252	1036.075764	13
7	698.346780	349.677028	681.320231	341.163753	680.336215	340.671745	N	1992.102053	996.554665	1975.075504	988.041390	1974.091488	987.549382	12
8	1137.572106	569.289691	1120.545557	560.776416	1119.561541	560.284408	Q	1878.059126	939.533201	1861.032577	931.019927	1860.048561	930.527919	11
9	1266.614699	633.810988	1249.588150	625.297713	1248.604134	624.805705	E	***1438.833800***	719.920538	1421.807251	711.407264	1420.823235	710.915256	10
10	**1705.840025**	853.423651	1688.813476	844.910376	1687.829460	844.418368	Q	***1309.791207***	655.399242	1292.764658	646.885967	1291.780642	646.393959	9
11	**1804.908439**	902.957858	1787.881890	894.444583	1786.897874	893.952575	V	***870.565881***	435.786579	853.539332	427.273304	852.555316	426.781296	8
12	1891.940467	946.473872	1874.913918	937.960597	1873.929902	937.468589	S	***771.497467***	386.252372	754.470918	377.739097	753.486902	377.247089	7
13	1988.993231	995.000254	1971.966682	986.486979	1970.982666	985.994971	P	***684.465439***	342.736358	667.438890	334.223083	666.454874	333.731075	6
14	2102.077295	1051.542285	2085.050746	1043.029011	2084.066730	1042.537003	L	587.412675	294.209976	570.386126	285.696701	569.402110	285.204693	5
15	2203.124974	1102.066125	2186.098425	1093.552850	2185.114409	1093.060842	T	***474.328611***	237.667944	457.302062	229.154669	456.318046	228.662661	4
16	2316.209038	1158.608157	2299.182489	1150.094882	2298.198473	1149.602874	L	373.280932	187.144104	356.254383	178.630830			3
17	2429.293102	1215.150189	2412.266553	1206.636914	2411.282537	1206.144906	L	***260.196868***	130.602072	243.170319	122.088798			2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.9	2574.391342	0.032240	QLTSGPNQEQVSPLTLLK
45.8	2574.391342	0.032240	QLTSGPNQEQVSPLTLLK
20.2	2574.391342	0.032240	QLTSGPNQEQVSPLTLLK

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

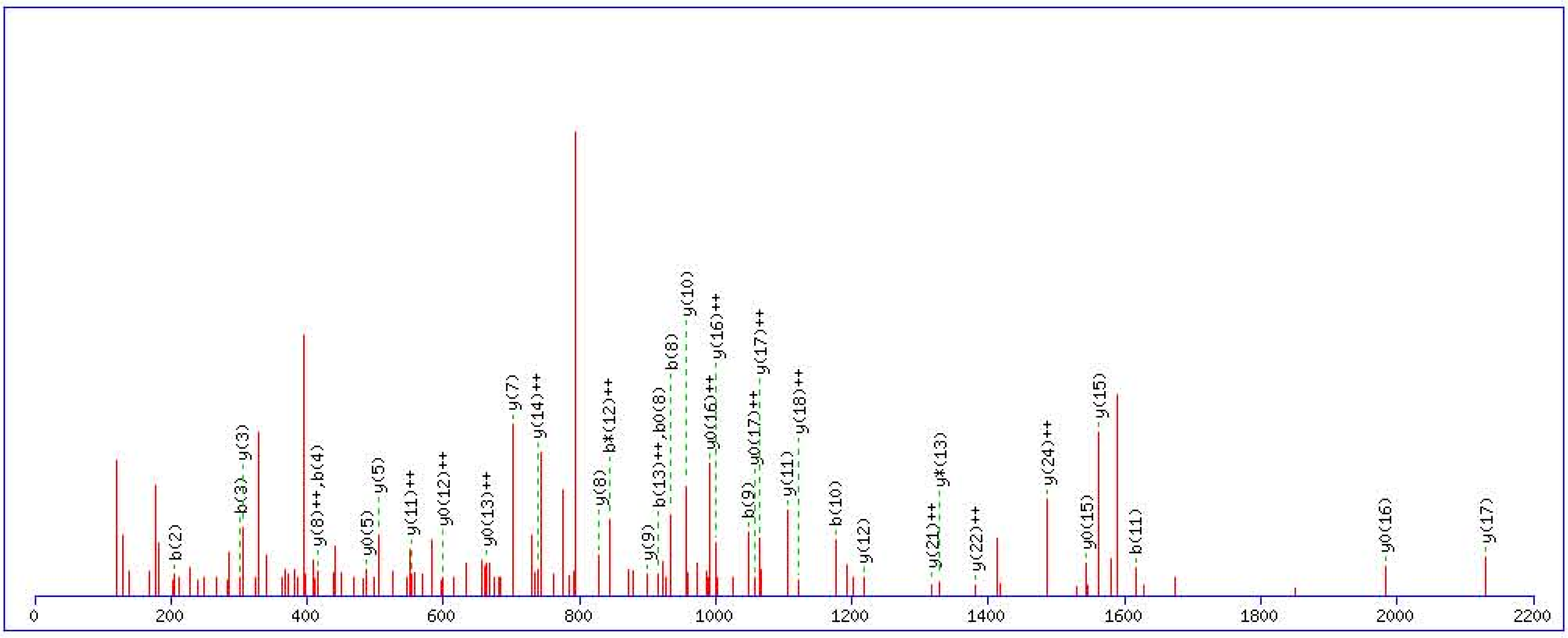
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFPIKEDFLEQSEQLFGAKPVSLTGK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

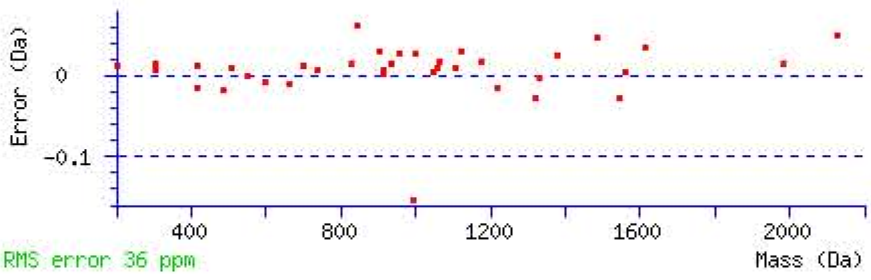
Match to Query 73208: 3175.697296 from(794.931600,4+) rtinseconds(2712) index(11496)
Title: Locus:1.1.1.3076.16 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

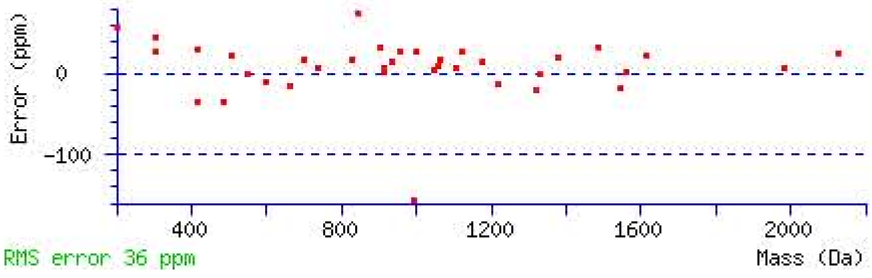


```
Monoisotopic mass of neutral peptide Mr(calc): 3175.662750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0022
Matches : 37/278 fragment ions using 93 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							26
2	**205.097154**	103.052215					F	3119.648573	1560.327924	3102.622024	1551.814650	3101.638008	1551.322642	25
3	**302.149918**	151.578597					P	2972.580159	1486.793717	2955.553610	1478.280443	2954.569594	1477.788435	24
4	**415.233982**	208.120629					I	2875.527395	1438.267335	2858.500846	1429.754061	2857.516830	1429.262053	23
5	543.328945	272.168111	526.302396	263.654836			K	2762.443331	1381.725303	2745.416782	1373.212029	2744.432766	1372.720021	22
6	672.371538	336.689407	655.344989	328.176133	654.360973	327.684125	E	2634.348368	1317.677822	2617.321819	1309.164547	2616.337803	1308.672539	21
7	787.398481	394.202879	770.371932	385.689604	769.387916	385.197596	D	2505.305775	1253.156525	2488.279226	1244.643251	2487.295210	1244.151243	20
8	**934.466895**	467.737086	917.440346	459.223811	916.456330	458.731803	F	2390.278832	1195.643054	2373.252283	1187.129779	2372.268267	1186.637771	19
9	**1047.550959**	524.279117	1030.524410	515.765843	1029.540394	515.273835	L	2243.210418	1122.108847	2226.183869	1113.595572	2225.199853	1113.103564	18
10	**1176.593552**	588.800414	1159.567003	580.287140	1158.582987	579.795132	E	***2130.126354***	1065.566815	2113.099805	1057.053540	2112.115789	1056.561532	17
11	**1615.818878**	808.413077	1598.792329	799.899803	1597.808313	799.407795	Q	2001.083761	1001.045519	1984.057212	992.532244	1983.073196	992.040236	16
12	1702.850906	851.929091	1685.824357	843.415817	1684.840341	842.923809	S	***1561.858435***	781.432856	1544.831886	772.919581	1543.847870	772.427573	15
13	1831.893499	916.450388	1814.866950	907.937113	1813.882934	907.445105	E	1474.826407	737.916842	1457.799858	729.403567	1456.815842	728.911559	14
14	1959.952077	980.479677	1942.925528	971.966402	1941.941512	971.474394	Q	1345.783814	673.395545	1328.757265	664.882271	1327.773249	664.390263	13
15	2073.036141	1037.021709	2056.009592	1028.508434	2055.025576	1028.016426	L	***1217.725236***	609.366256	1200.698687	600.852982	1199.714671	600.360974	12
16	2220.104555	1110.555916	2203.078006	1102.042641	2202.093990	1101.550633	F	***1104.641172***	552.824224	1087.614623	544.310949	1086.630607	543.818941	11
17	2277.126019	1139.066648	2260.099470	1130.553373	2259.115454	1130.061365	G	***957.572758***	479.290017	940.546209	470.776743	939.562193	470.284735	10
18	2348.163133	1174.585205	2331.136584	1166.071930	2330.152568	1165.579922	A	***900.551294***	450.779285	883.524745	442.266011	882.540729	441.774003	9
19	2476.258096	1238.632686	2459.231547	1230.119412	2458.247531	1229.627404	K	***829.514180***	415.260728	812.487631	406.747453	811.503615	406.255445	8
20	2573.310860	1287.159068	2556.284311	1278.645794	2555.300295	1278.153786	P	***701.419217***	351.213246	684.392668	342.699972	683.408652	342.207964	7
21	2672.379274	1336.693275	2655.352725	1328.180001	2654.368709	1327.687993	V	604.366453	302.686864	587.339904	294.173590	586.355888	293.681582	6
22	2759.411302	1380.209289	2742.384753	1371.696015	2741.400737	1371.204007	S	***505.298039***	253.152657	488.271490	244.639383	487.287474	244.147375	5
23	2872.495366	1436.751321	2855.468817	1428.238047	2854.484801	1427.746039	L	418.266011	209.636643	401.239462	201.123369	400.255446	200.631361	4
24	2973.543045	1487.275161	2956.516496	1478.761886	2955.532480	1478.269878	T	***305.181947***	153.094611	288.155398	144.581337	287.171382	144.089329	3
25	3030.564509	1515.785893	3013.537960	1507.272618	3012.553944	1506.780610	G	204.134268	102.570772	187.107719	94.057497			2
26							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 36 ppm



RMS error 36 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.0	3175.662750	0.034546	GFPIKEDFLEQSEQLFGAKPVSLTGK
24.4	3175.662750	0.034546	GFPIKEDFLEQSEQLFGAKPVSLTGK

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

{MATRIX SCIENCE}

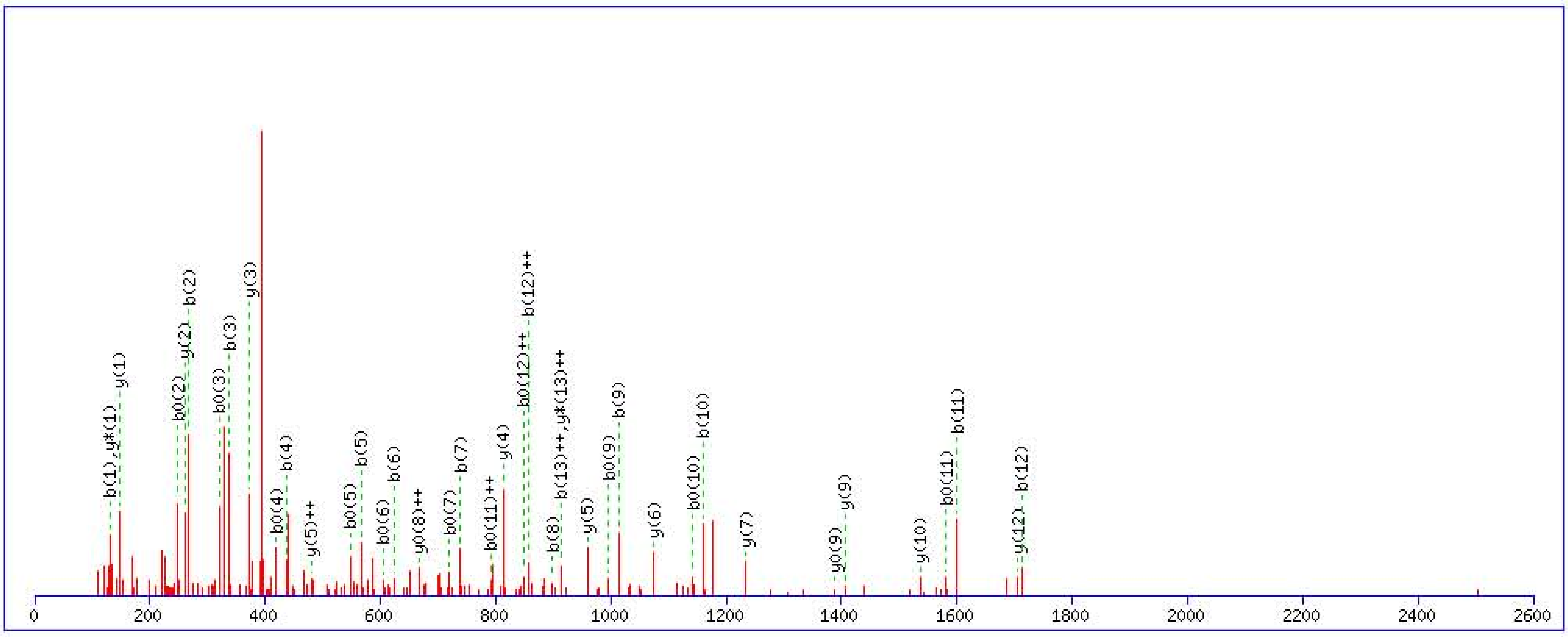
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHAVEGDCDFQLLK**
Found in **FETUA_HUMAN**, Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1

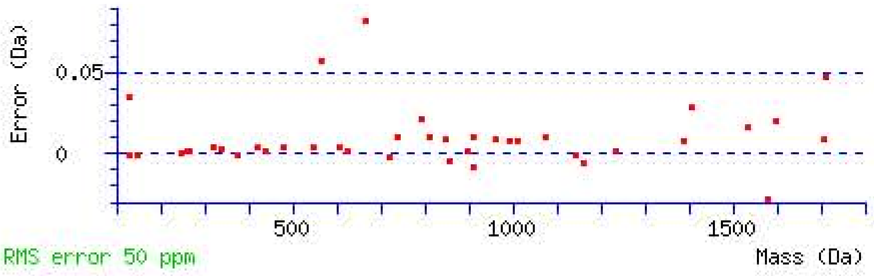
Match to Query 52300: 1970.939382 from(657.987070,3+) rtinseconds(2055) index(42474)
Title: Locus:1.1.1.2999.12 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

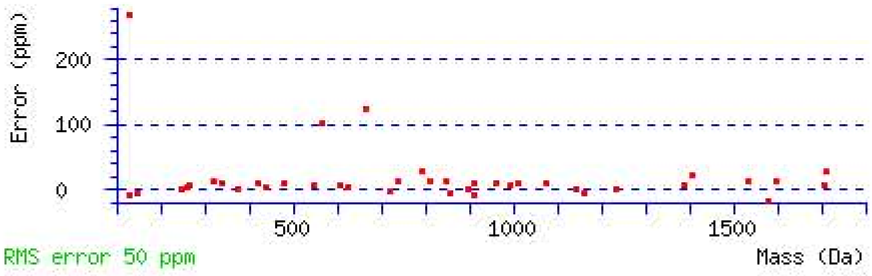
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1970.923019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 1.8e-006
Matches : 40/126 fragment ions using 71 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							14
2	***267.108781***	134.058028			249.098216	125.052746	H	1842.887704	921.947490	1825.861155	913.434216	1824.877139	912.942207	13
3	***338.145895***	169.576585			320.135330	160.571303	A	**1705.828792**	853.418034	1688.802243	844.904760	1687.818227	844.412752	12
4	***437.214309***	219.110792			419.203744	210.105510	V	1634.791678	817.899477	1617.765129	809.386203	1616.781113	808.894195	11
5	***566.256902***	283.632089			548.246337	274.626807	E	**1535.723264**	768.365270	1518.696715	759.851996	1517.712699	759.359988	10
6	***623.278366***	312.142821			605.267801	303.137539	G	**1406.680671**	703.843974	1389.654122	695.330699	1388.670106	694.838691	9
7	***738.305309***	369.656293			720.294744	360.651010	D	1349.659207	675.333241	1332.632658	666.819967	1331.648642	666.327959	8
8	***898.335958***	449.671617			880.325393	440.666335	C	**1234.632264**	617.819770	1217.605715	609.306496	1216.621699	608.814488	7
9	***1013.362901***	507.185089			995.352336	498.179806	D	**1074.601615**	537.804446	1057.575066	529.291171	1056.591050	528.799163	6
10	***1160.431315***	580.719296			1142.420750	571.714013	F	**959.574672**	480.290974	942.548123	471.777700			5
11	***1599.656641***	800.331959	1582.630092	791.818684	1581.646076	791.326676	Q	**812.506258**	406.756767	795.479709	398.243493			4
12	***1712.740705***	**856.873991**	1695.714156	848.360716	1694.730140	847.868708	L	**373.280932**	187.144104	356.254383	178.630829			3
13	1825.824769	**913.416023**	1808.798220	904.902748	1807.814204	904.410740	L	**260.196868**	130.602072	243.170319	122.088797			2
14							K	**147.112804**	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.5	1970.923019	0.016363	EHAVEGDCDFQLLK
5.0	1970.965729	-0.026347	EAINGQREDTGDQQGLLK
3.3	1970.959381	-0.019999	NEEKPVQMMFKQSTFK
2.7	1970.959396	-0.020014	DVQSAMDRYTAFLK
1.3	1970.963882	-0.024500	EHWLYPQQITTNQWK

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

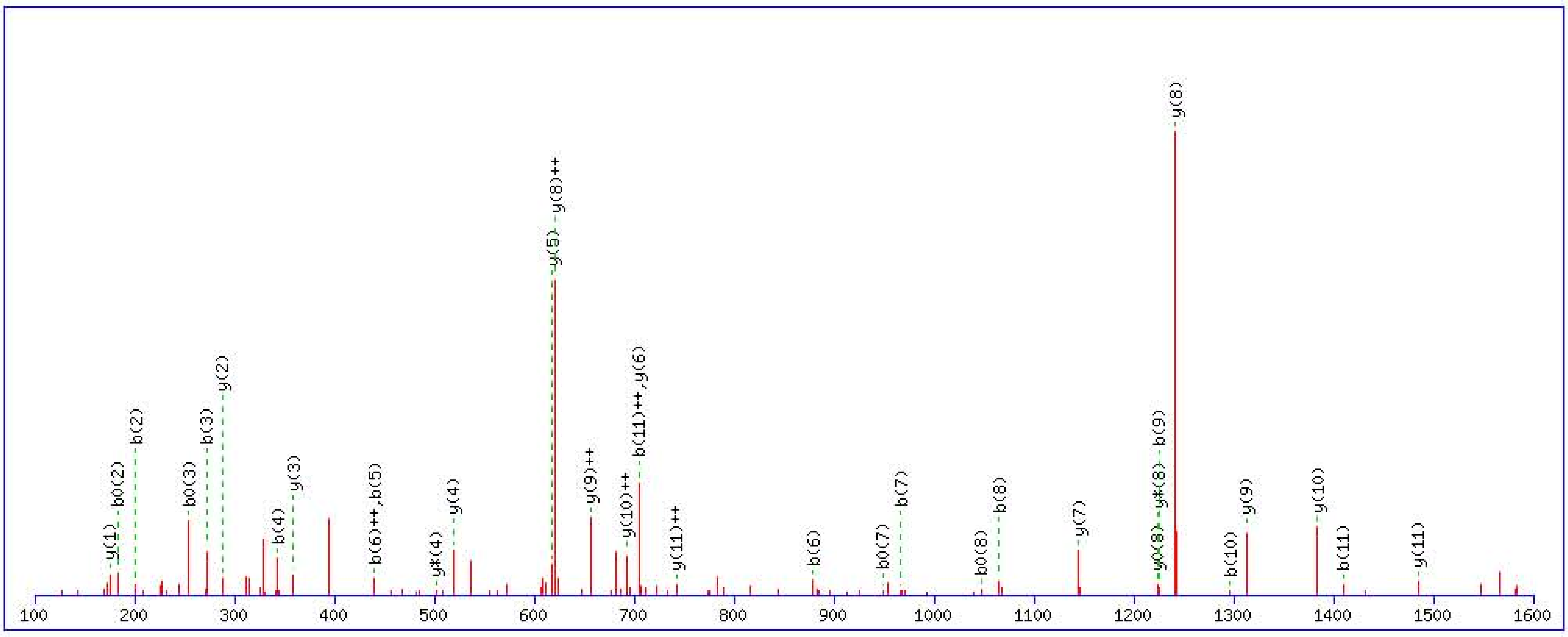
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTAAPQSVCALR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

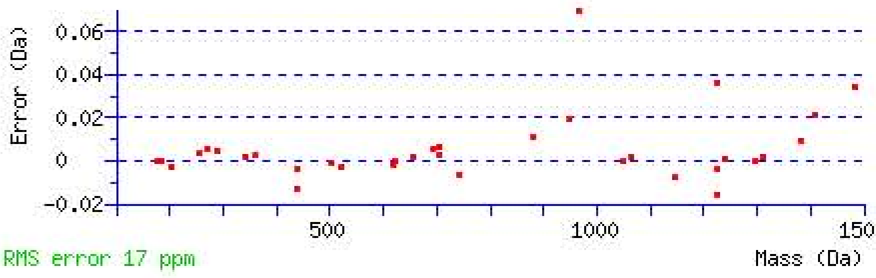
Match to Query 41197: 1582.841188 from(792.427870,2+) rtinseconds(1814) index(40818)
Title: Locus:1.1.1.2915.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

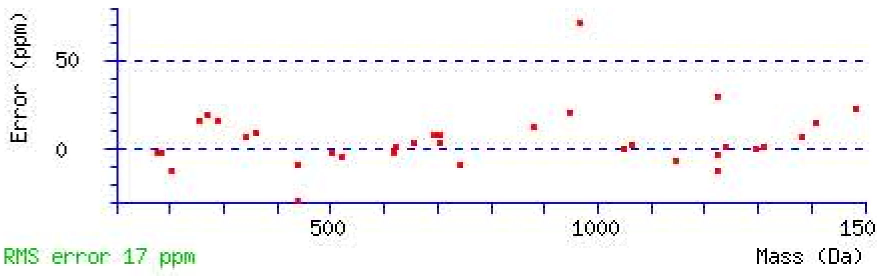
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1582.832352
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 2.7e-006
Matches : 34/110 fragment ions using 66 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							12
2	**201.123369**	101.065322			183.112804	92.060040	T	***1484.771218***	742.889247	1467.744669	734.375972	1466.760653	733.883964	11
3	**272.160483**	136.583879			254.149918	127.578597	A	***1383.723539***	692.365407	1366.696990	683.852133	1365.712974	683.360125	10
4	**343.197597**	172.102437			325.187032	163.097154	A	***1312.686425***	656.846850	1295.659876	648.333576	1294.675860	647.841568	9
5	**440.250361**	220.628819			422.239796	211.623536	P	***1241.649311***	621.328293	1224.622762	612.815019	1223.638746	612.323011	8
6	**879.475687**	**440.241482**	862.449138	431.728207	861.465122	431.236199	Q	***1144.596547***	572.801911	1127.569998	564.288637	1126.585982	563.796629	7
7	**966.507715**	483.757496	949.481166	475.244221	948.497150	474.752213	S	***705.371221***	353.189248	688.344672	344.675974	687.360656	344.183966	6
8	**1065.576129**	533.291703	1048.549580	524.778428	1047.565564	524.286420	V	***618.339193***	309.673234	601.312644	301.159960			5
9	**1225.606778**	613.307027	1208.580229	604.793753	1207.596213	604.301745	C	***519.270779***	260.139028	502.244230	251.625753			4
10	**1296.643892**	648.825584	1279.617343	640.312310	1278.633327	639.820302	A	***359.240130***	180.123703	342.213581	171.610428			3
11	**1409.727956**	**705.367616**	1392.701407	696.854342	1391.717391	696.362333	L	***288.203016***	144.605146	271.176467	136.091871			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.0	1582.832352	0.008836	VTAAPQSVCALR
8.1	1582.844040	-0.002852	APRHGPARDPGLPSR
3.3	1582.821564	0.019624	LSKAVATWHANTER
2.9	1582.836868	0.004320	LHTVDGHWVAPVPR
2.3	1582.846756	-0.005568	VTEVWTLPQVAGQR
1.9	1582.850067	-0.008879	AEQEASLQKLR
1.2	1582.853912	-0.012724	RPRDDAQISEKLR
1.1	1582.817535	0.023653	KTLSEETRQHQAR
1.0	1582.853912	-0.012724	RKPASGGLAASSSAPAR
0.7	1582.831451	0.009737	SAKELVEQDIQPAR

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

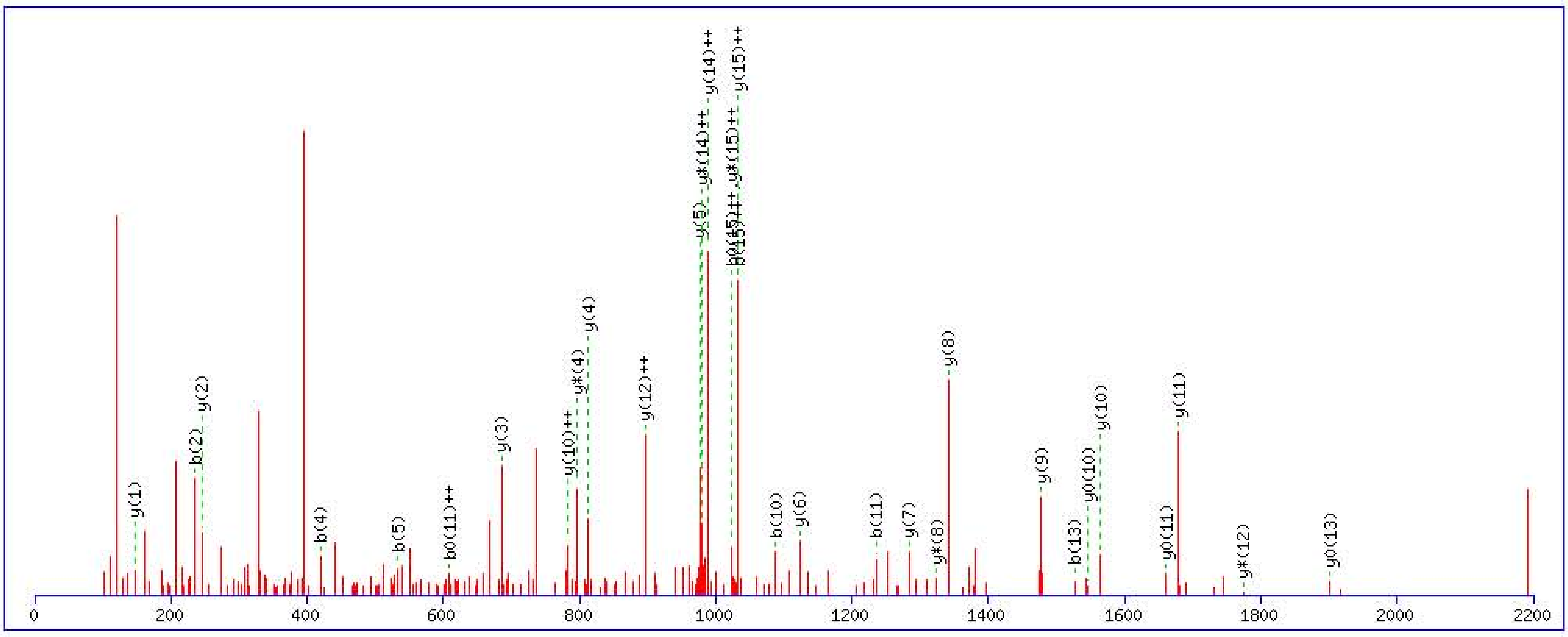
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSGQLNSHGCFYQQVK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

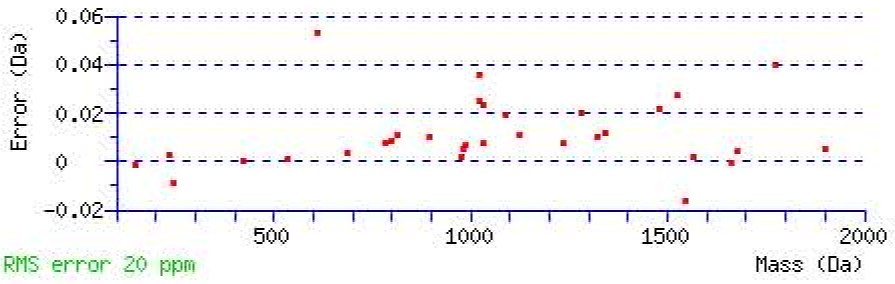
Match to Query 58315: 2210.056422 from(737.692750,3+) rtinseconds(1845) index(40970)
Title: Locus:1.1.1.2926.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

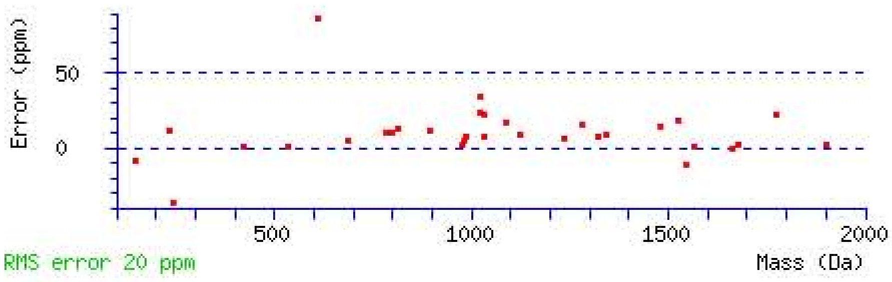
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2210.040131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00015
Matches : 32/154 fragment ions using 70 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							16
2	**235.107718**	118.057497			217.097153	109.052214	S	2063.978979	1032.493127	2046.952430	1023.979853	2045.968414	1023.487845	15
3	292.129182	146.568229			274.118617	137.562946	G	1976.946951	988.977114	1959.920402	980.463839	1958.936386	979.971831	14
4	**420.187760**	210.597518	403.161211	202.084243	402.177195	201.592235	Q	1919.925487	960.466382	1902.898938	951.953107	1901.914922	951.461099	13
5	**533.271824**	267.139550	516.245275	258.626276	515.261259	258.134268	L	1791.866909	896.437093	1774.840360	887.923818	1773.856344	887.431810	12
6	647.314751	324.161014	630.288202	315.647739	629.304186	315.155731	N	***1678.782845***	839.895061	1661.756296	831.381786	1660.772280	830.889778	11
7	734.346779	367.677028	717.320230	359.163753	716.336214	358.671745	S	***1564.739918***	782.873597	1547.713369	774.360323	1546.729353	773.868315	10
8	871.405691	436.206483	854.379142	427.693209	853.395126	427.201201	H	***1477.707890***	739.357583	1460.681341	730.844309			9
9	928.427155	464.717216	911.400606	456.203941	910.416590	455.711933	G	***1340.648978***	670.828127	1323.622429	662.314853			8
10	**1088.457804**	544.732540	1071.431255	536.219266	1070.447239	535.727257	C	***1283.627514***	642.317395	1266.600965	633.804121			7
11	**1235.526218**	618.266747	1218.499669	609.753473	1217.515653	609.261464	F	***1123.596865***	562.302071	1106.570316	553.788796			6
12	1398.589547	699.798412	1381.562998	691.285137	1380.578982	690.793129	Y	***976.528451***	488.767864	959.501902	480.254589			5
13	**1526.648125**	763.827700	1509.621576	755.314426	1508.637560	754.822418	Q	***813.465122***	407.236199	796.438573	398.722925			4
14	1965.873451	983.440364	1948.846902	974.927089	1947.862886	974.435081	Q	***685.406544***	343.206910	668.379995	334.693636			3
15	2064.941865	1032.974570	2047.915316	1024.461296	2046.931300	1023.969288	V	***246.181218***	123.594247	229.154669	115.080972			2
16							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.2	2210.040131	0.016291	FSGQLNSHGCFYQQVK
36.2	2210.040131	0.016291	FSGQLNSHGCFYQQVK
5.3	2210.058075	-0.001653	FSHLSRNMTMQRTMK
3.0	2210.058075	-0.001653	FSHLSRNMTMQRTMK
1.9	2210.045486	0.010936	MSMKEVDEQMLAIQSK

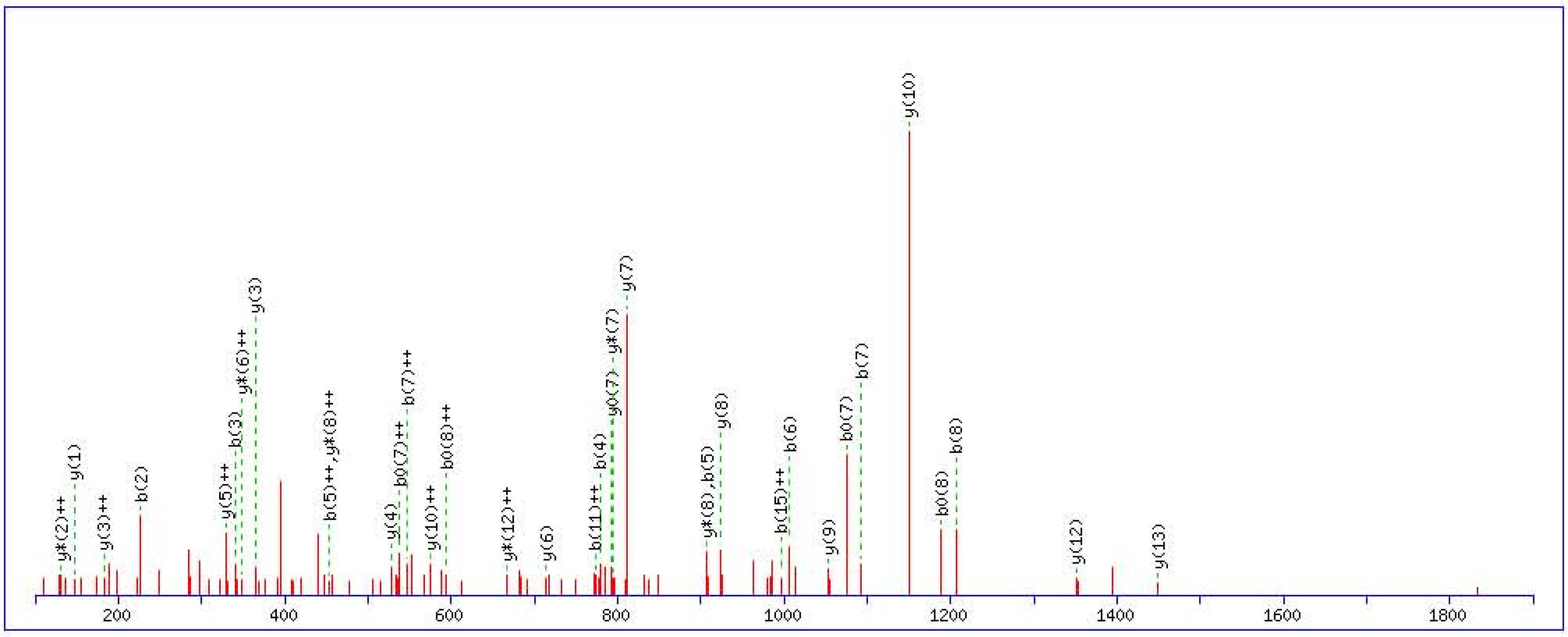
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLQQVSLPELPGEYSMK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

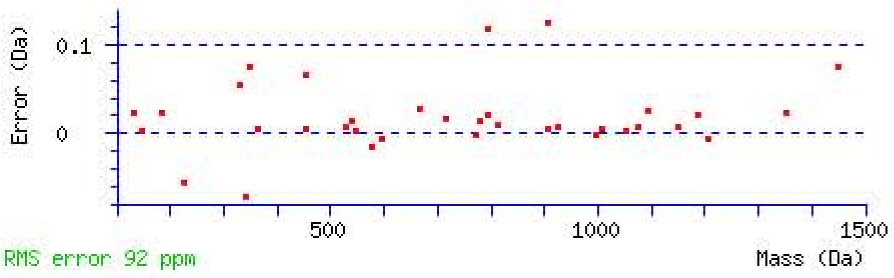
Match to Query 61731: 2355.283872 from(786.101900,3+) rtinseconds(2826) index(47538)
Title: Locus:1.1.1.3266.13 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

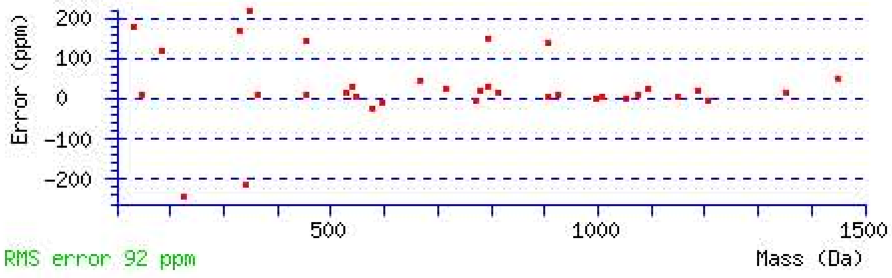
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2355.258179
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.00064
Matches : 35/182 fragment ions using 94 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							18
2	***227.175404***	114.091340					L	2243.181426	1122.094351	2226.154877	1113.581076	2225.170861	1113.089068	17
3	***340.259468***	170.633372					L	2130.097362	1065.552319	2113.070813	1057.039044	2112.086797	1056.547036	16
4	***779.484794***	390.246035	762.458245	381.732760			Q	2017.013298	1009.010287	1999.986749	1000.497013	1999.002733	1000.005005	15
5	***907.543372***	**454.275324**	890.516823	445.762049			Q	1577.787972	789.397624	1560.761423	780.884350	1559.777407	780.392342	14
6	***1006.611786***	503.809531	989.585237	495.296256			V	***1449.729394***	725.368335	1432.702845	716.855061	1431.718829	716.363053	13
7	***1093.643814***	**547.325545**	1076.617265	538.812271	1075.633249	538.320263	S	***1350.660980***	675.834128	1333.634431	667.320854	1332.650415	666.828846	12
8	***1206.727878***	603.867577	1189.701329	595.354303	1188.717313	594.862294	L	1263.628952	632.318114	1246.602403	623.804840	1245.618387	623.312832	11
9	1303.780642	652.393959	1286.754093	643.880685	1285.770077	643.388676	P	***1150.544888***	575.776082	1133.518339	567.262808	1132.534323	566.770800	10
10	1432.823235	716.915256	1415.796686	708.401981	1414.812670	707.909973	E	***1053.492124***	527.249700	1036.465575	518.736426	1035.481559	518.244418	9
11	1545.907299	**773.457288**	1528.880750	764.944013	1527.896734	764.452005	L	***924.449531***	462.728404	907.422982	454.215129	906.438966	453.723121	8
12	1642.960063	821.983670	1625.933514	813.470395	1624.949498	812.978387	P	***811.365467***	406.186372	794.338918	397.673097	793.354902	397.181089	7
13	1699.981527	850.494401	1682.954978	841.981127	1681.970962	841.489119	G	***714.312703***	357.659990	697.286154	349.146715	696.302138	348.654707	6
14	1829.024120	915.015698	1811.997571	906.502423	1811.013555	906.010415	E	657.291239	329.149258	640.264690	320.635983	639.280674	320.143975	5
15	1992.087449	**996.547362**	1975.060900	988.034088	1974.076884	987.542080	Y	***528.248646***	264.627961	511.222097	256.114687	510.238081	255.622679	4
16	2079.119477	1040.063376	2062.092928	1031.550102	2061.108912	1031.058094	S	***365.185317***	183.096297	348.158768	174.583022	347.174752	174.091014	3
17	2210.159962	1105.583619	2193.133413	1097.070344	2192.149397	1096.578336	M	278.153289	139.580282	261.126740	131.067008			2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.4	2355.258179	0.025693	LLLQQVSLPELPGEYSMK
29.3	2355.258179	0.025693	LLLQQVSLPELPGEYSMK
0.3	2355.273926	0.009946	LGLYTFVNLANFVKSWTNLR

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

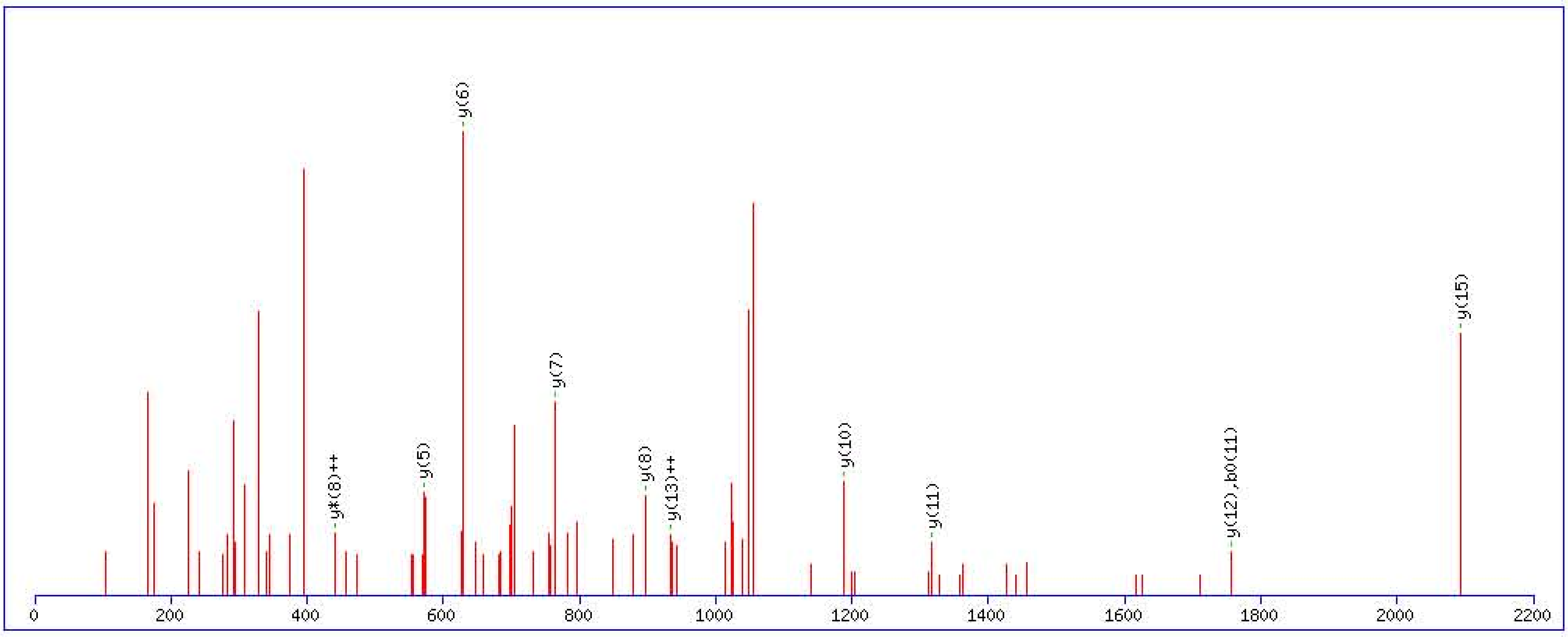
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

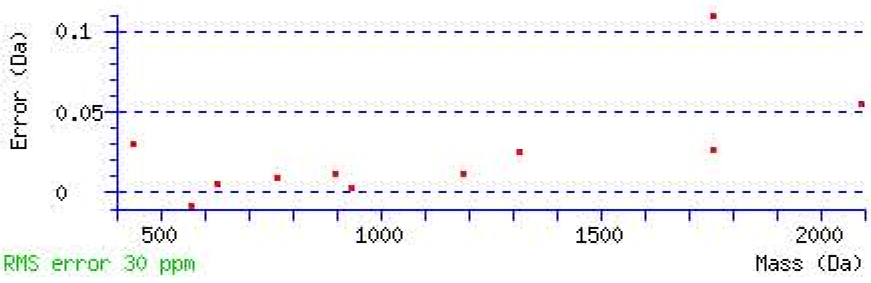
Match to Query 62368: 2400.087792 from(801.036540,3+) rtinseconds(1923) index(41606)
Title: Locus:1.1.1.2953.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

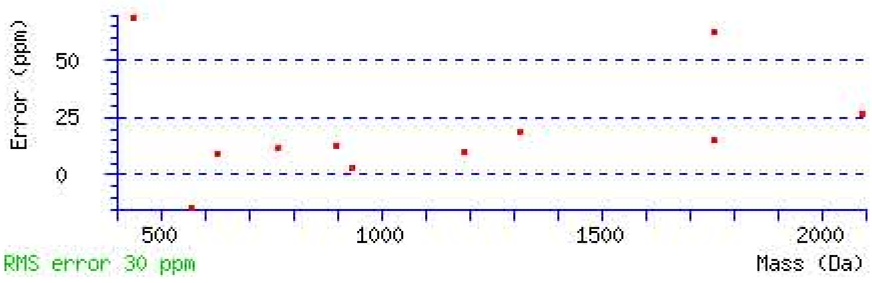
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2400.084686
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 44 **Expect:** 0.00036
Matches : 11/238 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.042676	74.524976					M							17
2	308.073325	154.540301					C	2254.056579	1127.531927	2237.030030	1119.018653	2236.046014	1118.526645	16
3	405.126089	203.066683					P	***2094.025930***	1047.516603	2076.999381	1039.003328	2076.015365	1038.511320	15
4	533.184667	267.095972	516.158118	258.582697			Q	1996.973166	998.990221	1979.946617	990.476947	1978.962601	989.984939	14
5	646.268731	323.638004	629.242182	315.124729			L	1868.914588	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	1085.494057	543.250667	1068.467508	534.737392			Q	***1755.830524***	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1213.552635	607.279956	1196.526086	598.766681			Q	***1316.605198***	658.806237	1299.578649	650.292963	1298.594633	649.800955	11
8	1376.615964	688.811620	1359.589415	680.298346			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1505.658557	753.332917	1488.632008	744.819642	1487.647992	744.327634	E	1025.483291	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1636.699042	818.853159	1619.672493	810.339885	1618.688477	809.847877	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	1773.757954	887.382615	1756.731405	878.869341	1755.747389	878.377333	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	1830.779418	915.893347	1813.752869	907.380073	1812.768853	906.888065	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	1927.832182	964.419729	1910.805633	955.906455	1909.821617	955.414447	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2056.874775	1028.941026	2039.848226	1020.427751	2038.864210	1019.935743	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2113.896239	1057.451758	2096.869690	1048.938483	2095.885674	1048.446475	G	345.224480	173.115878	328.197931	164.602603			3
16	2226.980303	1113.993790	2209.953754	1105.480515	2208.969738	1104.988507	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.5	2400.084686	0.003106	MCPQLQQYEMHGPEGLR
32.9	2400.084686	0.003106	MCPQLQQYEMHGPEGLR
32.7	2400.084686	0.003106	MCPQLQQYEMHGPEGLR
13.5	2400.084686	0.003106	MCPQLQQYEMHGPEGLR
10.4	2400.084686	0.003106	MCPQLQQYEMHGPEGLR
10.4	2400.084686	0.003106	MCPQLQQYEMHGPEGLR

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

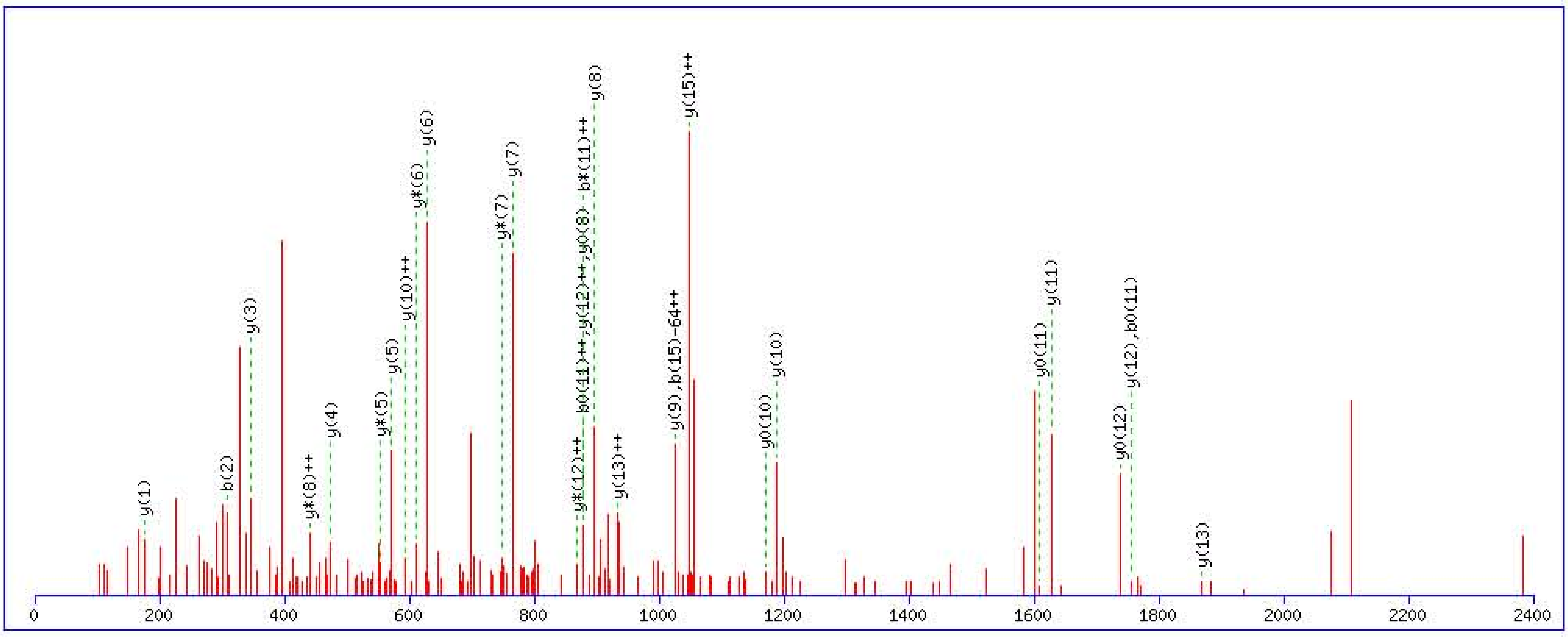
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

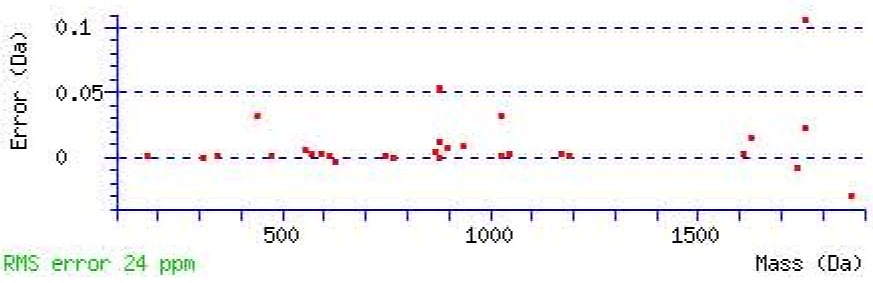
Match to Query 62372: 2400.095022 from(801.038950,3+) rtinseconds(1967) index(41940)
Title: Locus:1.1.1.2968.20 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

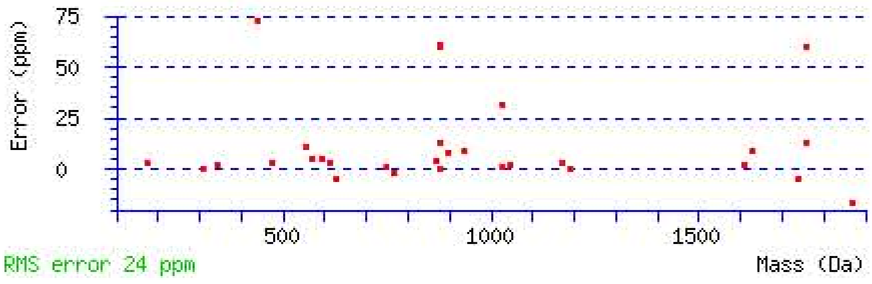
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2400.084686
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00093
Matches : 30/238 fragment ions using 75 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.042676	74.524976					M							17
2	308.073325	154.540301					C	2254.056579	1127.531927	2237.030030	1119.018653	2236.046014	1118.526645	16
3	405.126089	203.066683					P	2094.025930	1047.516603	2076.999381	1039.003328	2076.015365	1038.511320	15
4	533.184667	267.095972	516.158118	258.582697			Q	1996.973166	998.990221	1979.946617	990.476947	1978.962601	989.984939	14
5	646.268731	323.638004	629.242182	315.124729			L	***1868.914588***	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	774.327309	387.667293	757.300760	379.154018			Q	***1755.830524***	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1213.552635	607.279956	1196.526086	598.766681			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1376.615964	688.811620	1359.589415	680.298346			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1505.658557	753.332917	1488.632008	744.819642	1487.647992	744.327634	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1636.699042	818.853159	1619.672493	810.339885	1618.688477	809.847877	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	1773.757954	887.382615	1756.731405	878.869341	1755.747389	878.377333	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	1830.779418	915.893347	1813.752869	907.380073	1812.768853	906.888065	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	1927.832182	964.419729	1910.805633	955.906455	1909.821617	955.414447	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2056.874775	1028.941026	2039.848226	1020.427751	2038.864210	1019.935743	E	***474.267073***	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2113.896239	1057.451758	2096.869690	1048.938483	2095.885674	1048.446475	G	***345.224480***	173.115878	328.197931	164.602603			3
16	2226.980303	1113.993790	2209.953754	1105.480515	2208.969738	1104.988507	L	288.203016	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.9	2400.084686	0.010336	MCPQLQQYEMHGPEGLR
36.6	2400.084686	0.010336	MCPQLQQYEMHGPEGLR
17.7	2400.084686	0.010336	MCPQLQQYEMHGPEGLR
12.6	2400.084686	0.010336	MCPQLQQYEMHGPEGLR
11.7	2400.084686	0.010336	MCPQLQQYEMHGPEGLR
7.2	2400.084686	0.010336	MCPQLQQYEMHGPEGLR

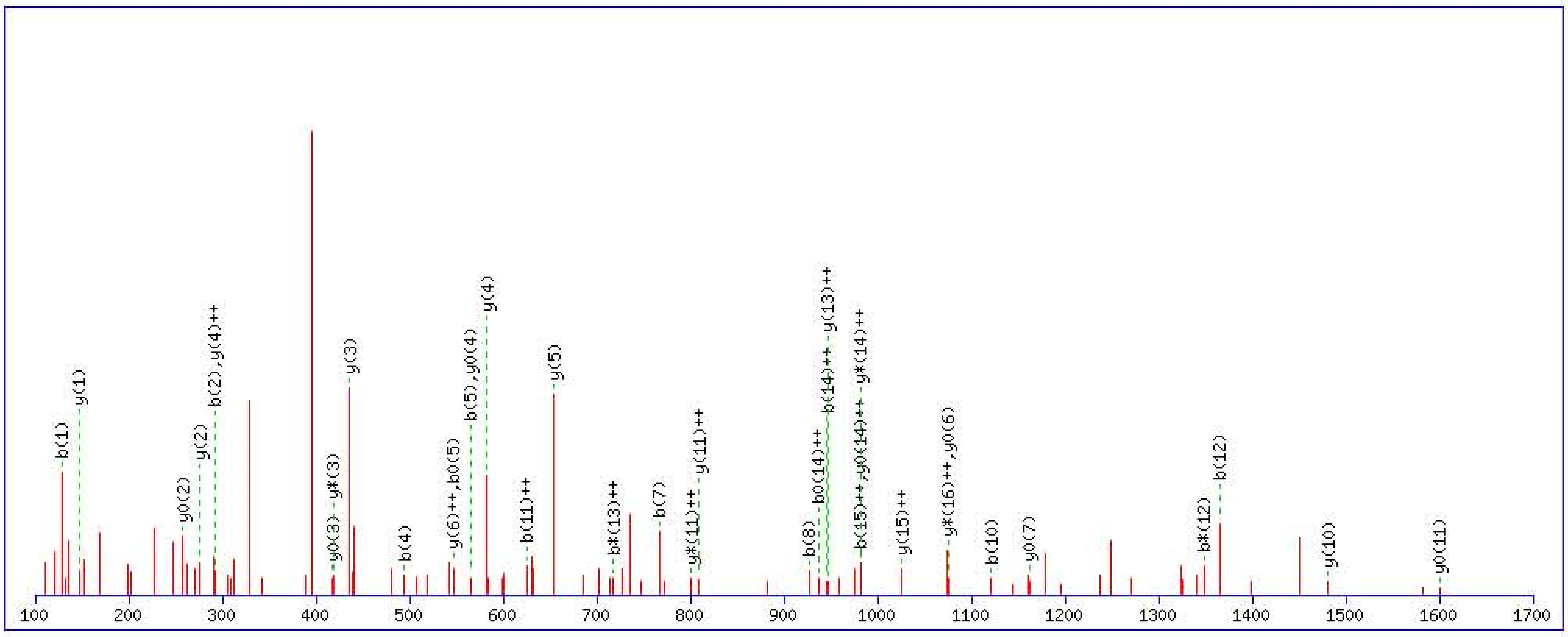
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KYSDASDCHGEDSQAFCEK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

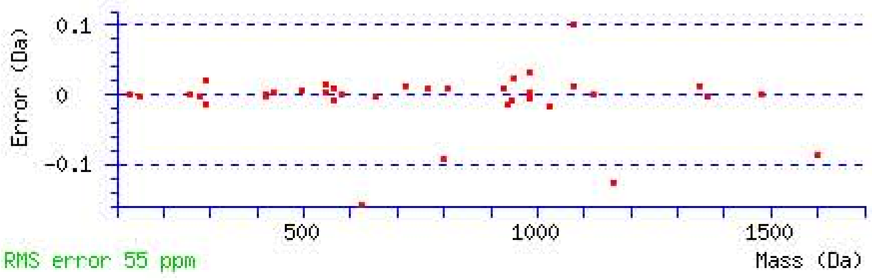
Match to Query 66032: 2544.041456 from(637.017640,4+) rtinseconds(1410) index(38175)
Title: Locus:1.1.1.2774.25 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

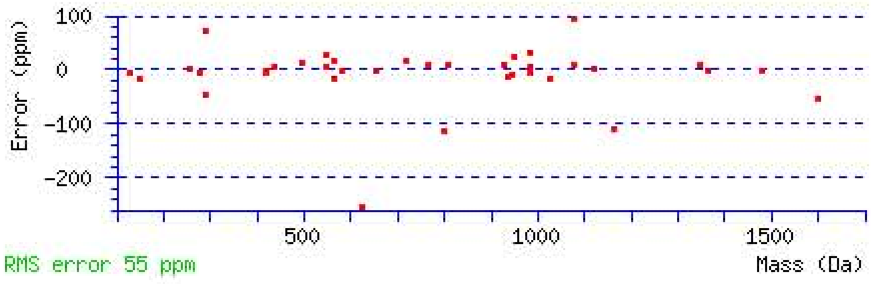


Monoisotopic mass of neutral peptide Mr(calc): 2544.035553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0035
Matches : 37/210 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							19
2	***292.165568***	146.586422	275.139019	138.073148			Y	2416.947874	1208.977575	2399.921325	1200.464300	2398.937309	1199.972292	18
3	379.197596	190.102436	362.171047	181.589162	361.187031	181.097154	S	2253.884545	1127.445910	2236.857996	1118.932636	2235.873980	1118.440628	17
4	***494.224539***	247.615908	477.197990	239.102633	476.213974	238.610625	D	2166.852517	1083.929896	2149.825968	1075.416622	2148.841952	1074.924614	16
5	***565.261653***	283.134465	548.235104	274.621190	547.251088	274.129182	A	2051.825574	1026.416425	2034.799025	1017.903150	2033.815009	1017.411142	15
6	652.293681	326.650479	635.267132	318.137204	634.283116	317.645196	S	1980.788460	990.897868	1963.761911	982.384594	1962.777895	981.892586	14
7	***767.320624***	384.163950	750.294075	375.650676	749.310059	375.158668	D	1893.756432	947.381854	1876.729883	938.868580	1875.745867	938.376572	13
8	***927.351273***	464.179275	910.324724	455.666000	909.340708	455.173992	C	1778.729489	889.868383	1761.702940	881.355108	1760.718924	880.863100	12
9	1064.410185	532.708731	1047.383636	524.195456	1046.399620	523.703448	H	1618.698840	809.853058	1601.672291	801.339784	1600.688275	800.847776	11
10	***1121.431649***	561.219463	1104.405100	552.706188	1103.421084	552.214180	G	***1481.639928***	741.323602	1464.613379	732.810328	1463.629363	732.318320	10
11	1250.474242	**625.740759**	1233.447693	617.227485	1232.463677	616.735477	E	1424.618464	712.812870	1407.591915	704.299596	1406.607899	703.807588	9
12	***1365.501185***	683.254231	1348.474636	674.740956	1347.490620	674.248948	D	1295.575871	648.291574	1278.549322	639.778299	1277.565306	639.286291	8
13	1452.533213	726.770245	1435.506664	718.256970	1434.522648	717.764962	S	1180.548928	590.778102	1163.522379	582.264828	1162.538363	581.772820	7
14	1891.758539	**946.382908**	1874.731990	937.869633	1873.747974	937.377625	Q	1093.516900	547.262088	1076.490351	538.748814	1075.506335	538.256806	6
15	1962.795653	**981.901465**	1945.769104	973.388190	1944.785088	972.896182	A	***654.291574***	327.649425	637.265025	319.136151	636.281009	318.644143	5
16	2109.864067	1055.435671	2092.837518	1046.922397	2091.853502	1046.430389	F	***583.254460***	292.130868	566.227911	283.617594	565.243895	283.125586	4
17	2269.894716	1135.450996	2252.868167	1126.937721	2251.884151	1126.445713	C	***436.186046***	218.596661	419.159497	210.083386	418.175481	209.591378	3
18	2398.937309	1199.972292	2381.910760	1191.459018	2380.926744	1190.967010	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
19							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 55 ppm



RMS error 55 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.0	2544.035553	0.005903	KYSDASDCHGEDSQAFCEK

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

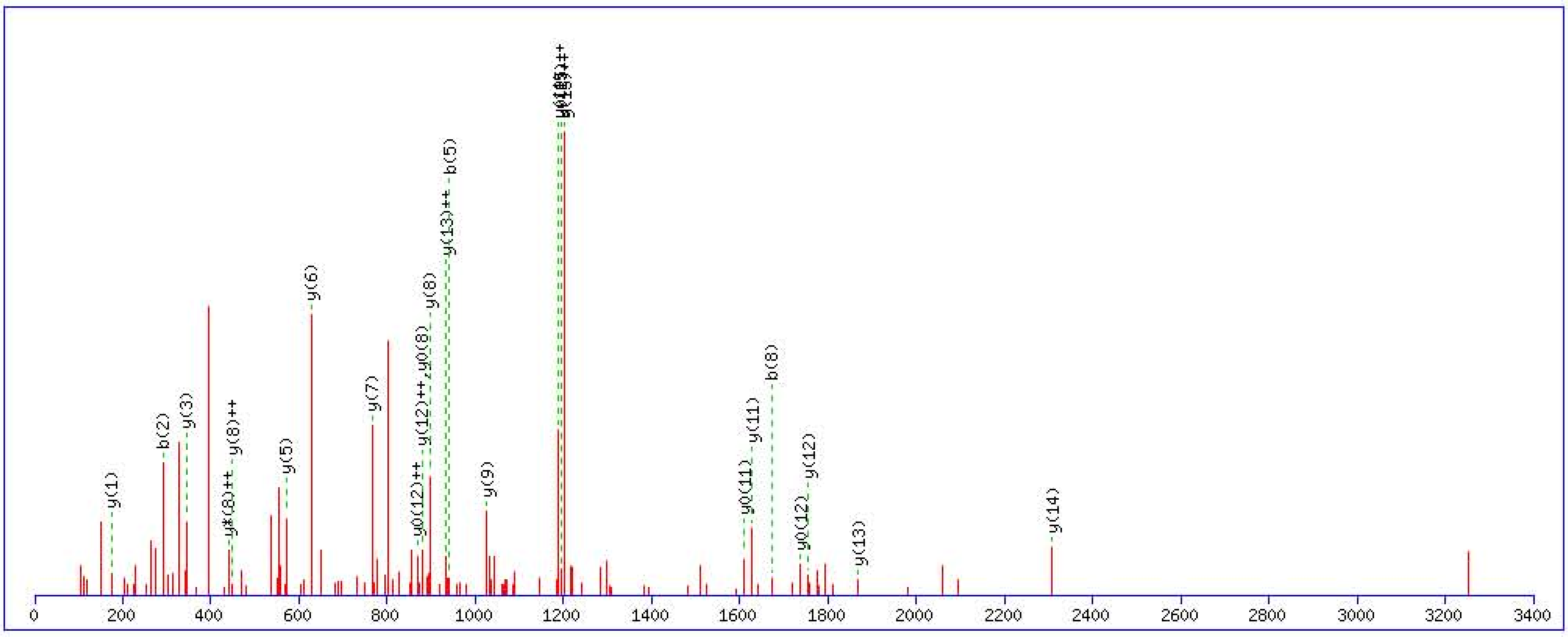
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

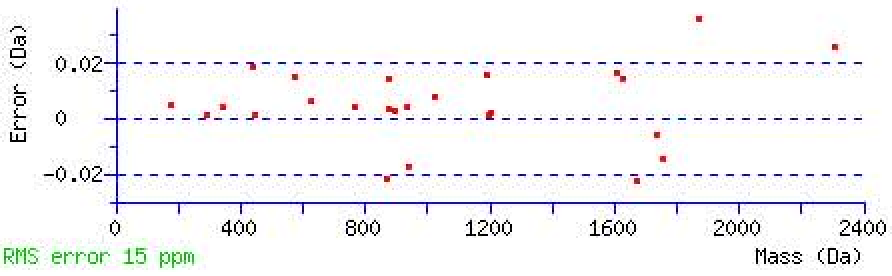
Match to Query 67443: 2695.282392 from(899.434740,3+) rtinseconds(2202) index(43445)
Title: Locus:1.1.1.3050.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

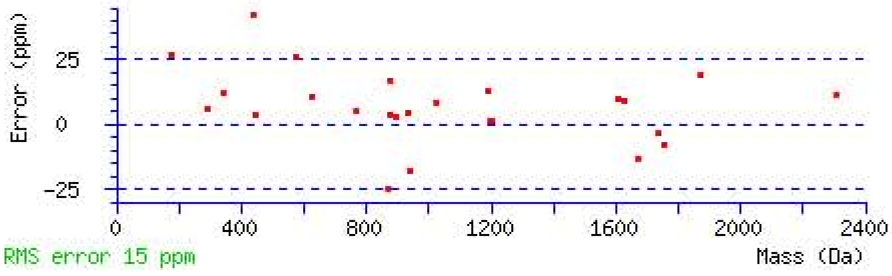
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2695.256516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.0027
Matches : 25/164 fragment ions using 72 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							17
2	**292.078410**	146.542843					C	2565.223327	1283.115301	2548.196778	1274.602027	2547.212762	1274.110019	16
3	389.131174	195.069225					P	2405.192678	1203.099977	2388.166129	1194.586702	2387.182113	1194.094694	15
4	828.356500	414.681888	811.329951	406.168614			Q	***2308.139914***	1154.573595	2291.113365	1146.060320	2290.129349	1145.568312	14
5	**941.440564**	471.223920	924.414015	462.710646			L	***1868.914588***	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	1069.499142	535.253209	1052.472593	526.739935			Q	***1755.830524***	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1508.724468	754.865872	1491.697919	746.352598			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	**1671.787797**	836.397537	1654.761248	827.884262			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1800.830390	900.918833	1783.803841	892.405559	1782.819825	891.913551	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1931.870875	966.439076	1914.844326	957.925801	1913.860310	957.433793	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2068.929787	1034.968531	2051.903238	1026.455257	2050.919222	1025.963249	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2125.951251	1063.479263	2108.924702	1054.965989	2107.940686	1054.473981	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2223.004015	1112.005645	2205.977466	1103.492371	2204.993450	1103.000363	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2352.046608	1176.526942	2335.020059	1168.013667	2334.036043	1167.521659	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2409.068072	1205.037674	2392.041523	1196.524399	2391.057507	1196.032391	G	***345.224480***	173.115878	328.197931	164.602603			3
16	2522.152136	1261.579706	2505.125587	1253.066431	2504.141571	1252.574424	L	288.203016	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.7	2695.256516	0.025876	MCPQLQQYEMHGPEGLR
32.2	2695.256516	0.025876	MCPQLQQYEMHGPEGLR
28.2	2695.256516	0.025876	MCPQLQQYEMHGPEGLR

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

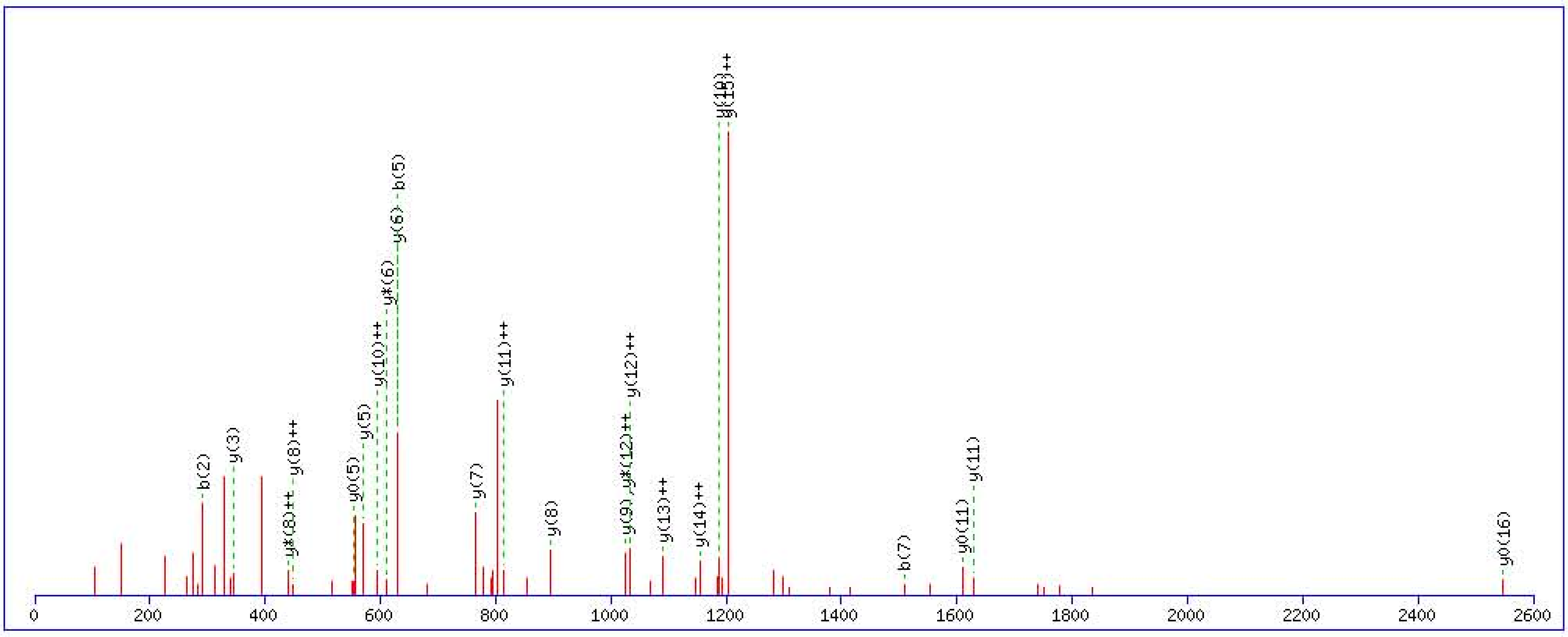
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

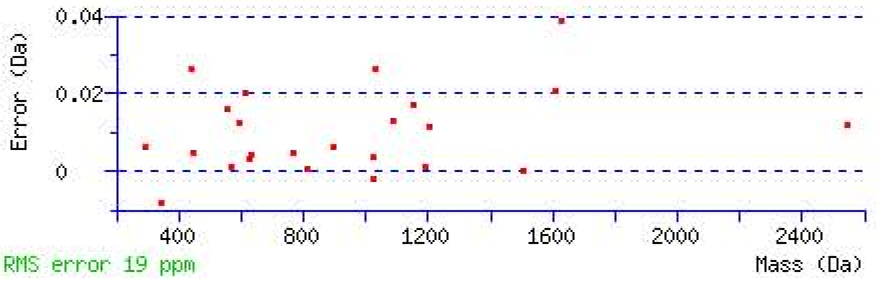
Match to Query 67445: 2695.282722 from(899.434850,3+) rtinseconds(2175) index(43266)
Title: Locus:1.1.1.3041.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

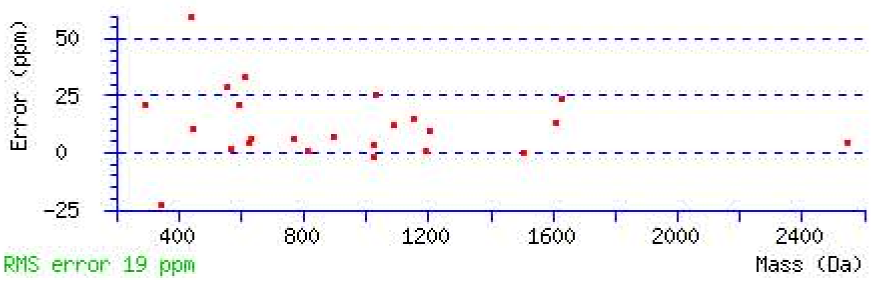
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2695.256516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0059
Matches : 24/164 fragment ions using 52 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							17
2	**292.078410**	146.542843					C	2565.223327	1283.115301	2548.196778	1274.602027	2547.212762	1274.110019	16
3	389.131174	195.069225					P	2405.192678	1203.099977	2388.166129	1194.586702	2387.182113	1194.094694	15
4	517.189752	259.098514	500.163203	250.585240			Q	2308.139914	1154.573595	2291.113365	1146.060320	2290.129349	1145.568312	14
5	**630.273816**	315.640546	613.247267	307.127272			L	2180.081336	1090.544306	2163.054787	1082.031031	2162.070771	1081.539023	13
6	1069.499142	535.253209	1052.472593	526.739935			Q	2066.997272	1034.002274	2049.970723	1025.488999	2048.986707	1024.996991	12
7	**1508.724468**	754.865872	1491.697919	746.352598			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1671.787797	836.397537	1654.761248	827.884262			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1800.830390	900.918833	1783.803841	892.405559	1782.819825	891.913551	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1931.870875	966.439076	1914.844326	957.925801	1913.860310	957.433793	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2068.929787	1034.968531	2051.903238	1026.455257	2050.919222	1025.963249	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2125.951251	1063.479263	2108.924702	1054.965989	2107.940686	1054.473981	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2223.004015	1112.005645	2205.977466	1103.492371	2204.993450	1103.000363	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2352.046608	1176.526942	2335.020059	1168.013667	2334.036043	1167.521659	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2409.068072	1205.037674	2392.041523	1196.524399	2391.057507	1196.032391	G	***345.224480***	173.115878	328.197931	164.602603			3
16	2522.152136	1261.579706	2505.125587	1253.066431	2504.141571	1252.574424	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.3	2695.256516	0.026206	MCPQLQQYEMHGPEGLR
24.1	2695.256516	0.026206	MCPQLQQYEMHGPEGLR
18.3	2695.256516	0.026206	MCPQLQQYEMHGPEGLR

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

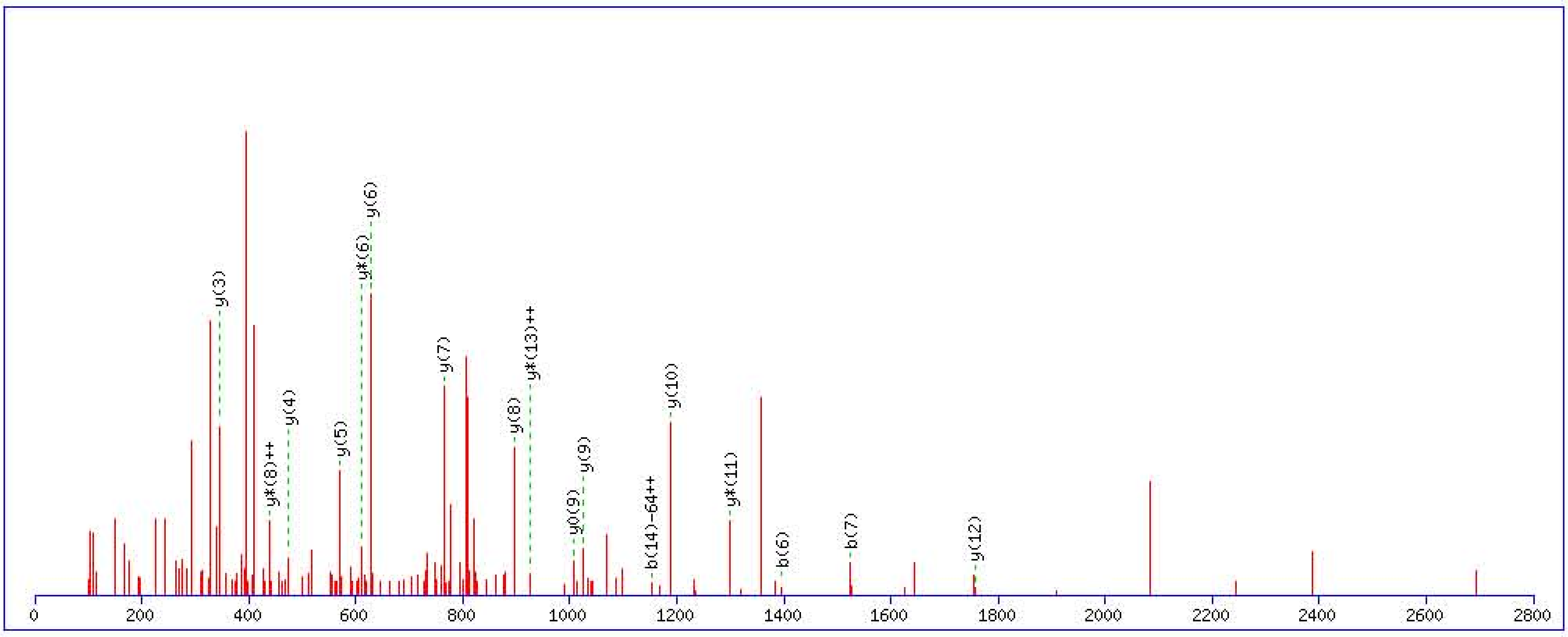
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

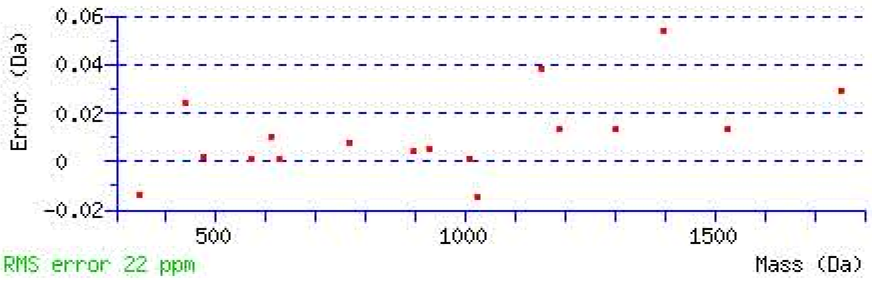
Match to Query 67628: 2711.267176 from(678.824070,4+) rtinseconds(2026) index(42295)
Title: Locus:1.1.1.2989.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

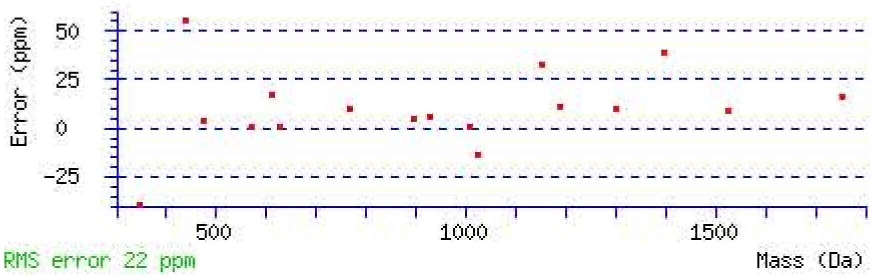
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2711.251434
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q4 : Biotin:Thermo-21345 (Q)
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.033
Matches : 17/238 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.042676	74.524976					M							17
2	308.073325	154.540301					C	2565.223327	1283.115302	2548.196778	1274.602027	2547.212762	1274.110019	16
3	405.126089	203.066683					P	2405.192678	1203.099977	2388.166129	1194.586702	2387.182113	1194.094694	15
4	844.351415	422.679346	827.324866	414.166071			Q	2308.139914	1154.573595	2291.113365	1146.060320	2290.129349	1145.568312	14
5	957.435479	479.221378	940.408930	470.708103			L	1868.914588	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	**1396.660805**	698.834041	1379.634256	690.320766			Q	***1755.830524***	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	**1524.719383**	762.863330	1507.692834	754.350055			Q	1316.605198	658.806237	1299.578649	650.292963	1298.594633	649.800955	11
8	1687.782712	844.394994	1670.756163	835.881720			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1816.825305	908.916291	1799.798756	900.403016	1798.814740	899.911008	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1947.865790	974.436533	1930.839241	965.923259	1929.855225	965.431251	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2084.924702	1042.965989	2067.898153	1034.452715	2066.914137	1033.960707	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2141.946166	1071.476721	2124.919617	1062.963446	2123.935601	1062.471439	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2238.998930	1120.003103	2221.972381	1111.489828	2220.988365	1110.997821	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2368.041523	1184.524400	2351.014974	1176.011125	2350.030958	1175.519117	E	***474.267073***	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2425.062987	1213.035132	2408.036438	1204.521857	2407.052422	1204.029849	G	***345.224480***	173.115878	328.197931	164.602603			3
16	2538.147051	1269.577164	2521.120502	1261.063889	2520.136486	1260.571881	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.0	2711.251434	0.015742	MCPQLQQYEMHGPEGLR
21.9	2711.251434	0.015742	MCPQLQQYEMHGPEGLR
15.3	2711.251434	0.015742	MCPQLQQYEMHGPEGLR
14.8	2711.251434	0.015742	MCPQLQQYEMHGPEGLR
8.0	2711.251434	0.015742	MCPQLQQYEMHGPEGLR
0.1	2711.251434	0.015742	MCPQLQQYEMHGPEGLR

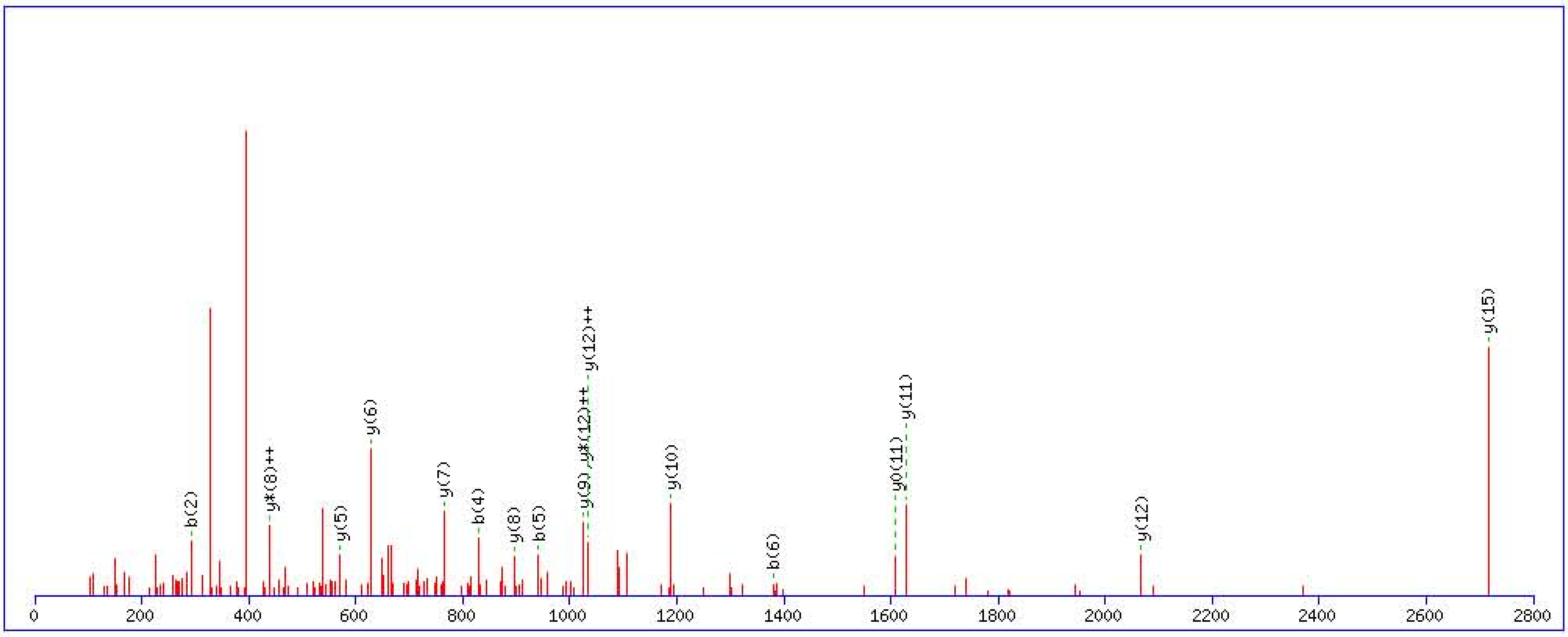
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

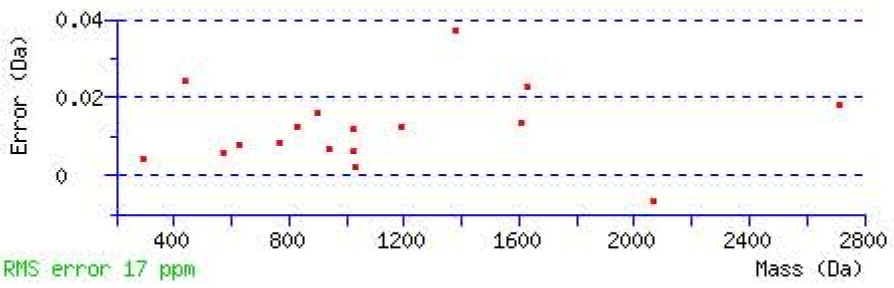
Match to Query 71708: 3006.457936 from(752.621760,4+) rtinseconds(2325) index(44198)
Title: Locus:1.1.1.3093.17 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

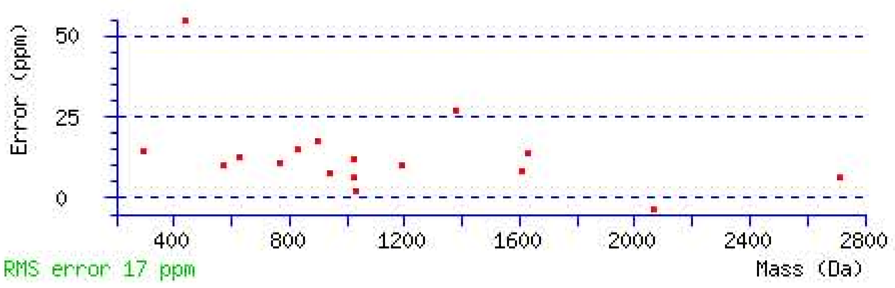
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3006.423264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Q6     : Biotin:Thermo-21345 (Q)
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.03
Matches : 17/164 fragment ions using 39 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.047761	66.527518					M							17
2	**292.078410**	146.542843					C	2876.390075	1438.698675	2859.363526	1430.185401	2858.379510	1429.693393	16
3	389.131174	195.069225					P	***2716.359426***	1358.683351	2699.332877	1350.170076	2698.348861	1349.678068	15
4	**828.356500**	414.681888	811.329951	406.168614			Q	2619.306662	1310.156969	2602.280113	1301.643694	2601.296097	1301.151686	14
5	**941.440564**	471.223920	924.414015	462.710646			L	2180.081336	1090.544306	2163.054787	1082.031031	2162.070771	1081.539023	13
6	**1380.665890**	690.836583	1363.639341	682.323309			Q	***2066.997272***	1034.002274	2049.970723	1025.488999	2048.986707	1024.996991	12
7	1819.891216	910.449246	1802.864667	901.935972			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1982.954545	991.980911	1965.927996	983.467636			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	2111.997138	1056.502207	2094.970589	1047.988932	2093.986573	1047.496925	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	2243.037623	1122.022450	2226.011074	1113.509175	2225.027058	1113.017167	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2380.096535	1190.551906	2363.069986	1182.038631	2362.085970	1181.546623	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2437.117999	1219.062637	2420.091450	1210.549363	2419.107434	1210.057355	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2534.170763	1267.589019	2517.144214	1259.075745	2516.160198	1258.583737	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2663.213356	1332.110316	2646.186807	1323.597041	2645.202791	1323.105034	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2720.234820	1360.621048	2703.208271	1352.107773	2702.224255	1351.615766	G	345.224480	173.115878	328.197931	164.602603			3
16	2833.318884	1417.163080	2816.292335	1408.649806	2815.308319	1408.157798	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.7	3006.423264	0.034672	MCPQLQQYEMHGPEGLR

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

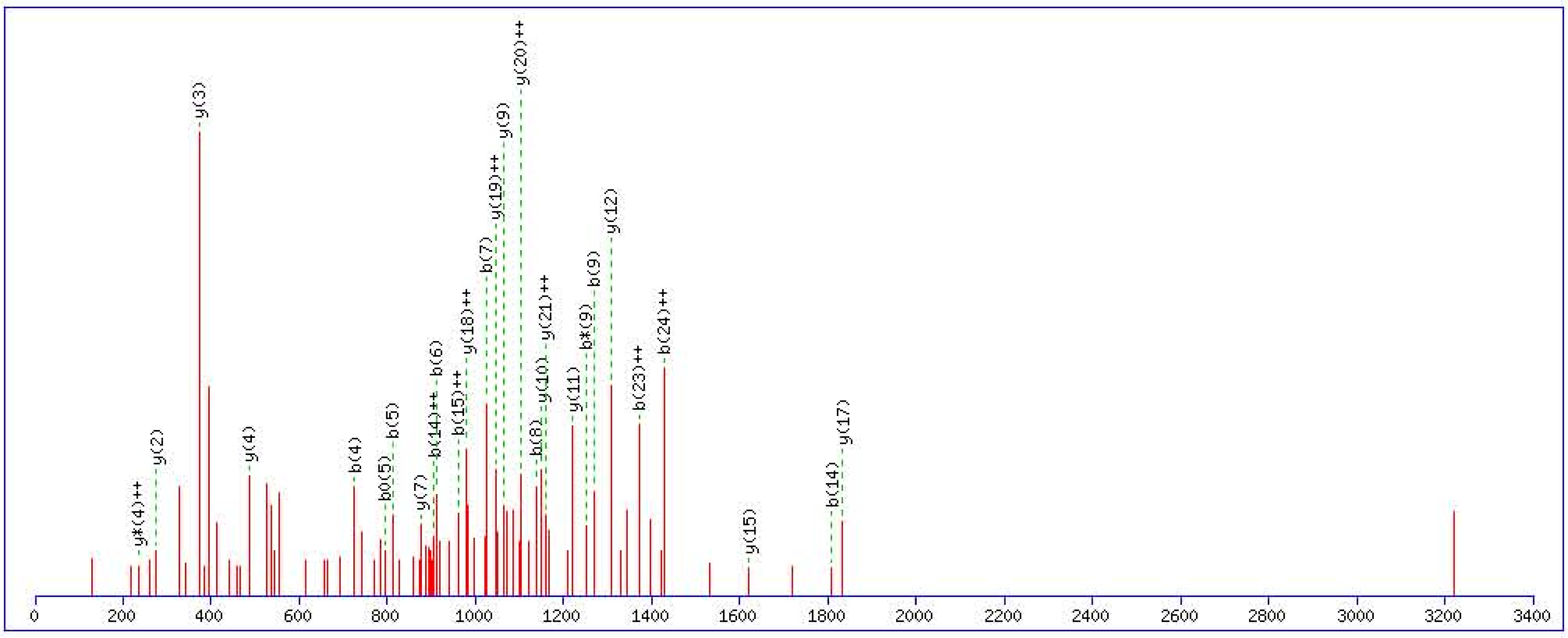
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVDQSVLLMKPDAELSASSVYNLLPEK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

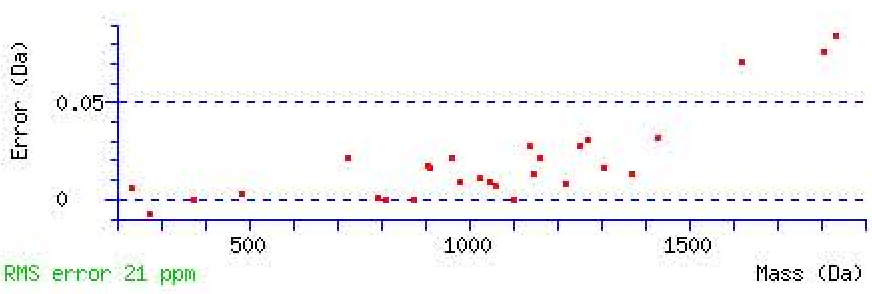
Match to Query 74341: 3227.724822 from(1076.915550,3+) rtinseconds(2742) index(46923)
Title: Locus:1.1.1.3237.25 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

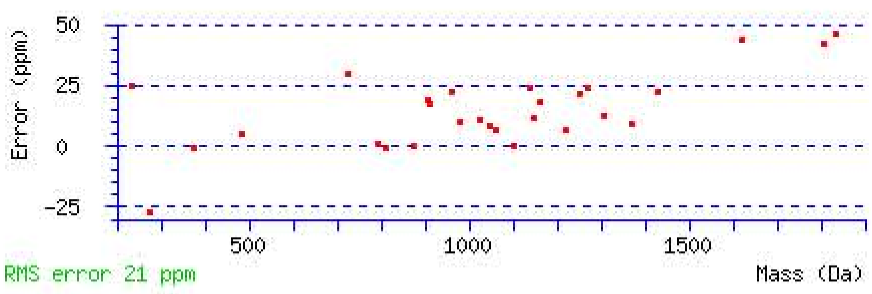
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3227.682129
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 7.3e-005
Matches : 28/300 fragment ions using 57 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	72.044390	36.525833					A							27
2	171.112804	86.060040					V	3157.652336	1579.329806	3140.625787	1570.816531	3139.641771	1570.324523	26
3	286.139747	143.573512			268.129182	134.568229	D	3058.583922	1529.795599	3041.557373	1521.282324	3040.573357	1520.790316	25
4	***725.365073***	363.186175	708.338524	354.672900	707.354508	354.180892	Q	2943.556979	1472.282127	2926.530430	1463.768853	2925.546414	1463.276845	24
5	***812.397101***	406.702189	795.370552	398.188914	794.386536	397.696906	S	2504.331653	1252.669464	2487.305104	1244.156190	2486.321088	1243.664182	23
6	***911.465515***	456.236396	894.438966	447.723121	893.454950	447.231113	V	2417.299625	1209.153451	2400.273076	1200.640176	2399.289060	1200.148168	22
7	***1024.549579***	512.778427	1007.523030	504.265153	1006.539014	503.773145	L	2318.231211	1159.619243	2301.204662	1151.105969	2300.220646	1150.613961	21
8	***1137.633643***	569.320459	1120.607094	560.807185	1119.623078	560.315177	L	2205.147147	1103.077212	2188.120598	1094.563937	2187.136582	1094.071929	20
9	***1268.674128***	634.840702	1251.647579	626.327428	1250.663563	625.835419	M	2092.063083	1046.535179	2075.036534	1038.021905	2074.052518	1037.529897	19
10	1396.769091	698.888183	1379.742542	690.374909	1378.758526	689.882901	K	1961.022598	981.014937	1943.996049	972.501663	1943.012033	972.009655	18
11	1493.821855	747.414565	1476.795306	738.901291	1475.811290	738.409283	P	***1832.927635***	916.967456	1815.901086	908.454181	1814.917070	907.962173	17
12	1608.848798	804.928037	1591.822249	796.414763	1590.838233	795.922755	D	1735.874871	868.441074	1718.848322	859.927799	1717.864306	859.435791	16
13	1679.885912	840.446594	1662.859363	831.933320	1661.875347	831.441311	A	***1620.847928***	810.927602	1603.821379	802.414328	1602.837363	801.922320	15
14	***1808.928505***	**904.967891**	1791.901956	896.454616	1790.917940	895.962608	E	1549.810814	775.409045	1532.784265	766.895771	1531.800249	766.403763	14
15	1922.012569	**961.509923**	1904.986020	952.996648	1904.002004	952.504640	L	1420.768221	710.887749	1403.741672	702.374474	1402.757656	701.882466	13
16	2009.044597	1005.025937	1992.018048	996.512662	1991.034032	996.020654	S	***1307.684157***	654.345717	1290.657608	645.832442	1289.673592	645.340434	12
17	2080.081711	1040.544493	2063.055162	1032.031219	2062.071146	1031.539211	A	***1220.652129***	610.829703	1203.625580	602.316428	1202.641564	601.824420	11
18	2167.113739	1084.060507	2150.087190	1075.547233	2149.103174	1075.055225	S	***1149.615015***	575.311146	1132.588466	566.797871	1131.604450	566.305863	10
19	2254.145767	1127.576521	2237.119218	1119.063247	2236.135202	1118.571239	S	***1062.582987***	531.795132	1045.556438	523.281857	1044.572422	522.789849	9
20	2353.214181	1177.110728	2336.187632	1168.597454	2335.203616	1168.105446	V	975.550959	488.279118	958.524410	479.765843	957.540394	479.273835	8
21	2516.277510	1258.642393	2499.250961	1250.129118	2498.266945	1249.637110	Y	***876.482545***	438.744911	859.455996	430.231636	858.471980	429.739628	7
22	2630.320437	1315.663856	2613.293888	1307.150582	2612.309872	1306.658574	N	713.419216	357.213246	696.392667	348.699972	695.408651	348.207964	6
23	2743.404501	**1372.205888**	2726.377952	1363.692614	2725.393936	1363.200606	L	599.376289	300.191783	582.349740	291.678508	581.365724	291.186500	5
24	2856.488565	**1428.747921**	2839.462016	1420.234646	2838.478000	1419.742638	L	***486.292225***	243.649751	469.265676	235.136476	468.281660	234.644468	4
25	2953.541329	1477.274303	2936.514780	1468.761028	2935.530764	1468.269020	P	***373.208161***	187.107719	356.181612	178.594444	355.197596	178.102436	3
26	3082.583922	1541.795599	3065.557373	1533.282325	3064.573357	1532.790317	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
27							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.4	3227.682129	0.042693	AVDQSVLLMKPDAELSASSVYNLLPEK

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

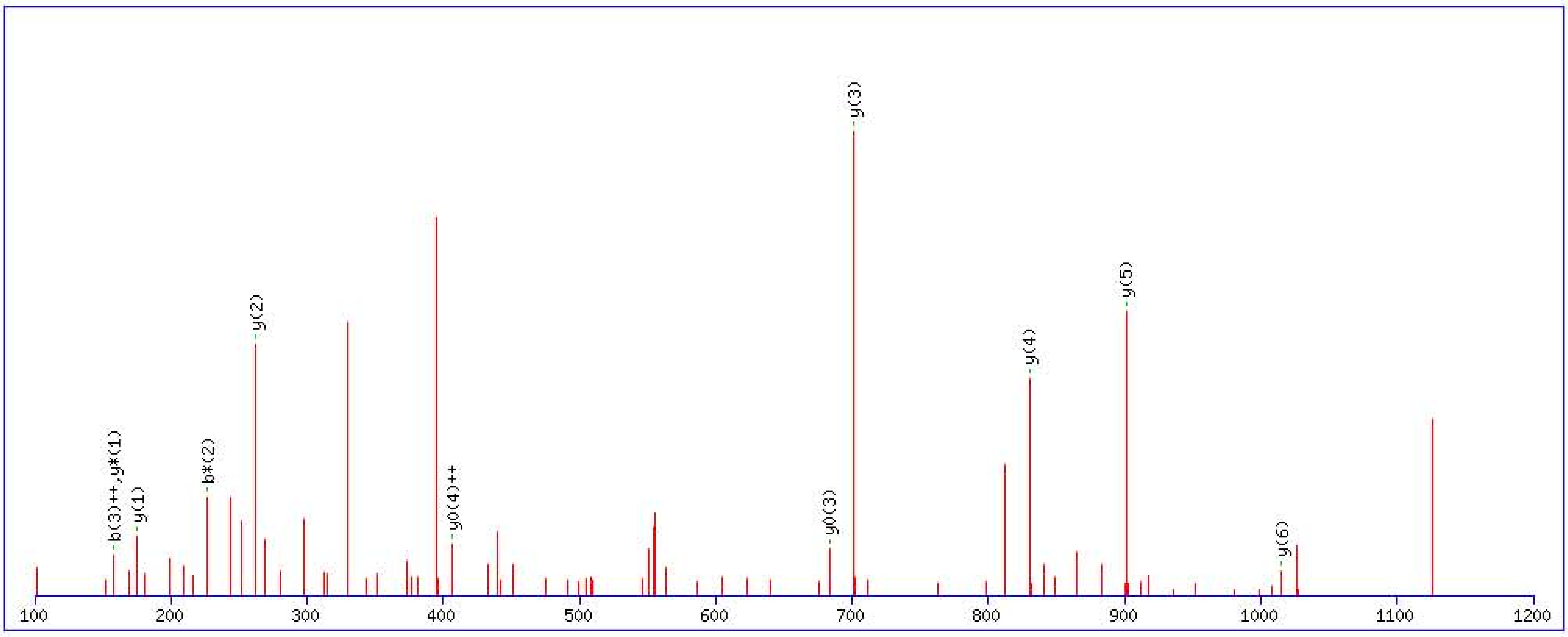
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENAEQSR**
Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

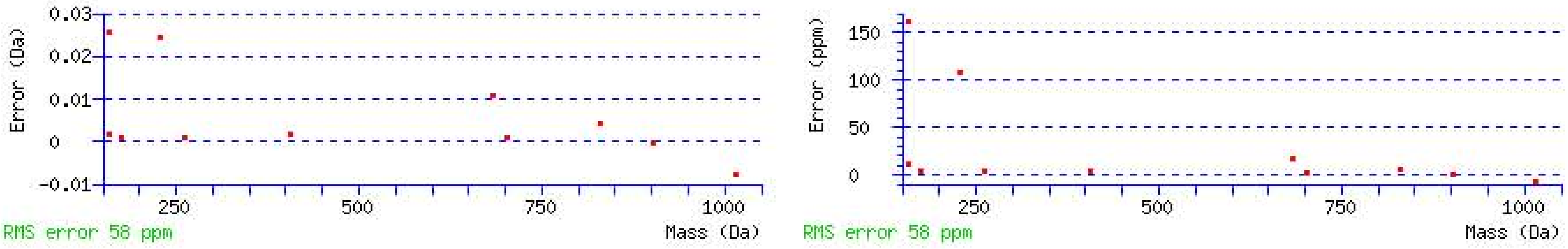
Match to Query 25467: 1143.535948 from(572.775250,2+) rtinseconds(1117) index(36288)
Title: Locus:1.1.1.2672.16 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1143.534225
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0054
Matches : 11/68 fragment ions using 21 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.049869	65.528572			112.039304	56.523290	E							7
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	N	***1015.498940***	508.253108	998.472391	499.739834	997.488375	499.247826	6
3	315.129910	158.068593	298.103361	149.555319	297.119345	149.063311	A	***901.456013***	451.231645	884.429464	442.718370	883.445448	442.226362	5
4	444.172503	222.589890	427.145954	214.076615	426.161938	213.584607	E	***830.418899***	415.713088	813.392350	407.199813	812.408334	406.707805	4
5	883.397829	442.202553	866.371280	433.689278	865.387264	433.197270	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
6	970.429857	485.718567	953.403308	477.205292	952.419292	476.713284	S	***262.150980***	131.579128	245.124431	123.065853	244.140415	122.573845	2
7							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.5	1143.534225	0.001723	ENAEQSR
13.2	1143.549500	-0.013552	WQEQSR
11.2	1143.552017	-0.016069	VDDGTGREAPK
6.3	1143.552002	-0.016054	SSSALDSPAGPR
4.6	1143.551987	-0.016039	ELNGSEAATPR
4.4	1143.549316	-0.013368	SRSRSHSGDR
4.1	1143.526840	0.009108	EGEGASAPRDR
3.1	1143.549500	-0.013552	EQWSQR
2.5	1143.530899	0.005049	TPFPDSSTHR
1.6	1143.551987	-0.016039	EQGNIEEAVR

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

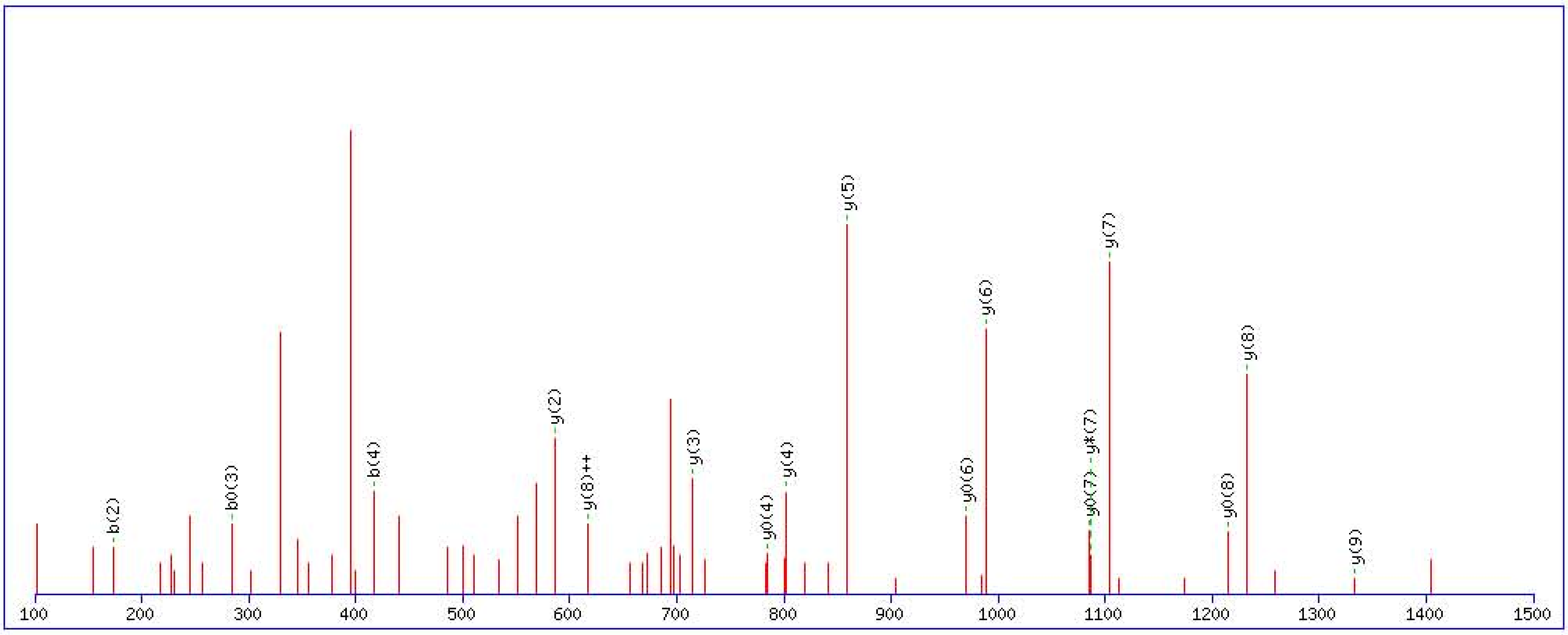
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATEDEGSEQK**
Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

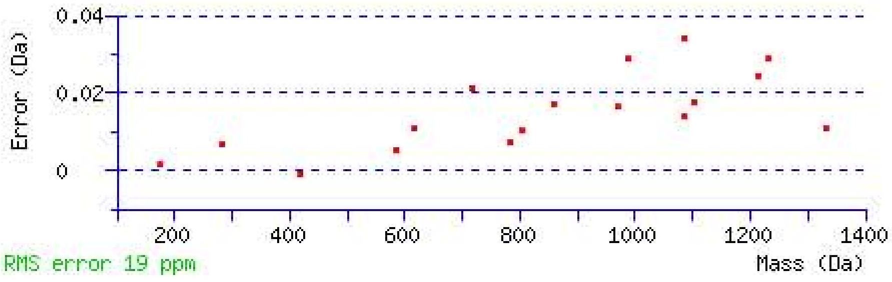
Match to Query 35315: 1403.644348 from(702.829450,2+) rtinseconds(1183) index(19051)
Title: Locus:1.1.1.2366.19 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

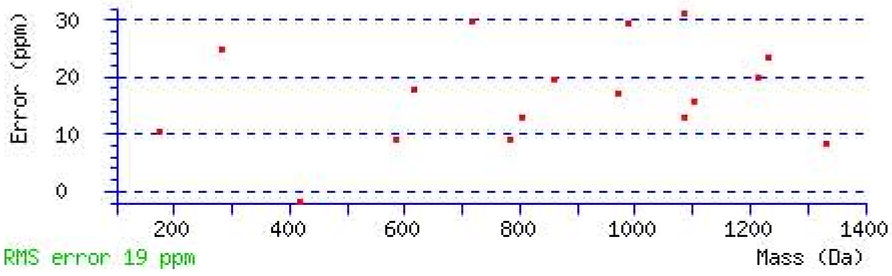
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1500 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1403.623840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 60 **Expect:** 9.8e-006
Matches : 17/86 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							10
2	**173.092069**	87.049672			155.081504	78.044390	T	***1333.594023***	667.300650	1316.567474	658.787375	1315.583458	658.295367	9
3	302.134662	151.570969			284.124097	142.565687	E	***1232.546344***	616.776810	1215.519795	608.263536	1214.535779	607.771528	8
4	**417.161605**	209.084441			399.151040	200.079158	D	***1103.503751***	552.255514	1086.477202	543.742239	1085.493186	543.250231	7
5	546.204198	273.605737			528.193633	264.600455	E	***988.476808***	494.742042	971.450259	486.228768	970.466243	485.736760	6
6	603.225662	302.116469			585.215097	293.111187	G	***859.434215***	430.220746	842.407666	421.707471	841.423650	421.215463	5
7	690.257690	345.632483			672.247125	336.627201	S	***802.412751***	401.710014	785.386202	393.196739	784.402186	392.704731	4
8	819.300283	410.153780			801.289718	401.148497	E	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
9	1258.525609	629.766443	1241.499060	621.253168	1240.515044	620.761160	Q	***586.338130***	293.672703	569.311581	285.159428			2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.0	1403.623840	0.020508	ATEDEGSEQK
9.2	1403.652832	-0.008484	LTSDEEGEPSGKR
7.4	1403.642929	0.001419	EAESWSQIGNQR
0.8	1403.650345	-0.005997	ATLKDSGSYFCR

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

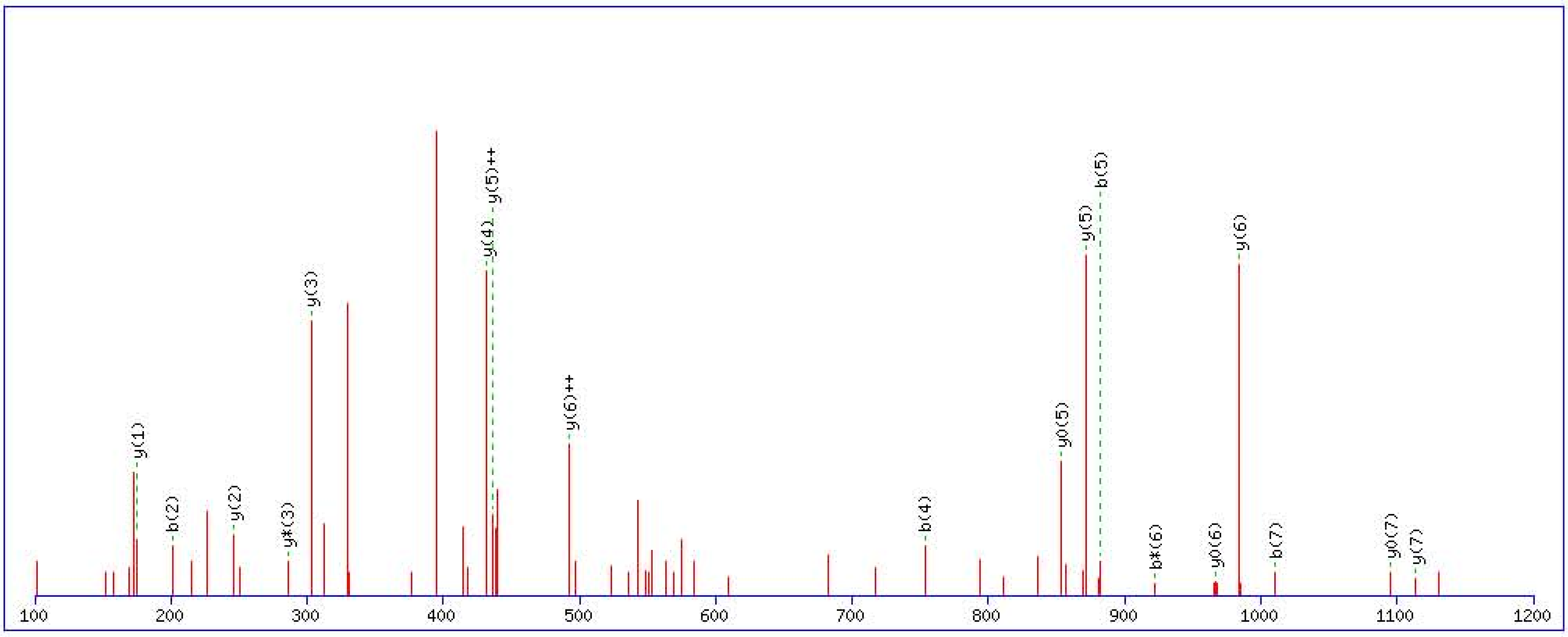
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AELQEGAR**
Found in **APOA1_HUMAN**, Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1

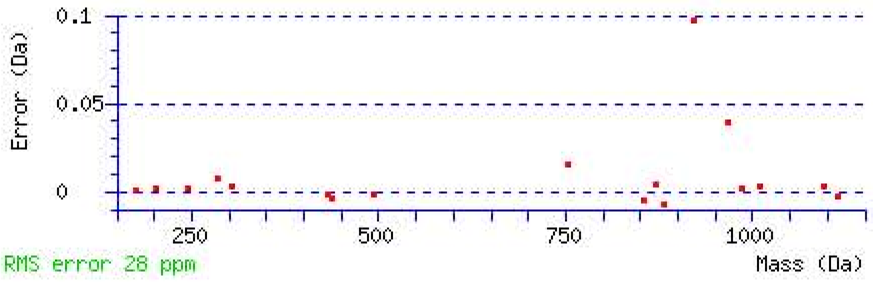
Match to Query 27181: 1183.606088 from(592.810320,2+) rtinseconds(1441) index(38444)
Title: Locus:1.1.1.2785.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

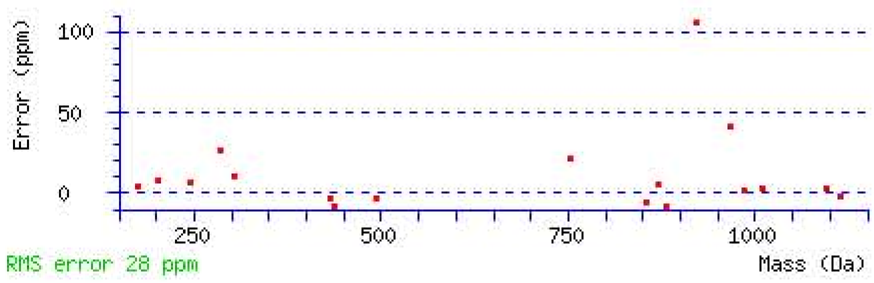
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1183.601913
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0014
Matches : 18/70 fragment ions using 37 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							8
2	**201.086983**	101.047130			183.076418	92.041847	E	***1113.572106***	557.289691	1096.545557	548.776417	1095.561541	548.284409	7
3	314.171047	157.589161			296.160482	148.583879	L	***984.529513***	492.768395	967.502964	484.255120	966.518948	483.763112	6
4	**753.396373**	377.201825	736.369824	368.688550	735.385808	368.196542	Q	***871.445449***	436.226363	854.418900	427.713088	853.434884	427.221080	5
5	**882.438966**	441.723121	865.412417	433.209847	864.428401	432.717839	E	***432.220123***	216.613699	415.193574	208.100425	414.209558	207.608417	4
6	939.460430	470.233853	922.433881	461.720579	921.449865	461.228571	G	***303.177530***	152.092403	286.150981	143.579128			3
7	**1010.497544**	505.752410	993.470995	497.239136	992.486979	496.747128	A	***246.156066***	123.581671	229.129517	115.068396			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.0	1183.601913	0.004175	AELQEGAR
12.1	1183.613815	-0.007727	FHFEALPPAR
10.2	1183.601913	0.004175	EALEQQR
6.9	1183.601913	0.004175	QLAEQER
5.9	1183.601913	0.004175	ELQAEAGR
5.5	1183.601913	0.004175	LQEAQER
5.5	1183.617172	-0.011084	AQLEAWR
5.1	1183.619690	-0.013602	TDPRPDAATIK
3.7	1183.601913	0.004175	EALEQQR
3.3	1183.609802	-0.003714	ATPHFSGLAAGR

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

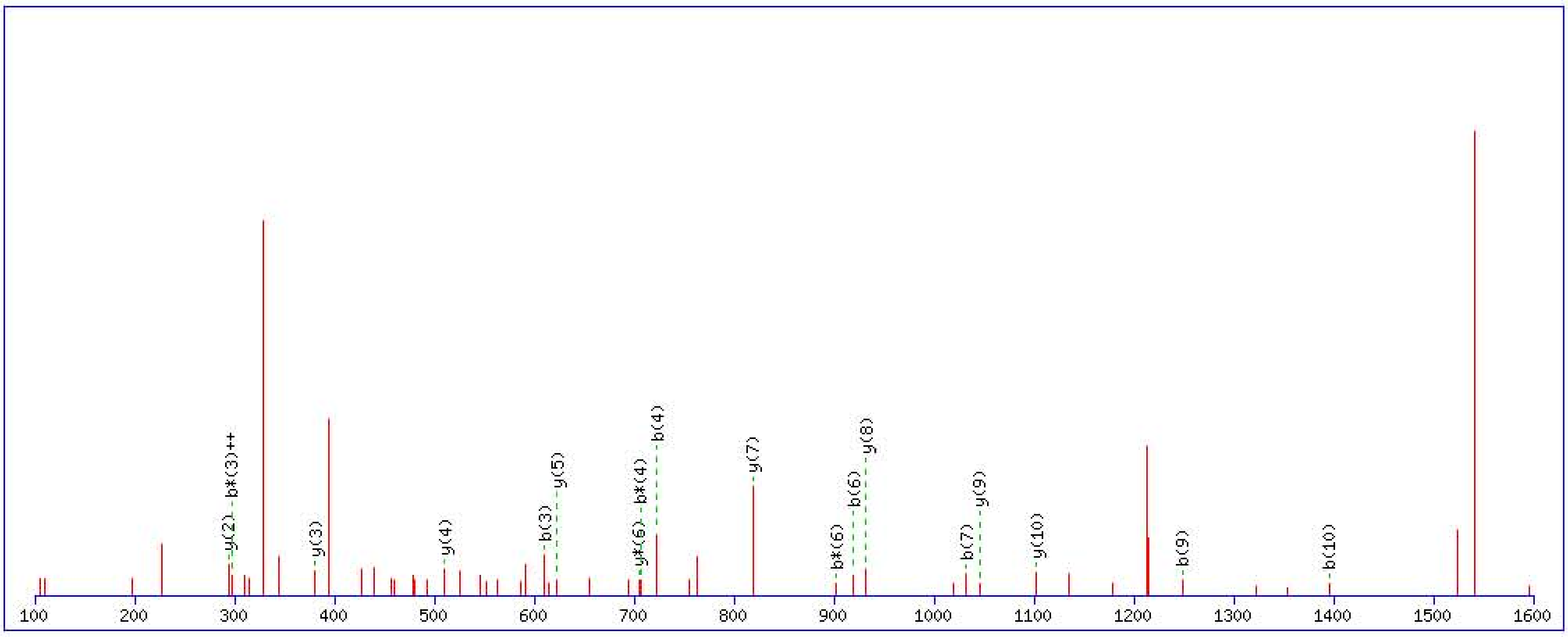
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGLLPVLESFK**
Found in **APOA1_HUMAN**, Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1

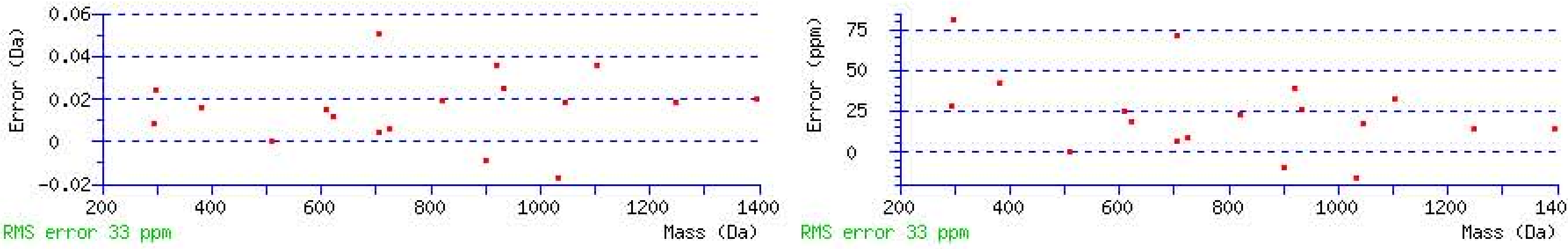
Match to Query 39736: 1540.882908 from(771.448730,2+) rtinseconds(2782) index(11927)
Title: Locus:1.1.1.3100.10 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1540.868713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0018
Matches : 18/102 fragment ions using 43 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							11
2	497.254066	249.130671	480.227517	240.617396			G	***1102.650673***	551.828975	1085.624124	543.315700	1084.640108	542.823692	10
3	**610.338130**	305.672703	593.311581	297.159428			L	***1045.629209***	523.318243	1028.602660	514.804968	1027.618644	514.312960	9
4	**723.422194**	362.214735	706.395645	353.701461			L	***932.545145***	466.776211	915.518596	458.262936	914.534580	457.770928	8
5	820.474958	410.741117	803.448409	402.227843			P	***819.461081***	410.234179	802.434532	401.720904	801.450516	401.228896	7
6	**919.543372**	460.275324	902.516823	451.762049			V	722.408317	361.707797	705.381768	353.194522	704.397752	352.702514	6
7	**1032.627436**	516.817356	1015.600887	508.304082			L	***623.339903***	312.173590	606.313354	303.660315	605.329338	303.168307	5
8	1161.670029	581.338653	1144.643480	572.825378	1143.659464	572.333370	E	***510.255839***	255.631558	493.229290	247.118283	492.245274	246.626275	4
9	**1248.702057**	624.854667	1231.675508	616.341392	1230.691492	615.849384	S	***381.213246***	191.110261	364.186697	182.596987	363.202681	182.104979	3
10	**1395.770471**	698.388874	1378.743922	689.875599	1377.759906	689.383591	F	***294.181218***	147.594247	277.154669	139.080973			2
11							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.8	1540.868713	0.014195	QGLLPVLESFK
15.2	1540.894531	-0.011623	QAVLSMVRKAK
0.0	1540.864700	0.018208	KVTVGKDDIQK
0.0	1540.893677	-0.010769	LKSVDVGLQGLREK

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

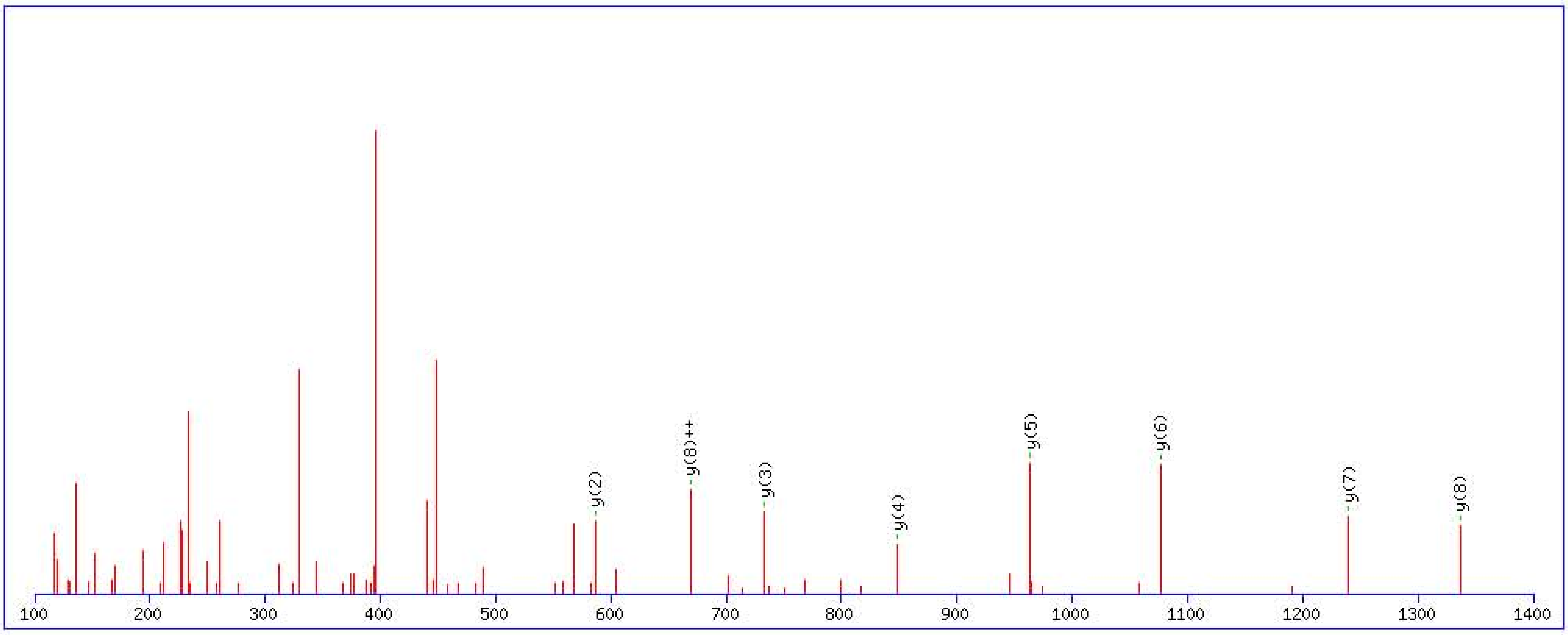
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQPYLDDFQK**
Found in **APOA1_HUMAN**, Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1

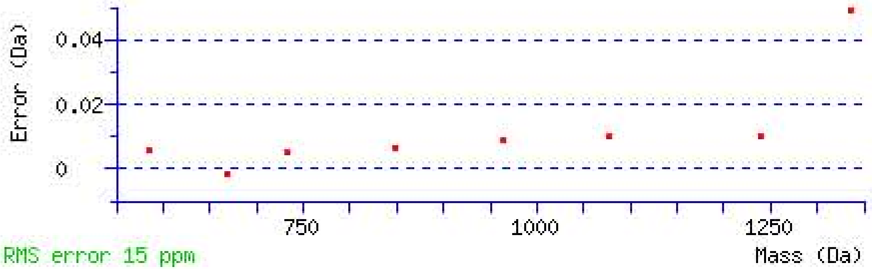
Match to Query 40356: 1562.787252 from(521.936360,3+) rtinseconds(2160) index(43157)
Title: Locus:1.1.1.3036.7 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

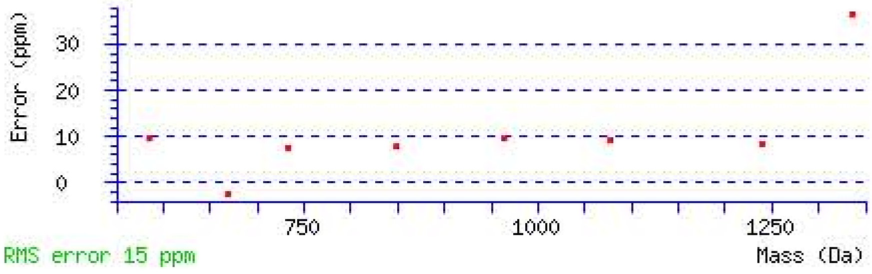
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1562.780304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00069
Matches : 8/90 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							10
2	228.134268	114.570772	211.107719	106.057498			Q	1464.719165	732.863221	1447.692616	724.349946	1446.708600	723.857938	9
3	325.187032	163.097154	308.160483	154.583879			P	***1336.660587***	668.833932	1319.634038	660.320657	1318.650022	659.828649	8
4	488.250361	244.628818	471.223812	236.115544			Y	***1239.607823***	620.307550	1222.581274	611.794275	1221.597258	611.302267	7
5	601.334425	301.170851	584.307876	292.657576			L	***1076.544494***	538.775885	1059.517945	530.262611	1058.533929	529.770603	6
6	716.361368	358.684322	699.334819	350.171047	698.350803	349.679039	D	***963.460430***	482.233853	946.433881	473.720579	945.449865	473.228571	5
7	831.388311	416.197793	814.361762	407.684519	813.377746	407.192511	D	***848.433487***	424.720382	831.406938	416.207107	830.422922	415.715099	4
8	978.456725	489.732000	961.430176	481.218726	960.446160	480.726718	F	***733.406544***	367.206910	716.379995	358.693636			3
9	1417.682051	709.344664	1400.655502	700.831389	1399.671486	700.339381	Q	***586.338130***	293.672703	569.311581	285.159429			2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.6	1562.780304	0.006948	VQPYLDDFQK

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

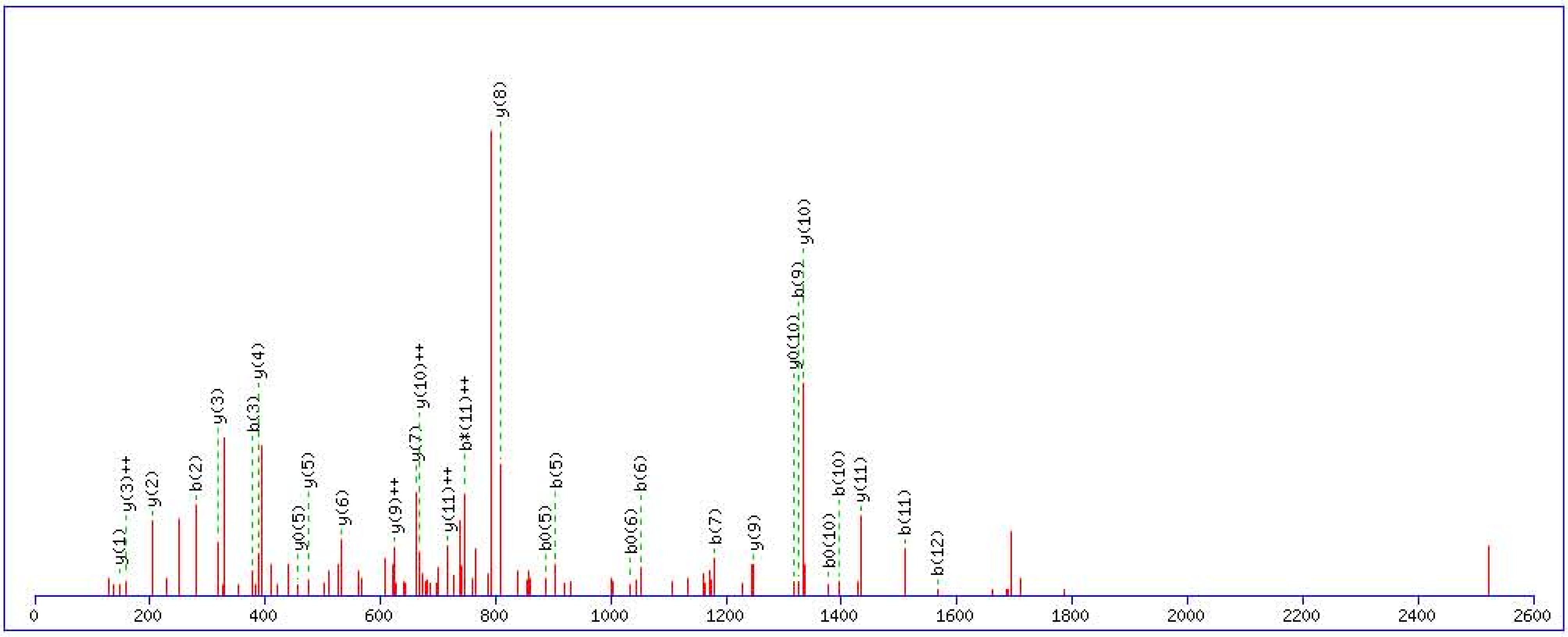
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DYVSQFEGSALGK**
Found in **APOA1_HUMAN**, Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1

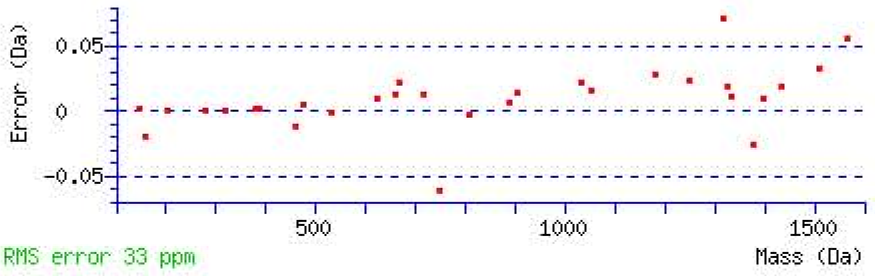
Match to Query 46079: 1710.841768 from(856.428160,2+) rtinseconds(2372) index(44553)
Title: Locus:1.1.1.3109.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

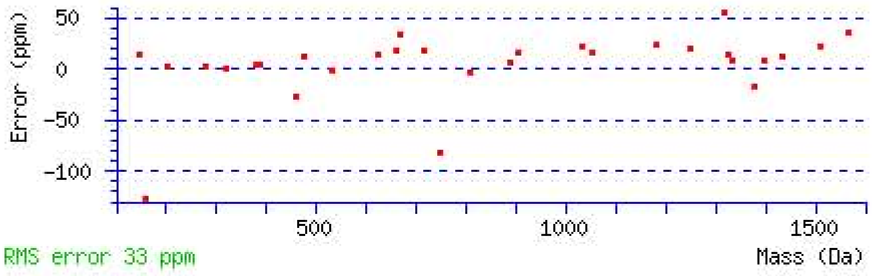
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1710.828705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 5e-005
Matches : 30/128 fragment ions using 79 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							13
2	**279.097548**	140.052412			261.086983	131.047130	Y	1596.809042	798.908159	1579.782493	790.394884	1578.798477	789.902876	12
3	**378.165962**	189.586619			360.155397	180.581337	V	***1433.745713***	717.376495	1416.719164	708.863220	1415.735148	708.371212	11
4	465.197990	233.102633			447.187425	224.097351	S	***1334.677299***	667.842288	1317.650750	659.329013	1316.666734	658.837005	10
5	**904.423316**	452.715296	887.396767	444.202022	886.412751	443.710014	Q	***1247.645271***	624.326273	1230.618722	615.812999	1229.634706	615.320991	9
6	**1051.491730**	526.249503	1034.465181	517.736229	1033.481165	517.244221	F	***808.419945***	404.713610	791.393396	396.200336	790.409380	395.708328	8
7	**1180.534323**	590.770800	1163.507774	582.257525	1162.523758	581.765517	E	***661.351531***	331.179403	644.324982	322.666129	643.340966	322.174121	7
8	1237.555787	619.281532	1220.529238	610.768257	1219.545222	610.276249	G	***532.308938***	266.658107	515.282389	258.144832	514.298373	257.652824	6
9	**1324.587815**	662.797546	1307.561266	654.284271	1306.577250	653.792263	S	***475.287474***	238.147375	458.260925	229.634100	457.276909	229.142092	5
10	**1395.624929**	698.316103	1378.598380	689.802828	1377.614364	689.310820	A	***388.255446***	194.631361	371.228897	186.118086			4
11	**1508.708993**	754.858135	1491.682444	746.344860	1490.698428	745.852852	L	***317.218332***	159.112804	300.191783	150.599529			3
12	**1565.730457**	783.368866	1548.703908	774.855592	1547.719892	774.363584	G	***204.134268***	102.570772	187.107719	94.057497			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.5	1710.828705	0.013063	DYVSQFEGSALGK
3.5	1710.835907	0.005861	ASRKGSFGEMGEQTVK
2.7	1710.833420	0.008348	YDPVWMTVTRKCR

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

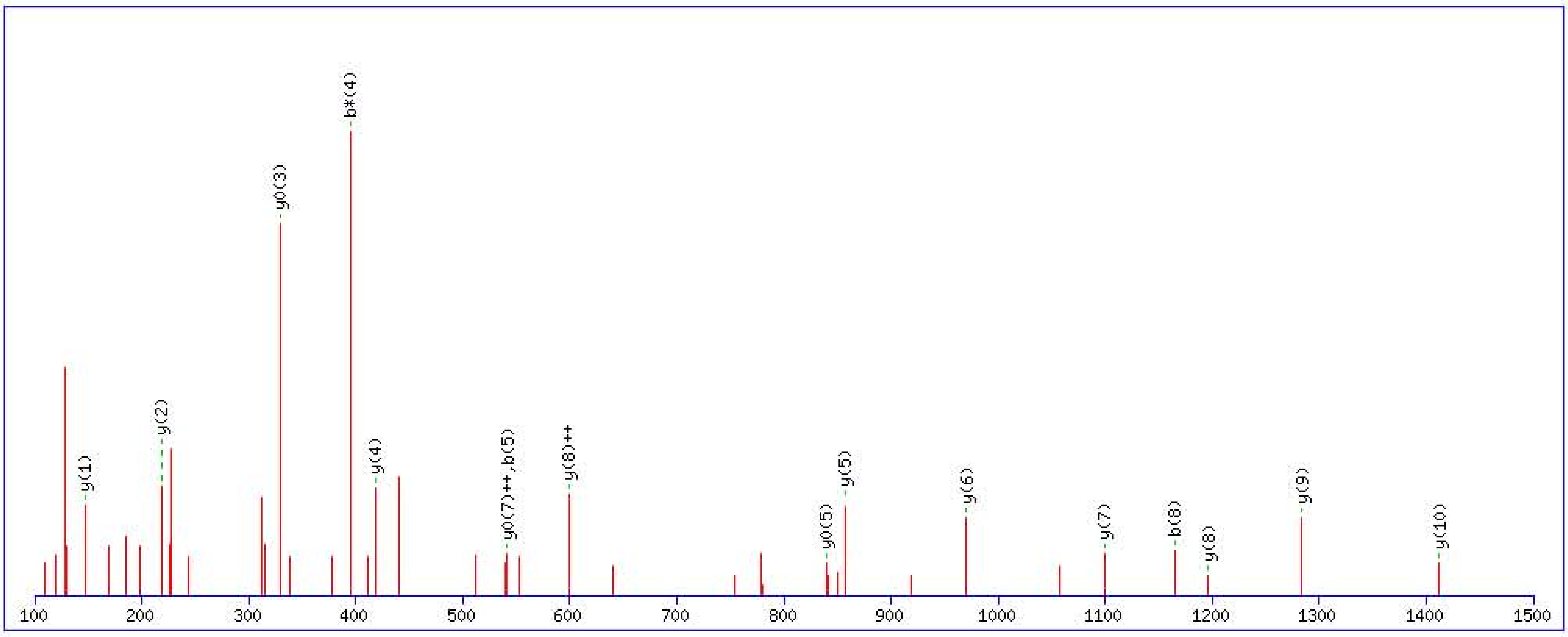
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VKSPELQAEAK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

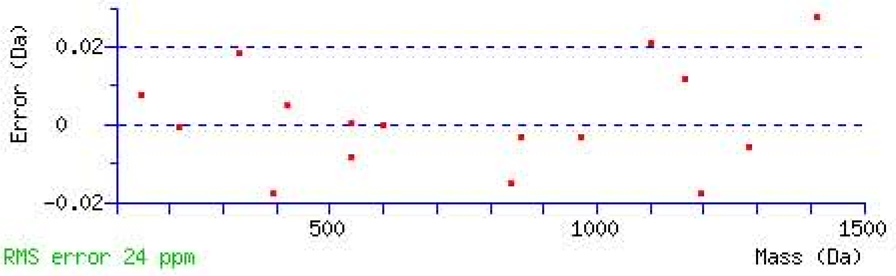
Match to Query 38997: 1509.820992 from(504.280940,3+) rtinseconds(1429) index(38339)
Title: Locus:1.1.1.2781.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

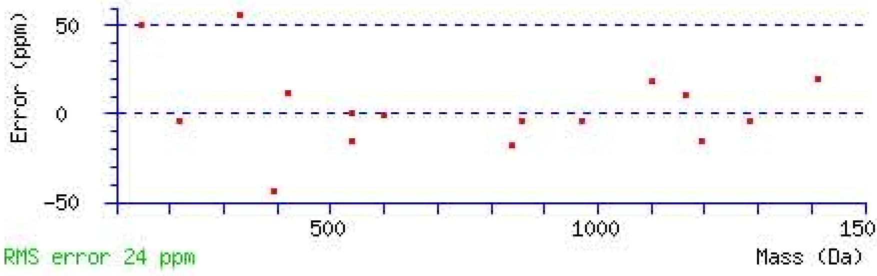
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1509.822464
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 4.1e-006
Matches : 16/110 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							11
2	228.170653	114.588965	211.144104	106.075690			K	***1411.761363***	706.384319	1394.734814	697.871045	1393.750798	697.379037	10
3	315.202681	158.104979	298.176132	149.591704	297.192116	149.099696	S	***1283.666400***	642.336838	1266.639851	633.823563	1265.655835	633.331555	9
4	412.255445	206.631361	395.228896	198.118086	394.244880	197.626078	P	***1196.634372***	598.820824	1179.607823	590.307549	1178.623807	589.815541	8
5	**541.298038**	271.152657	524.271489	262.639383	523.287473	262.147375	E	***1099.581608***	550.294442	1082.555059	541.781167	1081.571043	541.289159	7
6	654.382102	327.694689	637.355553	319.181415	636.371537	318.689407	L	***970.539015***	485.773145	953.512466	477.259871	952.528450	476.767863	6
7	1093.607428	547.307352	1076.580879	538.794078	1075.596863	538.302070	Q	***857.454951***	429.231113	840.428402	420.717839	839.444386	420.225831	5
8	**1164.644542**	582.825909	1147.617993	574.312635	1146.633977	573.820627	A	***418.229625***	209.618450	401.203076	201.105176	400.219060	200.613168	4
9	1293.687135	647.347205	1276.660586	638.833931	1275.676570	638.341923	E	347.192511	174.099893	330.165962	165.586619	329.181946	165.094611	3
10	1364.724249	682.865762	1347.697700	674.352488	1346.713684	673.860480	A	***218.149918***	109.578597	201.123369	101.065322			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.5	1509.822464	-0.001472	VKSPELQAEAK
8.5	1509.822479	-0.001487	AQELTLQTPAK
5.2	1509.803848	0.017144	KGEVLPEEQGPSIK
4.5	1509.822464	-0.001472	QVLLAQAEAEK
4.3	1509.803879	0.017113	TGGLDLPSPPTGASLK
3.9	1509.833679	-0.012687	QAELEAARLAK
3.5	1509.830338	-0.009346	DQAFKAIRSFLSK
0.7	1509.822479	-0.001487	QTLEVPQKEK

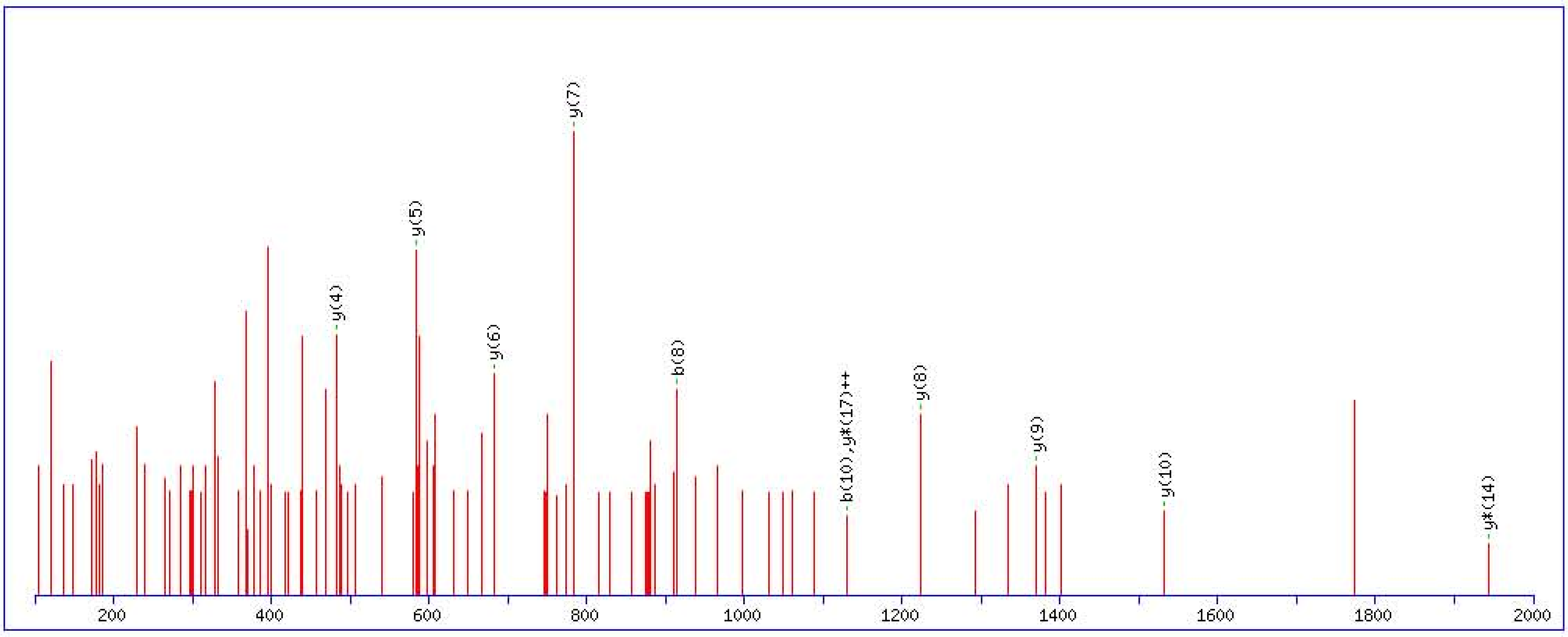
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPCVESLVSQYFQTVTDYGK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

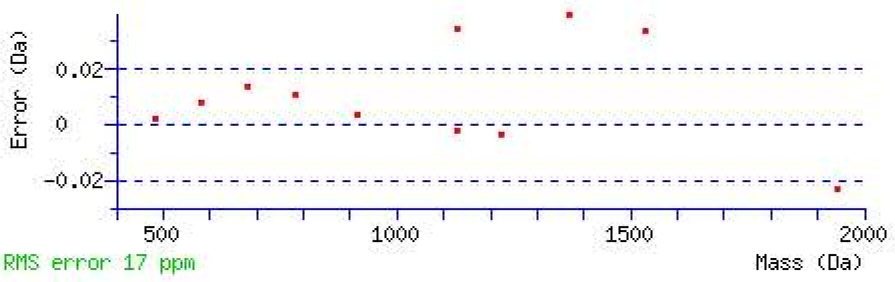
Match to Query 67131: 2660.280972 from(887.767600,3+) rtinseconds(3124) index(49837)
Title: Locus:1.1.1.3367.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

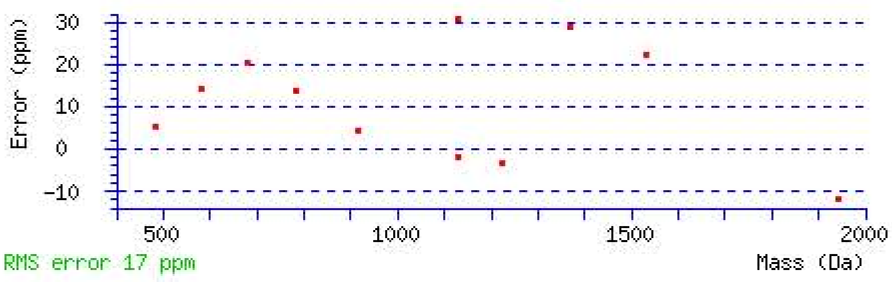
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2660.250244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.006
Matches : 11/204 fragment ions using 16 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							20
2	227.102633	114.054954			209.092068	105.049672	P	2532.214913	1266.611094	2515.188364	1258.097820	2514.204348	1257.605812	19
3	387.133282	194.070279			369.122717	185.064997	C	2435.162149	1218.084712	2418.135600	1209.571438	2417.151584	1209.079430	18
4	486.201696	243.604486			468.191131	234.599204	V	2275.131500	1138.069388	2258.104951	1129.556113	2257.120935	1129.064105	17
5	615.244289	308.125783			597.233724	299.120500	E	2176.063086	1088.535181	2159.036537	1080.021906	2158.052521	1079.529898	16
6	702.276317	351.641797			684.265752	342.636514	S	2047.020493	1024.013885	2029.993944	1015.500610	2029.009928	1015.008602	15
7	815.360381	408.183829			797.349816	399.178546	L	1959.988465	980.497871	1942.961916	971.984596	1941.977900	971.492588	14
8	**914.428795**	457.718036			896.418230	448.712753	V	1846.904401	923.955839	1829.877852	915.442564	1828.893836	914.950556	13
9	1001.460823	501.234050			983.450258	492.228767	S	1747.835987	874.421632	1730.809438	865.908357	1729.825422	865.416349	12
10	**1129.519401**	565.263339	1112.492852	556.750064	1111.508836	556.258056	Q	1660.803959	830.905618	1643.777410	822.392343	1642.793394	821.900335	11
11	1292.582730	646.795003	1275.556181	638.281729	1274.572165	637.789721	Y	***1532.745381***	766.876329	1515.718832	758.363054	1514.734816	757.871046	10
12	1439.651144	720.329210	1422.624595	711.815936	1421.640579	711.323928	F	***1369.682052***	685.344664	1352.655503	676.831390	1351.671487	676.339382	9
13	1878.876470	939.941873	1861.849921	931.428599	1860.865905	930.936591	Q	***1222.613638***	611.810457	1205.587089	603.297183	1204.603073	602.805175	8
14	1979.924149	990.465713	1962.897600	981.952438	1961.913584	981.460430	T	***783.388312***	392.197794	766.361763	383.684519	765.377747	383.192511	7
15	2078.992563	1039.999920	2061.966014	1031.486645	2060.981998	1030.994637	V	***682.340633***	341.673954	665.314084	333.160680	664.330068	332.668672	6
16	2180.040242	1090.523759	2163.013693	1082.010484	2162.029677	1081.518476	T	***583.272219***	292.139747	566.245670	283.626473	565.261654	283.134465	5
17	2295.067185	1148.037230	2278.040636	1139.523956	2277.056620	1139.031948	D	***482.224540***	241.615908	465.197991	233.102633	464.213975	232.610625	4
18	2458.130514	1229.568895	2441.103965	1221.055620	2440.119949	1220.563612	Y	367.197597	184.102436	350.171048	175.589162			3
19	2515.151978	1258.079627	2498.125429	1249.566352	2497.141413	1249.074344	G	204.134268	102.570772	187.107719	94.057497			2
20							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.1	2660.250244	0.030728	EPCVESLVSQYFQTVTDYGK
3.6	2660.250244	0.030728	EPCVESLVSQYFQTVTDYGK

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

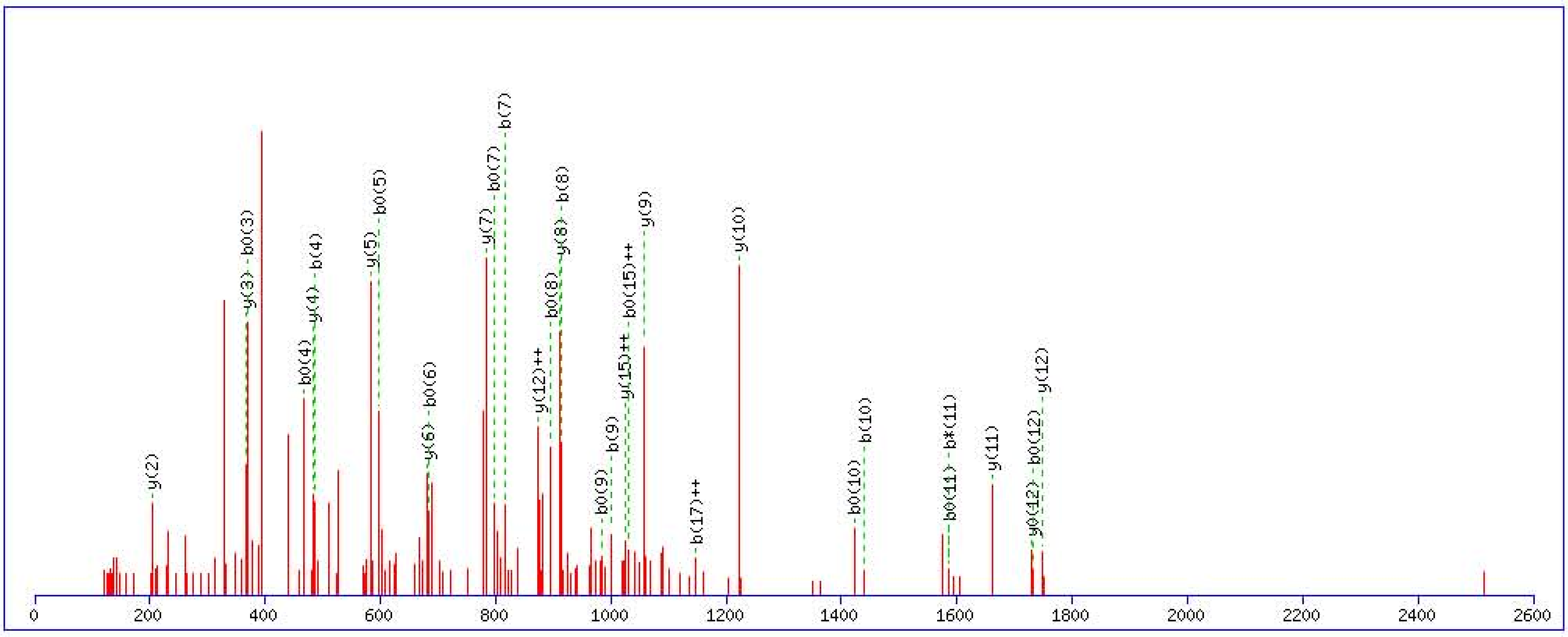
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPCVESLVSQYFQTVTDYGK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

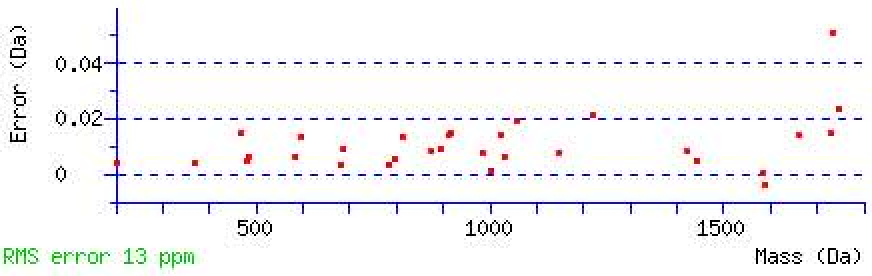
Match to Query 67135: 2660.283612 from(887.768480,3+) rtinseconds(3144) index(50011)
Title: Locus:1.1.1.3374.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

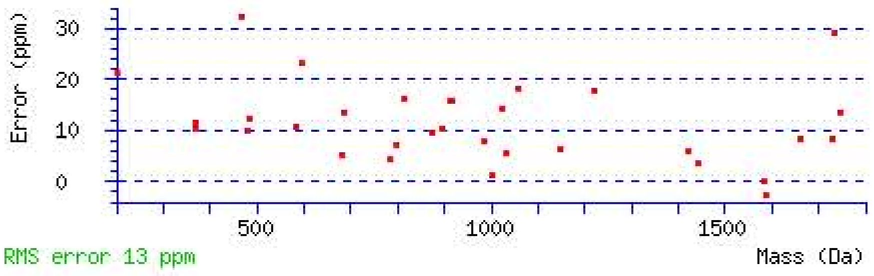
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2660.250244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00017
Matches : 32/204 fragment ions using 60 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							20
2	227.102633	114.054954			209.092068	105.049672	P	2532.214913	1266.611094	2515.188364	1258.097820	2514.204348	1257.605812	19
3	387.133282	194.070279			369.122717	185.064997	C	2435.162149	1218.084712	2418.135600	1209.571438	2417.151584	1209.079430	18
4	**486.201696**	243.604486			468.191131	234.599204	V	2275.131500	1138.069388	2258.104951	1129.556113	2257.120935	1129.064105	17
5	615.244289	308.125783			597.233724	299.120500	E	2176.063086	1088.535181	2159.036537	1080.021906	2158.052521	1079.529898	16
6	702.276317	351.641797			684.265752	342.636514	S	2047.020493	1024.013884	2029.993944	1015.500610	2029.009928	1015.008602	15
7	**815.360381**	408.183829			797.349816	399.178546	L	1959.988465	980.497870	1942.961916	971.984596	1941.977900	971.492588	14
8	**914.428795**	457.718036			896.418230	448.712753	V	1846.904401	923.955838	1829.877852	915.442564	1828.893836	914.950556	13
9	**1001.460823**	501.234050			983.450258	492.228767	S	***1747.835987***	874.421631	1730.809438	865.908357	1729.825422	865.416349	12
10	**1440.686149**	720.846712	1423.659600	712.333438	1422.675584	711.841430	Q	***1660.803959***	830.905617	1643.777410	822.392343	1642.793394	821.900335	11
11	1603.749478	802.378377	1586.722929	793.865103	1585.738913	793.373094	Y	***1221.578633***	611.292954	1204.552084	602.779680	1203.568068	602.287672	10
12	1750.817892	875.912584	1733.791343	867.399310	1732.807327	866.907302	F	***1058.515304***	529.761290	1041.488755	521.248015	1040.504739	520.756007	9
13	1878.876470	939.941873	1861.849921	931.428599	1860.865905	930.936590	Q	***911.446890***	456.227083	894.420341	447.713808	893.436325	447.221800	8
14	1979.924149	990.465713	1962.897600	981.952438	1961.913584	981.460430	T	***783.388312***	392.197794	766.361763	383.684519	765.377747	383.192511	7
15	2078.992563	1039.999919	2061.966014	1031.486645	2060.981998	1030.994637	V	***682.340633***	341.673954	665.314084	333.160680	664.330068	332.668672	6
16	2180.040242	1090.523759	2163.013693	1082.010484	2162.029677	1081.518476	T	***583.272219***	292.139747	566.245670	283.626473	565.261654	283.134465	5
17	2295.067185	1148.037230	2278.040636	1139.523956	2277.056620	1139.031948	D	***482.224540***	241.615908	465.197991	233.102633	464.213975	232.610625	4
18	2458.130514	1229.568895	2441.103965	1221.055620	2440.119949	1220.563612	Y	***367.197597***	184.102436	350.171048	175.589162			3
19	2515.151978	1258.079627	2498.125429	1249.566352	2497.141413	1249.074344	G	***204.134268***	102.570772	187.107719	94.057497			2
20							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.4	2660.250244	0.033368	EPCVESLVSQYFQTVTDYGK
23.3	2660.250244	0.033368	EPCVESLVSQYFQTVTDYGK

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

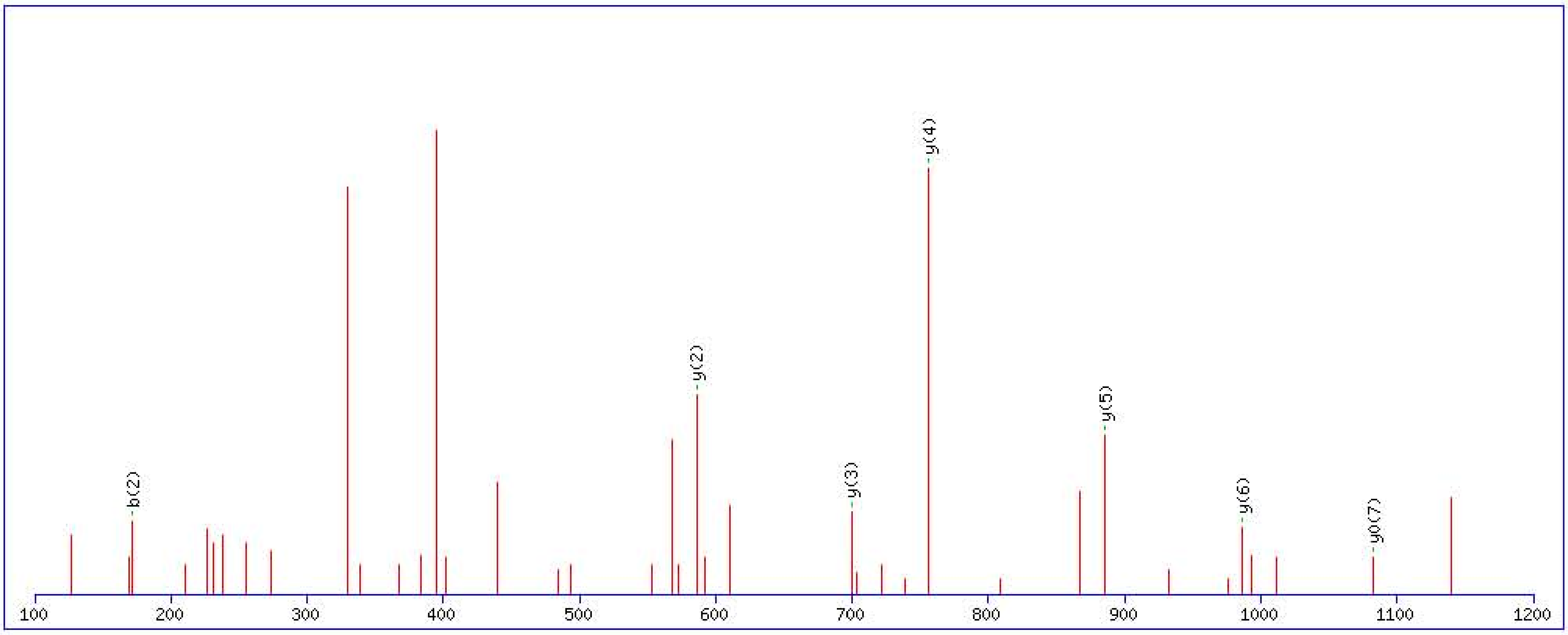
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNTEGLQK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

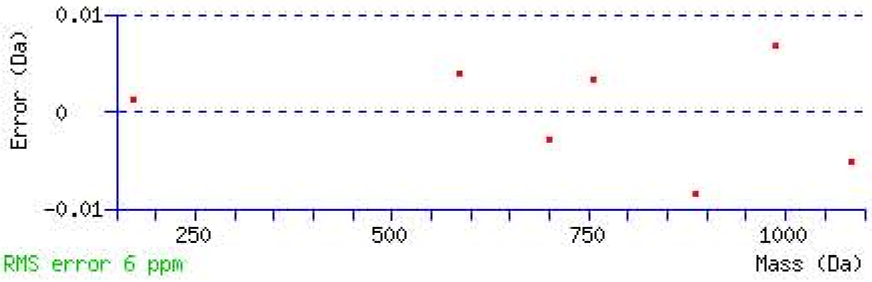
Match to Query 25937: 1156.592108 from(579.303330,2+) rtinseconds(1386) index(37996)
Title: Locus:1.1.1.2766.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

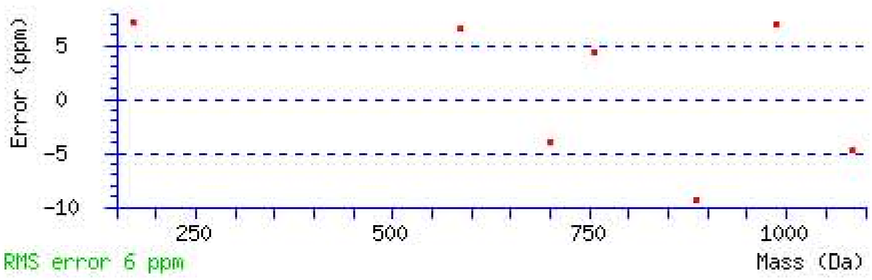
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1156.591034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0048
Matches : 7/70 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	58.028740	29.518008					G							8
2	172.071667	86.539471	155.045118	78.026197			N	1100.576857	550.792067	1083.550308	542.278792	1082.566292	541.786784	7
3	273.119346	137.063311	256.092797	128.550037	255.108781	128.058029	T	***986.533930***	493.770603	969.507381	485.257329	968.523365	484.765321	6
4	402.161939	201.584608	385.135390	193.071333	384.151374	192.579325	E	***885.486251***	443.246764	868.459702	434.733489	867.475686	434.241481	5
5	459.183403	230.095339	442.156854	221.582065	441.172838	221.090057	G	***756.443658***	378.725467	739.417109	370.212193			4
6	572.267467	286.637372	555.240918	278.124097	554.256902	277.632089	L	***699.422194***	350.214735	682.395645	341.701461			3
7	1011.492793	506.250035	994.466244	497.736760	993.482228	497.244752	Q	***586.338130***	293.672703	569.311581	285.159429			2
8							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.1	1156.591034	0.001074	GNTEGLQK

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

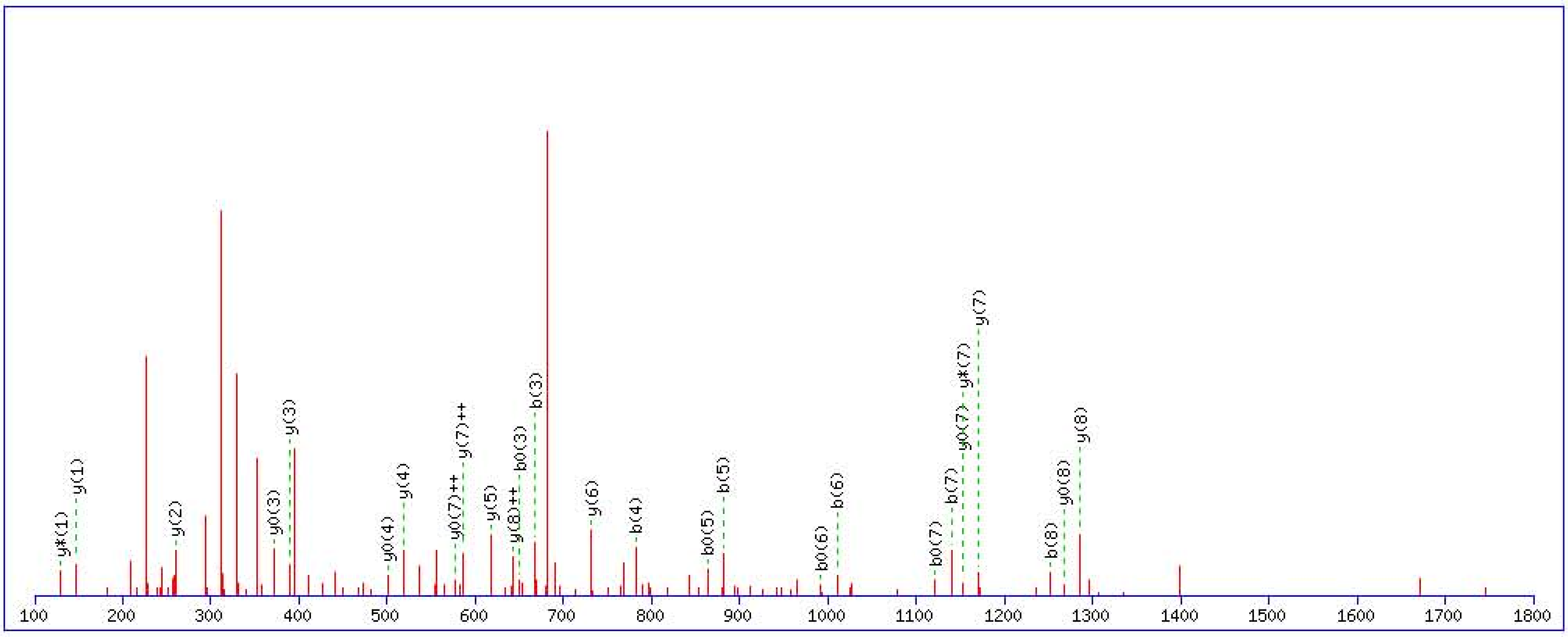
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDQNVEELK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

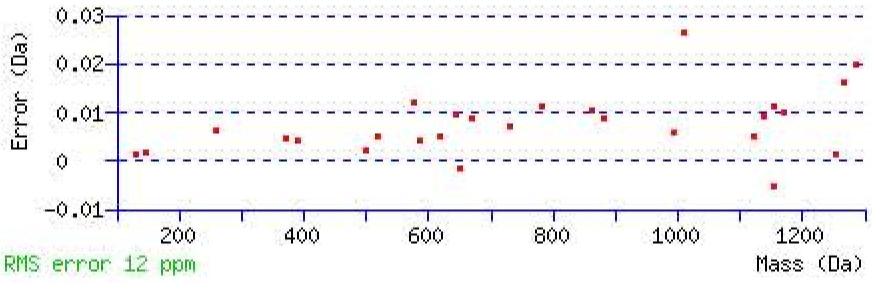
Match to Query 34520: 1397.732288 from(699.873420,2+) rtinseconds(1832) index(77278)
Title: Locus:1.1.1.2852.15 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

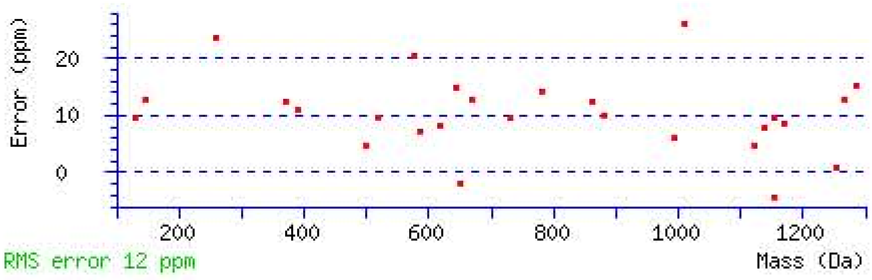
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1397.722427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.0069
Matches : 27/86 fragment ions using 58 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							9
2	229.118283	115.062779			211.107718	106.057497	D	***1285.645664***	643.326470	1268.619115	634.813196	1267.635099	634.321187	8
3	**668.343609**	334.675443	651.317060	326.162168	650.333044	325.670160	Q	***1170.618721***	585.812998	1153.592172	577.299724	1152.608156	576.807716	7
4	**782.386536**	391.696906	765.359987	383.183631	764.375971	382.691623	N	***731.393395***	366.200335	714.366846	357.687061	713.382830	357.195053	6
5	**881.454950**	441.231113	864.428401	432.717838	863.444385	432.225830	V	***617.350468***	309.178872	600.323919	300.665597	599.339903	300.173589	5
6	**1010.497543**	505.752410	993.470994	497.239135	992.486978	496.747127	E	***518.282054***	259.644665	501.255505	251.131390	500.271489	250.639382	4
7	**1139.540136**	570.273706	1122.513587	561.760431	1121.529571	561.268423	E	***389.239461***	195.123368	372.212912	186.610094	371.228896	186.118086	3
8	**1252.624200**	626.815738	1235.597651	618.302463	1234.613635	617.810455	L	***260.196868***	130.602072	243.170319	122.088797			2
9							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.0	1397.722427	0.009861	IDQNVEELK
15.4	1397.751404	-0.019116	QAEPELDLRSIK
9.7	1397.723785	0.008503	LFVSHMIDKHR
8.8	1397.744873	-0.012585	MLEKARHQELK
6.7	1397.744873	-0.012585	QRREEELK
4.6	1397.744873	-0.012585	QEERRELK
3.4	1397.747589	-0.015301	LEPMIVPDLDLK
3.2	1397.740204	-0.007916	VEGDLKGPEVDIK
3.2	1397.740204	-0.007916	VEGDLKGPEVDLK
2.9	1397.733658	-0.001370	QNITNQLEK

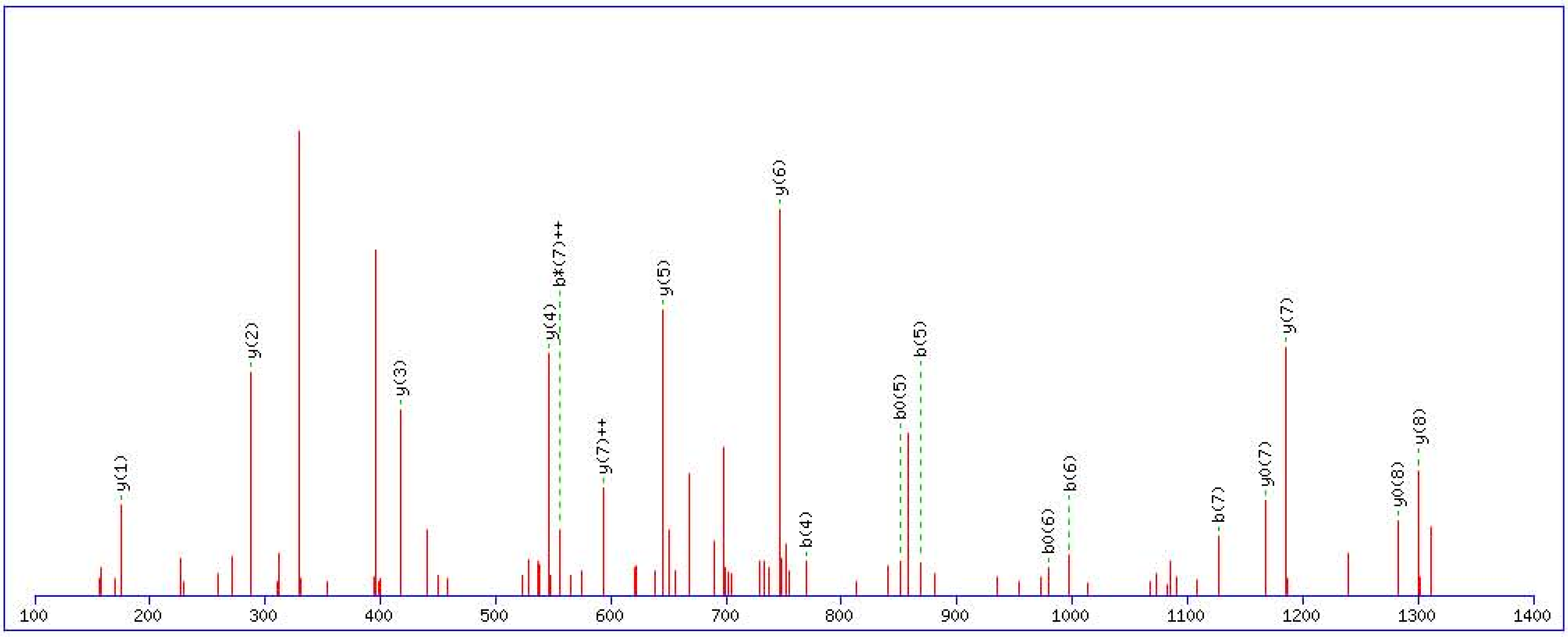
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDQTVEELR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

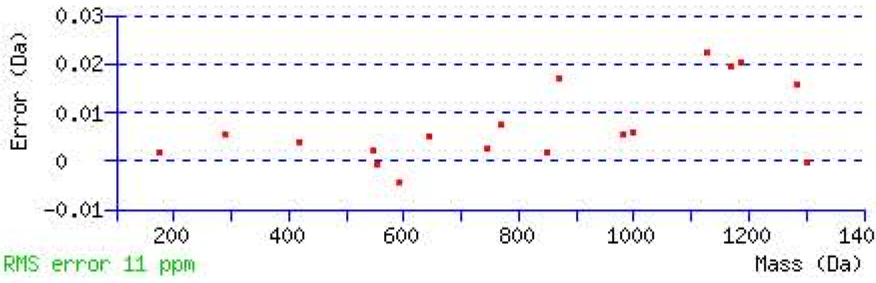
Match to Query 35557: 1412.741588 from(707.378070,2+) rtinseconds(1877) index(41215)
Title: Locus:1.1.1.2937.24 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

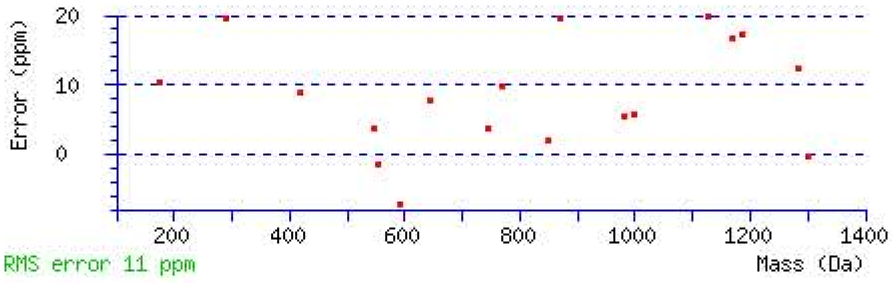
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1412.733337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 9.1e-006
Matches : 18/86 fragment ions using 24 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							9
2	229.118283	115.062779			211.107718	106.057497	D	***1300.656564***	650.831920	1283.630015	642.318646	1282.645999	641.826638	8
3	668.343609	334.675443	651.317060	326.162168	650.333044	325.670160	Q	***1185.629621***	593.318449	1168.603072	584.805174	1167.619056	584.313166	7
4	**769.391288**	385.199282	752.364739	376.686008	751.380723	376.194000	T	***746.404295***	373.705786	729.377746	365.192511	728.393730	364.700503	6
5	**868.459702**	434.733489	851.433153	426.220215	850.449137	425.728207	V	***645.356616***	323.181946	628.330067	314.668672	627.346051	314.176664	5
6	**997.502295**	499.254786	980.475746	490.741511	979.491730	490.249503	E	***546.288202***	273.647739	529.261653	265.134465	528.277637	264.642457	4
7	**1126.544888**	563.776082	1109.518339	555.262808	1108.534323	554.770800	E	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
8	1239.628952	620.318114	1222.602403	611.804840	1221.618387	611.312832	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 IDQTVEELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.4	1412.733337	0.008251	IDQTVEELR
13.1	1412.744537	-0.002949	IPPEKMRELER
10.4	1412.741211	0.000377	KVTIYSFTGNQR
9.7	1412.734665	0.006923	MPADWRQQLLR
5.0	1412.741196	0.000392	SSLHYKPTPDLR
4.0	1412.737167	0.004421	ARPEDVISEGRGK
3.9	1412.759857	-0.018269	LIPFPGGAVGCGIR
3.6	1412.756470	-0.014882	DLRSVFFNFIR
3.6	1412.748398	-0.006810	LVDNIQRNTNAR
3.3	1412.748596	-0.007008	SQLLMLFDKFR

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

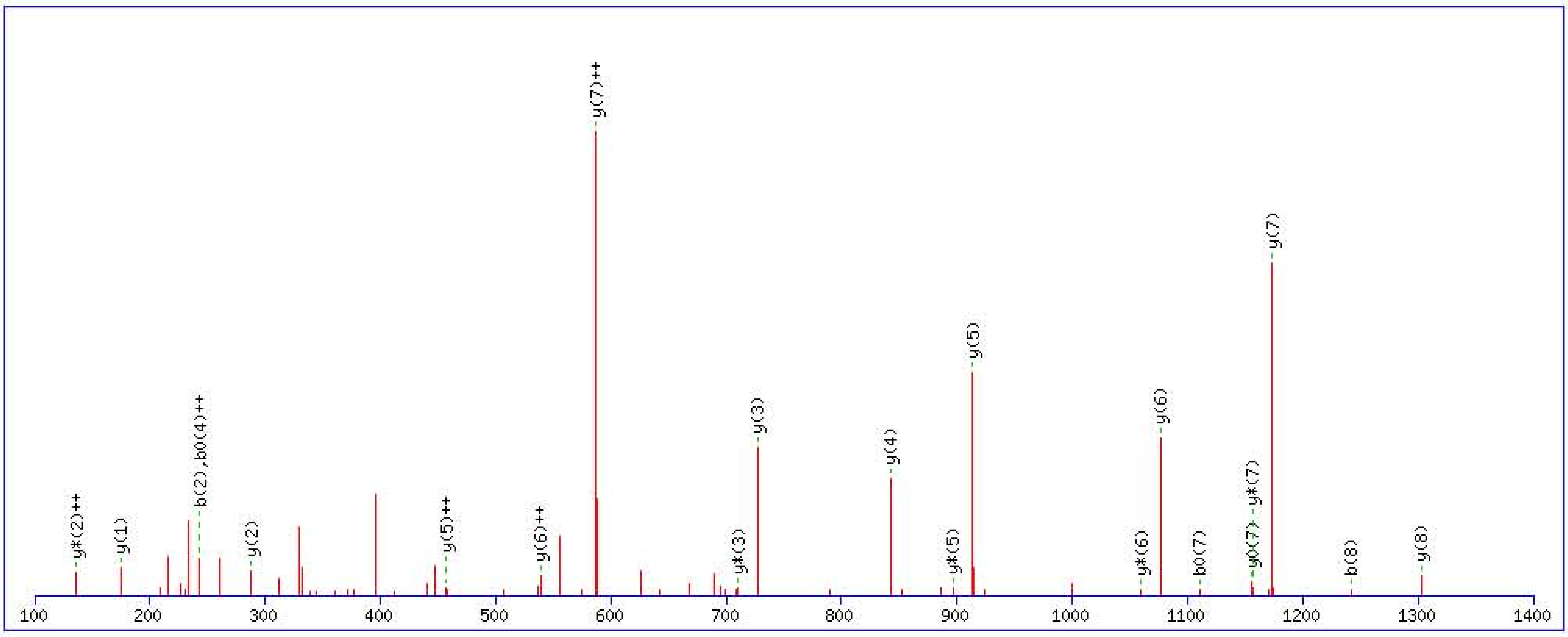
Mascot Search Results

Peptide View

MS/MS Fragmentation of LEPYADQLR
Found in APOA4_HUMAN, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

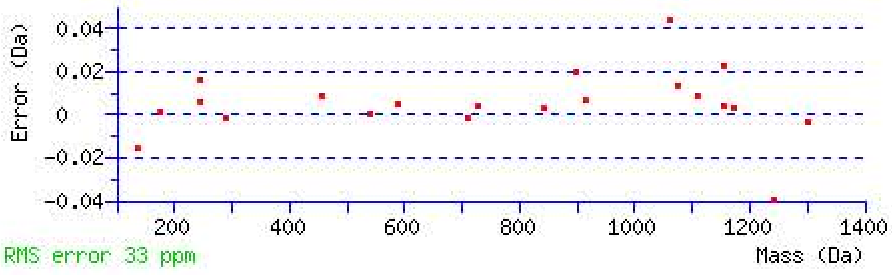
Match to Query 35599: 1414.735168 from(708.374860,2+) rtinseconds(1955) index(41855)
Title: Locus:1.1.1.2964.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

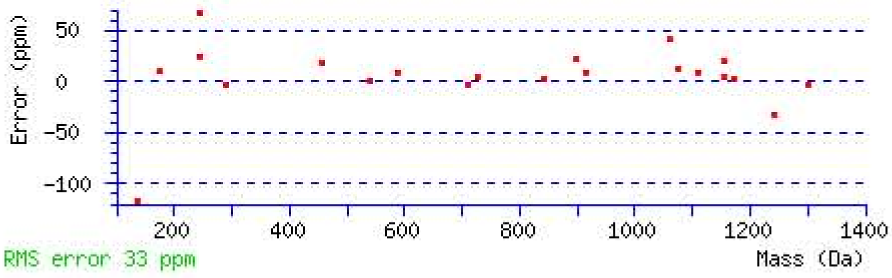
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1414.727844
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00065
Matches : 21/76 fragment ions using 47 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							9
2	**243.133933**	122.070605			225.123368	113.065322	E	***1302.651085***	651.829181	1285.624536	643.315906	1284.640520	642.823898	8
3	340.186697	170.596987			322.176132	161.591704	P	***1173.608492***	587.307884	1156.581943	578.794610	1155.597927	578.302602	7
4	503.250026	252.128651			485.239461	243.123369	Y	***1076.555728***	538.781502	1059.529179	530.268228	1058.545163	529.776220	6
5	574.287140	287.647208			556.276575	278.641926	A	***913.492399***	457.249838	896.465850	448.736563	895.481834	448.244555	5
6	689.314083	345.160680			671.303518	336.155397	D	***842.455285***	421.731281	825.428736	413.218006	824.444720	412.725998	4
7	1128.539409	564.773343	1111.512860	556.260068	1110.528844	555.768060	Q	***727.428342***	364.217809	710.401793	355.704535			3
8	**1241.623473**	621.315375	1224.596924	612.802100	1223.612908	612.310092	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 LEPYADQLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.7	1414.727844	0.007324	LEPYADQLR
6.2	1414.752777	-0.017609	KNIESARAELER
6.2	1414.735931	-0.000763	LMRGLLHCMIR
5.2	1414.716400	0.018768	LEEDARLEERR
5.1	1414.731216	0.003952	LMELQEAVR
1.6	1414.741547	-0.006379	LEKENLEERQK
1.3	1414.735062	0.000106	IQLMQEVDRQR
1.3	1414.731689	0.003479	NKAEFHQSVISR
0.5	1414.741577	-0.006409	ELDVEVSRLEAR
0.5	1414.741577	-0.006409	LETVQADNIREK

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

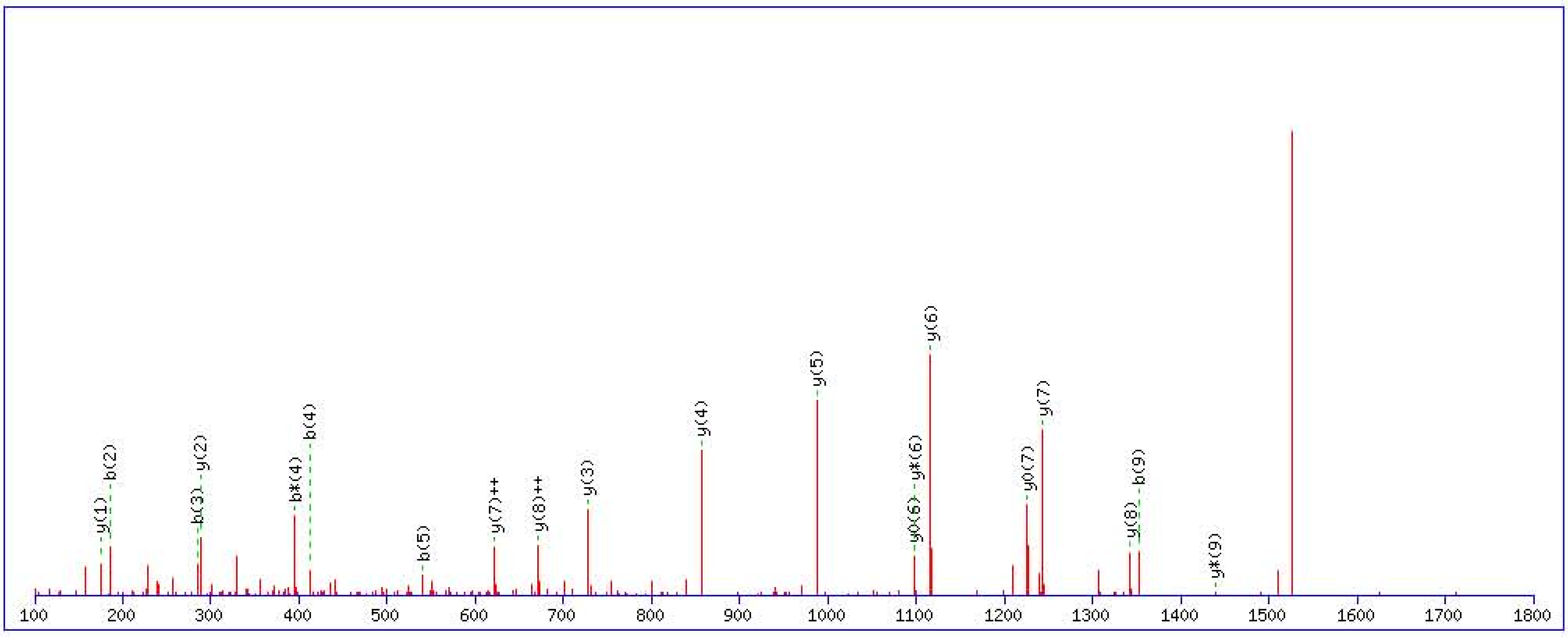
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALVQQMEQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

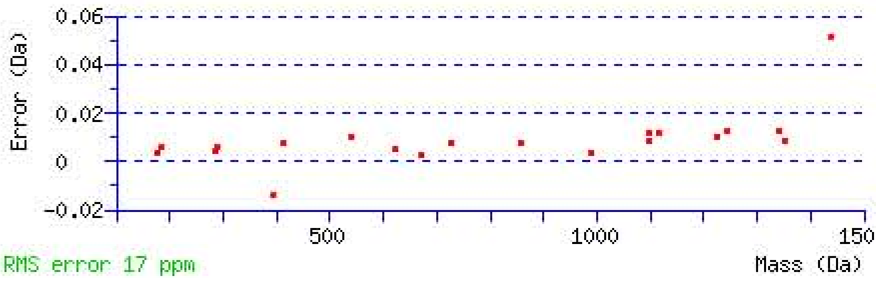
Match to Query 39386: 1525.825968 from(763.920260,2+) rtinseconds(2103) index(79211)
Title: Locus:1.1.1.2946.25 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

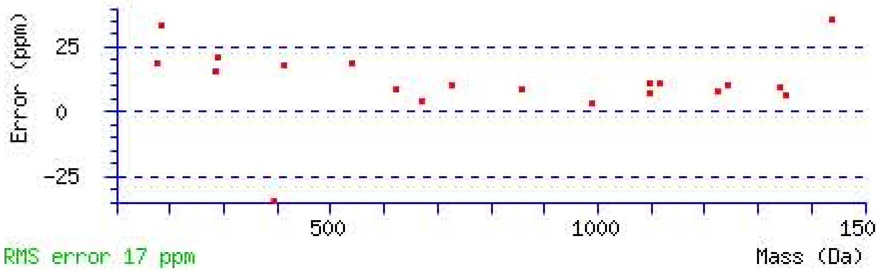
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1525.810867
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 8.9e-006
Matches : 20/84 fragment ions using 29 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	72.044390	36.525833					A							10
2	**185.128454**	93.067865					L	1455.781054	728.394165	1438.754505	719.880890	1437.770489	719.388882	9
3	**284.196868**	142.602072					V	***1342.696990***	671.852133	1325.670441	663.338858	1324.686425	662.846850	8
4	**412.255446**	206.631361	395.228897	198.118087			Q	***1243.628576***	622.317926	1226.602027	613.804651	1225.618011	613.312643	7
5	**540.314024**	270.660650	523.287475	262.147376			Q	***1115.569998***	558.288637	1098.543449	549.775362	1097.559433	549.283354	6
6	671.354509	336.180893	654.327960	327.667618			M	***987.511420***	494.259348	970.484871	485.746073	969.500855	485.254065	5
7	800.397102	400.702189	783.370553	392.188915	782.386537	391.696907	E	***856.470935***	428.739105	839.444386	420.225831	838.460370	419.733823	4
8	1239.622428	620.314852	1222.595879	611.801578	1221.611863	611.309569	Q	***727.428342***	364.217809	710.401793	355.704534			3
9	**1352.706492**	676.856884	1335.679943	668.343609	1334.695927	667.851601	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.8	1525.810867	0.015101	ALVQQMEQLR
25.8	1525.810867	0.015101	ALVQQMEQLR
11.2	1525.810867	0.015101	ALVQQMEQLR
10.6	1525.803482	0.022486	VNTPAGSSQKAR
5.7	1525.803467	0.022501	SPPSPRSSMAAVALR
5.5	1525.807495	0.018473	WPPQQLMLSAALR
5.5	1525.814682	0.011286	LARASEQERR
5.1	1525.843887	-0.017919	QFSLLSQHKK
4.7	1525.846390	-0.020422	SLKGEAITDGPGILR
2.6	1525.814697	0.011271	ERQRTEQLR

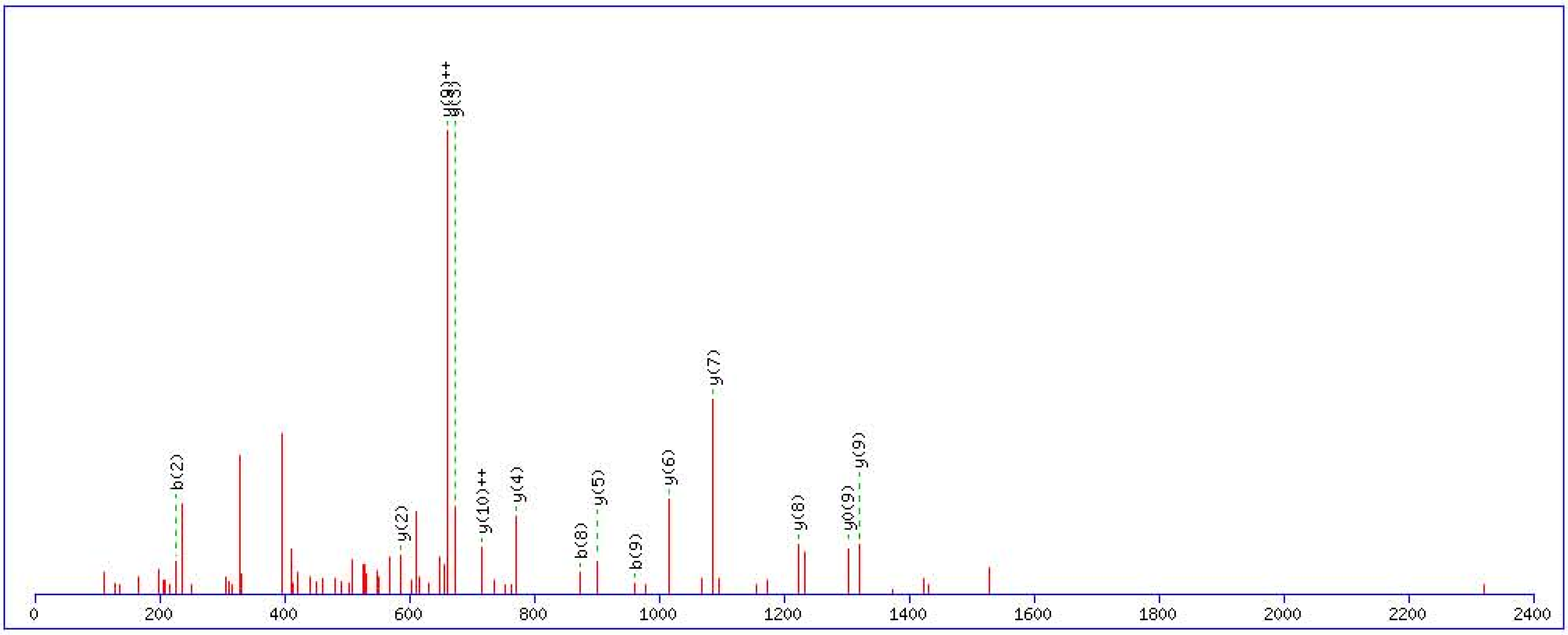
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPHANEVSQK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

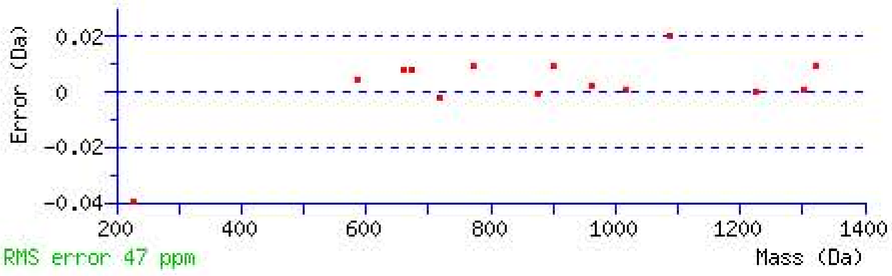
Match to Query 39849: 1545.835768 from(773.925160,2+) rtinseconds(1517) index(75365)
Title: Locus:1.1.1.2742.11 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

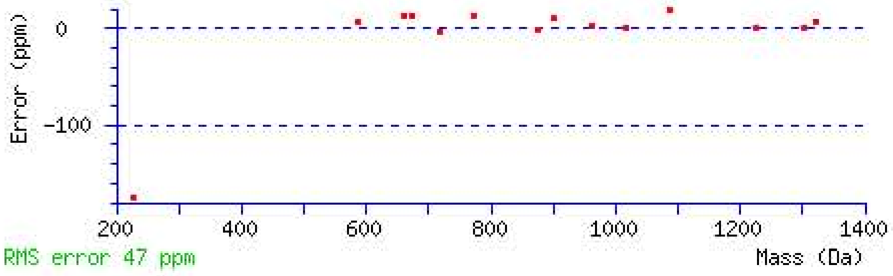
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 0 to 2400 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1545.833710
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 3.9e-005
Matches : 14/94 fragment ions using 29 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							11
2	**227.175404**	114.091340					L	1433.756946	717.382111	1416.730397	708.868837	1415.746381	708.376828	10
3	324.228168	162.617722					P	***1320.672882***	660.840079	1303.646333	652.326804	1302.662317	651.834796	9
4	461.287080	231.147178					H	***1223.620118***	612.313697	1206.593569	603.800422	1205.609553	603.308414	8
5	532.324194	266.665735					A	***1086.561206***	543.784241	1069.534657	535.270966	1068.550641	534.778958	7
6	646.367121	323.687199	629.340572	315.173924			N	***1015.524092***	508.265684	998.497543	499.752409	997.513527	499.260401	6
7	775.409714	388.208495	758.383165	379.695221	757.399149	379.203213	E	***901.481165***	451.244220	884.454616	442.730946	883.470600	442.238938	5
8	**874.478128**	437.742702	857.451579	429.229427	856.467563	428.737419	V	***772.438572***	386.722924	755.412023	378.209649	754.428007	377.717641	4
9	**961.510156**	481.258716	944.483607	472.745441	943.499591	472.253433	S	***673.370158***	337.188717	656.343609	328.675442	655.359593	328.183434	3
10	1400.735482	700.871379	1383.708933	692.358104	1382.724917	691.866096	Q	***586.338130***	293.672703	569.311581	285.159428			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.4	1545.833710	0.002058	LLPHANEVSQK
0.3	1545.832352	0.003416	LLSEVMEELEKVK

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

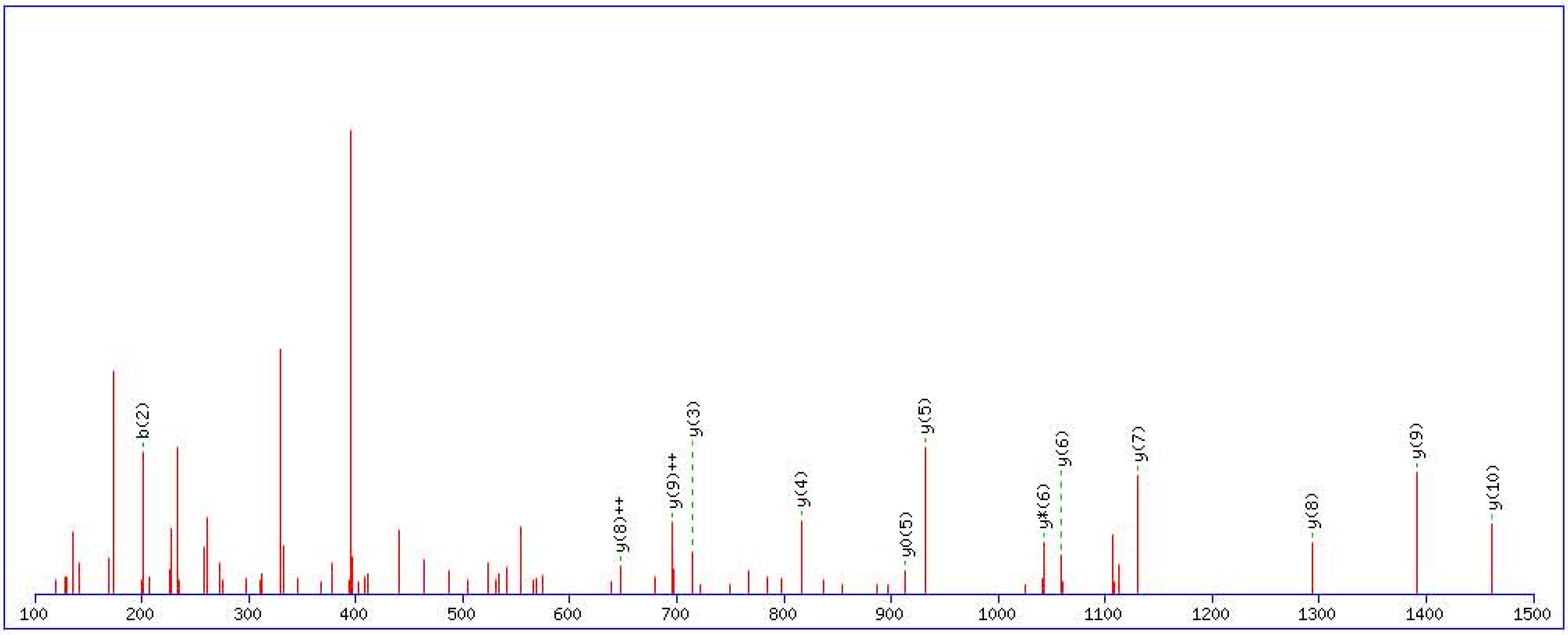
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLAPYAQDTQEK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

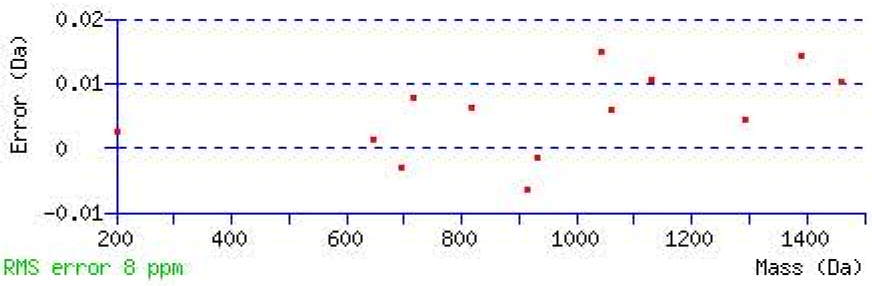
Match to Query 44862: 1660.815732 from(554.612520,3+) rtinseconds(1710) index(40151)
Title: Locus:1.1.1.2879.13 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

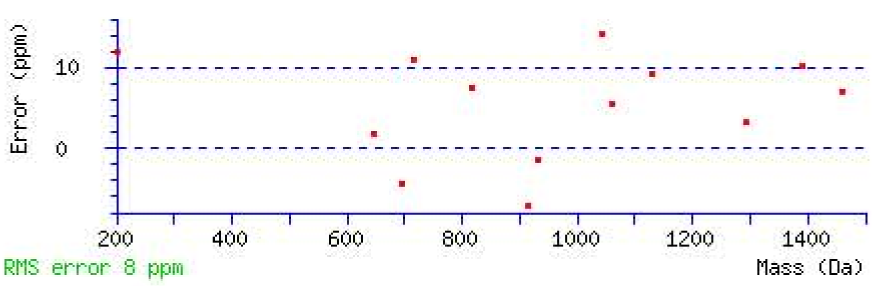
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1660.813034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.0082
Matches : 13/118 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	88.039304	44.523290			70.028739	35.518008	S							12
2	201.123368	101.065322			183.112803	92.060039	L	1574.788308	787.897792	1557.761759	779.384518	1556.777743	778.892510	11
3	272.160482	136.583879			254.149917	127.578596	A	***1461.704244***	731.355760	1444.677695	722.842486	1443.693679	722.350478	10
4	369.213246	185.110261			351.202681	176.104978	P	***1390.667130***	695.837203	1373.640581	687.323929	1372.656565	686.831921	9
5	532.276575	266.641926			514.266010	257.636643	Y	***1293.614366***	647.310821	1276.587817	638.797547	1275.603801	638.305539	8
6	603.313689	302.160483			585.303124	293.155200	A	***1130.551037***	565.779157	1113.524488	557.265882	1112.540472	556.773874	7
7	731.372267	366.189772	714.345718	357.676497	713.361702	357.184489	Q	***1059.513923***	530.260600	1042.487374	521.747325	1041.503358	521.255317	6
8	846.399210	423.703243	829.372661	415.189969	828.388645	414.697961	D	***931.455345***	466.231311	914.428796	457.718036	913.444780	457.226028	5
9	947.446889	474.227083	930.420340	465.713808	929.436324	465.221800	T	***816.428402***	408.717839	799.401853	400.204565	798.417837	399.712557	4
10	1386.672215	693.839746	1369.645666	685.326471	1368.661650	684.834463	Q	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
11	1515.714808	758.361042	1498.688259	749.847768	1497.704243	749.355760	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.4	1660.813034	0.002698	SLAPYAQDTQEK
14.9	1660.813034	0.002698	SLAPYAQDTQEK

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

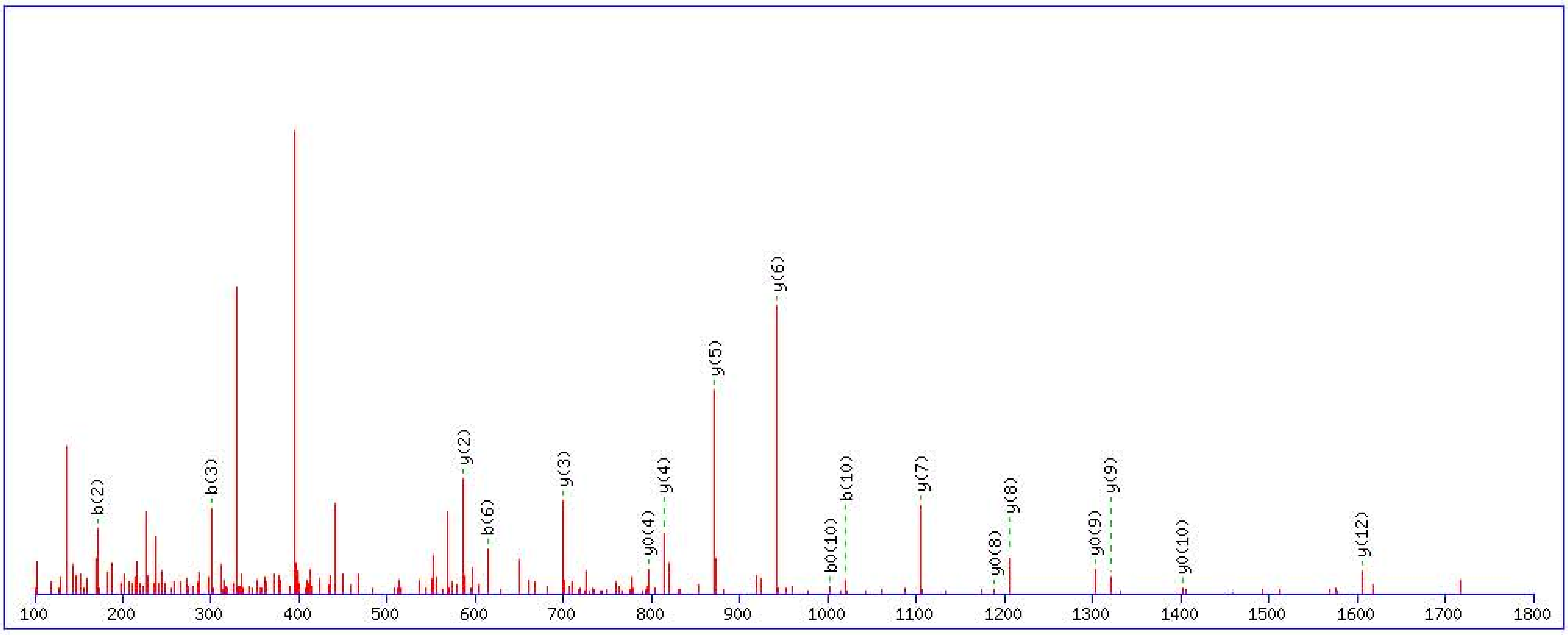
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGEVNTYAGDLQK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

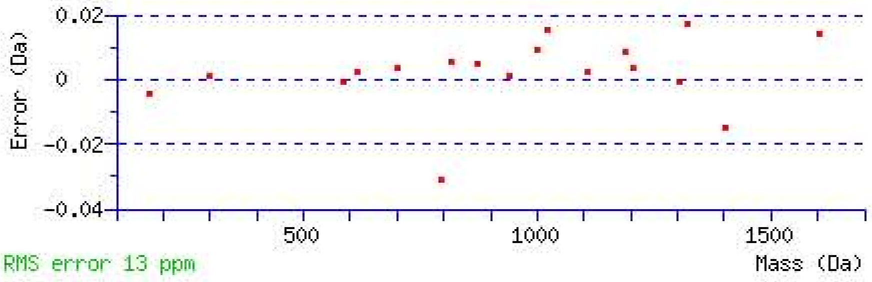
Match to Query 46261: 1717.877892 from(573.633240,3+) rtinseconds(1971) index(41954)
Title: Locus:1.1.1.2970.2 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

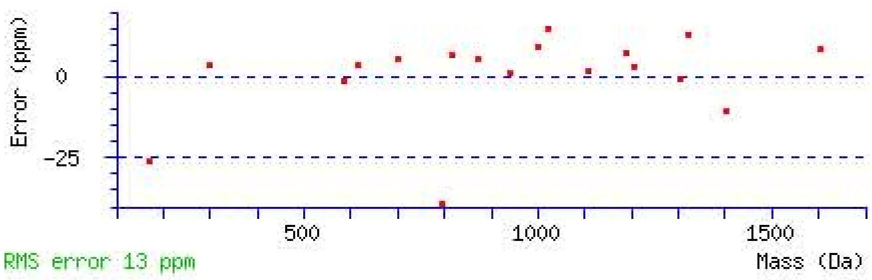
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1717.870895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 0.00011
Matches : 18/126 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	114.091340	57.549308					L							13
2	**171.112804**	86.060040					G	***1605.794121***	803.400699	1588.767572	794.887424	1587.783556	794.395416	12
3	**300.155397**	150.581336			282.144832	141.576054	E	1548.772657	774.889967	1531.746108	766.376692	1530.762092	765.884684	11
4	399.223811	200.115544			381.213246	191.110261	V	1419.730064	710.368670	1402.703515	701.855396	1401.719499	701.363388	10
5	513.266738	257.137007	496.240189	248.623733	495.256173	248.131725	N	***1320.661650***	660.834463	1303.635101	652.321189	1302.651085	651.829181	9
6	**614.314417**	307.660847	597.287868	299.147572	596.303852	298.655564	T	***1206.618723***	603.813000	1189.592174	595.299725	1188.608158	594.807717	8
7	777.377746	389.192511	760.351197	380.679237	759.367181	380.187229	Y	***1105.571044***	553.289160	1088.544495	544.775886	1087.560479	544.283878	7
8	848.414860	424.711068	831.388311	416.197794	830.404295	415.705786	A	***942.507715***	471.757496	925.481166	463.244221	924.497150	462.752213	6
9	905.436324	453.221800	888.409775	444.708526	887.425759	444.216518	G	***871.470601***	436.238939	854.444052	427.725664	853.460036	427.233656	5
10	**1020.463267**	510.735272	1003.436718	502.221997	1002.452702	501.729989	D	***814.449137***	407.728207	797.422588	399.214932	796.438572	398.722924	4
11	1133.547331	567.277304	1116.520782	558.764029	1115.536766	558.272021	L	***699.422194***	350.214735	682.395645	341.701461			3
12	1572.772657	786.889967	1555.746108	778.376692	1554.762092	777.884684	Q	***586.338130***	293.672703	569.311581	285.159429			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.0	1717.870895	0.006997	LGEVNTYAGDLQK

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

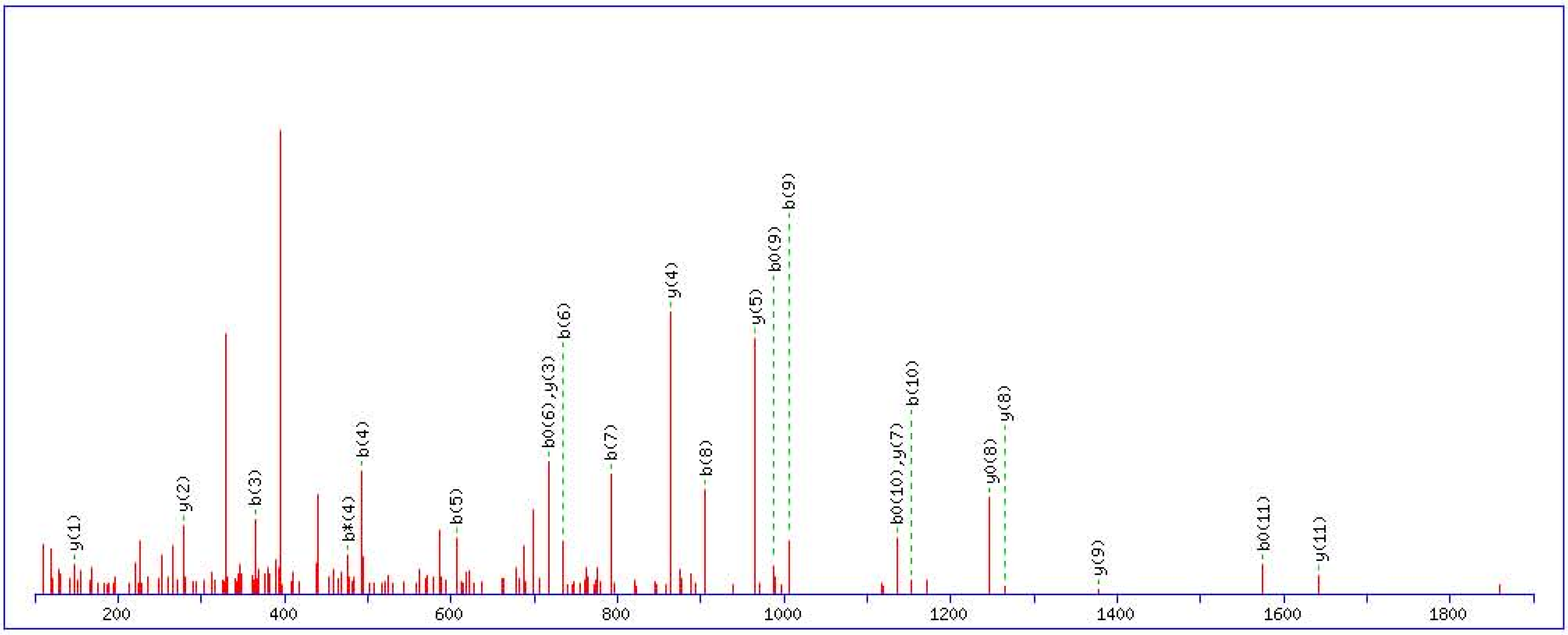
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNHQLEGLTFQMK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

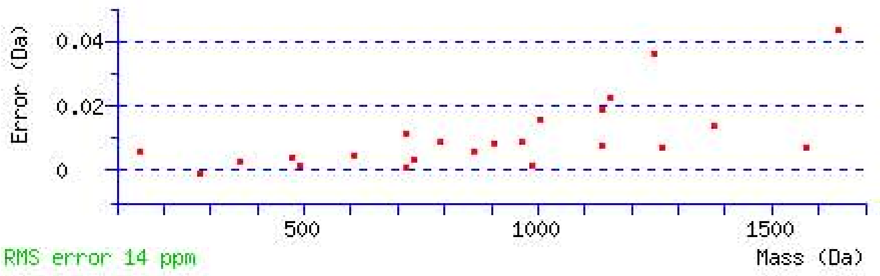
Match to Query 50044: 1868.977632 from(623.999820,3+) rtinseconds(2129) index(42909)
Title: Locus:1.1.1.3025.10 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

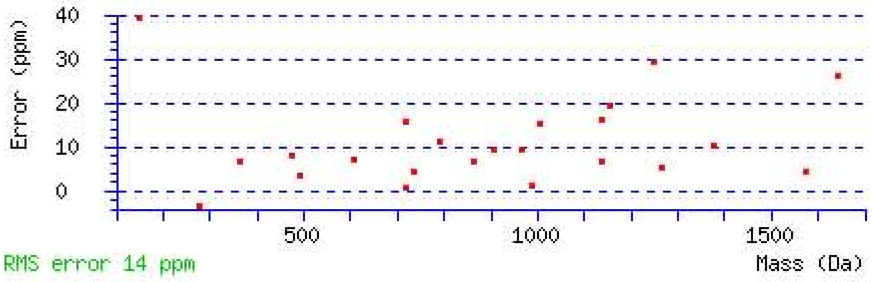
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1868.964081
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 59 **Expect:** 3.7e-005
Matches : 23/124 fragment ions using 36 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							13
2	228.134267	114.570771	211.107718	106.057497			N	1756.887310	878.947293	1739.860761	870.434019	1738.876745	869.942011	12
3	***365.193179***	183.100227	348.166630	174.586953			H	***1642.844383***	821.925830	1625.817834	813.412555	1624.833818	812.920547	11
4	***493.251757***	247.129516	476.225208	238.616242			Q	1505.785471	753.396374	1488.758922	744.883099	1487.774906	744.391091	10
5	***606.335821***	303.671549	589.309272	295.158274			L	***1377.726893***	689.367085	1360.700344	680.853810	1359.716328	680.361802	9
6	***735.378414***	368.192845	718.351865	359.679571	717.367849	359.187563	E	***1264.642829***	632.825053	1247.616280	624.311778	1246.632264	623.819770	8
7	***792.399878***	396.703577	775.373329	388.190303	774.389313	387.698295	G	***1135.600236***	568.303756	1118.573687	559.790482	1117.589671	559.298474	7
8	***905.483942***	453.245609	888.457393	444.732335	887.473377	444.240327	L	1078.578772	539.793024	1061.552223	531.279750	1060.568207	530.787742	6
9	***1006.531621***	503.769449	989.505072	495.256174	988.521056	494.764166	T	***965.494708***	483.250992	948.468159	474.737718	947.484143	474.245710	5
10	***1153.600035***	577.303656	1136.573486	568.790381	1135.589470	568.298373	F	***864.447029***	432.727153	847.420480	424.213878			4
11	1592.825361	796.916319	1575.798812	788.403044	1574.814796	787.911036	Q	***717.378615***	359.192946	700.352066	350.679671			3
12	1723.865846	862.436561	1706.839297	853.923287	1705.855281	853.431279	M	***278.153289***	139.580282	261.126740	131.067008			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.8	1868.964081	0.013551	LNHQLEGLTFQMK

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

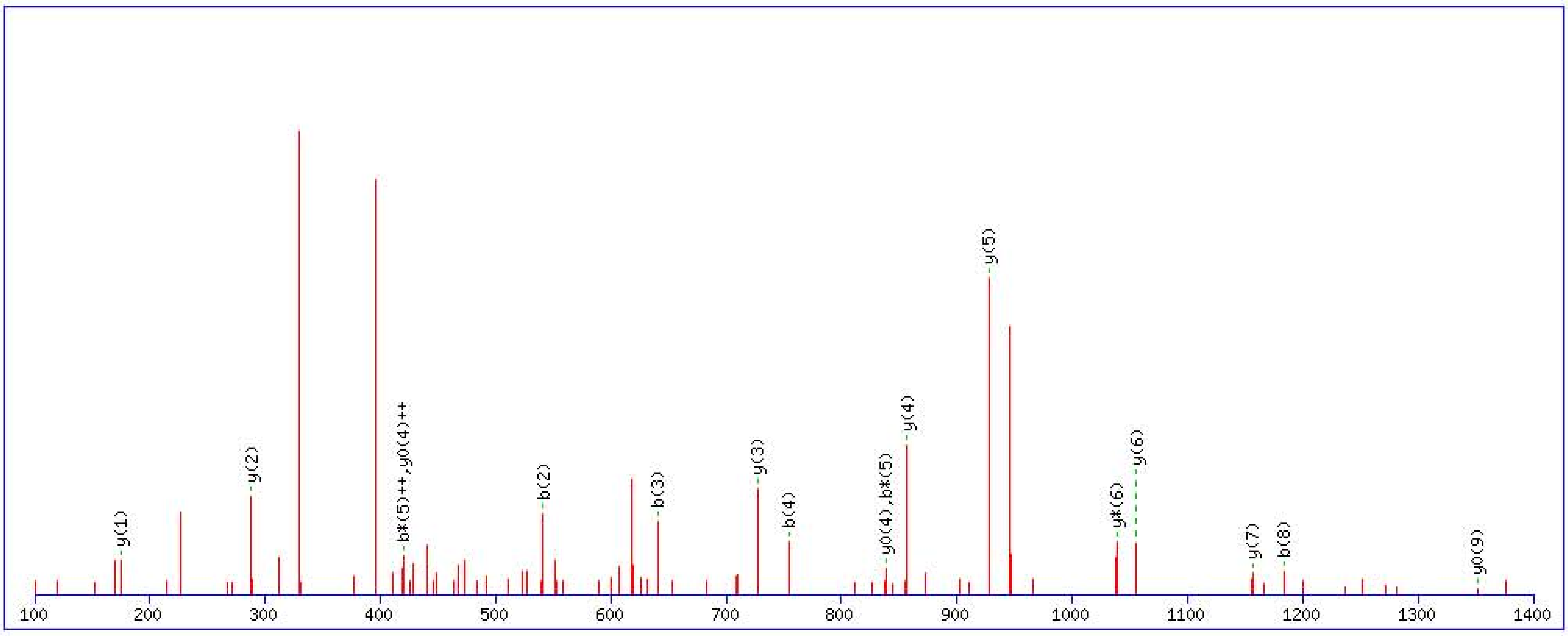
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQVNTQAEQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

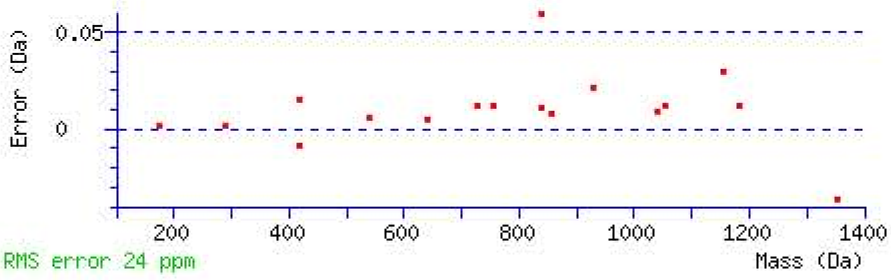
Match to Query 50799: 1909.001502 from(637.341110,3+) rtinseconds(1918) index(77847)
Title: Locus:1.1.1.2882.18 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

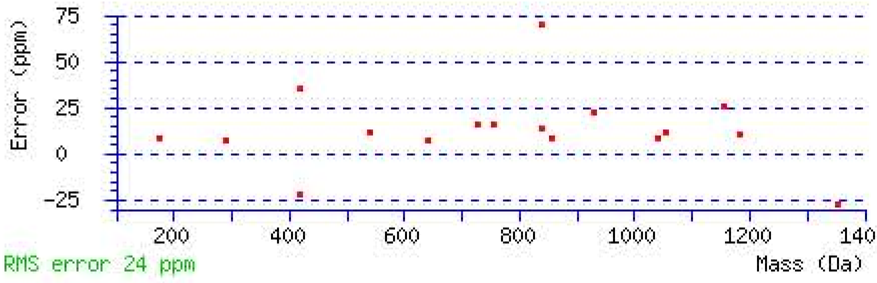
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1908.991364
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.00052
Matches : 17/112 fragment ions using 26 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							11
2	***541.280281***	271.143779	524.253732	262.630504	523.269716	262.138496	Q	1808.950973	904.979125	1791.924424	896.465850	1790.940408	895.973842	10
3	***640.348695***	320.677986	623.322146	312.164711	622.338130	311.672703	V	1369.725647	685.366462	1352.699098	676.853187	1351.715082	676.361179	9
4	***754.391622***	377.699449	737.365073	369.186174	736.381057	368.694166	N	1270.657233	635.832255	1253.630684	627.318980	1252.646668	626.826972	8
5	855.439301	428.223289	838.412752	419.710014	837.428736	419.218006	T	***1156.614306***	578.810791	1139.587757	570.297517	1138.603741	569.805509	7
6	983.497879	492.252578	966.471330	483.739303	965.487314	483.247295	Q	***1055.566627***	528.286952	1038.540078	519.773677	1037.556062	519.281669	6
7	1054.534993	527.771135	1037.508444	519.257860	1036.524428	518.765852	A	***927.508049***	464.257663	910.481500	455.744388	909.497484	455.252380	5
8	***1183.577586***	592.292431	1166.551037	583.779157	1165.567021	583.287149	E	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
9	1622.802912	811.905094	1605.776363	803.391820	1604.792347	802.899812	Q	***727.428342***	364.217809	710.401793	355.704535			3
10	1735.886976	868.447126	1718.860427	859.933852	1717.876411	859.441844	L	***288.203016***	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.2	1908.991364	0.010138	TQVNTQAEQLR
14.6	1908.991364	0.010138	TQVNTQAEQLR
9.1	1908.991364	0.010138	TQVNTQAEQLR
1.2	1909.015610	-0.014108	SSIALTAPDAAADPKEKPK

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

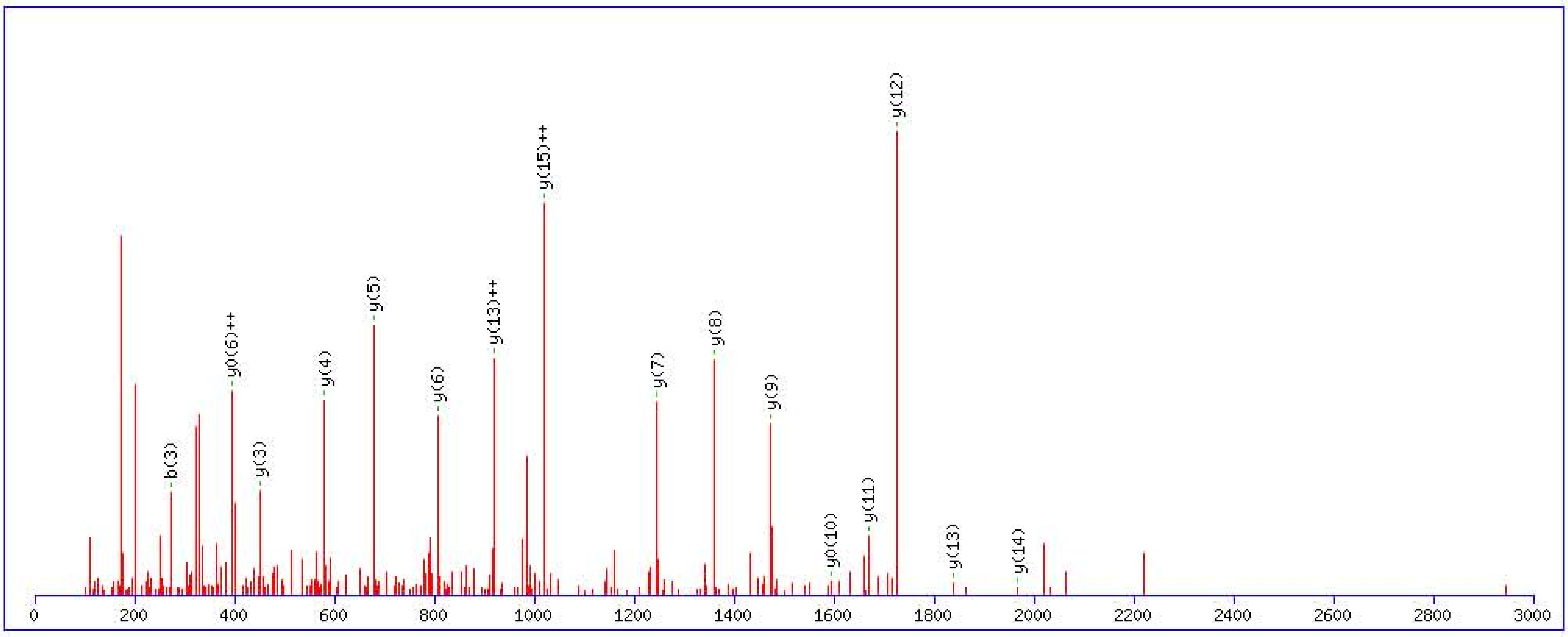
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLAELGGHLDQQVEEFR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

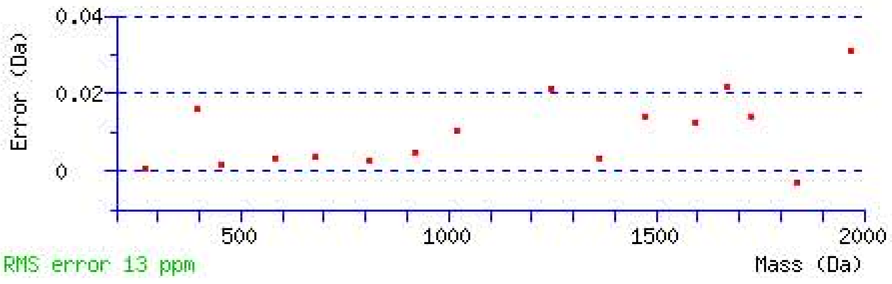
Match to Query 59082: 2238.125382 from(747.049070,3+) rtinseconds(2222) index(43573)
Title: Locus:1.1.1.3057.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

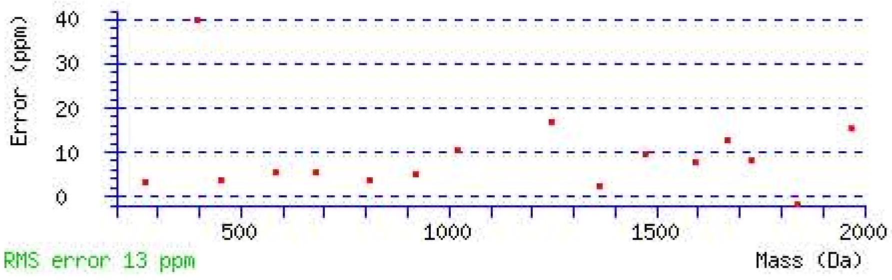
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2238.110291
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 88  Expect: 8.9e-009
Matches : 16/168 fragment ions using 21 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**							**17**
2	201.123368	101.065322			183.112803	92.060039	**L**	2152.085552	1076.546414	2135.059003	1068.033139	2134.074987	1067.541131	**16**
3	272.160482	136.583879			254.149917	127.578596	**A**	2039.001488	1020.004382	2021.974939	1011.491108	2020.990923	1010.999100	**15**
4	401.203075	201.105175			383.192510	192.099893	**E**	***1967.964374***	984.485825	1950.937825	975.972551	1949.953809	975.480543	**14**
5	514.287139	257.647208			496.276574	248.641925	**L**	***1838.921781***	919.964529	1821.895232	911.451254	1820.911216	910.959246	**13**
6	571.308603	286.157940			553.298038	277.152657	**G**	***1725.837717***	863.422497	1708.811168	854.909222	1707.827152	854.417214	**12**
7	628.330067	314.668672			610.319502	305.663389	**G**	***1668.816253***	834.911765	1651.789704	826.398490	1650.805688	825.906482	**11**
8	765.388979	383.198128			747.378414	374.192845	**H**	1611.794789	806.401033	1594.768240	797.887758	1593.784224	797.395750	**10**
9	878.473043	439.740160			860.462478	430.734877	**L**	***1474.735877***	737.871577	1457.709328	729.358302	1456.725312	728.866294	**9**
10	993.499986	497.253631			975.489421	488.248349	**D**	***1361.651813***	681.329545	1344.625264	672.816270	1343.641248	672.324262	**8**
11	1432.725312	716.866294	1415.698763	708.353020	1414.714747	707.861012	**Q**	***1246.624870***	623.816073	1229.598321	615.302799	1228.614305	614.810791	**7**
12	1560.783890	780.895583	1543.757341	772.382309	1542.773325	771.890301	**Q**	***807.399544***	404.203410	790.372995	395.690136	789.388979	395.198128	**6**
13	1659.852304	830.429790	1642.825755	821.916516	1641.841739	821.424508	**V**	***679.340966***	340.174121	662.314417	331.660846	661.330401	331.168838	**5**
14	1788.894897	894.951087	1771.868348	886.437812	1770.884332	885.945804	**E**	***580.272552***	290.639914	563.246003	282.126639	562.261987	281.634631	**4**
15	1917.937490	959.472383	1900.910941	950.959109	1899.926925	950.467101	**E**	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	**3**
16	2065.005904	1033.006590	2047.979355	1024.493316	2046.995339	1024.001307	**F**	322.187366	161.597321	305.160817	153.084046			**2**
17							**R**	175.118952	88.063114	158.092403	79.549839			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.4	2238.110291	0.015091	SLAELGGHLDQQVEEFR
69.8	2238.110291	0.015091	SLAELGGHLDQQVEEFR
2.5	2238.146637	-0.021255	AYGCGRTELAIKLLEYEPR

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

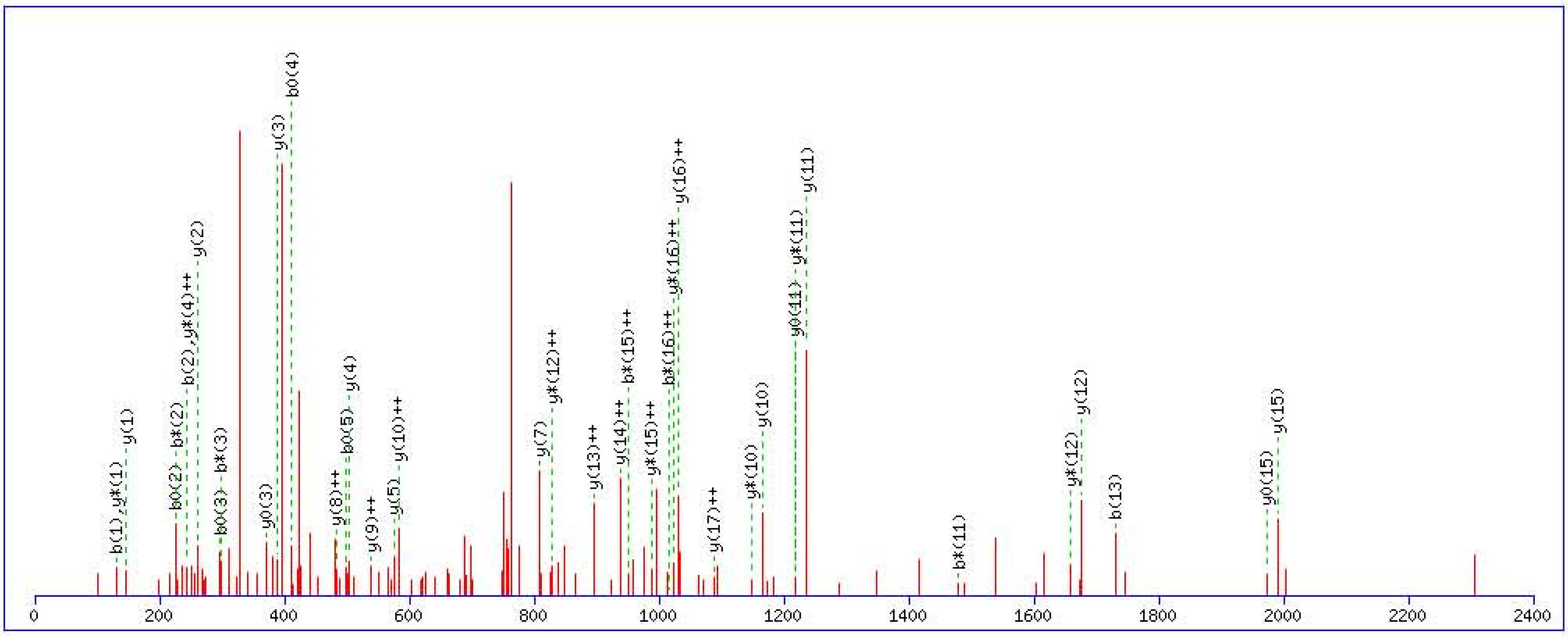
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENADSLQASLRPHADELK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

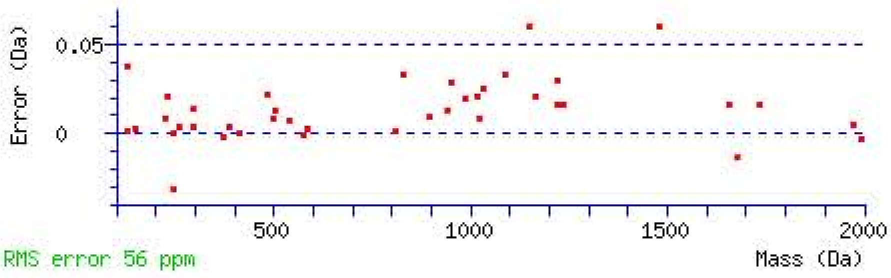
Match to Query 60761: 2304.182082 from(769.067970,3+) rtinseconds(1884) index(77566)
Title: Locus:1.1.1.2870.23 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

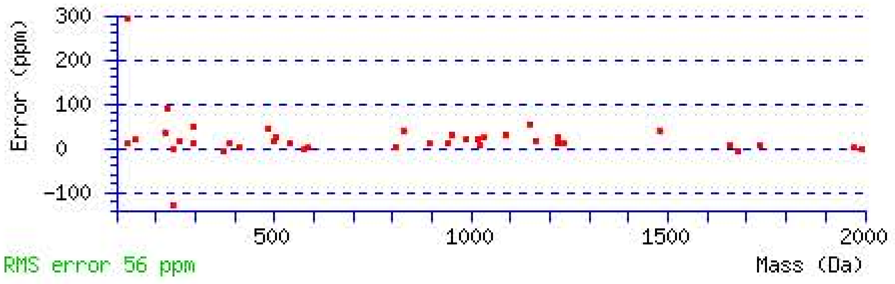
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2304.153183
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0052
Matches : 40/198 fragment ions using 112 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	**244.092796**	122.550036	227.066247	114.036762	226.082231	113.544754	N	2176.117913	1088.562594	2159.091364	1080.049320	2158.107348	1079.557312	17
3	315.129910	158.068593	298.103361	149.555319	297.119345	149.063311	A	2062.074986	1031.541131	2045.048437	1023.027856	2044.064421	1022.535848	16
4	430.156853	215.582065	413.130304	207.068790	412.146288	206.576782	D	***1991.037872***	996.022574	1974.011323	987.509300	1973.027307	987.017292	15
5	517.188881	259.098079	500.162332	250.584804	499.178316	250.092796	S	1876.010929	938.509103	1858.984380	929.995828	1858.000364	929.503820	14
6	630.272945	315.640111	613.246396	307.126836	612.262380	306.634828	L	1788.978901	894.993089	1771.952352	886.479814	1770.968336	885.987806	13
7	1069.498271	535.252774	1052.471722	526.739499	1051.487706	526.247491	Q	***1675.894837***	838.451057	1658.868288	829.937782	1657.884272	829.445774	12
8	1140.535385	570.771331	1123.508836	562.258056	1122.524820	561.766048	A	***1236.669511***	618.838394	1219.642962	610.325119	1218.658946	609.833111	11
9	1227.567413	614.287345	1210.540864	605.774070	1209.556848	605.282062	S	***1165.632397***	583.319837	1148.605848	574.806562	1147.621832	574.314554	10
10	1340.651477	670.829377	1323.624928	662.316102	1322.640912	661.824094	L	1078.600369	539.803823	1061.573820	531.290548	1060.589804	530.798540	9
11	1496.752588	748.879932	1479.726039	740.366658	1478.742023	739.874650	R	965.516305	483.261791	948.489756	474.748516	947.505740	474.256508	8
12	1593.805352	797.406314	1576.778803	788.893040	1575.794787	788.401032	P	***809.415194***	405.211235	792.388645	396.697961	791.404629	396.205953	7
13	**1730.864264**	865.935770	1713.837715	857.422496	1712.853699	856.930488	H	712.362430	356.684853	695.335881	348.171579	694.351865	347.679571	6
14	1801.901378	901.454327	1784.874829	892.941053	1783.890813	892.449045	A	***575.303518***	288.155397	558.276969	279.642123	557.292953	279.150115	5
15	1916.928321	958.967799	1899.901772	950.454524	1898.917756	949.962516	D	***504.266404***	252.636840	487.239855	244.123566	486.255839	243.631558	4
16	2045.970914	1023.489095	2028.944365	1014.975821	2027.960349	1014.483813	E	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
17	2159.054978	1080.031127	2142.028429	1071.517852	2141.044413	1071.025844	L	***260.196868***	130.602072	243.170319	122.088798			2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.1	2304.153183	0.028899	ENADSLQASLRPHADELK

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

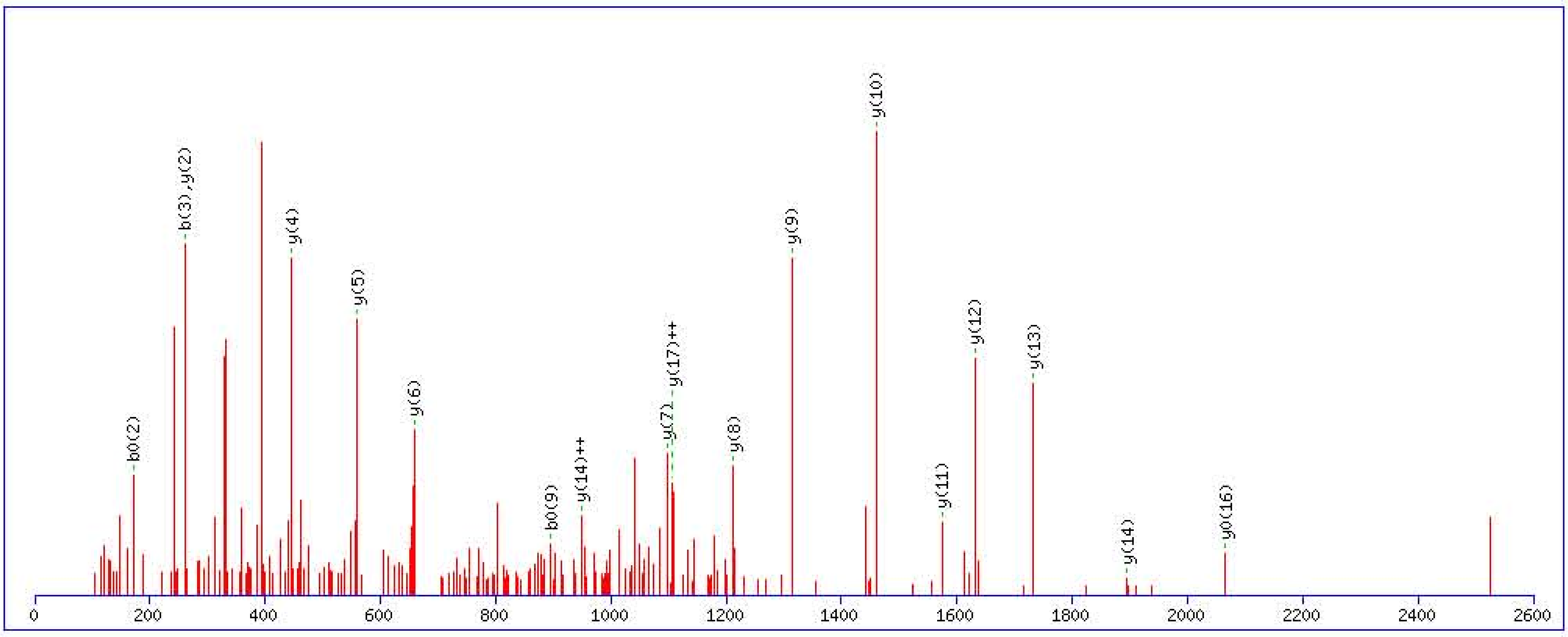
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STAAMSTYTGIFTDQVLSVLK**
Found in **APOC2_HUMAN**, Apolipoprotein C-II OS=Homo sapiens GN=APOC2 PE=1 SV=1

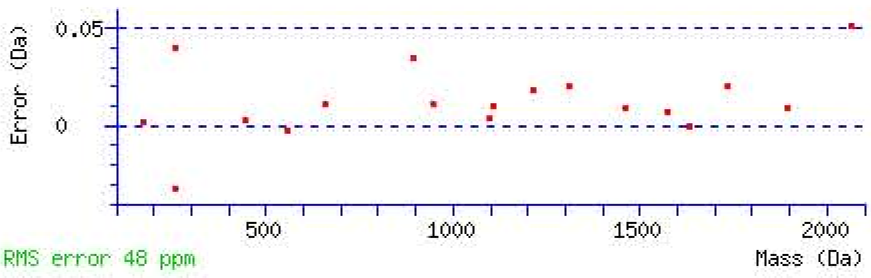
Match to Query 66023: 2543.333772 from(848.785200,3+) rtinseconds(3201) index(50486)
Title: Locus:1.1.1.3393.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

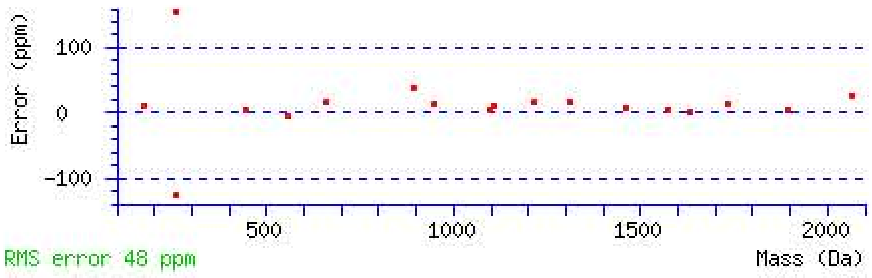
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2543.301544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 97  Expect: 1.9e-009
Matches : 18/206 fragment ions using 21 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							21
2	189.086983	95.047129			171.076418	86.041847	T	2457.276785	1229.142030	2440.250236	1220.628756	2439.266220	1220.136748	20
3	260.124097	130.565686			242.113532	121.560404	A	2356.229106	1178.618191	2339.202557	1170.104916	2338.218541	1169.612908	19
4	331.161211	166.084243			313.150646	157.078961	A	2285.191992	1143.099634	2268.165443	1134.586359	2267.181427	1134.094351	18
5	462.201696	231.604486			444.191131	222.599203	M	2214.154878	1107.581077	2197.128329	1099.067802	2196.144313	1098.575794	17
6	549.233724	275.120500			531.223159	266.115217	S	2083.114393	1042.060834	2066.087844	1033.547560	2065.103828	1033.055552	16
7	650.281403	325.644340			632.270838	316.639057	T	1996.082365	998.544821	1979.055816	990.031546	1978.071800	989.539538	15
8	813.344732	407.176004			795.334167	398.170722	Y	***1895.034686***	948.020981	1878.008137	939.507707	1877.024121	939.015699	14
9	914.392411	457.699844			896.381846	448.694561	T	***1731.971357***	866.489317	1714.944808	857.976042	1713.960792	857.484034	13
10	971.413875	486.210576			953.403310	477.205293	G	***1630.923678***	815.965477	1613.897129	807.452203	1612.913113	806.960195	12
11	1084.497939	542.752608			1066.487374	533.747325	I	***1573.902214***	787.454745	1556.875665	778.941471	1555.891649	778.449463	11
12	1231.566353	616.286815			1213.555788	607.281532	F	***1460.818150***	730.912713	1443.791601	722.399439	1442.807585	721.907431	10
13	1332.614032	666.810654			1314.603467	657.805372	T	***1313.749736***	657.378506	1296.723187	648.865232	1295.739171	648.373224	9
14	1447.640975	724.324126			1429.630410	715.318843	D	***1212.702057***	606.854667	1195.675508	598.341392	1194.691492	597.849384	8
15	1886.866301	943.936789	1869.839752	935.423514	1868.855736	934.931506	Q	***1097.675114***	549.341195	1080.648565	540.827921	1079.664549	540.335913	7
16	1985.934715	993.470996	1968.908166	984.957721	1967.924150	984.465713	V	***658.449788***	329.728532	641.423239	321.215258	640.439223	320.723250	6
17	2099.018779	1050.013027	2081.992230	1041.499753	2081.008214	1041.007745	L	***559.381374***	280.194325	542.354825	271.681051	541.370809	271.189043	5
18	2186.050807	1093.529041	2169.024258	1085.015767	2168.040242	1084.523759	S	***446.297310***	223.652293	429.270761	215.139019	428.286745	214.647011	4
19	2285.119221	1143.063248	2268.092672	1134.549974	2267.108656	1134.057966	V	359.265282	180.136279	342.238733	171.623004			3
20	2398.203285	1199.605280	2381.176736	1191.092006	2380.192720	1190.599998	L	***260.196868***	130.602072	243.170319	122.088798			2
21							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
96.9	2543.301544	0.032228	STAAMSTYTGIFTDQVLSVLK
3.8	2543.370712	-0.036940	ELEFNEIKTQVELATGQLGLRR

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

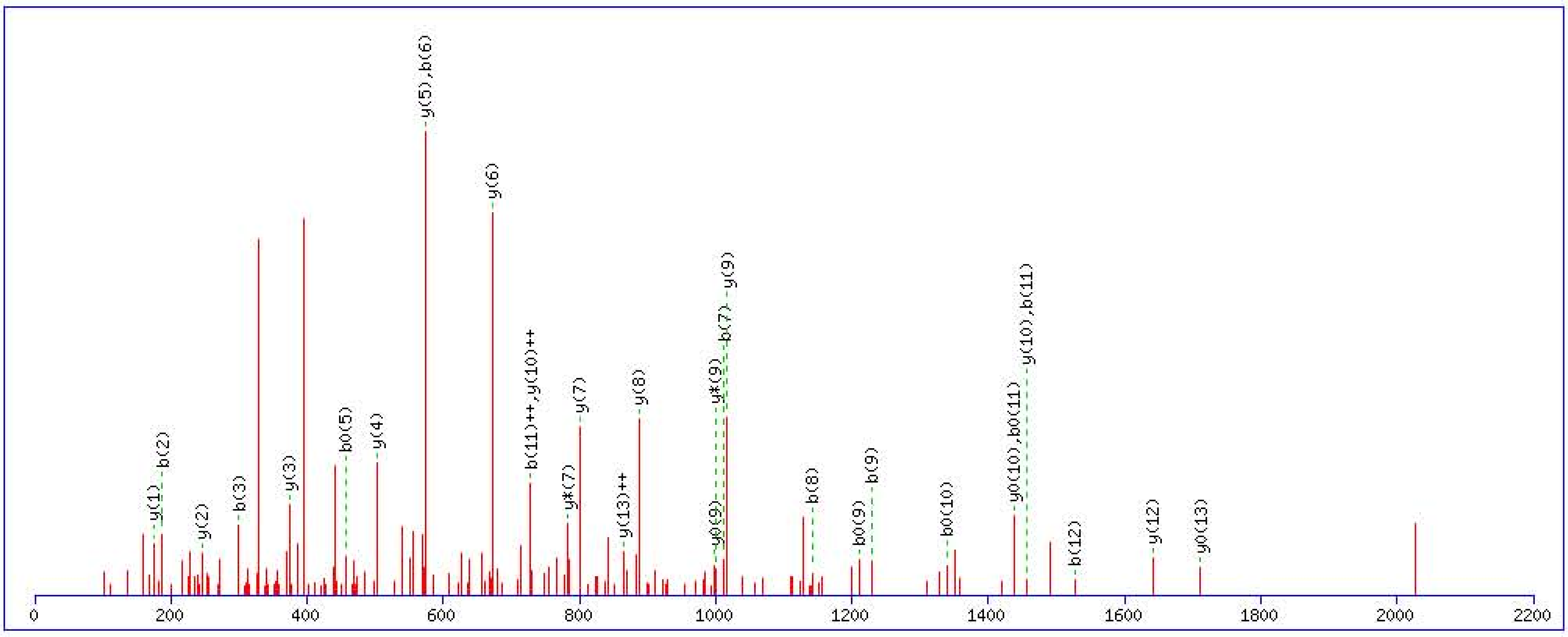
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

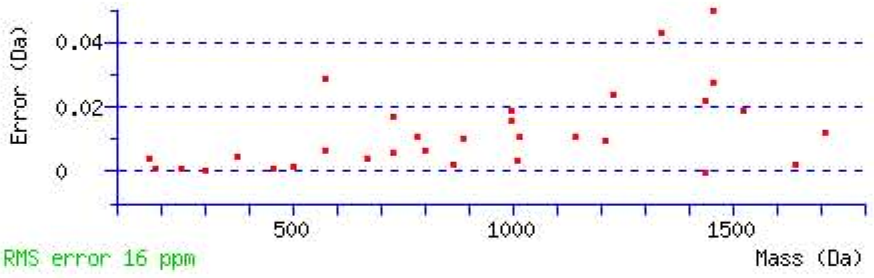
Match to Query 54415: 2027.020122 from(676.680650,3+) rtinseconds(1943) index(41776)
Title: Locus:1.1.1.2960.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

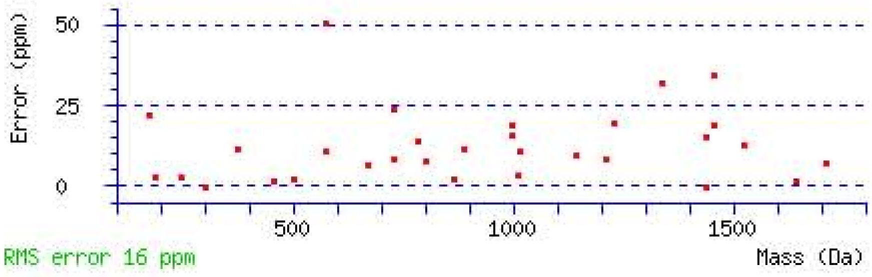
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 70  Expect: 2.5e-006
Matches : 31/154 fragment ions using 44 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.034219	58.520748			98.023654	49.515465	D							16
2	**187.071333**	94.039304			169.060768	85.034022	A	1912.990923	956.999100	1895.964374	948.485825	1894.980358	947.993817	15
3	**300.155397**	150.581336			282.144832	141.576054	L	1841.953809	921.480543	1824.927260	912.967268	1823.943244	912.475260	14
4	387.187425	194.097351			369.176860	185.092068	S	1728.869745	864.938511	1711.843196	856.425236	1710.859180	855.933228	13
5	474.219453	237.613364			456.208888	228.608082	S	***1641.837717***	821.422497	1624.811168	812.909222	1623.827152	812.417214	12
6	**573.287867**	287.147572			555.277302	278.142289	V	1554.805689	777.906483	1537.779140	769.393208	1536.795124	768.901200	11
7	**1012.513193**	506.760235	995.486644	498.246960	994.502628	497.754952	Q	***1455.737275***	728.372276	1438.710726	719.859001	1437.726710	719.366993	10
8	**1141.555786**	571.281531	1124.529237	562.768257	1123.545221	562.276249	E	***1016.511949***	508.759613	999.485400	500.246338	998.501384	499.754330	9
9	**1228.587814**	614.797545	1211.561265	606.284271	1210.577249	605.792263	S	***887.469356***	444.238316	870.442807	435.725042	869.458791	435.233034	8
10	1356.646392	678.826834	1339.619843	670.313560	1338.635827	669.821552	Q	***800.437328***	400.722302	783.410779	392.209028			7
11	**1455.714806**	728.361041	1438.688257	719.847767	1437.704241	719.355759	V	***672.378750***	336.693013	655.352201	328.179739			6
12	**1526.751920**	763.879598	1509.725371	755.366324	1508.741355	754.874316	A	***573.310336***	287.158806	556.283787	278.645532			5
13	1654.810498	827.908887	1637.783949	819.395613	1636.799933	818.903605	Q	***502.273222***	251.640249	485.246673	243.126975			4
14	1782.869076	891.938176	1765.842527	883.424902	1764.858511	882.932894	Q	***374.214644***	187.610960	357.188095	179.097686			3
15	1853.906190	927.456733	1836.879641	918.943459	1835.895625	918.451451	A	***246.156066***	123.581671	229.129517	115.068396			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.0	2027.010574	0.009548	DALSSVQESQVAQQAR
45.7	2027.010574	0.009548	DALSSVQESQVAQQAR
31.7	2027.010574	0.009548	DALSSVQESQVAQQAR
26.8	2027.010574	0.009548	DALSSVQESQVAQQAR

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

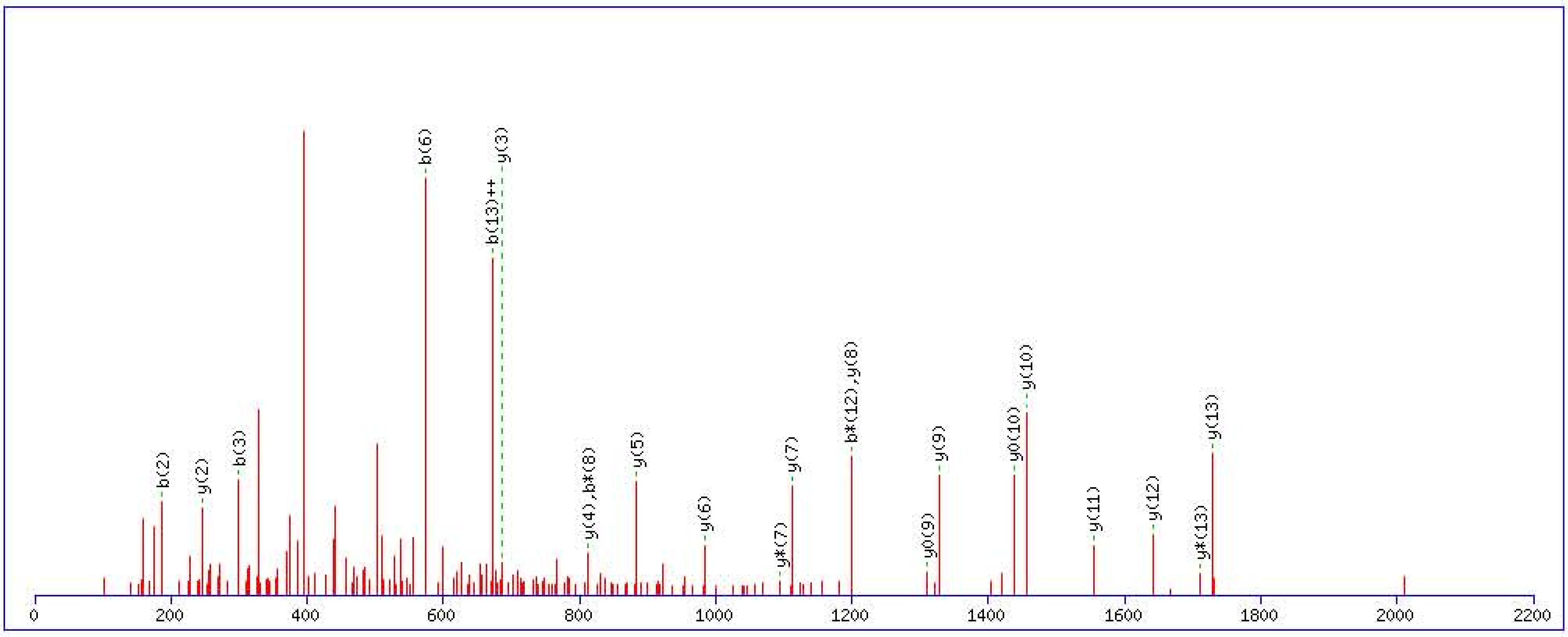
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

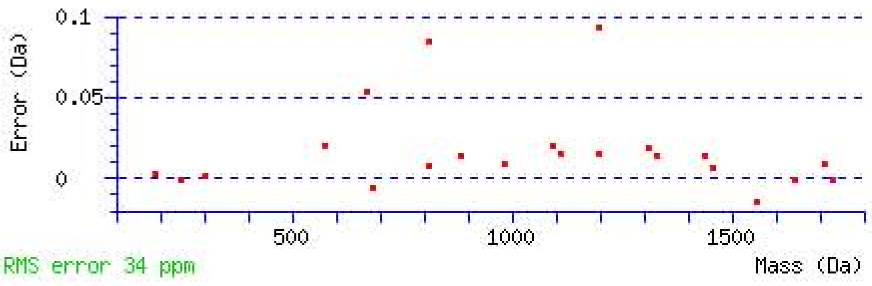
Match to Query 54416: 2027.021442 from(676.681090,3+) rtinseconds(1931) index(41676)
Title: Locus:1.1.1.2956.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

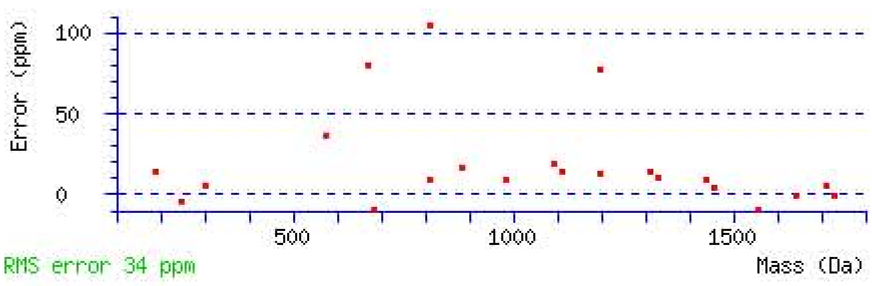
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 87  Expect: 5.3e-008
Matches : 22/154 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	116.034219	58.520748			98.023654	49.515465	D							16
2	**187.071333**	94.039304			169.060768	85.034022	A	1912.990923	956.999100	1895.964374	948.485825	1894.980358	947.993817	15
3	**300.155397**	150.581336			282.144832	141.576054	L	1841.953809	921.480543	1824.927260	912.967268	1823.943244	912.475260	14
4	387.187425	194.097351			369.176860	185.092068	S	***1728.869745***	864.938511	1711.843196	856.425236	1710.859180	855.933228	13
5	474.219453	237.613364			456.208888	228.608082	S	***1641.837717***	821.422497	1624.811168	812.909222	1623.827152	812.417214	12
6	**573.287867**	287.147572			555.277302	278.142289	V	***1554.805689***	777.906483	1537.779140	769.393208	1536.795124	768.901200	11
7	701.346445	351.176861	684.319896	342.663586	683.335880	342.171578	Q	***1455.737275***	728.372276	1438.710726	719.859001	1437.726710	719.366993	10
8	830.389038	415.698157	813.362489	407.184883	812.378473	406.692875	E	***1327.678697***	664.342987	1310.652148	655.829712	1309.668132	655.337704	9
9	917.421066	459.214171	900.394517	450.700897	899.410501	450.208889	S	***1198.636104***	599.821690	1181.609555	591.308416	1180.625539	590.816408	8
10	1045.479644	523.243460	1028.453095	514.730186	1027.469079	514.238178	Q	***1111.604076***	556.305676	1094.577527	547.792402			7
11	1144.548058	572.777667	1127.521509	564.264393	1126.537493	563.772385	V	***983.545498***	492.276387	966.518949	483.763113			6
12	1215.585172	608.296224	1198.558623	599.782950	1197.574607	599.290942	A	***884.477084***	442.742180	867.450535	434.228906			5
13	1343.643750	672.325513	1326.617201	663.812239	1325.633185	663.320230	Q	***813.439970***	407.223623	796.413421	398.710349			4
14	1782.869076	891.938176	1765.842527	883.424902	1764.858511	882.932894	Q	***685.381392***	343.194334	668.354843	334.681060			3
15	1853.906190	927.456733	1836.879641	918.943459	1835.895625	918.451451	A	***246.156066***	123.581671	229.129517	115.068396			2
16							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.0	2027.010574	0.010868	DALSSVQESQVAQQAR
83.0	2027.010574	0.010868	DALSSVQESQVAQQAR
82.4	2027.010574	0.010868	DALSSVQESQVAQQAR
43.0	2027.010574	0.010868	DALSSVQESQVAQQAR

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

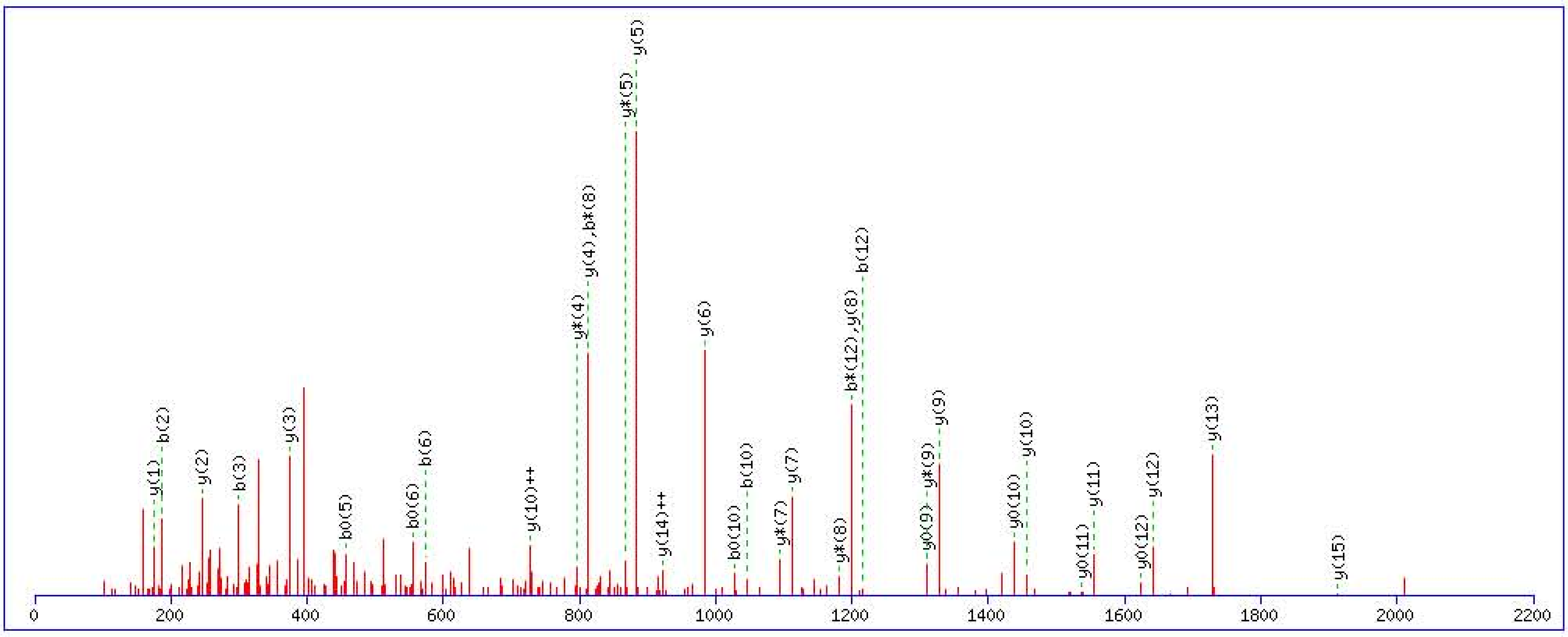
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

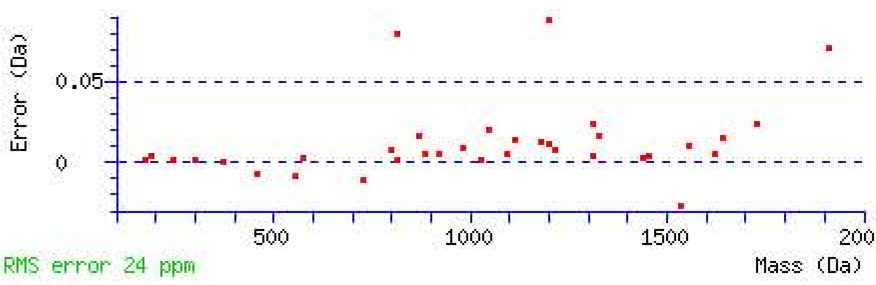
Match to Query 54419: 2027.023482 from(676.681770,3+) rtinseconds(1871) index(41160)
Title: Locus:1.1.1.2935.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

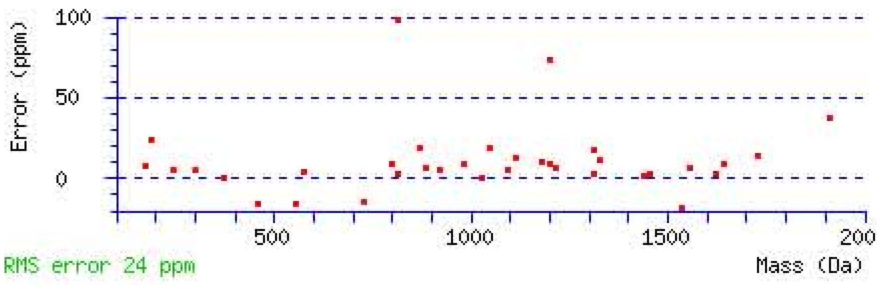
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 107  Expect: 9.4e-011
Matches : 35/154 fragment ions using 51 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							16
2	**187.071333**	94.039304			169.060768	85.034022	A	***1912.990923***	956.999100	1895.964374	948.485825	1894.980358	947.993817	15
3	**300.155397**	150.581336			282.144832	141.576054	L	1841.953809	921.480543	1824.927260	912.967268	1823.943244	912.475260	14
4	387.187425	194.097351			369.176860	185.092068	S	***1728.869745***	864.938511	1711.843196	856.425236	1710.859180	855.933228	13
5	474.219453	237.613364			456.208888	228.608082	S	***1641.837717***	821.422497	1624.811168	812.909222	1623.827152	812.417214	12
6	**573.287867**	287.147572			555.277302	278.142289	V	***1554.805689***	777.906483	1537.779140	769.393208	1536.795124	768.901200	11
7	701.346445	351.176861	684.319896	342.663586	683.335880	342.171578	Q	***1455.737275***	728.372276	1438.710726	719.859001	1437.726710	719.366993	10
8	830.389038	415.698157	813.362489	407.184883	812.378473	406.692875	E	***1327.678697***	664.342987	1310.652148	655.829712	1309.668132	655.337704	9
9	917.421066	459.214171	900.394517	450.700897	899.410501	450.208889	S	***1198.636104***	599.821690	1181.609555	591.308416	1180.625539	590.816408	8
10	**1045.479644**	523.243460	1028.453095	514.730186	1027.469079	514.238178	Q	***1111.604076***	556.305676	1094.577527	547.792402			7
11	1144.548058	572.777667	1127.521509	564.264393	1126.537493	563.772385	V	***983.545498***	492.276387	966.518949	483.763113			6
12	**1215.585172**	608.296224	1198.558623	599.782950	1197.574607	599.290942	A	***884.477084***	442.742180	867.450535	434.228906			5
13	1654.810498	827.908887	1637.783949	819.395613	1636.799933	818.903605	Q	***813.439970***	407.223623	796.413421	398.710349			4
14	1782.869076	891.938176	1765.842527	883.424902	1764.858511	882.932894	Q	***374.214644***	187.610960	357.188095	179.097686			3
15	1853.906190	927.456733	1836.879641	918.943459	1835.895625	918.451451	A	***246.156066***	123.581671	229.129517	115.068396			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
107.5	2027.010574	0.012908	DALSSVQESQVAQQAR
93.3	2027.010574	0.012908	DALSSVQESQVAQQAR
70.5	2027.010574	0.012908	DALSSVQESQVAQQAR
32.8	2027.010574	0.012908	DALSSVQESQVAQQAR
0.5	2027.029633	-0.006151	QEESEHSHKHLIELRR

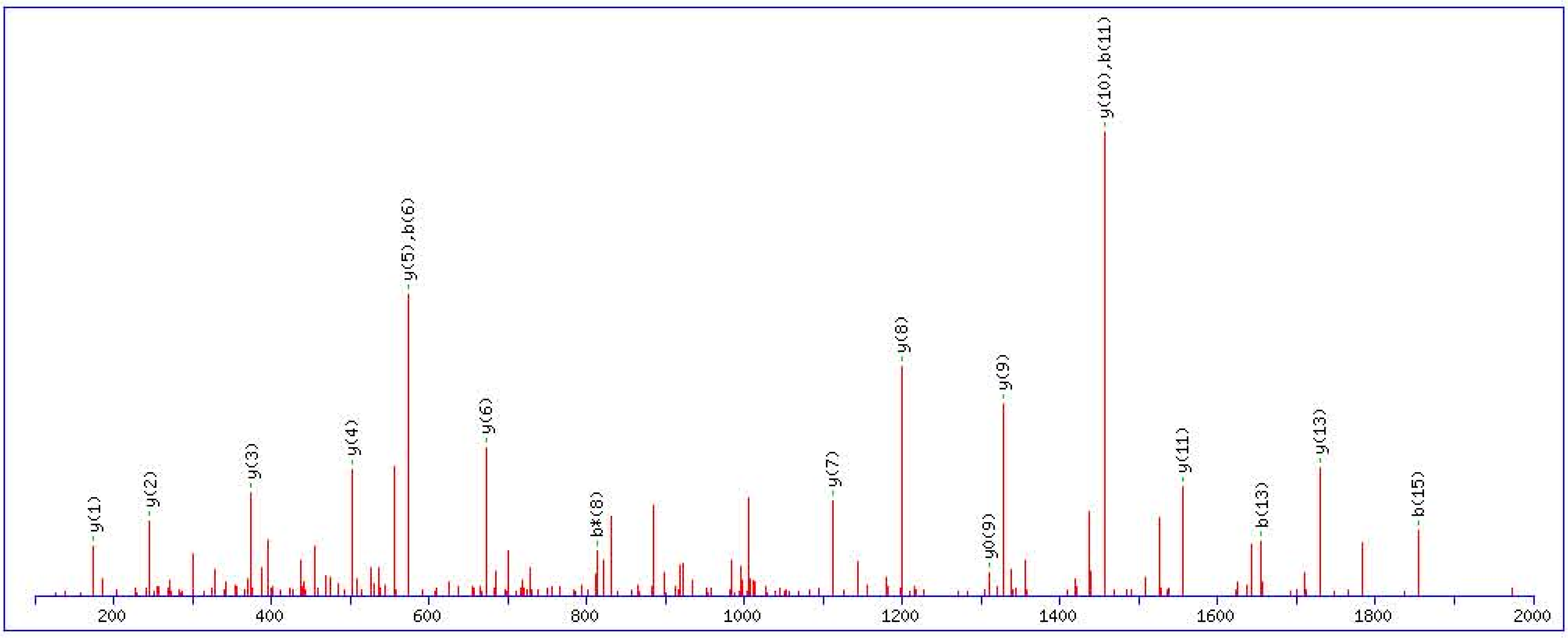
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

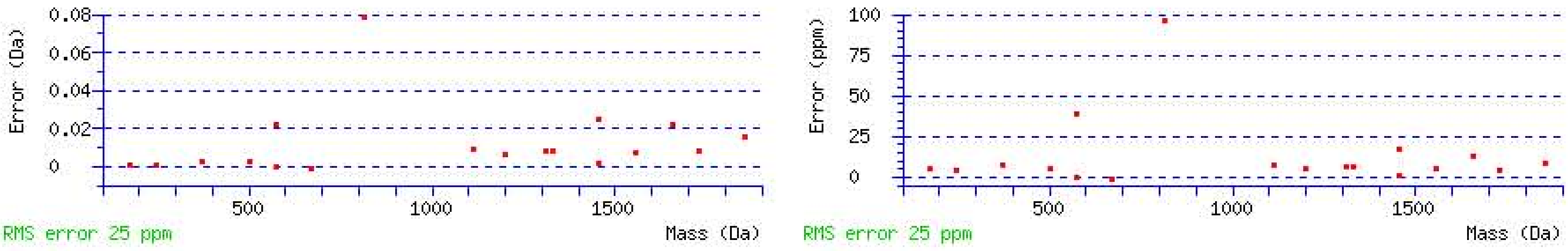
Match to Query 54421: 2027.028188 from(1014.521370,2+) rtinseconds(1923) index(41609)
Title: Locus:1.1.1.2953.26 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 118 **Expect:** 4.7e-011
Matches : 18/154 fragment ions using 19 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.034219	58.520748			98.023654	49.515465	D							16
2	187.071333	94.039304			169.060768	85.034022	A	1912.990923	956.999100	1895.964374	948.485825	1894.980358	947.993817	15
3	300.155397	150.581336			282.144832	141.576054	L	1841.953809	921.480543	1824.927260	912.967268	1823.943244	912.475260	14
4	387.187425	194.097351			369.176860	185.092068	S	***1728.869745***	864.938511	1711.843196	856.425236	1710.859180	855.933228	13
5	474.219453	237.613364			456.208888	228.608082	S	1641.837717	821.422497	1624.811168	812.909222	1623.827152	812.417214	12
6	**573.287867**	287.147572			555.277302	278.142289	V	***1554.805689***	777.906483	1537.779140	769.393208	1536.795124	768.901200	11
7	701.346445	351.176861	684.319896	342.663586	683.335880	342.171578	Q	***1455.737275***	728.372276	1438.710726	719.859001	1437.726710	719.366993	10
8	830.389038	415.698157	813.362489	407.184883	812.378473	406.692875	E	***1327.678697***	664.342987	1310.652148	655.829712	1309.668132	655.337704	9
9	917.421066	459.214171	900.394517	450.700897	899.410501	450.208889	S	***1198.636104***	599.821690	1181.609555	591.308416	1180.625539	590.816408	8
10	1356.646392	678.826834	1339.619843	670.313560	1338.635827	669.821551	Q	***1111.604076***	556.305676	1094.577527	547.792402			7
11	**1455.714806**	728.361041	1438.688257	719.847767	1437.704241	719.355758	V	***672.378750***	336.693013	655.352201	328.179739			6
12	1526.751920	763.879598	1509.725371	755.366324	1508.741355	754.874315	A	***573.310336***	287.158806	556.283787	278.645532			5
13	**1654.810498**	827.908887	1637.783949	819.395613	1636.799933	818.903605	Q	***502.273222***	251.640249	485.246673	243.126975			4
14	1782.869076	891.938176	1765.842527	883.424902	1764.858511	882.932894	Q	***374.214644***	187.610960	357.188095	179.097686			3
15	**1853.906190**	927.456733	1836.879641	918.943459	1835.895625	918.451451	A	***246.156066***	123.581671	229.129517	115.068396			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
117.7	2027.010574	0.017614	DALSSVQESQVAQQAR
99.5	2027.010574	0.017614	DALSSVQESQVAQQAR
91.5	2027.010574	0.017614	DALSSVQESQVAQQAR
63.5	2027.010574	0.017614	DALSSVQESQVAQQAR
13.2	2027.021805	0.006383	VASVESQGQEISGNRR
4.4	2027.017960	0.010228	MFELTLRGMSEALVDKR
3.7	2027.029633	-0.001445	QEESEHSHKHLIELRR
3.4	2027.041092	-0.012904	RTFVSKESPHWQSK
3.0	2027.021805	0.006383	VASVESQGQEISGNRR
2.6	2027.039520	-0.011332	GLERALEEAANSGGLNLSAR

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

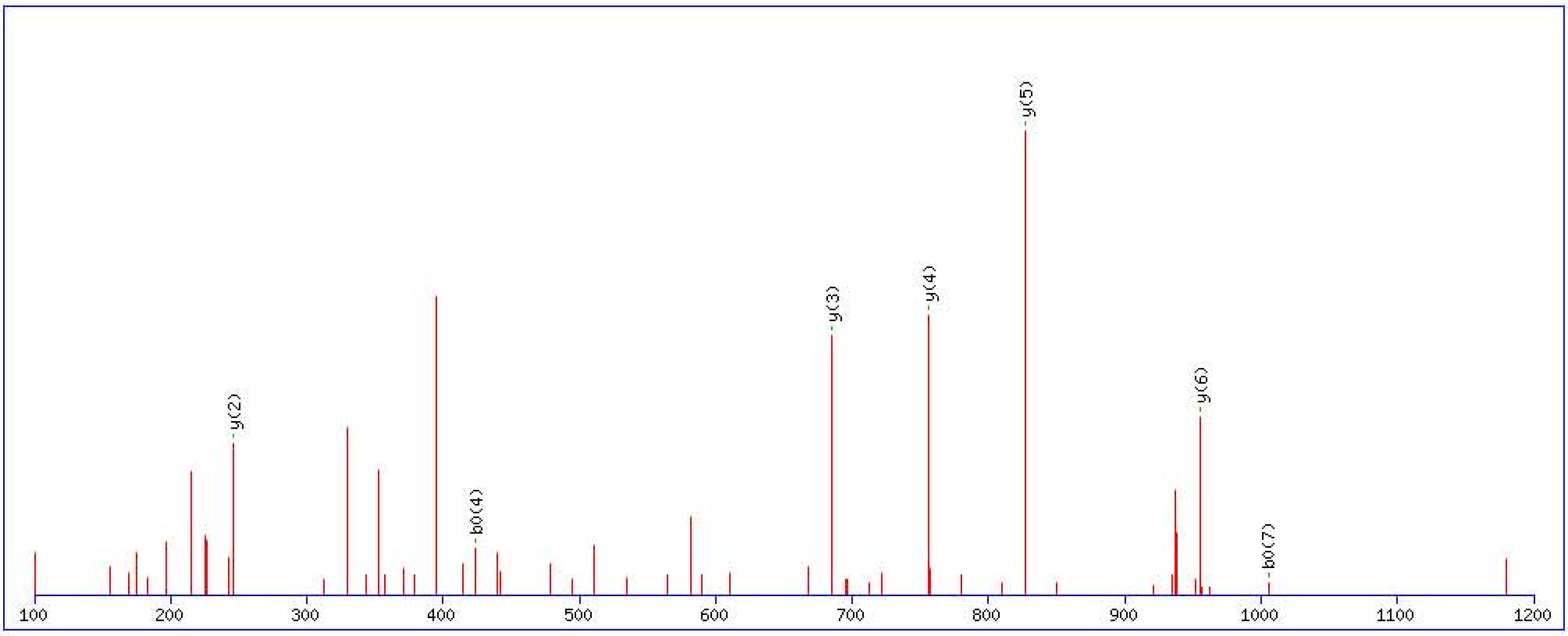
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELQAAQAR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

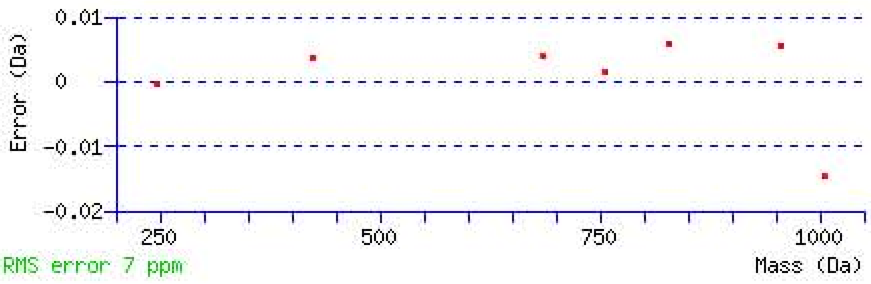
Match to Query 27618: 1196.632548 from(599.323550,2+) rtinseconds(1432) index(38370)
Title: Locus:1.1.1.2782.20 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

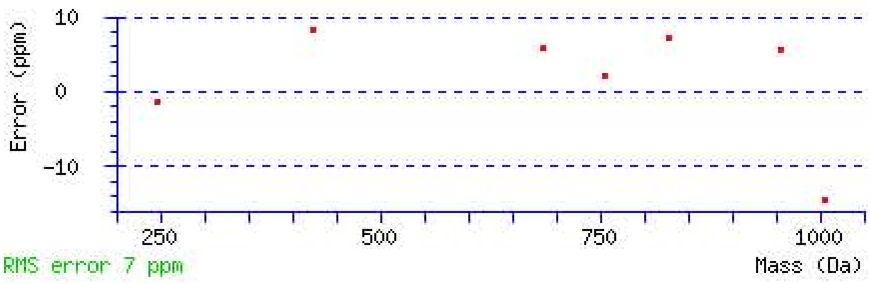
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1196.633545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.004
Matches : 7/66 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					8
2	243.133933	122.070605			225.123368	113.065322	L	1068.598262	534.802769	1051.571713	526.289495	7
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	Q	***955.514198***	478.260737	938.487649	469.747463	6
4	442.229625	221.618450	425.203076	213.105176	424.219060	212.613168	A	***827.455620***	414.231448	810.429071	405.718174	5
5	513.266739	257.137008	496.240190	248.623733	495.256174	248.131725	A	***756.418506***	378.712891	739.391957	370.199617	4
6	952.492065	476.749671	935.465516	468.236396	934.481500	467.744388	Q	***685.381392***	343.194334	668.354843	334.681060	3
7	1023.529179	512.268227	1006.502630	503.754953	1005.518614	503.262945	A	***246.156066***	123.581671	229.129517	115.068397	2
8							R	175.118952	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.3	1196.633545	-0.000997	ELQAAQAR
5.7	1196.614914	0.017634	ELQQAELPNR
3.6	1196.633575	-0.001027	QASTQVPR

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

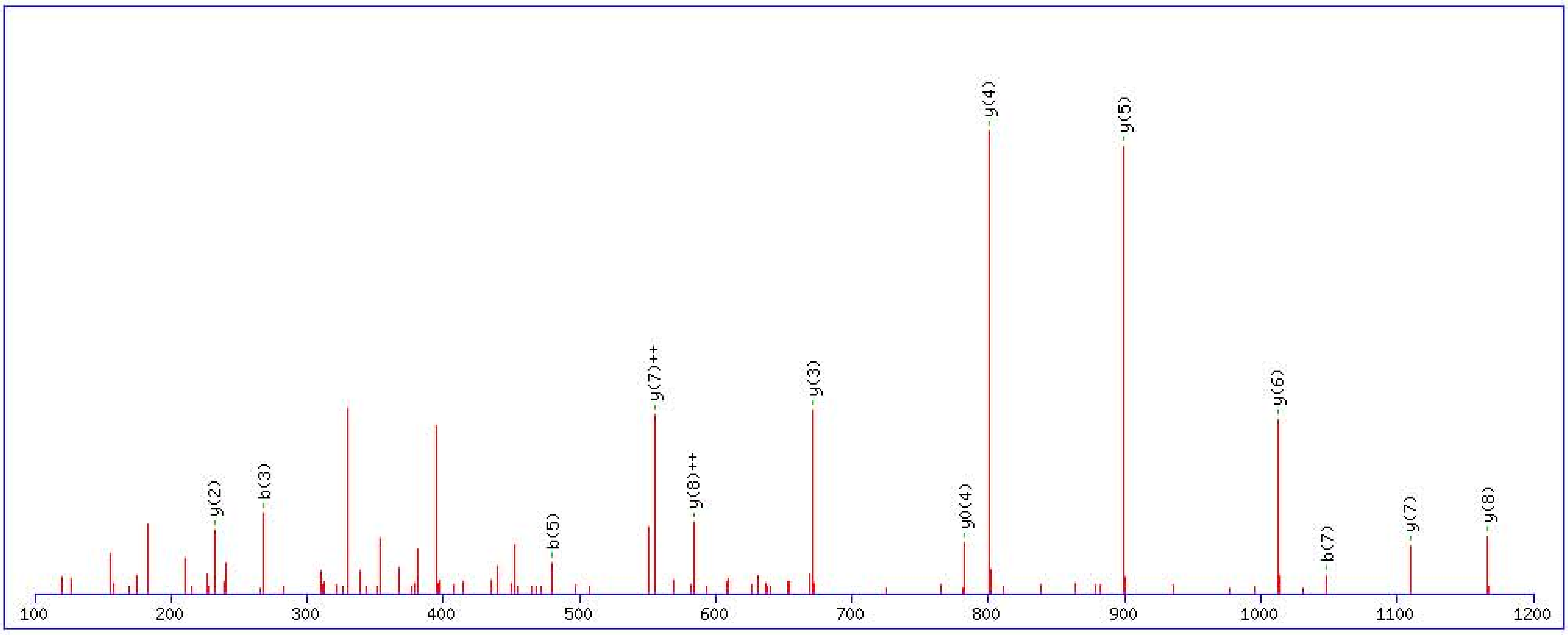
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGPLVEQGR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

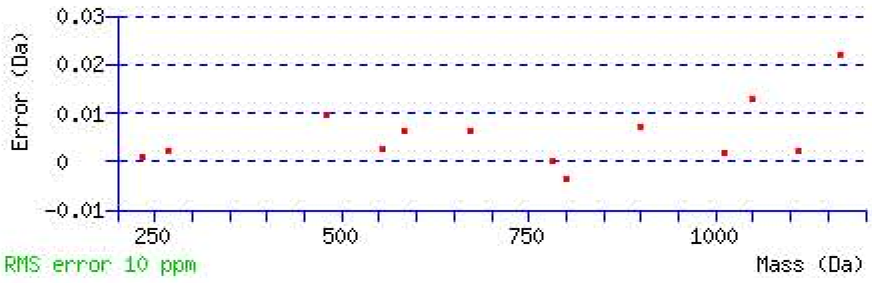
Match to Query 30184: 1278.717328 from(640.365940,2+) rtinseconds(1935) index(41703)
Title: Locus:1.1.1.2957.20 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

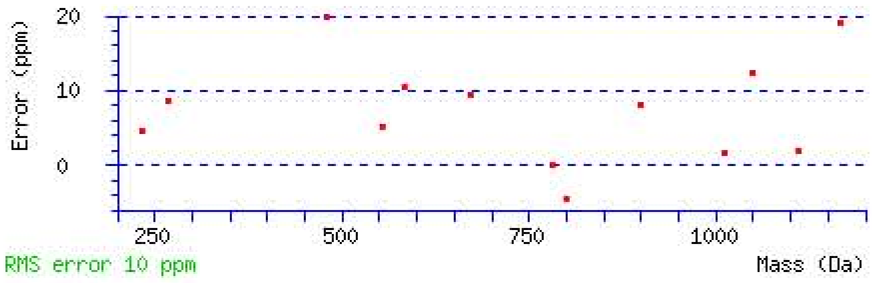
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1278.711823
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 5.5e-005
Matches : 13/68 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	114.091340	57.549308					L							9
2	171.112804	86.060040					G	***1166.635041***	583.821159	1149.608492	575.307884	1148.624476	574.815876	8
3	**268.165568**	134.586422					P	***1109.613577***	555.310426	1092.587028	546.797152	1091.603012	546.305144	7
4	381.249632	191.128454					L	***1012.560813***	506.784044	995.534264	498.270770	994.550248	497.778762	6
5	**480.318046**	240.662661					V	***899.476749***	450.242012	882.450200	441.728738	881.466184	441.236730	5
6	609.360639	305.183958			591.350074	296.178675	E	***800.408335***	400.707805	783.381786	392.194531	782.397770	391.702523	4
7	**1048.585965**	524.796621	1031.559416	516.283346	1030.575400	515.791338	Q	***671.365742***	336.186509	654.339193	327.673234			3
8	1105.607429	553.307352	1088.580880	544.794078	1087.596864	544.302070	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 LGPLVEQGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.7	1278.711823	0.005505	LGPLVEQGR
2.3	1278.729584	-0.012256	IVIVPSLNPDGR

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

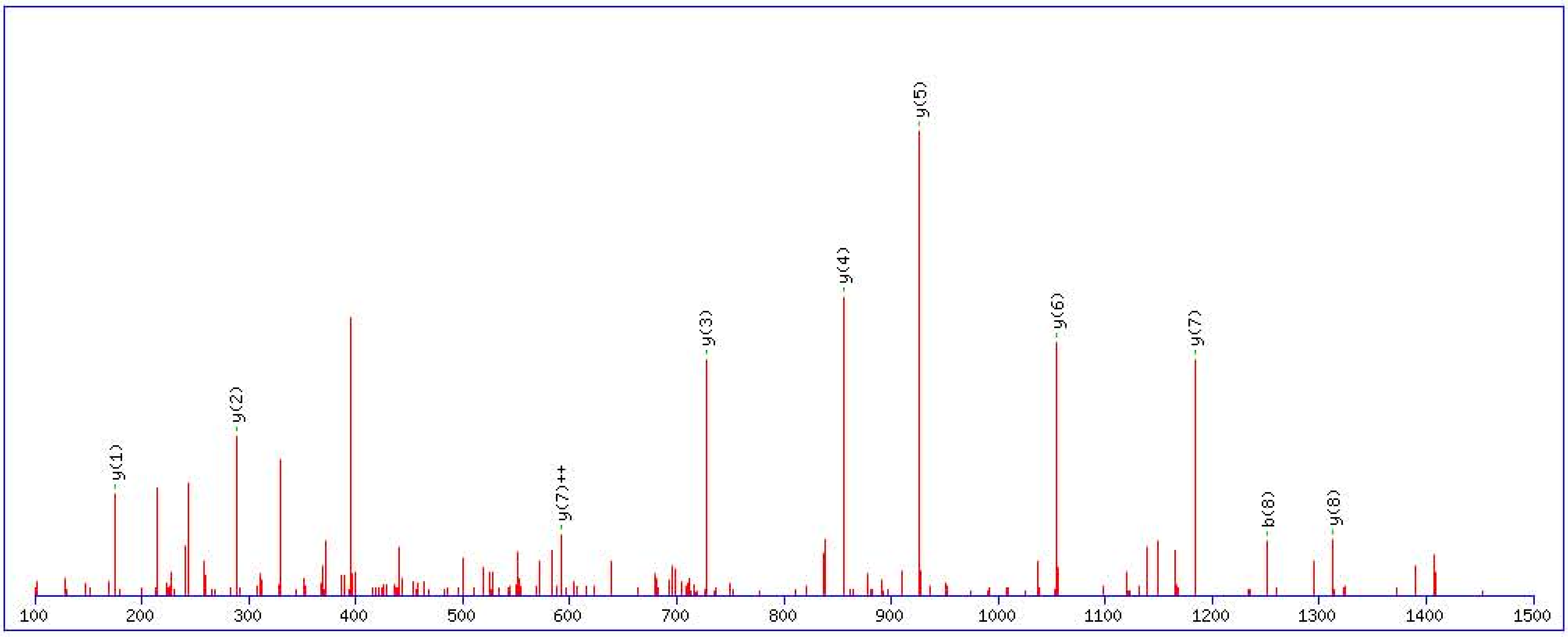
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEEQAQQIR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

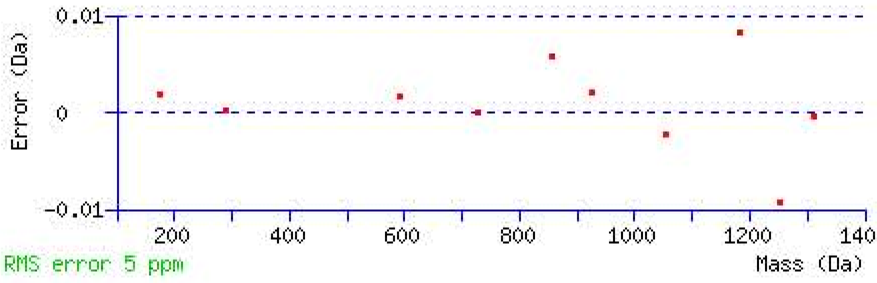
Match to Query 36155: 1424.747968 from(713.381260,2+) rtinseconds(1519) index(38994)
Title: Locus:1.1.1.2812.24 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

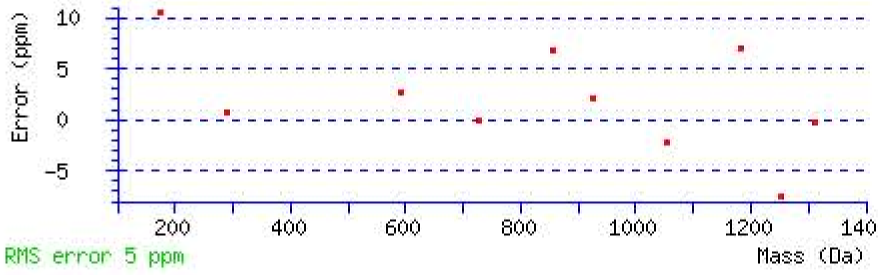
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1424.744553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 71 **Expect:** 2.1e-006
Matches : 10/76 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							9
2	243.133933	122.070605			225.123368	113.065322	E	*1312.667798*	656.837537	1295.641249	648.324263	1294.657233	647.832255	8
3	372.176526	186.591901			354.165961	177.586619	E	*1183.625205*	592.316241	1166.598656	583.802966	1165.614640	583.310958	7
4	500.235104	250.621190	483.208555	242.107916	482.224539	241.615908	Q	*1054.582612*	527.794944	1037.556063	519.281670			6
5	571.272218	286.139747	554.245669	277.626473	553.261653	277.134465	A	*926.524034*	463.765655	909.497485	455.252381			5
6	699.330796	350.169036	682.304247	341.655762	681.320231	341.163754	Q	*855.486920*	428.247098	838.460371	419.733824			4
7	1138.556122	569.781699	1121.529573	561.268425	1120.545557	560.776417	Q	*727.428342*	364.217809	710.401793	355.704535			3
8	1251.640186	626.323731	1234.613637	617.810457	1233.629621	617.318449	I	*288.203016*	144.605146	271.176467	136.091871			2
9							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.6	1424.744553	0.003415	LEEQAQQIR
54.3	1424.744553	0.003415	LEEQAQQIR
25.6	1424.744553	0.003415	LEEQAQQIR
16.9	1424.733322	0.014646	LEQETEPLR
15.1	1424.745438	0.002530	QMQQIR
13.2	1424.767014	-0.019046	EERRQQLR
10.0	1424.730667	0.017301	QPGCAVPQSGRLR
7.4	1424.744583	0.003385	QLSGDQPTIR
6.5	1424.726807	0.021161	QMNLQQQPK
6.4	1424.745438	0.002530	QMQQIR

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

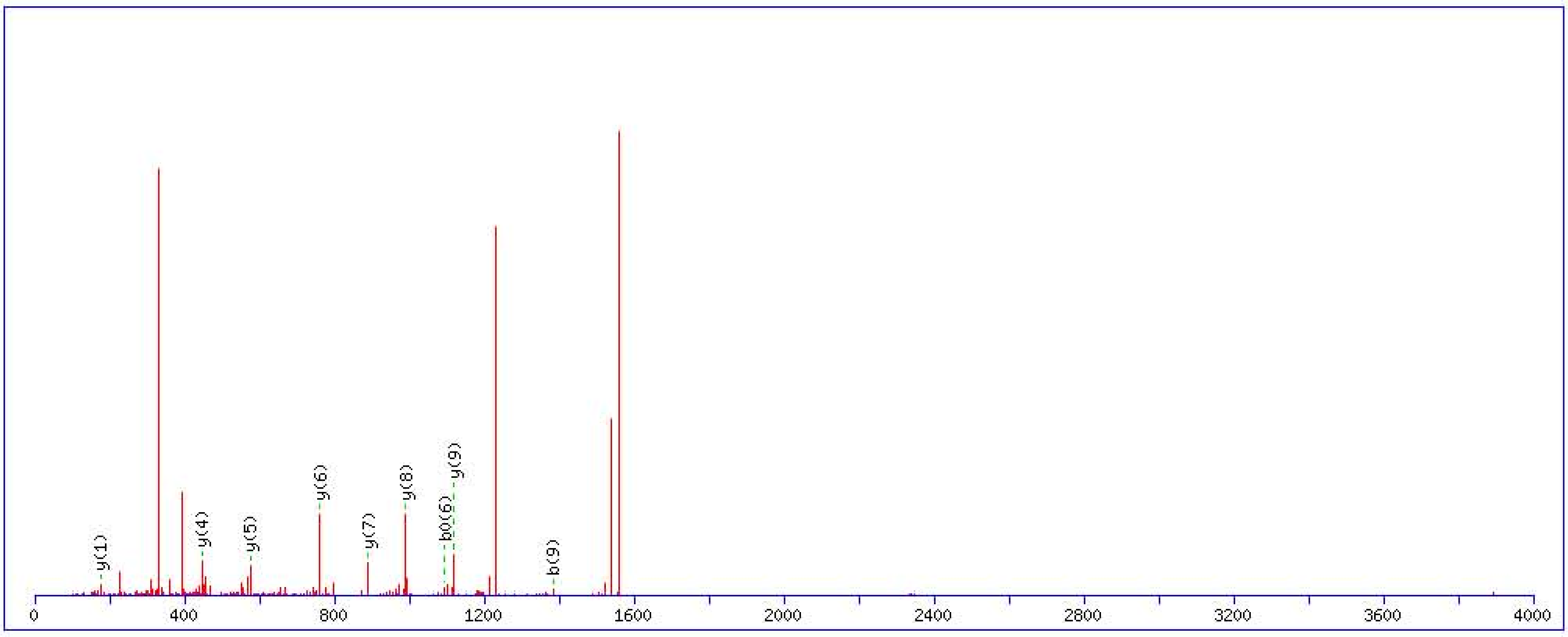
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQTEWQSGQR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

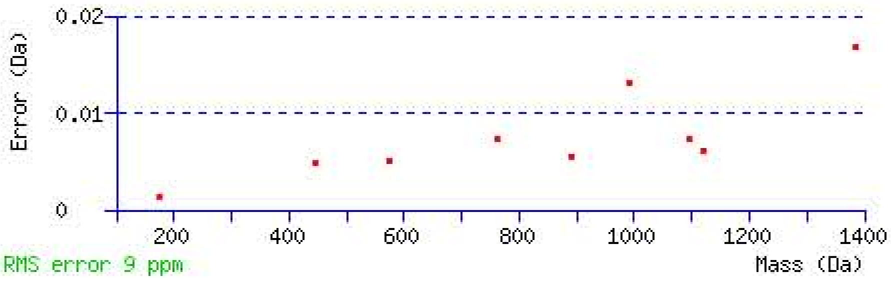
Match to Query 40109: 1557.748268 from(779.881410,2+) rtinseconds(1526) index(57129)
Title: Locus:1.1.1.2837.20 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

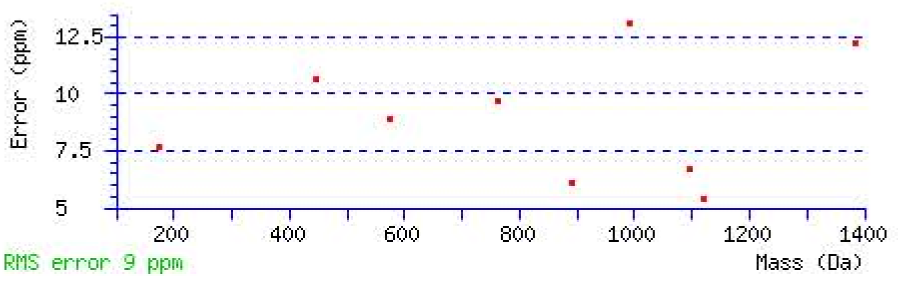
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1557.735809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0011
Matches : 9/98 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							10
2	568.291180	284.649228	551.264631	276.135954			Q	***1119.517763***	560.262520	1102.491214	551.749245	1101.507198	551.257237	9
3	669.338859	335.173068	652.312310	326.659793	651.328294	326.167785	T	***991.459185***	496.233231	974.432636	487.719956	973.448620	487.227948	8
4	798.381452	399.694364	781.354903	391.181090	780.370887	390.689082	E	***890.411506***	445.709391	873.384957	437.196117	872.400941	436.704109	7
5	984.460765	492.734021	967.434216	484.220746	966.450200	483.728738	W	***761.368913***	381.188095	744.342364	372.674820	743.358348	372.182812	6
6	1112.519343	556.763310	1095.492794	548.250035	1094.508778	547.758027	Q	***575.289600***	288.148438	558.263051	279.635164	557.279035	279.143156	5
7	1199.551371	600.279324	1182.524822	591.766049	1181.540806	591.274041	S	***447.231022***	224.119149	430.204473	215.605875	429.220457	215.113867	4
8	1256.572835	628.790056	1239.546286	620.276781	1238.562270	619.784773	G	360.198994	180.603135	343.172445	172.089860			3
9	1384.631413	692.819345	1367.604864	684.306070	1366.620848	683.814062	Q	303.177530	152.092403	286.150981	143.579129			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.1	1557.735809	0.012459	QQTEWQSGQR
28.9	1557.735809	0.012459	QQTEWQSGQR
9.2	1557.747040	0.001228	AFSHCSSLTKHQR
6.0	1557.746567	0.001701	QMSSPQSR
5.2	1557.742340	0.005928	TQSFEIPQPDSGPR
3.6	1557.760925	-0.012657	AKEEAEWQTR
3.6	1557.756897	-0.008629	MAASAAAAELQASGGPR
3.6	1557.749496	-0.001228	QAEATRQAAAQEER
2.9	1557.745697	0.002571	GSSLFMDTEKSGKR
1.7	1557.756912	-0.008644	SSDRLDEAAQR

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

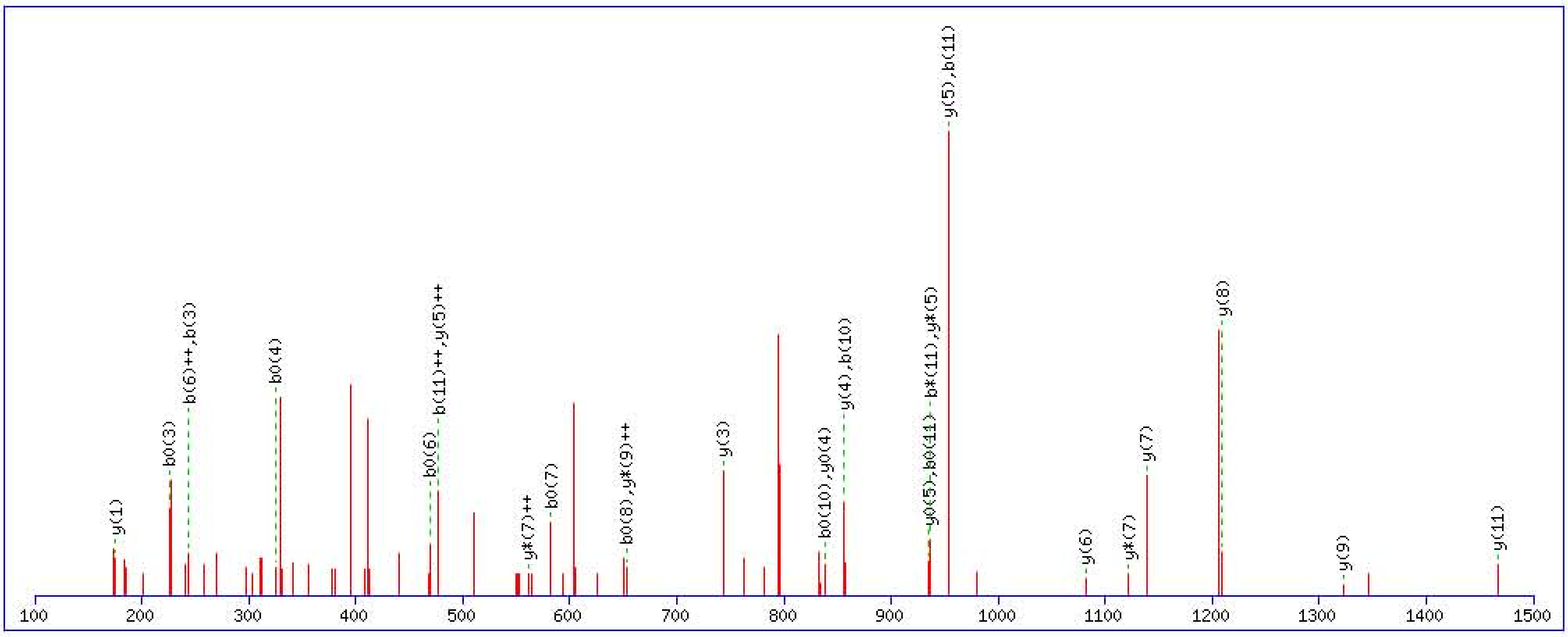
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AATVGSLAGQPLQER**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

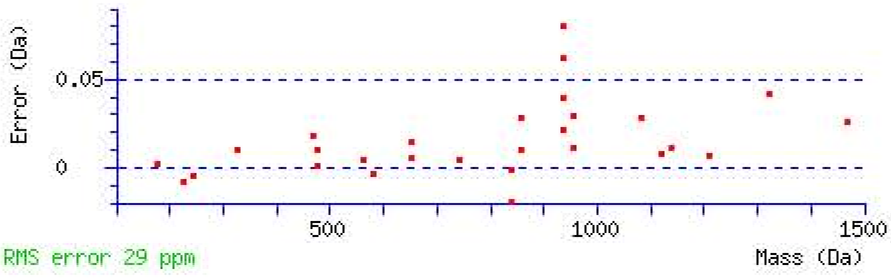
Match to Query 48573: 1807.968792 from(603.663540,3+) rtinseconds(1943) index(41772)
Title: Locus:1.1.1.2960.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

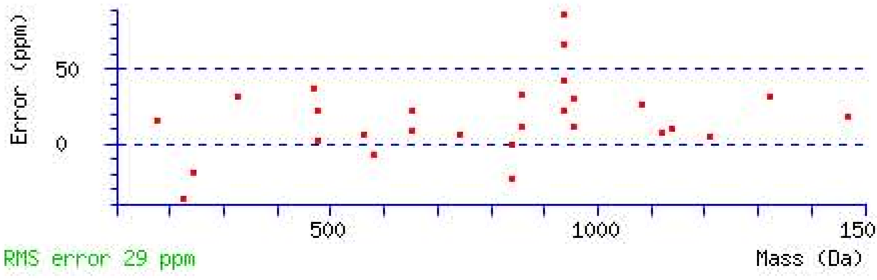
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1807.961441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0056
Matches : 29/144 fragment ions using 52 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							15
2	143.081504	72.044390					A	1737.931618	869.469447	1720.905069	860.956173	1719.921053	860.464165	14
3	**244.129183**	122.568230			226.118618	113.562947	T	1666.894504	833.950890	1649.867955	825.437616	1648.883939	824.945608	13
4	343.197597	172.102437			325.187032	163.097154	V	1565.846825	783.427051	1548.820276	774.913776	1547.836260	774.421768	12
5	400.219061	200.613169			382.208496	191.607886	G	***1466.778411***	733.892844	1449.751862	725.379569	1448.767846	724.887561	11
6	487.251089	**244.129183**			469.240524	235.123900	S	1409.756947	705.382112	1392.730398	696.868837	1391.746382	696.376829	10
7	600.335153	300.671215			582.324588	291.665932	L	***1322.724919***	661.866098	1305.698370	653.352823	1304.714354	652.860815	9
8	671.372267	336.189772			653.361702	327.184489	A	***1209.640855***	605.324066	1192.614306	596.810791	1191.630290	596.318783	8
9	728.393731	364.700504			710.383166	355.695221	G	***1138.603741***	569.805509	1121.577192	561.292234	1120.593176	560.800226	7
10	**856.452309**	428.729793	839.425760	420.216518	838.441744	419.724510	Q	***1081.582277***	541.294777	1064.555728	532.781502	1063.571712	532.289494	6
11	**953.505073**	**477.256175**	936.478524	468.742900	935.494508	468.250892	P	***953.523699***	477.265488	936.497150	468.752213	935.513134	468.260205	5
12	1066.589137	533.798207	1049.562588	525.284932	1048.578572	524.792924	L	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
13	1505.814463	753.410870	1488.787914	744.897595	1487.803898	744.405587	Q	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
14	1634.857056	817.932166	1617.830507	809.418892	1616.846491	808.926884	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.3	1807.961441	0.007351	AATVGSLAGQPLQER
11.7	1807.947510	0.021282	VGLAQIAAMDISRGNHR
2.8	1807.942795	0.025997	ENKDQLESVLEVLHR
1.3	1807.961441	0.007351	AATVGSLAGQPLQER

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

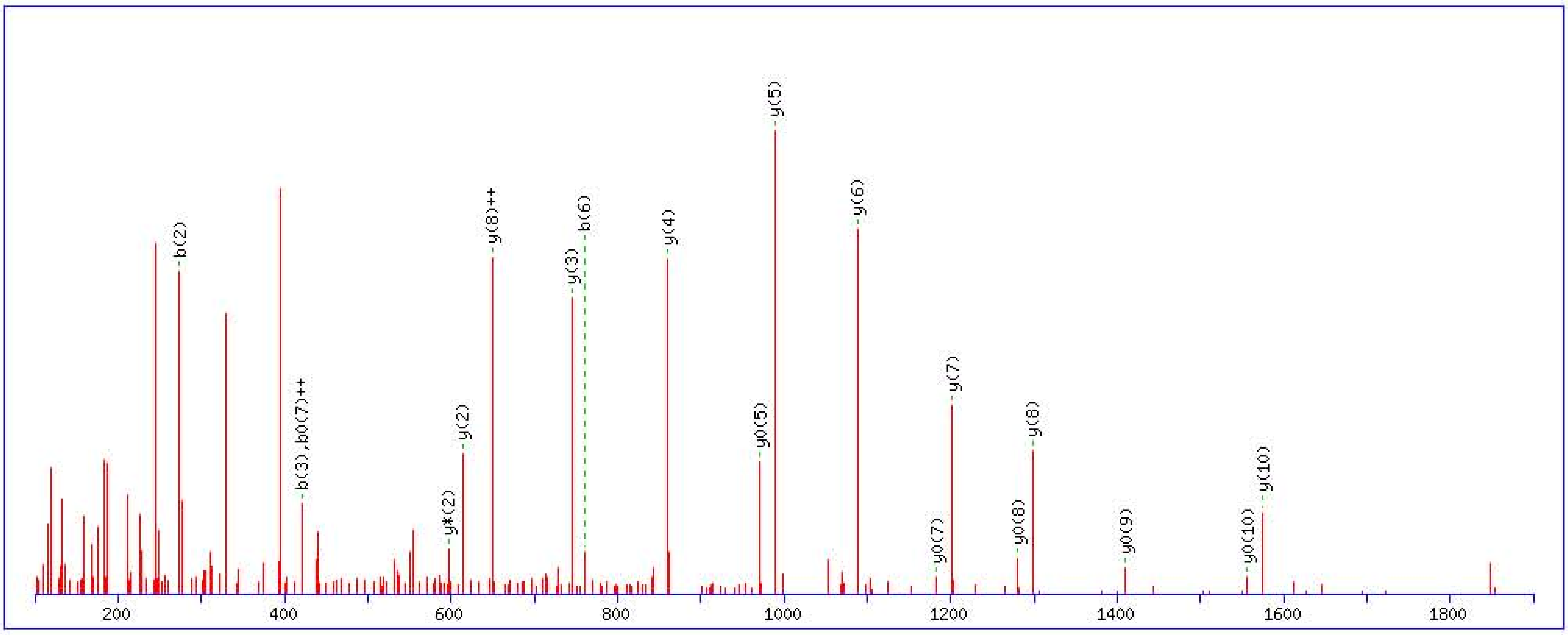
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SWFEPLVEDMQR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

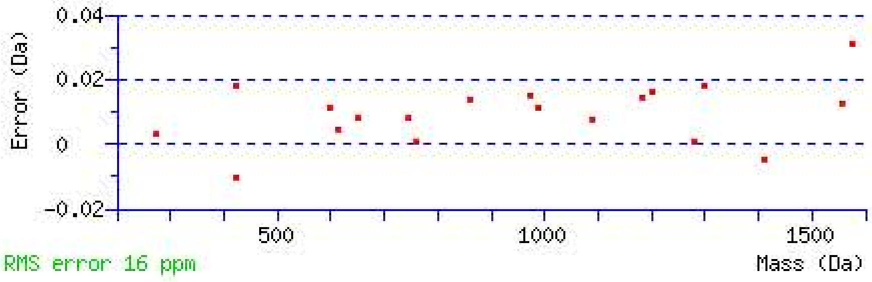
Match to Query 49436: 1846.890372 from(616.637400,3+) rtinseconds(2799) index(47353)
Title: Locus:1.1.1.3257.2 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

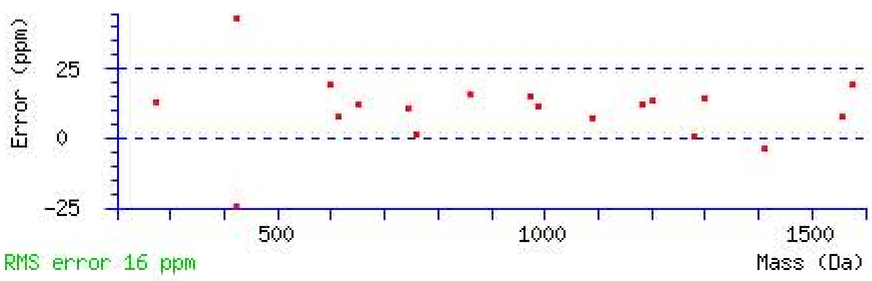
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1846.874603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0014
Matches : 19/106 fragment ions using 33 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							12
2	**274.118617**	137.562947			256.108052	128.557664	W	1760.849861	880.928568	1743.823312	872.415294	1742.839296	871.923286	11
3	**421.187031**	211.097153			403.176466	202.091871	F	***1574.770548***	787.888912	1557.743999	779.375638	1556.759983	778.883629	10
4	550.229624	275.618450			532.219059	266.613168	E	1427.702134	714.354705	1410.675585	705.841431	1409.691569	705.349422	9
5	647.282388	324.144832			629.271823	315.139550	P	***1298.659541***	649.833409	1281.632992	641.320134	1280.648976	640.828126	8
6	**760.366452**	380.686864			742.355887	371.681582	L	***1201.606777***	601.307027	1184.580228	592.793752	1183.596212	592.301744	7
7	859.434866	430.221071			841.424301	421.215789	V	***1088.522713***	544.764995	1071.496164	536.251720	1070.512148	535.759712	6
8	988.477459	494.742368			970.466894	485.737085	E	***989.454299***	495.230788	972.427750	486.717513	971.443734	486.225505	5
9	1103.504402	552.255839			1085.493837	543.250557	D	***860.411706***	430.709491	843.385157	422.196216	842.401141	421.704208	4
10	1234.544887	617.776082			1216.534322	608.770799	M	***745.384763***	373.196020	728.358214	364.682745			3
11	1673.770213	837.388745	1656.743664	828.875470	1655.759648	828.383462	Q	***614.344278***	307.675777	597.317729	299.162503			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.4	1846.874603	0.015769	SWFEPLVEDMQR

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

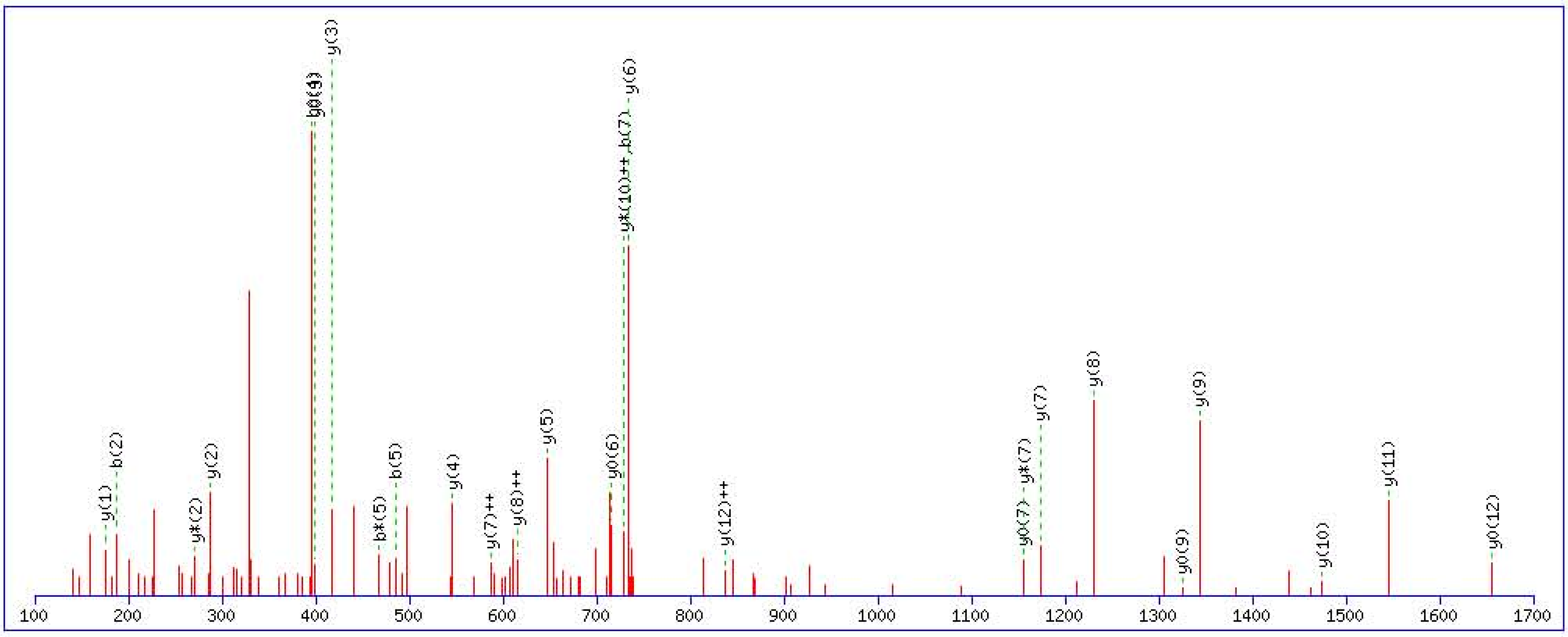
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEVQAMLGQSTEELR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

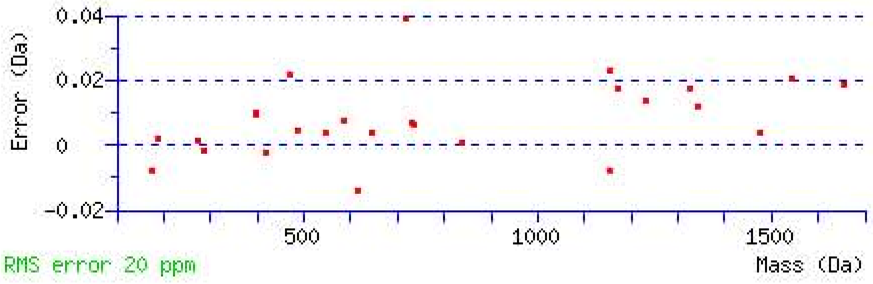
Match to Query 51923: 1957.972992 from(653.664940,3+) rtinseconds(2238) index(43690)
Title: Locus:1.1.1.3063.11 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

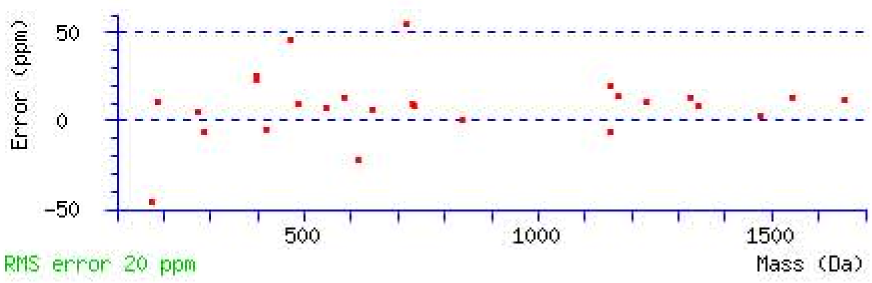
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1957.960114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 5.5e-005
Matches : 27/156 fragment ions using 55 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							15
2	**187.071333**	94.039305			169.060768	85.034022	E	1901.945947	951.476612	1884.919398	942.963337	1883.935382	942.471329	14
3	286.139747	143.573512			268.129182	134.568229	V	1772.903354	886.955315	1755.876805	878.442041	1754.892789	877.950033	13
4	414.198325	207.602801	397.171776	199.089526	396.187760	198.597518	Q	1673.834940	837.421108	1656.808391	828.907834	1655.824375	828.415825	12
5	**485.235439**	243.121357	468.208890	234.608083	467.224874	234.116075	A	***1545.776362***	773.391819	1528.749813	764.878545	1527.765797	764.386537	11
6	616.275924	308.641600	599.249375	300.128326	598.265359	299.636318	M	***1474.739248***	737.873262	1457.712699	729.359988	1456.728683	728.867980	10
7	**729.359988**	365.183632	712.333439	356.670358	711.349423	356.178350	L	***1343.698763***	672.353020	1326.672214	663.839745	1325.688198	663.347737	9
8	786.381452	393.694364	769.354903	385.181090	768.370887	384.689082	G	***1230.614699***	615.810988	1213.588150	607.297713	1212.604134	606.805705	8
9	1225.606778	613.307027	1208.580229	604.793753	1207.596213	604.301745	Q	***1173.593235***	587.300256	1156.566686	578.786981	1155.582670	578.294973	7
10	1312.638806	656.823041	1295.612257	648.309767	1294.628241	647.817759	S	***734.367909***	367.687593	717.341360	359.174318	716.357344	358.682310	6
11	1413.686485	707.346881	1396.659936	698.833606	1395.675920	698.341598	T	***647.335881***	324.171579	630.309332	315.658304	629.325316	315.166296	5
12	1542.729078	771.868177	1525.702529	763.354903	1524.718513	762.862895	E	***546.288202***	273.647739	529.261653	265.134464	528.277637	264.642456	4
13	1671.771671	836.389474	1654.745122	827.876199	1653.761106	827.384191	E	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
14	1784.855735	892.931506	1767.829186	884.418231	1766.845170	883.926223	L	***288.203016***	144.605146	271.176467	136.091871			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.1	1957.960114	0.012878	GEVQAMLGQSTEELR
8.9	1957.960114	0.012878	GEVQAMLGQSTEELR

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

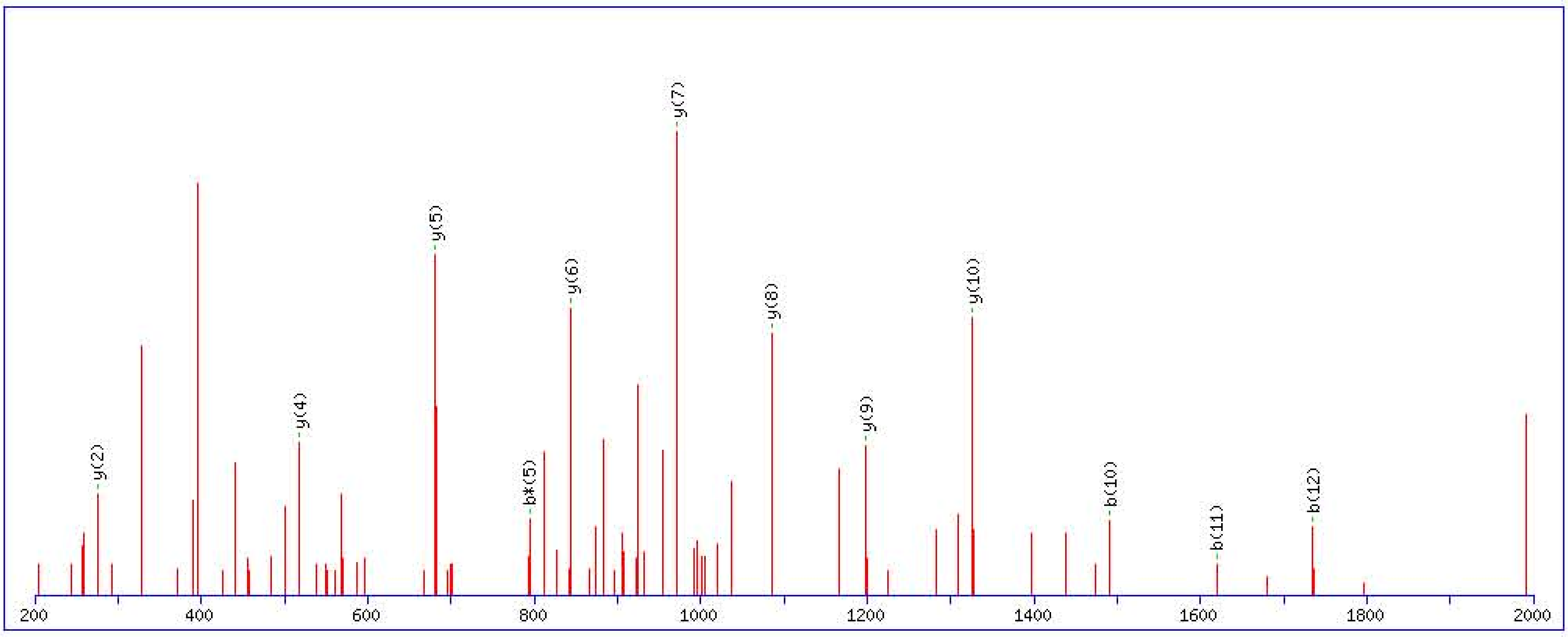
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGVQQLIQYYQDQK**
Found in **APOF_HUMAN**, Apolipoprotein F OS=Homo sapiens GN=APOF PE=1 SV=2

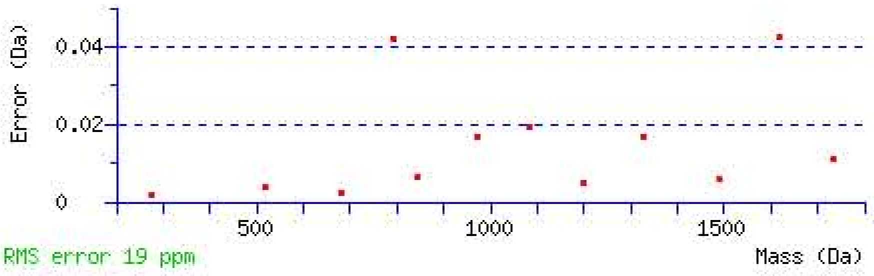
Match to Query 54001: 2008.035448 from(1005.025000,2+) rtinseconds(2469) index(45067)
Title: Locus:1.1.1.3143.26 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

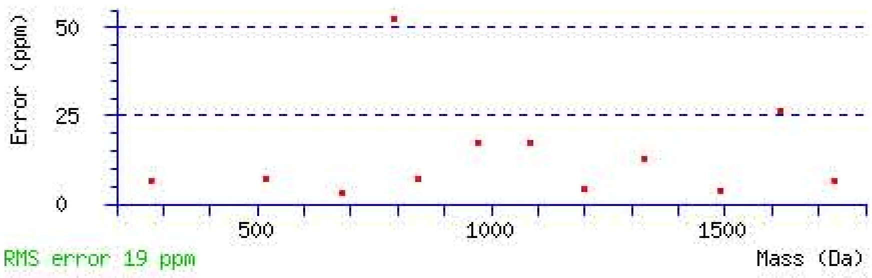
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2008.008789
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 62 **Expect:** 4.7e-006
Matches : 12/146 fragment ions using 16 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							14
2	145.060768	73.034022			127.050203	64.028740	G	1921.984049	961.495663	1904.957500	952.982388	1903.973484	952.490380	13
3	244.129182	122.568229			226.118617	113.562947	V	1864.962585	932.984931	1847.936036	924.471656	1846.952020	923.979648	12
4	683.354508	342.180892	666.327959	333.667618	665.343943	333.175610	Q	1765.894171	883.450724	1748.867622	874.937449	1747.883606	874.445441	11
5	811.413086	406.210181	794.386537	397.696907	793.402521	397.204899	Q	***1326.668845***	663.838061	1309.642296	655.324786	1308.658280	654.832778	10
6	924.497150	462.752213	907.470601	454.238939	906.486585	453.746931	L	***1198.610267***	599.808772	1181.583718	591.295497	1180.599702	590.803489	9
7	1037.581214	519.294245	1020.554665	510.780971	1019.570649	510.288963	I	***1085.526203***	543.266740	1068.499654	534.753465	1067.515638	534.261457	8
8	1165.639792	583.323534	1148.613243	574.810260	1147.629227	574.318252	Q	***972.442139***	486.724708	955.415590	478.211433	954.431574	477.719425	7
9	1328.703121	664.855199	1311.676572	656.341924	1310.692556	655.849916	Y	***844.383561***	422.695419	827.357012	414.182144	826.372996	413.690136	6
10	**1491.766450**	746.386863	1474.739901	737.873589	1473.755885	737.381581	Y	***681.320232***	341.163754	664.293683	332.650480	663.309667	332.158472	5
11	**1619.825028**	810.416152	1602.798479	801.902878	1601.814463	801.410870	Q	***518.256903***	259.632090	501.230354	251.118815	500.246338	250.626807	4
12	**1734.851971**	867.929624	1717.825422	859.416349	1716.841406	858.924341	D	390.198325	195.602800	373.171776	187.089526	372.187760	186.597518	3
13	1862.910549	931.958913	1845.884000	923.445638	1844.899984	922.953630	Q	***275.171382***	138.089329	258.144833	129.576054			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.5	2008.008789	0.026659	SGVQQLIQYYQDQK
52.5	2008.008789	0.026659	SGVQQLIQYYQDQK
31.6	2008.008789	0.026659	SGVQQLIQYYQDQK
8.3	2008.008789	0.026659	SGVQQLIQYYQDQK
5.3	2008.053009	-0.017561	WAEKPAFGTPLEEHLKR
3.4	2008.008789	0.026659	SGVQQLIQYYQDQK
3.0	2008.005630	0.029818	ITQRMVCAGYKEGGK
2.1	2008.012146	0.023302	LCEQDKVVHALEEK
0.5	2008.030762	0.004686	ASVMLFMKGNKQEAK
0.2	2008.033752	0.001696	SSSFSRSGPGSQLNTKLQK

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

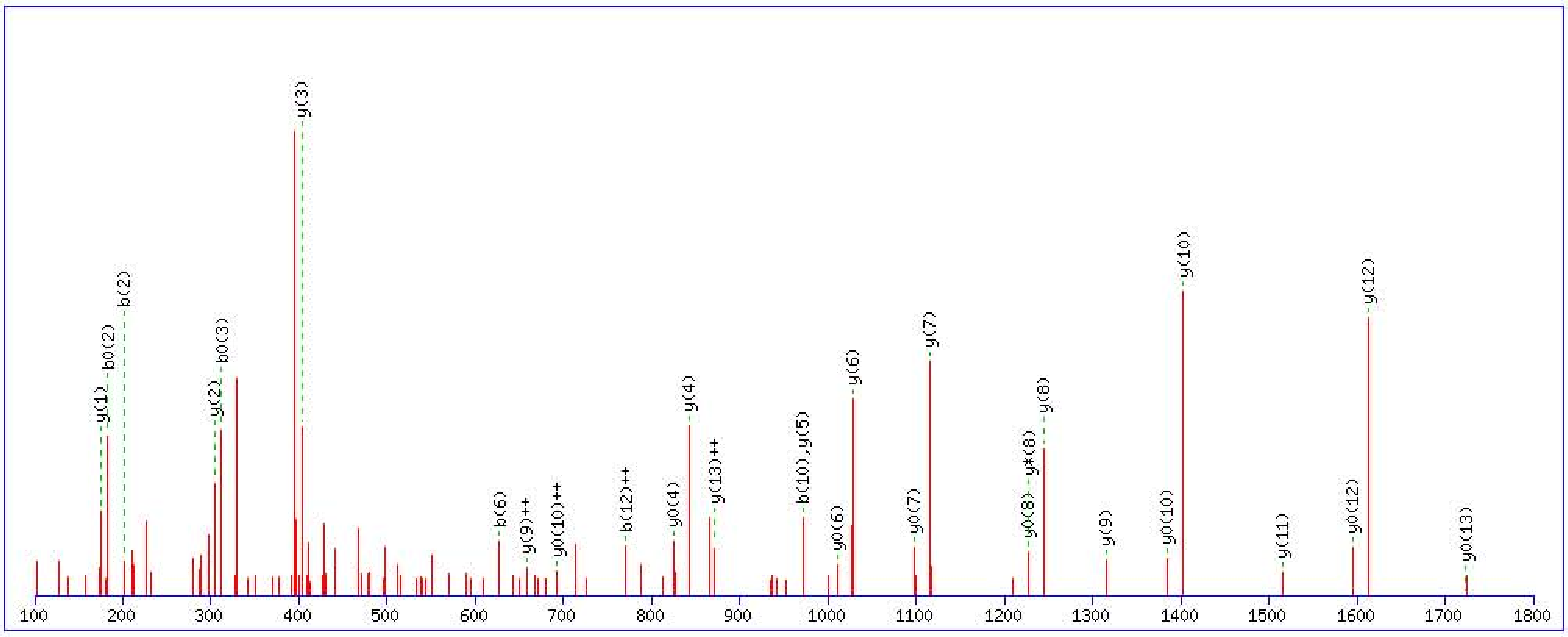
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTEPISAESGEQVER**
Found in **APOL1_HUMAN**, Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5

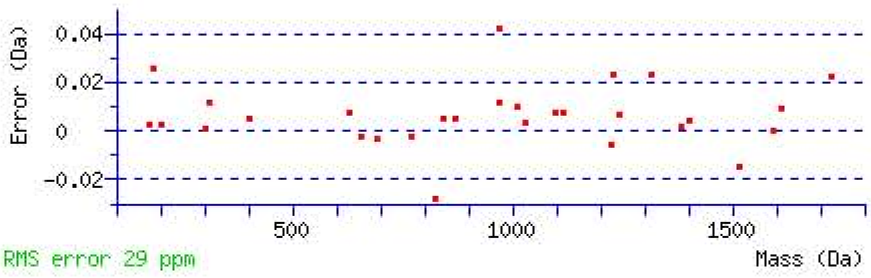
Match to Query 51534: 1940.958492 from(647.993440,3+) rtinseconds(1704) index(40107)
Title: Locus:1.1.1.2877.9 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

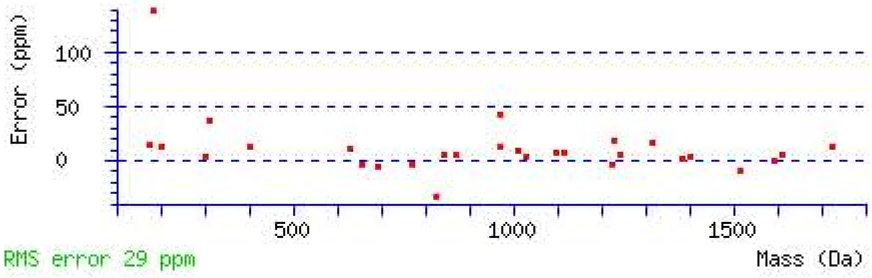
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1940.951324
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 71 **Expect:** 1.9e-006
Matches : 29/142 fragment ions using 53 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							15
2	**201.123369**	101.065322			183.112804	92.060040	T	1842.890205	921.948741	1825.863656	913.435466	1824.879640	912.943458	14
3	330.165962	165.586619			312.155397	156.581336	E	1741.842526	871.424901	1724.815977	862.911627	1723.831961	862.419619	13
4	427.218726	214.113001			409.208161	205.107719	P	***1612.799933***	806.903605	1595.773384	798.390330	1594.789368	797.898322	12
5	540.302790	270.655033			522.292225	261.649751	I	***1515.747169***	758.377223	1498.720620	749.863948	1497.736604	749.371940	11
6	**627.334818**	314.171047			609.324253	305.165765	S	***1402.663105***	701.835191	1385.636556	693.321916	1384.652540	692.829908	10
7	698.371932	349.689604			680.361367	340.684322	A	***1315.631077***	658.319177	1298.604528	649.805902	1297.620512	649.313894	9
8	827.414525	414.210901			809.403960	405.205618	E	***1244.593963***	622.800620	1227.567414	614.287345	1226.583398	613.795337	8
9	914.446553	457.726915			896.435988	448.721632	S	***1115.551370***	558.279323	1098.524821	549.766049	1097.540805	549.274041	7
10	**971.468017**	486.237647			953.457452	477.232364	G	***1028.519342***	514.763309	1011.492793	506.250035	1010.508777	505.758027	6
11	1100.510610	550.758943			1082.500045	541.753661	E	***971.497878***	486.252577	954.471329	477.739303	953.487313	477.247295	5
12	1539.735936	770.371606	1522.709387	761.858332	1521.725371	761.366324	Q	***842.455285***	421.731281	825.428736	413.218006	824.444720	412.725998	4
13	1638.804350	819.905813	1621.777801	811.392539	1620.793785	810.900531	V	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
14	1767.846943	884.427110	1750.820394	875.913835	1749.836378	875.421827	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.2	1940.951324	0.007168	VTEPISAESGEQVER
10.0	1940.962540	-0.004048	LLNDQEEEGTQRAK
5.8	1940.937378	0.021114	SNNLEREQEQLDR

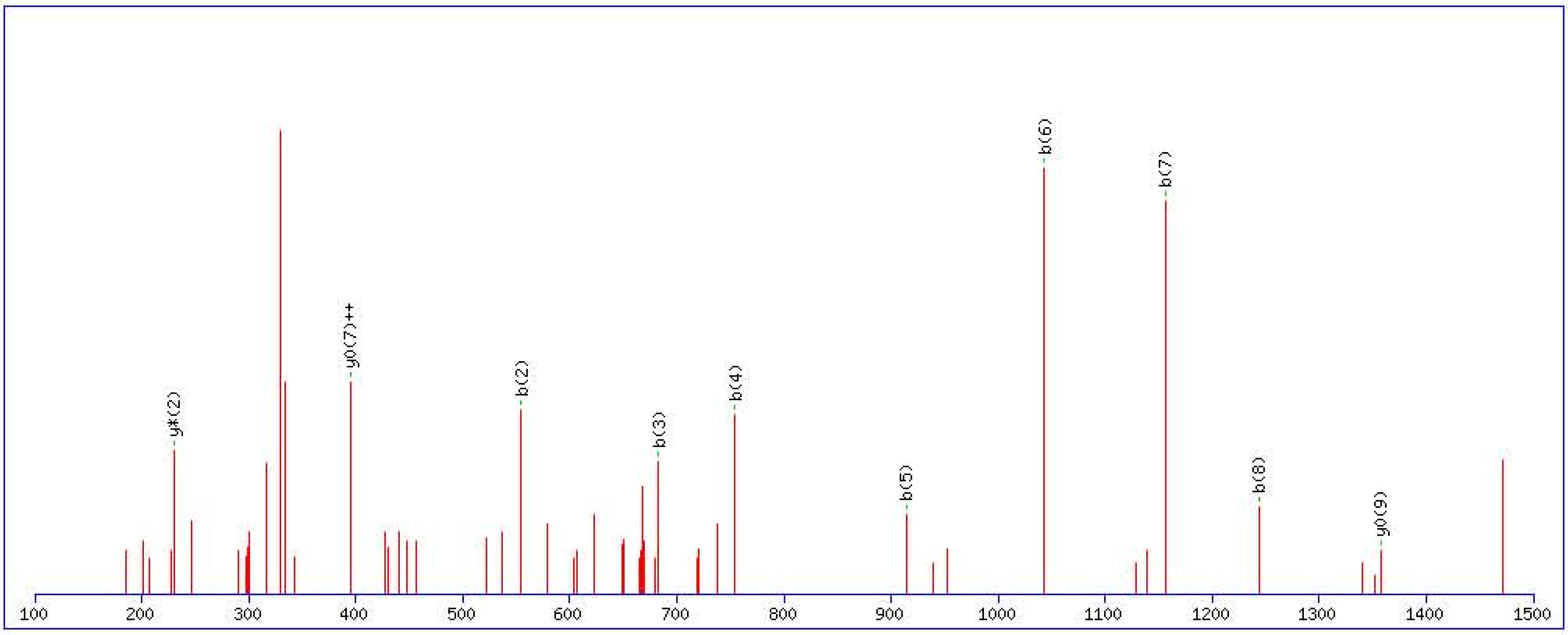
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of NQEACELSNN
Found in APOM_HUMAN, Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2

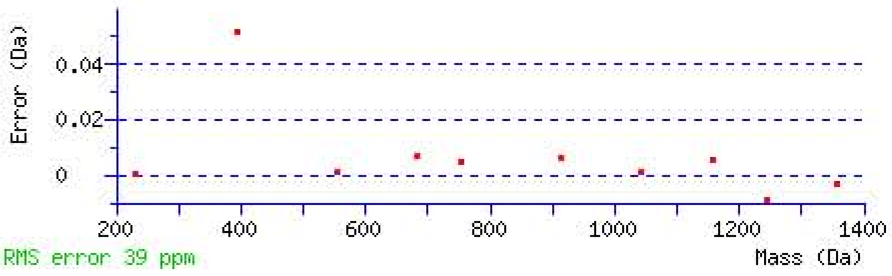
Match to Query 38261: 1488.638068 from(745.326310,2+) rtinseconds(1639) index(39711)
Title: Locus:1.1.1.2854.22 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

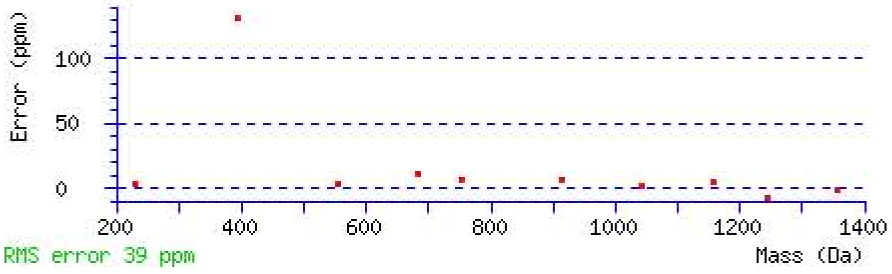
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1488.633682
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 6.8e-007
Matches : 11/100 fragment ions using 12 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							10
2	***554.275529***	277.641403	537.248980	269.128128			Q	1375.598062	688.302669	1358.571513	679.789395	1357.587497	679.297387	9
3	***683.318122***	342.162699	666.291573	333.649425	665.307557	333.157417	E	936.372736	468.690006	919.346187	460.176732	918.362171	459.684724	8
4	***754.355236***	377.681256	737.328687	369.167982	736.344671	368.675974	A	807.330143	404.168710	790.303594	395.655435	789.319578	395.163427	7
5	***914.385885***	457.696581	897.359336	449.183306	896.375320	448.691298	C	736.293029	368.650153	719.266480	360.136878	718.282464	359.644870	6
6	***1043.428478***	522.217877	1026.401929	513.704603	1025.417913	513.212595	E	576.262380	288.634828	559.235831	280.121554	558.251815	279.629546	5
7	***1156.512542***	578.759909	1139.485993	570.246635	1138.501977	569.754626	L	447.219787	224.113531	430.193238	215.600257	429.209222	215.108249	4
8	***1243.544570***	622.275923	1226.518021	613.762649	1225.534005	613.270641	S	334.135723	167.571499	317.109174	159.058225	316.125158	158.566217	3
9	***1357.587497***	679.297387	1340.560948	670.784112	1339.576932	670.292104	N	247.103695	124.055485	230.077146	115.542211			2
10							N	133.060768	67.034022	116.034219	58.520747			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.1	1488.633682	0.004386	NQEACELSNN

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

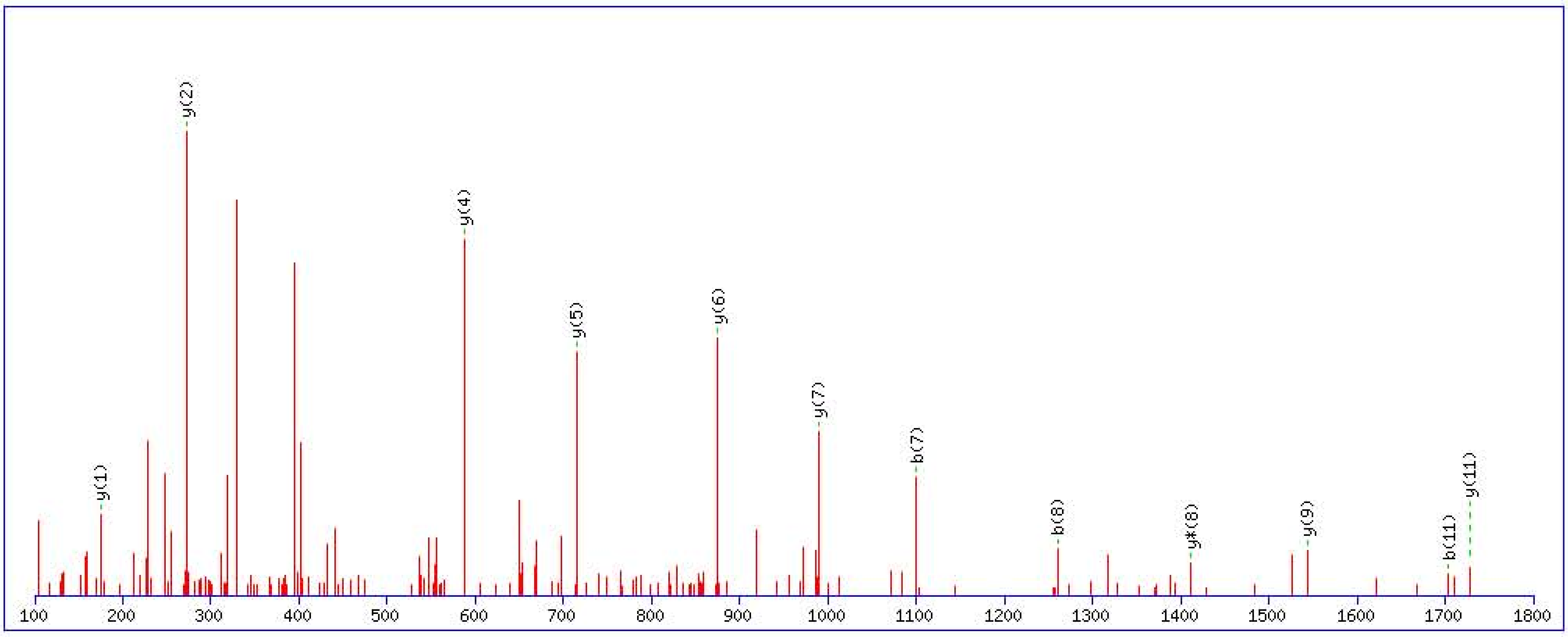
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SCALDQNCQWEPR**
Found in **ATRN_HUMAN**, Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

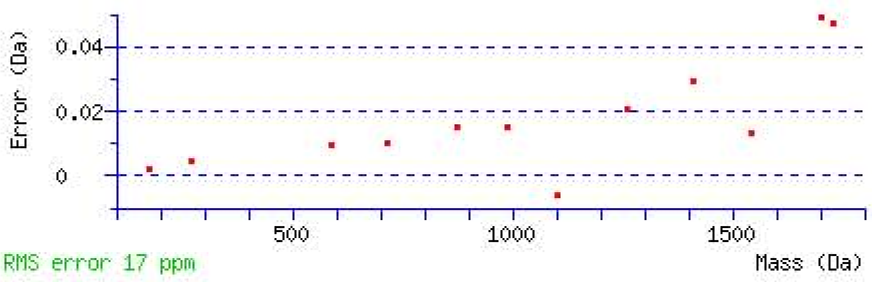
Match to Query 52342: 1973.871282 from(658.964370,3+) rtinseconds(1968) index(6828)
Title: Locus:1.1.1.2817.12 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

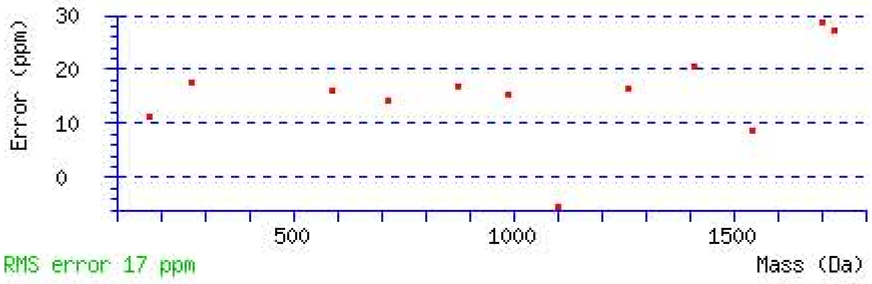
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1973.854614
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 57 **Expect:** 1.3e-005
Matches : 12/130 fragment ions using 17 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							13
2	248.069953	124.538614			230.059388	115.533332	C	1887.829872	944.418574	1870.803323	935.905300	1869.819307	935.413292	12
3	319.107067	160.057171			301.096502	151.051889	A	***1727.799223***	864.403250	1710.772674	855.889975	1709.788658	855.397967	11
4	432.191131	216.599203			414.180566	207.593921	L	1656.762109	828.884693	1639.735560	820.371418	1638.751544	819.879410	10
5	547.218074	274.112675			529.207509	265.107393	D	***1543.678045***	772.342661	1526.651496	763.829386	1525.667480	763.337378	9
6	986.443400	493.725338	969.416851	485.212064	968.432835	484.720056	Q	1428.651102	714.829189	1411.624553	706.315915	1410.640537	705.823907	8
7	**1100.486327**	550.746802	1083.459778	542.233527	1082.475762	541.741519	N	***989.425776***	495.216526	972.399227	486.703252	971.415211	486.211244	7
8	**1260.516976**	630.762126	1243.490427	622.248852	1242.506411	621.756844	C	***875.382849***	438.195063	858.356300	429.681788	857.372284	429.189780	6
9	1388.575554	694.791415	1371.549005	686.278141	1370.564989	685.786133	Q	***715.352200***	358.179738	698.325651	349.666464	697.341635	349.174456	5
10	1574.654867	787.831072	1557.628318	779.317797	1556.644302	778.825789	W	***587.293622***	294.150449	570.267073	285.637174	569.283057	285.145166	4
11	**1703.697460**	852.352368	1686.670911	843.839094	1685.686895	843.347086	E	401.214309	201.110792	384.187760	192.597518	383.203744	192.105510	3
12	1800.750224	900.878750	1783.723675	892.365476	1782.739659	891.873468	P	***272.171716***	136.589496	255.145167	128.076221			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.6	1973.854614	0.016668	SCALDQNCQWEPR
19.3	1973.854614	0.016668	SCALDQNCQWEPR
6.7	1973.853729	0.017553	DSPETGEEMGRAEGAWPR

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

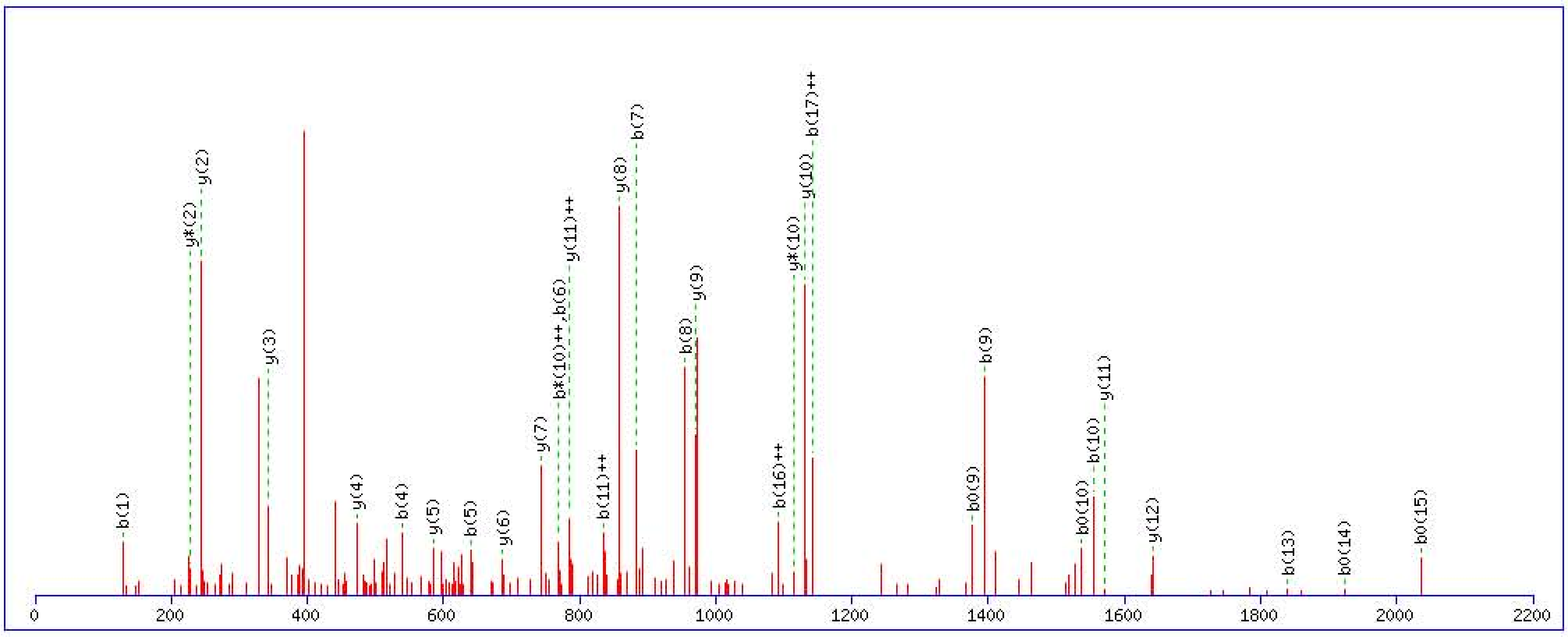
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KCSYTEDAQCIDGTIEVPK**
Found in **APOH_HUMAN**, Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3

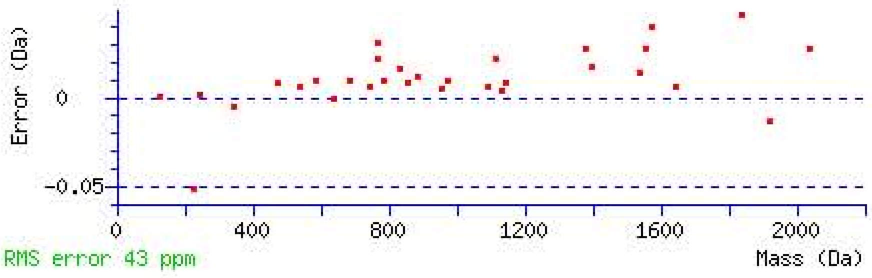
Match to Query 65810: 2524.191162 from(842.404330,3+) rtinseconds(1980) index(78354)
Title: Locus:1.1.1.2903.23 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

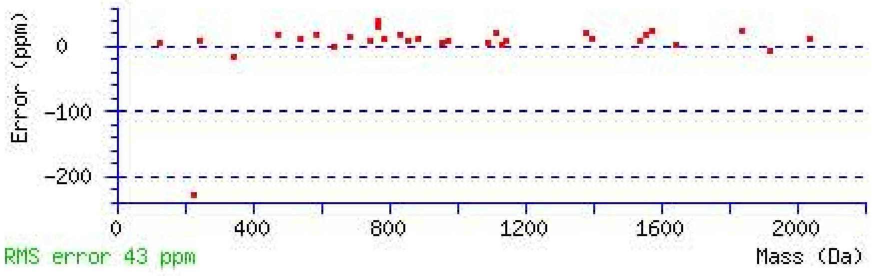
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2524.164780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 5.7e-006
Matches : 31/206 fragment ions using 55 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							19
2	289.132888	145.070082	272.106339	136.556808			C	2397.077099	1199.042187	2380.050550	1190.528913	2379.066534	1190.036905	18
3	376.164916	188.586096	359.138367	180.072822	358.154351	179.580814	S	2237.046450	1119.026863	2220.019901	1110.513588	2219.035885	1110.021580	17
4	***539.228245***	270.117761	522.201696	261.604486	521.217680	261.112478	Y	2150.014422	1075.510849	2132.987873	1066.997574	2132.003857	1066.505566	16
5	***640.275924***	320.641600	623.249375	312.128326	622.265359	311.636318	T	1986.951093	993.979185	1969.924544	985.465910	1968.940528	984.973902	15
6	***769.318517***	385.162897	752.291968	376.649622	751.307952	376.157614	E	1885.903414	943.455345	1868.876865	934.942071	1867.892849	934.450063	14
7	***884.345460***	442.676368	867.318911	434.163094	866.334895	433.671086	D	1756.860821	878.934049	1739.834272	870.420774	1738.850256	869.928766	13
8	***955.382574***	478.194925	938.356025	469.681650	937.372009	469.189642	A	***1641.833878***	821.420577	1624.807329	812.907303	1623.823313	812.415295	12
9	***1394.607900***	697.807588	1377.581351	689.294314	1376.597335	688.802306	Q	***1570.796764***	785.902020	1553.770215	777.388746	1552.786199	776.896738	11
10	***1554.638549***	777.822913	1537.612000	769.309638	1536.627984	768.817630	C	***1131.571438***	566.289357	1114.544889	557.776083	1113.560873	557.284075	10
11	1667.722613	**834.364945**	1650.696064	825.851670	1649.712048	825.359662	I	***971.540789***	486.274033	954.514240	477.760758	953.530224	477.268750	9
12	1782.749556	891.878416	1765.723007	883.365142	1764.738991	882.873134	D	***858.456725***	429.732001	841.430176	421.218726	840.446160	420.726718	8
13	***1839.771020***	920.389148	1822.744471	911.875874	1821.760455	911.383866	G	***743.429782***	372.218529	726.403233	363.705255	725.419217	363.213247	7
14	1940.818699	970.912988	1923.792150	962.399713	1922.808134	961.907705	T	***686.408318***	343.707797	669.381769	335.194523	668.397753	334.702515	6
15	2053.902763	1027.455019	2036.876214	1018.941745	2035.892198	1018.449737	I	***585.360639***	293.183958	568.334090	284.670683	567.350074	284.178675	5
16	2182.945356	**1091.976316**	2165.918807	1083.463041	2164.934791	1082.971034	E	***472.276575***	236.641925	455.250026	228.128651	454.266010	227.636643	4
17	2282.013770	**1141.510523**	2264.987221	1132.997248	2264.003205	1132.505240	V	***343.233982***	172.120629	326.207433	163.607354			3
18	2379.066534	1190.036905	2362.039985	1181.523630	2361.055969	1181.031622	P	***244.165568***	122.586422	227.139019	114.073148			2
19							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.9	2524.164780	0.026382	KCSYTEDAQCIDGTIEVPK

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

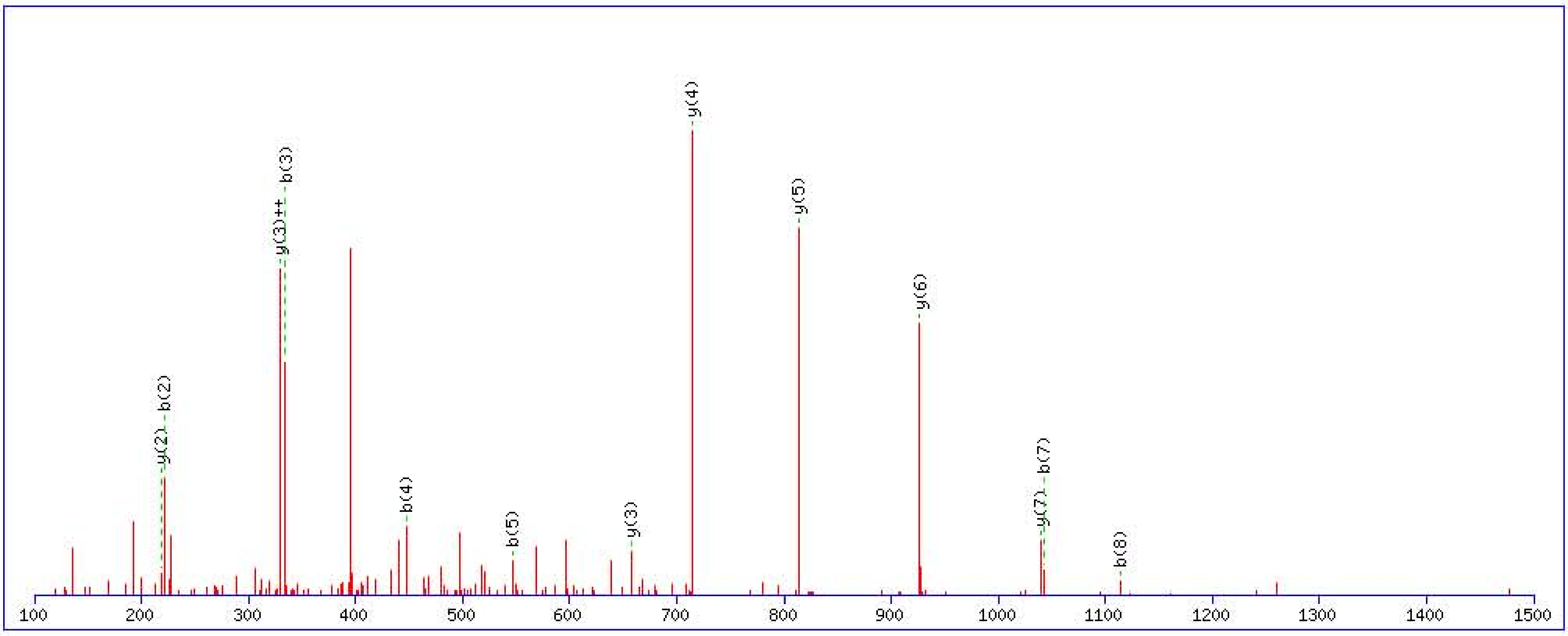
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GYILVGQAK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

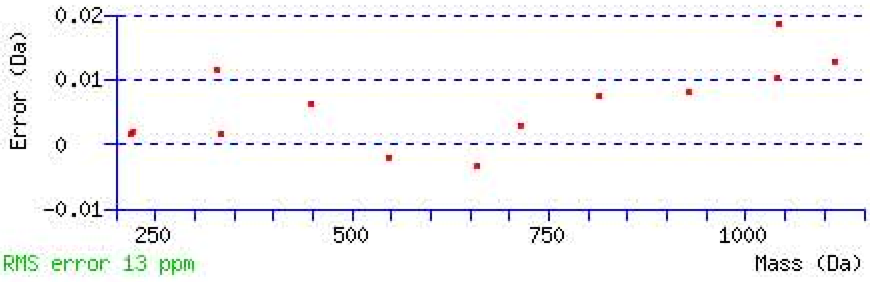
Match to Query 29498: 1258.717068 from(630.365810,2+) rtinseconds(2035) index(42338)
Title: Locus:1.1.1.2992.11 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

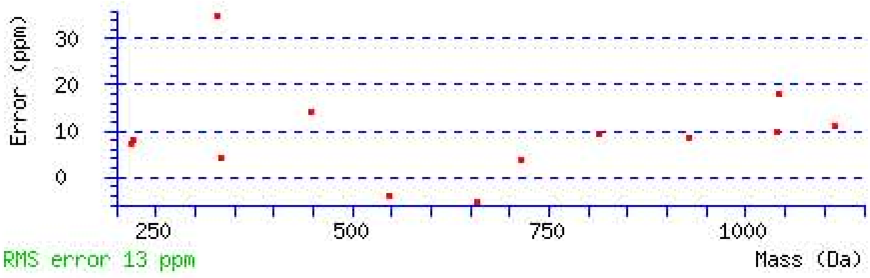
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1258.710754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.018
Matches : 13/52 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	58.028740	29.518008			G					9
2	*221.092069*	111.049673			Y	1202.696579	601.851928	1185.670030	593.338653	8
3	*334.176133*	167.591704			I	*1039.633250*	520.320263	1022.606701	511.806989	7
4	*447.260197*	224.133737			L	*926.549186*	463.778231	909.522637	455.264957	6
5	*546.328611*	273.667944			V	*813.465122*	407.236199	796.438573	398.722925	5
6	603.350075	302.178676			G	*714.396708*	357.701992	697.370159	349.188718	4
7	*1042.575401*	521.791339	1025.548852	513.278064	Q	*657.375244*	329.191260	640.348695	320.677986	3
8	*1113.612515*	557.309896	1096.585966	548.796621	A	*218.149918*	109.578597	201.123369	101.065322	2
9					K	147.112804	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.1	1258.710754	0.006314	GYILVGQAK
9.8	1258.721970	-0.004902	GYILQAKR
6.4	1258.717941	-0.000873	RILAKVQEMR
0.6	1258.706726	0.010342	QIAVKVEKCGK

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

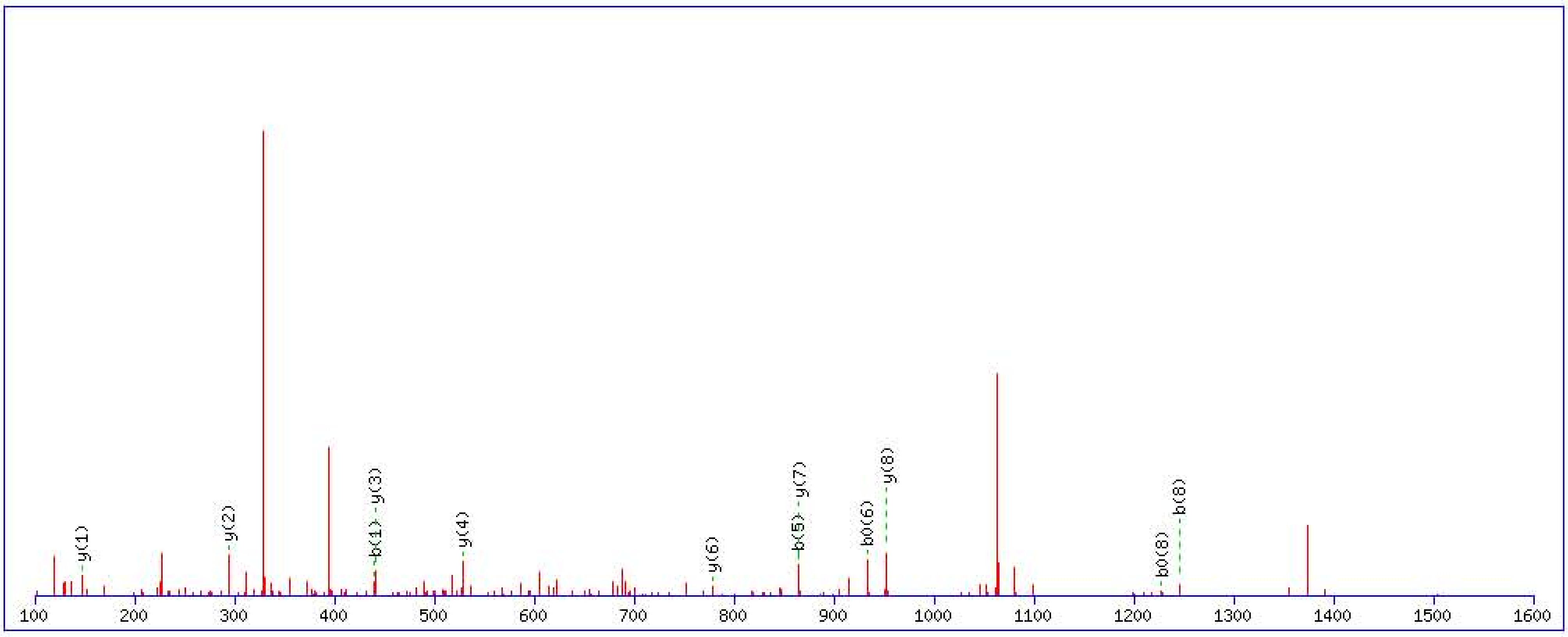
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSSSYSFFK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

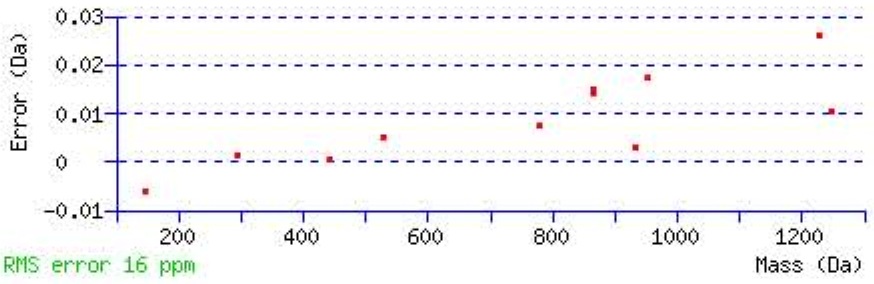
Match to Query 34176: 1390.673988 from(696.344270,2+) rtinseconds(2118) index(42848)
Title: Locus:1.1.1.3021.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

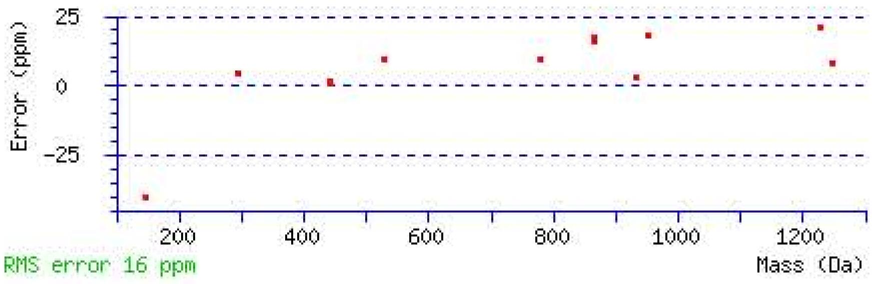
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1390.659119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0014
Matches : 12/88 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**440.232602**	220.619939	423.206053	212.106664			**Q**							9
2	527.264630	264.135953	510.238081	255.622679	509.254065	255.130671	**S**	***952.441073***	476.724175	935.414524	468.210900	934.430508	467.718892	8
3	614.296658	307.651967	597.270109	299.138692	596.286093	298.646684	**S**	***865.409045***	433.208161	848.382496	424.694886	847.398480	424.202878	7
4	701.328686	351.167981	684.302137	342.654706	683.318121	342.162698	**S**	***778.377017***	389.692147	761.350468	381.178872	760.366452	380.686864	6
5	**864.392015**	432.699645	847.365466	424.186371	846.381450	423.694363	**Y**	691.344989	346.176133	674.318440	337.662858	673.334424	337.170850	5
6	951.424043	476.215659	934.397494	467.702385	933.413478	467.210377	**S**	***528.281660***	264.644468	511.255111	256.131194	510.271095	255.639186	4
7	1098.492457	549.749866	1081.465908	541.236592	1080.481892	540.744584	**F**	***441.249632***	221.128454	424.223083	212.615180			3
8	**1245.560871**	623.284073	1228.534322	614.770799	1227.550306	614.278791	**F**	***294.181218***	147.594247	277.154669	139.080973			2
9							**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.2	1390.659119	0.014869	QSSSYSFFK
8.4	1390.691467	-0.017479	VTKEMNEFIHK
5.9	1390.657547	0.016441	EEGAASTAEEAAKK
4.0	1390.670135	0.003853	YRNQESKSSHR
3.8	1390.655075	0.018913	IHEQDQLYSMK
2.9	1390.659088	0.014900	YFSKKEWEMK
2.4	1390.669678	0.004310	CAPASIRLMDNK
2.0	1390.676208	-0.002220	AEKSSSTDQK
1.8	1390.694839	-0.020851	SLKSDMMSHLVK
1.8	1390.694839	-0.020851	SLKSDMMSHLVK

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

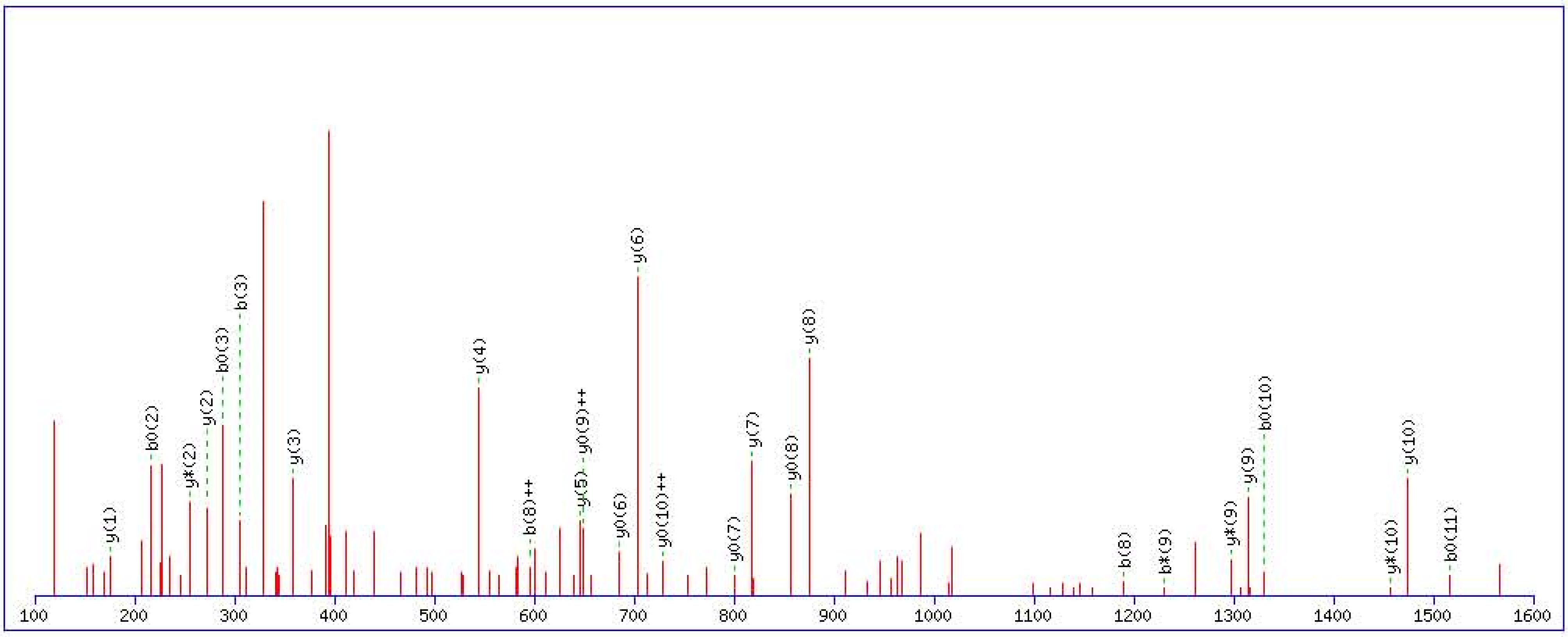
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSAICQGDGTWSPR**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

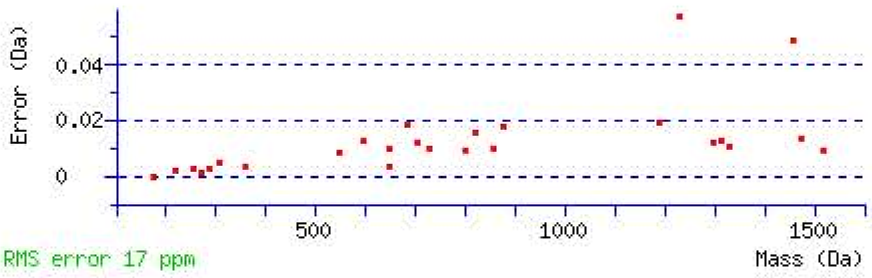
Match to Query 50437: 1891.887852 from(631.636560,3+) rtinseconds(2124) index(42876)
Title: Locus:1.1.1.3023.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

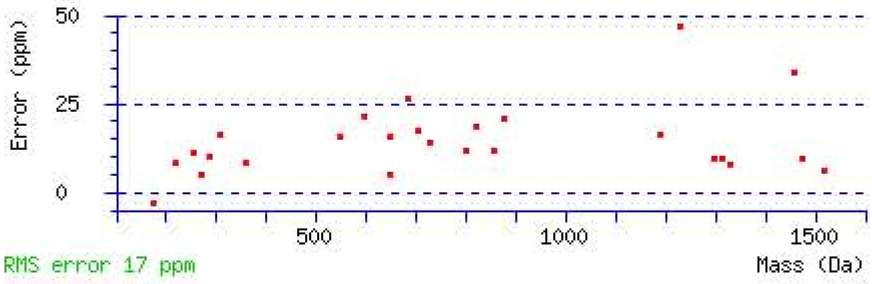
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1891.870941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 42 **Expect:** 0.00089
Matches : 26/140 fragment ions using 61 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							14
2	235.107718	118.057497			217.097153	109.052214	S	1745.809788	873.408532	1728.783239	864.895258	1727.799223	864.403250	13
3	**306.144832**	153.576054			288.134267	144.570772	A	1658.777760	829.892518	1641.751211	821.379244	1640.767195	820.887236	12
4	419.228896	210.118086			401.218331	201.112804	I	1587.740646	794.373961	1570.714097	785.860687	1569.730081	785.368678	11
5	579.259545	290.133411			561.248980	281.128128	C	***1474.656582***	737.831929	1457.630033	729.318655	1456.646017	728.826647	10
6	1018.484871	509.746074	1001.458322	501.232799	1000.474306	500.740791	Q	***1314.625933***	657.816605	1297.599384	649.303330	1296.615368	648.811322	9
7	1075.506335	538.256806	1058.479786	529.743531	1057.495770	529.251523	G	***875.400607***	438.203942	858.374058	429.690667	857.390042	429.198659	8
8	**1190.533278**	595.770277	1173.506729	587.257003	1172.522713	586.764995	D	***818.379143***	409.693210	801.352594	401.179935	800.368578	400.687927	7
9	1247.554742	624.281009	1230.528193	615.767735	1229.544177	615.275727	G	***703.352200***	352.179738	686.325651	343.666464	685.341635	343.174456	6
10	1348.602421	674.804849	1331.575872	666.291574	1330.591856	665.799566	T	***646.330736***	323.669006	629.304187	315.155732	628.320171	314.663724	5
11	1534.681734	767.844505	1517.655185	759.331231	1516.671169	758.839223	W	***545.283057***	273.145167	528.256508	264.631892	527.272492	264.139884	4
12	1621.713762	811.360519	1604.687213	802.847245	1603.703197	802.355237	S	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
13	1718.766526	859.886901	1701.739977	851.373627	1700.755961	850.881619	P	***272.171716***	136.589496	255.145167	128.076221			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.2	1891.870941	0.016911	FSAICQGDGTWSPR

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

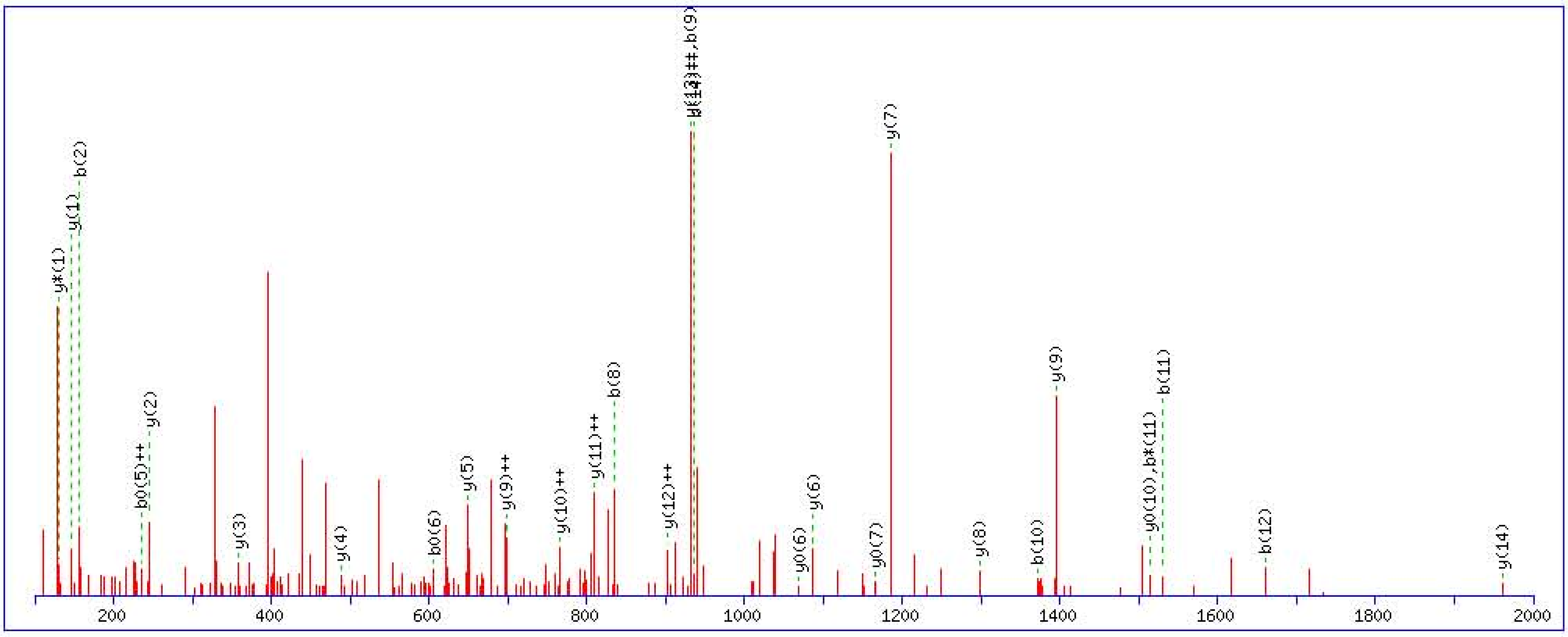
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVGWSHPLPQCEIVK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

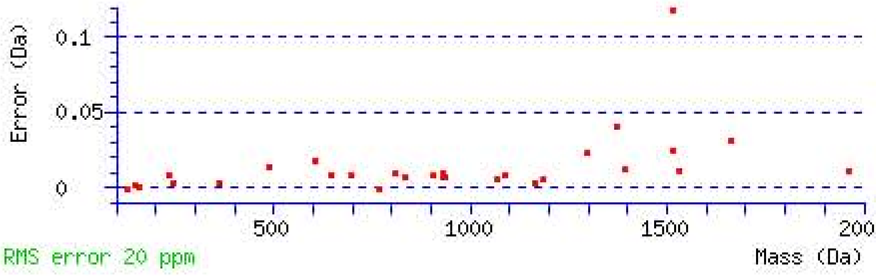
Match to Query 54214: 2017.042332 from(673.354720,3+) rtinseconds(2046) index(42411)
Title: Locus:1.1.1.2996.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

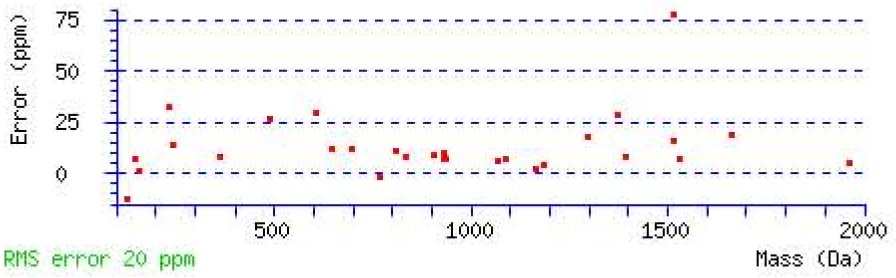


```
Monoisotopic mass of neutral peptide Mr(calc): 2017.027771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.032
Matches : 29/136 fragment ions using 91 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							15
2	**157.097154**	79.052215					V	***1961.013573***	981.010425	1943.987024	972.497150	1943.003008	972.005142	14
3	214.118618	107.562947					G	1861.945159	931.476217	1844.918610	922.962943	1843.934594	922.470935	13
4	400.197931	200.602603					W	1804.923695	902.965486	1787.897146	894.452211	1786.913130	893.960203	12
5	487.229959	244.118617			469.219394	235.113335	S	1618.844382	809.925829	1601.817833	801.412555	1600.833817	800.920547	11
6	624.288871	312.648074			606.278306	303.642791	H	1531.812354	766.409815	1514.785805	757.896541	1513.801789	757.404532	10
7	721.341635	361.174456			703.331070	352.169173	P	***1394.753442***	697.880359	1377.726893	689.367085	1376.742877	688.875076	9
8	**834.425699**	417.716488			816.415134	408.711205	L	***1297.700678***	649.353977	1280.674129	640.840703	1279.690113	640.348694	8
9	**931.478463**	466.242870			913.467898	457.237587	P	***1184.616614***	592.811945	1167.590065	584.298670	1166.606049	583.806662	7
10	**1370.703789**	685.855532	1353.677240	677.342258	1352.693224	676.850250	Q	***1087.563850***	544.285563	1070.537301	535.772288	1069.553285	535.280280	6
11	**1530.734438**	765.870857	1513.707889	757.357583	1512.723873	756.865574	C	***648.338524***	324.672900	631.311975	316.159626	630.327959	315.667618	5
12	**1659.777031**	830.392153	1642.750482	821.878879	1641.766466	821.386871	E	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.652293	4
13	1772.861095	886.934185	1755.834546	878.420911	1754.850530	877.928903	I	***359.265282***	180.136279	342.238733	171.623004			3
14	1871.929509	936.468392	1854.902960	927.955118	1853.918944	927.463110	V	***246.181218***	123.594247	229.154669	115.080973			2
15							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 20 ppm



RMS error 20 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.8	2017.027771	0.014561	GVGWSHPLPQCEIVK

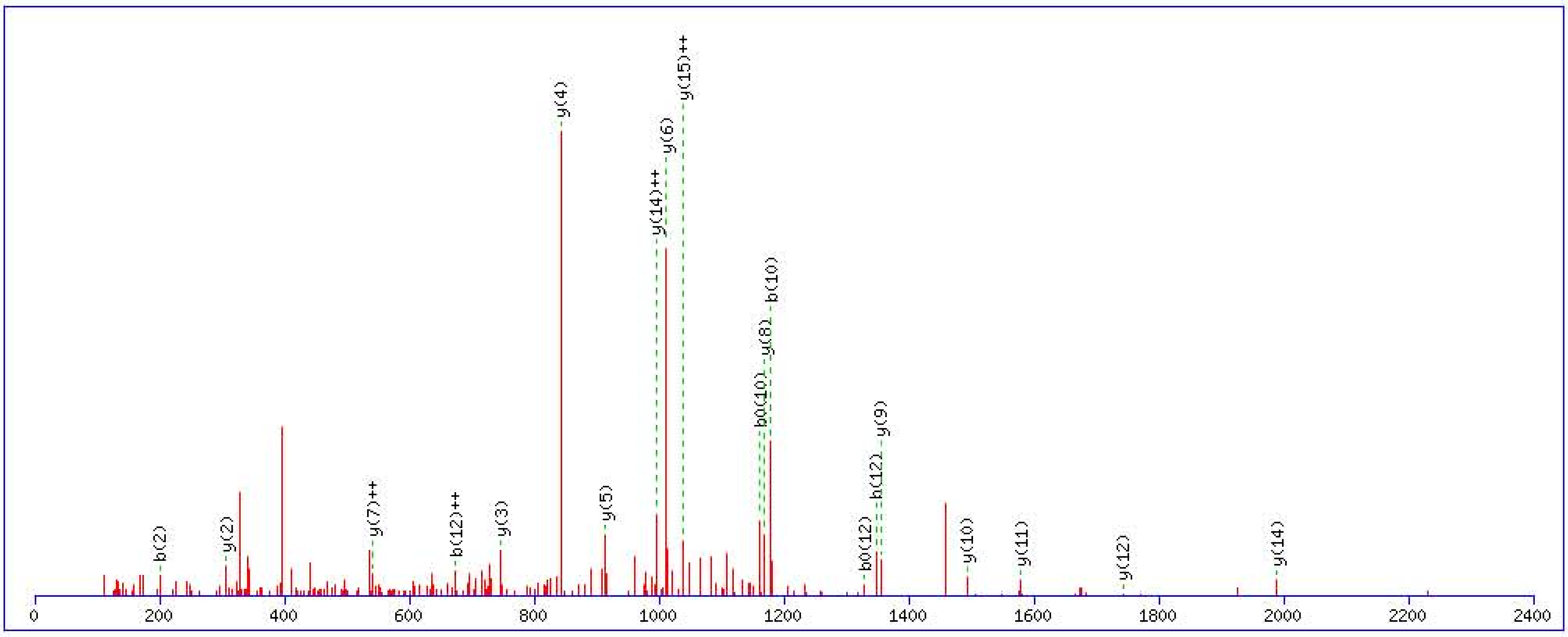
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSCSYSHWSAPAPQCK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

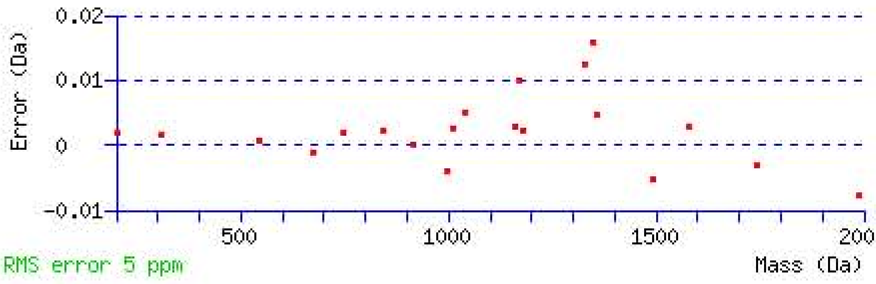
Match to Query 57931: 2188.996542 from(730.672790,3+) rtinseconds(1750) index(40439)
Title: Locus:1.1.1.2893.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

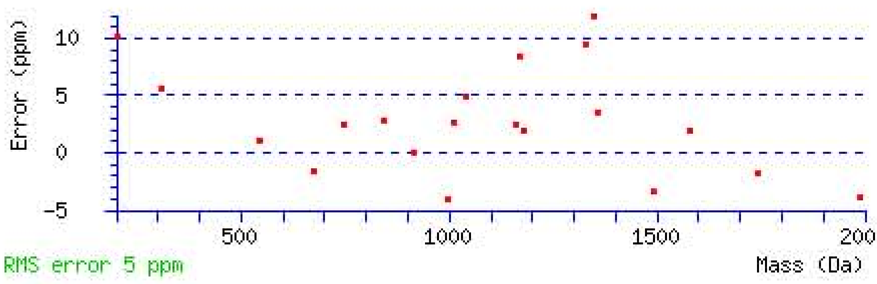
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2188.985626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00033
Matches : 20/138 fragment ions using 53 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	114.091340	57.549308					L							16
2	**201.123368**	101.065322			183.112803	92.060039	S	2076.908850	1038.958063	2059.882301	1030.444788	2058.898285	1029.952780	15
3	361.154017	181.080647			343.143452	172.075364	C	***1989.876822***	995.442049	1972.850273	986.928775	1971.866257	986.436767	14
4	448.186045	224.596660			430.175480	215.591378	S	1829.846173	915.426725	1812.819624	906.913450	1811.835608	906.421442	13
5	611.249374	306.128325			593.238809	297.123043	Y	***1742.814145***	871.910711	1725.787596	863.397436	1724.803580	862.905428	12
6	698.281402	349.644339			680.270837	340.639056	S	***1579.750816***	790.379046	1562.724267	781.865772	1561.740251	781.373764	11
7	835.340314	418.173795			817.329749	409.168512	H	***1492.718788***	746.863032	1475.692239	738.349758	1474.708223	737.857750	10
8	1021.419627	511.213452			1003.409062	502.208169	W	***1355.659876***	678.333576	1338.633327	669.820302	1337.649311	669.328294	9
9	1108.451655	554.729466			1090.441090	545.724183	S	***1169.580563***	585.293920	1152.554014	576.780645	1151.569998	576.288637	8
10	**1179.488769**	590.248023			1161.478204	581.242740	A	1082.548535	541.777906	1065.521986	533.264631			7
11	1276.541533	638.774405			1258.530968	629.769122	P	***1011.511421***	506.259349	994.484872	497.746074			6
12	**1347.578647**	674.292962			1329.568082	665.287679	A	***914.458657***	457.732967	897.432108	449.219692			5
13	1444.631411	722.819344			1426.620846	713.814061	P	***843.421543***	422.214410	826.394994	413.701135			4
14	1883.856737	942.432007	1866.830188	933.918732	1865.846172	933.426724	Q	***746.368779***	373.688028	729.342230	365.174753			3
15	2043.887386	1022.447331	2026.860837	1013.934057	2025.876821	1013.442049	C	***307.143453***	154.075365	290.116904	145.562090			2
16							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.5	2188.985626	0.010916	LSCSYSHWSAPAPQCK

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

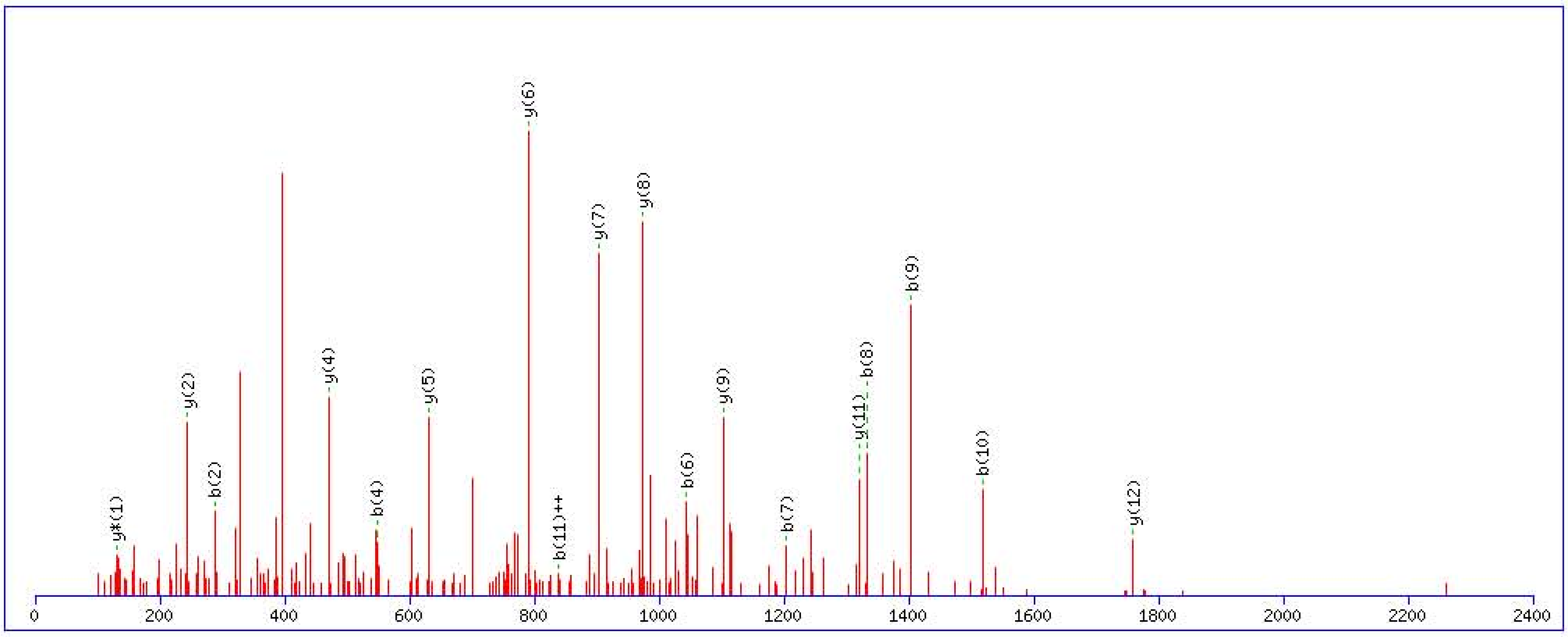
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WTPYQGCEALCCPEPK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

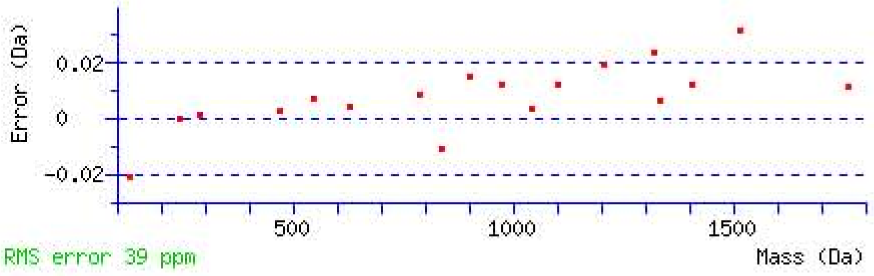
Match to Query 60818: 2306.025882 from(769.682570,3+) rtinseconds(2093) index(42701)
Title: Locus:1.1.1.3012.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

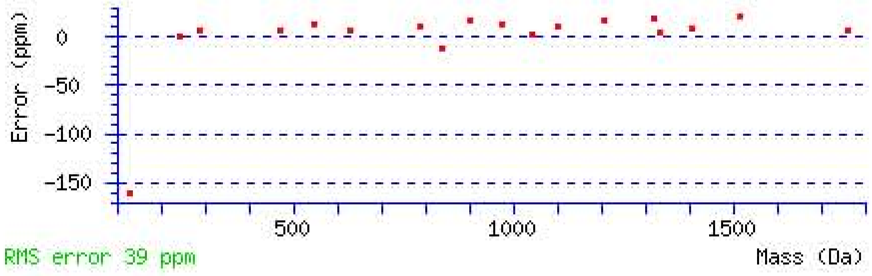


Monoisotopic mass of neutral peptide Mr(calc): 2305.999237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 48 **Expect:** 0.00013
Matches : 18/166 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932					W							16
2	***288.134268***	144.570772			270.123703	135.565490	T	2120.927205	1060.967240	2103.900656	1052.453966	2102.916640	1051.961958	15
3	385.187032	193.097154			367.176467	184.091872	P	2019.879526	1010.443401	2002.852977	1001.930127	2001.868961	1001.438119	14
4	***548.250361***	274.628819			530.239796	265.623536	Y	1922.826762	961.917019	1905.800213	953.403745	1904.816197	952.911737	13
5	987.475687	494.241482	970.449138	485.728207	969.465122	485.236199	Q	***1759.763433***	880.385355	1742.736884	871.872080	1741.752868	871.380072	12
6	***1044.497151***	522.752214	1027.470602	514.238939	1026.486586	513.746931	G	***1320.538107***	660.772692	1303.511558	652.259417	1302.527542	651.767409	11
7	***1204.527800***	602.767538	1187.501251	594.254264	1186.517235	593.762256	C	1263.516643	632.261960	1246.490094	623.748685	1245.506078	623.256677	10
8	***1333.570393***	667.288835	1316.543844	658.775560	1315.559828	658.283552	E	***1103.485994***	552.246635	1086.459445	543.733361	1085.475429	543.241353	9
9	***1404.607507***	702.807392	1387.580958	694.294117	1386.596942	693.802109	A	***974.443401***	487.725339	957.416852	479.212064	956.432836	478.720056	8
10	***1517.691571***	759.349424	1500.665022	750.836149	1499.681006	750.344141	L	***903.406287***	452.206782	886.379738	443.693507	885.395722	443.201499	7
11	1677.722220	839.364748	1660.695671	830.851474	1659.711655	830.359466	C	***790.322223***	395.664750	773.295674	387.151475	772.311658	386.659467	6
12	1837.752869	919.380073	1820.726320	910.866798	1819.742304	910.374790	C	***630.291574***	315.649425	613.265025	307.136151	612.281009	306.644143	5
13	1934.805633	967.906455	1917.779084	959.393180	1916.795068	958.901172	P	***470.260925***	235.634101	453.234376	227.120826	452.250360	226.628818	4
14	2063.848226	1032.427751	2046.821677	1023.914477	2045.837661	1023.422469	E	373.208161	187.107719	356.181612	178.594444	355.197596	178.102436	3
15	2160.900990	1080.954133	2143.874441	1072.440858	2142.890425	1071.948850	P	***244.165568***	122.586422	227.139019	114.073148			2
16							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 39 ppm



RMS error 39 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.5	2305.999237	0.026645	WTPYQGCEALCCPEPK

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

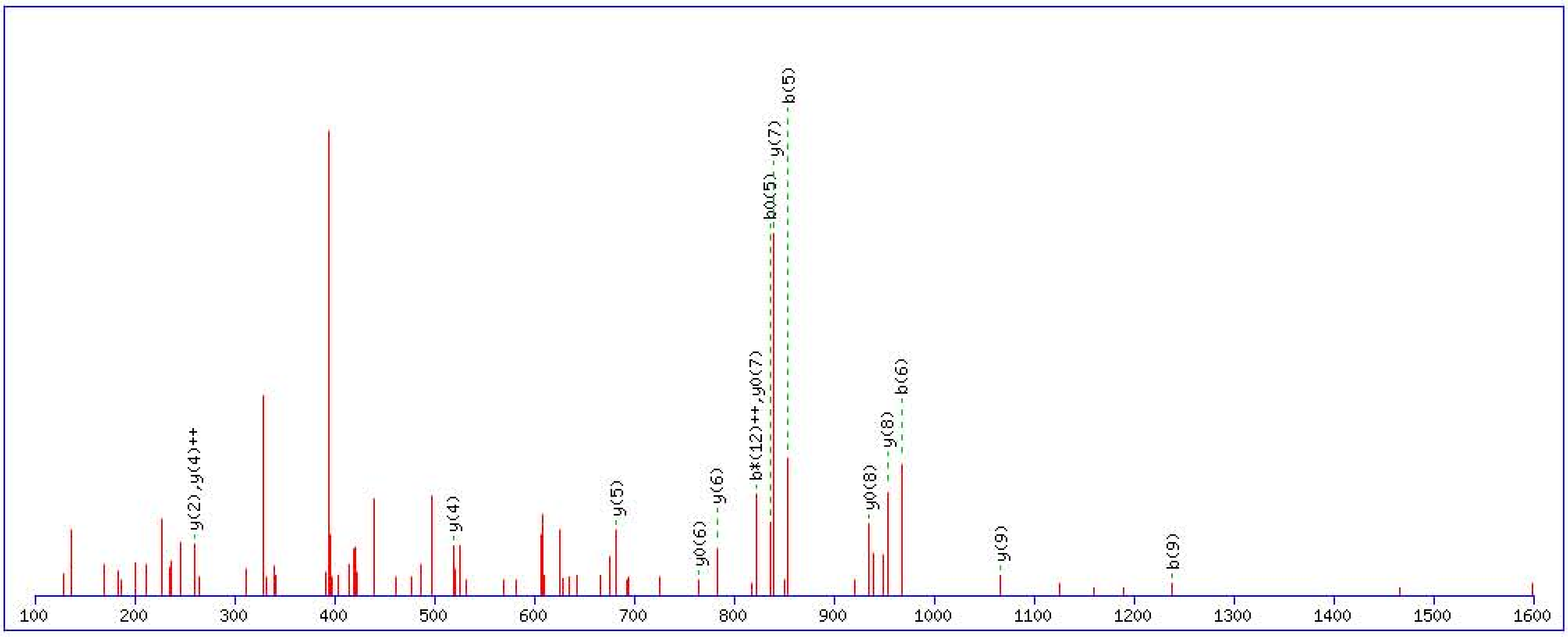
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVEGQILGTYVCIK**
Found in **C4BPB_HUMAN**, C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1

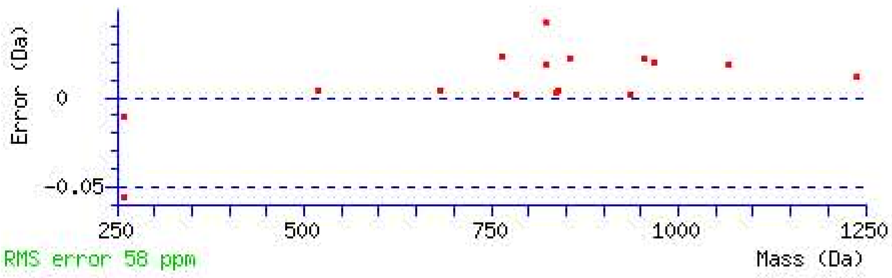
Match to Query 51002: 1919.012082 from(640.677970,3+) rtinseconds(2459) index(44987)
Title: Locus:1.1.1.3140.6 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

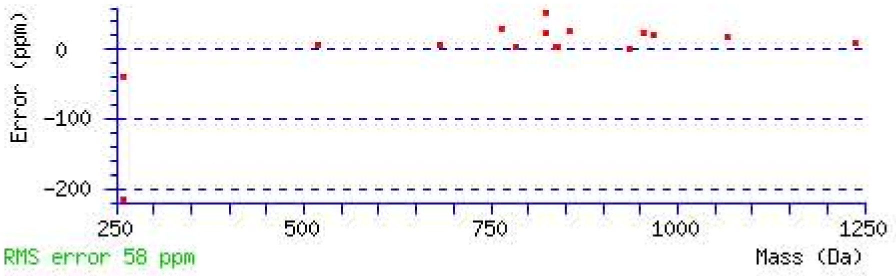
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1918.989639
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.06
Matches : 16/138 fragment ions using 34 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							14
2	229.118283	115.062780			211.107718	106.057497	V	1790.954328	895.980802	1773.927779	887.467528	1772.943763	886.975520	13
3	358.160876	179.584076			340.150311	170.578794	E	1691.885914	846.446595	1674.859365	837.933321	1673.875349	837.441313	12
4	415.182340	208.094808			397.171775	199.089526	G	1562.843321	781.925299	1545.816772	773.412024	1544.832756	772.920016	11
5	**854.407666**	427.707471	837.381117	419.194197	836.397101	418.702189	Q	1505.821857	753.414567	1488.795308	744.901292	1487.811292	744.409284	10
6	**967.491730**	484.249503	950.465181	475.736229	949.481165	475.244221	I	***1066.596531***	533.801904	1049.569982	525.288629	1048.585966	524.796621	9
7	1080.575794	540.791535	1063.549245	532.278261	1062.565229	531.786253	L	***953.512467***	477.259872	936.485918	468.746597	935.501902	468.254589	8
8	1137.597258	569.302267	1120.570709	560.788993	1119.586693	560.296985	G	***840.428403***	420.717840	823.401854	412.204565	822.417838	411.712557	7
9	**1238.644937**	619.826107	1221.618388	611.312832	1220.634372	610.820824	T	***783.406939***	392.207108	766.380390	383.693833	765.396374	383.201825	6
10	1401.708266	701.357771	1384.681717	692.844497	1383.697701	692.352489	Y	***682.359260***	341.683268	665.332711	333.169994			5
11	1500.776680	750.891978	1483.750131	742.378704	1482.766115	741.886696	V	***519.295931***	260.151604	502.269382	251.638329			4
12	1660.807329	830.907303	1643.780780	822.394028	1642.796764	821.902020	C	420.227517	210.617396	403.200968	202.104122			3
13	1773.891393	887.449335	1756.864844	878.936060	1755.880828	878.444052	I	***260.196868***	130.602072	243.170319	122.088797			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.0	1918.989639	0.022443	EVEGQILGTYVCIK

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

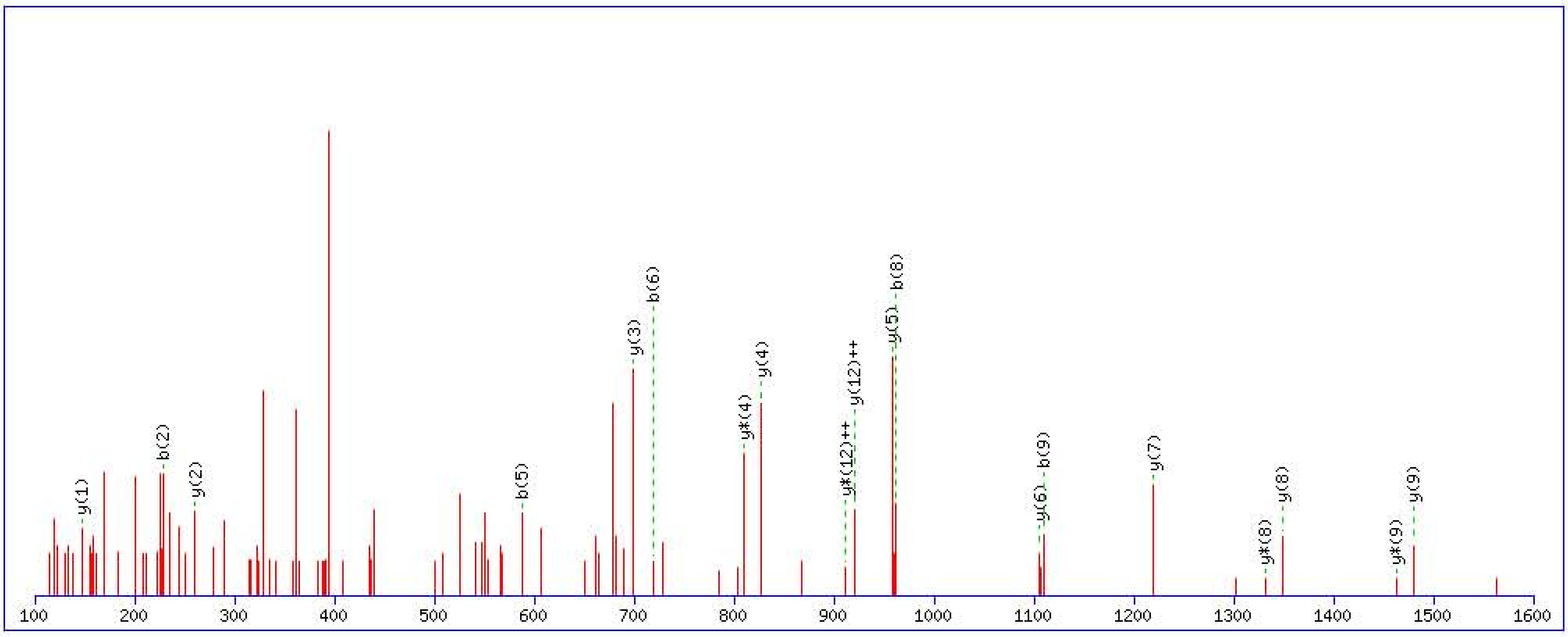
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLCEAMENFMQQLK**
Found in **C4BPB_HUMAN**, C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1

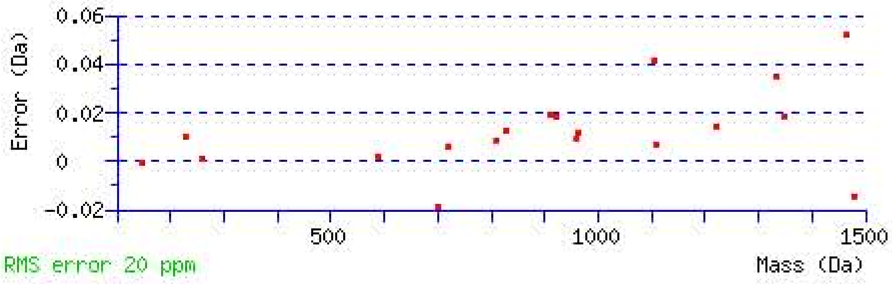
Match to Query 55365: 2065.965972 from(689.662600,3+) rtinseconds(3066) index(49347)
Title: Locus:1.1.1.3348.4 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

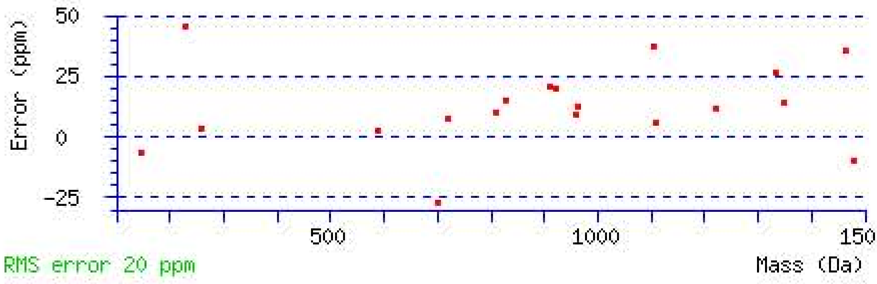
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2065.945709
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0045
Matches : 19/136 fragment ions using 45 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							14
2	**228.134267**	114.570771	211.107718	106.057497			L	1952.910096	976.958686	1935.883547	968.445412	1934.899531	967.953404	13
3	388.164916	194.586096	371.138367	186.072822			C	1839.826032	920.416654	1822.799483	911.903380	1821.815467	911.411371	12
4	517.207509	259.107393	500.180960	250.594118	499.196944	250.102110	E	1679.795383	840.401329	1662.768834	831.888055	1661.784818	831.396047	11
5	**588.244623**	294.625950	571.218074	286.112675	570.234058	285.620667	A	1550.752790	775.880033	1533.726241	767.366759	1532.742225	766.874751	10
6	**719.285108**	360.146192	702.258559	351.632918	701.274543	351.140910	M	***1479.715676***	740.361476	1462.689127	731.848202	1461.705111	731.356194	9
7	848.327701	424.667489	831.301152	416.154214	830.317136	415.662206	E	***1348.675191***	674.841234	1331.648642	666.327959	1330.664626	665.835951	8
8	**962.370628**	481.688952	945.344079	473.175678	944.360063	472.683670	N	***1219.632598***	610.319937	1202.606049	601.806663			7
9	**1109.439042**	555.223159	1092.412493	546.709885	1091.428477	546.217876	F	***1105.589671***	553.298474	1088.563122	544.785199			6
10	1240.479527	620.743402	1223.452978	612.230127	1222.468962	611.738119	M	***958.521257***	479.764267	941.494708	471.250992			5
11	1368.538105	684.772690	1351.511556	676.259416	1350.527540	675.767408	Q	***827.480772***	414.244024	810.454223	405.730750			4
12	1807.763431	904.385354	1790.736882	895.872079	1789.752866	895.380071	Q	***699.422194***	350.214735	682.395645	341.701461			3
13	1920.847495	960.927386	1903.820946	952.414111	1902.836930	951.922103	L	***260.196868***	130.602072	243.170319	122.088797			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.3	2065.945709	0.020263	NLCEAMENFMQQLK
26.2	2065.945709	0.020263	NLCEAMENFMQQLK

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

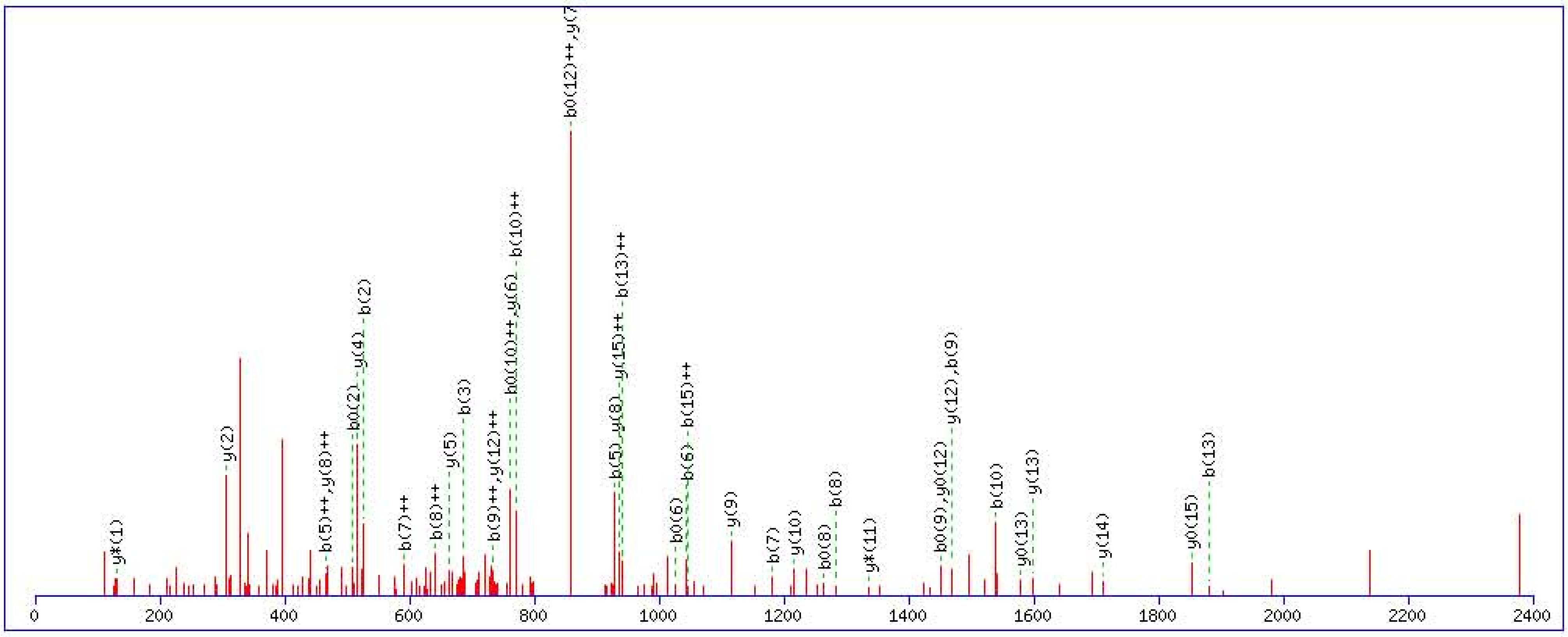
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQCLEDHTWAPPFPICK**
Found in **C4BPB_HUMAN**, C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1

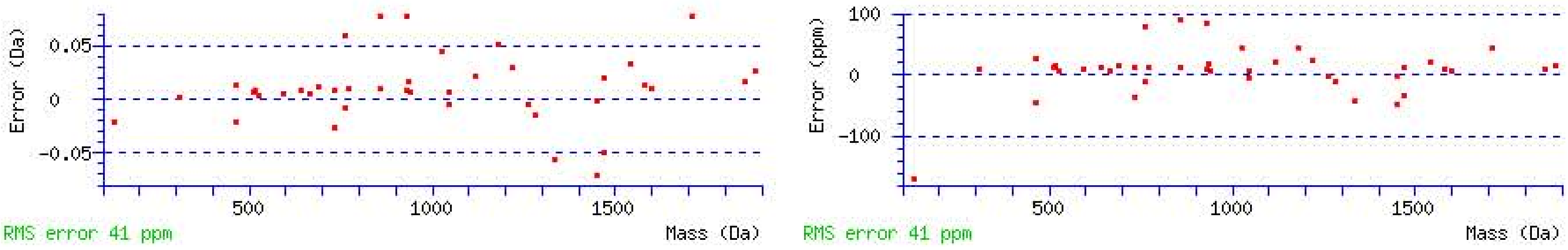
Match to Query 62265: 2396.138742 from(799.720190,3+) rtinseconds(2319) index(44154)
Title: Locus:1.1.1.3091.17 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2396.111572
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 47 **Expect:** 0.00038
Matches : 41/172 fragment ions using 75 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							17
2	***527.264630***	264.135953	510.238081	255.622679	509.254065	255.130671	Q	2310.086816	1155.547046	2293.060267	1147.033771	2292.076251	1146.541763	16
3	***687.295279***	344.151278	670.268730	335.638003	669.284714	335.145995	C	1870.861490	935.934383	1853.834941	927.421109	1852.850925	926.929101	15
4	800.379343	400.693310	783.352794	392.180035	782.368778	391.688027	L	***1710.830841***	855.919058	1693.804292	847.405784	1692.820276	846.913776	14
5	***929.421936***	**465.214606**	912.395387	456.701332	911.411371	456.209324	E	***1597.746777***	799.377026	1580.720228	790.863752	1579.736212	790.371744	13
6	***1044.448879***	522.728078	1027.422330	514.214803	1026.438314	513.722795	D	***1468.704184***	734.855730	1451.677635	726.342456	1450.693619	725.850447	12
7	***1181.507791***	**591.257534**	1164.481242	582.744259	1163.497226	582.252251	H	1353.677241	677.342258	1336.650692	668.828984	1335.666676	668.336976	11
8	***1282.555470***	**641.781373**	1265.528921	633.268099	1264.544905	632.776091	T	***1216.618329***	608.812802	1199.591780	600.299528	1198.607764	599.807520	10
9	***1468.634783***	**734.821030**	1451.608234	726.307755	1450.624218	725.815747	W	***1115.570650***	558.288963	1098.544101	549.775689			9
10	***1539.671897***	**770.339587**	1522.645348	761.826312	1521.661332	761.334304	A	***929.491337***	465.249306	912.464788	456.736032			8
11	1636.724661	818.865969	1619.698112	810.352694	1618.714096	809.860686	P	***858.454223***	429.730750	841.427674	421.217475			7
12	1733.777425	867.392351	1716.750876	858.879076	1715.766860	858.387068	P	***761.401459***	381.204367	744.374910	372.691093			6
13	***1880.845839***	**940.926558**	1863.819290	932.413283	1862.835274	931.921275	F	***664.348695***	332.677985	647.322146	324.164711			5
14	1977.898603	989.452940	1960.872054	980.939665	1959.888038	980.447657	P	***517.280281***	259.143778	500.253732	250.630504			4
15	2090.982667	**1045.994971**	2073.956118	1037.481697	2072.972102	1036.989689	I	420.227517	210.617396	403.200968	202.104122			3
16	2251.013316	1126.010296	2233.986767	1117.497021	2233.002751	1117.005013	C	***307.143453***	154.075364	290.116904	145.562090			2
17							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.5	2396.111572	0.027170	SQCLEDHTWAPPFPICK

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

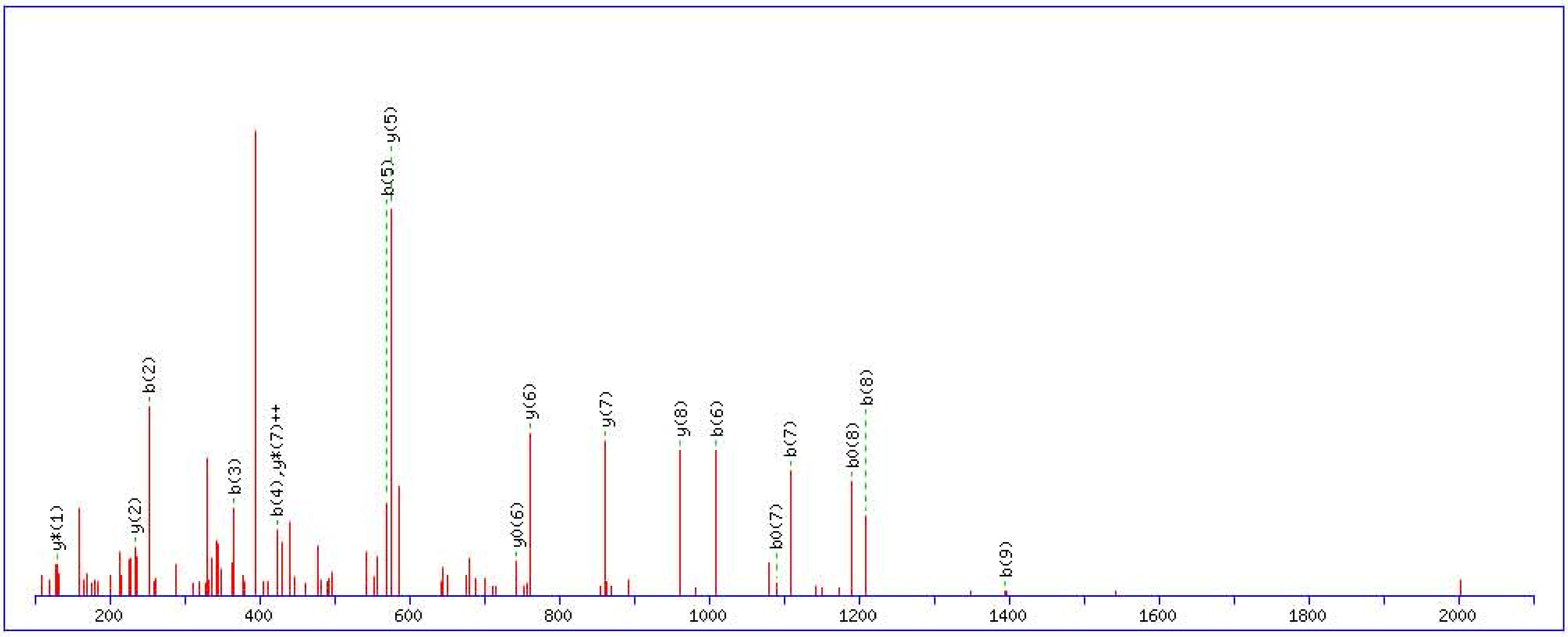
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DHLGFQVTWPDESK**
Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

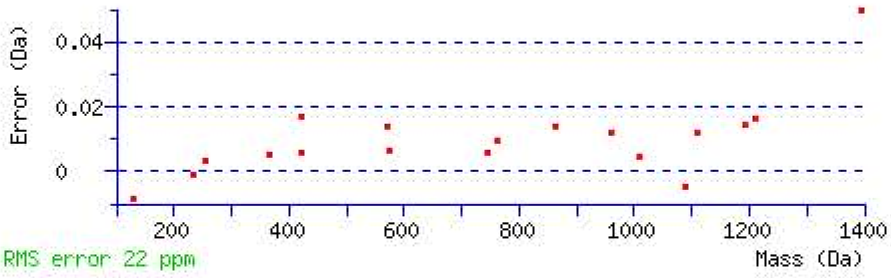
Match to Query 52253: 1968.955362 from(657.325730,3+) rtinseconds(2284) index(43962)
Title: Locus:1.1.1.3079.9 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

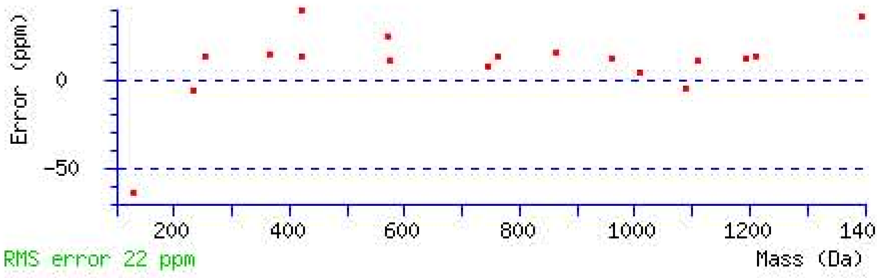
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1968.940399
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.0027
Matches : 18/144 fragment ions using 37 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							14
2	***253.093131***	127.050203			235.082566	118.044921	H	1854.920718	927.963997	1837.894169	919.450723	1836.910153	918.958715	13
3	***366.177195***	183.592235			348.166630	174.586953	L	1717.861806	859.434541	1700.835257	850.921267	1699.851241	850.429259	12
4	***423.198659***	212.102967			405.188094	203.097685	G	1604.777742	802.892509	1587.751193	794.379235	1586.767177	793.887227	11
5	***570.267073***	285.637175			552.256508	276.631892	F	1547.756278	774.381777	1530.729729	765.868503	1529.745713	765.376495	10
6	***1009.492399***	505.249838	992.465850	496.736563	991.481834	496.244555	Q	1400.687864	700.847570	1383.661315	692.334296	1382.677299	691.842288	9
7	***1108.560813***	554.784045	1091.534264	546.270770	1090.550248	545.778762	V	**961.462538**	481.234907	944.435989	472.721633	943.451973	472.229625	8
8	***1209.608492***	605.307884	1192.581943	596.794610	1191.597927	596.302602	T	**862.394124**	431.700700	845.367575	423.187426	844.383559	422.695418	7
9	***1395.687805***	698.347541	1378.661256	689.834266	1377.677240	689.342258	W	**761.346445**	381.176861	744.319896	372.663586	743.335880	372.171578	6
10	1492.740569	746.873923	1475.714020	738.360648	1474.730004	737.868640	P	**575.267132**	288.137204	558.240583	279.623930	557.256567	279.131922	5
11	1607.767512	804.387394	1590.740963	795.874120	1589.756947	795.382112	D	478.214368	239.610822	461.187819	231.097548	460.203803	230.605540	4
12	1736.810105	868.908691	1719.783556	860.395416	1718.799540	859.903408	E	363.187425	182.097351	346.160876	173.584076	345.176860	173.092068	3
13	1823.842133	912.424705	1806.815584	903.911430	1805.831568	903.419422	S	**234.144832**	117.576054	217.118283	109.062780	216.134267	108.570772	2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.3	1968.940399	0.014963	DHLGFQVTWPDESK
8.9	1968.949585	0.005777	EGQMESVEAAMSSKTLKK

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

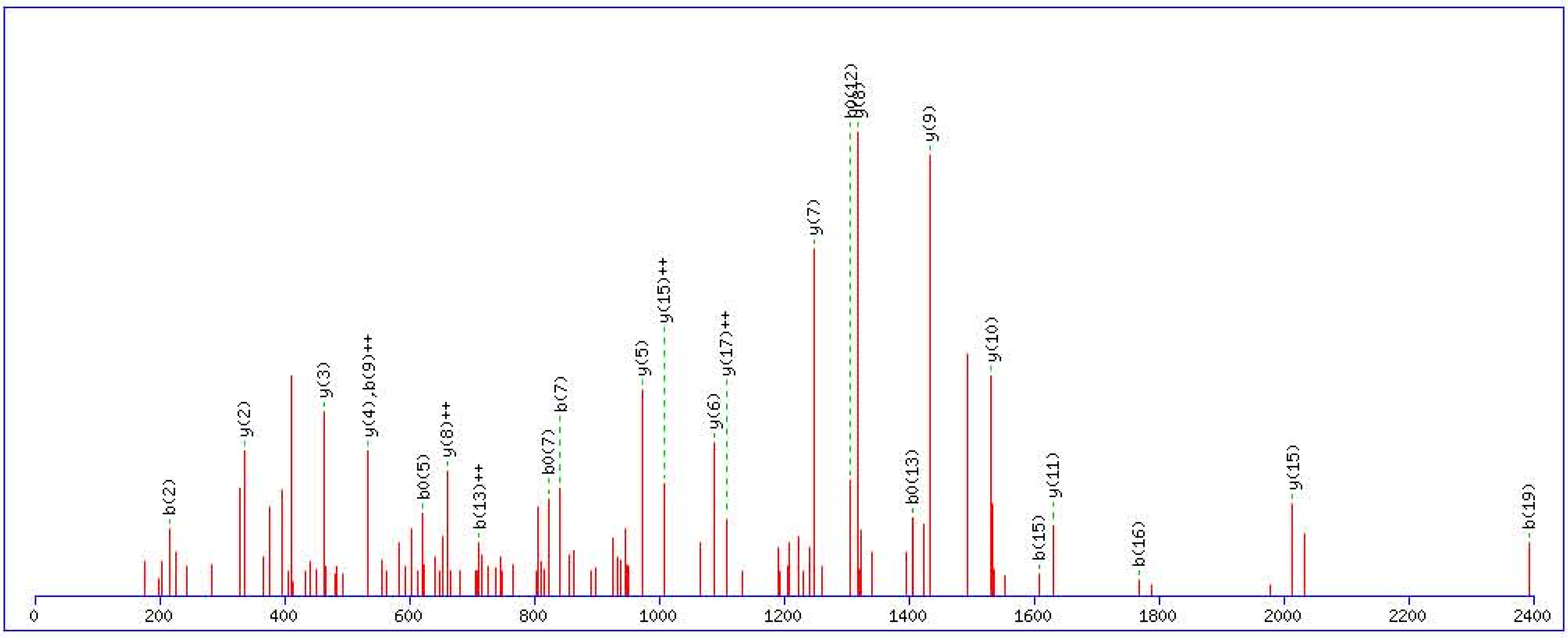
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQCTYSNPEGTVVLACDQAQCR**
Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

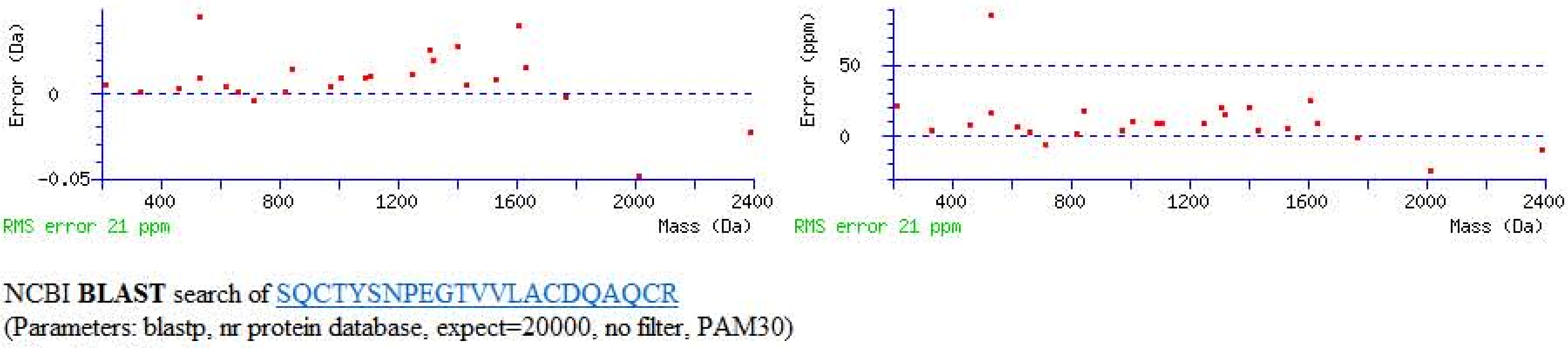
Match to Query 69839: 2854.278822 from(952.433550,3+) rtinseconds(2038) index(42362)
Title: Locus:1.1.1.2993.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2854.250671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 71  Expect: 6.6e-007
Matches : 25/240 fragment ions using 35 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							22
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	Q	2768.225907	1384.616591	2751.199358	1376.103317	2750.215342	1375.611309	21
3	376.128531	188.567904	359.101982	180.054629	358.117966	179.562621	C	2640.167329	1320.587302	2623.140780	1312.074028	2622.156764	1311.582020	20
4	477.176210	239.091743	460.149661	230.578469	459.165645	230.086461	T	2480.136680	1240.571978	2463.110131	1232.058703	2462.126115	1231.566695	19
5	640.239539	320.623408	623.212990	312.110133	622.228974	311.618125	Y	2379.089001	1190.048138	2362.062452	1181.534864	2361.078436	1181.042856	18
6	727.271567	364.139422	710.245018	355.626147	709.261002	355.134139	S	2216.025672	1108.516474	2198.999123	1100.003199	2198.015107	1099.511191	17
7	**841.314494**	421.160885	824.287945	412.647611	823.303929	412.155603	N	2128.993644	1065.000460	2111.967095	1056.487185	2110.983079	1055.995177	16
8	938.367258	469.687267	921.340709	461.173993	920.356693	460.681985	P	***2014.950717***	1007.978997	1997.924168	999.465722	1996.940152	998.973714	15
9	1067.409851	**534.208564**	1050.383302	525.695289	1049.399286	525.203281	E	1917.897953	959.452615	1900.871404	950.939340	1899.887388	950.447332	14
10	1124.431315	562.719296	1107.404766	554.206021	1106.420750	553.714013	G	1788.855360	894.931318	1771.828811	886.418044	1770.844795	885.926036	13
11	1225.478994	613.243135	1208.452445	604.729861	1207.468429	604.237853	T	1731.833896	866.420586	1714.807347	857.907312	1713.823331	857.415304	12
12	1324.547408	662.777342	1307.520859	654.264068	1306.536843	653.772060	V	***1630.786217***	815.896747	1613.759668	807.383472	1612.775652	806.891464	11
13	1423.615822	**712.311549**	1406.589273	703.798275	1405.605257	703.306267	V	***1531.717803***	766.362540	1514.691254	757.849265	1513.707238	757.357257	10
14	1536.699886	768.853581	1519.673337	760.340307	1518.689321	759.848299	L	***1432.649389***	716.828333	1415.622840	708.315058	1414.638824	707.823050	9
15	**1607.737000**	804.372138	1590.710451	795.858864	1589.726435	795.366856	A	***1319.565325***	660.286301	1302.538776	651.773026	1301.554760	651.281018	8
16	**1767.767649**	884.387463	1750.741100	875.874188	1749.757084	875.382180	C	***1248.528211***	624.767744	1231.501662	616.254469	1230.517646	615.762461	7
17	1882.794592	941.900934	1865.768043	933.387660	1864.784027	932.895652	D	***1088.497562***	544.752419	1071.471013	536.239145	1070.486997	535.747137	6
18	2322.019918	1161.513597	2304.993369	1153.000322	2304.009353	1152.508314	Q	***973.470619***	487.238948	956.444070	478.725673			5
19	**2393.057032**	1197.032154	2376.030483	1188.518879	2375.046467	1188.026872	A	***534.245293***	267.626285	517.218744	259.113010			4
20	2521.115610	1261.061443	2504.089061	1252.548169	2503.105045	1252.056161	Q	***463.208179***	232.107727	446.181630	223.594453			3
21	2681.146259	1341.076768	2664.119710	1332.563493	2663.135694	1332.071485	C	***335.149601***	168.078438	318.123052	159.565164			2
22							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.8	2854.250671	0.028151	SQCTYSNPEGTVVLACDQAQCR
54.0	2854.250671	0.028151	SQCTYSNPEGTVVLACDQAQCR
1.1	2854.250671	0.028151	SQCTYSNPEGTVVLACDQAQCR

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

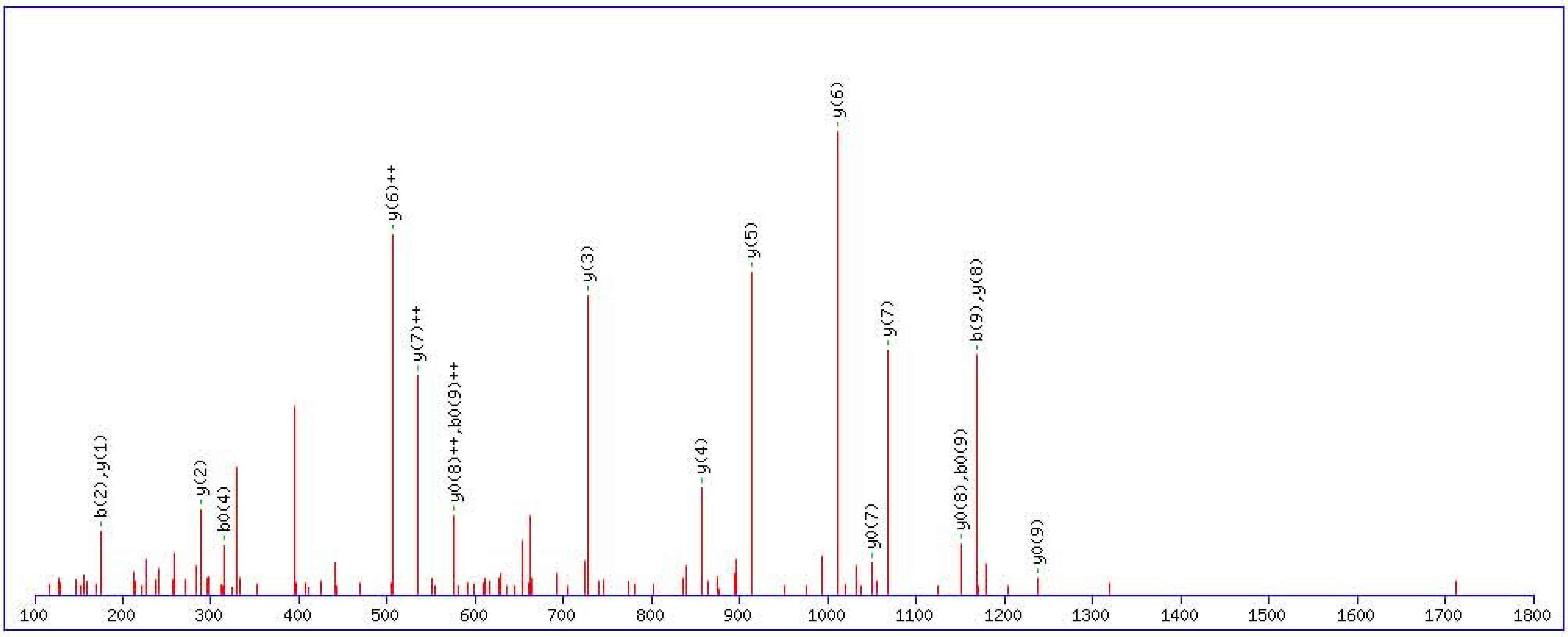
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSTGPGEQLR**
Found in **COMP_HUMAN**, Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2

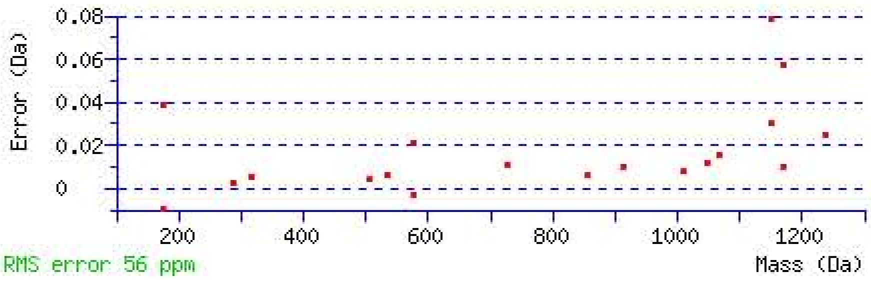
Match to Query 31826: 1341.675568 from(671.845060,2+) rtinseconds(1526) index(57126)
Title: Locus:1.1.1.2837.17 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

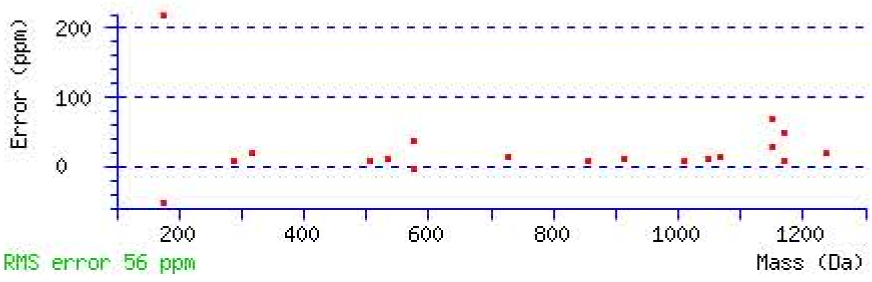
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1341.671082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 9.7e-006
Matches : 19/88 fragment ions using 24 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							10
2	**175.071332**	88.039304			157.060767	79.034021	S	1255.646334	628.326805	1238.619785	619.813530	1237.635769	619.321522	9
3	276.119011	138.563144			258.108446	129.557861	T	***1168.614306***	584.810791	1151.587757	576.297517	1150.603741	575.805508	8
4	333.140475	167.073875			315.129910	158.068593	G	***1067.566627***	534.286951	1050.540078	525.773677	1049.556062	525.281669	7
5	430.193239	215.600258			412.182674	206.594975	P	***1010.545163***	505.776219	993.518614	497.262945	992.534598	496.770937	6
6	487.214703	244.110989			469.204138	235.105707	G	***913.492399***	457.249837	896.465850	448.736563	895.481834	448.244555	5
7	616.257296	308.632286			598.246731	299.627004	E	***856.470935***	428.739105	839.444386	420.225831	838.460370	419.733823	4
8	1055.482622	528.244949	1038.456073	519.731675	1037.472057	519.239667	Q	***727.428342***	364.217809	710.401793	355.704534			3
9	**1168.566686**	584.786981	1151.540137	576.273707	1150.556121	575.781698	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.0	1341.671082	0.004486	SSTGPGEQLR
13.1	1341.663681	0.011887	SSHKDSPRDVSK
9.9	1341.674911	0.000657	TSPERREPGTGR
9.2	1341.663651	0.011917	ESARDPKPEASR
7.5	1341.693512	-0.017944	ASEQERRR
5.9	1341.688828	-0.013260	DDAQLSGLPSALR
5.7	1341.682297	-0.006729	ASEQDVRAR
5.7	1341.682297	-0.006729	LQEGRDASR
5.0	1341.686340	-0.010772	GSGIQWDLR
1.6	1341.671051	0.004517	ASQEEQIAR

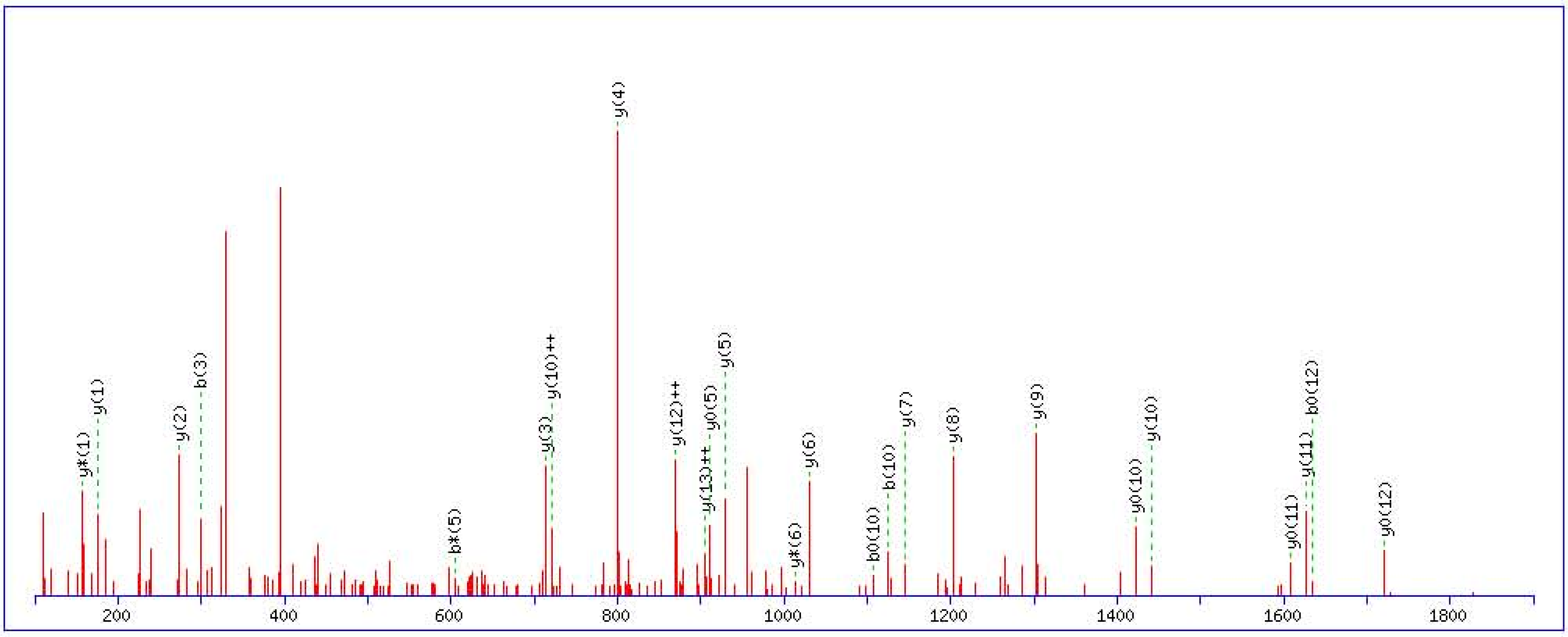
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NALWHTGDTESQVR**
Found in **COMP_HUMAN**, Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2

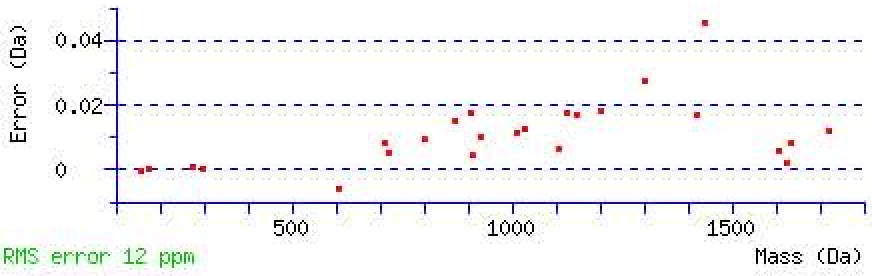
Match to Query 51136: 1923.940872 from(642.320900,3+) rtinseconds(1732) index(58582)
Title: Locus:1.1.1.2909.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

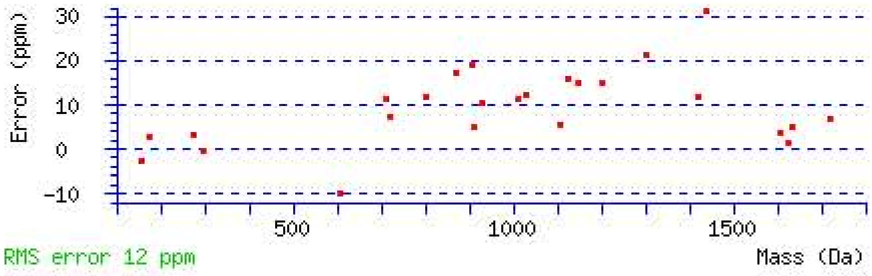
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1923.926132
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1.4e-005
Matches : 25/140 fragment ions using 49 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							14
2	186.087317	93.547296	169.060768	85.034022			A	1810.890481	905.948879	1793.863932	897.435604	1792.879916	896.943596	13
3	**299.171381**	150.089328	282.144832	141.576054			L	1739.853367	870.430322	1722.826818	861.917047	1721.842802	861.425039	12
4	485.250694	243.128985	468.224145	234.615711			W	***1626.769303***	813.888290	1609.742754	805.375015	1608.758738	804.883007	11
5	622.309606	311.658441	605.283057	303.145167			H	***1440.689990***	720.848633	1423.663441	712.335359	1422.679425	711.843351	10
6	723.357285	362.182281	706.330736	353.669006	705.346720	353.176998	T	***1303.631078***	652.319177	1286.604529	643.805903	1285.620513	643.313895	9
7	780.378749	390.693013	763.352200	382.179738	762.368184	381.687730	G	***1202.583399***	601.795338	1185.556850	593.282063	1184.572834	592.790055	8
8	895.405692	448.206484	878.379143	439.693210	877.395127	439.201202	D	***1145.561935***	573.284606	1128.535386	564.771331	1127.551370	564.279323	7
9	996.453371	498.730324	979.426822	490.217049	978.442806	489.725041	T	***1030.534992***	515.771134	1013.508443	507.257860	1012.524427	506.765852	6
10	**1125.495964**	563.251620	1108.469415	554.738346	1107.485399	554.246337	E	***929.487313***	465.247295	912.460764	456.734020	911.476748	456.242012	5
11	1212.527992	606.767634	1195.501443	598.254360	1194.517427	597.762352	S	***800.444720***	400.725998	783.418171	392.212724	782.434155	391.720716	4
12	1651.753318	826.380297	1634.726769	817.867023	1633.742753	817.375015	Q	***713.412692***	357.209984	696.386143	348.696710			3
13	1750.821732	875.914504	1733.795183	867.401230	1732.811167	866.909222	V	***274.187366***	137.597321	257.160817	129.084047			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.7	1923.926132	0.014740	NALWHTGDTESQVR

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

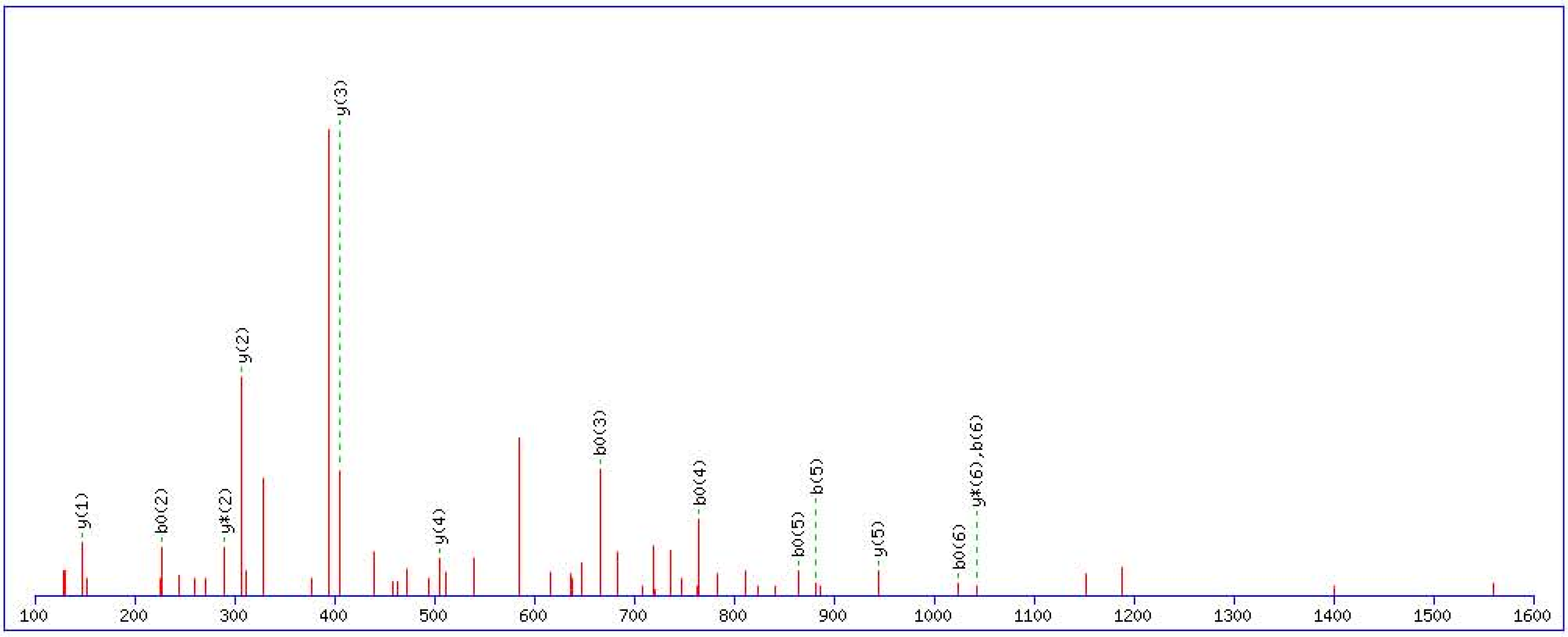
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDQVVCK**
Found in **CD5L_HUMAN**, CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1

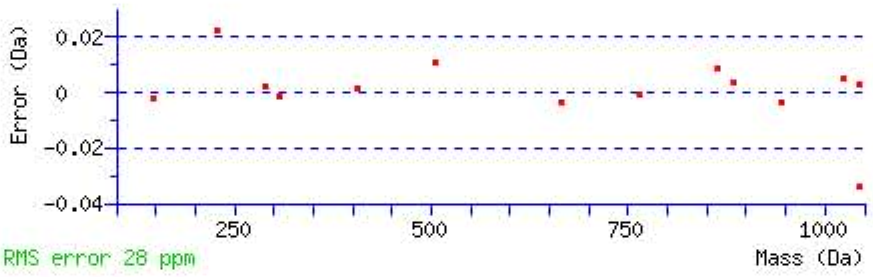
Match to Query 27309: 1187.566688 from(594.790620,2+) rtinseconds(1424) index(38297)
Title: Locus:1.1.1.2779.22 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

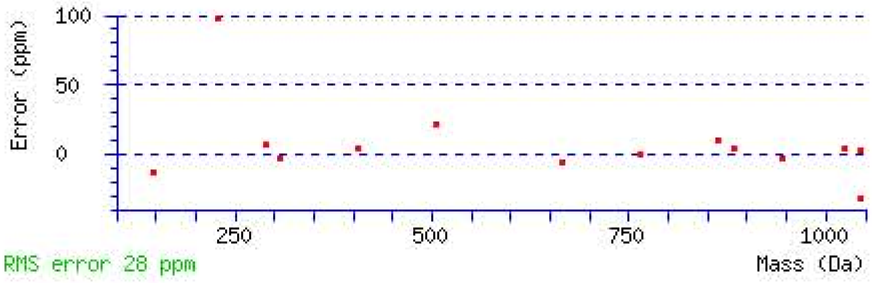
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1187.567871
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0051
Matches : 14/58 fragment ions using 20 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							7
2	245.076812	123.042044			227.066247	114.036762	D	1059.532550	530.269913	1042.506001	521.756639	1041.521985	521.264631	6
3	684.302138	342.654707	667.275589	334.141433	666.291573	333.649425	Q	***944.505607***	472.756442	927.479058	464.243167			5
4	783.370552	392.188914	766.344003	383.675639	765.359987	383.183631	V	***505.280281***	253.143778	488.253732	244.630504			4
5	**882.438966**	441.723121	865.412417	433.209846	864.428401	432.717838	V	***406.211867***	203.609571	389.185318	195.096297			3
6	**1042.469615**	521.738446	1025.443066	513.225171	1024.459050	512.733163	C	***307.143453***	154.075365	290.116904	145.562090			2
7							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.4	1187.567871	-0.001183	EDQVVCK
9.4	1187.567841	-0.001153	QAEIECK
8.5	1187.567841	-0.001153	QAIEECK
8.4	1187.557968	0.008720	QASFHCK
7.8	1187.553955	0.012733	VVHRQDMCK
5.2	1187.553940	0.012748	KSGPSCKHCK
3.9	1187.549225	0.017463	QDEDKDK
2.0	1187.564499	0.002189	FCSLSFQATK
1.4	1187.564499	0.002189	TEGKFCATFK
0.3	1187.579086	-0.012398	ANSIQGCK

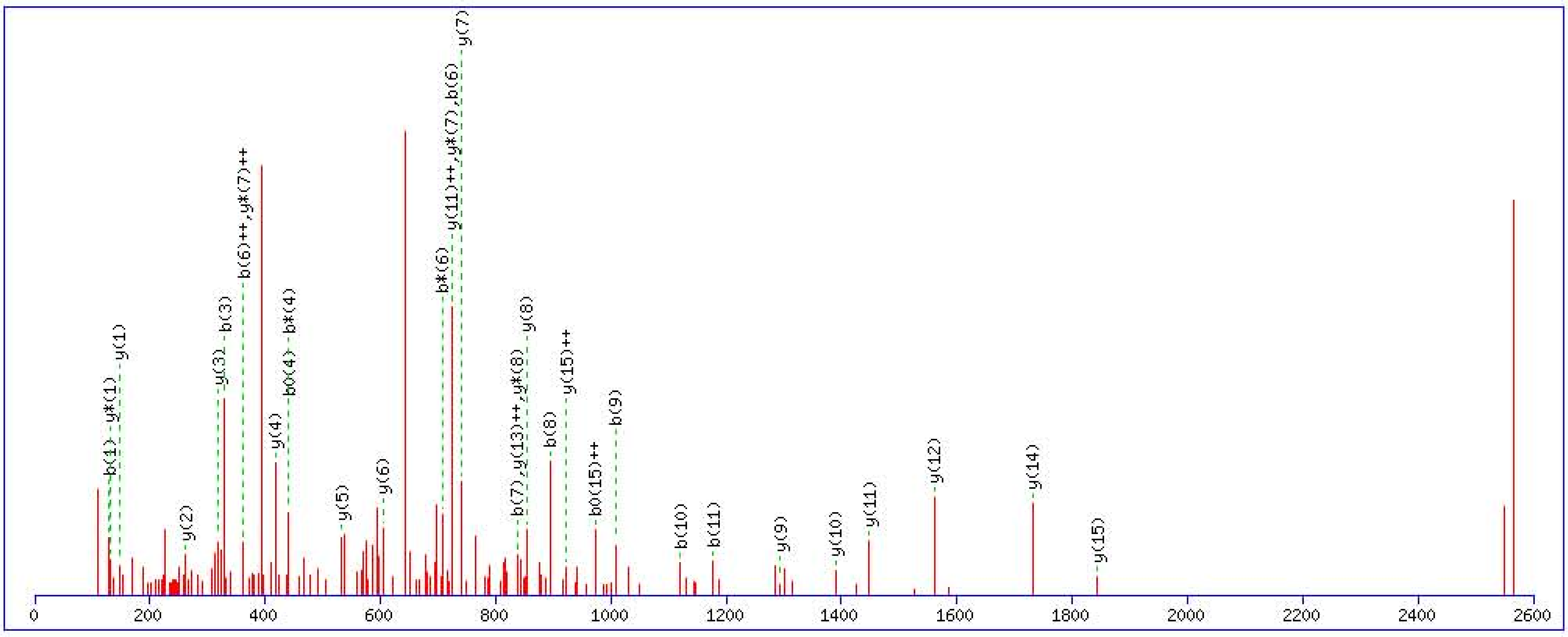
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KAEEEHLGILGPQLHADVGDK**
Found in **CERU_HUMAN**, Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1

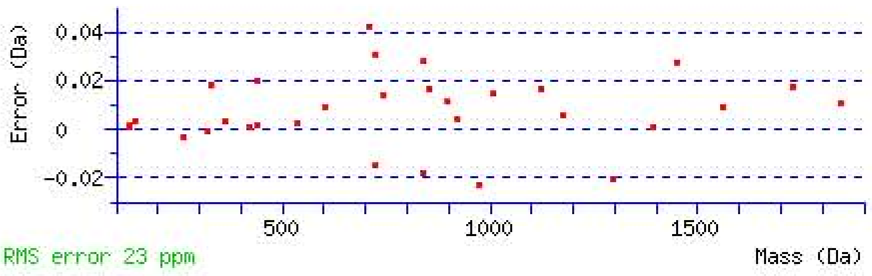
Match to Query 66214: 2566.341296 from(642.592600,4+) rtinseconds(1912) index(59868)
Title: Locus:1.1.1.2971.14 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

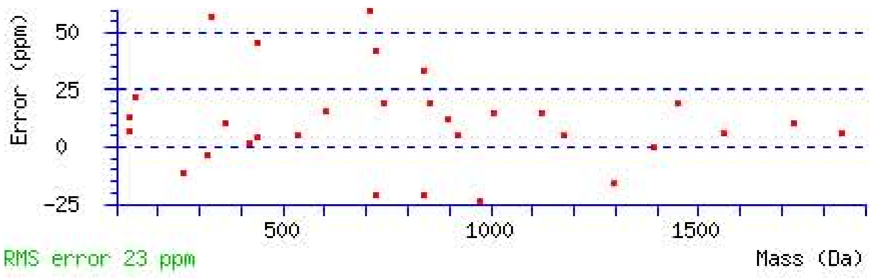
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2566.321335
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 70  Expect: 2.7e-006
Matches : 34/234 fragment ions using 67 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	**129.102239**	65.054757	112.075690	56.541483			K							21
2	200.139353	100.573315	183.112804	92.060040			A	2439.233673	1220.120474	2422.207124	1211.607200	2421.223108	1211.115192	20
3	**329.181946**	165.094611	312.155397	156.581336	311.171381	156.089328	E	2368.196559	1184.601917	2351.170010	1176.088643	2350.185994	1175.596635	19
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	E	2239.153966	1120.080621	2222.127417	1111.567346	2221.143401	1111.075338	18
5	587.267132	294.137204	570.240583	285.623930	569.256567	285.131922	E	2110.111373	1055.559324	2093.084824	1047.046050	2092.100808	1046.554042	17
6	**724.326044**	362.666660	707.299495	354.153386	706.315479	353.661378	H	1981.068780	991.038028	1964.042231	982.524753	1963.058215	982.032745	16
7	**837.410108**	419.208692	820.383559	410.695418	819.399543	410.203410	L	***1844.009868***	922.508572	1826.983319	913.995297	1825.999303	913.503289	15
8	**894.431572**	447.719424	877.405023	439.206150	876.421007	438.714142	G	***1730.925804***	865.966540	1713.899255	857.453265	1712.915239	856.961257	14
9	**1007.515636**	504.261456	990.489087	495.748182	989.505071	495.256174	I	1673.904340	837.455808	1656.877791	828.942533	1655.893775	828.450525	13
10	**1120.599700**	560.803488	1103.573151	552.290214	1102.589135	551.798205	L	***1560.820276***	780.913776	1543.793727	772.400501	1542.809711	771.908493	12
11	**1177.621164**	589.314220	1160.594615	580.800946	1159.610599	580.308937	G	***1447.736212***	724.371744	1430.709663	715.858469	1429.725647	715.366461	11
12	1274.673928	637.840602	1257.647379	629.327328	1256.663363	628.835319	P	***1390.714748***	695.861012	1373.688199	687.347737	1372.704183	686.855729	10
13	1713.899254	857.453265	1696.872705	848.939991	1695.888689	848.447983	Q	***1293.661984***	647.334630	1276.635435	638.821355	1275.651419	638.329347	9
14	1826.983318	913.995297	1809.956769	905.482023	1808.972753	904.990015	L	***854.436658***	427.721967	837.410109	419.208692	836.426093	418.716684	8
15	1964.042230	982.524753	1947.015681	974.011479	1946.031665	973.519471	H	***741.352594***	371.179935	724.326045	362.666660	723.342029	362.174652	7
16	2035.079344	1018.043310	2018.052795	1009.530036	2017.068779	1009.038028	A	***604.293682***	302.650479	587.267133	294.137204	586.283117	293.645196	6
17	2150.106287	1075.556781	2133.079738	1067.043507	2132.095722	1066.551499	D	***533.256568***	267.131922	516.230019	258.618647	515.246003	258.126639	5
18	2249.174701	1125.090988	2232.148152	1116.577714	2231.164136	1116.085706	V	***418.229625***	209.618450	401.203076	201.105176	400.219060	200.613168	4
19	2306.196165	1153.601720	2289.169616	1145.088446	2288.185600	1144.596438	G	***319.161211***	160.084243	302.134662	151.570969	301.150646	151.078961	3
20	2421.223108	1211.115192	2404.196559	1202.601917	2403.212543	1202.109909	D	***262.139747***	131.573511	245.113198	123.060237	244.129182	122.568229	2
21							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.8	2566.321335	0.019961	KAEEEHLGILGPQLHADVGDK

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

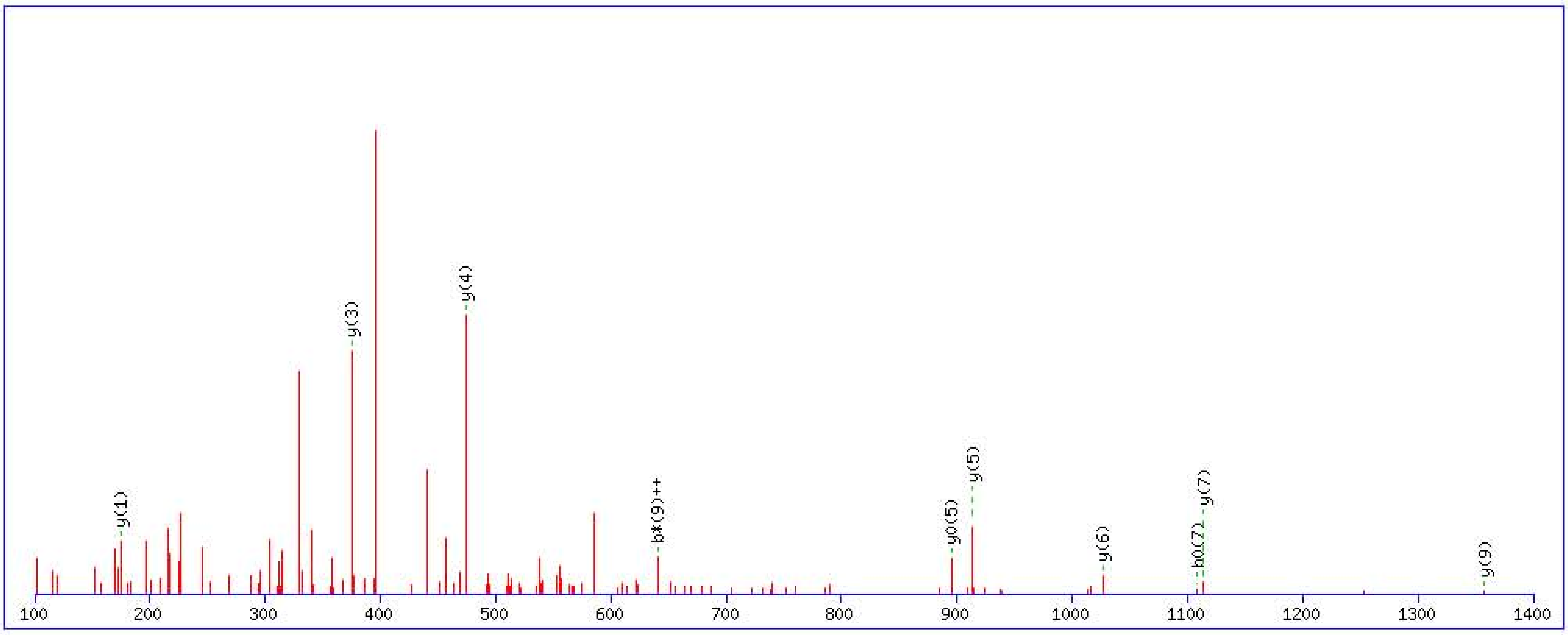
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELDESLQVAER**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

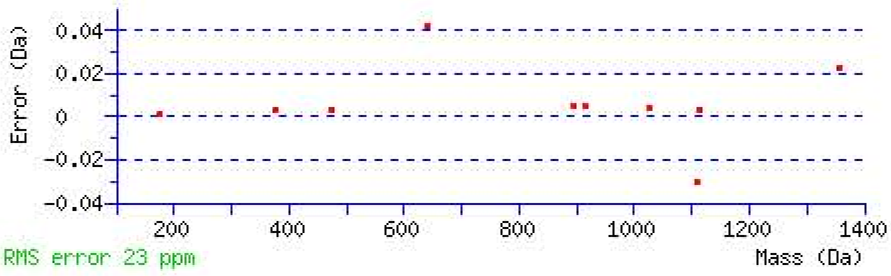
Match to Query 42154: 1598.802222 from(533.941350,3+) rtinseconds(1940) index(41744)
Title: Locus:1.1.1.2959.11 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

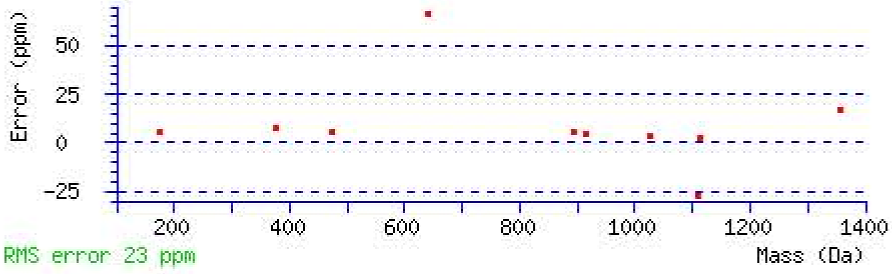
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1598.797379
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0031
Matches : 10/106 fragment ions using 24 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							11
2	243.133933	122.070605			225.123368	113.065322	L	1470.762091	735.884684	1453.735542	727.371409	1452.751526	726.879401	10
3	358.160876	179.584076			340.150311	170.578794	D	***1357.678027***	679.342652	1340.651478	670.829377	1339.667462	670.337369	9
4	487.203469	244.105373			469.192904	235.100090	E	1242.651084	621.829180	1225.624535	613.315906	1224.640519	612.823898	8
5	574.235497	287.621387			556.224932	278.616104	S	***1113.608491***	557.307884	1096.581942	548.794609	1095.597926	548.302601	7
6	687.319561	344.163419			669.308996	335.158136	L	***1026.576463***	513.791870	1009.549914	505.278595	1008.565898	504.786587	6
7	1126.544887	563.776082	1109.518338	555.262807	1108.534322	554.770799	Q	***913.492399***	457.249838	896.465850	448.736563	895.481834	448.244555	5
8	1225.613301	613.310289	1208.586752	604.797014	1207.602736	604.305006	V	***474.267073***	237.637175	457.240524	229.123900	456.256508	228.631892	4
9	1296.650415	648.828846	1279.623866	640.315571	1278.639850	639.823563	A	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
10	1425.693008	713.350142	1408.666459	704.836868	1407.682443	704.344860	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.9	1598.797379	0.004843	ELDESLQVAER
0.2	1598.812439	-0.010217	EQQRLREGEEGLR
0.2	1598.812439	-0.010217	EQRRLQEGEEGIR

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

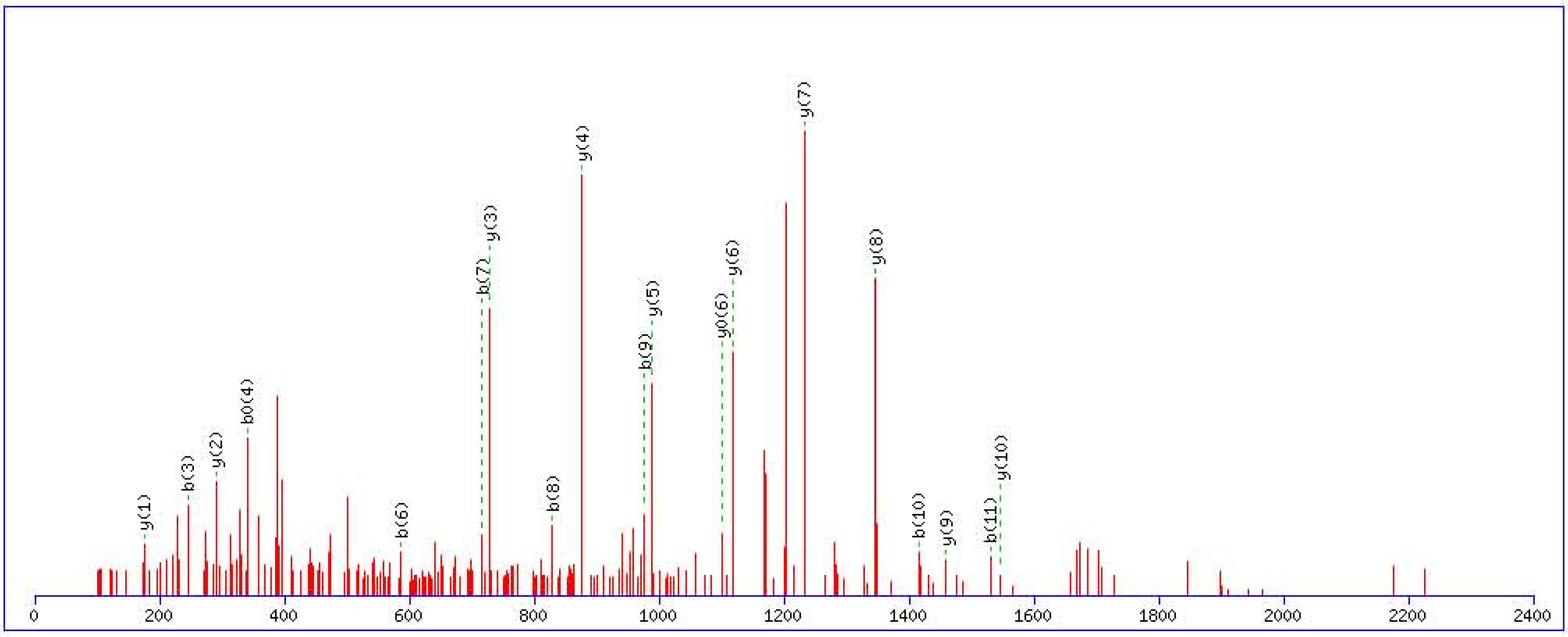
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASSIIDELFQDR**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

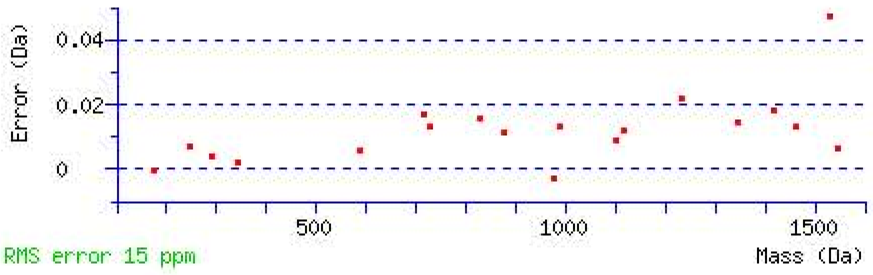
Match to Query 45941: 1703.862168 from(852.938360,2+) rtinseconds(2801) index(47357)
Title: Locus:1.1.1.3257.6 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

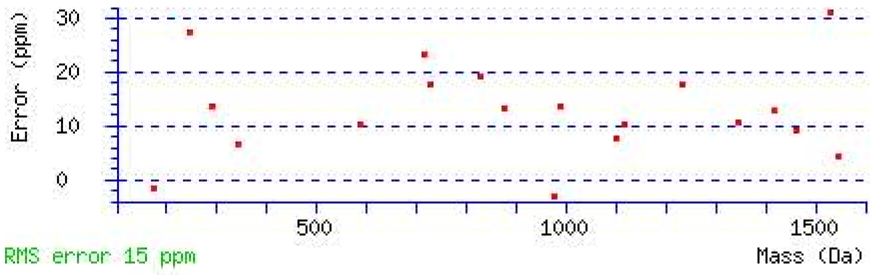


```
Monoisotopic mass of neutral peptide Mr(calc): 1703.855240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 1e-006
Matches : 19/110 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							12
2	159.076418	80.041847			141.065853	71.036564	S	1633.825419	817.416348	1616.798870	808.903073	1615.814854	808.411065	11
3	**246.108446**	123.557861			228.097881	114.552578	S	***1546.793391***	773.900333	1529.766842	765.387059	1528.782826	764.895051	10
4	359.192510	180.099893			341.181945	171.094610	I	***1459.761363***	730.384320	1442.734814	721.871045	1441.750798	721.379037	9
5	472.276574	236.641925			454.266009	227.636642	I	***1346.677299***	673.842288	1329.650750	665.329013	1328.666734	664.837005	8
6	**587.303517**	294.155397			569.292952	285.150114	D	***1233.593235***	617.300256	1216.566686	608.786981	1215.582670	608.294973	7
7	**716.346110**	358.676693			698.335545	349.671411	E	***1118.566292***	559.786784	1101.539743	551.273510	1100.555727	550.781501	6
8	**829.430174**	415.218725			811.419609	406.213443	L	***989.523699***	495.265488	972.497150	486.752213	971.513134	486.260205	5
9	**976.498588**	488.752932			958.488023	479.747650	F	***876.439635***	438.723456	859.413086	430.210181	858.429070	429.718173	4
10	**1415.723914**	708.365595	1398.697365	699.852321	1397.713349	699.360312	Q	***729.371221***	365.189249	712.344672	356.675974	711.360656	356.183966	3
11	**1530.750857**	765.879067	1513.724308	757.365792	1512.740292	756.873784	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
12							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 15 ppm



RMS error 15 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.3	1703.855240	0.006928	ASSIIDELFQDR
5.1	1703.859070	0.003098	RWDELETTTQAKAR
2.5	1703.866455	-0.004287	NNNLSKDHYMLIVK
1.5	1703.881088	-0.018920	VQTSIAVCKLQACAR
1.4	1703.874313	-0.012145	NRGYLADPAKFPEAR

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

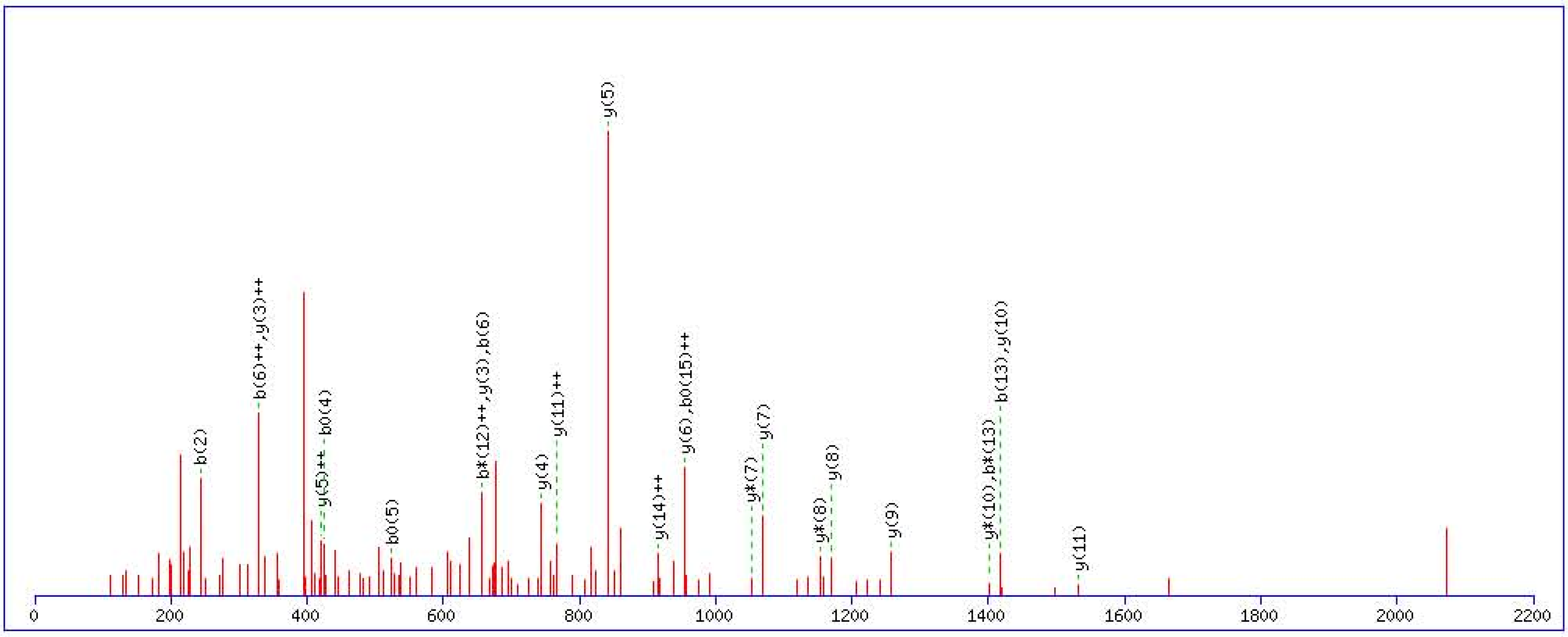
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EILSVDCSTNNPSQAK**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

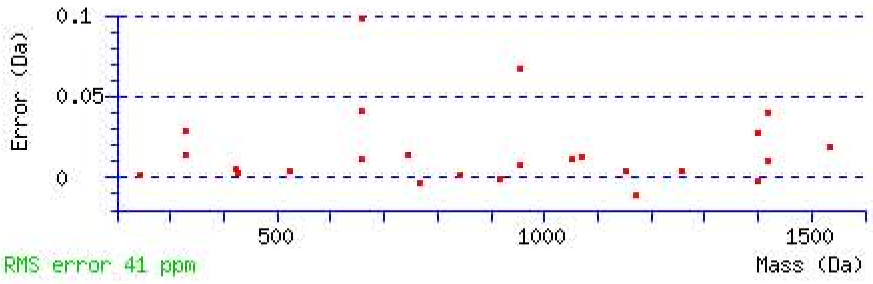
Match to Query 55460: 2072.998782 from(692.006870,3+) rtinseconds(1797) index(40728)
Title: Locus:1.1.1.2909.12 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

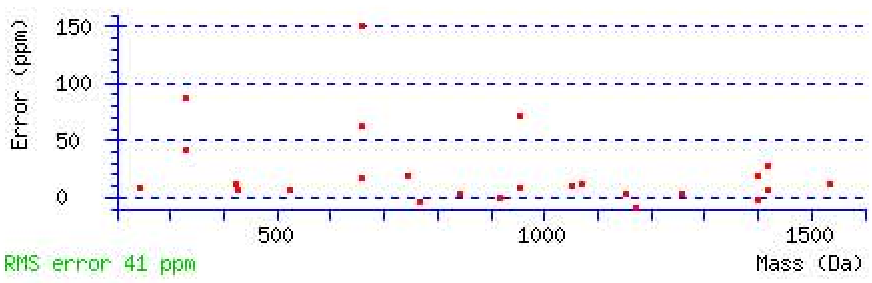
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2072.987061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 58 **Expect:** 3.5e-005
Matches : 25/156 fragment ions using 29 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							16
2	**243.133933**	122.070605			225.123368	113.065322	I	1944.951759	972.979517	1927.925210	964.466243	1926.941194	963.974235	15
3	356.217997	178.612637			338.207432	169.607354	L	1831.867695	916.437485	1814.841146	907.924211	1813.857130	907.432203	14
4	443.250025	222.128650			425.239460	213.123368	S	1718.783631	859.895454	1701.757082	851.382179	1700.773066	850.890171	13
5	542.318439	271.662858			524.307874	262.657575	V	1631.751603	816.379439	1614.725054	807.866165	1613.741038	807.374157	12
6	**657.345382**	329.176329			639.334817	320.171046	D	***1532.683189***	766.845233	1515.656640	758.331958	1514.672624	757.839950	11
7	817.376031	409.191654			799.365466	400.186371	C	***1417.656246***	709.331761	1400.629697	700.818487	1399.645681	700.326479	10
8	904.408059	452.707668			886.397494	443.702385	S	***1257.625597***	629.316437	1240.599048	620.803162	1239.615032	620.311154	9
9	1005.455738	503.231507			987.445173	494.226225	T	***1170.593569***	585.800422	1153.567020	577.287148	1152.583004	576.795140	8
10	1119.498665	560.252971	1102.472116	551.739696	1101.488100	551.247688	N	***1069.545890***	535.276583	1052.519341	526.763309	1051.535325	526.271301	7
11	1233.541592	617.274434	1216.515043	608.761160	1215.531027	608.269152	N	***955.502963***	478.255119	938.476414	469.741845	937.492398	469.249837	6
12	1330.594356	665.800816	1313.567807	657.287542	1312.583791	656.795534	P	***841.460036***	421.233656	824.433487	412.720381	823.449471	412.228373	5
13	**1417.626384**	709.316830	1400.599835	700.803556	1399.615819	700.311548	S	***744.407272***	372.707274	727.380723	364.193999	726.396707	363.701991	4
14	1856.851710	928.929493	1839.825161	920.416219	1838.841145	919.924211	Q	***657.375244***	329.191260	640.348695	320.677985			3
15	1927.888824	964.448050	1910.862275	955.934776	1909.878259	955.442768	A	218.149918	109.578597	201.123369	101.065322			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.7	2072.987061	0.011721	EILSVDCSTNNPSQAK

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

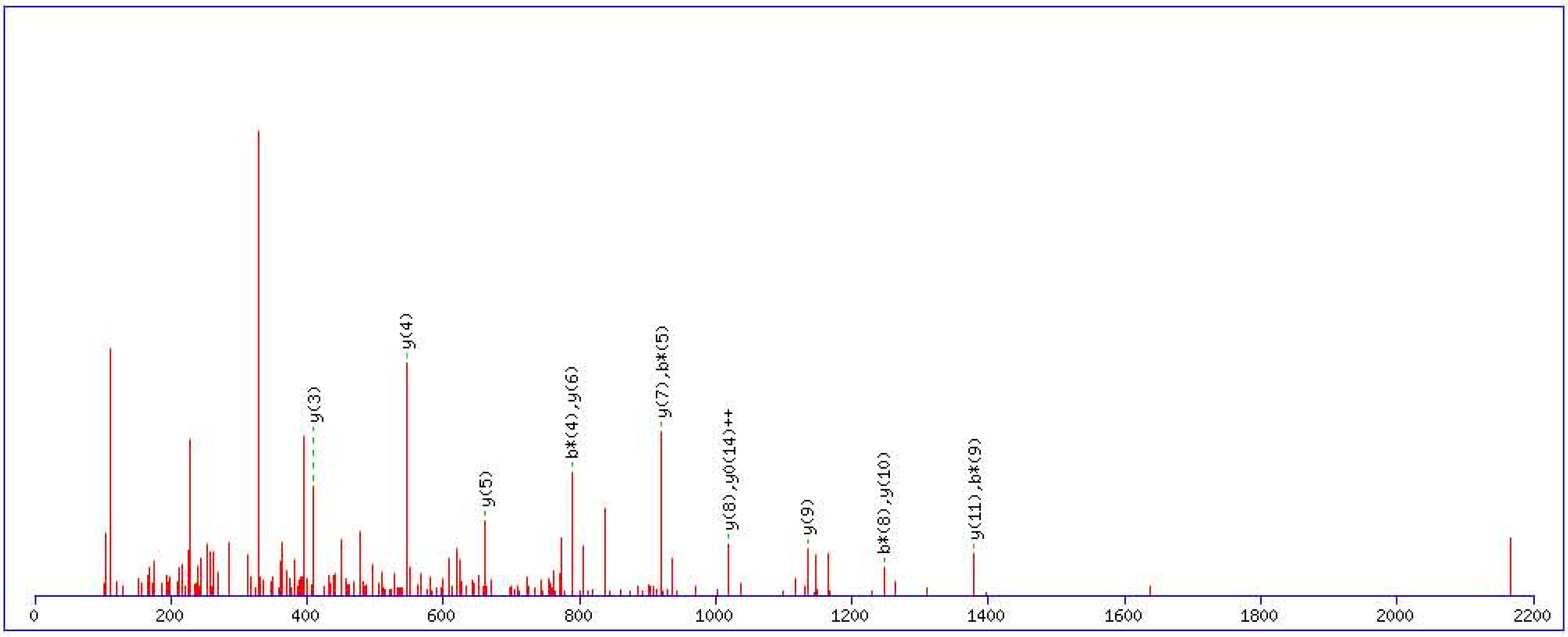
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQTHMLDVMQDHFSR**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

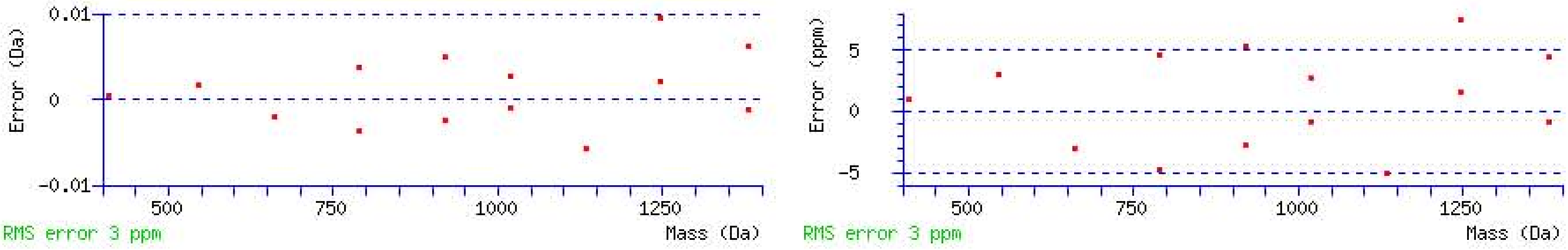
Match to Query 57785: 2183.013736 from(546.760710,4+) rtinseconds(1986) index(42032)
Title: Locus:1.1.1.2975.12 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2183.007446
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 62 **Expect:** 8e-006
Matches : 14/162 fragment ions using 15 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	129.065854	65.036565	112.039305	56.523291			Q							15
2	568.291180	284.649228	551.264631	276.135954			Q	2055.956135	1028.481705	2038.929586	1019.968431	2037.945570	1019.476423	14
3	669.338859	335.173068	652.312310	326.659793	651.328294	326.167785	T	1616.730809	808.869043	1599.704260	800.355768	1598.720244	799.863760	13
4	806.397771	403.702524	789.371222	395.189249	788.387206	394.697241	H	1515.683130	758.345203	1498.656581	749.831929	1497.672565	749.339921	12
5	937.438256	469.222766	920.411707	460.709492	919.427691	460.217484	M	***1378.624218***	689.815747	1361.597669	681.302473	1360.613653	680.810465	11
6	1050.522320	525.764798	1033.495771	517.251524	1032.511755	516.759516	L	***1247.583733***	624.295505	1230.557184	615.782230	1229.573168	615.290222	10
7	1165.549263	583.278270	1148.522714	574.764995	1147.538698	574.272987	D	***1134.499669***	567.753473	1117.473120	559.240198	1116.489104	558.748190	9
8	1264.617677	632.812477	1247.591128	624.299202	1246.607112	623.807194	V	***1019.472726***	510.240001	1002.446177	501.726727	1001.462161	501.234719	8
9	1395.658162	698.332719	1378.631613	689.819445	1377.647597	689.327437	M	***920.404312***	460.705794	903.377763	452.192520	902.393747	451.700512	7
10	1523.716740	762.362008	1506.690191	753.848734	1505.706175	753.356726	Q	***789.363827***	395.185552	772.337278	386.672277	771.353262	386.180269	6
11	1638.743683	819.875480	1621.717134	811.362205	1620.733118	810.870197	D	***661.305249***	331.156263	644.278700	322.642988	643.294684	322.150980	5
12	1775.802595	888.404936	1758.776046	879.891661	1757.792030	879.399653	H	***546.278306***	273.642791	529.251757	265.129517	528.267741	264.637509	4
13	1922.871009	961.939143	1905.844460	953.425868	1904.860444	952.933860	F	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	3
14	2009.903037	1005.455157	1992.876488	996.941882	1991.892472	996.449874	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
15							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.4	2183.007446	0.006290	QQTHMLDVMQDHFSR
62.4	2183.007446	0.006290	QQTHMLDVMQDHFSR

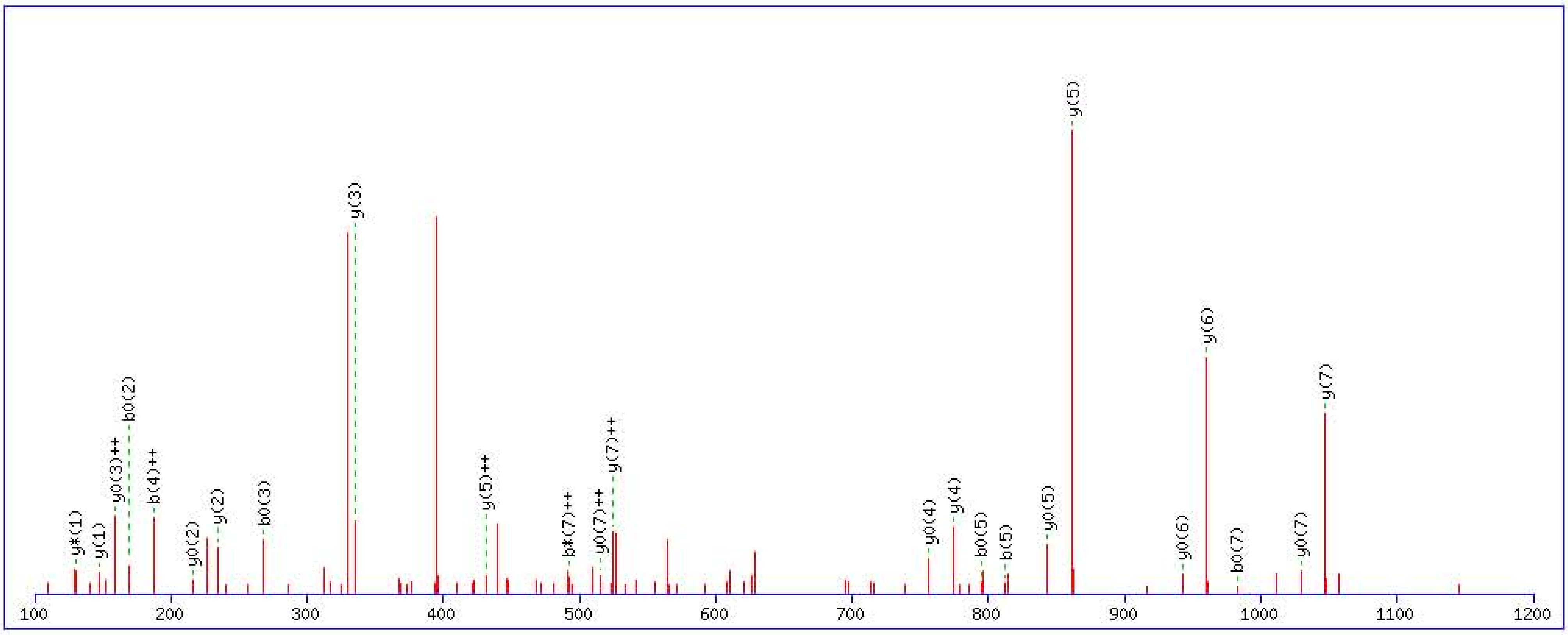
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSVSQTSK**
Found in **FA9_HUMAN**, Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2

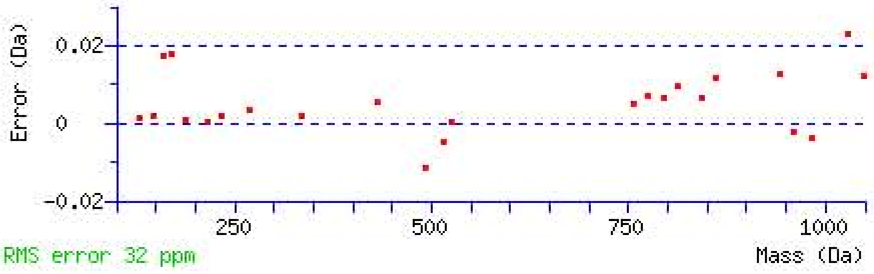
Match to Query 25574: 1145.616688 from(573.815620,2+) rtinseconds(1380) index(56053)
Title: Locus:1.1.1.2786.20 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

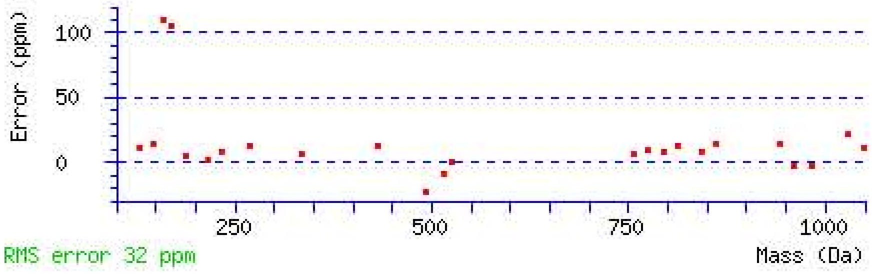
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1145.611450
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.0067
Matches : 25/72 fragment ions using 57 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							8
2	**187.107718**	94.057497			169.097153	85.052214	S	***1047.550307***	524.278792	1030.523758	515.765517	1029.539742	515.273509	7
3	286.176132	143.591704			268.165567	134.586422	V	***960.518279***	480.762778	943.491730	472.249503	942.507714	471.757495	6
4	373.208160	187.107718			355.197595	178.102435	S	***861.449865***	431.228571	844.423316	422.715296	843.439300	422.223288	5
5	**812.433486**	406.720381	795.406937	398.207107	794.422921	397.715099	Q	***774.417837***	387.712557	757.391288	379.199282	756.407272	378.707274	4
6	913.481165	457.244221	896.454616	448.730946	895.470600	448.238938	T	***335.192511***	168.099893	318.165962	159.586619	317.181946	159.094611	3
7	1000.513193	500.760235	983.486644	492.246960	982.502628	491.754952	S	***234.144832***	117.576054	217.118283	109.062779	216.134267	108.570771	2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.6	1145.611450	0.005238	VSVSQTSK
8.0	1145.629196	-0.012508	GEVLGLSSSLGK
5.5	1145.604019	0.012669	REQLSDASLK
2.6	1145.629181	-0.012493	VAKEVVEASSK
2.3	1145.611420	0.005268	KSIMVQSPEK

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

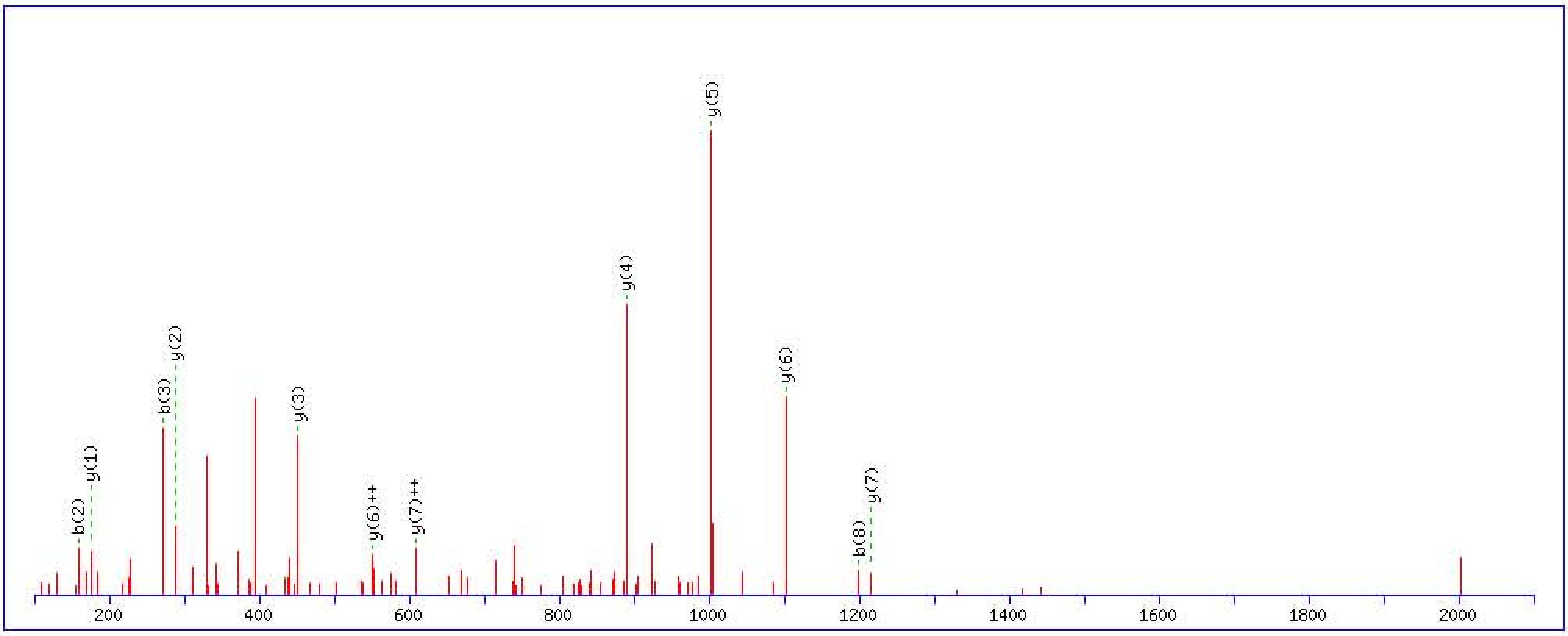
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SALVLQYLR**
Found in **FA9_HUMAN**, Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2

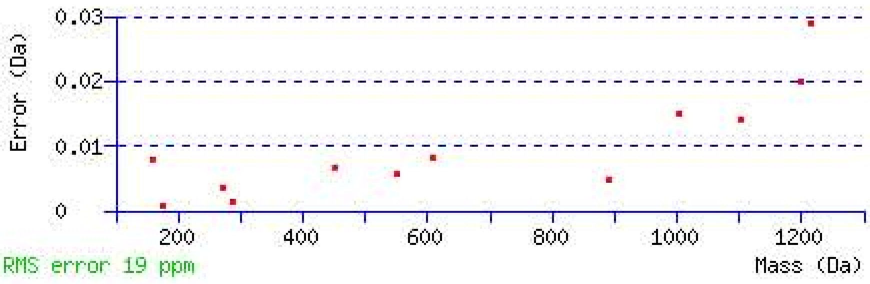
Match to Query 33630: 1372.803748 from(687.409150,2+) rtinseconds(2382) index(63327)
Title: Locus:1.1.1.3134.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

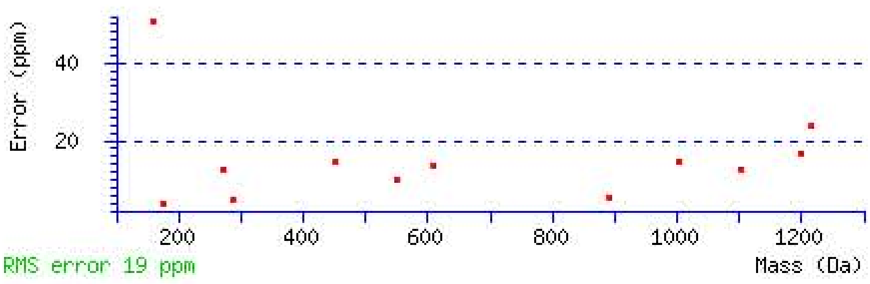
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1372.790054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 44 **Expect:** 0.00026
Matches : 12/70 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					9
2	**159.076418**	80.041847			141.065853	71.036564	A	1286.765327	643.886301	1269.738778	635.373027	8
3	**272.160482**	136.583879			254.149917	127.578597	L	***1215.728213***	608.367744	1198.701664	599.854470	7
4	371.228896	186.118086			353.218331	177.112804	V	***1102.644149***	551.825713	1085.617600	543.312438	6
5	484.312960	242.660118			466.302395	233.654836	L	***1003.575735***	502.291505	986.549186	493.778231	5
6	923.538286	462.272781	906.511737	453.759507	905.527721	453.267499	Q	***890.491671***	445.749473	873.465122	437.236199	4
7	1086.601615	543.804446	1069.575066	535.291171	1068.591050	534.799163	Y	***451.266345***	226.136810	434.239796	217.623536	3
8	**1199.685679**	600.346477	1182.659130	591.833203	1181.675114	591.341195	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 SALVLQYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.1	1372.790054	0.013694	SALVLQYLR
5.7	1372.819046	-0.015298	QNLVIKDKFIR
0.5	1372.790039	0.013709	KELQILYR
0.3	1372.793900	0.009848	TERRVPFSLLR
0.2	1372.790039	0.013709	IIEKYQLR

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

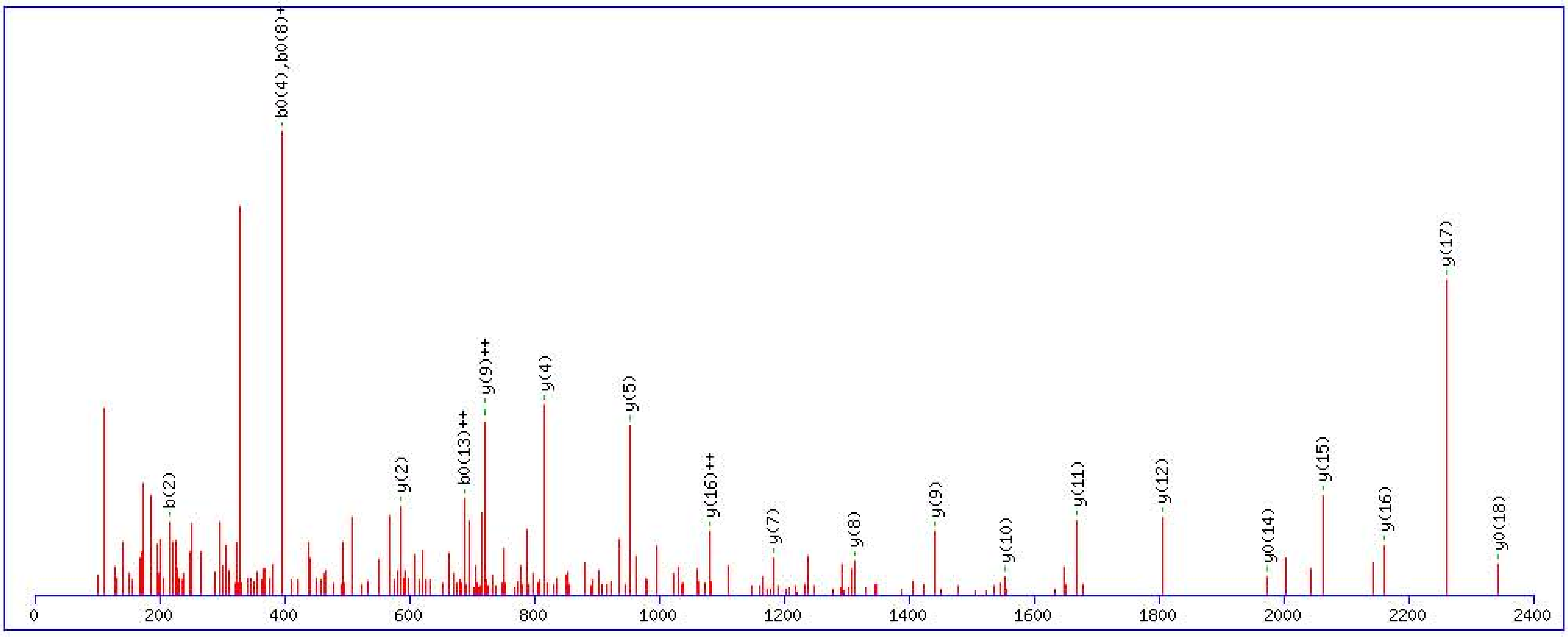
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITVVAGEHNIEETEHTEQK**
Found in **FA9_HUMAN**, Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2

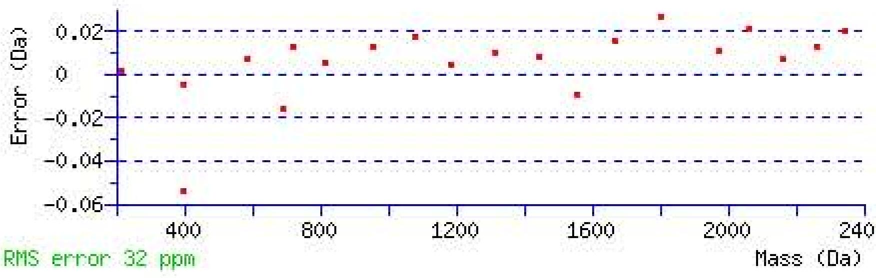
Match to Query 64536: 2474.225496 from(619.563650,4+) rtinseconds(1580) index(57494)
Title: Locus:1.1.1.2856.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

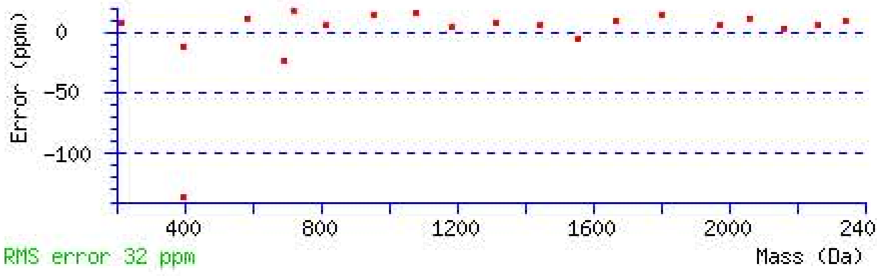
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2474.211121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 97  Expect: 5.1e-009
Matches : 20/194 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	114.091340	57.549308					I							19
2	215.139019	108.073147			197.128454	99.067865	T	2362.134353	1181.570814	2345.107804	1173.057540	2344.123788	1172.565532	18
3	314.207433	157.607354			296.196868	148.602072	V	***2261.086674***	1131.046975	2244.060125	1122.533700	2243.076109	1122.041692	17
4	413.275847	207.141561			395.265282	198.136279	V	***2162.018260***	1081.512768	2144.991711	1072.999493	2144.007695	1072.507485	16
5	484.312961	242.660119			466.302396	233.654836	A	***2062.949846***	1031.978561	2045.923297	1023.465286	2044.939281	1022.973278	15
6	541.334425	271.170851			523.323860	262.165568	G	1991.912732	996.460004	1974.886183	987.946730	1973.902167	987.454722	14
7	670.377018	335.692147			652.366453	326.686865	E	1934.891268	967.949272	1917.864719	959.435998	1916.880703	958.943990	13
8	807.435930	404.221603			789.425365	395.216321	H	***1805.848675***	903.427976	1788.822126	894.914701	1787.838110	894.422693	12
9	921.478857	461.243067	904.452308	452.729792	903.468292	452.237784	N	***1668.789763***	834.898520	1651.763214	826.385245	1650.779198	825.893237	11
10	1034.562921	517.785099	1017.536372	509.271824	1016.552356	508.779816	I	***1554.746836***	777.877056	1537.720287	769.363782	1536.736271	768.871774	10
11	1163.605514	582.306395	1146.578965	573.793121	1145.594949	573.301113	E	***1441.662772***	721.335024	1424.636223	712.821750	1423.652207	712.329742	9
12	1292.648107	646.827692	1275.621558	638.314417	1274.637542	637.822409	E	***1312.620179***	656.813728	1295.593630	648.300453	1294.609614	647.808445	8
13	1393.695786	697.351531	1376.669237	688.838257	1375.685221	688.346249	T	***1183.577586***	592.292431	1166.551037	583.779157	1165.567021	583.287149	7
14	1522.738379	761.872828	1505.711830	753.359553	1504.727814	752.867545	E	1082.529907	541.768592	1065.503358	533.255317	1064.519342	532.763309	6
15	1659.797291	830.402284	1642.770742	821.889009	1641.786726	821.397001	H	***953.487314***	477.247295	936.460765	468.734021	935.476749	468.242013	5
16	1760.844970	880.926123	1743.818421	872.412849	1742.834405	871.920841	T	***816.428402***	408.717839	799.401853	400.204565	798.417837	399.712557	4
17	1889.887563	945.447420	1872.861014	936.934145	1871.876998	936.442137	E	715.380723	358.194000	698.354174	349.680725	697.370158	349.188717	3
18	2329.112889	1165.060082	2312.086340	1156.546808	2311.102324	1156.054800	Q	***586.338130***	293.672703	569.311581	285.159429			2
19							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
97.2	2474.211121	0.014375	ITVVAGEHNIEETEHTEQK

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

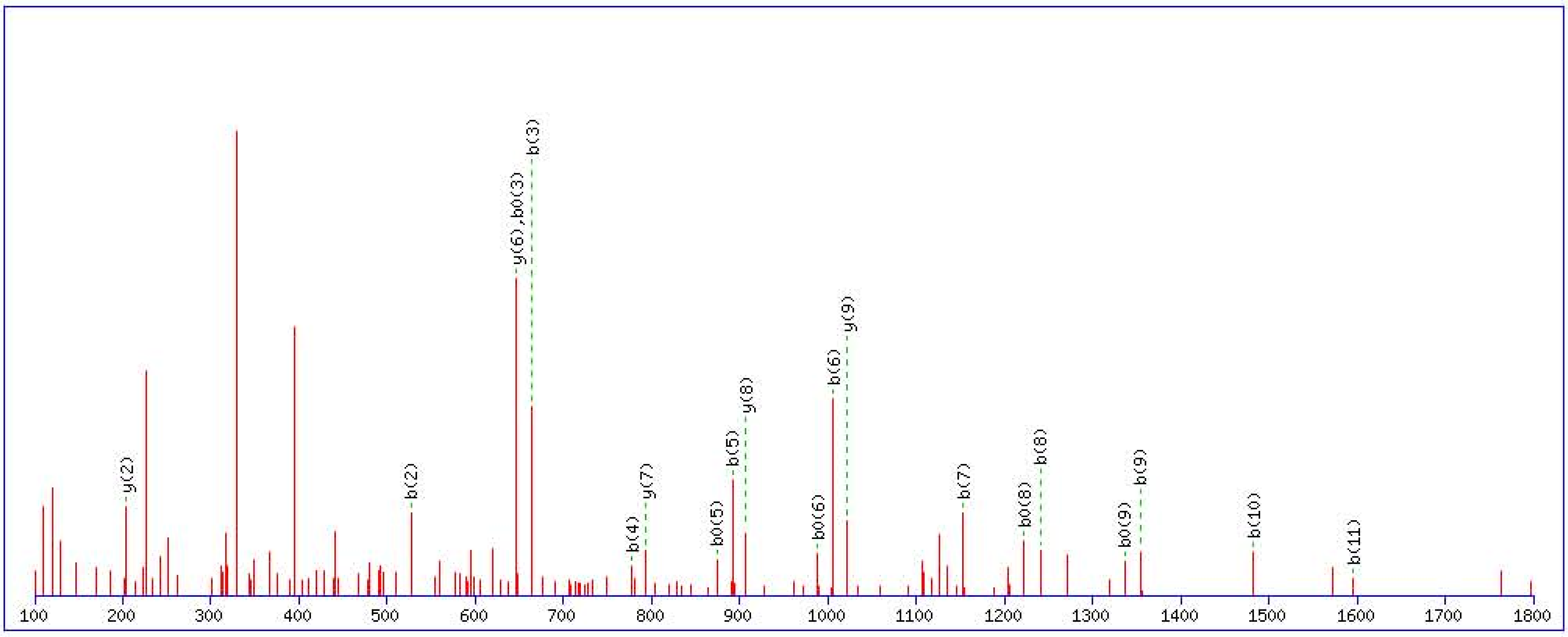
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQHLDNFSNQIGK**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

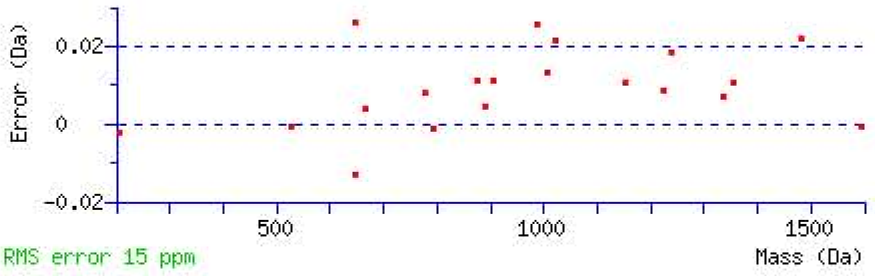
Match to Query 48359: 1797.896052 from(600.305960,3+) rtinseconds(1735) index(58608)
Title: Locus:1.1.1.2910.10 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

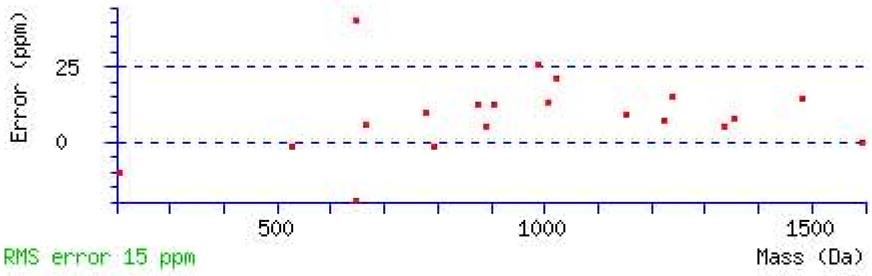
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1797.883194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 5.2e-007
Matches : 20/132 fragment ions using 31 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							13
2	***527.264630***	264.135953	510.238081	255.622679	509.254065	255.130671	Q	1711.858451	856.432863	1694.831902	847.919589	1693.847886	847.427581	12
3	***664.323542***	332.665409	647.296993	324.152134	646.312977	323.660126	H	1272.633125	636.820200	1255.606576	628.306926	1254.622560	627.814918	11
4	***777.407606***	389.207441	760.381057	380.694166	759.397041	380.202159	L	1135.574213	568.290744	1118.547664	559.777470	1117.563648	559.285462	10
5	***892.434549***	446.720913	875.408000	438.207638	874.423984	437.715630	D	**1022.490149**	511.748712	1005.463600	503.235438	1004.479584	502.743430	9
6	***1006.477476***	503.742376	989.450927	495.229101	988.466911	494.737093	N	**907.463206**	454.235241	890.436657	445.721966	889.452641	445.229958	8
7	***1153.545890***	577.276583	1136.519341	568.763308	1135.535325	568.271300	F	**793.420279**	397.213777	776.393730	388.700503	775.409714	388.208495	7
8	***1240.577918***	620.792597	1223.551369	612.279323	1222.567353	611.787314	S	**646.351865**	323.679570	629.325316	315.166296	628.341300	314.674288	6
9	***1354.620845***	677.814060	1337.594296	669.300786	1336.610280	668.808778	N	559.319837	280.163556	542.293288	271.650282			5
10	***1482.679423***	741.843349	1465.652874	733.330075	1464.668858	732.838067	Q	445.276910	223.142093	428.250361	214.628818			4
11	***1595.763487***	798.385381	1578.736938	789.872107	1577.752922	789.380099	I	317.218332	159.112804	300.191783	150.599529			3
12	1652.784951	826.896113	1635.758402	818.382839	1634.774386	817.890831	G	**204.134268**	102.570772	187.107719	94.057497			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.0	1797.883194	0.012858	SQHLDNFSNQIGK
2.0	1797.872604	0.023448	KWDFSKYYVSNFSK

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

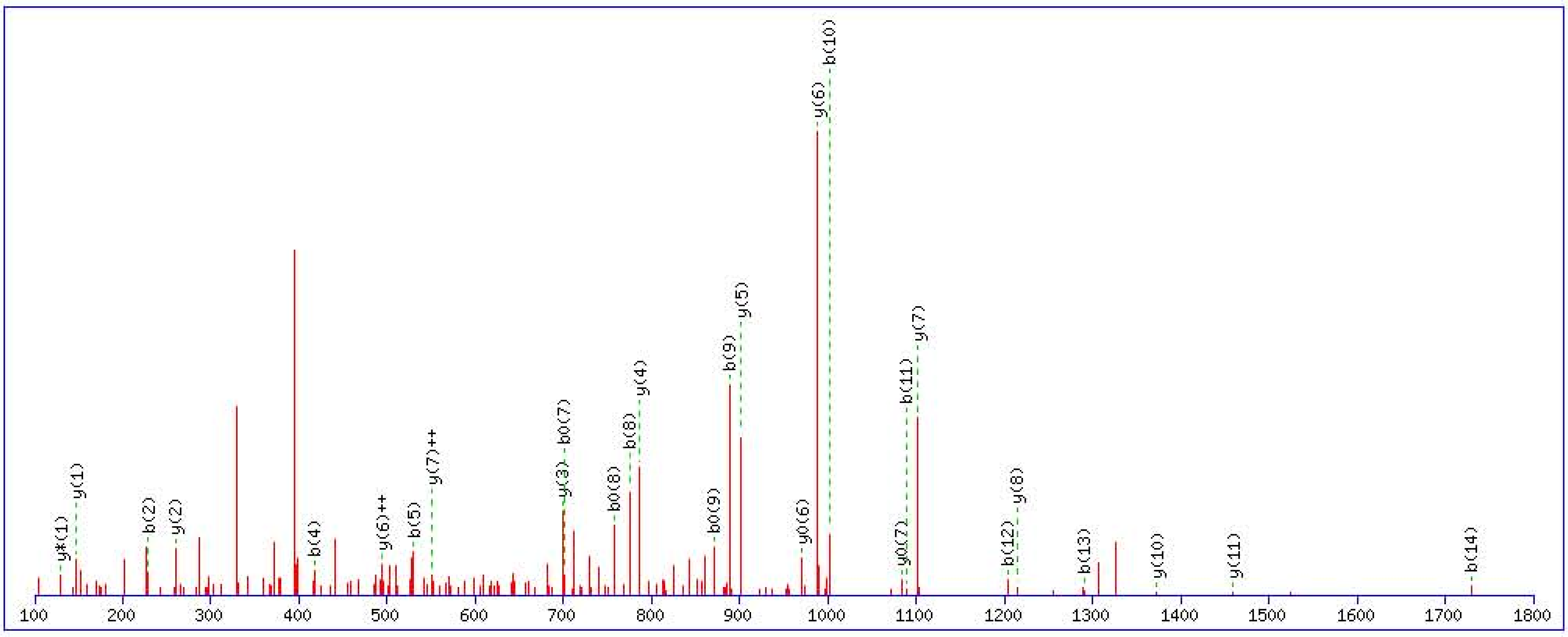
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPMGLSTGIISDSQIK**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

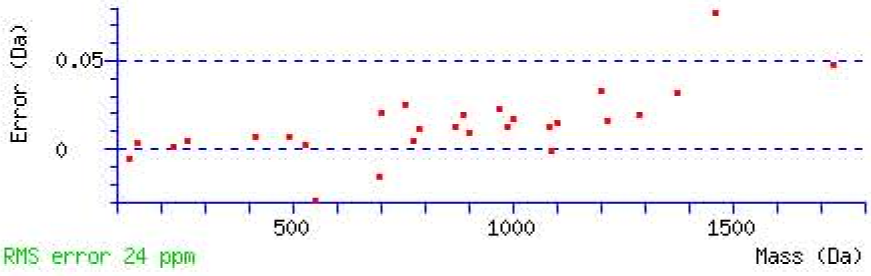
Match to Query 52595: 1988.036712 from(663.686180,3+) rtinseconds(2440) index(63646)
Title: Locus:1.1.1.3154.7 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

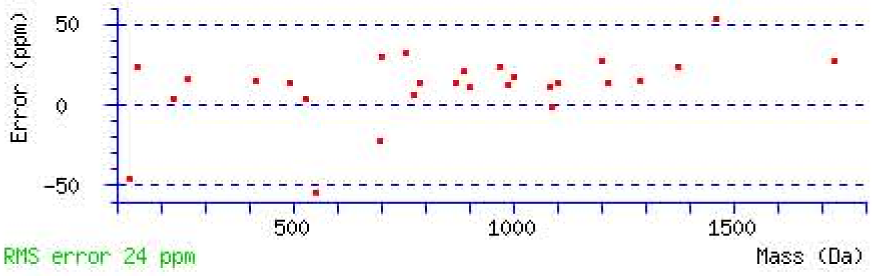
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1988.014465
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 4.8e-006
Matches : 28/138 fragment ions using 51 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							16
2	***229.100525***	115.053900					P	1857.981269	929.494273	1840.954720	920.980998	1839.970704	920.488990	15
3	360.141010	180.574143					M	1760.928505	880.967891	1743.901956	872.454616	1742.917940	871.962608	14
4	***417.162474***	209.084875					G	1629.888020	815.447648	1612.861471	806.934374	1611.877455	806.442366	13
5	***530.246538***	265.626907					L	1572.866556	786.936916	1555.840007	778.423642	1554.855991	777.931634	12
6	617.278566	309.142921			599.268001	300.137638	S	***1459.782492***	730.394884	1442.755943	721.881610	1441.771927	721.389602	11
7	718.326245	359.666761			700.315680	350.661478	T	***1372.750464***	686.878870	1355.723915	678.365596	1354.739899	677.873588	10
8	***775.347709***	388.177493			757.337144	379.172210	G	1271.702785	636.355031	1254.676236	627.841756	1253.692220	627.349748	9
9	***888.431773***	444.719525			870.421208	435.714242	I	***1214.681321***	607.844299	1197.654772	599.331024	1196.670756	598.839016	8
10	***1001.515837***	501.261557			983.505272	492.256274	I	***1101.597257***	551.302267	1084.570708	542.788992	1083.586692	542.296984	7
11	***1088.547865***	544.777571			1070.537300	535.772288	S	***988.513193***	494.760235	971.486644	486.246960	970.502628	485.754952	6
12	***1203.574808***	602.291042			1185.564243	593.285760	D	***901.481165***	451.244221	884.454616	442.730946	883.470600	442.238938	5
13	***1290.606836***	645.807056			1272.596271	636.801774	S	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
14	***1729.832162***	865.419719	1712.805613	856.906445	1711.821597	856.414437	Q	***699.422194***	350.214735	682.395645	341.701461			3
15	1842.916226	921.961751	1825.889677	913.448477	1824.905661	912.956469	I	***260.196868***	130.602072	243.170319	122.088797			2
16							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.9	1988.014465	0.022247	MPMGLSTGIISDSQIK
5.0	1988.047485	-0.010773	YDVSSQVISQLK
4.0	1988.054688	-0.017975	EVGKILCTDCATRPKLK
1.5	1988.051331	-0.014619	MTHKLVFLEDGTSQVRK

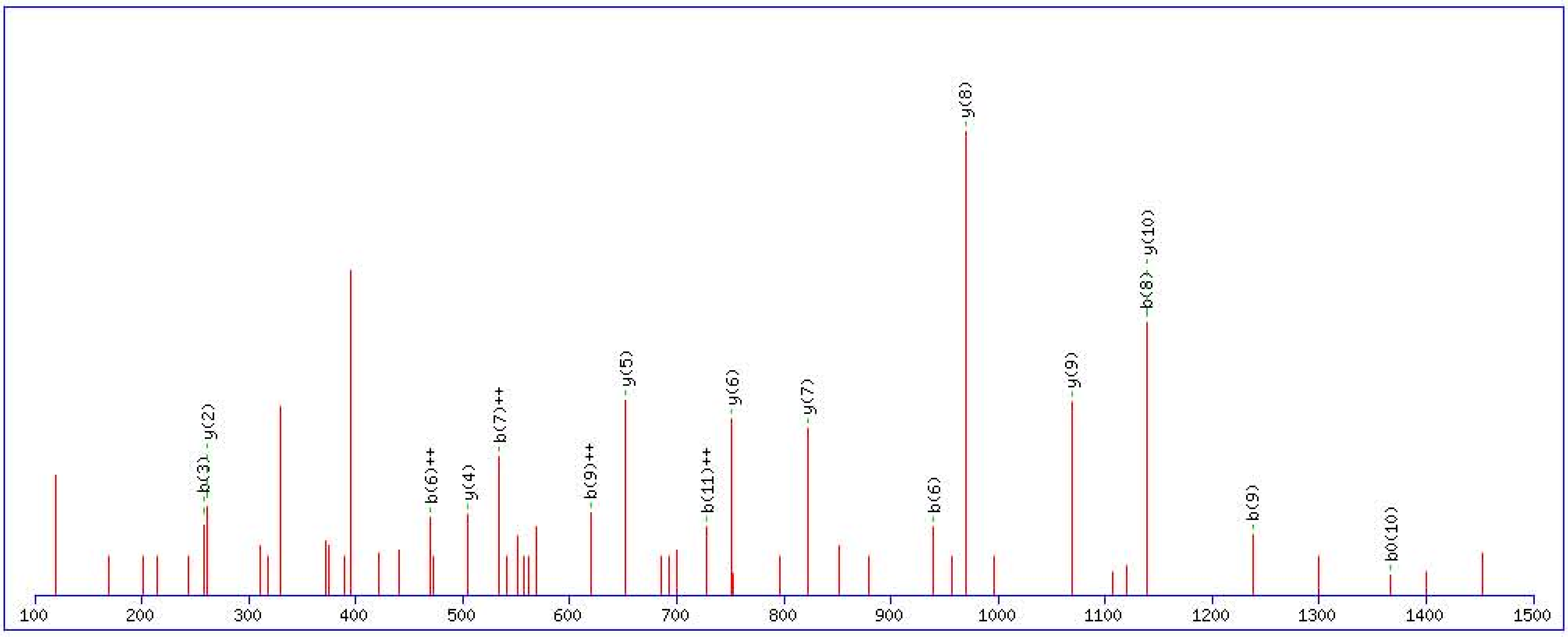
Mascot Search Results

Peptide View

MS/MS Fragmentation of AADIEQQAVFAVFDENK
Found in FA5_HUMAN, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

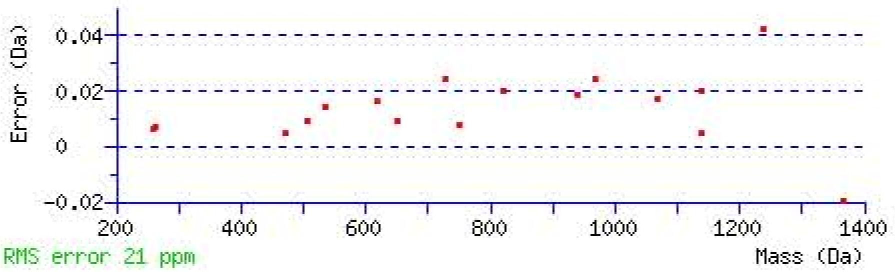
Match to Query 58219: 2205.110232 from(736.044020,3+) rtinseconds(2735) index(65587)
Title: Locus:1.1.1.3256.11 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

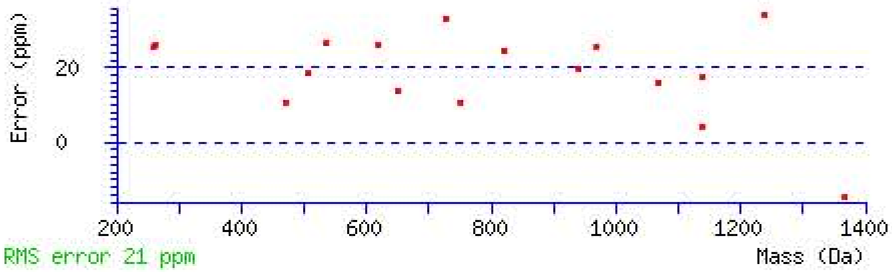
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2205.077591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00027
Matches : 17/174 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	72.044390	36.525833					A							17
2	143.081504	72.044390					A	2135.047769	1068.027522	2118.021220	1059.514248	2117.037204	1059.022240	16
3	**258.108447**	129.557862			240.097882	120.552579	D	2064.010655	1032.508965	2046.984106	1023.995691	2046.000090	1023.503683	15
4	371.192511	186.099894			353.181946	177.094611	I	1948.983712	974.995494	1931.957163	966.482220	1930.973147	965.990212	14
5	500.235104	250.621190			482.224539	241.615908	E	1835.899648	918.453462	1818.873099	909.940188	1817.889083	909.448180	13
6	**939.460430**	**470.233853**	922.433881	461.720579	921.449865	461.228571	Q	1706.857055	853.932166	1689.830506	845.418891	1688.846490	844.926883	12
7	1067.519008	**534.263142**	1050.492459	525.749868	1049.508443	525.257860	Q	1267.631729	634.319503	1250.605180	625.806228	1249.621164	625.314220	11
8	**1138.556122**	569.781699	1121.529573	561.268425	1120.545557	560.776416	A	***1139.573151***	570.290214	1122.546602	561.776939	1121.562586	561.284931	10
9	**1237.624536**	**619.315906**	1220.597987	610.802632	1219.613971	610.310624	V	***1068.536037***	534.771657	1051.509488	526.258382	1050.525472	525.766374	9
10	1384.692950	692.850113	1367.666401	684.336839	1366.682385	683.844831	F	***969.467623***	485.237450	952.441074	476.724175	951.457058	476.232167	8
11	1455.730064	**728.368670**	1438.703515	719.855396	1437.719499	719.363388	A	***822.399209***	411.703243	805.372660	403.189968	804.388644	402.697960	7
12	1554.798478	777.902877	1537.771929	769.389603	1536.787913	768.897595	V	***751.362095***	376.184686	734.335546	367.671411	733.351530	367.179403	6
13	1701.866892	851.437084	1684.840343	842.923810	1683.856327	842.431802	F	***652.293681***	326.650479	635.267132	318.137204	634.283116	317.645196	5
14	1816.893835	908.950556	1799.867286	900.437281	1798.883270	899.945273	D	***505.225267***	253.116271	488.198718	244.602997	487.214702	244.110989	4
15	1945.936428	973.471852	1928.909879	964.958578	1927.925863	964.466570	E	390.198324	195.602800	373.171775	187.089525	372.187759	186.597517	3
16	2059.979355	1030.493315	2042.952806	1021.980041	2041.968790	1021.488033	N	***261.155731***	131.081503	244.129182	122.568229			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	2205.077591	0.032641	AADIEQQAVFAVFDENK
47.7	2205.077591	0.032641	AADIEQQAVFAVFDENK
9.2	2205.080063	0.030169	EKENDELDIQLKVFDENK
3.4	2205.129929	-0.019697	YPGRNGAQMMVHIVFKVAR
0.4	2205.115311	-0.005079	FLPPPGYAPCHEAVLPRER

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

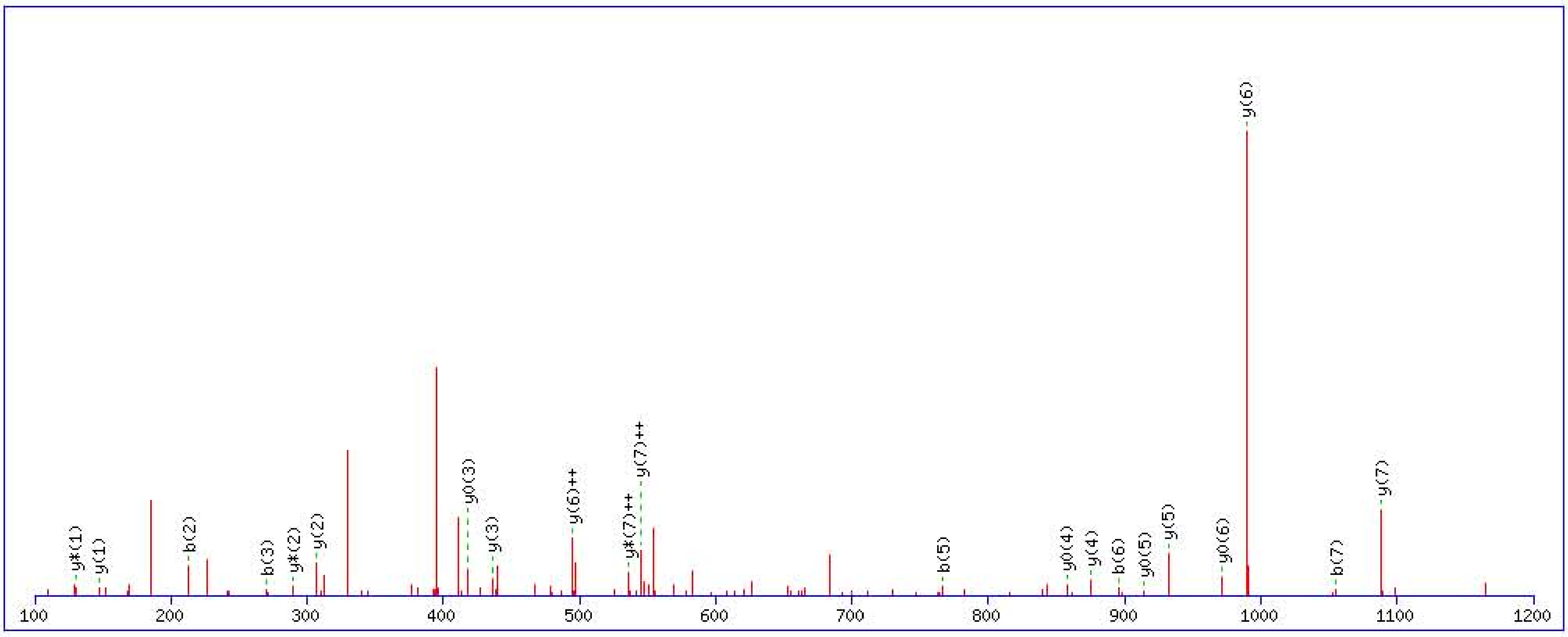
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVGGQECK**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

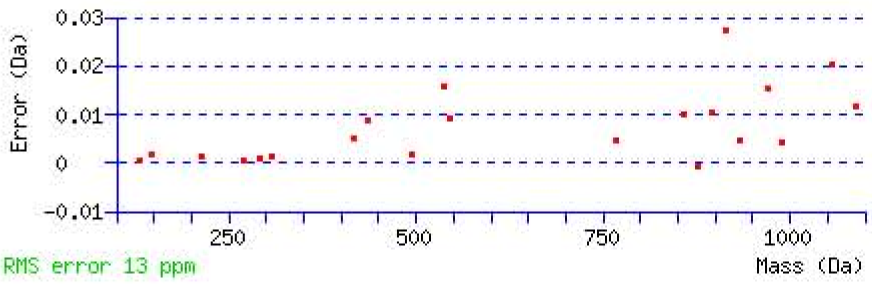
Match to Query 27696: 1200.606228 from(601.310390,2+) rtinseconds(1391) index(56148)
Title: Locus:1.1.1.2790.15 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

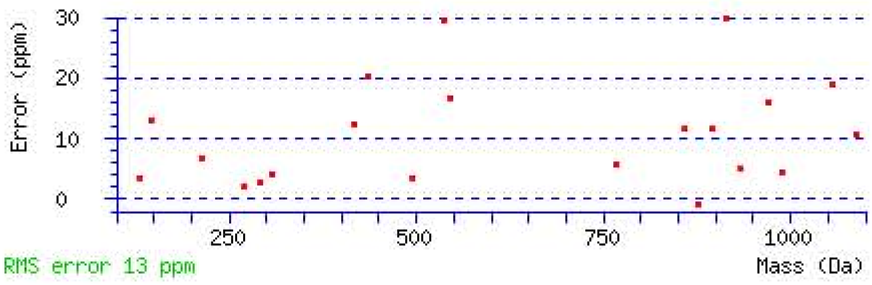
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1200.599503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.0063
Matches : 21/62 fragment ions using 59 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							8
2	**213.159754**	107.083515					V	***1088.522714***	544.764995	1071.496165	536.251721	1070.512149	535.759713	7
3	**270.181218**	135.594247					G	***989.454300***	495.230788	972.427751	486.717514	971.443735	486.225506	6
4	327.202682	164.104979					G	***932.432836***	466.720056	915.406287	458.206782	914.422271	457.714774	5
5	**766.428008**	383.717642	749.401459	375.204368			Q	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
6	**895.470601**	448.238939	878.444052	439.725664	877.460036	439.233656	E	***436.186046***	218.596661	419.159497	210.083386	418.175481	209.591378	3
7	**1055.501250**	528.254263	1038.474701	519.740989	1037.490685	519.248981	C	***307.143453***	154.075364	290.116904	145.562090			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	1200.599503	0.006725	IVGGQECK
4.6	1200.621048	-0.014820	IRQKEEENR
3.5	1200.599503	0.006725	LIQGDGCK
2.0	1200.598587	0.007641	ILADLEEENR
1.9	1200.607376	-0.001148	HTGVKPFQCK
0.6	1200.609863	-0.003635	QTVEADVNGLR
0.5	1200.599487	0.006741	LLNDQCK
0.2	1200.596100	0.010128	LVKYMYDNR

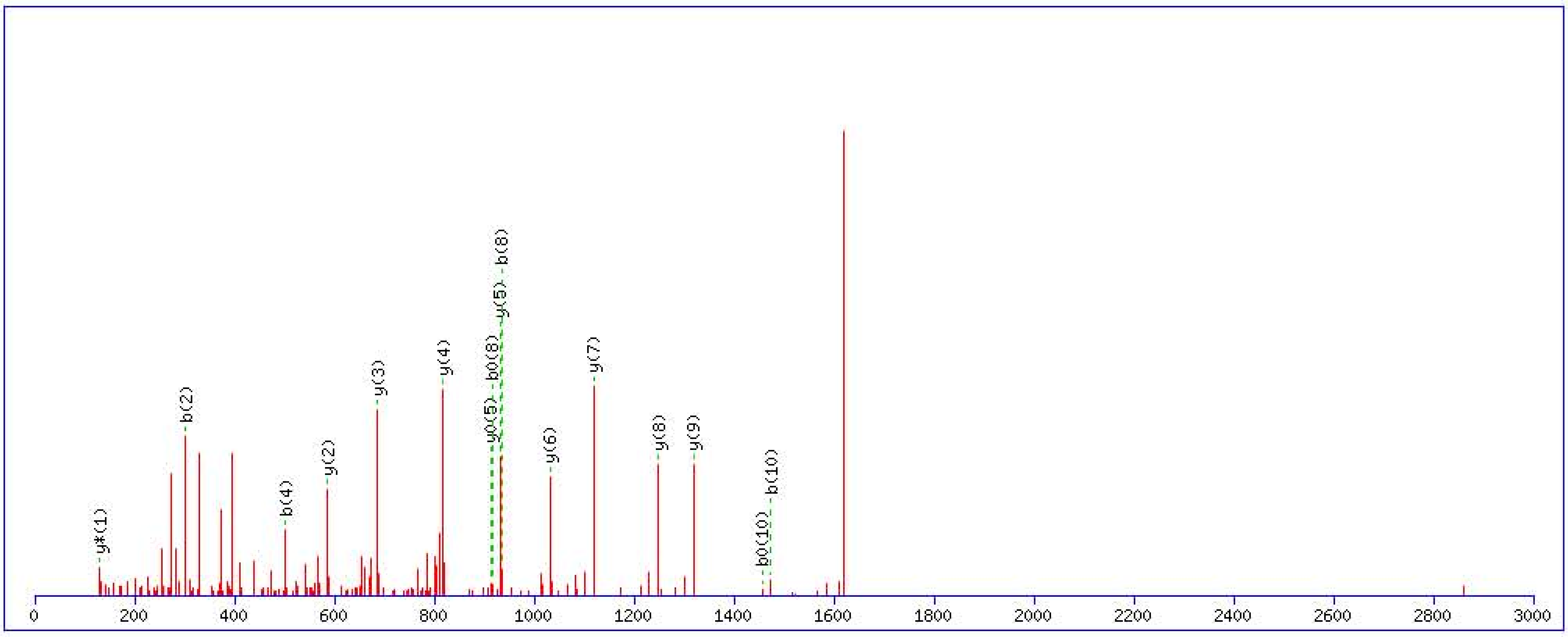
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DWAESTLMTQK**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

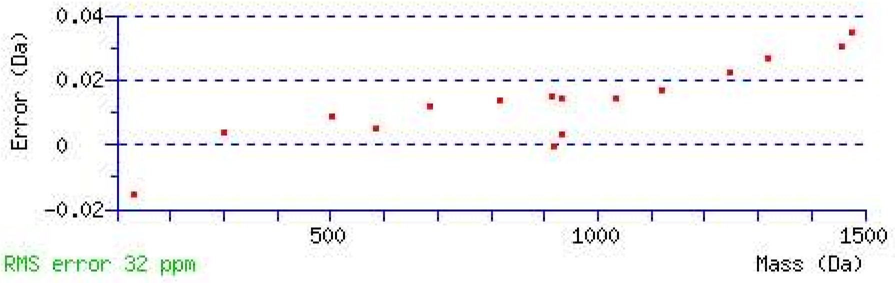
Match to Query 43013: 1619.787048 from(810.900800,2+) rtinseconds(2245) index(62332)
Title: Locus:1.1.1.3086.22 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

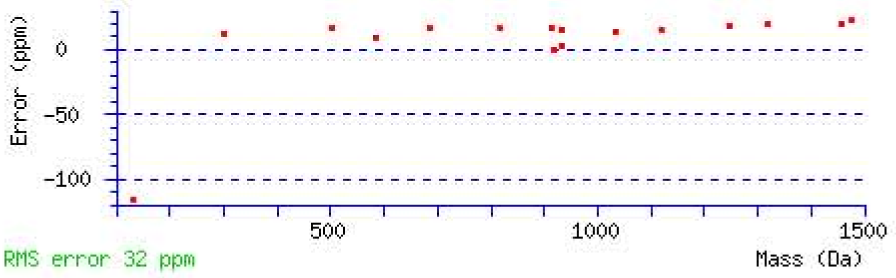
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1619.768738
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00015
Matches : 16/98 fragment ions using 28 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							11
2	**302.113532**	151.560404			284.102967	142.555122	W	1505.749085	753.378180	1488.722536	744.864906	1487.738520	744.372898	10
3	373.150646	187.078961			355.140081	178.073679	A	***1319.669772***	660.338524	1302.643223	651.825250	1301.659207	651.333241	9
4	**502.193239**	251.600258			484.182674	242.594975	E	***1248.632658***	624.819967	1231.606109	616.306693	1230.622093	615.814685	8
5	589.225267	295.116272			571.214702	286.110989	S	***1119.590065***	560.298671	1102.563516	551.785396	1101.579500	551.293388	7
6	690.272946	345.640111			672.262381	336.634829	T	***1032.558037***	516.782657	1015.531488	508.269382	1014.547472	507.777374	6
7	803.357010	402.182143			785.346445	393.176861	L	***931.510358***	466.258817	914.483809	457.745543	913.499793	457.253535	5
8	**934.397495**	467.702386			916.386930	458.697103	M	***818.426294***	409.716785	801.399745	401.203510	800.415729	400.711502	4
9	1035.445174	518.226225			1017.434609	509.220942	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
10	**1474.670500**	737.838888	1457.643951	729.325614	1456.659935	728.833605	Q	***586.338130***	293.672703	569.311581	285.159429			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.0	1619.768738	0.018310	DWAESTLMTQK
9.8	1619.783340	0.003708	MLGNEICLCIVGNK
5.9	1619.805099	-0.018051	IMQEYQLEQK
5.1	1619.793686	-0.006638	MEQPTSSINGEKRK
3.3	1619.793716	-0.006668	LVCAVGSRNGTEETK

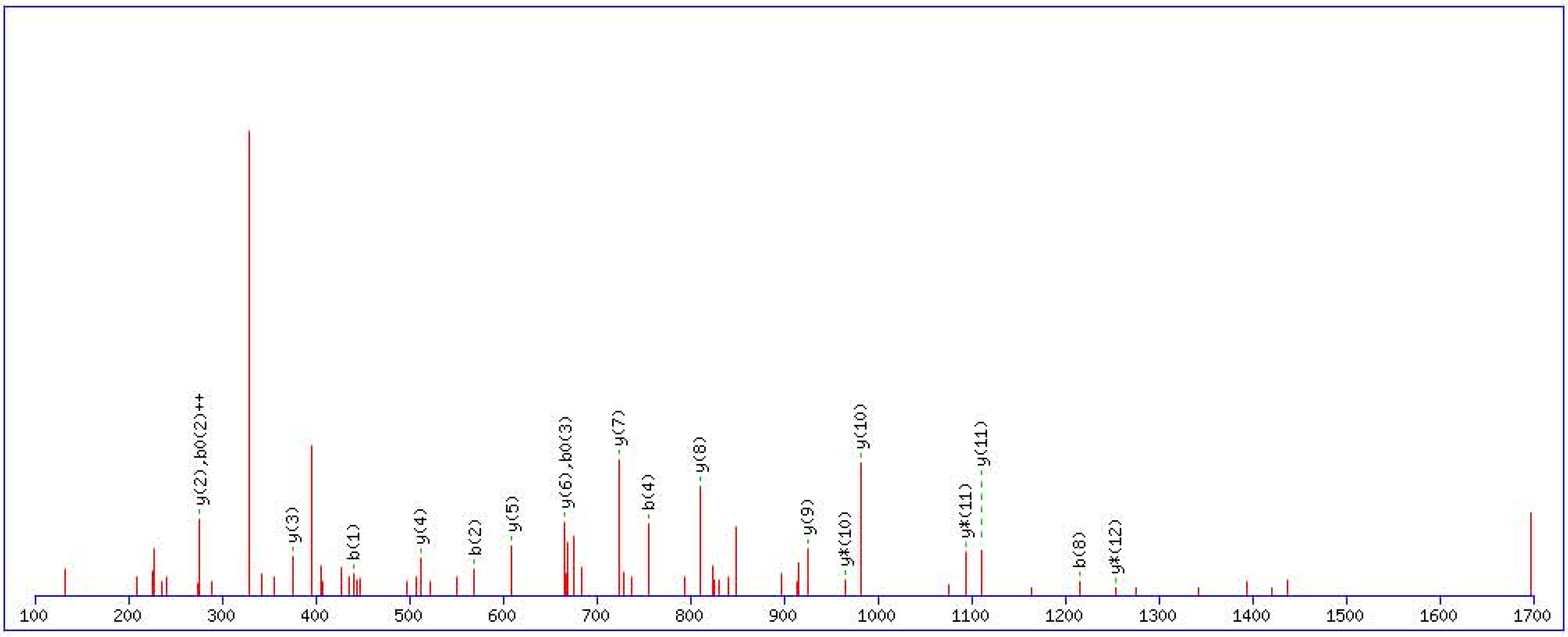
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEDACQGDSGGPHVTR**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

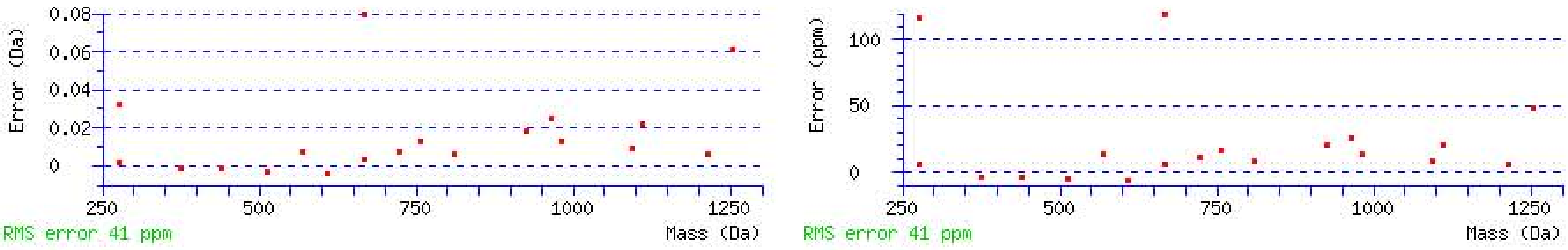
Match to Query 54344: 2023.897032 from(675.639620,3+) rtinseconds(1280) index(55403)
Title: Locus:1.1.1.2751.25 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2023.884033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1     : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 2e-006
Matches : 19/176 fragment ions using 28 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	**440.232602**	220.619939	423.206053	212.106664			Q							16
2	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	E	1585.665961	793.336618	1568.639412	784.823344	1567.655396	784.331336	15
3	684.302138	342.654707	667.275589	334.141433	666.291573	333.649425	D	1456.623368	728.815322	1439.596819	720.302047	1438.612803	719.810039	14
4	**755.339252**	378.173264	738.312703	369.659989	737.328687	369.167982	A	1341.596425	671.301851	1324.569876	662.788576	1323.585860	662.296568	13
5	915.369901	458.188589	898.343352	449.675314	897.359336	449.183306	C	1270.559311	635.783294	1253.532762	627.270019	1252.548746	626.778011	12
6	1043.428479	522.217877	1026.401930	513.704603	1025.417914	513.212595	Q	***1110.528662***	555.767969	1093.502113	547.254695	1092.518097	546.762686	11
7	1100.449943	550.728609	1083.423394	542.215335	1082.439378	541.723327	G	***982.470084***	491.738680	965.443535	483.225406	964.459519	482.733398	10
8	**1215.476886**	608.242081	1198.450337	599.728807	1197.466321	599.236798	D	***925.448620***	463.227948	908.422071	454.714674	907.438055	454.222666	9
9	1302.508914	651.758095	1285.482365	643.244821	1284.498349	642.752813	S	***810.421677***	405.714477	793.395128	397.201202	792.411112	396.709194	8
10	1359.530378	680.268827	1342.503829	671.755553	1341.519813	671.263544	G	***723.389649***	362.198463	706.363100	353.685188	705.379084	353.193180	7
11	1416.551842	708.779559	1399.525293	700.266284	1398.541277	699.774276	G	***666.368185***	333.687731	649.341636	325.174456	648.357620	324.682448	6
12	1513.604606	757.305941	1496.578057	748.792667	1495.594041	748.300658	P	***609.346721***	305.176999	592.320172	296.663724	591.336156	296.171716	5
13	1650.663518	825.835397	1633.636969	817.322122	1632.652953	816.830114	H	***512.293957***	256.650617	495.267408	248.137342	494.283392	247.645334	4
14	1749.731932	875.369604	1732.705383	866.856330	1731.721367	866.364321	V	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.115878	3
15	1850.779611	925.893443	1833.753062	917.380169	1832.769046	916.888161	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
16							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.2	2023.884033	0.012999	QEDACQGDSGGPHVTR
49.4	2023.884033	0.012999	QEDACQGDSGGPHVTR

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

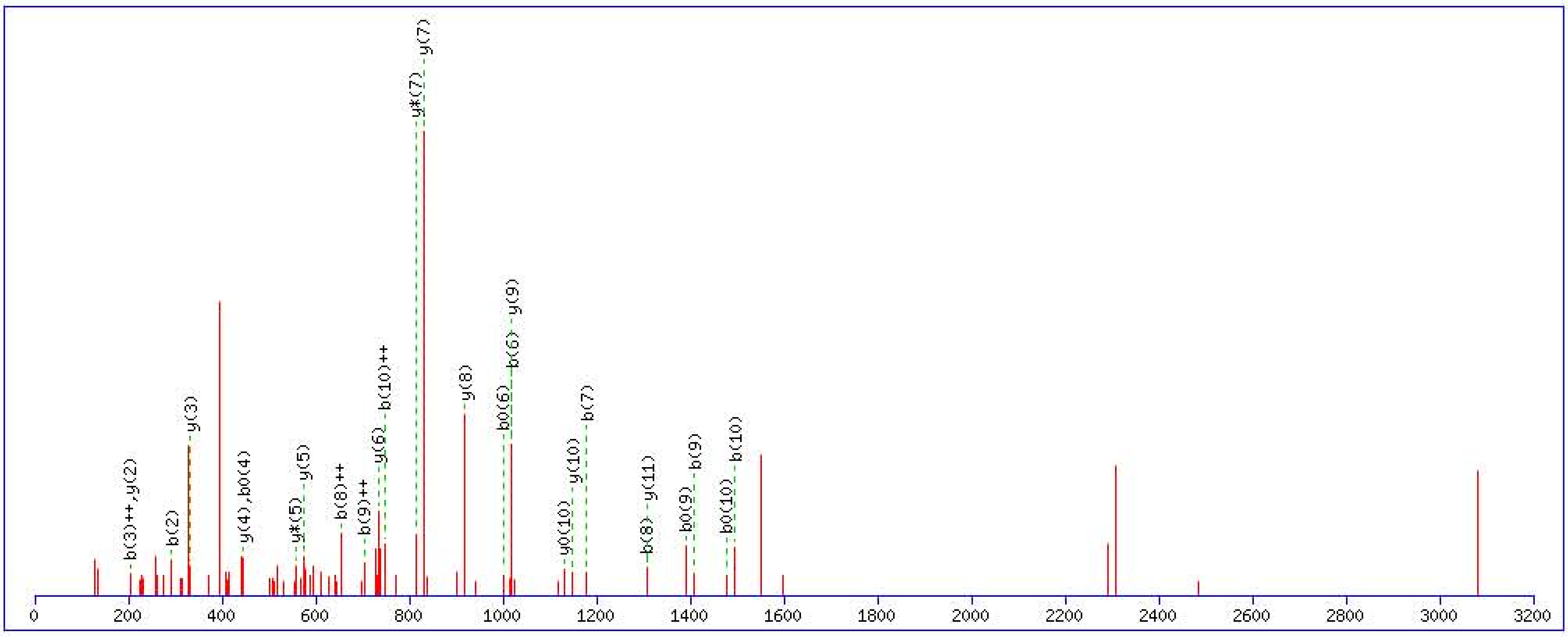
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YKDGDQCETSPCQNQGK**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

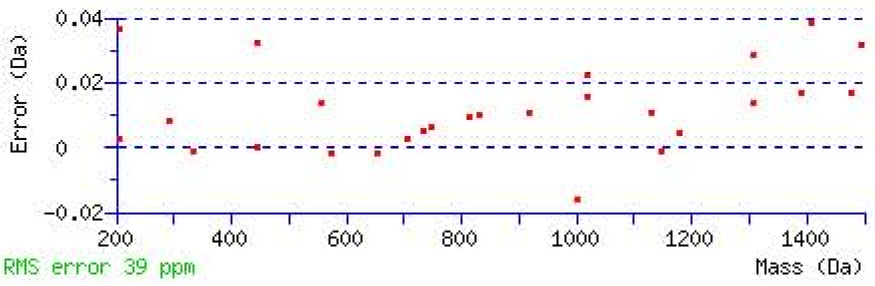
Match to Query 61242: 2325.000132 from(776.007320,3+) rtinseconds(1242) index(55139)
Title: Locus:1.1.1.2738.23 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

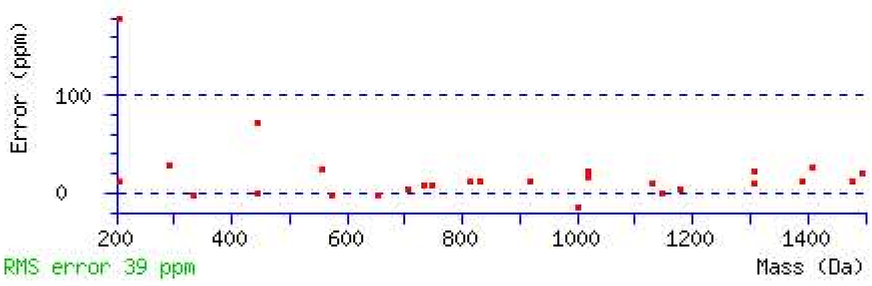
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2324.982407
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 2.8e-006
Matches : 27/172 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					**Y**							**17**
2	**292.165568**	146.586422	275.139019	138.073148			**K**	2162.926352	1081.966814	2145.899803	1073.453539	2144.915787	1072.961531	**16**
3	407.192511	**204.099894**	390.165962	195.586619	389.181946	195.094611	**D**	2034.831389	1017.919333	2017.804840	1009.406058	2016.820824	1008.914050	**15**
4	464.213975	232.610626	447.187426	224.097351	446.203410	223.605343	**G**	1919.804446	960.405861	1902.777897	951.892587	1901.793881	951.400579	**14**
5	579.240918	290.124097	562.214369	281.610823	561.230353	281.118815	**D**	1862.782982	931.895129	1845.756433	923.381855	1844.772417	922.889847	**13**
6	**1018.466244**	509.736760	1001.439695	501.223486	1000.455679	500.731478	**Q**	1747.756039	874.381658	1730.729490	865.868383	1729.745474	865.376375	**12**
7	**1178.496893**	589.752085	1161.470344	581.238810	1160.486328	580.746802	**C**	***1308.530713***	654.768995	1291.504164	646.255720	1290.520148	645.763712	**11**
8	**1307.539486**	**654.273381**	1290.512937	645.760107	1289.528921	645.268098	**E**	***1148.500064***	574.753670	1131.473515	566.240396	1130.489499	565.748388	**10**
9	**1408.587165**	**704.797220**	1391.560616	696.283946	1390.576600	695.791938	**T**	***1019.457471***	510.232374	1002.430922	501.719099	1001.446906	501.227091	**9**
10	**1495.619193**	**748.313235**	1478.592644	739.799960	1477.608628	739.307952	**S**	***918.409792***	459.708534	901.383243	451.195260	900.399227	450.703252	**8**
11	1592.671957	796.839617	1575.645408	788.326342	1574.661392	787.834334	**P**	***831.377764***	416.192520	814.351215	407.679246			**7**
12	1752.702606	876.854941	1735.676057	868.341667	1734.692041	867.849659	**C**	***734.325000***	367.666138	717.298451	359.152864			**6**
13	1880.761184	940.884230	1863.734635	932.370956	1862.750619	931.878948	**Q**	***574.294351***	287.650814	557.267802	279.137539			**5**
14	1994.804111	997.905694	1977.777562	989.392419	1976.793546	988.900411	**N**	***446.235773***	223.621524	429.209224	215.108250			**4**
15	2122.862689	1061.934982	2105.836140	1053.421708	2104.852124	1052.929700	**Q**	***332.192846***	166.600061	315.166297	158.086787			**3**
16	2179.884153	1090.445714	2162.857604	1081.932440	2161.873588	1081.440432	**G**	***204.134268***	102.570772	187.107719	94.057497			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.0	2324.982407	0.017725	YKDGDQCETSPCQNQGK

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

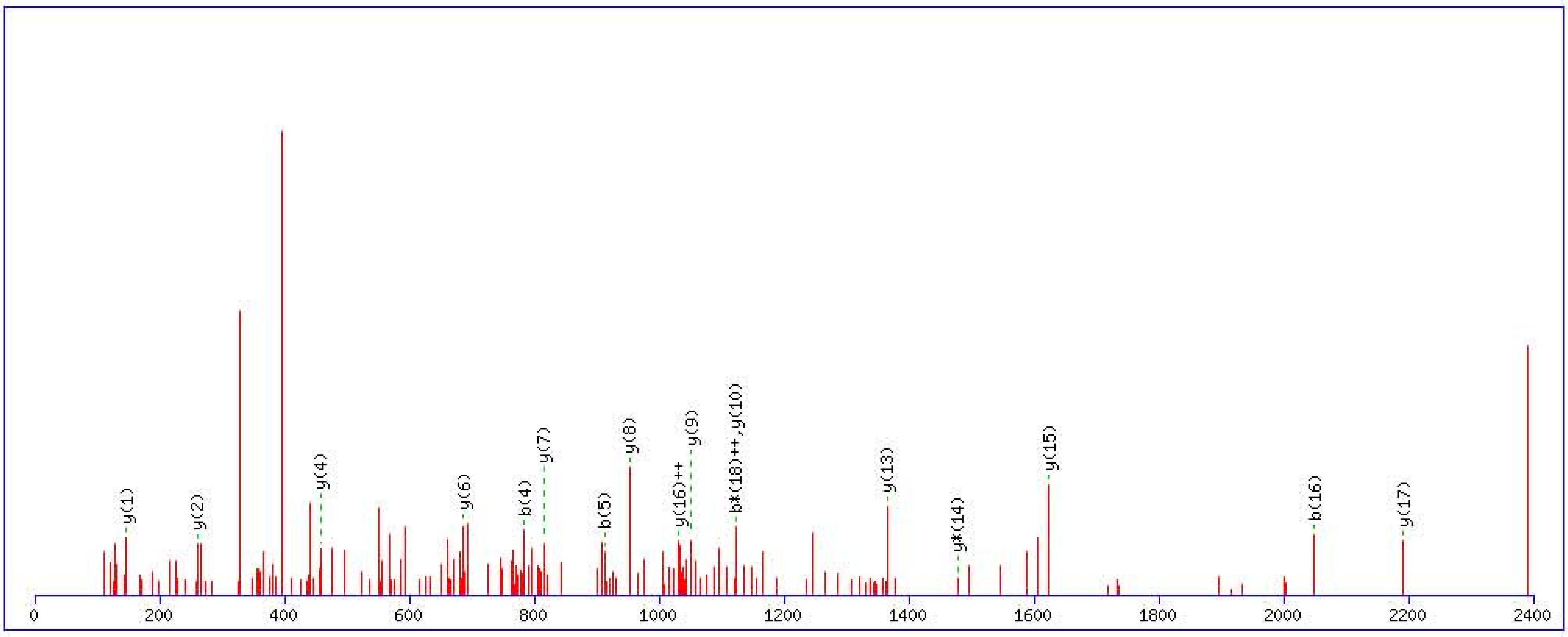
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NTEQEEGGEAVHEVEVVIK**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

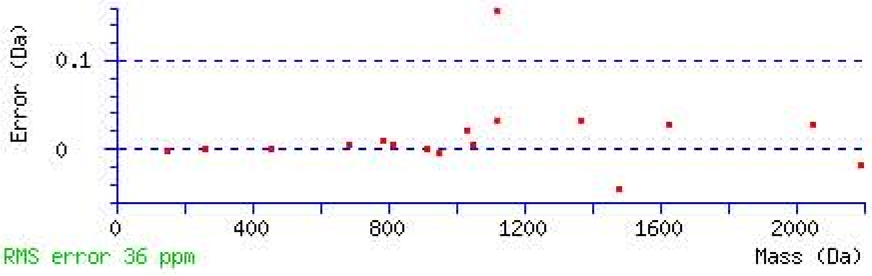
Match to Query 62541: 2406.204642 from(803.075490,3+) rtinseconds(2161) index(61662)
Title: Locus:1.1.1.3057.17 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

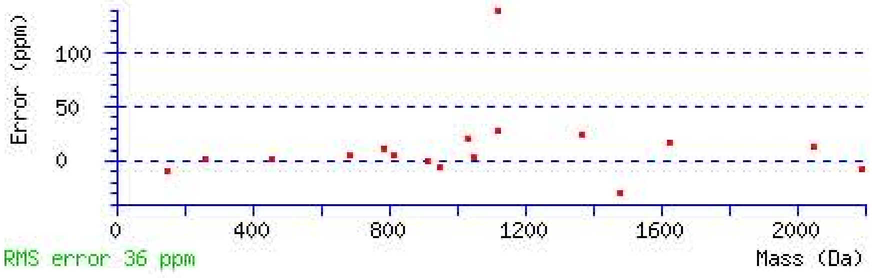
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2406.173676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 4.7e-005
Matches : 17/206 fragment ions using 40 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							19
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	T	2293.138041	1147.072658	2276.111492	1138.559384	2275.127476	1138.067376	18
3	345.140475	173.073875	328.113926	164.560601	327.129910	164.068593	E	***2192.090362***	1096.548819	2175.063813	1088.035544	2174.079797	1087.543536	17
4	**784.365801**	392.686539	767.339252	384.173264	766.355236	383.681256	Q	2063.047769	1032.027522	2046.021220	1023.514248	2045.037204	1023.022240	16
5	**913.408394**	457.207835	896.381845	448.694561	895.397829	448.202553	E	***1623.822443***	812.414860	1606.795894	803.901585	1605.811878	803.409577	15
6	1042.450987	521.729131	1025.424438	513.215857	1024.440422	512.723849	E	1494.779850	747.893563	1477.753301	739.380289	1476.769285	738.888281	14
7	1099.472451	550.239863	1082.445902	541.726589	1081.461886	541.234581	G	***1365.737257***	683.372267	1348.710708	674.858992	1347.726692	674.366984	13
8	1156.493915	578.750595	1139.467366	570.237321	1138.483350	569.745313	G	1308.715793	654.861535	1291.689244	646.348260	1290.705228	645.856252	12
9	1285.536508	643.271892	1268.509959	634.758618	1267.525943	634.266609	E	1251.694329	626.350803	1234.667780	617.837528	1233.683764	617.345520	11
10	1356.573622	678.790449	1339.547073	670.277175	1338.563057	669.785166	A	***1122.651736***	561.829506	1105.625187	553.316232	1104.641171	552.824224	10
11	1455.642036	728.324656	1438.615487	719.811382	1437.631471	719.319373	V	***1051.614622***	526.310949	1034.588073	517.797675	1033.604057	517.305667	9
12	1592.700948	796.854112	1575.674399	788.340838	1574.690383	787.848829	H	***952.546208***	476.776742	935.519659	468.263468	934.535643	467.771460	8
13	1721.743541	861.375409	1704.716992	852.862134	1703.732976	852.370126	E	***815.487296***	408.247286	798.460747	399.734012	797.476731	399.242004	7
14	1820.811955	910.909616	1803.785406	902.396341	1802.801390	901.904333	V	***686.444703***	343.725990	669.418154	335.212715	668.434138	334.720707	6
15	1949.854548	975.430912	1932.827999	966.917638	1931.843983	966.425630	E	587.376289	294.191783	570.349740	285.678508	569.365724	285.186500	5
16	**2048.922962**	1024.965119	2031.896413	1016.451845	2030.912397	1015.959837	V	***458.333696***	229.670486	441.307147	221.157212			4
17	2147.991376	1074.499326	2130.964827	1065.986051	2129.980811	1065.494043	V	359.265282	180.136279	342.238733	171.623005			3
18	2261.075440	1131.041358	2244.048891	1122.528083	2243.064875	1122.036075	I	***260.196868***	130.602072	243.170319	122.088798			2
19							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.2	2406.173676	0.030966	NTEQEEGGEAVHEVEVVIK
2.1	2406.218338	-0.013696	EPVQMELSPPMGVVQK

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

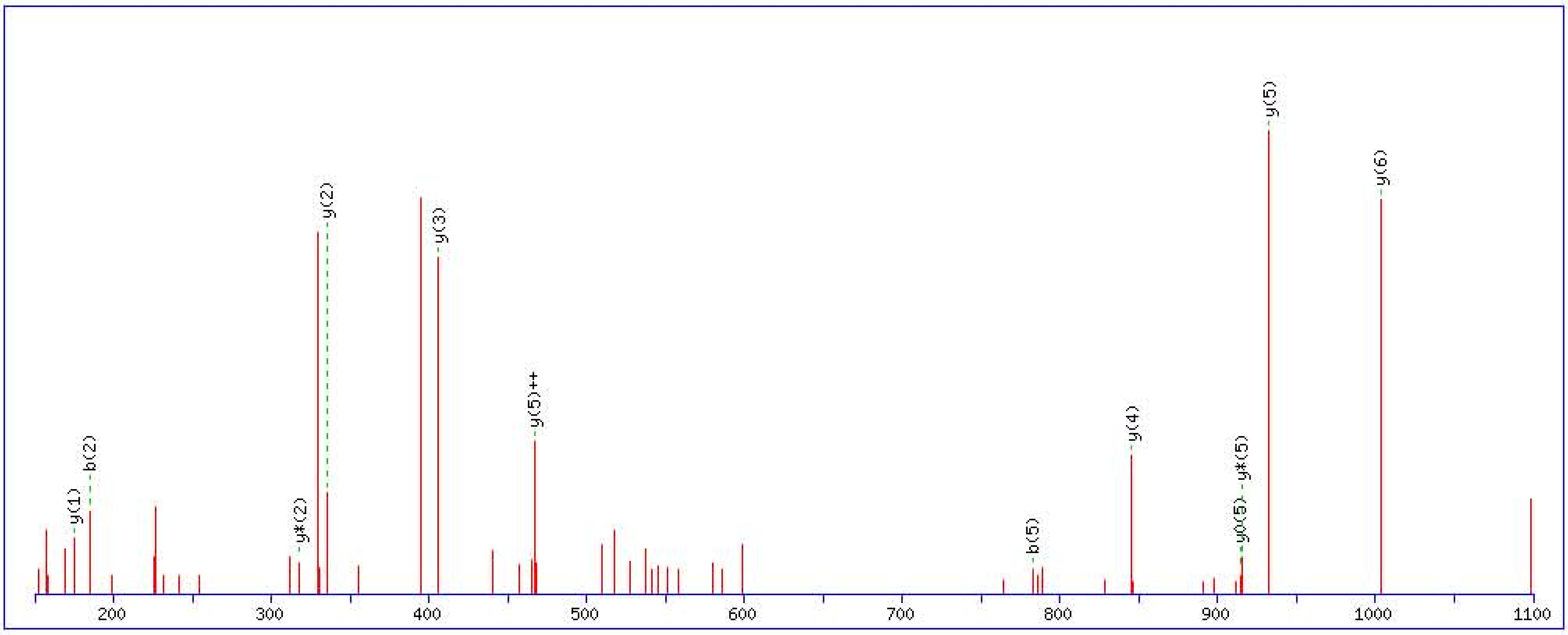
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LASQACR**
Found in **FA12_HUMAN**, Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

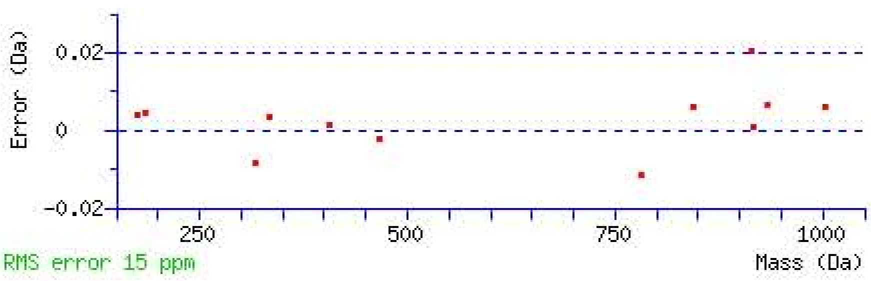
Match to Query 23570: 1115.563268 from(558.788910,2+) rtinseconds(1344) index(74004)
Title: Locus:1.1.1.2682.23 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

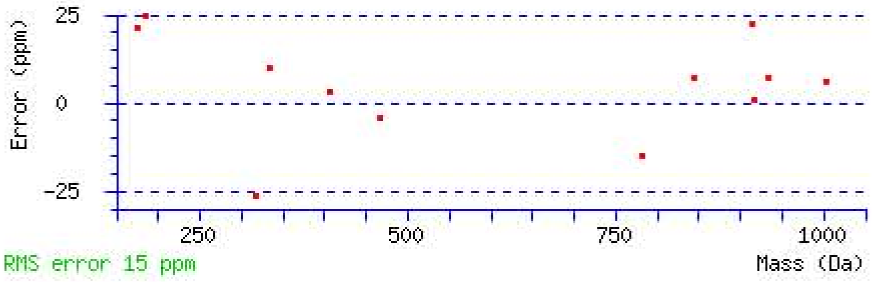
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1115.557953
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.032
Matches : 12/54 fragment ions using 30 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							7
2	**185.128454**	93.067865					A	***1003.481183***	502.244230	986.454634	493.730955	985.470618	493.238947	6
3	272.160482	136.583879			254.149917	127.578596	S	***932.444069***	466.725673	915.417520	458.212398	914.433504	457.720390	5
4	711.385808	356.196542	694.359259	347.683268	693.375243	347.191260	Q	***845.412041***	423.209659	828.385492	414.696384			4
5	**782.422922**	391.715099	765.396373	383.201824	764.412357	382.709816	A	***406.186715***	203.596995	389.160166	195.083721			3
6	942.453571	471.730424	925.427022	463.217149	924.443006	462.725141	C	***335.149601***	168.078438	318.123052	159.565164			2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.7	1115.557953	0.005315	LASQACR
11.1	1115.579544	-0.016276	LAGSRRDGER
1.6	1115.550552	0.012716	LAAGSRCPER
1.6	1115.546722	0.016546	LAQDACK

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

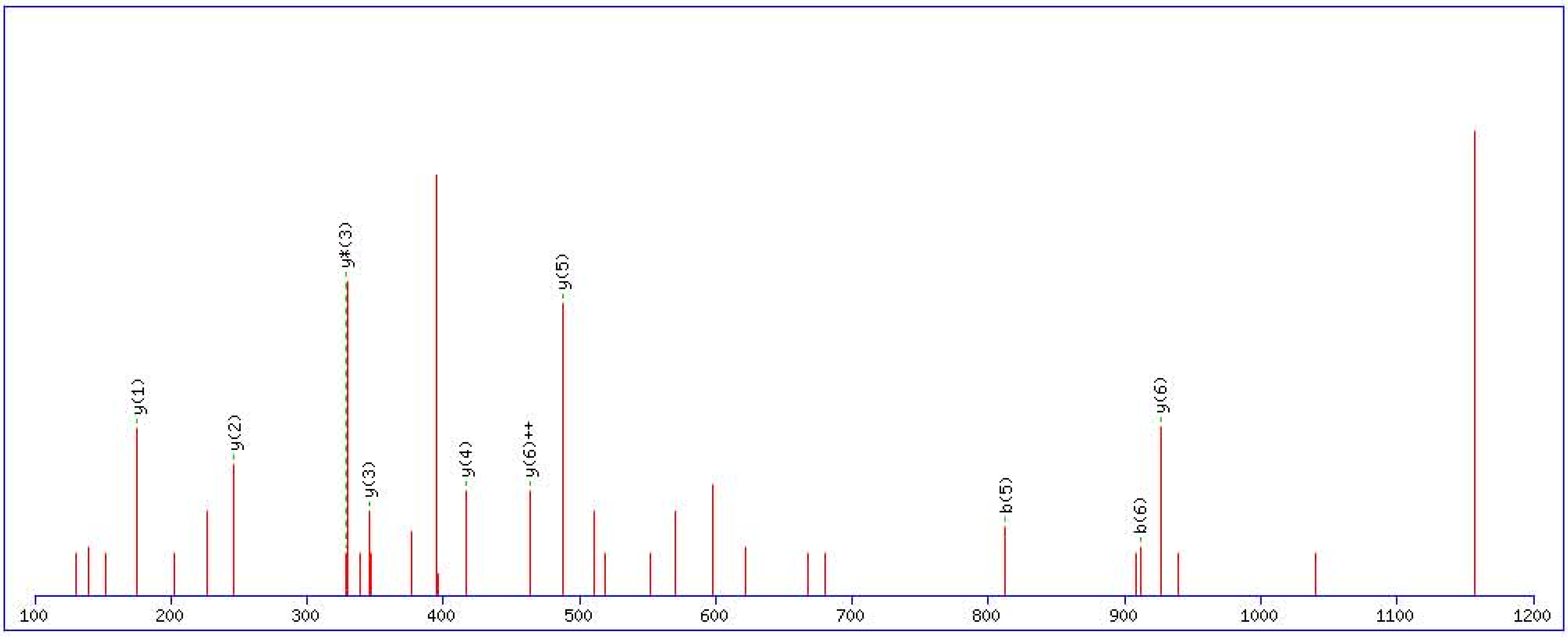
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEQAAVAR**
Found in **FA12_HUMAN**, Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

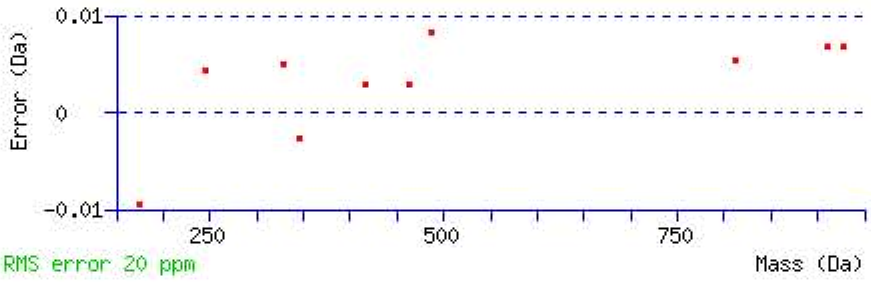
Match to Query 25917: 1155.607748 from(578.811150,2+) rtinseconds(1352) index(37819)
Title: Locus:1.1.1.2754.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

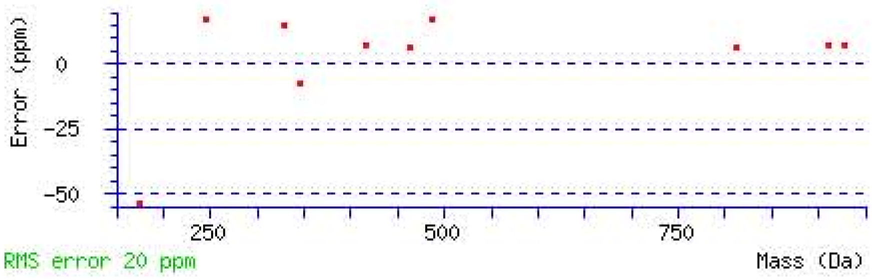


```
Monoisotopic mass of neutral peptide Mr(calc): 1155.607010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.019
Matches : 10/68 fragment ions using 23 most intense peaks   (help)
```

#	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							8
2	231.097548	116.052412			213.086983	107.047130	E	1055.566627	528.286951	1038.540078	519.773677	1037.556062	519.281669	7
3	670.322874	335.665075	653.296325	327.151801	652.312309	326.659793	Q	***926.524034***	463.765655	909.497485	455.252380			6
4	741.359988	371.183632	724.333439	362.670358	723.349423	362.178350	A	***487.298708***	244.152992	470.272159	235.639717			5
5	**812.397102**	406.702189	795.370553	398.188915	794.386537	397.696907	A	***416.261594***	208.634435	399.235045	200.121160			4
6	**911.465516**	456.236396	894.438967	447.723121	893.454951	447.231113	V	***345.224480***	173.115878	328.197931	164.602603			3
7	982.502630	491.754953	965.476081	483.241678	964.492065	482.749670	A	***246.156066***	123.581671	229.129517	115.068396			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 20 ppm



RMS error 20 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.7	1155.607010	0.000738	TEQAAVAR
11.5	1155.607025	0.000723	VQDSAVAR
8.2	1155.624771	-0.017023	LQSLPEGSLGR
2.2	1155.622269	-0.014521	QAWLTAR
1.0	1155.610855	-0.003107	GAGAGLSRPGSAR
0.4	1155.624756	-0.017008	ELEQQLAAVR
0.4	1155.610840	-0.003092	GELPRDSRAR
0.4	1155.624771	-0.017023	NLLDVIDQAR
0.3	1155.599594	0.008154	QAQGALAAAEAR
0.1	1155.603653	0.004095	FSEITPHAVR

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

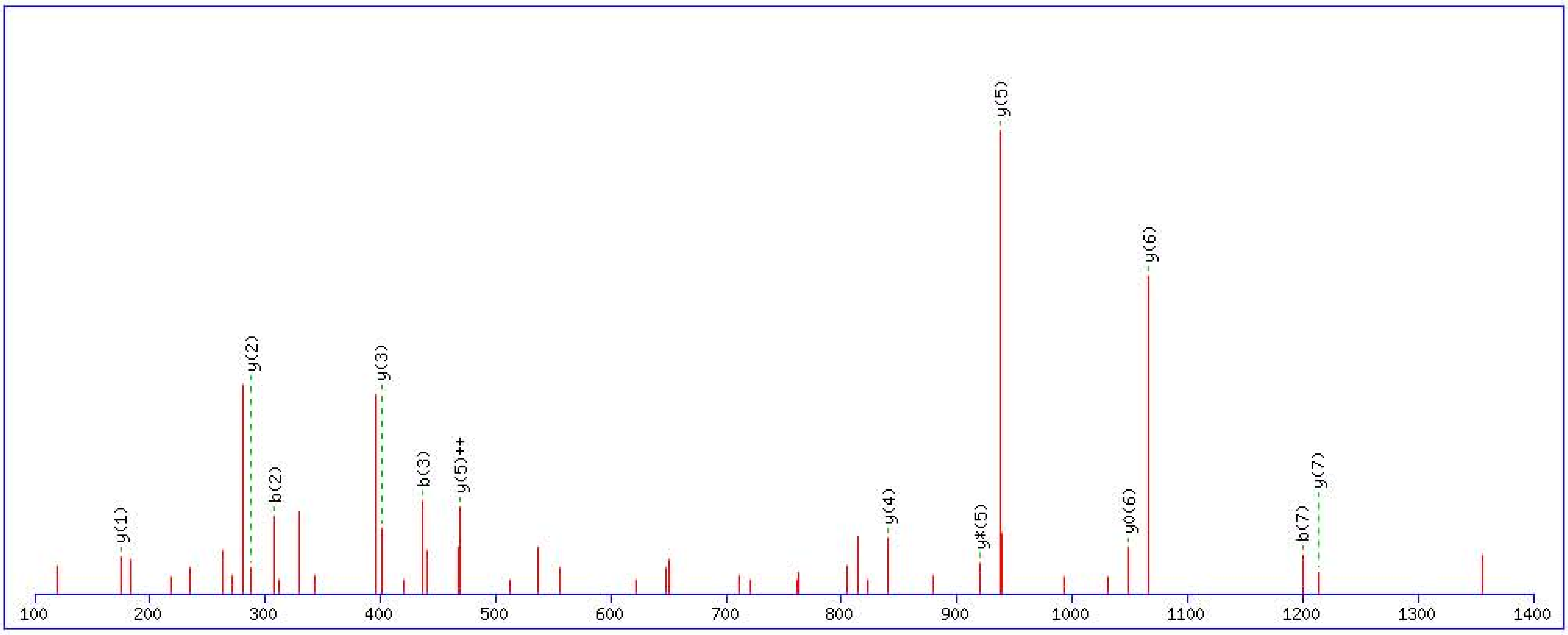
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CFEPQLLR**
Found in **FA12_HUMAN**, Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

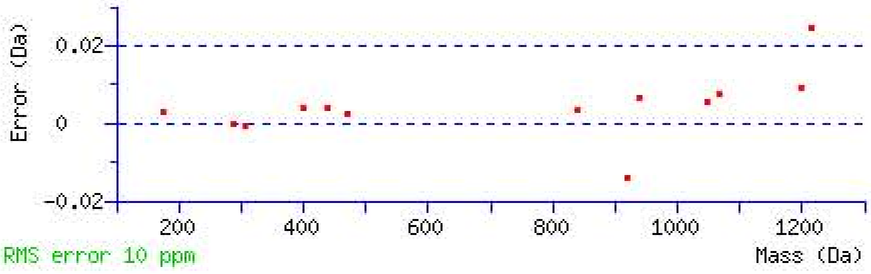
Match to Query 33619: 1372.712708 from(687.363630,2+) rtinseconds(2194) index(79893)
Title: Locus:1.1.1.2978.8 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

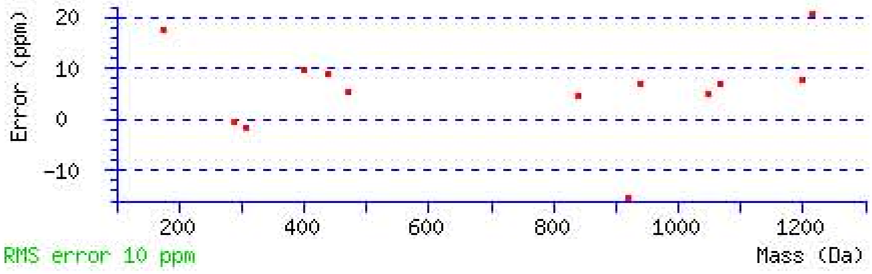
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1372.699539
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.027
Matches : 13/62 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600					C							8
2	**308.106339**	154.556807					F	***1213.676177***	607.341726	1196.649628	598.828452	1195.665612	598.336444	7
3	**437.148932**	219.078104			419.138367	210.072822	E	***1066.607763***	533.807519	1049.581214	525.294245	1048.597198	524.802237	6
4	534.201696	267.604486			516.191131	258.599204	P	***937.565170***	469.286223	920.538621	460.772948			5
5	973.427022	487.217149	956.400473	478.703875	955.416457	478.211867	Q	***840.512406***	420.759841	823.485857	412.246566			4
6	1086.511086	543.759181	1069.484537	535.245907	1068.500521	534.753898	L	***401.287080***	201.147178	384.260531	192.633903			3
7	**1199.595150**	600.301213	1182.568601	591.787939	1181.584585	591.295930	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 CFEPQLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.3	1372.699539	0.013169	CFEPQLLR
9.9	1372.710770	0.001938	QPRMLDFR
2.1	1372.703369	0.009339	NPPKQEGHR
2.1	1372.717331	-0.004623	QGLPVVMPVFDR
0.3	1372.692123	0.020585	HIGNPEYLMKR

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

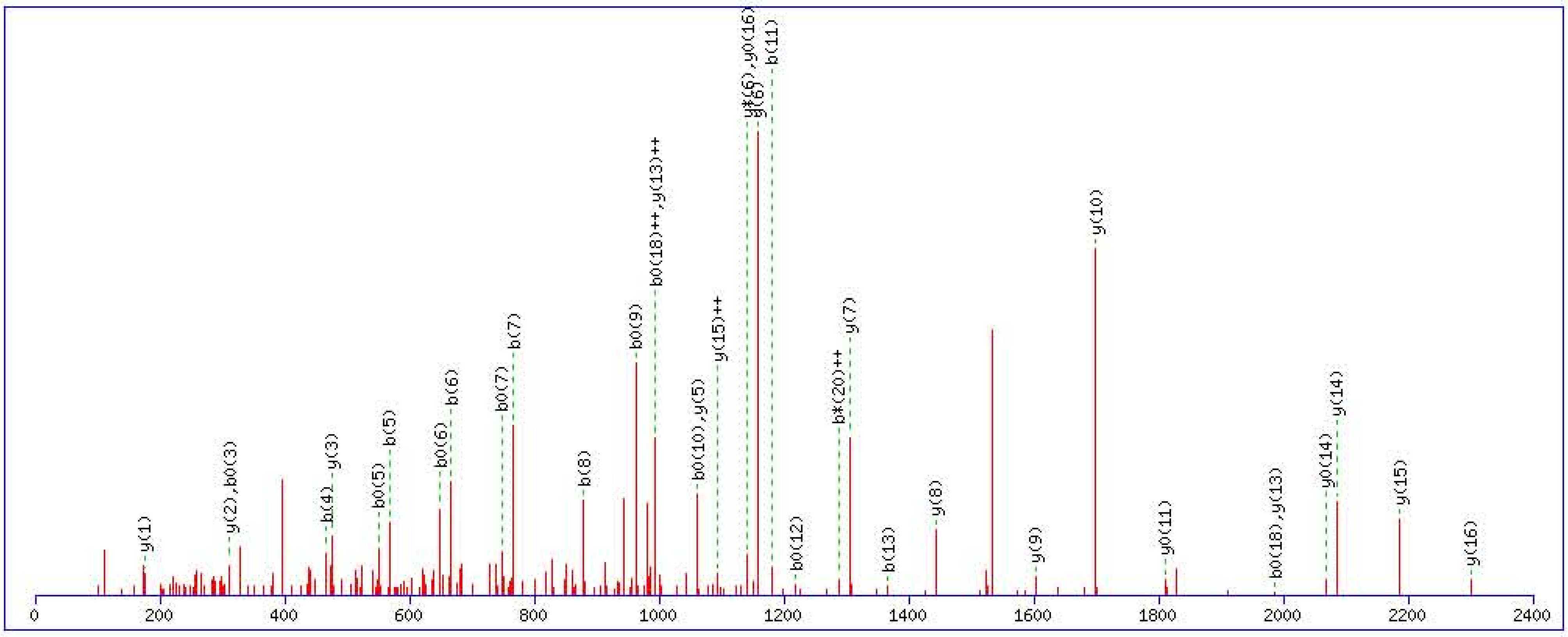
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEEHTVVLTVTGEPCHFPFQYHR**
Found in **FA12_HUMAN**, Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

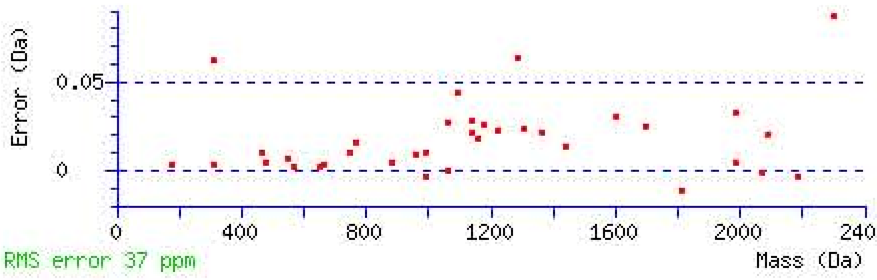
Match to Query 72157: 3064.503216 from(767.133080,4+) rtinseconds(2128) index(79391)
Title: Locus:1.1.1.2955.14 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

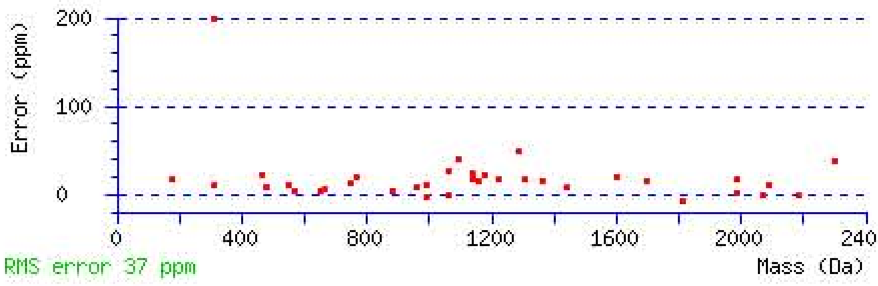
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3064.468796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20 : Biotin:Thermo-21345 (Q)
Ions Score: 72 **Expect:** 1.7e-006
Matches : 36/204 fragment ions using 57 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							23
2	201.086983	101.047130			183.076418	92.041847	E	2994.438934	1497.723105	2977.412385	1489.209830	2976.428369	1488.717822	22
3	330.129576	165.568426			312.119011	156.563144	E	2865.396341	1433.201808	2848.369792	1424.688534	2847.385776	1424.196526	21
4	***467.188488***	234.097882			449.177923	225.092599	H	2736.353748	1368.680512	2719.327199	1360.167237	2718.343183	1359.675229	20
5	***568.236167***	284.621722			550.225602	275.616439	T	2599.294836	1300.151056	2582.268287	1291.637781	2581.284271	1291.145773	19
6	***667.304581***	334.155929			649.294016	325.150646	V	2498.247157	1249.627216	2481.220608	1241.113942	2480.236592	1240.621934	18
7	***766.372995***	383.690136			748.362430	374.684853	V	2399.178743	1200.093009	2382.152194	1191.579735	2381.168178	1191.087727	17
8	***879.457059***	440.232168			861.446494	431.226885	L	***2300.110329***	1150.558802	2283.083780	1142.045528	2282.099764	1141.553520	16
9	980.504738	490.756007			962.494173	481.750724	T	***2187.026265***	1094.016770	2169.999716	1085.503496	2169.015700	1085.011488	15
10	1079.573152	540.290214			1061.562587	531.284931	V	***2085.978586***	1043.492931	2068.952037	1034.979656	2067.968021	1034.487648	14
11	***1180.620831***	590.814054			1162.610266	581.808771	T	***1986.910172***	993.958724	1969.883623	985.445450	1968.899607	984.953442	13
12	1237.642295	619.324785			1219.631730	610.319503	G	1885.862493	943.434885	1868.835944	934.921610	1867.851928	934.429602	12
13	***1366.684888***	683.846082			1348.674323	674.840800	E	1828.841029	914.924153	1811.814480	906.410878	1810.830464	905.918870	11
14	1463.737652	732.372464			1445.727087	723.367182	P	***1699.798436***	850.402856	1682.771887	841.889582			10
15	1623.768301	812.387789			1605.757736	803.382506	C	***1602.745672***	801.876474	1585.719123	793.363200			9
16	1760.827213	880.917245			1742.816648	871.911962	H	***1442.715023***	721.861150	1425.688474	713.347875			8
17	1907.895627	954.451452			1889.885062	945.446169	F	***1305.656111***	653.331694	1288.629562	644.818419			7
18	2004.948391	1002.977834			1986.937826	993.972551	P	***1158.587697***	579.797487	1141.561148	571.284212			6
19	2152.016805	1076.512040			2134.006240	1067.506758	F	***1061.534933***	531.271105	1044.508384	522.757830			5
20	2591.242131	1296.124703	2574.215582	1287.611429	2573.231566	1287.119421	Q	914.466519	457.736898	897.439970	449.223623			4
21	2754.305460	1377.656368	2737.278911	1369.143093	2736.294895	1368.651085	Y	***475.241193***	238.124234	458.214644	229.610960			3
22	2891.364372	1446.185824	2874.337823	1437.672549	2873.353807	1437.180541	H	***312.177864***	156.592570	295.151315	148.079295			2
23							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.8	3064.468796	0.034420	AEEHTVVLTVTGEPCHFPFQYHR

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

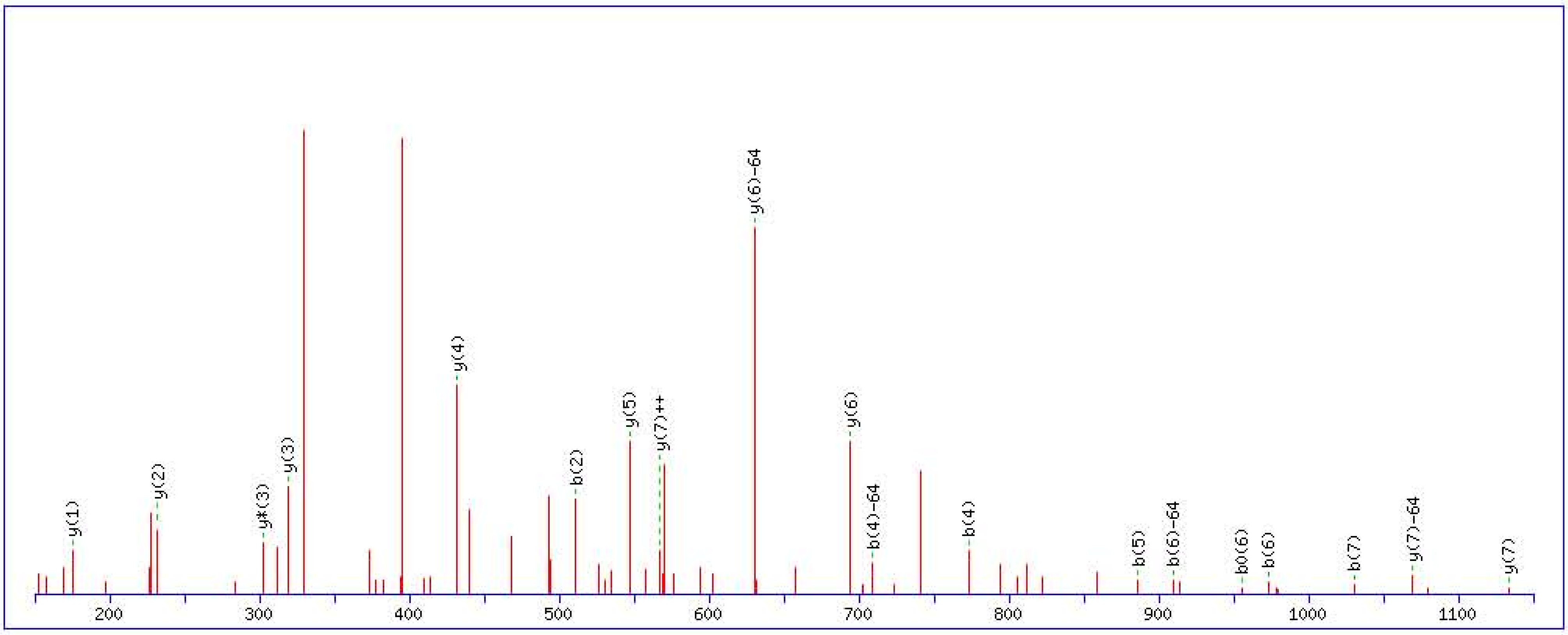
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQMDLSGR**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

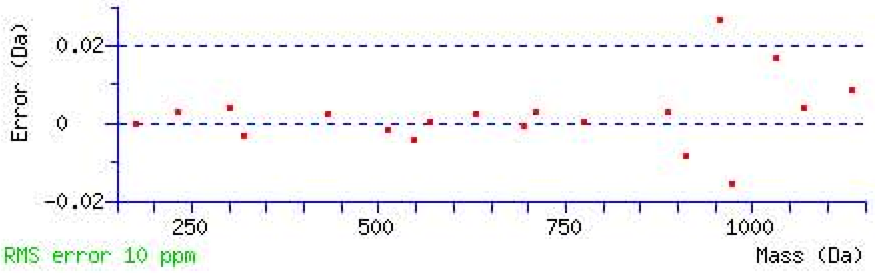
Match to Query 27745: 1203.576568 from(602.795560,2+) rtinseconds(1432) index(38371)
Title: Locus:1.1.1.2782.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

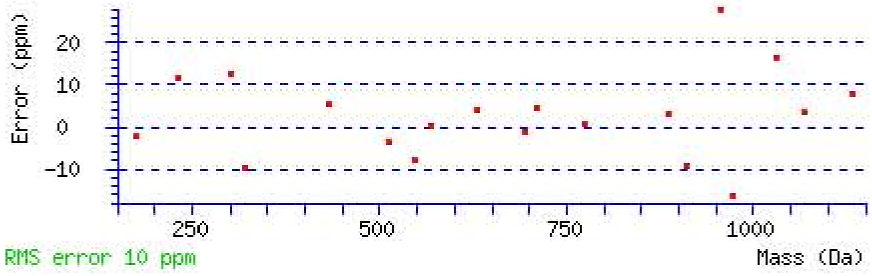
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1203.574005
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
M3      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 47  Expect: 0.00013
Matches : 19/112 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							8
2	**511.269716**	256.138496	494.243167	247.625221			Q	***1133.544177***	567.275727	1116.517628	558.762452	1115.533612	558.270444	7
3	658.305116	329.656196	641.278567	321.142922			M	***694.318851***	347.663064	677.292302	339.149789	676.308286	338.657781	6
4	**773.332059**	387.169668	756.305510	378.656393	755.321494	378.164385	D	***547.283451***	274.145364	530.256902	265.632089	529.272886	265.140081	5
5	**886.416123**	443.711700	869.389574	435.198425	868.405558	434.706417	L	***432.256508***	216.631892	415.229959	208.118617	414.245943	207.626609	4
6	**973.448151**	487.227713	956.421602	478.714439	955.437586	478.222431	S	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	3
7	**1030.469615**	515.738446	1013.443066	507.225171	1012.459050	506.733163	G	***232.140416***	116.573846	215.113867	108.060571			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.2	1203.574005	0.002563	AQMDLSGR
5.5	1203.577820	-0.001252	EAQQRQAAMR
5.2	1203.581848	-0.005280	ALCSAAQAAWR
1.4	1203.584351	-0.007783	SGSPISSEERR
0.6	1203.573090	0.003478	ETAAAAEEKER

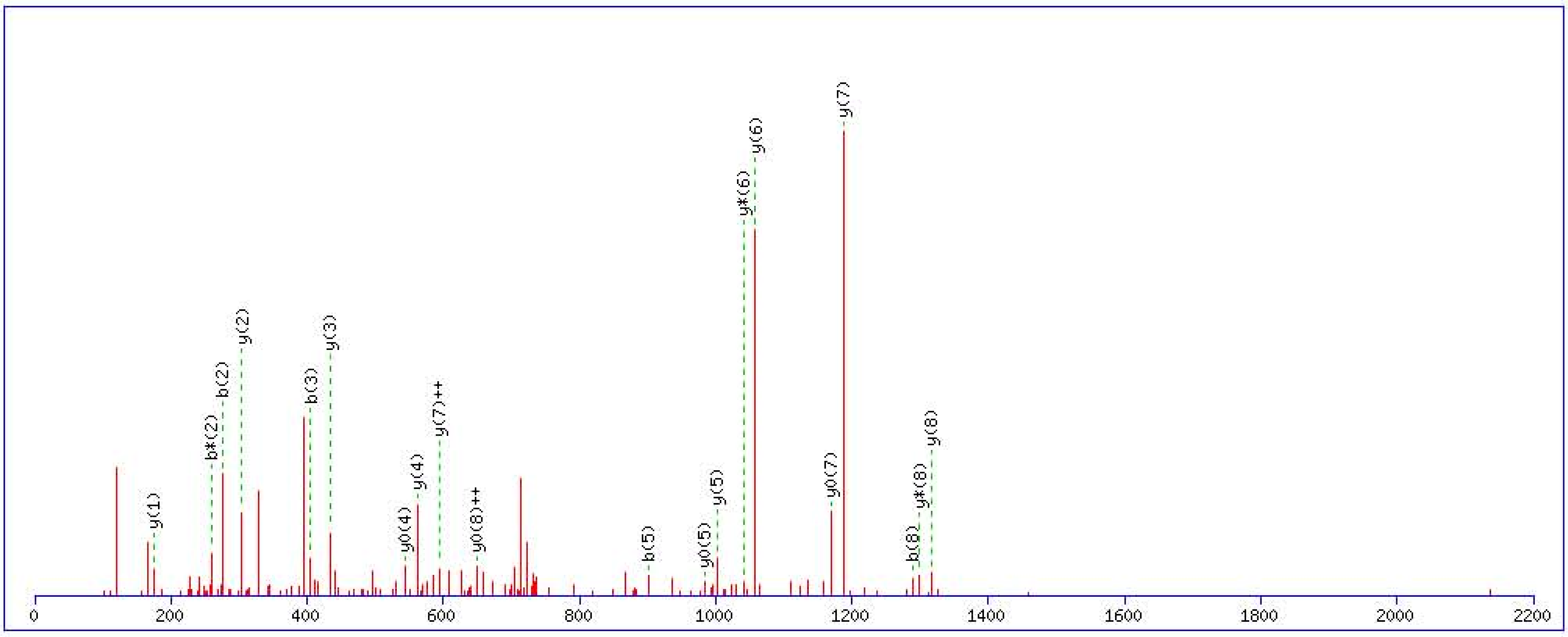
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQEGQEEER**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

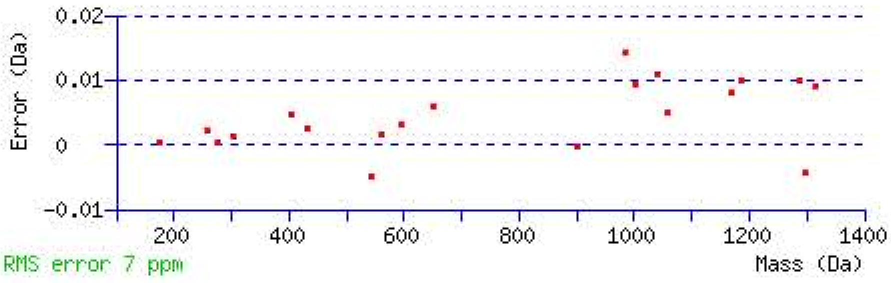
Match to Query 37384: 1461.661288 from(731.837920,2+) rtinseconds(1433) index(38375)
Title: Locus:1.1.1.2782.25 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

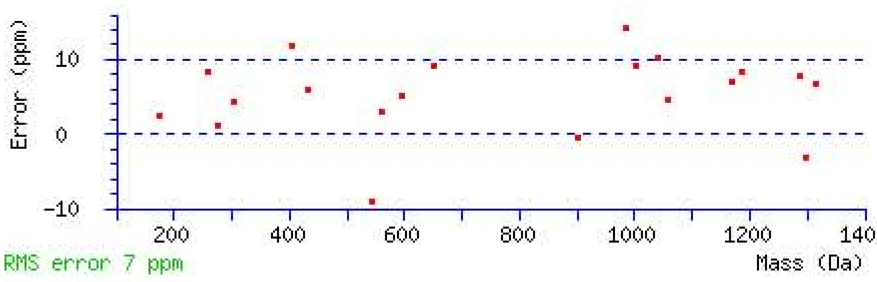
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1461.655807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00029
Matches : 20/88 fragment ions using 40 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.075690	74.541483					F							9
2	**276.134268**	138.570772	259.107719	130.057497			Q	***1315.594692***	658.300984	1298.568143	649.787710	1297.584127	649.295702	8
3	**405.176861**	203.092068	388.150312	194.578794	387.166296	194.086786	E	***1187.536114***	594.271695	1170.509565	585.758421	1169.525549	585.266413	7
4	462.198325	231.602800	445.171776	223.089526	444.187760	222.597518	G	***1058.493521***	529.750399	1041.466972	521.237124	1040.482956	520.745116	6
5	**901.423651**	451.215464	884.397102	442.702189	883.413086	442.210181	Q	***1001.472057***	501.239667	984.445508	492.726392	983.461492	492.234384	5
6	1030.466244	515.736760	1013.439695	507.223485	1012.455679	506.731477	E	***562.246731***	281.627004	545.220182	273.113729	544.236166	272.621721	4
7	1159.508837	580.258057	1142.482288	571.744782	1141.498272	571.252774	E	***433.204138***	217.105707	416.177589	208.592433	415.193573	208.100425	3
8	**1288.551430**	644.779353	1271.524881	636.266079	1270.540865	635.774071	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.7	1461.655807	0.005481	FQEGQEEER
11.9	1461.640564	0.020724	NSGTQSDGEEK
7.9	1461.655807	0.005481	FQEGQEEER
6.8	1461.640564	0.020724	VMTDVAGNPEEER
3.7	1461.648392	0.012896	HREELSDYEER
2.5	1461.677811	-0.016523	MSQMASVPER
0.4	1461.676956	-0.015668	MSGQVGDLSPSQEK
0.4	1461.647049	0.014239	EEEGEEKQVEK

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

{MATRIX}
{SCIENCE}

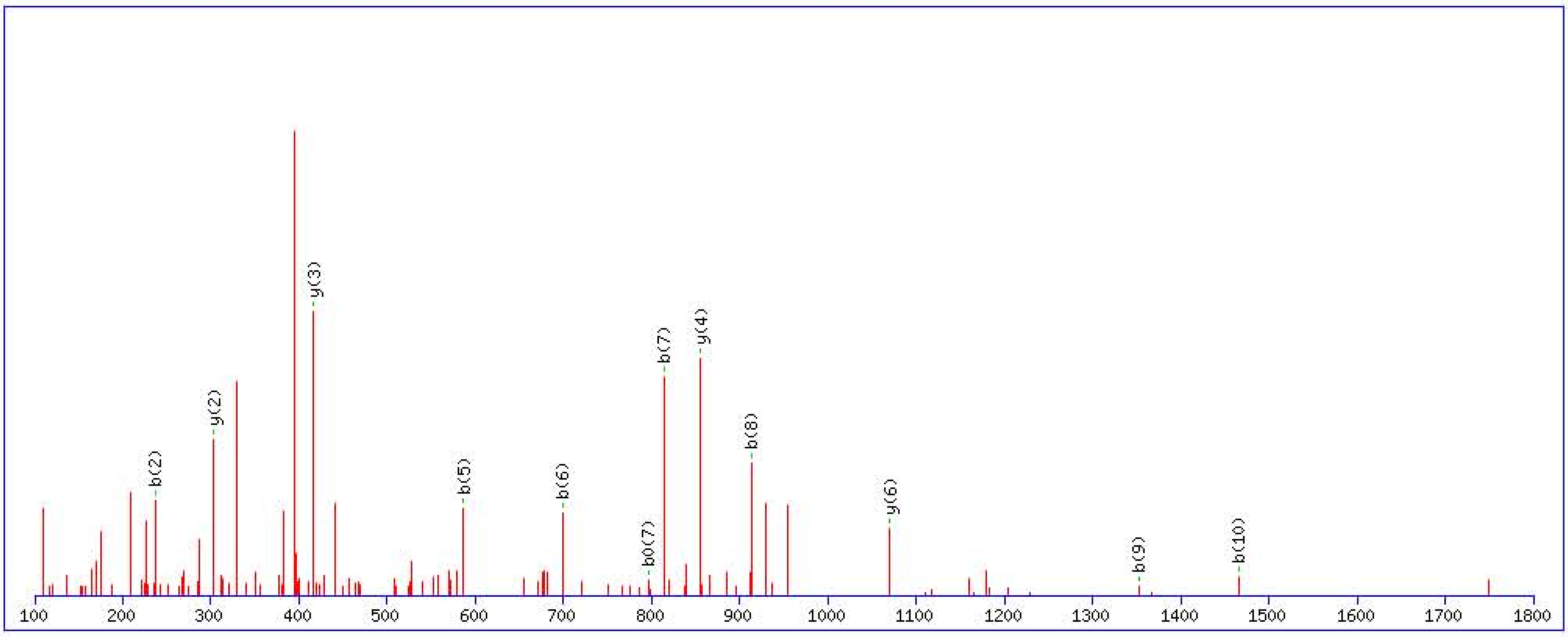
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HVYGELDVQIQR**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

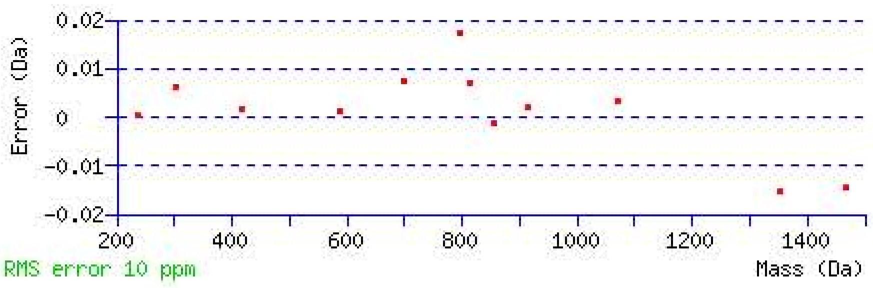
Match to Query 47640: 1766.922522 from(589.981450,3+) rtinseconds(1910) index(41502)
Title: Locus:1.1.1.2949.11 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

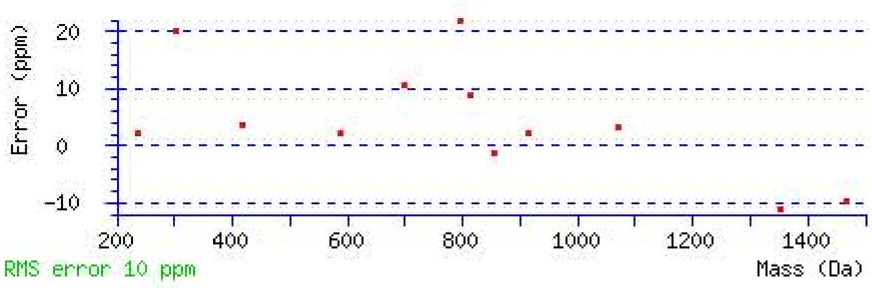
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1766.913773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0047
Matches : 12/98 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	138.066188	69.536732					H							12
2	***237.134602***	119.070939					V	1630.862141	815.934708	1613.835592	807.421434	1612.851576	806.929426	11
3	400.197931	200.602603					Y	1531.793727	766.400501	1514.767178	757.887227	1513.783162	757.395219	10
4	457.219395	229.113335					G	1368.730398	684.868837	1351.703849	676.355563	1350.719833	675.863554	9
5	***586.261988***	293.634632			568.251423	284.629349	E	1311.708934	656.358105	1294.682385	647.844830	1293.698369	647.352822	8
6	***699.346052***	350.176664			681.335487	341.171382	L	1182.666341	591.836808	1165.639792	583.323534	1164.655776	582.831526	7
7	***814.372995***	407.690136			796.362430	398.684853	D	**1069.582277**	535.294776	1052.555728	526.781502	1051.571712	526.289494	6
8	***913.441409***	457.224342			895.430844	448.219060	V	954.555334	477.781305	937.528785	469.268030			5
9	***1352.666735***	676.837006	1335.640186	668.323731	1334.656170	667.831723	Q	**855.486920**	428.247098	838.460371	419.733823			4
10	***1465.750799***	733.379037	1448.724250	724.865763	1447.740234	724.373755	I	**416.261594**	208.634435	399.235045	200.121160			3
11	1593.809377	797.408326	1576.782828	788.895052	1575.798812	788.403044	Q	**303.177530**	152.092403	286.150981	143.579128			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.6	1766.913773	0.008749	HVYGELDVQIQR
14.3	1766.913773	0.008749	HVYGELDVQIQR
8.5	1766.946976	-0.024454	QDMARQLRK
4.3	1766.946106	-0.023584	SQEQLIRLQGER
3.7	1766.934906	-0.012384	QITSPVSGINGDIR

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

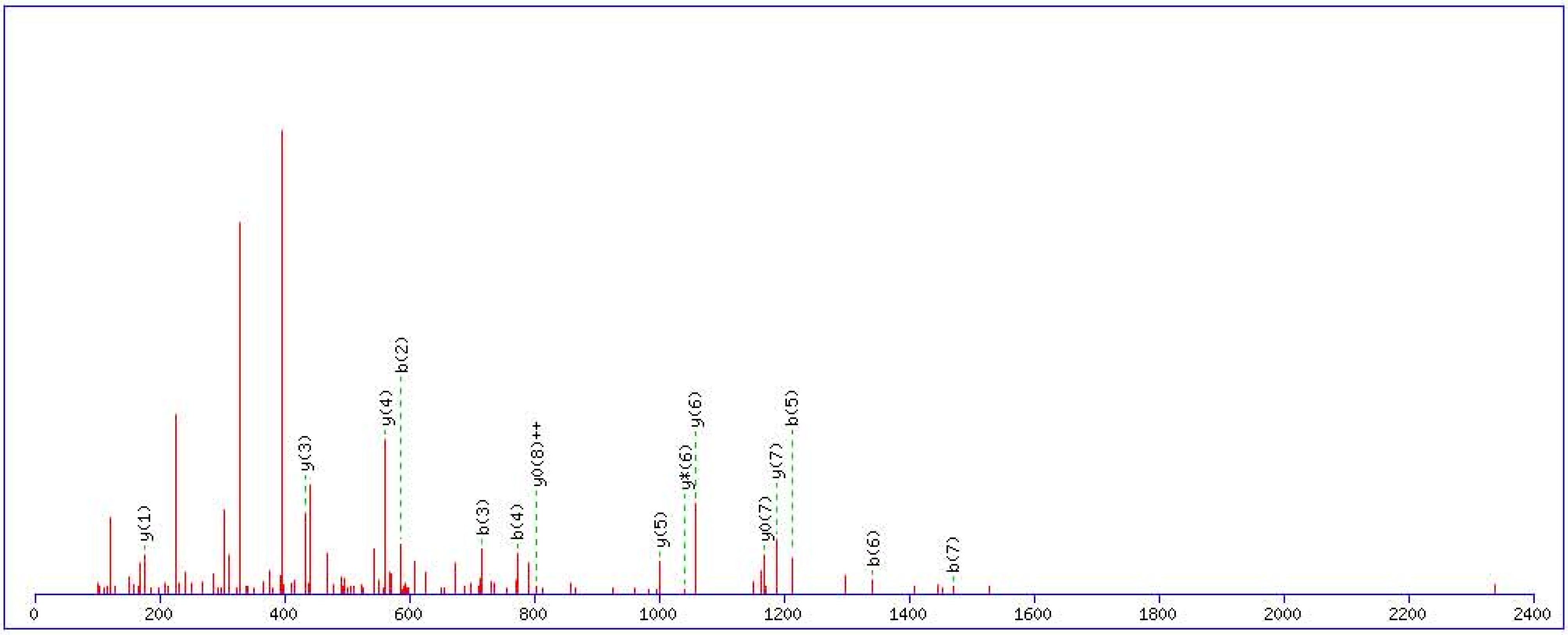
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQEGQEEER**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

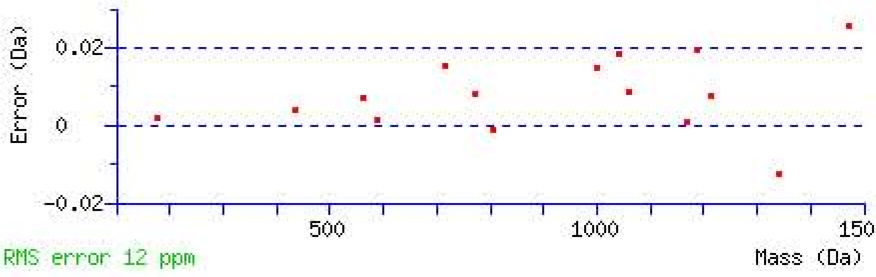
Match to Query 47829: 1772.831472 from(591.951100,3+) rtinseconds(1838) index(77295)
Title: Locus:1.1.1.2854.9 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

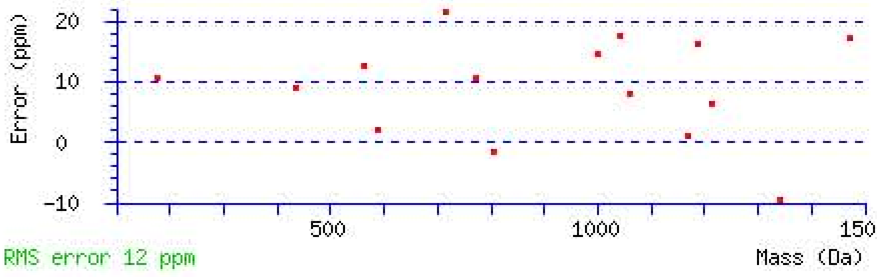
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1772.822556
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0029
Matches : 15/88 fragment ions using 28 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							9
2	***587.301016***	294.154146	570.274467	285.640872			Q	1626.761440	813.884358	1609.734891	805.371084	1608.750875	804.879076	8
3	***716.343609***	358.675443	699.317060	350.162168	698.333044	349.670160	E	***1187.536114***	594.271695	1170.509565	585.758421	1169.525549	585.266413	7
4	***773.365073***	387.186175	756.338524	378.672900	755.354508	378.180892	G	***1058.493521***	529.750399	1041.466972	521.237124	1040.482956	520.745116	6
5	***1212.590399***	606.798837	1195.563850	598.285563	1194.579834	597.793555	Q	***1001.472057***	501.239667	984.445508	492.726392	983.461492	492.234384	5
6	***1341.632992***	671.320134	1324.606443	662.806860	1323.622427	662.314852	E	***562.246731***	281.627004	545.220182	273.113729	544.236166	272.621721	4
7	***1470.675585***	735.841431	1453.649036	727.328156	1452.665020	726.836148	E	***433.204138***	217.105707	416.177589	208.592433	415.193573	208.100425	3
8	1599.718178	800.362727	1582.691629	791.849453	1581.707613	791.357445	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.8	1772.822556	0.008916	FQEGQEEER
2.7	1772.828873	0.002599	QAEQEATVAREEQER

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

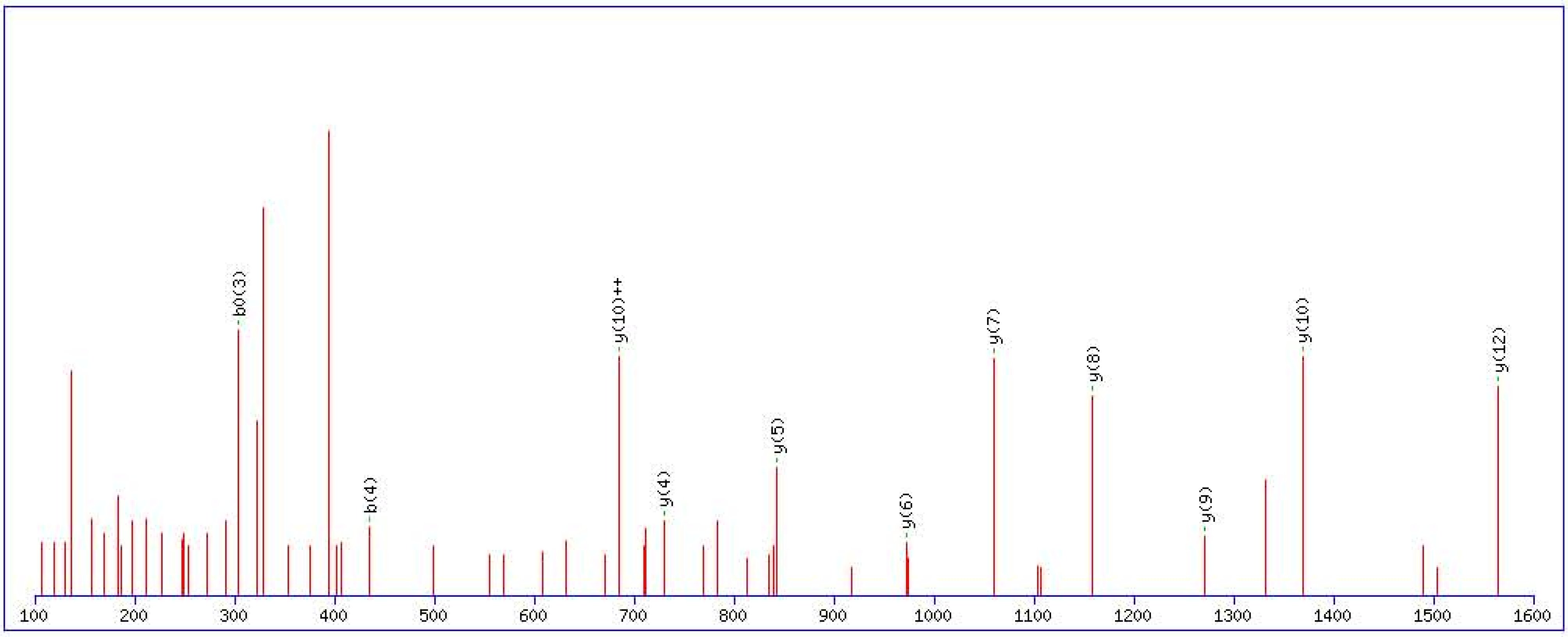
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTYIPVPIVSELQSGK**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

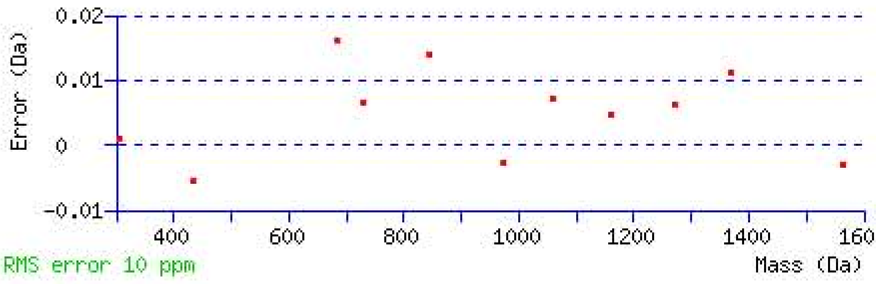
Match to Query 52872: 1998.104142 from(667.041990,3+) rtinseconds(2729) index(46808)
Title: Locus:1.1.1.3233.10 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

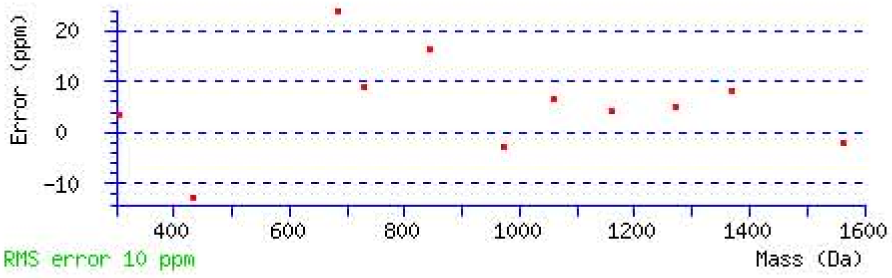
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1998.085983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 3.3e-005
Matches : 11/150 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							16
2	159.076419	80.041847			141.065854	71.036565	T	1942.071799	971.539538	1925.045250	963.026263	1924.061234	962.534255	15
3	322.139748	161.573512			304.129183	152.568230	Y	1841.024120	921.015698	1823.997571	912.502424	1823.013555	912.010416	14
4	435.223812	218.115544			417.213247	209.110262	I	1677.960791	839.484034	1660.934242	830.970759	1659.950226	830.478751	13
5	532.276576	266.641926			514.266011	257.636644	P	***1564.876727***	782.942002	1547.850178	774.428727	1546.866162	773.936719	12
6	631.344990	316.176133			613.334425	307.170851	V	1467.823963	734.415620	1450.797414	725.902345	1449.813398	725.410337	11
7	728.397754	364.702515			710.387189	355.697233	P	***1368.755549***	684.881413	1351.729000	676.368138	1350.744984	675.876130	10
8	841.481818	421.244547			823.471253	412.239265	I	***1271.702785***	636.355031	1254.676236	627.841756	1253.692220	627.349748	9
9	940.550232	470.778754			922.539667	461.773472	V	***1158.618721***	579.812999	1141.592172	571.299724	1140.608156	570.807716	8
10	1027.582260	514.294768			1009.571695	505.289486	S	***1059.550307***	530.278792	1042.523758	521.765517	1041.539742	521.273509	7
11	1156.624853	578.816065			1138.614288	569.810782	E	***972.518279***	486.762777	955.491730	478.249503	954.507714	477.757495	6
12	1269.708917	635.358096			1251.698352	626.352814	L	***843.475686***	422.241481	826.449137	413.728207	825.465121	413.236199	5
13	1708.934243	854.970759	1691.907694	846.457485	1690.923678	845.965477	Q	***730.391622***	365.699449	713.365073	357.186175	712.381057	356.694167	4
14	1795.966271	898.486774	1778.939722	889.973499	1777.955706	889.481491	S	291.166296	146.086786	274.139747	137.573512	273.155731	137.081504	3
15	1852.987735	926.997505	1835.961186	918.484231	1834.977170	917.992223	G	204.134268	102.570772	187.107719	94.057497			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.9	1998.085983	0.018159	GTYIPVPIVSELQSGK
0.1	1998.099731	0.004411	GDEVVVELVENGKKVTVGK

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

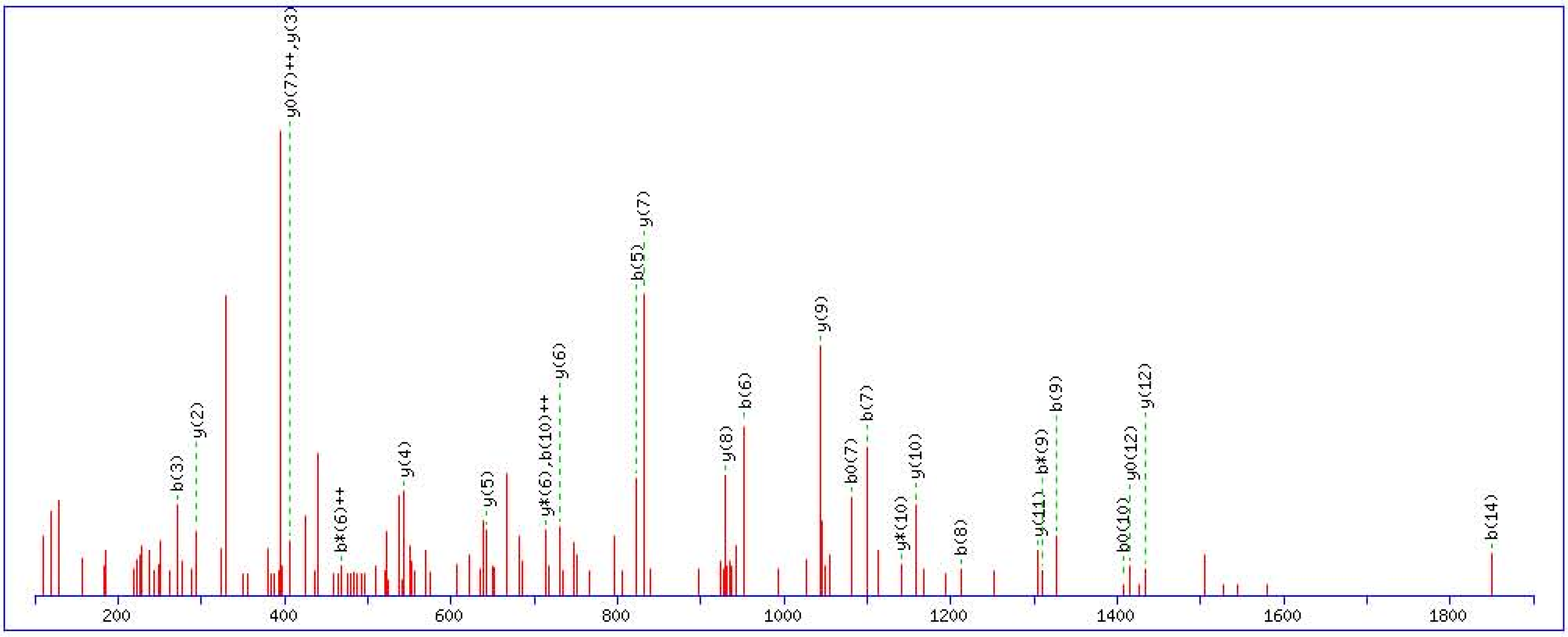
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVNLQEFLNVTSVHLFK**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

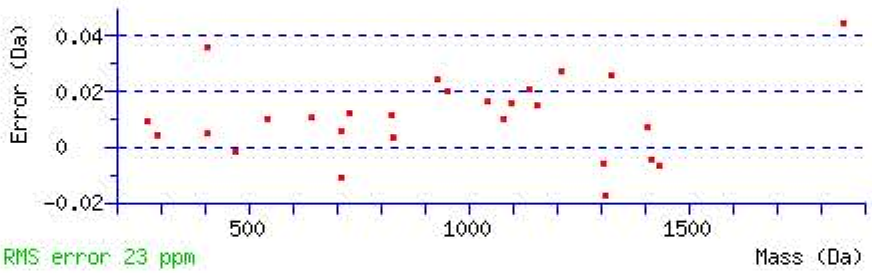
Match to Query 59447: 2255.238642 from(752.753490,3+) rtinseconds(2967) index(48700)
Title: Locus:1.1.1.3314.10 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

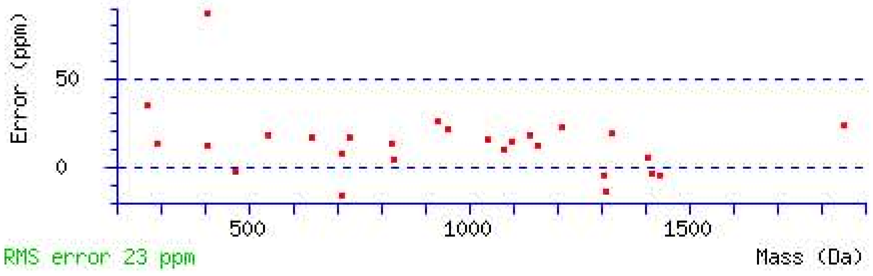
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2255.213654
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 1.1e-005
Matches : 27/168 fragment ions using 45 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							17
2	157.097154	79.052215					V	2199.199458	1100.103367	2182.172909	1091.590092	2181.188893	1091.098084	16
3	**271.140081**	136.073679	254.113532	127.560404			N	2100.131044	1050.569160	2083.104495	1042.055885	2082.120479	1041.563877	15
4	384.224145	192.615711	367.197596	184.102436			L	1986.088117	993.547697	1969.061568	985.034422	1968.077552	984.542414	14
5	**823.449471**	412.228374	806.422922	403.715099			Q	1873.004053	937.005665	1855.977504	928.492390	1854.993488	928.000382	13
6	**952.492064**	476.749670	935.465515	468.236396	934.481499	467.744388	E	***1433.778727***	717.393002	1416.752178	708.879727	1415.768162	708.387719	12
7	**1099.560478**	550.283877	1082.533929	541.770603	1081.549913	541.278595	F	***1304.736134***	652.871705	1287.709585	644.358431	1286.725569	643.866423	11
8	**1212.644542**	606.825909	1195.617993	598.312635	1194.633977	597.820627	L	***1157.667720***	579.337498	1140.641171	570.824224	1139.657155	570.332216	10
9	**1326.687469**	663.847373	1309.660920	655.334098	1308.676904	654.842090	N	***1044.583656***	522.795466	1027.557107	514.282192	1026.573091	513.790184	9
10	1425.755883	713.381580	1408.729334	704.868305	1407.745318	704.376297	V	***930.540729***	465.774003	913.514180	457.260728	912.530164	456.768720	8
11	1526.803562	763.905419	1509.777013	755.392145	1508.792997	754.900137	T	***831.472315***	416.239796	814.445766	407.726521	813.461750	407.234513	7
12	1613.835590	807.421433	1596.809041	798.908159	1595.825025	798.416151	S	***730.424636***	365.715956	713.398087	357.202682	712.414071	356.710674	6
13	1712.904004	856.955640	1695.877455	848.442366	1694.893439	847.950358	V	***643.392608***	322.199942	626.366059	313.686668			5
14	**1849.962916**	925.485096	1832.936367	916.971822	1831.952351	916.479814	H	***544.324194***	272.665735	527.297645	264.152461			4
15	1963.046980	982.027128	1946.020431	973.513854	1945.036415	973.021846	L	***407.265282***	204.136279	390.238733	195.623004			3
16	2110.115394	1055.561335	2093.088845	1047.048060	2092.104829	1046.556052	F	***294.181218***	147.594247	277.154669	139.080973			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.4	2255.213654	0.024988	GVNLQEFLNVTSVHLFK

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

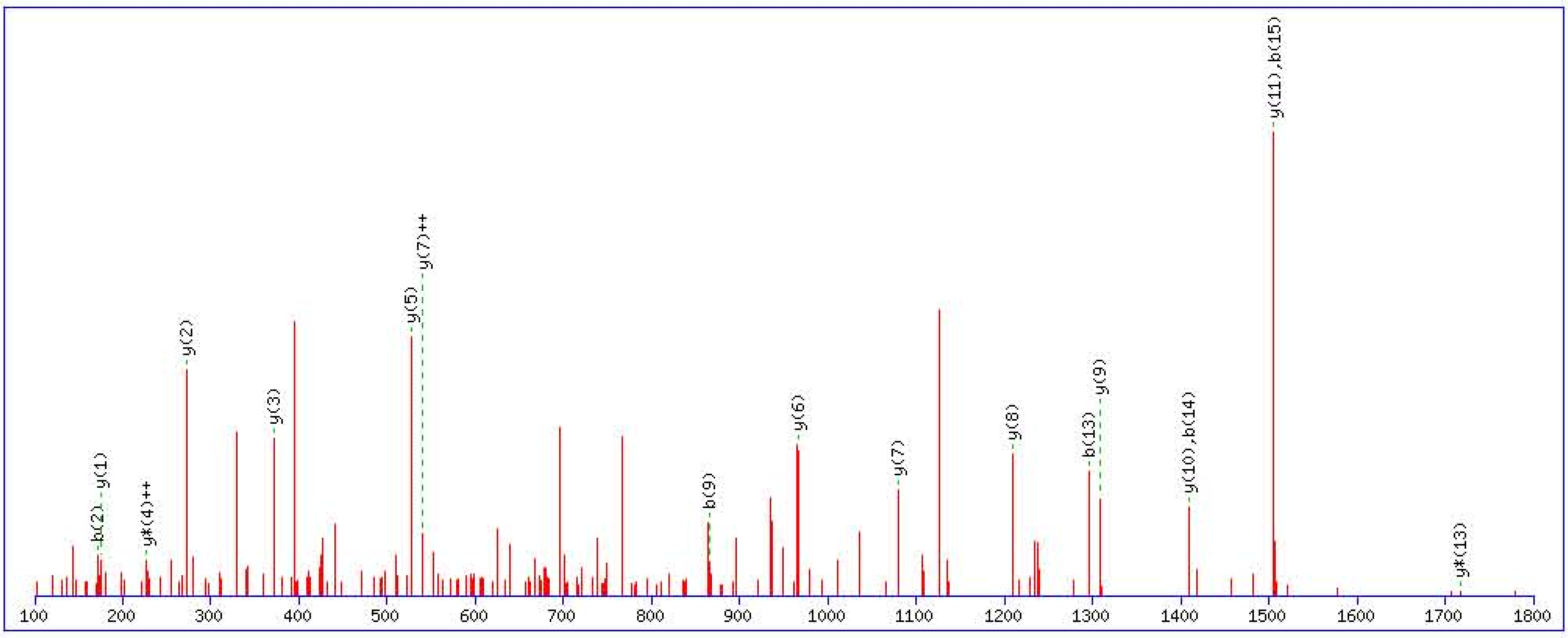
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVPPNNSNAAEDDLPTVELQGVVPR**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

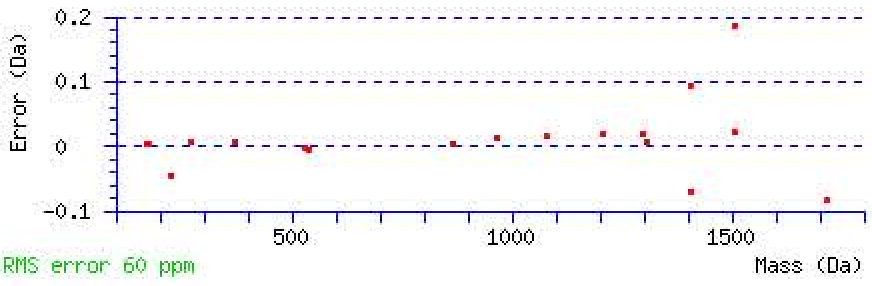
Match to Query 70682: 2912.508016 from(729.134280,4+) rtinseconds(2456) index(9982)
Title: Locus:1.1.1.2987.15 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

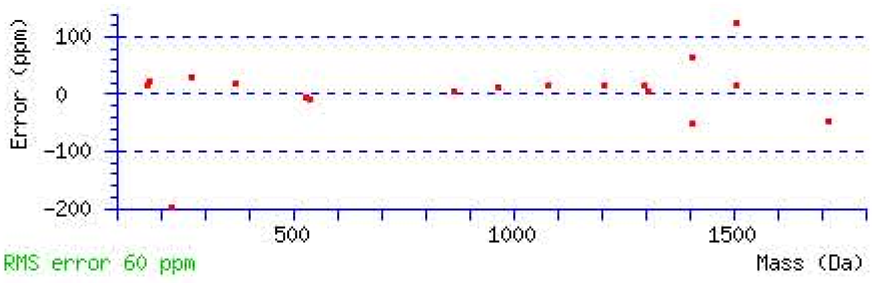
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2912.470200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.027
Matches : 18/254 fragment ions using 47 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							25
2	**171.112804**	86.060040					V	2842.440370	1421.723823	2825.413821	1413.210548	2824.429805	1412.718540	24
3	268.165568	134.586422					P	2743.371956	1372.189616	2726.345407	1363.676341	2725.361391	1363.184333	23
4	365.218332	183.112804					P	2646.319192	1323.663234	2629.292643	1315.149959	2628.308627	1314.657951	22
5	479.261259	240.134267	462.234710	231.620993			N	2549.266428	1275.136852	2532.239879	1266.623577	2531.255863	1266.131569	21
6	593.304186	297.155731	576.277637	288.642457			N	2435.223501	1218.115388	2418.196952	1209.602114	2417.212936	1209.110106	20
7	680.336214	340.671745	663.309665	332.158471	662.325649	331.666463	S	2321.180574	1161.093925	2304.154025	1152.580650	2303.170009	1152.088642	19
8	794.379141	397.693209	777.352592	389.179934	776.368576	388.687926	N	2234.148546	1117.577911	2217.121997	1109.064636	2216.137981	1108.572628	18
9	**865.416255**	433.211766	848.389706	424.698491	847.405690	424.206483	A	2120.105619	1060.556447	2103.079070	1052.043173	2102.095054	1051.551165	17
10	936.453369	468.730323	919.426820	460.217048	918.442804	459.725040	A	2049.068505	1025.037890	2032.041956	1016.524616	2031.057940	1016.032608	16
11	1065.495962	533.251619	1048.469413	524.738345	1047.485397	524.246336	E	1978.031391	989.519333	1961.004842	981.006059	1960.020826	980.514051	15
12	1180.522905	590.765091	1163.496356	582.251816	1162.512340	581.759808	D	1848.988798	924.998037	1831.962249	916.484762	1830.978233	915.992754	14
13	**1295.549848**	648.278562	1278.523299	639.765288	1277.539283	639.273280	D	1733.961855	867.484565	1716.935306	858.971291	1715.951290	858.479283	13
14	**1408.633912**	704.820594	1391.607363	696.307320	1390.623347	695.815312	L	1618.934912	809.971094	1601.908363	801.457819	1600.924347	800.965811	12
15	**1505.686676**	753.346976	1488.660127	744.833702	1487.676111	744.341694	P	***1505.850848***	753.429062	1488.824299	744.915787	1487.840283	744.423779	11
16	1606.734355	803.870816	1589.707806	795.357541	1588.723790	794.865533	T	***1408.798084***	704.902680	1391.771535	696.389405	1390.787519	695.897397	10
17	1705.802769	853.405023	1688.776220	844.891748	1687.792204	844.399740	V	***1307.750405***	654.378840	1290.723856	645.865566	1289.739840	645.373558	9
18	1834.845362	917.926319	1817.818813	909.413045	1816.834797	908.921037	E	***1208.681991***	604.844633	1191.655442	596.331359	1190.671426	595.839351	8
19	1947.929426	974.468351	1930.902877	965.955077	1929.918861	965.463069	L	***1079.639398***	540.323337	1062.612849	531.810062			7
20	2387.154752	1194.081014	2370.128203	1185.567739	2369.144187	1185.075731	Q	***966.555334***	483.781305	949.528785	475.268030			6
21	2444.176216	1222.591746	2427.149667	1214.078471	2426.165651	1213.586463	G	***527.330008***	264.168642	510.303459	255.655367			5
22	2543.244630	1272.125953	2526.218081	1263.612678	2525.234065	1263.120670	V	470.308544	235.657910	453.281995	227.144635			4
23	2642.313044	1321.660160	2625.286495	1313.146885	2624.302479	1312.654877	V	***371.240130***	186.123703	354.213581	177.610428			3
24	2739.365808	1370.186542	2722.339259	1361.673267	2721.355243	1361.181259	P	***272.171716***	136.589496	255.145167	128.076221			2
25							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.9	2912.470200	0.037816	AVPPNNSNAAEDDLPTVELQGVVPR

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

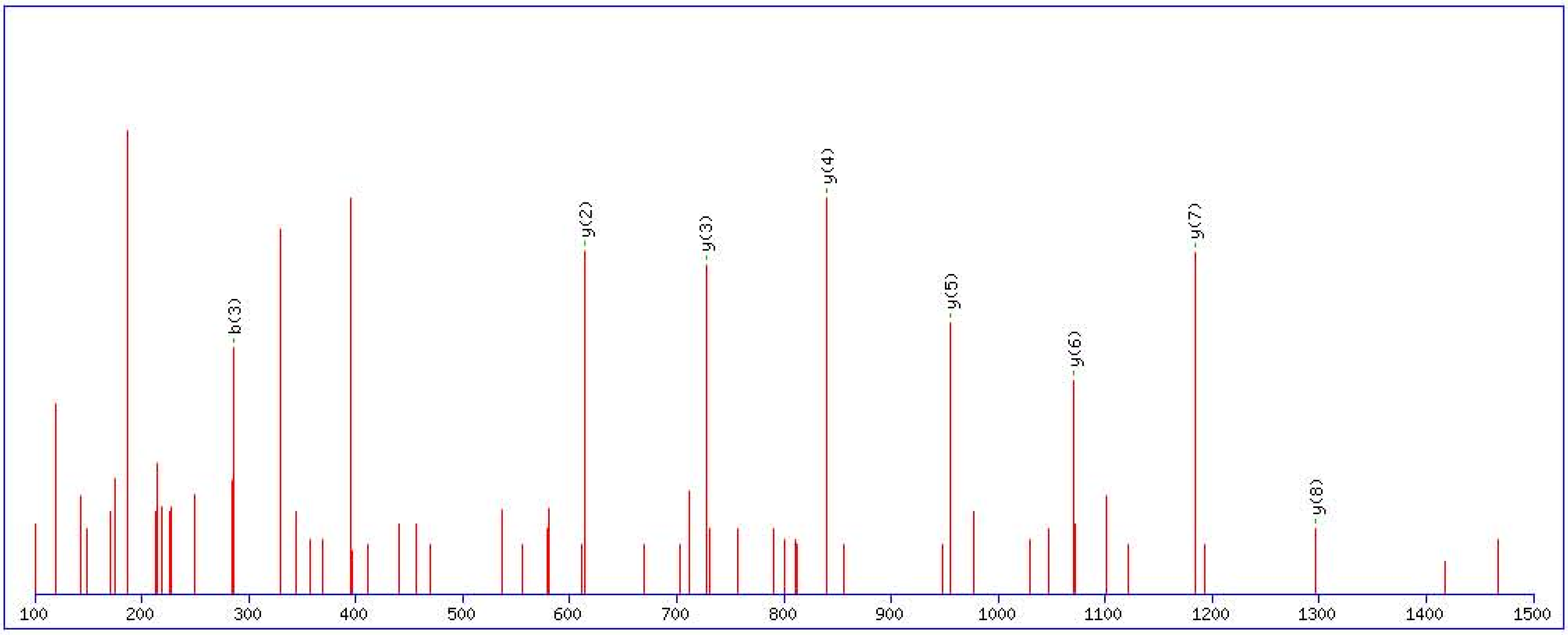
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TIAVLLDDILQR**
Found in **CC126_HUMAN**, Coiled-coil domain-containing protein 126 OS=Homo sapiens GN=CCDC126 PE=2 SV=2

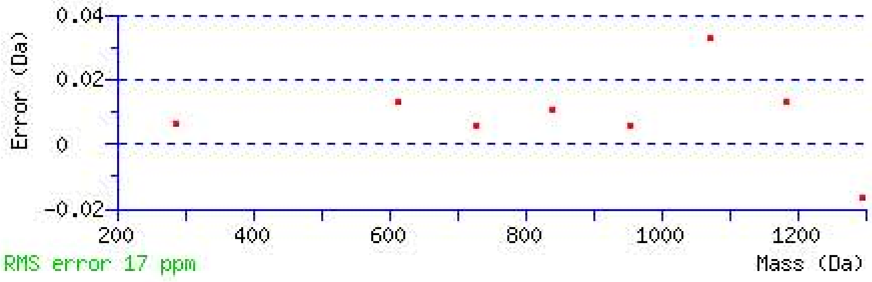
Match to Query 23729: 1679.988672 from(561.003500,3+) rtinseconds(3072) index(13910)
Title: Locus:1.1.1.3199.5 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

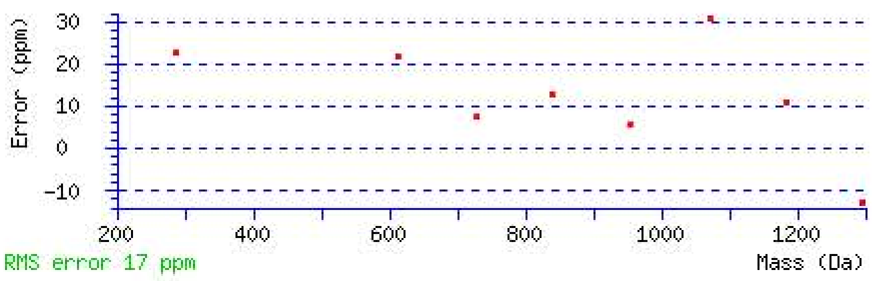
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1679.964401
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00033
Matches : 8/104 fragment ions using 13 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.054955	51.531116			84.044390	42.525833	T							12
2	215.139019	108.073147			197.128454	99.067865	I	1579.924012	790.465644	1562.897463	781.952370	1561.913447	781.460361	11
3	**286.176133**	143.591704			268.165568	134.586422	A	1466.839948	733.923612	1449.813399	725.410338	1448.829383	724.918330	10
4	385.244547	193.125912			367.233982	184.120629	V	1395.802834	698.405055	1378.776285	689.891780	1377.792269	689.399772	9
5	498.328611	249.667944			480.318046	240.662661	L	***1296.734420***	648.870848	1279.707871	640.357574	1278.723855	639.865566	8
6	611.412675	306.209976			593.402110	297.204693	L	***1183.650356***	592.328816	1166.623807	583.815541	1165.639791	583.323533	7
7	726.439618	363.723447			708.429053	354.718165	D	***1070.566292***	535.786784	1053.539743	527.273510	1052.555727	526.781501	6
8	841.466561	421.236919			823.455996	412.231636	D	***955.539349***	478.273313	938.512800	469.760038	937.528784	469.268030	5
9	954.550625	477.778951			936.540060	468.773668	I	***840.512406***	420.759841	823.485857	412.246567			4
10	1067.634689	534.320983			1049.624124	525.315700	L	***727.428342***	364.217809	710.401793	355.704535			3
11	1506.860015	753.933646	1489.833466	745.420371	1488.849450	744.928363	Q	***614.344278***	307.675777	597.317729	299.162503			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.1	1679.964401	0.024271	TIAVLLDDILQR

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

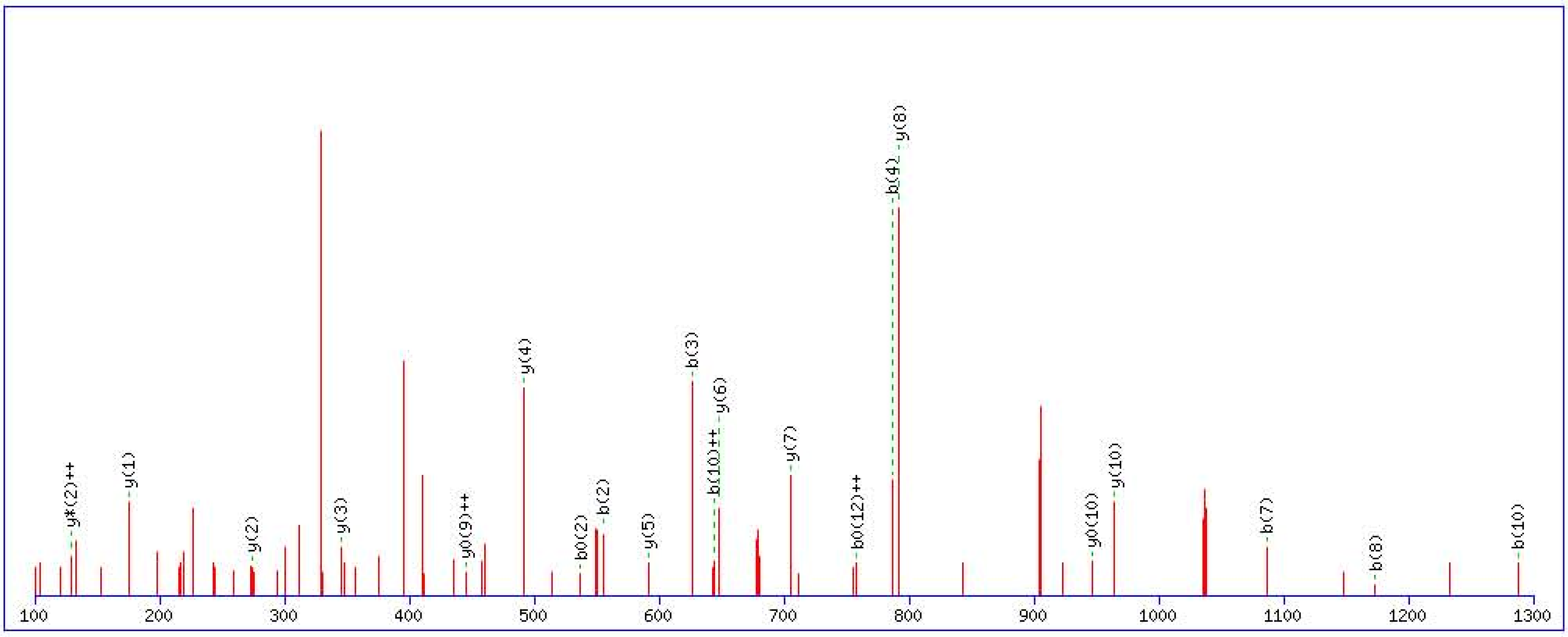
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDACQGDSGGVFAVR**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

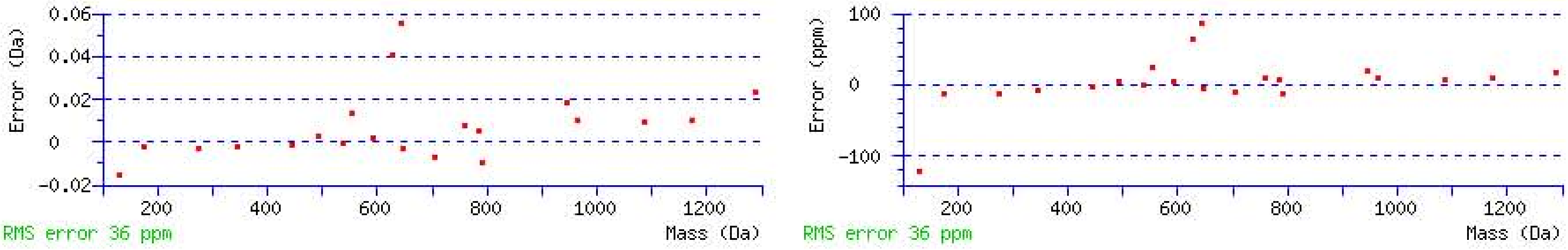
Match to Query 50211: 1876.864692 from(626.628840,3+) rtinseconds(1925) index(41623)
Title: Locus:1.1.1.2954.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1876.856033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0032
Matches : 21/152 fragment ions using 57 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							15
2	***555.259545***	278.133411	538.232996	269.620136	537.248980	269.128128	D	1438.637955	719.822616	1421.611406	711.309341	1420.627390	710.817333	14
3	***626.296659***	313.651968	609.270110	305.138693	608.286094	304.646685	A	1323.611012	662.309144	1306.584463	653.795870	1305.600447	653.303862	13
4	***786.327308***	393.667292	769.300759	385.154018	768.316743	384.662010	C	1252.573898	626.790587	1235.547349	618.277313	1234.563333	617.785305	12
5	914.385886	457.696581	897.359337	449.183307	896.375321	448.691299	Q	1092.543249	546.775263	1075.516700	538.261988	1074.532684	537.769980	11
6	971.407350	486.207313	954.380801	477.694039	953.396785	477.202031	G	***964.484671***	482.745974	947.458122	474.232699	946.474106	473.740691	10
7	***1086.434293***	543.720785	1069.407744	535.207510	1068.423728	534.715502	D	907.463207	454.235242	890.436658	445.721967	889.452642	445.229959	9
8	***1173.466321***	587.236799	1156.439772	578.723524	1155.455756	578.231516	S	***792.436264***	396.721770	775.409715	388.208496	774.425699	387.716488	8
9	1230.487785	615.747531	1213.461236	607.234256	1212.477220	606.742248	G	***705.404236***	353.205756	688.377687	344.692482			7
10	***1287.509249***	644.258263	1270.482700	635.744988	1269.498684	635.252980	G	***648.382772***	324.695024	631.356223	316.181750			6
11	1386.577663	693.792470	1369.551114	685.279195	1368.567098	684.787187	V	***591.361308***	296.184292	574.334759	287.671018			5
12	1533.646077	767.326677	1516.619528	758.813402	1515.635512	758.321394	F	***492.292894***	246.650085	475.266345	238.136811			4
13	1604.683191	802.845234	1587.656642	794.331959	1586.672626	793.839951	A	***345.224480***	173.115878	328.197931	164.602603			3
14	1703.751605	852.379441	1686.725056	843.866166	1685.741040	843.374158	V	***274.187366***	137.597321	257.160817	129.084047			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.6	1876.856033	0.008659	QDACQGDSGGVFAVR
28.6	1876.856033	0.008659	QDACQGDSGGVFAVR

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

{MATRIX} {SCIENCE}

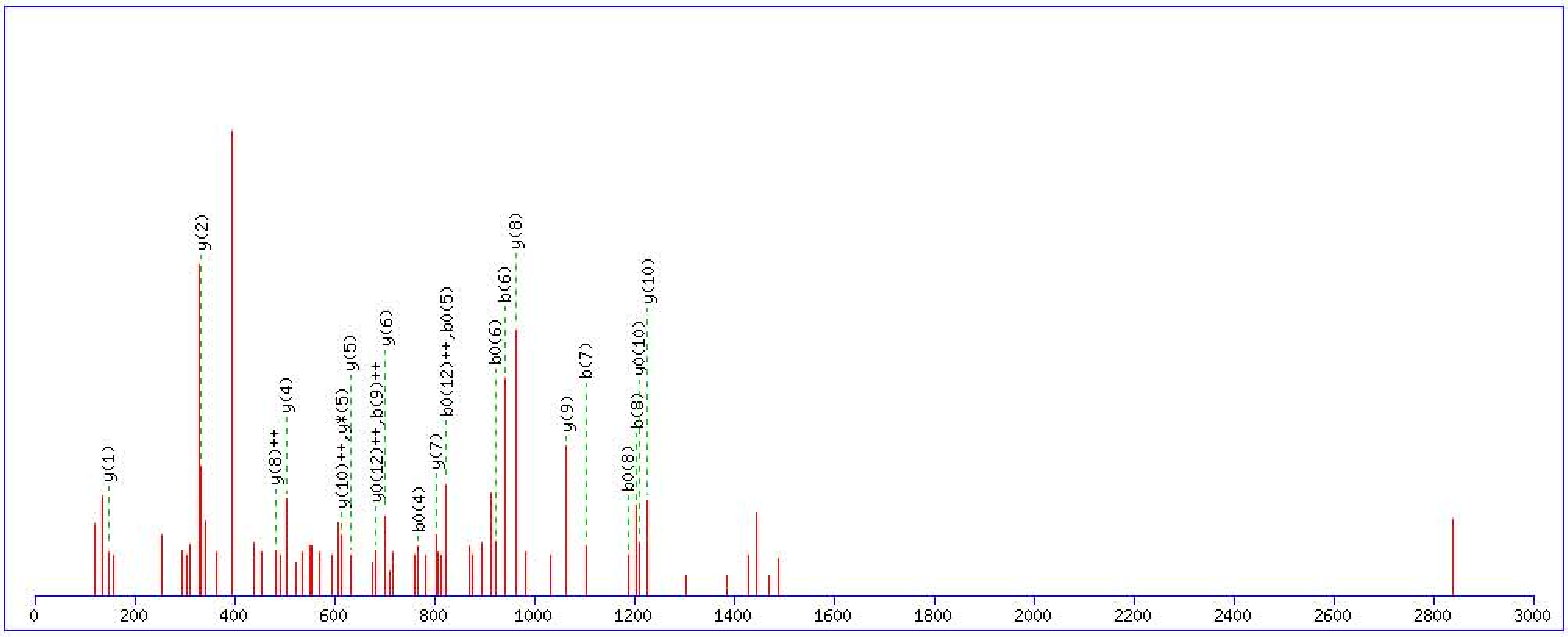
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESEQGVYTCTAQGIWK**
Found in **C1R_HUMAN**, Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2

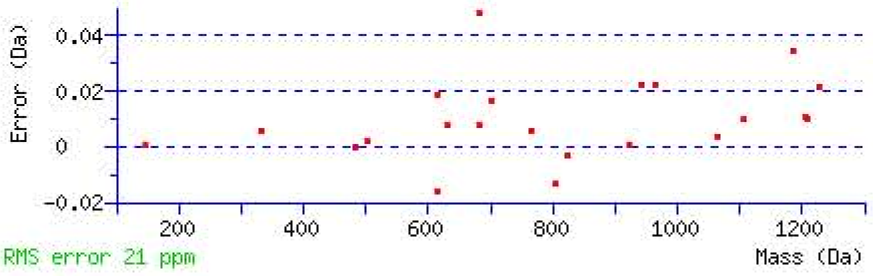
Match to Query 57376: 2167.026102 from(723.349310,3+) rtinseconds(2156) index(43122)
Title: Locus:1.1.1.3034.22 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

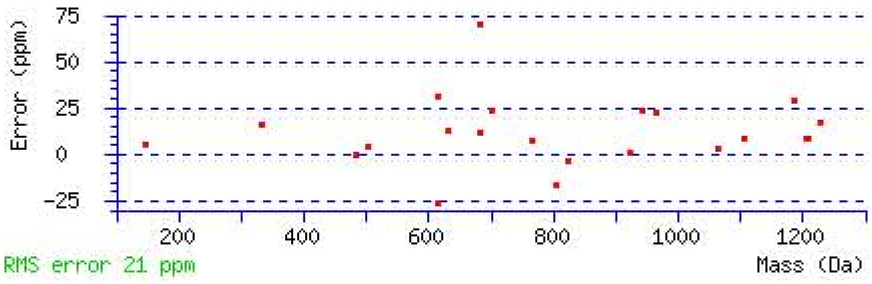
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2167.007813
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0066
Matches : 23/162 fragment ions using 49 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							16
2	217.081897	109.044586			199.071332	100.039304	S	2038.972498	1019.989887	2021.945949	1011.476613	2020.961933	1010.984604	15
3	346.124490	173.565883			328.113925	164.560600	E	1951.940470	976.473873	1934.913921	967.960599	1933.929905	967.468591	14
4	785.349816	393.178546	768.323267	384.665272	767.339251	384.173264	Q	1822.897877	911.952577	1805.871328	903.439302	1804.887312	902.947294	13
5	842.371280	421.689278	825.344731	413.176004	824.360715	412.683996	G	1383.672551	692.339913	1366.646002	683.826639	1365.661986	683.334631	12
6	**941.439694**	471.223485	924.413145	462.710211	923.429129	462.218203	V	1326.651087	663.829182	1309.624538	655.315907	1308.640522	654.823899	11
7	**1104.503023**	552.755150	1087.476474	544.241875	1086.492458	543.749867	Y	***1227.582673***	614.294975	1210.556124	605.781700	1209.572108	605.289692	10
8	**1205.550702**	603.278989	1188.524153	594.765715	1187.540137	594.273707	T	***1064.519344***	532.763310	1047.492795	524.250036	1046.508779	523.758028	9
9	1365.581351	683.294314	1348.554802	674.781039	1347.570786	674.289031	C	***963.471665***	482.239471	946.445116	473.726196	945.461100	473.234188	8
10	1466.629030	733.818153	1449.602481	725.304879	1448.618465	724.812871	T	***803.441016***	402.224146	786.414467	393.710872	785.430451	393.218864	7
11	1537.666144	769.336710	1520.639595	760.823436	1519.655579	760.331428	A	***702.393337***	351.700307	685.366788	343.187032			6
12	1665.724722	833.365999	1648.698173	824.852725	1647.714157	824.360717	Q	***631.356223***	316.181750	614.329674	307.668475			5
13	1722.746186	861.876731	1705.719637	853.363457	1704.735621	852.871449	G	***503.297645***	252.152460	486.271096	243.639186			4
14	1835.830250	918.418763	1818.803701	909.905489	1817.819685	909.413480	I	446.276181	223.641728	429.249632	215.128454			3
15	2021.909563	1011.458420	2004.883014	1002.945145	2003.898998	1002.453137	W	***333.192117***	167.099696	316.165568	158.586422			2
16							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.6	2167.007813	0.018289	ESEQGVYTCTAQGIWK

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

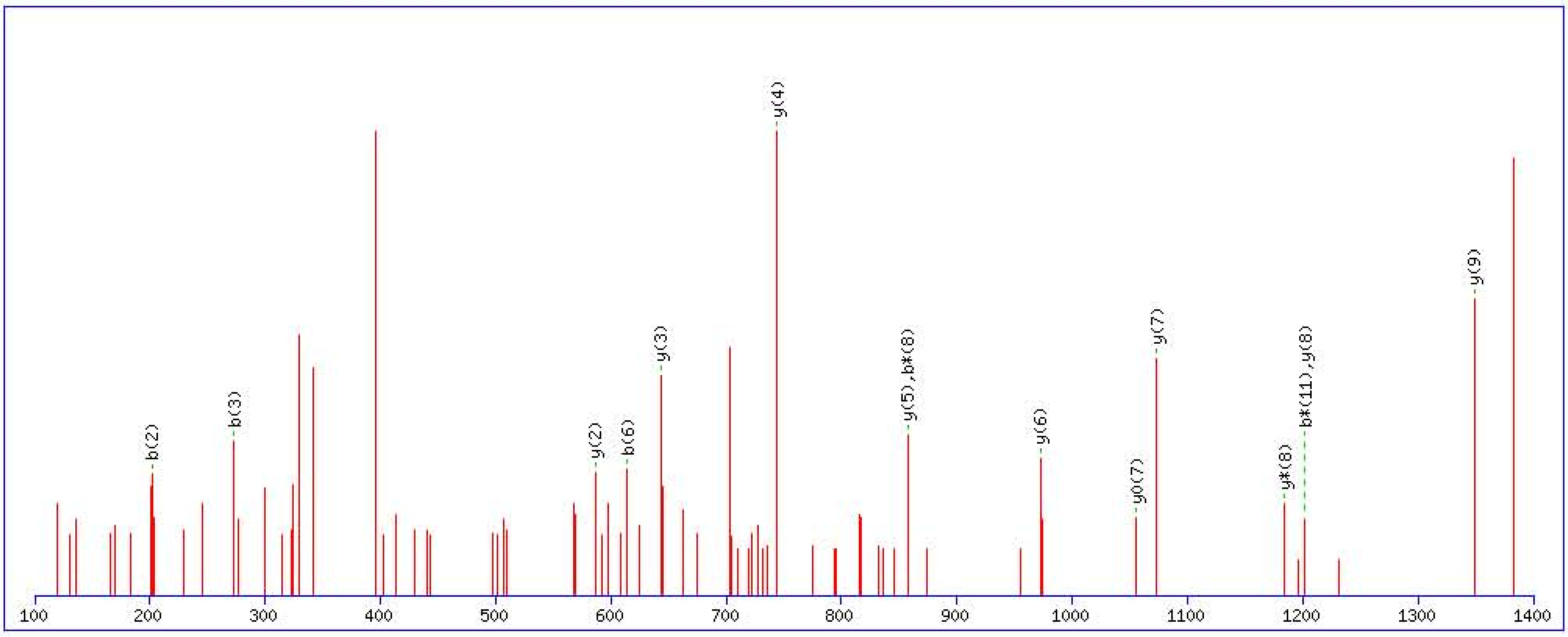
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SNALDIIFQTDLTGQK**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

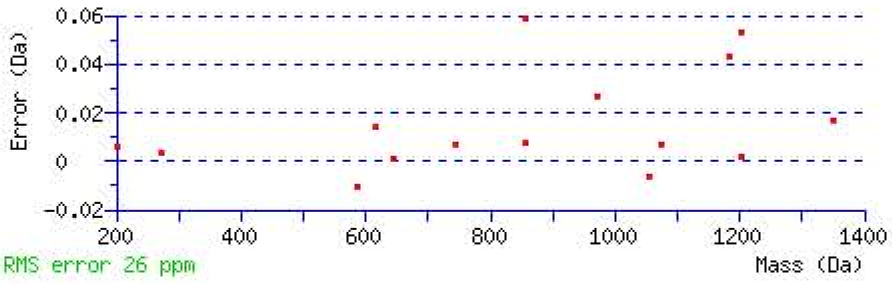
Match to Query 55521: 2074.097622 from(692.373150,3+) rtinseconds(2840) index(47657)
Title: Locus:1.1.1.3271.7 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

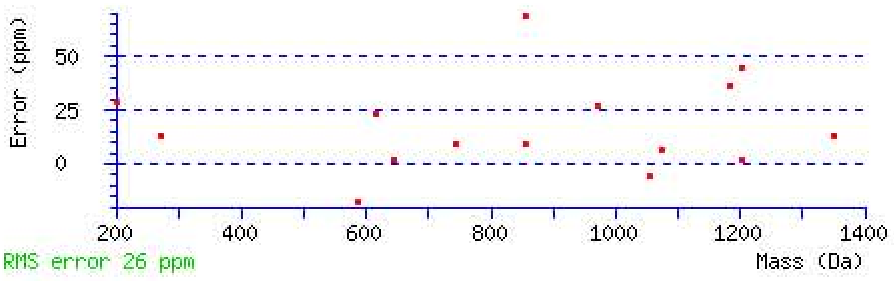
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2074.076874
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00073
Matches : 15/172 fragment ions using 25 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							16
2	**202.082231**	101.544753	185.055682	93.031479	184.071666	92.539471	N	1988.052127	994.529702	1971.025578	986.016427	1970.041562	985.524419	15
3	**273.119345**	137.063311	256.092796	128.550036	255.108780	128.058028	A	1874.009200	937.508238	1856.982651	928.994964	1855.998635	928.502956	14
4	386.203409	193.605343	369.176860	185.092068	368.192844	184.600060	L	1802.972086	901.989681	1785.945537	893.476407	1784.961521	892.984399	13
5	501.230352	251.118814	484.203803	242.605540	483.219787	242.113532	D	1689.888022	845.447649	1672.861473	836.934375	1671.877457	836.442367	12
6	**614.314416**	307.660846	597.287867	299.147572	596.303851	298.655564	I	1574.861079	787.934178	1557.834530	779.420903	1556.850514	778.928895	11
7	727.398480	364.202878	710.371931	355.689604	709.387915	355.197596	I	1461.777015	731.392146	1444.750466	722.878871	1443.766450	722.386863	10
8	874.466894	437.737085	857.440345	429.223811	856.456329	428.731803	F	***1348.692951***	674.850114	1331.666402	666.336839	1330.682386	665.844831	9
9	1002.525472	501.766374	985.498923	493.253100	984.514907	492.761092	Q	***1201.624537***	601.315907	1184.597988	592.802632	1183.613972	592.310624	8
10	1103.573151	552.290214	1086.546602	543.776939	1085.562586	543.284931	T	***1073.565959***	537.286618	1056.539410	528.773343	1055.555394	528.281335	7
11	1218.600094	609.803685	1201.573545	601.290411	1200.589529	600.798403	D	***972.518280***	486.762778	955.491731	478.249504	954.507715	477.757496	6
12	1331.684158	666.345717	1314.657609	657.832443	1313.673593	657.340435	L	***857.491337***	429.249307	840.464788	420.736032	839.480772	420.244024	5
13	1432.731837	716.869557	1415.705288	708.356282	1414.721272	707.864274	T	***744.407273***	372.707275	727.380724	364.194000	726.396708	363.701992	4
14	1489.753301	745.380289	1472.726752	736.867014	1471.742736	736.375006	G	***643.359594***	322.183435	626.333045	313.670161			3
15	1928.978627	964.992952	1911.952078	956.479677	1910.968062	955.987669	Q	***586.338130***	293.672703	569.311581	285.159429			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.3	2074.076874	0.020748	SNALDIIFQTDLTGQK
7.9	2074.076874	0.020748	SNALDIIFQTDLTGQK
7.8	2074.125122	-0.027500	ISVLPAYLSYDAPWPVRK

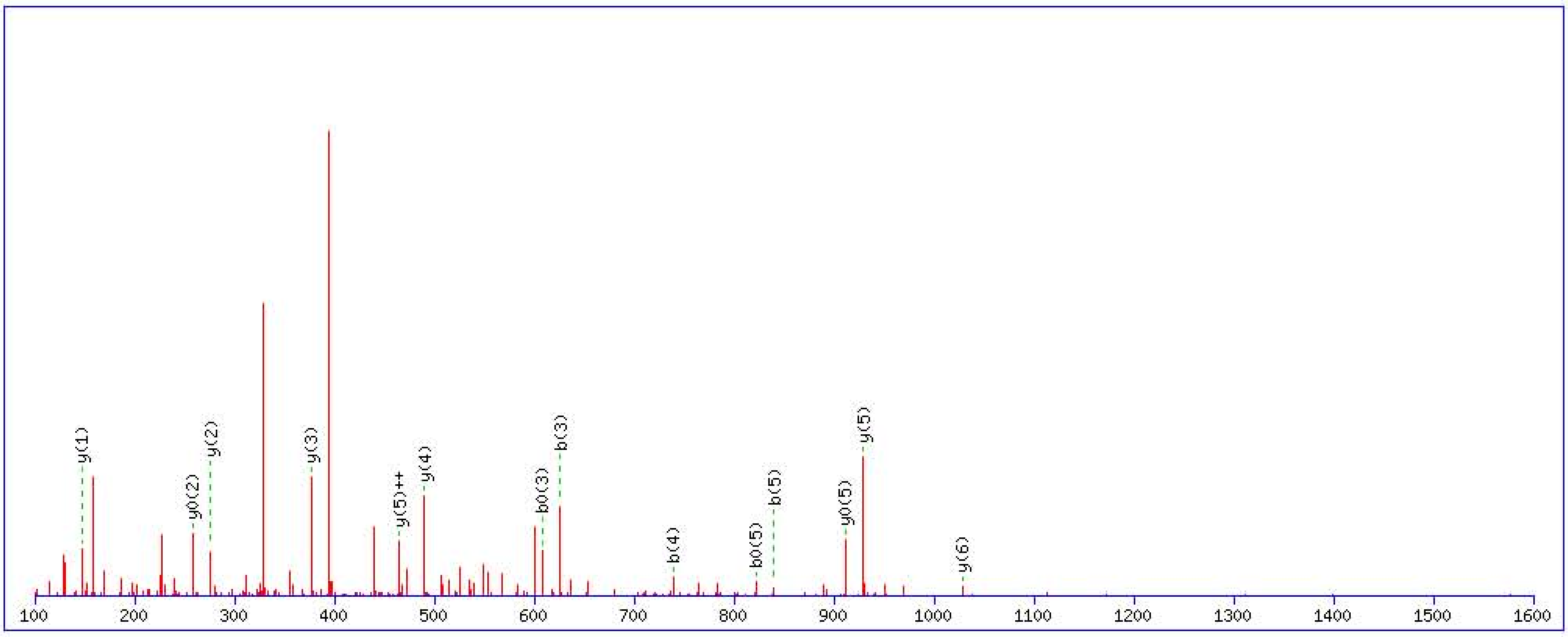
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVQLTEK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

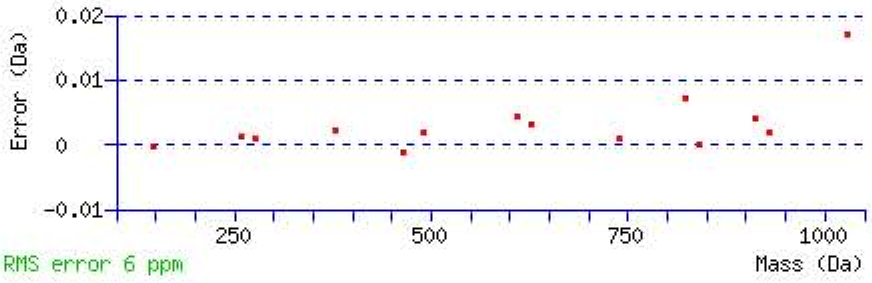
Match to Query 23557: 1114.606248 from(558.310400,2+) rtinseconds(1489) index(38785)
Title: Locus:1.1.1.2802.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

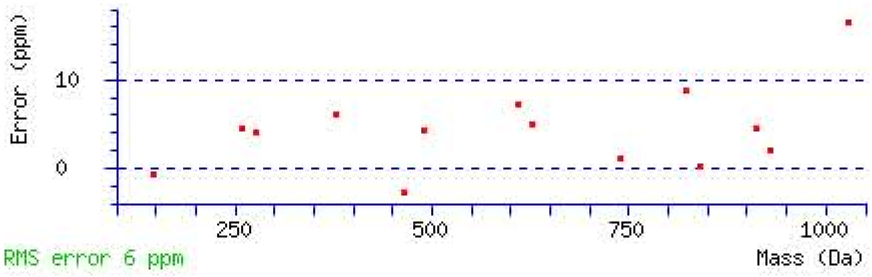
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1114.605621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.032
Matches : 14/66 fragment ions using 30 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**							7
2	187.107718	94.057497			169.097153	85.052214	**V**	***1028.580880***	514.794078	1011.554331	506.280804	1010.570315	505.788796	6
3	**626.333044**	313.670160	609.306495	305.156885	608.322479	304.664877	**Q**	***929.512466***	465.259871	912.485917	456.746597	911.501901	456.254589	5
4	**739.417108**	370.212192	722.390559	361.698917	721.406543	361.206909	**L**	***490.287140***	245.647208	473.260591	237.133934	472.276575	236.641926	4
5	**840.464787**	420.736032	823.438238	412.222757	822.454222	411.730749	**T**	***377.203076***	189.105176	360.176527	180.591902	359.192511	180.099894	3
6	969.507380	485.257328	952.480831	476.744054	951.496815	476.252046	**E**	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
7							**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	1114.605621	0.000627	SVQLTEK
16.2	1114.613480	-0.007232	SVFAKHGLEK
5.8	1114.609451	-0.003203	SVARLSPETR
4.4	1114.591690	0.014558	ASVHSMISRK
3.9	1114.598236	0.008012	SAVITSLDPGR
3.0	1114.609436	-0.003188	EGIKRQQEK
2.9	1114.609451	-0.003203	LLQSALGGNSR
2.3	1114.616837	-0.010589	SPRLLCIEK
1.3	1114.605621	0.000627	LQTSVEK

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

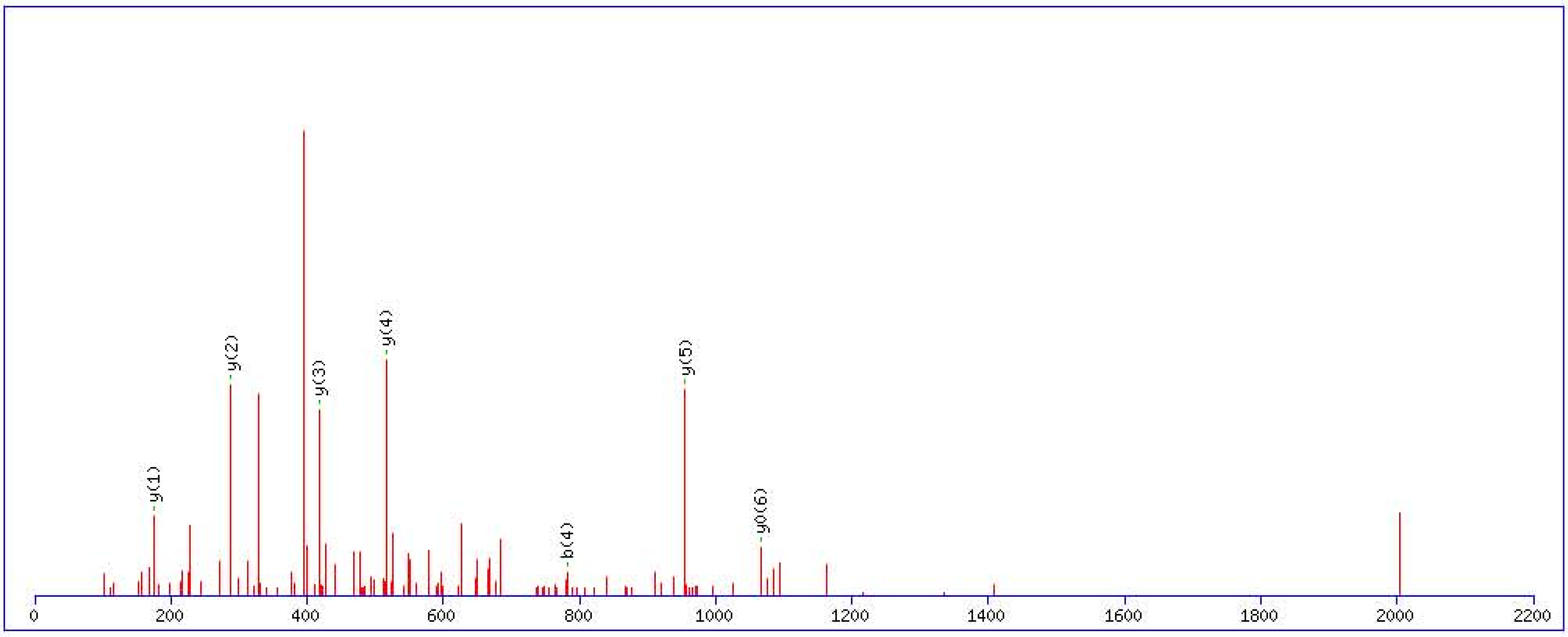
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NEQVEIR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

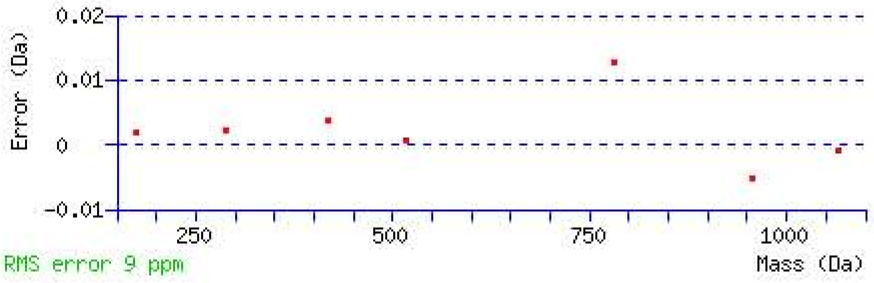
Match to Query 27643: 1197.619268 from(599.816910,2+) rtinseconds(1595) index(39486)
Title: Locus:1.1.1.2839.13 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

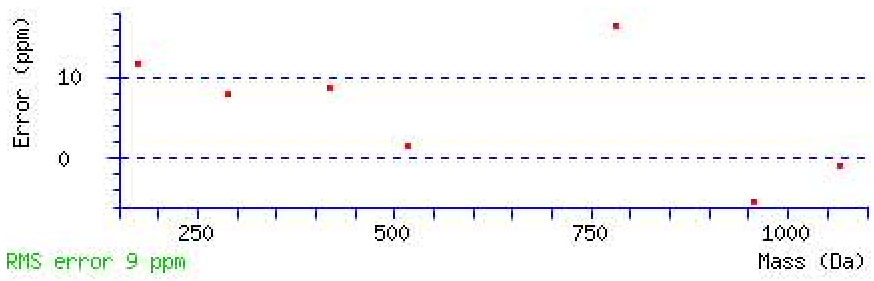
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1197.617569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0054
Matches : 7/66 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	115.050203	58.028740	98.023654	49.515465			N							7
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	E	1084.581942	542.794609	1067.555393	534.281335	**1066.571377**	533.789327	6
3	683.318122	342.162699	666.291573	333.649425	665.307557	333.157417	Q	***955.539349***	478.273313	938.512800	469.760038	937.528784	469.268030	5
4	**782.386536**	391.696906	765.359987	383.183632	764.375971	382.691624	V	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
5	911.429129	456.218203	894.402580	447.704928	893.418564	447.212920	E	***417.245609***	209.126443	400.219060	200.613168	399.235044	200.121160	3
6	1024.513193	512.760235	1007.486644	504.246960	1006.502628	503.754952	I	***288.203016***	144.605146	271.176467	136.091872			2
7							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.6	1197.617569	0.001699	NEQVEIR
14.7	1197.636215	-0.016947	GVSQMPLR
9.4	1197.617569	0.001699	QEVNELR
9.0	1197.617569	0.001699	NQEDLLR
8.1	1197.625443	-0.006175	WGSSLVKHER
7.9	1197.617569	0.001699	LQDNELR
5.9	1197.621399	-0.002131	EKHSTQAKNR
4.3	1197.628815	-0.009547	QLSMQVHALR
2.2	1197.617584	0.001684	QDLDQLR
1.6	1197.635315	-0.016047	AAAAAETPEVLR

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

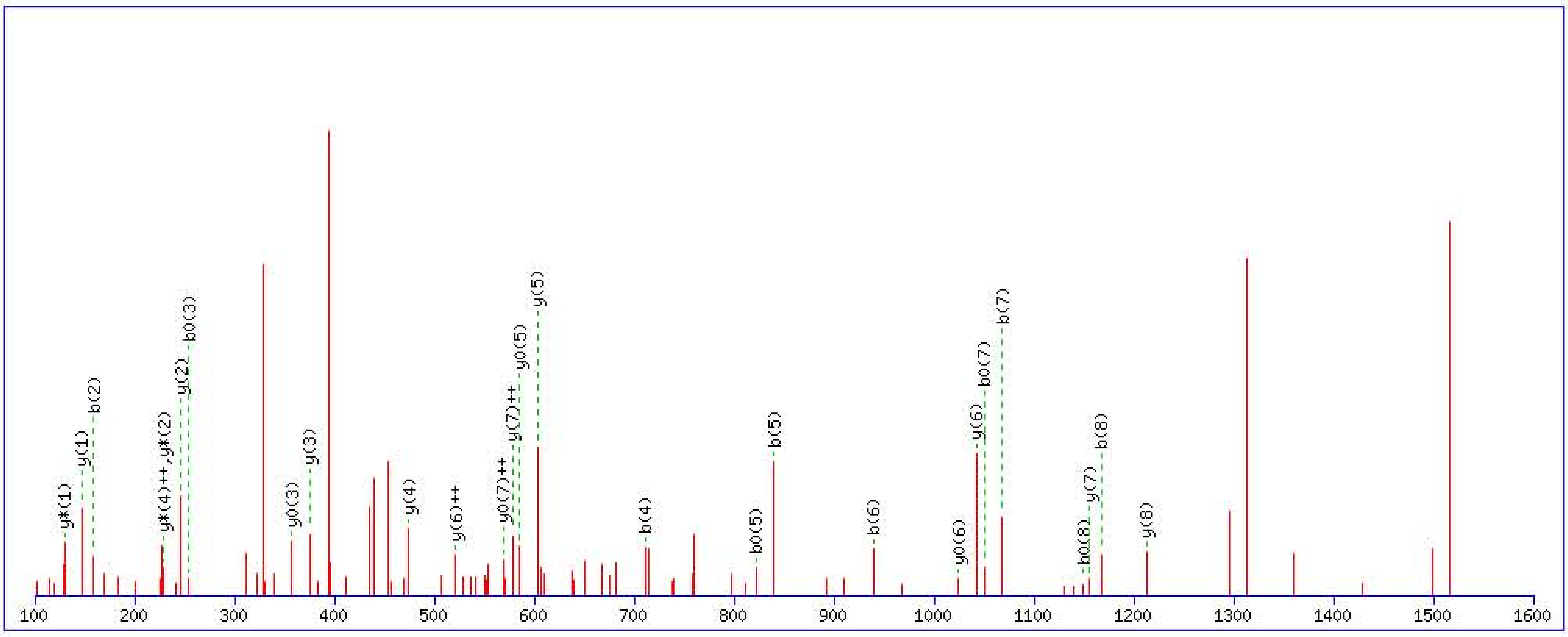
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGLQEVEVK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

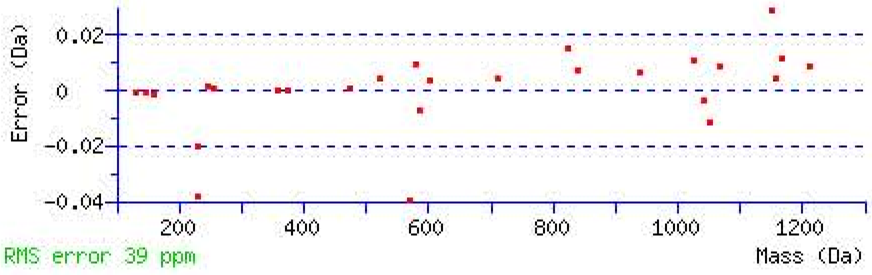
Match to Query 31201: 1312.713028 from(657.363790,2+) rtinseconds(1796) index(40727)
Title: Locus:1.1.1.2909.11 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

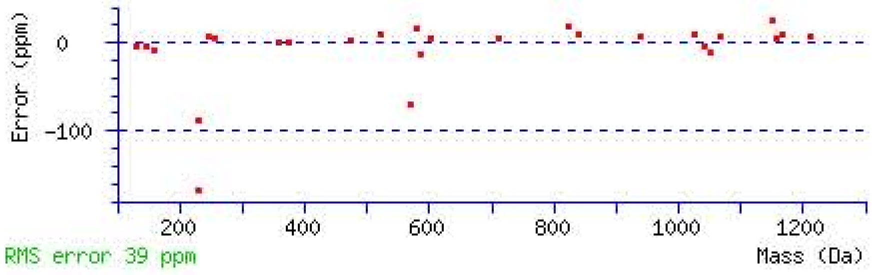
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1312.706070
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 50 **Expect:** 0.0001
Matches : 27/86 fragment ions using 45 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							9
2	**159.076419**	80.041847			141.065854	71.036565	G	***1212.665672***	606.836474	1195.639123	598.323200	1194.655107	597.831192	8
3	272.160483	136.583879			254.149918	127.578597	L	***1155.644208***	578.325742	1138.617659	569.812468	1137.633643	569.320460	7
4	**711.385809**	356.196543	694.359260	347.683268	693.375244	347.191260	Q	***1042.560144***	521.783710	1025.533595	513.270436	1024.549579	512.778428	6
5	**840.428402**	420.717839	823.401853	412.204565	822.417837	411.712557	E	***603.334818***	302.171047	586.308269	293.657773	585.324253	293.165765	5
6	**939.496816**	470.252046	922.470267	461.738772	921.486251	461.246764	V	***474.292225***	237.649751	457.265676	229.136476	456.281660	228.644468	4
7	**1068.539409**	534.773343	1051.512860	526.260068	1050.528844	525.768060	E	***375.223811***	188.115544	358.197262	179.602269	357.213246	179.110261	3
8	**1167.607823**	584.307550	1150.581274	575.794275	1149.597258	575.302267	V	***246.181218***	123.594247	229.154669	115.080973			2
9							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.6	1312.706070	0.006958	TGLQEVEVK
6.8	1312.699524	0.013504	TIMHLMINNVK
5.7	1312.732544	-0.019516	VHLKWKMEVK
5.5	1312.728516	-0.015488	KPQRGMPKVEK
3.9	1312.721130	-0.008102	QVEVLTNQRAR
2.9	1312.717300	-0.004272	ASLQTVDIR
2.1	1312.721115	-0.008087	KKPQRDSQAQK
1.4	1312.713913	-0.000885	KVFEKYTTAAR
1.2	1312.732346	-0.019318	EARQRVQSLAR
1.1	1312.728546	-0.015518	QGSRGTAVVK

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

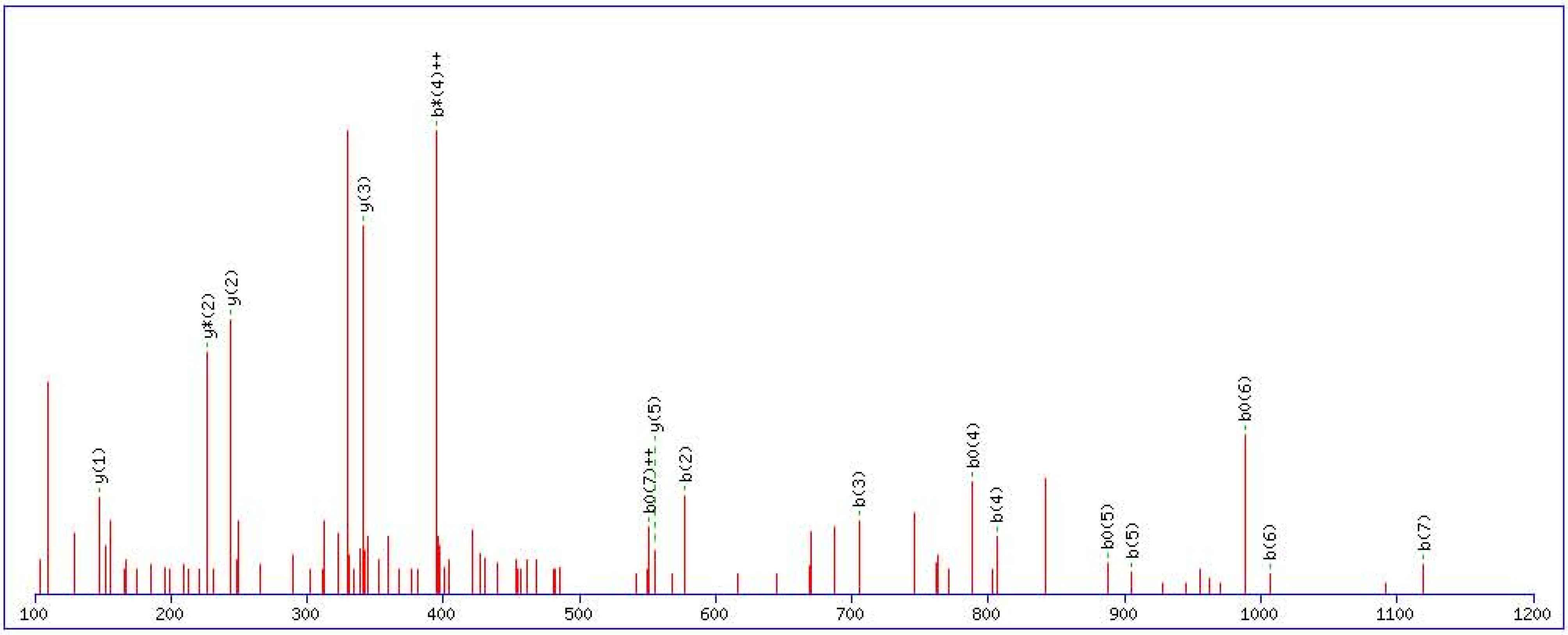
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQQTVTIPPK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

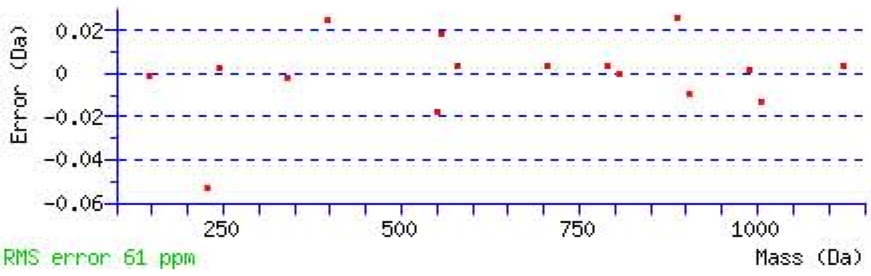
Match to Query 37318: 1458.798192 from(487.273340,3+) rtinseconds(1523) index(39032)
Title: Locus:1.1.1.2814.12 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

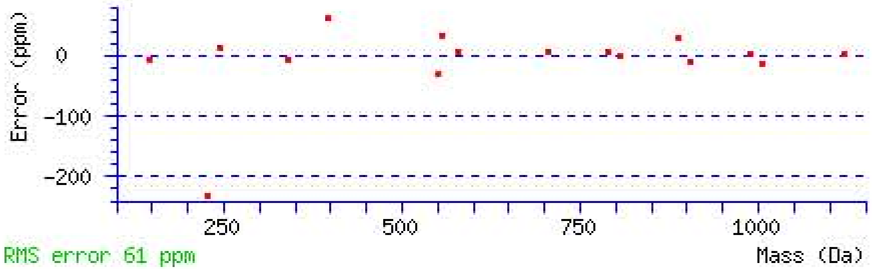
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1458.801712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.015
Matches : 16/92 fragment ions using 30 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							10
2	***577.291514***	289.149395	560.264965	280.636121			Q	1322.750072	661.878674	1305.723523	653.365400	1304.739507	652.873392	9
3	***705.350092***	353.178684	688.323543	344.665410			Q	883.524746	442.266011	866.498197	433.752737	865.514181	433.260729	8
4	***806.397771***	403.702524	789.371222	395.189249	788.387206	394.697241	T	755.466168	378.236722	738.439619	369.723448	737.455603	369.231440	7
5	***905.466185***	453.236731	888.439636	444.723456	887.455620	444.231448	V	654.418489	327.712883	637.391940	319.199608	636.407924	318.707600	6
6	***1006.513864***	503.760570	989.487315	495.247296	988.503299	494.755288	T	***555.350075***	278.178676	538.323526	269.665401	537.339510	269.173393	5
7	***1119.597928***	560.302602	1102.571379	551.789328	1101.587363	551.297319	I	454.302396	227.654836	437.275847	219.141561			4
8	1216.650692	608.828984	1199.624143	600.315710	1198.640127	599.823701	P	***341.218332***	171.112804	324.191783	162.599530			3
9	1313.703456	657.355366	1296.676907	648.842092	1295.692891	648.350083	P	***244.165568***	122.586422	227.139019	114.073148			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.6	1458.801712	-0.003520	HQQTVTIPPK
24.1	1458.801712	-0.003520	HQQTVTIPPK

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

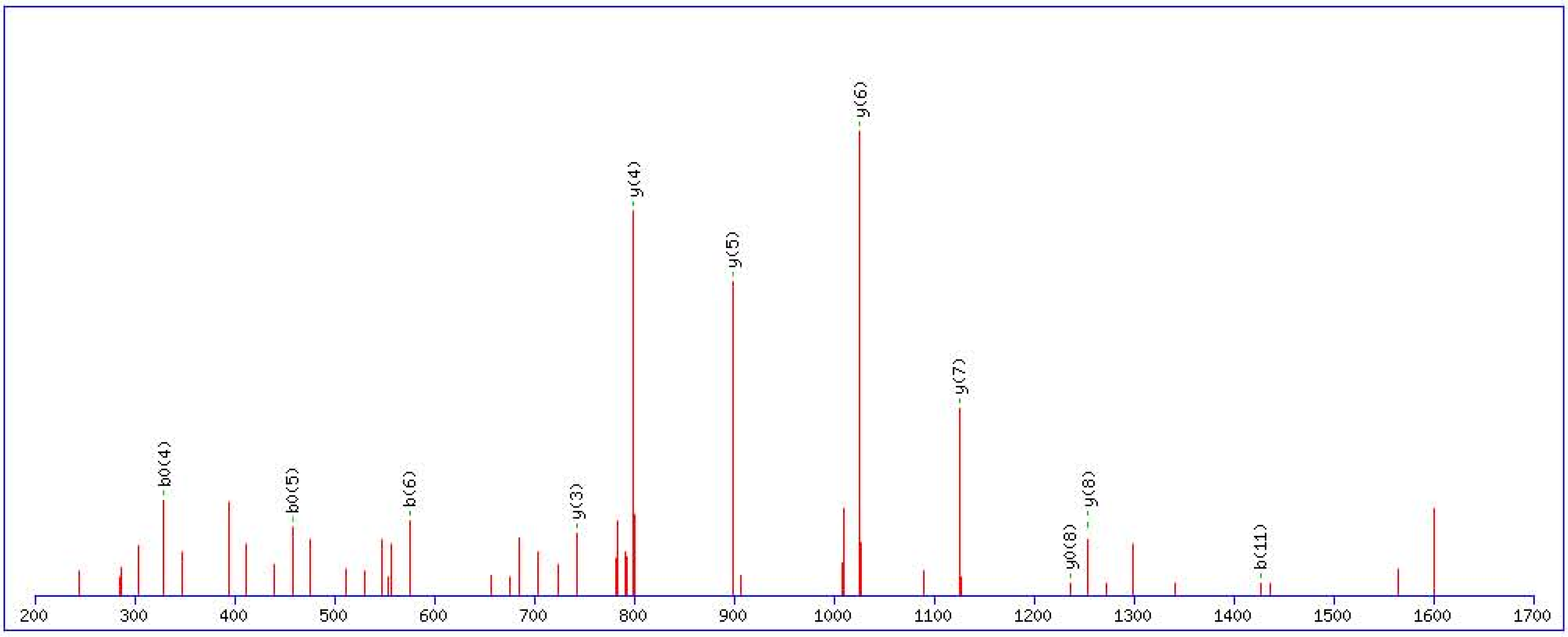
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

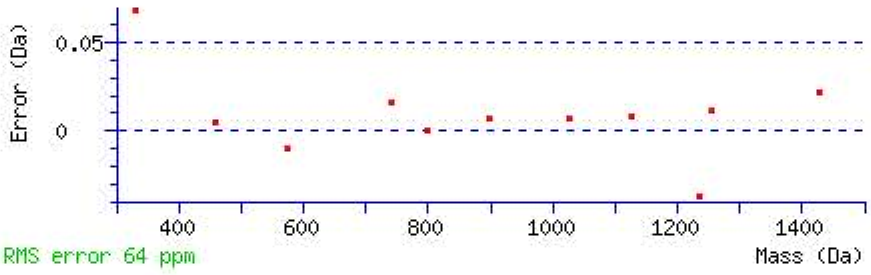
Match to Query 42186: 1599.775288 from(800.894920,2+) rtinseconds(1512) index(38942)
Title: Locus:1.1.1.2810.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

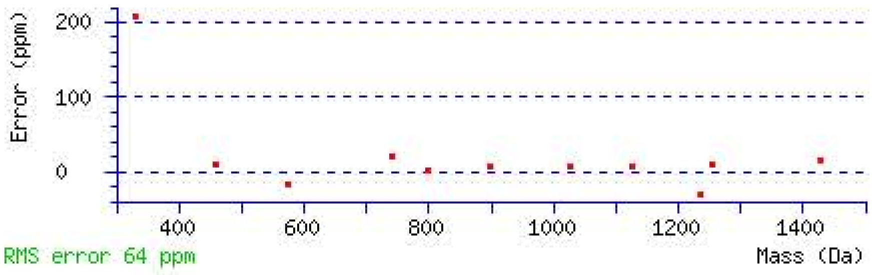
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1599.767517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 8.7e-005
Matches : 11/106 fragment ions using 13 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							12
2	145.060768	73.034022			127.050203	64.028740	G	1513.742754	757.375015	1496.716205	748.861741	1495.732189	748.369733	11
3	232.092796	116.550036			214.082231	107.544753	S	1456.721290	728.864283	1439.694741	720.351009	1438.710725	719.859001	10
4	347.119739	174.063507			329.109174	165.058225	D	1369.689262	685.348269	1352.662713	676.834995	1351.678697	676.342987	9
5	476.162332	238.584804			458.151767	229.579522	E	***1254.662319***	627.834798	1237.635770	619.321523	1236.651754	618.829515	8
6	**575.230746**	288.119011			557.220181	279.113729	V	***1125.619726***	563.313501	1108.593177	554.800227			7
7	703.289324	352.148300	686.262775	343.635026	685.278759	343.143018	Q	***1026.551312***	513.779294	1009.524763	505.266020			6
8	802.357738	401.682507	785.331189	393.169233	784.347173	392.677225	V	***898.492734***	449.750005	881.466185	441.236731			5
9	859.379202	430.193239	842.352653	421.679965	841.368637	421.187957	G	***799.424320***	400.215798	782.397771	391.702524			4
10	987.437780	494.222528	970.411231	485.709254	969.427215	485.217246	Q	***742.402856***	371.705066	725.376307	363.191792			3
11	**1426.663106**	713.835191	1409.636557	705.321917	1408.652541	704.829909	Q	614.344278	307.675777	597.317729	299.162503			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.9	1599.767517	0.007771	SGSDEVQVGQQR
52.9	1599.767517	0.007771	SGSDEVQVGQQR
18.6	1599.767517	0.007771	SGSDEVQVGQQR
11.5	1599.796677	-0.021389	DINDNPPIFPMTVK
7.3	1599.774872	0.000416	MAKEAIFQDTMRK
1.2	1599.767471	0.007817	AMNAANLNIPPSDTR
0.1	1599.753769	0.021519	ASTFSCIMQKWGGK

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

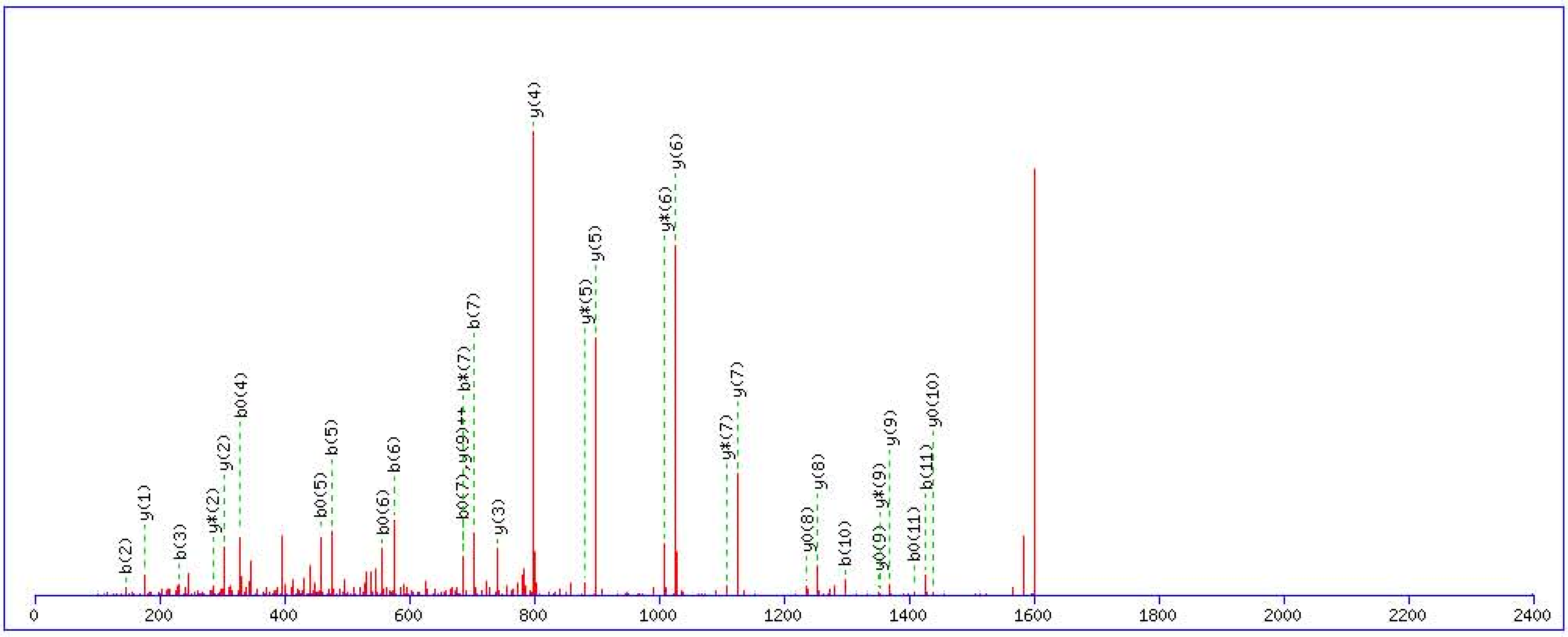
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

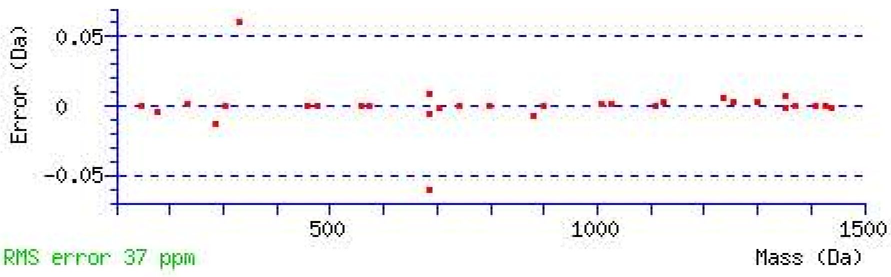
Match to Query 42187: 1599.775288 from(800.894920,2+) rtinseconds(1501) index(38859)
Title: Locus:1.1.1.2806.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

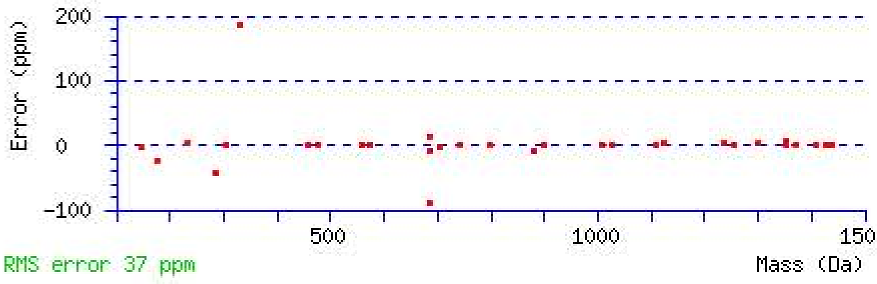


Monoisotopic mass of neutral peptide Mr(calc): 1599.767517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 6.6e-006
Matches : 31/106 fragment ions using 45 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							12
2	**145.060768**	73.034022			127.050203	64.028740	G	1513.742754	757.375015	1496.716205	748.861741	1495.732189	748.369733	11
3	**232.092796**	116.550036			214.082231	107.544753	S	1456.721290	728.864283	1439.694741	720.351009	1438.710725	719.859001	10
4	347.119739	174.063507			329.109174	165.058225	D	***1369.689262***	685.348269	1352.662713	676.834995	1351.678697	676.342987	9
5	**476.162332**	238.584804			458.151767	229.579522	E	***1254.662319***	627.834798	1237.635770	619.321523	1236.651754	618.829515	8
6	**575.230746**	288.119011			557.220181	279.113729	V	***1125.619726***	563.313501	1108.593177	554.800227			7
7	**703.289324**	352.148300	686.262775	343.635026	685.278759	343.143018	Q	***1026.551312***	513.779294	1009.524763	505.266020			6
8	802.357738	401.682507	785.331189	393.169233	784.347173	392.677225	V	***898.492734***	449.750005	881.466185	441.236731			5
9	859.379202	430.193239	842.352653	421.679965	841.368637	421.187957	G	***799.424320***	400.215798	782.397771	391.702524			4
10	**1298.604528**	649.805902	1281.577979	641.292628	1280.593963	640.800620	Q	***742.402856***	371.705066	725.376307	363.191792			3
11	**1426.663106**	713.835191	1409.636557	705.321917	1408.652541	704.829909	Q	***303.177530***	152.092403	286.150981	143.579129			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 37 ppm



RMS error 37 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.1	1599.767517	0.007771	SGSDEVQVGQQR
56.9	1599.767517	0.007771	SGSDEVQVGQQR
33.1	1599.767517	0.007771	SGSDEVQVGQQR
11.4	1599.767471	0.007817	AMNAANLNIPPSDTR
7.0	1599.792648	-0.017360	SSAEVTPDLQSR
5.5	1599.779388	-0.004100	RFPDFSYITQNGR
4.8	1599.767502	0.007786	LHMLSSVDLNGQDR
2.4	1599.771515	0.003773	YVTSAPMPEPQAPGR
1.4	1599.753769	0.021519	MPKFSMPGFKGEGR
1.0	1599.793976	-0.018688	QRSSGIWENGR

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

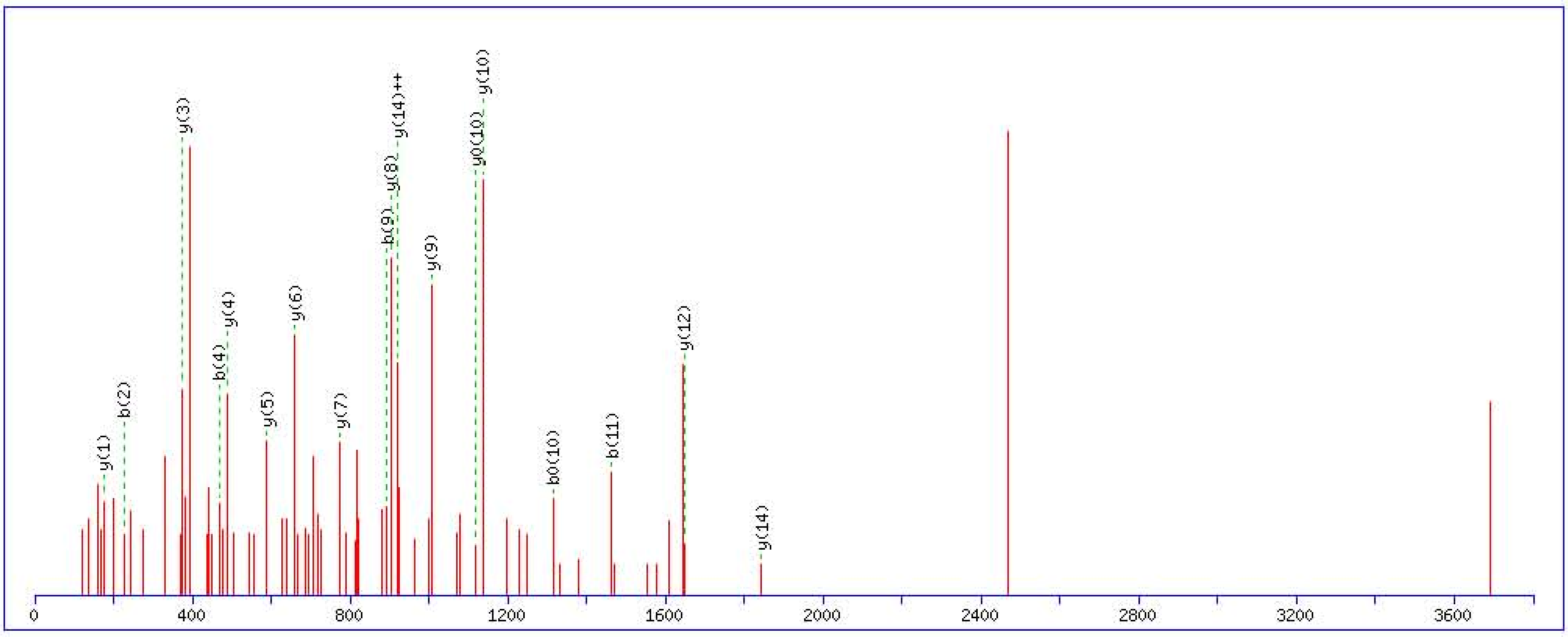
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLQGTPVAQMTEDAVDAER**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

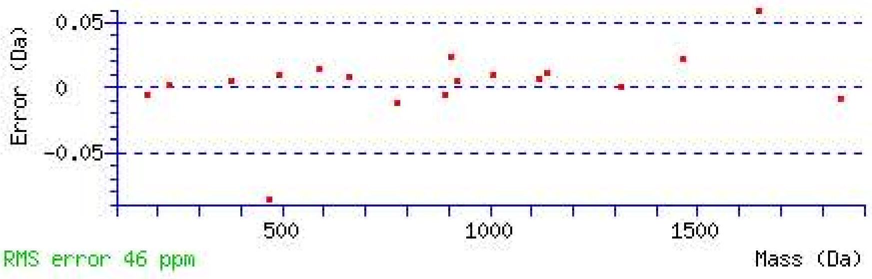
Match to Query 44492: 2467.267962 from(823.429930,3+) rtinseconds(2668) index(46295)
Title: Locus:1.1.1.3212.22 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

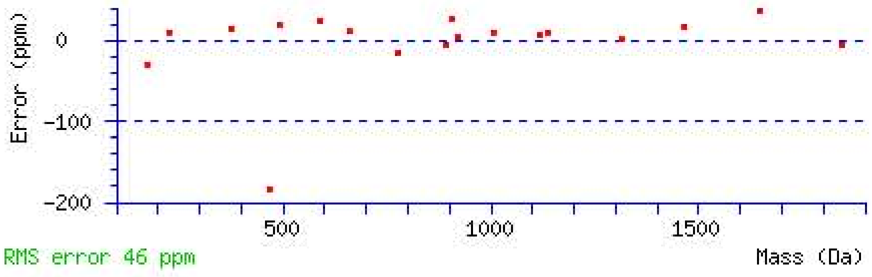
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2467.245071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.0026
Matches : 18/210 fragment ions using 46 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							20
2	**227.175404**	114.091340					L	2355.168297	1178.087786	2338.141748	1169.574512	2337.157732	1169.082504	19
3	340.259468	170.633372					L	2242.084233	1121.545754	2225.057684	1113.032480	2224.073668	1112.540472	18
4	**468.318046**	234.662661	451.291497	226.149386			Q	2129.000169	1065.003722	2111.973620	1056.490448	2110.989604	1055.998440	17
5	525.339510	263.173393	508.312961	254.660119			G	2000.941591	1000.974434	1983.915042	992.461159	1982.931026	991.969151	16
6	626.387189	313.697233	609.360640	305.183958	608.376624	304.691950	T	1943.920127	972.463702	1926.893578	963.950427	1925.909562	963.458419	15
7	723.439953	362.223615	706.413404	353.710340	705.429388	353.218332	P	***1842.872448***	921.939862	1825.845899	913.426588	1824.861883	912.934580	14
8	822.508367	411.757822	805.481818	403.244547	804.497802	402.752539	V	1745.819684	873.413480	1728.793135	864.900206	1727.809119	864.408198	13
9	**893.545481**	447.276379	876.518932	438.763104	875.534916	438.271096	A	***1646.751270***	823.879273	1629.724721	815.365999	1628.740705	814.873991	12
10	1332.770807	666.889042	1315.744258	658.375767	1314.760242	657.883759	Q	1575.714156	788.360716	1558.687607	779.847442	1557.703591	779.355434	11
11	**1463.811292**	732.409284	1446.784743	723.896010	1445.800727	723.404002	M	***1136.488830***	568.748053	1119.462281	560.234779	1118.478265	559.742771	10
12	1564.858971	782.933124	1547.832422	774.419849	1546.848406	773.927841	T	***1005.448345***	503.227811	988.421796	494.714536	987.437780	494.222528	9
13	1693.901564	847.454420	1676.875015	838.941146	1675.890999	838.449138	E	***904.400666***	452.703971	887.374117	444.190697	886.390101	443.698689	8
14	1808.928507	904.967892	1791.901958	896.454617	1790.917942	895.962609	D	***775.358073***	388.182675	758.331524	379.669400	757.347508	379.177392	7
15	1879.965621	940.486449	1862.939072	931.973174	1861.955056	931.481166	A	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.663921	6
16	1979.034035	990.020656	1962.007486	981.507381	1961.023470	981.015373	V	***589.294016***	295.150646	572.267467	286.637372	571.283451	286.145364	5
17	2094.060978	1047.534127	2077.034429	1039.020852	2076.050413	1038.528844	D	***490.225602***	245.616439	473.199053	237.103165	472.215037	236.611157	4
18	2165.098092	1083.052684	2148.071543	1074.539409	2147.087527	1074.047402	A	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
19	2294.140685	1147.573981	2277.114136	1139.060706	2276.130120	1138.568698	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.0	2467.245071	0.022891	ILLQGTPVAQMTEDAVDAER
29.3	2467.245071	0.022891	ILLQGTPVAQMTEDAVDAER

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

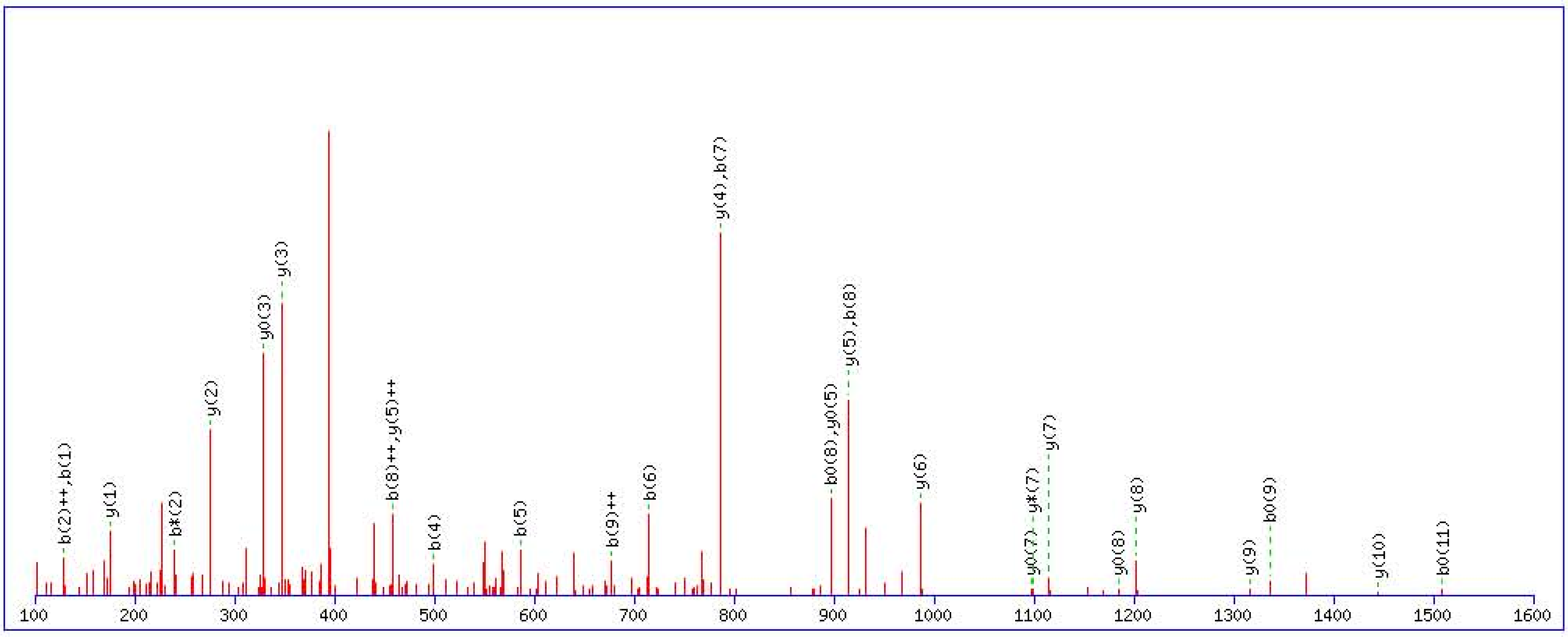
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KQELSEAEQATR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

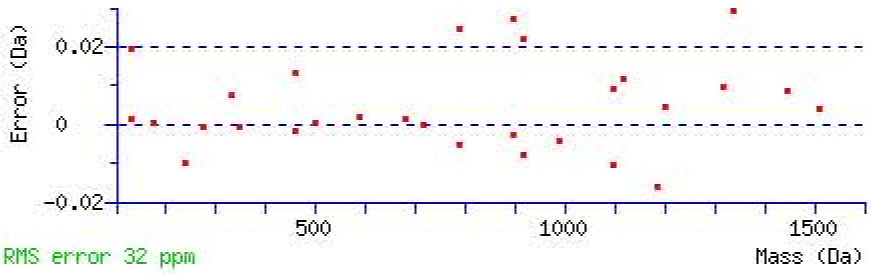
Match to Query 45809: 1699.857132 from(567.626320,3+) rtinseconds(1357) index(37846)
Title: Locus:1.1.1.2756.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

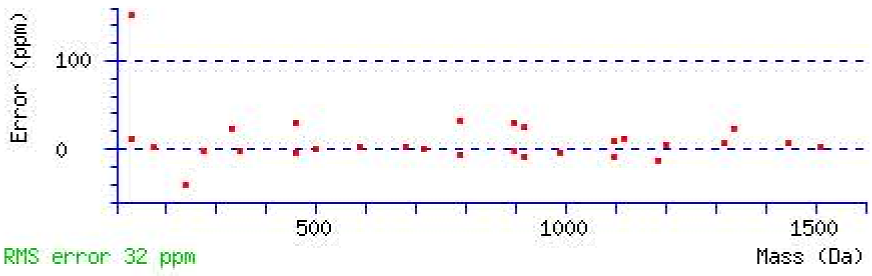
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1699.856277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 3e-006
Matches : 29/126 fragment ions using 39 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.102239**	65.054757	112.075690	56.541483			K							12
2	257.160817	**129.084047**	240.134268	120.570772			Q	1572.768634	786.887955	1555.742085	778.374681	1554.758069	777.882673	11
3	386.203410	193.605343	369.176861	185.092069	368.192845	184.600061	E	***1444.710056***	722.858666	1427.683507	714.345392	1426.699491	713.853384	10
4	**499.287474**	250.147375	482.260925	241.634101	481.276909	241.142093	L	***1315.667463***	658.337370	1298.640914	649.824095	1297.656898	649.332087	9
5	**586.319502**	293.663389	569.292953	285.150115	568.308937	284.658107	S	***1202.583399***	601.795338	1185.556850	593.282063	1184.572834	592.790055	8
6	**715.362095**	358.184686	698.335546	349.671411	697.351530	349.179403	E	***1115.551371***	558.279324	1098.524822	549.766049	1097.540806	549.274041	7
7	**786.399209**	393.703243	769.372660	385.189968	768.388644	384.697960	A	***986.508778***	493.758027	969.482229	485.244753	968.498213	484.752745	6
8	**915.441802**	**458.224539**	898.415253	449.711265	897.431237	449.219257	E	***915.471664***	458.239470	898.445115	449.726196	897.461099	449.234188	5
9	1354.667128	**677.837202**	1337.640579	669.323928	1336.656563	668.831920	Q	***786.429071***	393.718174	769.402522	385.204899	768.418506	384.712891	4
10	1425.704242	713.355759	1408.677693	704.842485	1407.693677	704.350477	A	***347.203745***	174.105510	330.177196	165.592236	329.193180	165.100228	3
11	1526.751921	763.879599	1509.725372	755.366324	1508.741356	754.874316	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.1	1699.856277	0.000855	KQELSEAEQATR
14.3	1699.856277	0.000855	KQELSEAEQATR
7.8	1699.881424	-0.024292	LSSKELQEQAEK
7.2	1699.845932	0.011200	QAMQEQLSK
6.8	1699.878754	-0.021622	ELQQRMQEEVVRR
6.1	1699.849792	0.007340	QEMRTTQLGPGR
4.5	1699.845932	0.011200	QAMQEQLSK
4.0	1699.874039	-0.016907	KEISVNDLNESSIPR
3.6	1699.874924	-0.017792	SQGMLALSISPNR
2.7	1699.849792	0.007340	QEMRTTQLGPGR

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

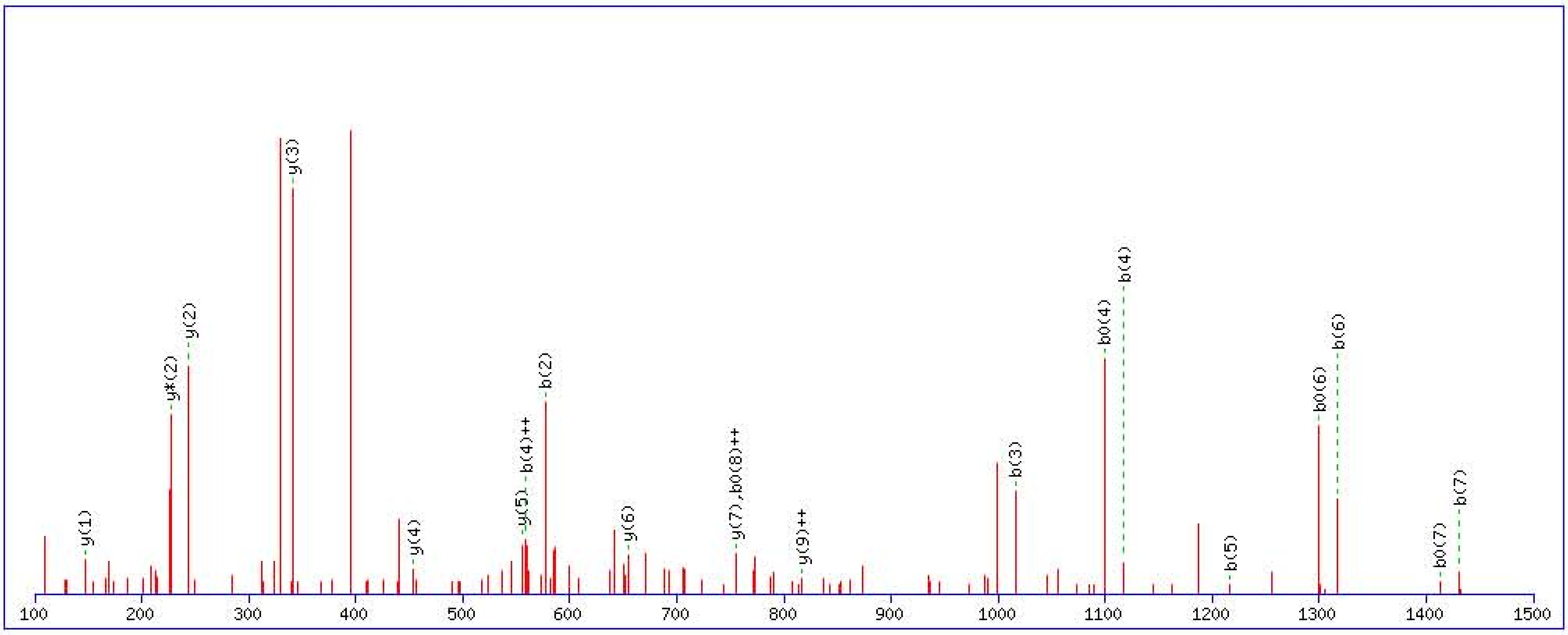
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQQTVTIPPK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

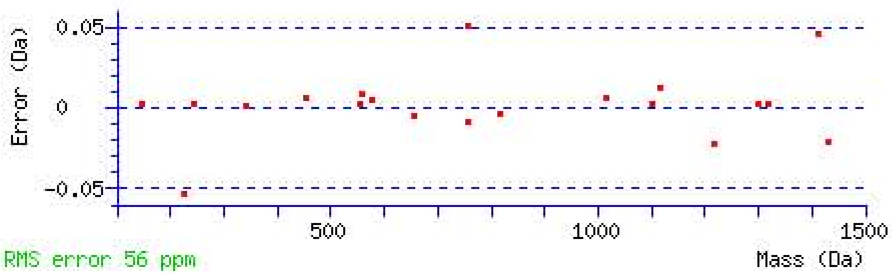
Match to Query 47759: 1769.974092 from(590.998640,3+) rtinseconds(1899) index(41399)
Title: Locus:1.1.1.2945.8 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

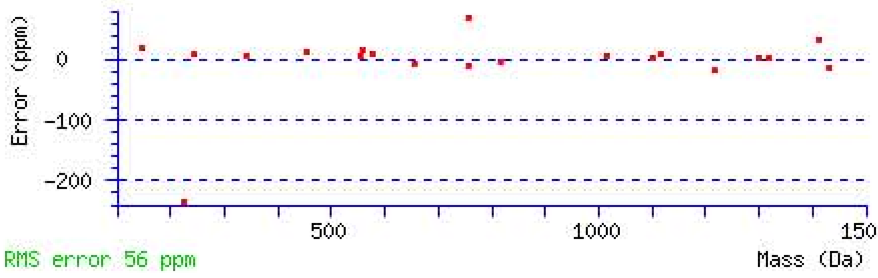
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1769.968460
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.028
Matches : 20/92 fragment ions using 40 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							10
2	***577.291514***	289.149395	560.264965	280.636121			Q	1633.916820	817.462048	1616.890271	808.948774	1615.906255	808.456766	9
3	***1016.516840***	508.762058	999.490291	500.248784			Q	1194.691494	597.849385	1177.664945	589.336111	1176.680929	588.844103	8
4	***1117.564519***	559.285898	1100.537970	550.772623	1099.553954	550.280615	T	***755.466168***	378.236722	738.439619	369.723448	737.455603	369.231440	7
5	***1216.632933***	608.820105	1199.606384	600.306830	1198.622368	599.814822	V	***654.418489***	327.712883	637.391940	319.199608	636.407924	318.707600	6
6	***1317.680612***	659.343944	1300.654063	650.830670	1299.670047	650.338662	T	***555.350075***	278.178676	538.323526	269.665401	537.339510	269.173393	5
7	***1430.764676***	715.885976	1413.738127	707.372702	1412.754111	706.880694	I	***454.302396***	227.654836	437.275847	219.141561			4
8	1527.817440	764.412358	1510.790891	755.899084	1509.806875	755.407076	P	***341.218332***	171.112804	324.191783	162.599530			3
9	1624.870204	812.938740	1607.843655	804.425466	1606.859639	803.933458	P	***244.165568***	122.586422	227.139019	114.073148			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	1769.968460	0.005632	HQQTVTIPPK
11.8	1769.961029	0.013063	WMLSRDRASTLPLPK

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

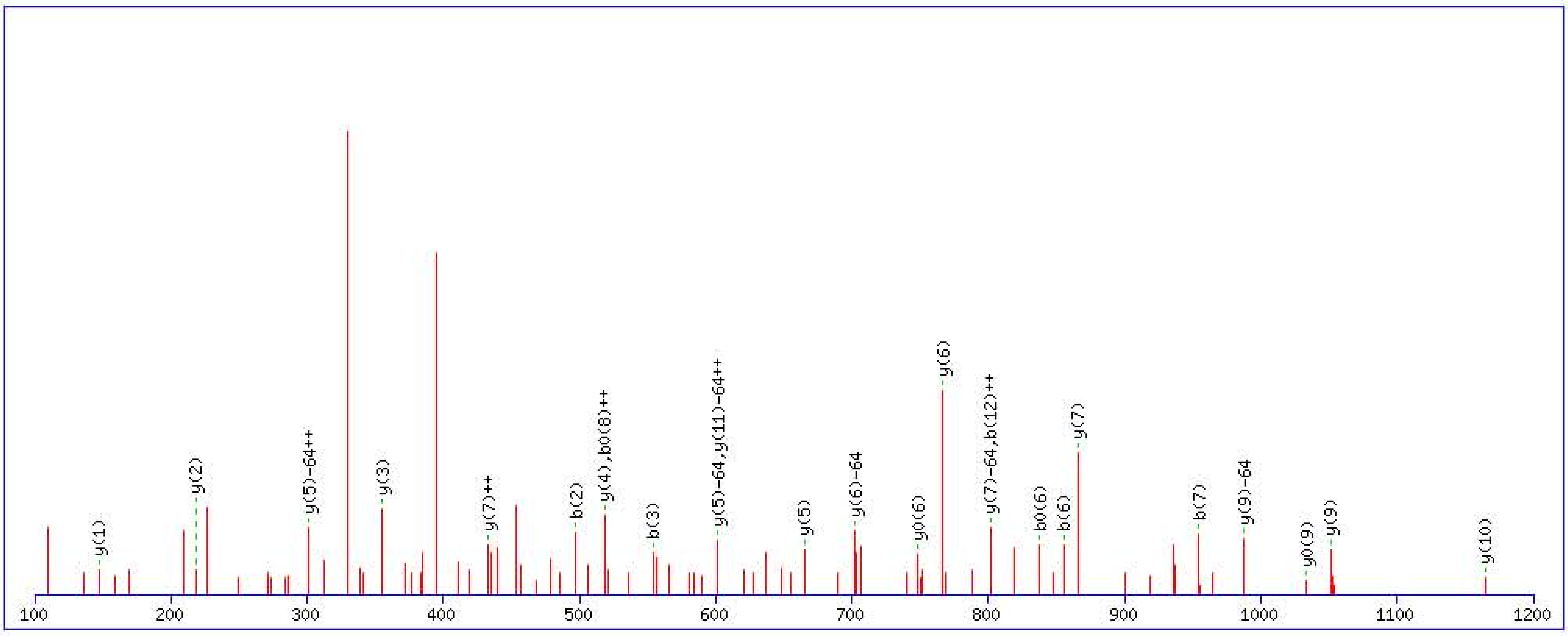
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQGTLSVVTMYHAK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

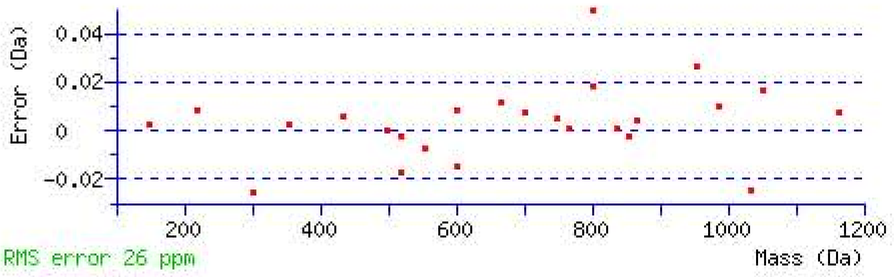
Match to Query 48895: 1817.924892 from(606.982240,3+) rtinseconds(1786) index(40676)
Title: Locus:1.1.1.2906.8 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

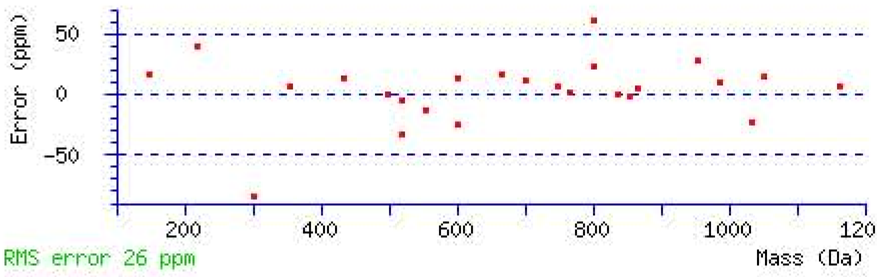
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1817.916824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
M10     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 61  Expect: 2.5e-005
Matches : 25/214 fragment ions using 31 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							14
2	**497.254066**	249.130671	480.227517	240.617397			Q	1761.902627	881.454952	1744.876078	872.941677	1743.892062	872.449669	13
3	**554.275530**	277.641403	537.248981	269.128129			G	1322.677301	661.842289	1305.650752	653.329014	1304.666736	652.837006	12
4	655.323209	328.165243	638.296660	319.651968	637.312644	319.159960	T	1265.655837	633.331557	1248.629288	624.818282	1247.645272	624.326274	11
5	768.407273	384.707275	751.380724	376.194000	750.396708	375.701992	L	***1164.608158***	582.807717	1147.581609	574.294443	1146.597593	573.802435	10
6	**855.439301**	428.223289	838.412752	419.710014	837.428736	419.218006	S	***1051.524094***	526.265685	1034.497545	517.752411	1033.513529	517.260403	9
7	**954.507715**	477.757496	937.481166	469.244221	936.497150	468.752213	V	964.492066	482.749671	947.465517	474.236397	946.481501	473.744389	8
8	1053.576129	527.291703	1036.549580	518.778428	1035.565564	518.286420	V	***865.423652***	433.215464	848.397103	424.702190	847.413087	424.210182	7
9	1154.623808	577.815542	1137.597259	569.302268	1136.613243	568.810260	T	***766.355238***	383.681257	749.328689	375.167983	748.344673	374.675975	6
10	1301.659208	651.333242	1284.632659	642.819968	1283.648643	642.327960	M	***665.307559***	333.157418	648.281010	324.644143			5
11	1464.722537	732.864907	1447.695988	724.351632	1446.711972	723.859624	Y	***518.272159***	259.639718	501.245610	251.126443			4
12	1601.781449	801.394363	1584.754900	792.881088	1583.770884	792.389080	H	***355.208830***	178.108053	338.182281	169.594778			3
13	1672.818563	836.912920	1655.792014	828.399645	1654.807998	827.907637	A	***218.149918***	109.578597	201.123369	101.065322			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.5	1817.916824	0.008068	GQGTLSVVTMYHAK

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

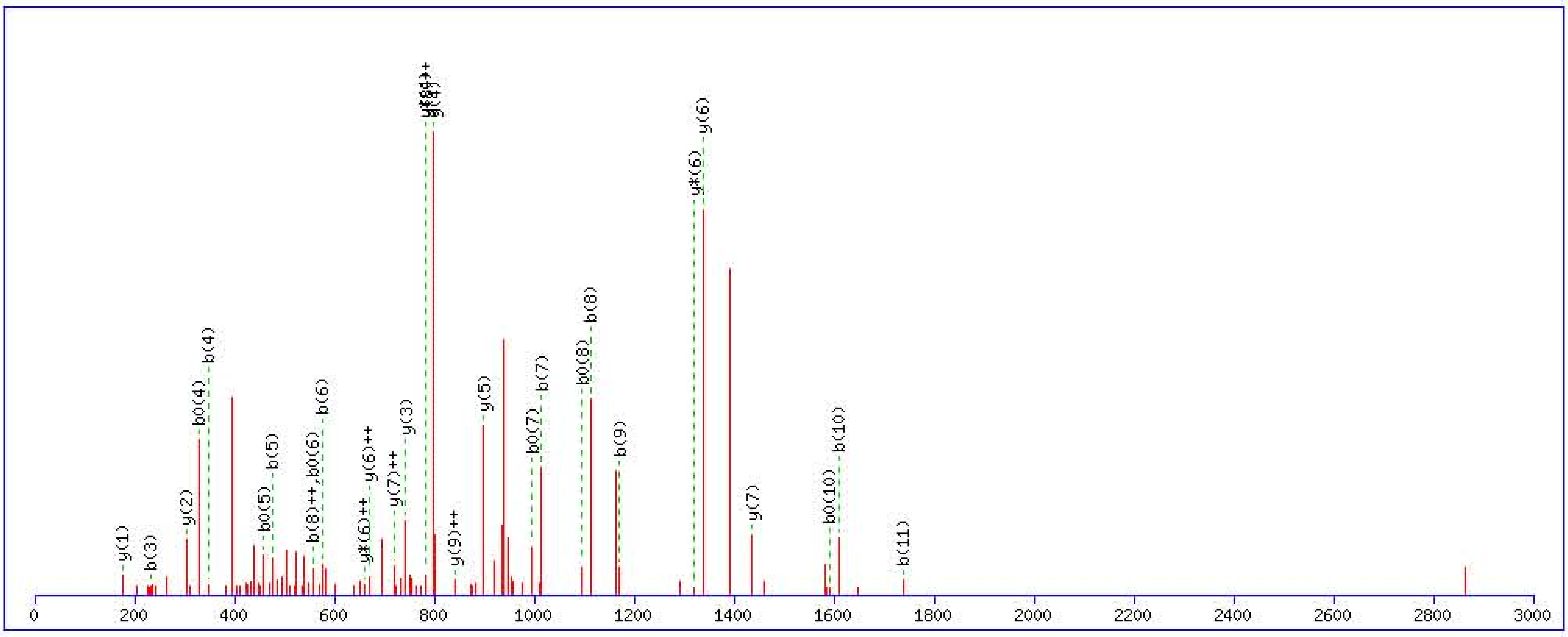
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

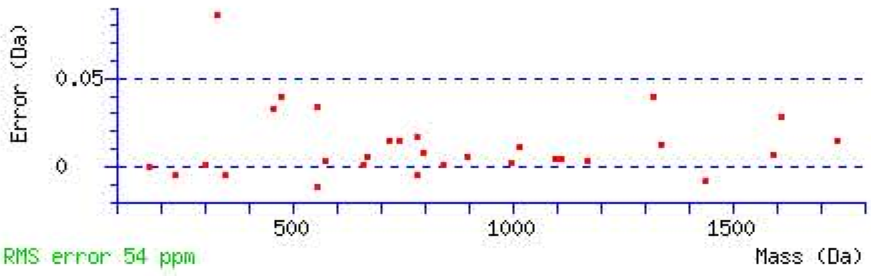
Match to Query 50875: 1910.940228 from(956.477390,2+) rtinseconds(1851) index(41009)
Title: Locus:1.1.1.2928.22 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

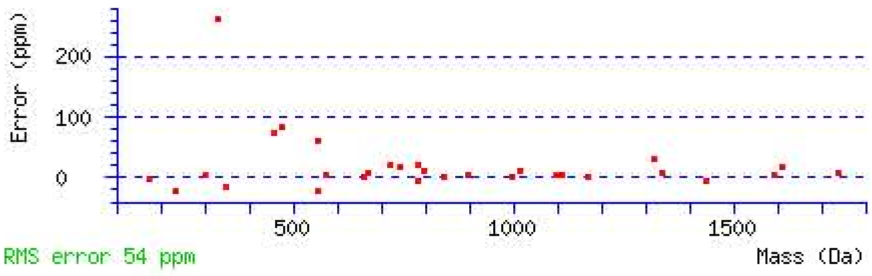
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1910.934265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.013
Matches : 30/106 fragment ions using 69 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							12
2	145.060768	73.034022			127.050203	64.028740	G	1824.909502	912.958389	1807.882953	904.445115	1806.898937	903.953107	11
3	***232.092796***	116.550036			214.082231	107.544753	S	1767.888038	884.447657	1750.861489	875.934383	1749.877473	875.442375	10
4	***347.119739***	174.063507			329.109174	165.058225	D	1680.856010	840.931643	1663.829461	832.418369	1662.845445	831.926361	9
5	***476.162332***	238.584804			458.151767	229.579522	E	1565.829067	783.418172	1548.802518	774.904897	1547.818502	774.412889	8
6	***575.230746***	288.119011			557.220181	279.113729	V	**1436.786474**	718.896875	1419.759925	710.383601			7
7	***1014.456072***	507.731674	997.429523	499.218400	996.445507	498.726392	Q	**1337.718060**	669.362668	1320.691511	660.849394			6
8	***1113.524486***	557.265881	1096.497937	548.752607	1095.513921	548.260599	V	**898.492734**	449.750005	881.466185	441.236731			5
9	***1170.545950***	585.776613	1153.519401	577.263339	1152.535385	576.771330	G	**799.424320**	400.215798	782.397771	391.702524			4
10	***1609.771276***	805.389276	1592.744727	796.876002	1591.760711	796.383994	Q	**742.402856**	371.705066	725.376307	363.191792			3
11	***1737.829854***	869.418565	1720.803305	860.905291	1719.819289	860.413283	Q	**303.177530**	152.092403	286.150981	143.579129			2
12							R	**175.118952**	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	1910.934265	0.005963	SGSDEVQVGQQR
31.6	1910.938263	0.001965	YVTSAPMPEPQAPGR
27.7	1910.934265	0.005963	SGSDEVQVGQQR
5.0	1910.934265	0.005963	SGSDEVQVGQQR
3.9	1910.930725	0.009503	AGSGGLGGGAGGGQGAGAGQGAALR
3.9	1910.963196	-0.022968	EQQRQEELEKQR
3.1	1910.913101	0.027127	TLNMDMFTWEPRKAR
2.7	1910.955811	-0.015583	RLAALGADPAARDSDAEGR
2.3	1910.957382	-0.017154	DPWRFGNTPVQQR
1.4	1910.938721	0.001507	QEAEGLALDSPWHRFR

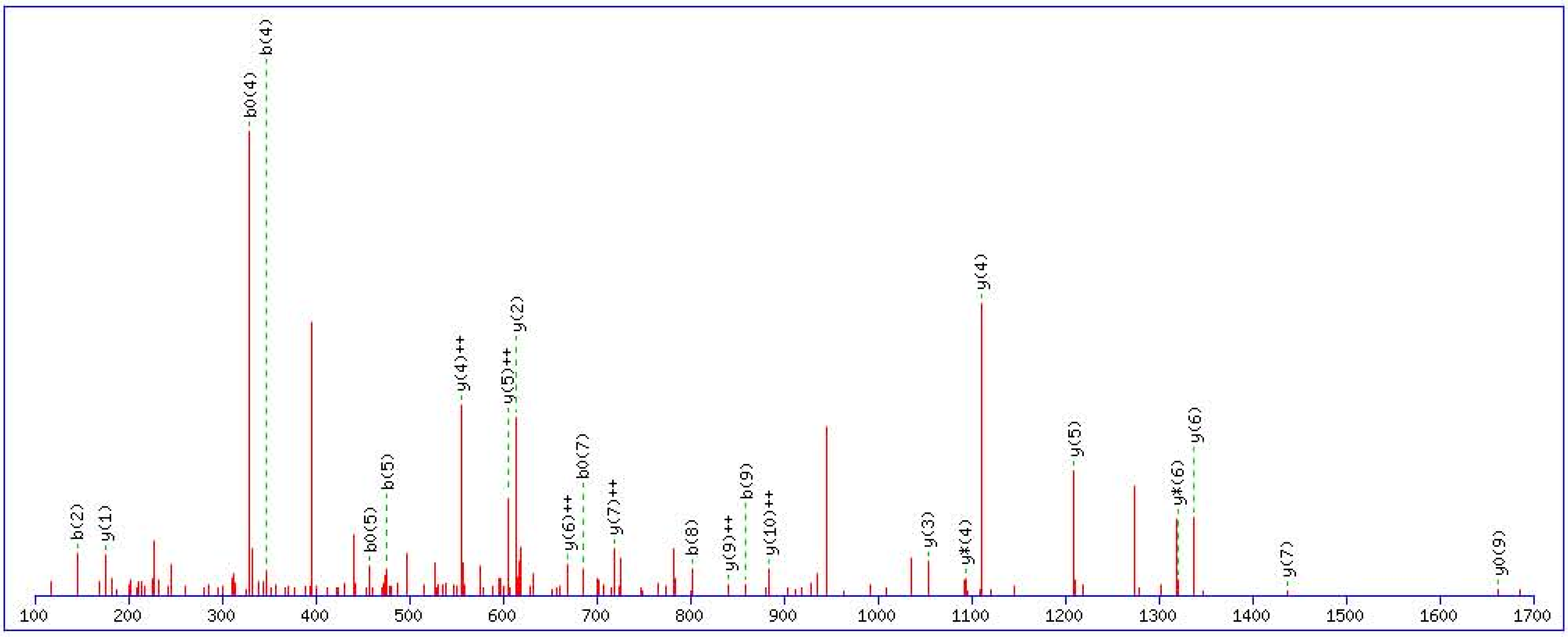
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

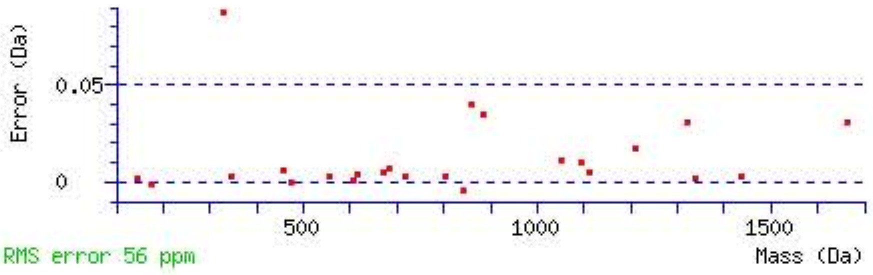
Match to Query 50876: 1910.943492 from(637.988440,3+) rtinseconds(1890) index(41325)
Title: Locus:1.1.1.2942.9 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

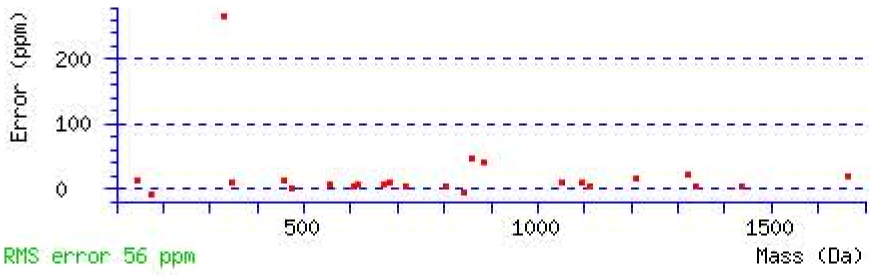
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1910.934265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.011
Matches : 24/106 fragment ions using 55 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							12
2	**145.060768**	73.034022			127.050203	64.028740	G	1824.909502	912.958389	1807.882953	904.445115	1806.898937	903.953107	11
3	232.092796	116.550036			214.082231	107.544753	S	1767.888038	884.447657	1750.861489	875.934383	1749.877473	875.442375	10
4	**347.119739**	174.063507			329.109174	165.058225	D	1680.856010	840.931643	1663.829461	832.418369	1662.845445	831.926361	9
5	**476.162332**	238.584804			458.151767	229.579522	E	1565.829067	783.418172	1548.802518	774.904897	1547.818502	774.412889	8
6	575.230746	288.119011			557.220181	279.113729	V	***1436.786474***	718.896875	1419.759925	710.383601			7
7	703.289324	352.148300	686.262775	343.635026	685.278759	343.143018	Q	***1337.718060***	669.362668	1320.691511	660.849394			6
8	**802.357738**	401.682507	785.331189	393.169233	784.347173	392.677225	V	***1209.659482***	605.333379	1192.632933	596.820105			5
9	**859.379202**	430.193239	842.352653	421.679965	841.368637	421.187957	G	***1110.591068***	555.799172	1093.564519	547.285898			4
10	1298.604528	649.805902	1281.577979	641.292628	1280.593963	640.800620	Q	***1053.569604***	527.288440	1036.543055	518.775166			3
11	1737.829854	869.418565	1720.803305	860.905291	1719.819289	860.413283	Q	***614.344278***	307.675777	597.317729	299.162503			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.0	1910.934265	0.009227	SGSDEVQVGQQR
6.0	1910.958542	-0.015050	TDDYGRDLSSVQTLLTK
5.9	1910.934265	0.009227	SGSDEVQVGQQR
3.9	1910.934265	0.009227	SGSDEVQVGQQR

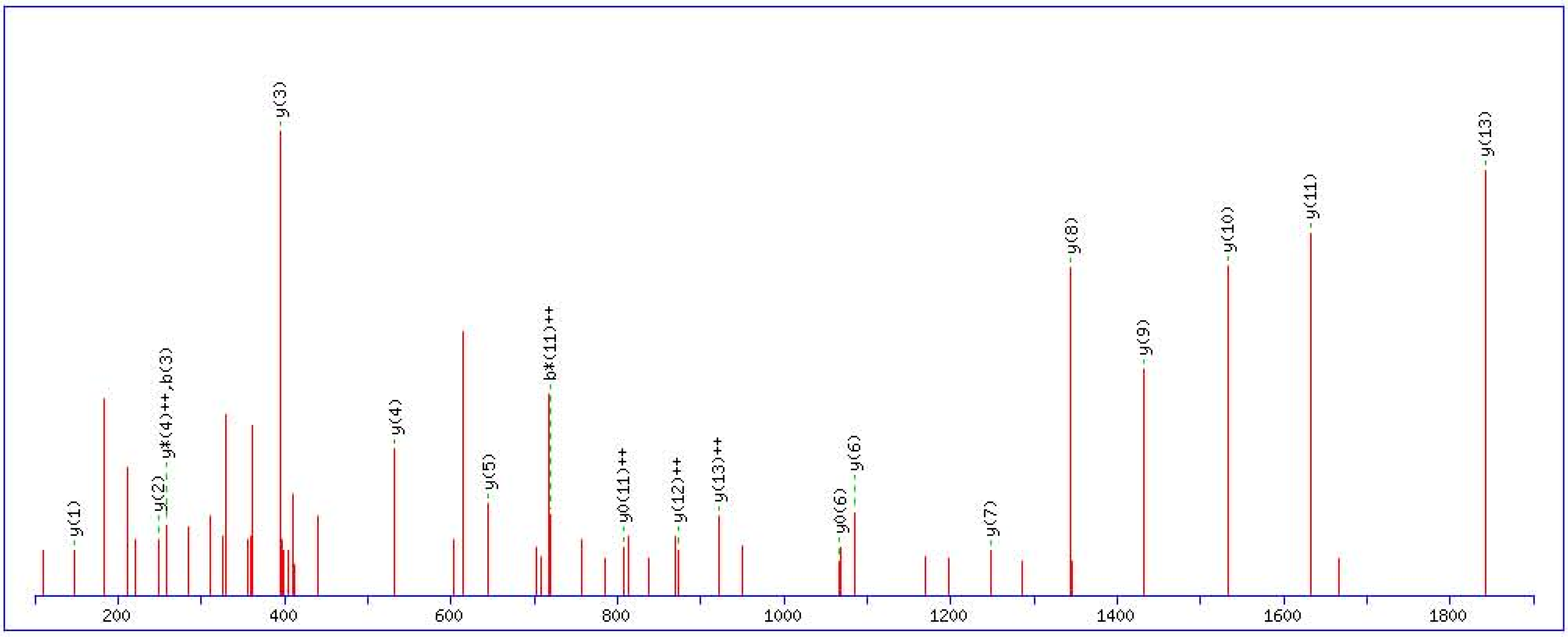
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGIPIVTSPYQIHFTK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

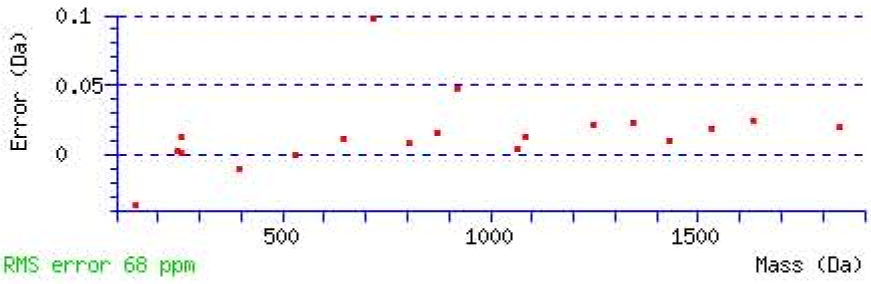
Match to Query 56011: 2098.150092 from(700.390640,3+) rtinseconds(2322) index(44177)
Title: Locus:1.1.1.3092.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

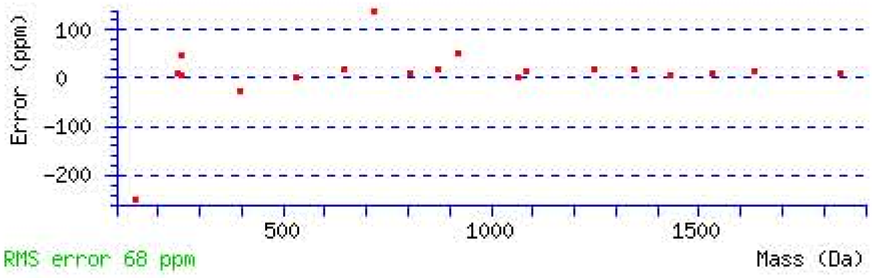
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2098.128525
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 1.8e-005
Matches : 19/158 fragment ions using 46 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							16
2	145.060768	73.034022			127.050203	64.028740	G	2012.103769	1006.555523	1995.077220	998.042248	1994.093204	997.550240	15
3	258.144832	129.576054			240.134267	120.570772	I	1955.082305	978.044791	1938.055756	969.531516	1937.071740	969.039508	14
4	355.197596	178.102436			337.187031	169.097154	P	***1841.998241***	921.502759	1824.971692	912.989484	1823.987676	912.497476	13
5	468.281660	234.644468			450.271095	225.639186	I	1744.945477	872.976377	1727.918928	864.463102	1726.934912	863.971094	12
6	567.350074	284.178675			549.339509	275.173393	V	***1631.861413***	816.434345	1614.834864	807.921070	1613.850848	807.429062	11
7	668.397753	334.702515			650.387188	325.697232	T	***1532.792999***	766.900138	1515.766450	758.386863	1514.782434	757.894855	10
8	755.429781	378.218529			737.419216	369.213246	S	***1431.745320***	716.376298	1414.718771	707.863024	1413.734755	707.371016	9
9	852.482545	426.744911			834.471980	417.739628	P	***1344.713292***	672.860284	1327.686743	664.347010	1326.702727	663.855002	8
10	1015.545874	508.276575			997.535309	499.271293	Y	***1247.660528***	624.333902	1230.633979	615.820628	1229.649963	615.328620	7
11	1454.771200	727.889238	1437.744651	719.375964	1436.760635	718.883956	Q	***1084.597199***	542.802238	1067.570650	534.288963	1066.586634	533.796955	6
12	1567.855264	784.431270	1550.828715	775.917996	1549.844699	775.425988	I	***645.371873***	323.189574	628.345324	314.676300	627.361308	314.184292	5
13	1704.914176	852.960726	1687.887627	844.447452	1686.903611	843.955444	H	***532.287809***	266.647542	515.261260	258.134268	514.277244	257.642260	4
14	1851.982590	926.494933	1834.956041	917.981659	1833.972025	917.489651	F	***395.228897***	198.118086	378.202348	189.604812	377.218332	189.112804	3
15	1953.030269	977.018773	1936.003720	968.505498	1935.019704	968.013490	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
16							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.5	2098.128525	0.021567	SGIPIVTSPYQIHFTK

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

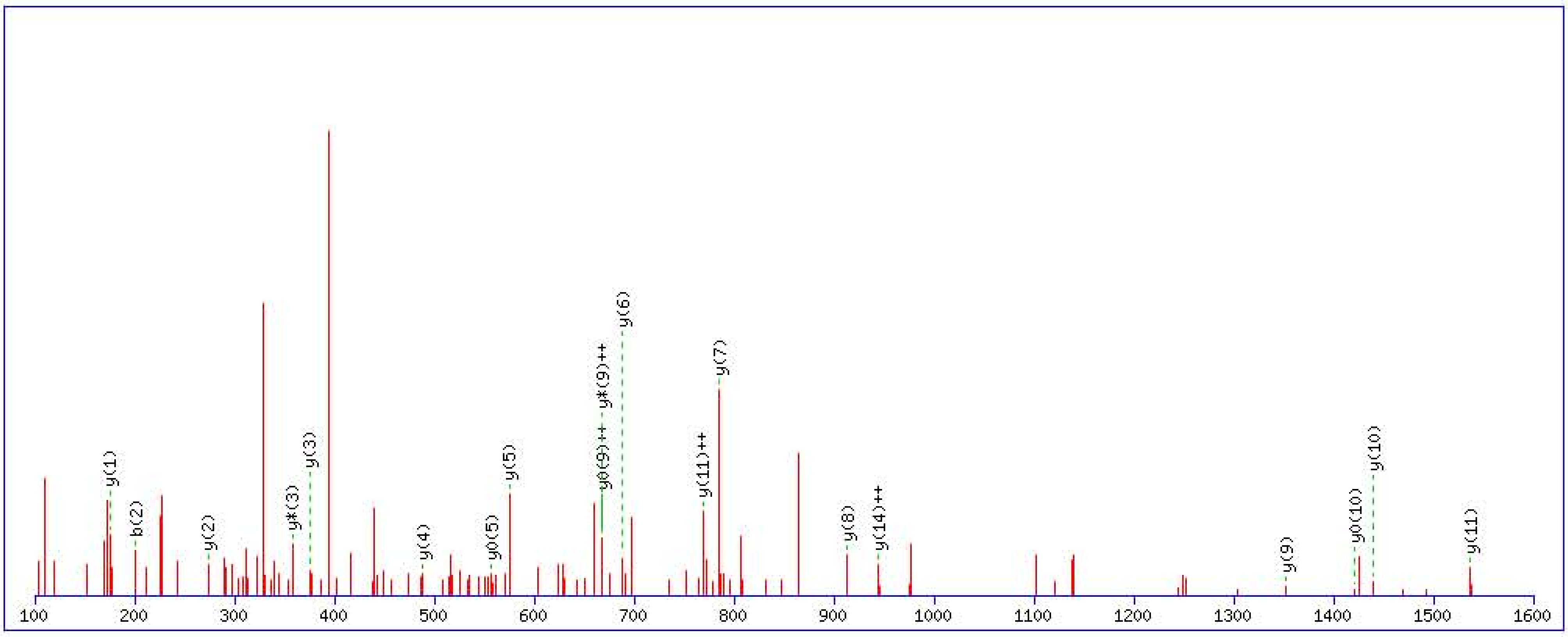
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSINTHPSQKPLSITVR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

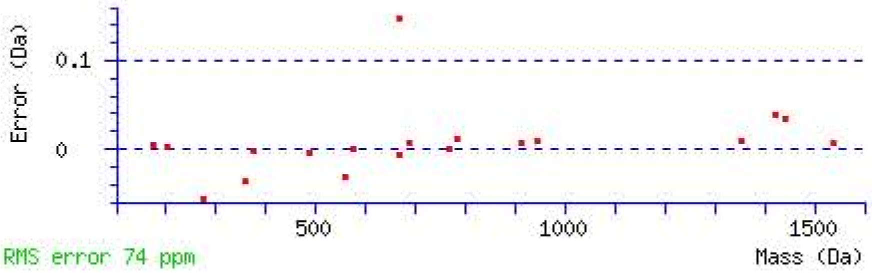
Match to Query 58173: 2201.243736 from(551.318210,4+) rtinseconds(1859) index(41062)
Title: Locus:1.1.1.2931.16 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

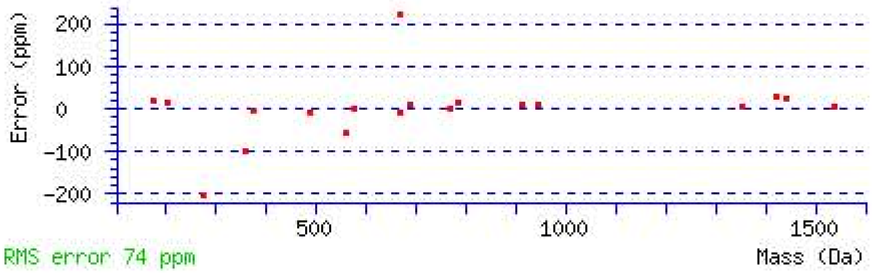
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2201.235428
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.013
Matches : 19/180 fragment ions using 75 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							17
2	201.123368	101.065322			183.112803	92.060039	S	2089.158656	1045.082966	2072.132107	1036.569691	2071.148091	1036.077683	16
3	314.207432	157.607354			296.196867	148.602071	I	2002.126628	1001.566952	1985.100079	993.053678	1984.116063	992.561669	15
4	428.250359	214.628818	411.223810	206.115543	410.239794	205.623535	N	1889.042564	945.024920	1872.016015	936.511646	1871.031999	936.019638	14
5	529.298038	265.152657	512.271489	256.639383	511.287473	256.147375	T	1774.999637	888.003456	1757.973088	879.490182	1756.989072	878.998174	13
6	666.356950	333.682113	649.330401	325.168838	648.346385	324.676830	H	1673.951958	837.479617	1656.925409	828.966343	1655.941393	828.474334	12
7	763.409714	382.208495	746.383165	373.695221	745.399149	373.203213	P	***1536.893046***	768.950161	1519.866497	760.436887	1518.882481	759.944878	11
8	850.441742	425.724509	833.415193	417.211234	832.431177	416.719226	S	***1439.840282***	720.423779	1422.813733	711.910505	1421.829717	711.418496	10
9	1289.667068	645.337172	1272.640519	636.823898	1271.656503	636.331889	Q	***1352.808254***	676.907765	1335.781705	668.394491	1334.797689	667.902483	9
10	1417.762031	709.384654	1400.735482	700.871379	1399.751466	700.379371	K	***913.582928***	457.295102	896.556379	448.781828	895.572363	448.289820	8
11	1514.814795	757.911036	1497.788246	749.397761	1496.804230	748.905753	P	***785.487965***	393.247621	768.461416	384.734346	767.477400	384.242338	7
12	1627.898859	814.453067	1610.872310	805.939793	1609.888294	805.447785	L	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
13	1714.930887	857.969082	1697.904338	849.455807	1696.920322	848.963799	S	***575.351137***	288.179207	558.324588	279.665932	557.340572	279.173924	5
14	1828.014951	914.511113	1810.988402	905.997839	1810.004386	905.505831	I	***488.319109***	244.663192	471.292560	236.149918	470.308544	235.657910	4
15	1929.062630	965.034953	1912.036081	956.521679	1911.052065	956.029670	T	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.115878	3
16	2028.131044	1014.569160	2011.104495	1006.055886	2010.120479	1005.563878	V	***274.187366***	137.597321	257.160817	129.084047			2
17							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.7	2201.235428	0.008308	LSINTHPSQKPLSITVR

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

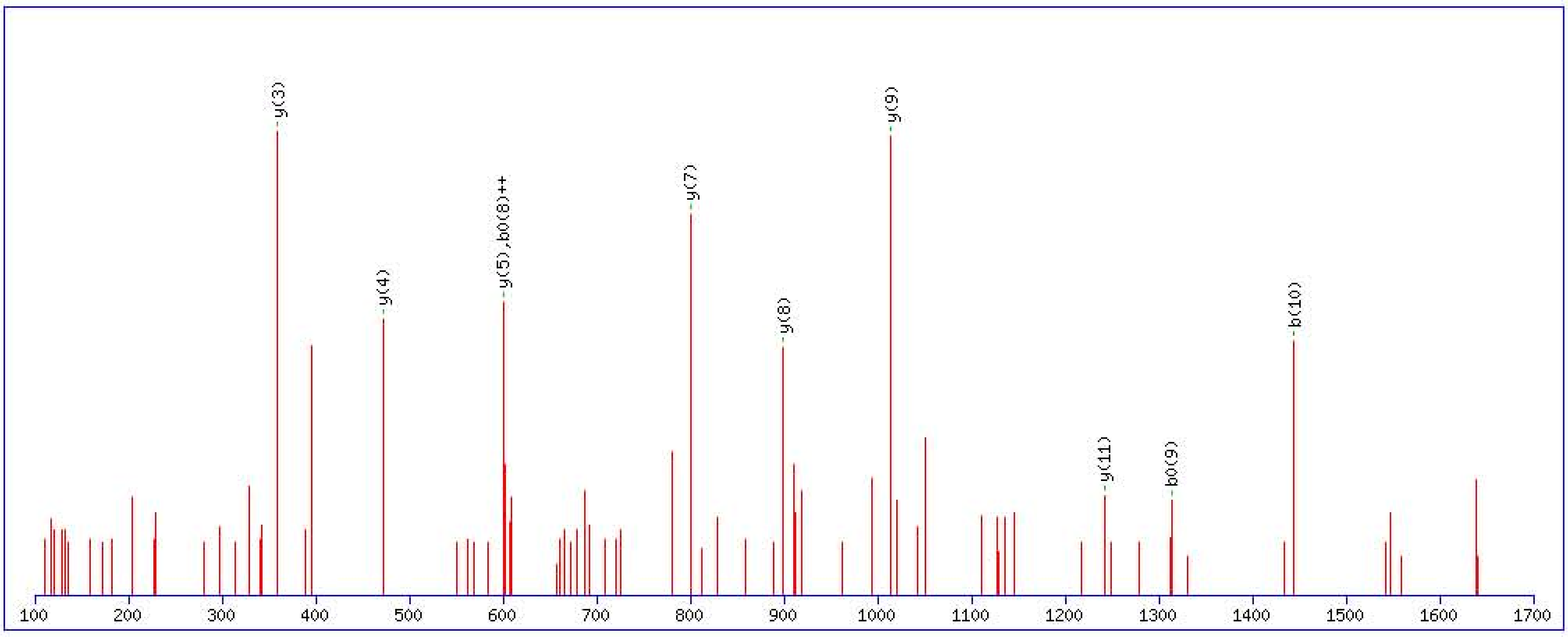
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAPDHQELNLDVSLQLPSR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

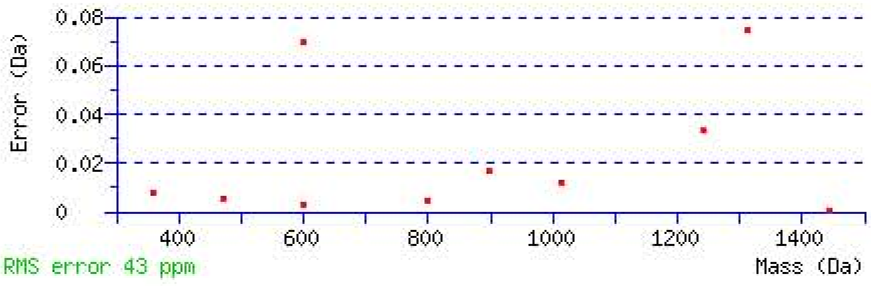
Match to Query 63990: 2457.252282 from(820.091370,3+) rtinseconds(2647) index(46121)
Title: Locus:1.1.1.3205.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

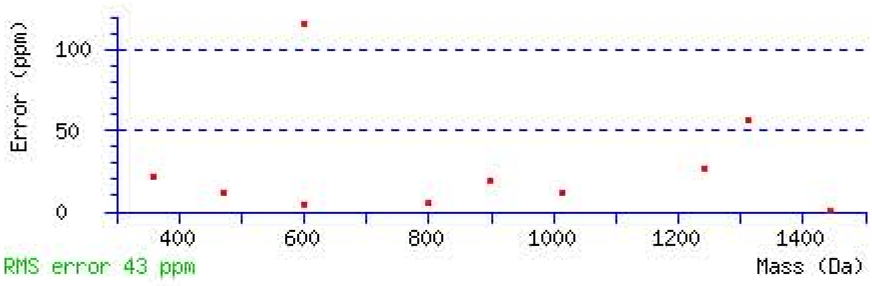
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2457.232193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0075
Matches : 10/204 fragment ions using 16 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							19
2	187.071333	94.039304			169.060768	85.034022	A	2343.212542	1172.109909	2326.185993	1163.596634	2325.201977	1163.104626	18
3	284.124097	142.565686			266.113532	133.560404	P	2272.175428	1136.591352	2255.148879	1128.078077	2254.164863	1127.586069	17
4	399.151040	200.079158			381.140475	191.073875	D	2175.122664	1088.064970	2158.096115	1079.551695	2157.112099	1079.059687	16
5	536.209952	268.608614			518.199387	259.603332	H	2060.095721	1030.551498	2043.069172	1022.038224	2042.085156	1021.546216	15
6	975.435278	488.221277	958.408729	479.708003	957.424713	479.215995	Q	1923.036809	962.022043	1906.010260	953.508768	1905.026244	953.016760	14
7	1104.477871	552.742574	1087.451322	544.229299	1086.467306	543.737291	E	1483.811483	742.409380	1466.784934	733.896105	1465.800918	733.404097	13
8	1217.561935	609.284606	1200.535386	600.771331	1199.551370	600.279323	L	1354.768890	677.888083	1337.742341	669.374809	1336.758325	668.882801	12
9	1331.604862	666.306069	1314.578313	657.792795	1313.594297	657.300786	N	***1241.684826***	621.346051	1224.658277	612.832777	1223.674261	612.340769	11
10	1444.688926	722.848101	1427.662377	714.334826	1426.678361	713.842818	L	1127.641899	564.324588	1110.615350	555.811313	1109.631334	555.319305	10
11	1559.715869	780.361572	1542.689320	771.848298	1541.705304	771.356290	D	***1014.557835***	507.782556	997.531286	499.269281	996.547270	498.777273	9
12	1658.784283	829.895780	1641.757734	821.382505	1640.773718	820.890497	V	***899.530892***	450.269084	882.504343	441.755810	881.520327	441.263802	8
13	1745.816311	873.411794	1728.789762	864.898519	1727.805746	864.406511	S	***800.462478***	400.734877	783.435929	392.221603	782.451913	391.729595	7
14	1858.900375	929.953825	1841.873826	921.440551	1840.889810	920.948543	L	713.430450	357.218863	696.403901	348.705589	695.419885	348.213581	6
15	1986.958953	993.983115	1969.932404	985.469840	1968.948388	984.977832	Q	***600.346386***	300.676831	583.319837	292.163557	582.335821	291.671549	5
16	2100.043017	1050.525146	2083.016468	1042.011872	2082.032452	1041.519864	L	***472.287808***	236.647542	455.261259	228.134268	454.277243	227.642260	4
17	2197.095781	1099.051528	2180.069232	1090.538254	2179.085216	1090.046246	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
18	2284.127809	1142.567542	2267.101260	1134.054268	2266.117244	1133.562260	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
19							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.6	2457.232193	0.020089	DAPDHQELNLDVSLQLPSR
9.0	2457.243423	0.008859	TGLSDAFMILNPSPDVPESRRR

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

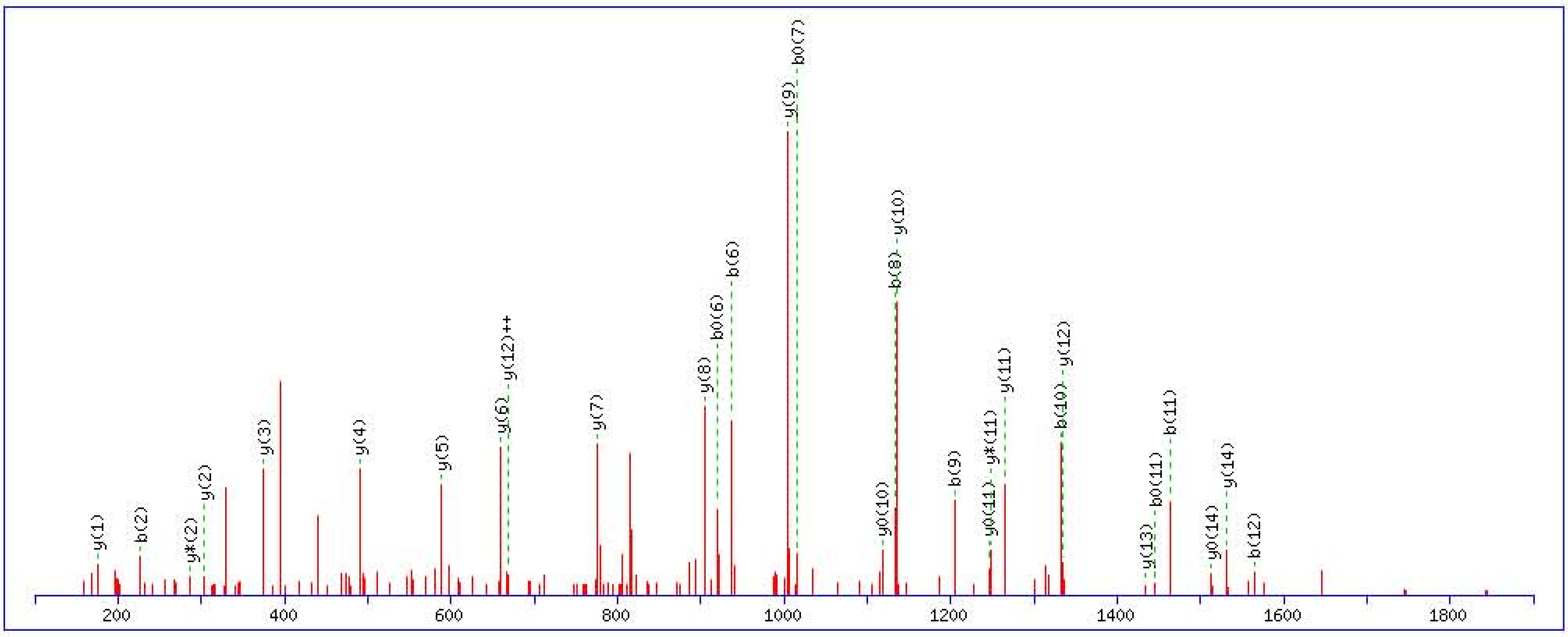
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLQGTPVAQMTEDAVDAER**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

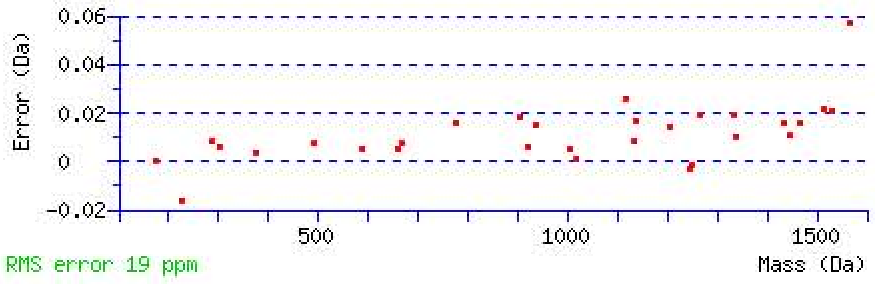
Match to Query 64320: 2467.275642 from(823.432490,3+) rtinseconds(2650) index(46142)
Title: Locus:1.1.1.3206.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

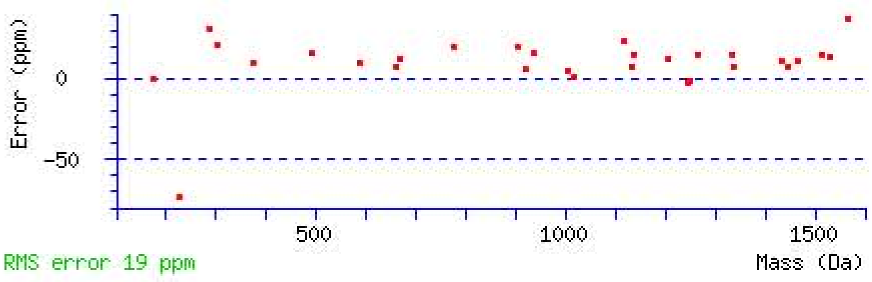
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2467.245071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 94 **Expect:** 1.2e-008
Matches : 30/210 fragment ions using 48 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							20
2	**227.175404**	114.091340					L	2355.168297	1178.087786	2338.141748	1169.574512	2337.157732	1169.082504	19
3	340.259468	170.633372					L	2242.084233	1121.545754	2225.057684	1113.032480	2224.073668	1112.540472	18
4	779.484794	390.246035	762.458245	381.732760			Q	2129.000169	1065.003722	2111.973620	1056.490448	2110.989604	1055.998440	17
5	836.506258	418.756767	819.479709	410.243493			G	1689.774843	845.391060	1672.748294	836.877785	1671.764278	836.385777	16
6	**937.553937**	469.280607	920.527388	460.767332	919.543372	460.275324	T	1632.753379	816.880328	1615.726830	808.367053	1614.742814	807.875045	15
7	1034.606701	517.806988	1017.580152	509.293714	1016.596136	508.801706	P	***1531.705700***	766.356488	1514.679151	757.843214	1513.695135	757.351206	14
8	**1133.675115**	567.341196	1116.648566	558.827921	1115.664550	558.335913	V	***1434.652936***	717.830106	1417.626387	709.316832	1416.642371	708.824824	13
9	**1204.712229**	602.859753	1187.685680	594.346478	1186.701664	593.854470	A	***1335.584522***	668.295899	1318.557973	659.782625	1317.573957	659.290617	12
10	**1332.770807**	666.889042	1315.744258	658.375767	1314.760242	657.883759	Q	***1264.547408***	632.777342	1247.520859	624.264068	1246.536843	623.772060	11
11	**1463.811292**	732.409284	1446.784743	723.896010	1445.800727	723.404002	M	***1136.488830***	568.748053	1119.462281	560.234779	1118.478265	559.742771	10
12	**1564.858971**	782.933124	1547.832422	774.419849	1546.848406	773.927841	T	***1005.448345***	503.227811	988.421796	494.714536	987.437780	494.222528	9
13	1693.901564	847.454420	1676.875015	838.941146	1675.890999	838.449138	E	***904.400666***	452.703971	887.374117	444.190697	886.390101	443.698689	8
14	1808.928507	904.967892	1791.901958	896.454617	1790.917942	895.962609	D	***775.358073***	388.182675	758.331524	379.669400	757.347508	379.177392	7
15	1879.965621	940.486449	1862.939072	931.973174	1861.955056	931.481166	A	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.663921	6
16	1979.034035	990.020656	1962.007486	981.507381	1961.023470	981.015373	V	***589.294016***	295.150646	572.267467	286.637372	571.283451	286.145364	5
17	2094.060978	1047.534127	2077.034429	1039.020852	2076.050413	1038.528844	D	***490.225602***	245.616439	473.199053	237.103165	472.215037	236.611157	4
18	2165.098092	1083.052684	2148.071543	1074.539409	2147.087527	1074.047402	A	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
19	2294.140685	1147.573981	2277.114136	1139.060706	2276.130120	1138.568698	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
93.9	2467.245071	0.030571	ILLQGTPVAQMTEDAVDAER
80.9	2467.245071	0.030571	ILLQGTPVAQMTEDAVDAER

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

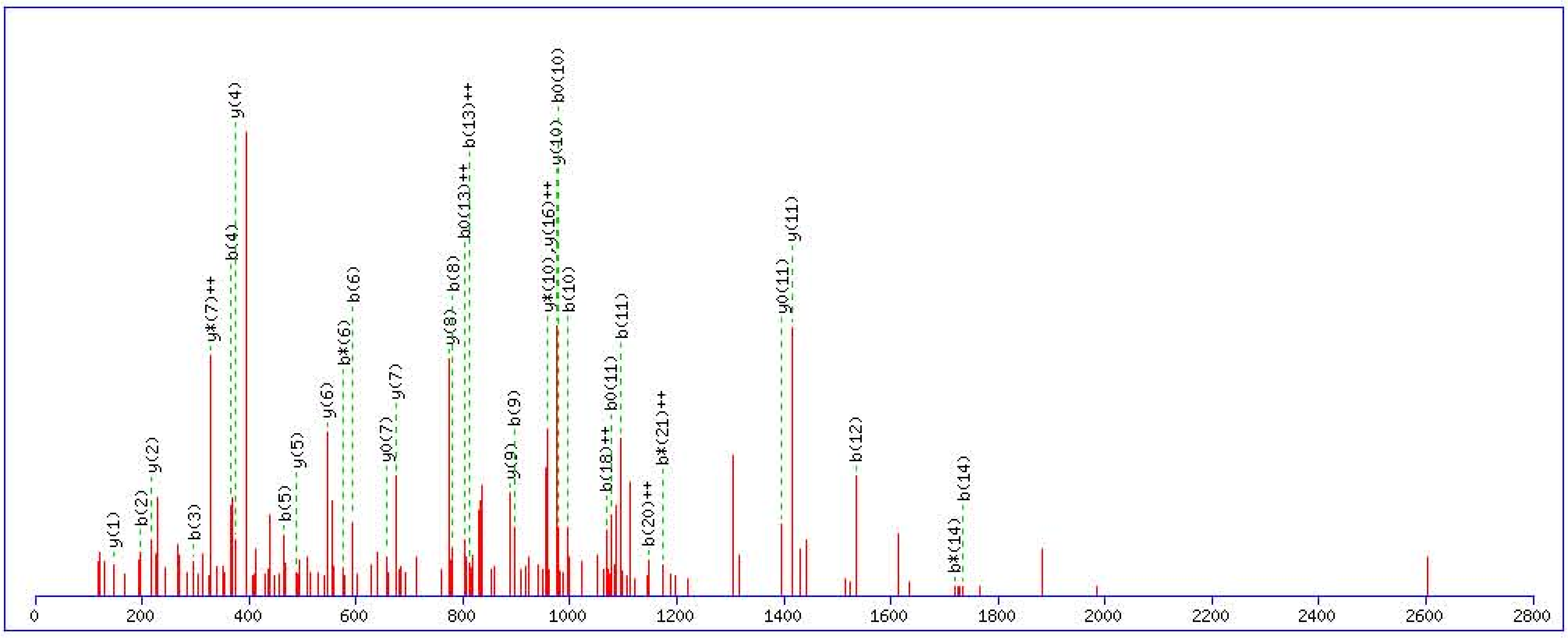
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPVAVQGEDTVQSLTQGDGVAK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

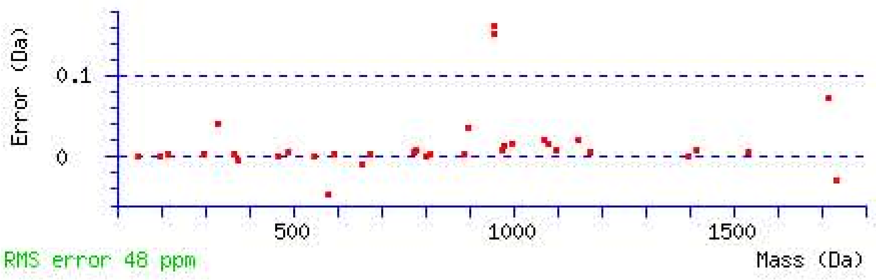
Match to Query 65599: 2508.311652 from(837.111160,3+) rtinseconds(2213) index(43518)
Title: Locus:1.1.1.3054.20 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

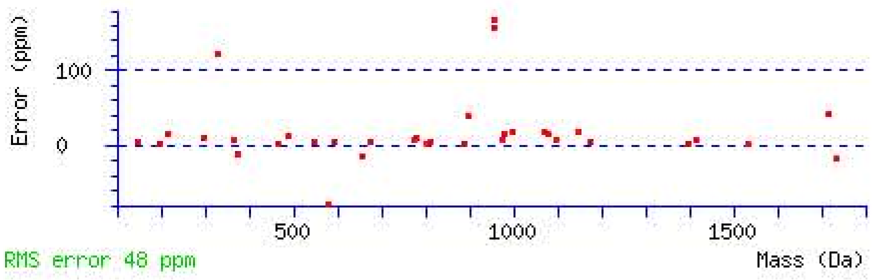


```
Monoisotopic mass of neutral peptide Mr(calc): 2508.289429
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00016
Matches : 35/220 fragment ions using 97 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							22
2	***197.128454***	99.067865					P	2410.228255	1205.617765	2393.201706	1197.104491	2392.217690	1196.612483	21
3	***296.196868***	148.602072					V	2313.175491	1157.091383	2296.148942	1148.578109	2295.164926	1148.086101	20
4	***367.233982***	184.120629					A	2214.107077	1107.557176	2197.080528	1099.043902	2196.096512	1098.551894	19
5	***466.302396***	233.654836					V	2143.069963	1072.038619	2126.043414	1063.525345	2125.059398	1063.033337	18
6	***594.360974***	297.684125	577.334425	289.170851			Q	2044.001549	1022.504413	2026.975000	1013.991138	2025.990984	1013.499130	17
7	651.382438	326.194857	634.355889	317.681583			G	1915.942971	958.475124	1898.916422	949.961849	1897.932406	949.469841	16
8	***780.425031***	390.716154	763.398482	382.202879	762.414466	381.710871	E	1858.921507	929.964391	1841.894958	921.451117	1840.910942	920.959109	15
9	***895.451974***	448.229625	878.425425	439.716351	877.441409	439.224343	D	1729.878914	865.443095	1712.852365	856.929821	1711.868349	856.437812	14
10	***996.499653***	498.753465	979.473104	490.240190	978.489088	489.748182	T	1614.851971	807.929623	1597.825422	799.416349	1596.841406	798.924341	13
11	***1095.568067***	548.287672	1078.541518	539.774397	1077.557502	539.282389	V	1513.804292	757.405784	1496.777743	748.892510	1495.793727	748.400502	12
12	***1534.793393***	767.900335	1517.766844	759.387060	1516.782828	758.895052	Q	***1414.735878***	707.871577	1397.709329	699.358303	1396.725313	698.866294	11
13	1621.825421	**811.416349**	1604.798872	802.903074	1603.814856	802.411066	S	***975.510552***	488.258914	958.484003	479.745639	957.499987	479.253631	10
14	***1734.909485***	867.958381	1717.882936	859.445106	1716.898920	858.953098	L	***888.478524***	444.742900	871.451975	436.229625	870.467959	435.737617	9
15	1835.957164	918.482220	1818.930615	909.968946	1817.946599	909.476938	T	***775.394460***	388.200868	758.367911	379.687593	757.383895	379.195585	8
16	1964.015742	982.511509	1946.989193	973.998235	1946.005177	973.506227	Q	***674.346781***	337.677029	657.320232	329.163754	656.336216	328.671746	7
17	2021.037206	1011.022241	2004.010657	1002.508967	2003.026641	1002.016959	G	***546.288203***	273.647739	529.261654	265.134465	528.277638	264.642457	6
18	2136.064149	**1068.535712**	2119.037600	1060.022438	2118.053584	1059.530430	D	***489.266739***	245.137007	472.240190	236.623733	471.256174	236.131725	5
19	2193.085613	1097.046444	2176.059064	1088.533170	2175.075048	1088.041162	G	***374.239796***	187.623536	357.213247	179.110261			4
20	2292.154027	**1146.580651**	2275.127478	1138.067377	2274.143462	1137.575369	V	317.218332	159.112804	300.191783	150.599530			3
21	2363.191141	1182.099208	2346.164592	1173.585934	2345.180576	1173.093926	A	***218.149918***	109.578597	201.123369	101.065323			2
22							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 48 ppm



RMS error 48 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.1	2508.289429	0.022223	VPVAVQGEDTVQSLTQGDGVAK
22.1	2508.289429	0.022223	VPVAVQGEDTVQSLTQGDGVAK
19.2	2508.289429	0.022223	VPVAVQGEDTVQSLTQGDGVAK

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

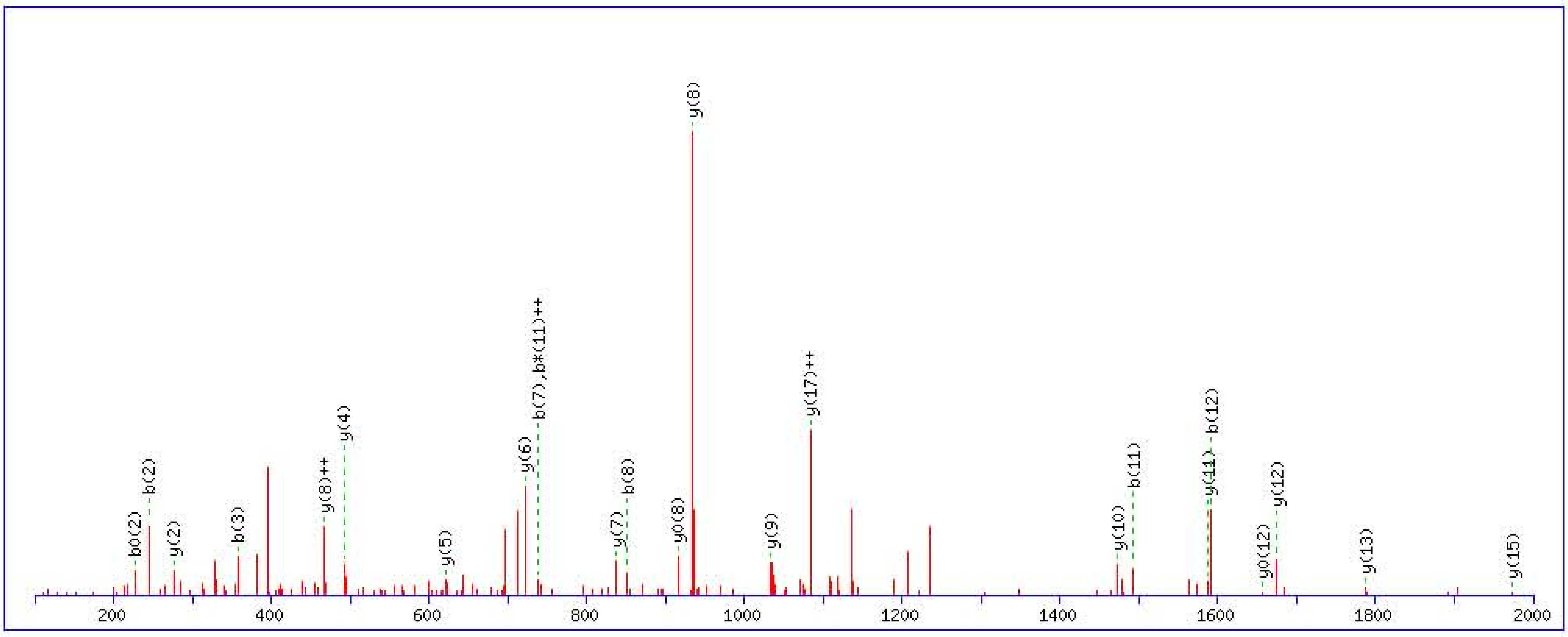
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDIPPADLSDQVPDTESETR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

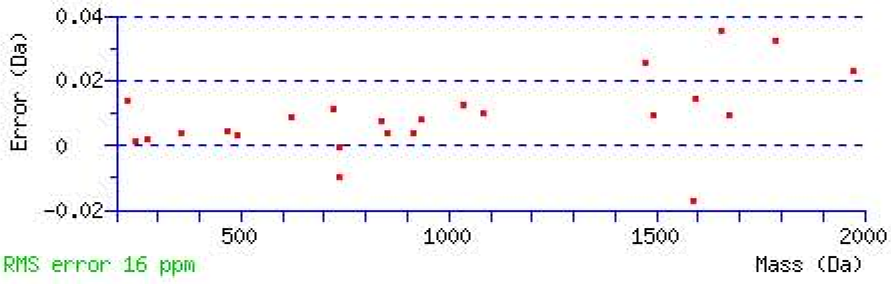
Match to Query 65811: 2524.195062 from(842.405630,3+) rtinseconds(2084) index(42656)
Title: Locus:1.1.1.3009.16 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

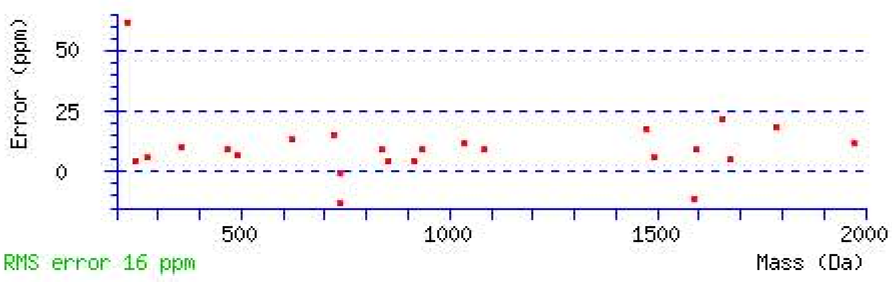
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2524.163910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 59 **Expect:** 2.6e-005
Matches : 24/206 fragment ions using 51 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							20
2	**245.076812**	123.042044			227.066247	114.036762	D	2396.128598	1198.567937	2379.102049	1190.054662	2378.118033	1189.562654	19
3	**358.160876**	179.584076			340.150311	170.578794	I	2281.101655	1141.054465	2264.075106	1132.541191	2263.091090	1132.049183	18
4	455.213640	228.110458			437.203075	219.105176	P	2168.017591	1084.512433	2150.991042	1075.999159	2150.007026	1075.507151	17
5	552.266404	276.636840			534.255839	267.631558	P	2070.964827	1035.986051	2053.938278	1027.472777	2052.954262	1026.980769	16
6	623.303518	312.155397			605.292953	303.150115	A	***1973.912063***	987.459670	1956.885514	978.946395	1955.901498	978.454387	15
7	**738.330461**	369.668869			720.319896	360.663586	D	1902.874949	951.941113	1885.848400	943.427838	1884.864384	942.935830	14
8	**851.414525**	426.210901			833.403960	417.205618	L	***1787.848006***	894.427641	1770.821457	885.914367	1769.837441	885.422359	13
9	938.446553	469.726915			920.435988	460.721632	S	***1674.763942***	837.885609	1657.737393	829.372335	1656.753377	828.880327	12
10	1053.473496	527.240386			1035.462931	518.235104	D	***1587.731914***	794.369595	1570.705365	785.856321	1569.721349	785.364313	11
11	**1492.698822**	746.853049	1475.672273	738.339775	1474.688257	737.847767	Q	***1472.704971***	736.856124	1455.678422	728.342849	1454.694406	727.850841	10
12	**1591.767236**	796.387256	1574.740687	787.873982	1573.756671	787.381974	V	***1033.479645***	517.243461	1016.453096	508.730186	1015.469080	508.238178	9
13	1688.820000	844.913638	1671.793451	836.400364	1670.809435	835.908356	P	***934.411231***	467.709254	917.384682	459.195979	916.400666	458.703971	8
14	1803.846943	902.427110	1786.820394	893.913835	1785.836378	893.421827	D	***837.358467***	419.182872	820.331918	410.669597	819.347902	410.177589	7
15	1904.894622	952.950949	1887.868073	944.437675	1886.884057	943.945667	T	***722.331524***	361.669400	705.304975	353.156125	704.320959	352.664117	6
16	2033.937215	1017.472246	2016.910666	1008.958971	2015.926650	1008.466963	E	***621.283845***	311.145560	604.257296	302.632286	603.273280	302.140278	5
17	2120.969243	1060.988259	2103.942694	1052.474985	2102.958678	1051.982977	S	***492.241252***	246.624264	475.214703	238.110989	474.230687	237.618981	4
18	2250.011836	1125.509556	2232.985287	1116.996281	2232.001271	1116.504274	E	405.209224	203.108250	388.182675	194.594975	387.198659	194.102967	3
19	2351.059515	1176.033395	2334.032966	1167.520121	2333.048950	1167.028113	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
20							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.6	2524.163910	0.031152	EDIPPADLSDQVPDTESETR

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

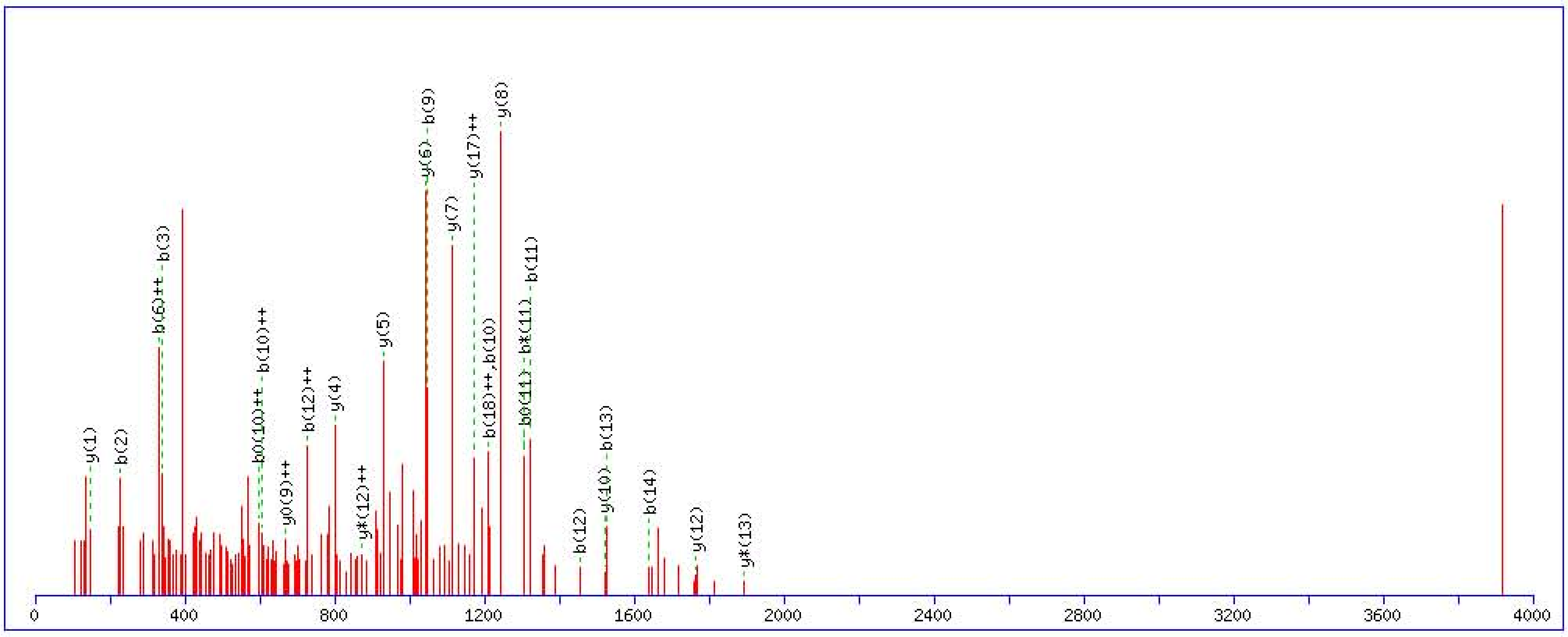
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQLSNDFDEYIMAIEQTIK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

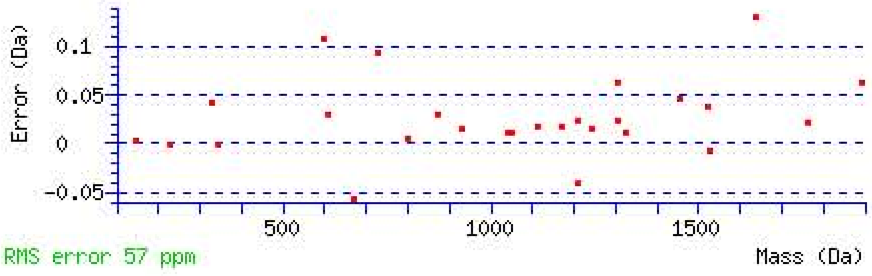
Match to Query 66219: 2567.293362 from(856.771730,3+) rtinseconds(3234) index(50759)
Title: Locus:1.1.1.3404.16 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

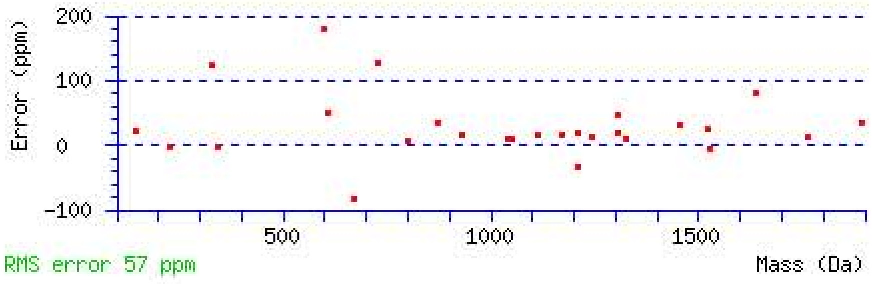
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2567.265121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0005
Matches : 27/204 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							19
2	***228.134268***	114.570772	211.107719	106.057498			Q	2469.204012	1235.105644	2452.177463	1226.592369	2451.193447	1226.100361	18
3	***341.218332***	171.112804	324.191783	162.599530			L	2341.145434	1171.076355	2324.118885	1162.563080	2323.134869	1162.071072	17
4	428.250360	214.628818	411.223811	206.115544	410.239795	205.623536	S	2228.061370	1114.534323	2211.034821	1106.021048	2210.050805	1105.529040	16
5	542.293287	271.650282	525.266738	263.137007	524.282722	262.644999	N	2141.029342	1071.018309	2124.002793	1062.505034	2123.018777	1062.013026	15
6	657.320230	**329.163753**	640.293681	320.650479	639.309665	320.158471	D	2026.986415	1013.996845	2009.959866	1005.483571	2008.975850	1004.991563	14
7	804.388644	402.697960	787.362095	394.184686	786.378079	393.692678	F	1911.959472	956.483374	1894.932923	947.970099	1893.948907	947.478091	13
8	919.415587	460.211432	902.389038	451.698157	901.405022	451.206149	D	***1764.891058***	882.949167	1747.864509	874.435893	1746.880493	873.943884	12
9	***1048.458180***	524.732728	1031.431631	516.219453	1030.447615	515.727445	E	1649.864115	825.435695	1632.837566	816.922421	1631.853550	816.430413	11
10	***1211.521509***	**606.264392**	1194.494960	597.751118	1193.510944	597.259110	Y	***1520.821522***	760.914399	1503.794973	752.401125	1502.810957	751.909116	10
11	***1324.605573***	662.806424	1307.579024	654.293150	1306.595008	653.801142	I	1357.758193	679.382734	1340.731644	670.869460	1339.747628	670.377452	9
12	***1455.646058***	**728.326667**	1438.619509	719.813392	1437.635493	719.321384	M	***1244.674129***	622.840703	1227.647580	614.327428	1226.663564	613.835420	8
13	***1526.683172***	763.845224	1509.656623	755.331949	1508.672607	754.839941	A	***1113.633644***	557.320460	1096.607095	548.807186	1095.623079	548.315178	7
14	***1639.767236***	820.387256	1622.740687	811.873981	1621.756671	811.381973	I	***1042.596530***	521.801903	1025.569981	513.288629	1024.585965	512.796621	6
15	1768.809829	884.908552	1751.783280	876.395278	1750.799264	875.903270	E	***929.512466***	465.259871	912.485917	456.746597	911.501901	456.254589	5
16	2208.035155	1104.521215	2191.008606	1096.007941	2190.024590	1095.515933	Q	***800.469873***	400.738575	783.443324	392.225300	782.459308	391.733292	4
17	2309.082834	1155.045055	2292.056285	1146.531780	2291.072269	1146.039772	T	361.244547	181.125911	344.217998	172.612637	343.233982	172.120629	3
18	2422.166898	**1211.587087**	2405.140349	1203.073812	2404.156333	1202.581804	I	260.196868	130.602072	243.170319	122.088798			2
19							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.7	2567.265121	0.028241	VQLSNDFDEYIMAIEQTIK
2.5	2567.264923	0.028439	IQSDLTSHEISLEEMKKHNQGK

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

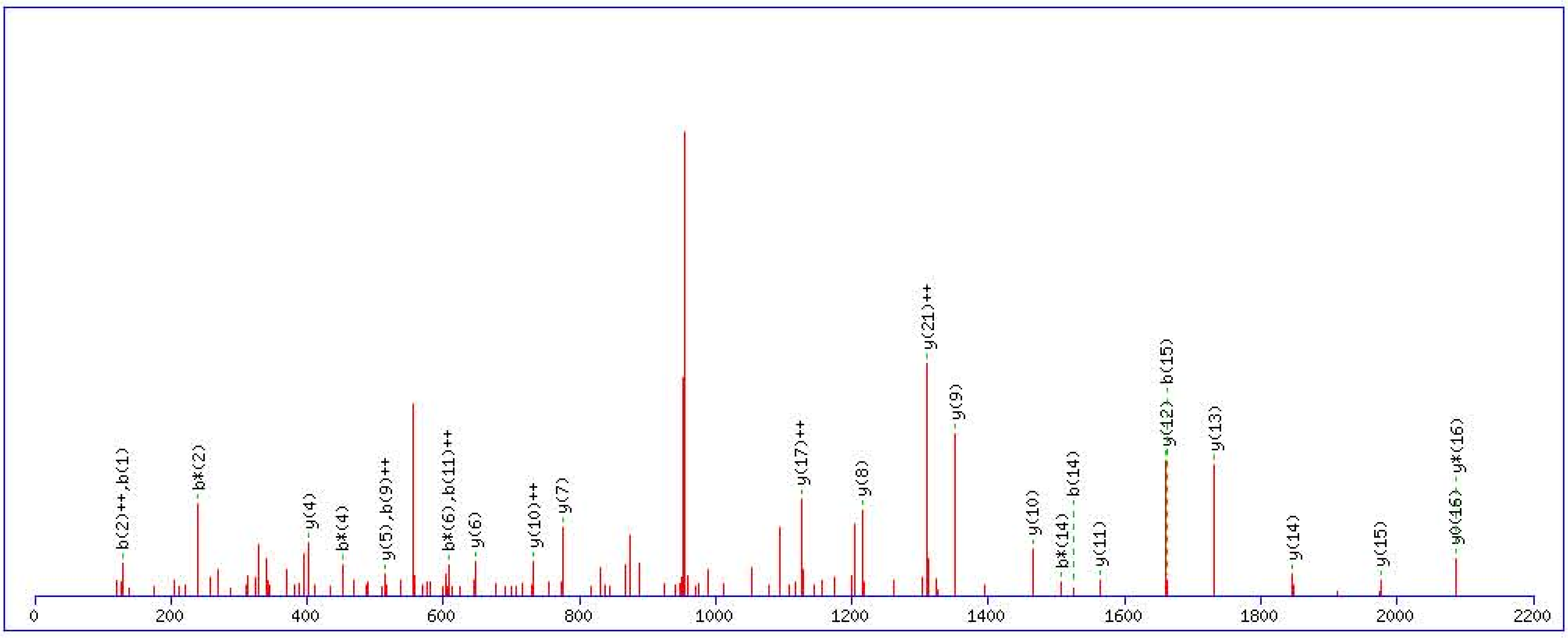
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QKPDGVFQEDAPVIHQEMIGGLR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

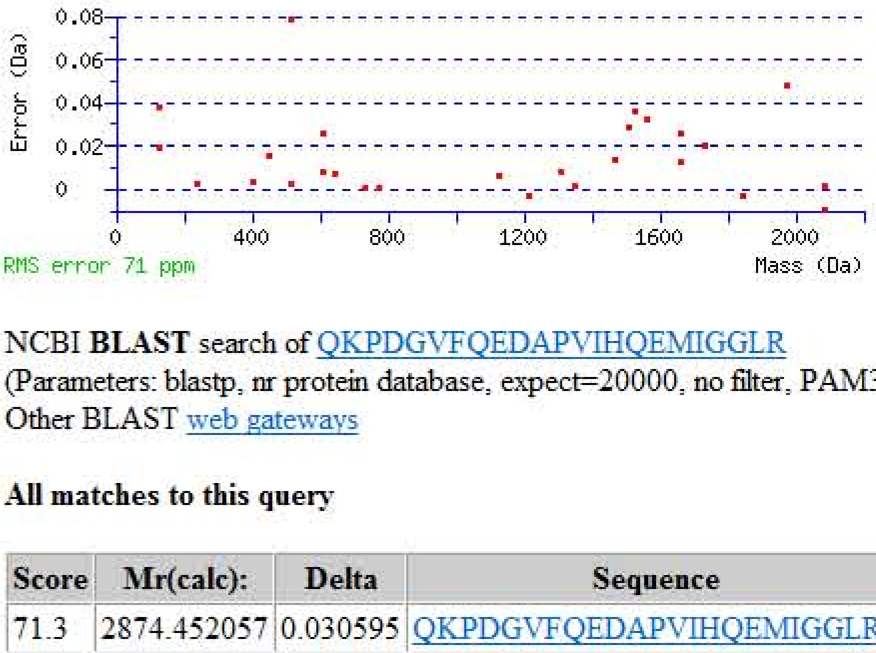
Match to Query 70215: 2874.482652 from(959.168160,3+) rtinseconds(2202) index(43447)
Title: Locus:1.1.1.3050.17 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

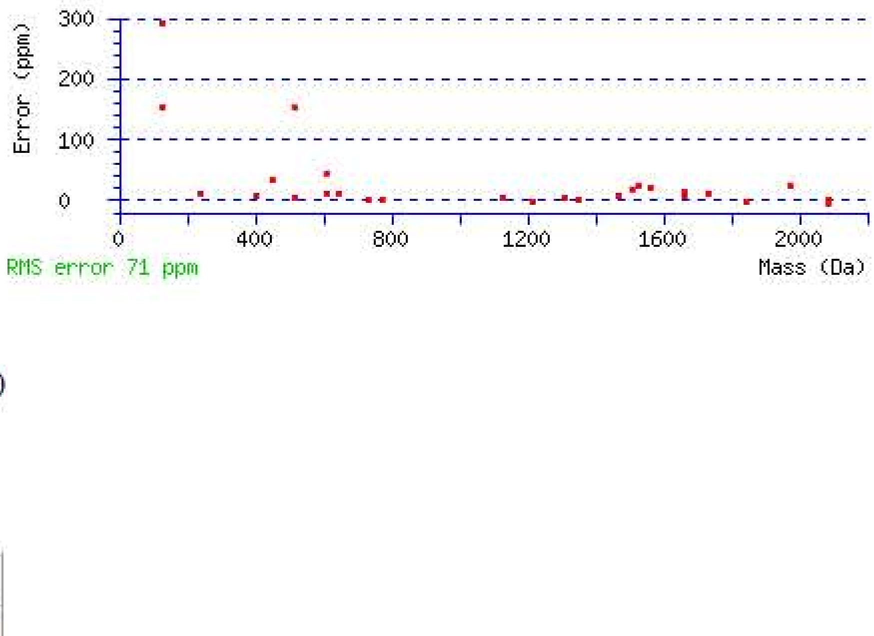
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2874.452057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 71 **Expect:** 5.1e-007
Matches : 27/246 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.065854**	65.036565	112.039305	56.523291			**Q**							**23**
2	257.160817	**129.084047**	240.134268	120.570772			**K**	2747.400756	1374.204016	2730.374207	1365.690741	2729.390191	1365.198733	**22**
3	354.213581	177.610429	337.187032	169.097154			**P**	2619.305793	1310.156534	2602.279244	1301.643260	2601.295228	1301.151252	**21**
4	469.240524	235.123900	452.213975	226.610626	451.229959	226.118618	**D**	2522.253029	1261.630152	2505.226480	1253.116878	2504.242464	1252.624870	**20**
5	526.261988	263.634632	509.235439	255.121358	508.251423	254.629350	**G**	2407.226086	1204.116681	2390.199537	1195.603406	2389.215521	1195.111398	**19**
6	625.330402	313.168839	608.303853	304.655565	607.319837	304.163557	**V**	2350.204622	1175.605949	2333.178073	1167.092674	2332.194057	1166.600666	**18**
7	772.398816	386.703046	755.372267	378.189772	754.388251	377.697764	**F**	2251.136208	1126.071742	2234.109659	1117.558467	2233.125643	1117.066459	**17**
8	900.457394	450.732335	883.430845	442.219061	882.446829	441.727053	**Q**	2104.067794	1052.537535	2087.041245	1044.024260	2086.057229	1043.532252	**16**
9	1029.499987	**515.253631**	1012.473438	506.740357	1011.489422	506.248349	**E**	***1976.009216***	988.508246	1958.982667	979.994972	1957.998651	979.502964	**15**
10	1144.526930	572.767103	1127.500381	564.253829	1126.516365	563.761821	**D**	***1846.966623***	923.986950	1829.940074	915.473675	1828.956058	914.981667	**14**
11	1215.564044	**608.285660**	1198.537495	599.772386	1197.553479	599.280377	**A**	***1731.939680***	866.473478	1714.913131	857.960204	1713.929115	857.468196	**13**
12	1312.616808	656.812042	1295.590259	648.298768	1294.606243	647.806760	**P**	***1660.902566***	830.954921	1643.876017	822.441647	1642.892001	821.949639	**12**
13	1411.685222	706.346249	1394.658673	697.832975	1393.674657	697.340967	**V**	***1563.849802***	782.428539	1546.823253	773.915265	1545.839237	773.423257	**11**
14	**1524.769286**	762.888281	1507.742737	754.375007	1506.758721	753.882998	**I**	***1464.781388***	732.894332	1447.754839	724.381058	1446.770823	723.889050	**10**
15	**1661.828198**	831.417737	1644.801649	822.904463	1643.817633	822.412454	**H**	***1351.697324***	676.352300	1334.670775	667.839026	1333.686759	667.347018	**9**
16	2101.053524	1051.030400	2084.026975	1042.517125	2083.042959	1042.025117	**Q**	***1214.638412***	607.822844	1197.611863	599.309570	1196.627847	598.817562	**8**
17	2230.096117	1115.551696	2213.069568	1107.038422	2212.085552	1106.546414	**E**	***775.413086***	388.210181	758.386537	379.696907	757.402521	379.204899	**7**
18	2361.136602	1181.071939	2344.110053	1172.558664	2343.126037	1172.066656	**M**	***646.370493***	323.688885	629.343944	315.175610			**6**
19	2474.220666	1237.613971	2457.194117	1229.100696	2456.210101	1228.608689	**I**	***515.330008***	258.168642	498.303459	249.655368			**5**
20	2531.242130	1266.124703	2514.215581	1257.611428	2513.231565	1257.119420	**G**	***402.245944***	201.626610	385.219395	193.113335			**4**
21	2588.263594	1294.635435	2571.237045	1286.122160	2570.253029	1285.630152	**G**	345.224480	173.115878	328.197931	164.602603			**3**
22	2701.347658	1351.177467	2684.321109	1342.664192	2683.337093	1342.172185	**L**	288.203016	144.605146	271.176467	136.091872			**2**
23							**R**	175.118952	88.063114	158.092403	79.549839			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.3	2874.452057	0.030595	QKPDGVFQEDAPVIHQEMIGGLR
10.7	2874.452057	0.030595	QKPDGVFQEDAPVIHQEMIGGLR
4.1	2874.459396	0.023256	QYIQLELPAFALACLMLMPHSEKR

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

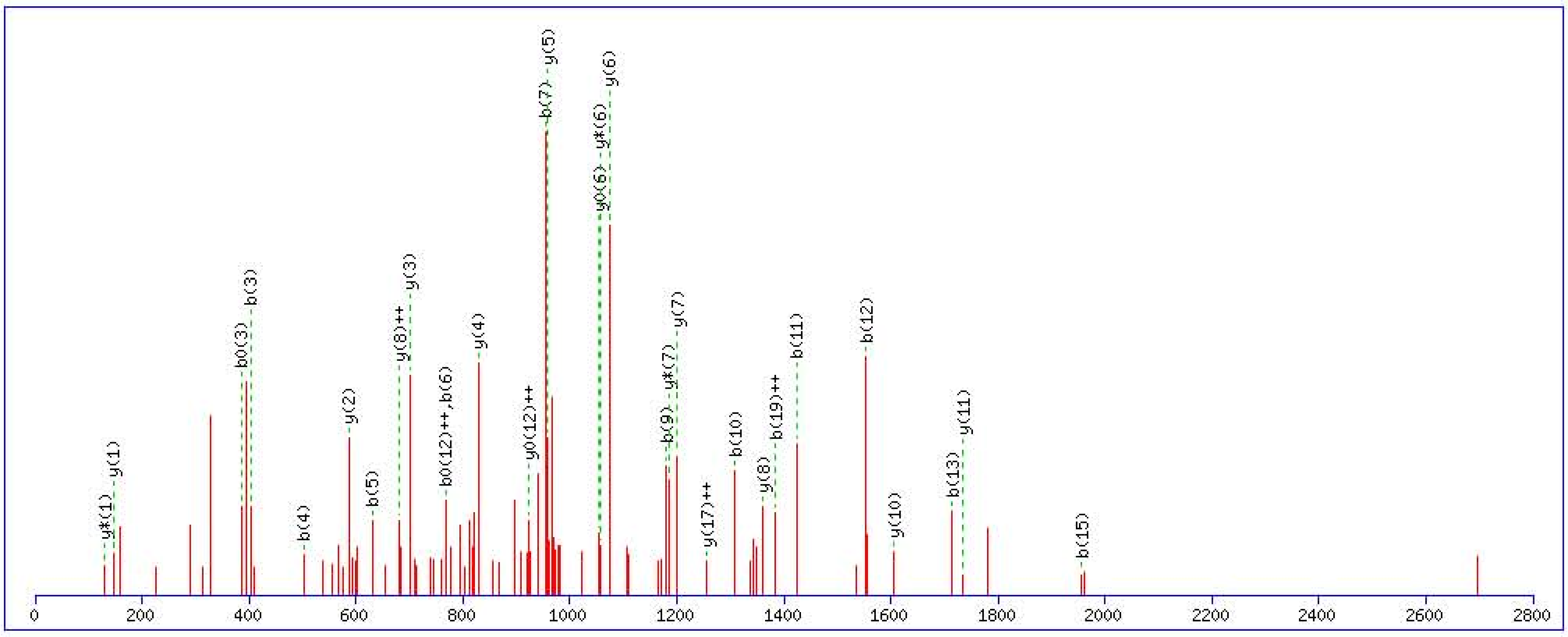
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTWVEHWPEEDECQDEENQK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

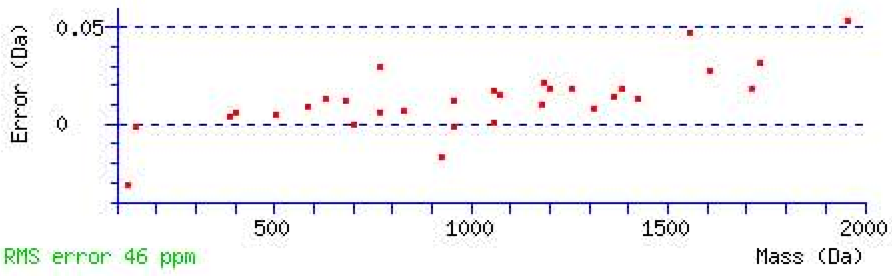
Match to Query 70712: 2913.221082 from(972.080970,3+) rtinseconds(2099) index(42739)
Title: Locus:1.1.1.3014.26 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

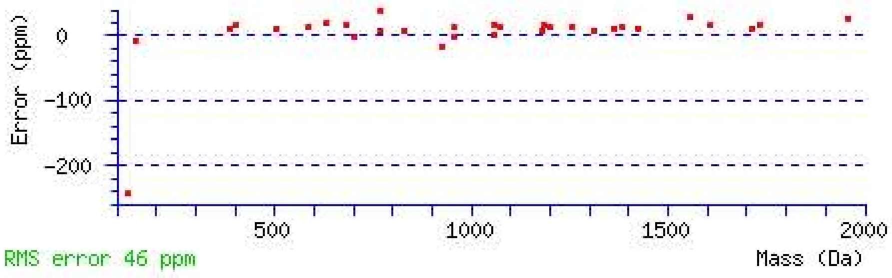
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2913.185776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19 : Biotin:Thermo-21345 (Q)
Ions Score: 79 **Expect:** 2.6e-008
Matches : 31/196 fragment ions using 46 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							20
2	217.081898	109.044587			199.071333	100.039304	T	2799.166123	1400.086699	2782.139574	1391.573425	2781.155558	1391.081417	19
3	***403.161211***	202.084244			385.150646	193.078961	W	2698.118444	1349.562860	2681.091895	1341.049585	2680.107879	1340.557577	18
4	***502.229625***	251.618451			484.219060	242.613168	V	2512.039131	1256.523203	2495.012582	1248.009929	2494.028566	1247.517921	17
5	***631.272218***	316.139747			613.261653	307.134465	E	2412.970717	1206.988996	2395.944168	1198.475722	2394.960152	1197.983714	16
6	***768.331130***	384.669203			750.320565	375.663921	H	2283.928124	1142.467700	2266.901575	1133.954425	2265.917559	1133.462417	15
7	***954.410443***	477.708860			936.399878	468.703577	W	2146.869212	1073.938244	2129.842663	1065.424969	2128.858647	1064.932961	14
8	1051.463207	526.235242			1033.452642	517.229959	P	1960.789899	980.898588	1943.763350	972.385313	1942.779334	971.893305	13
9	***1180.505800***	590.756538			1162.495235	581.751256	E	1863.737135	932.372206	1846.710586	923.858931	1845.726570	923.366923	12
10	***1309.548393***	655.277835			1291.537828	646.272552	E	***1734.694542***	867.850909	1717.667993	859.337635	1716.683977	858.845627	11
11	***1424.575336***	712.791306			1406.564771	703.786024	D	***1605.651949***	803.329613	1588.625400	794.816338	1587.641384	794.324330	10
12	***1553.617929***	777.312603			1535.607364	768.307320	E	1490.625006	745.816141	1473.598457	737.302867	1472.614441	736.810859	9
13	***1713.648578***	857.327927			1695.638013	848.322645	C	***1361.582413***	681.294845	1344.555864	672.781570	1343.571848	672.289562	8
14	1841.707156	921.357216	1824.680607	912.843942	1823.696591	912.351934	Q	***1201.551764***	601.279520	1184.525215	592.766246	1183.541199	592.274238	7
15	***1956.734099***	978.870688	1939.707550	970.357413	1938.723534	969.865405	D	***1073.493186***	537.250231	1056.466637	528.736957	1055.482621	528.244949	6
16	2085.776692	1043.391984	2068.750143	1034.878709	2067.766127	1034.386701	E	***958.466243***	479.736760	941.439694	471.223485	940.455678	470.731477	5
17	2214.819285	1107.913280	2197.792736	1099.400006	2196.808720	1098.907998	E	***829.423650***	415.215463	812.397101	406.702189	811.413085	406.210181	4
18	2328.862212	1164.934744	2311.835663	1156.421469	2310.851647	1155.929461	N	***700.381057***	350.694167	683.354508	342.180892			3
19	2768.087538	1384.547407	2751.060989	1376.034132	2750.076973	1375.542125	Q	***586.338130***	293.672703	569.311581	285.159429			2
20							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.3	2913.185776	0.035306	DTWVEHWPEEDECQDEENQK
39.3	2913.185776	0.035306	DTWVEHWPEEDECQDEENQK

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

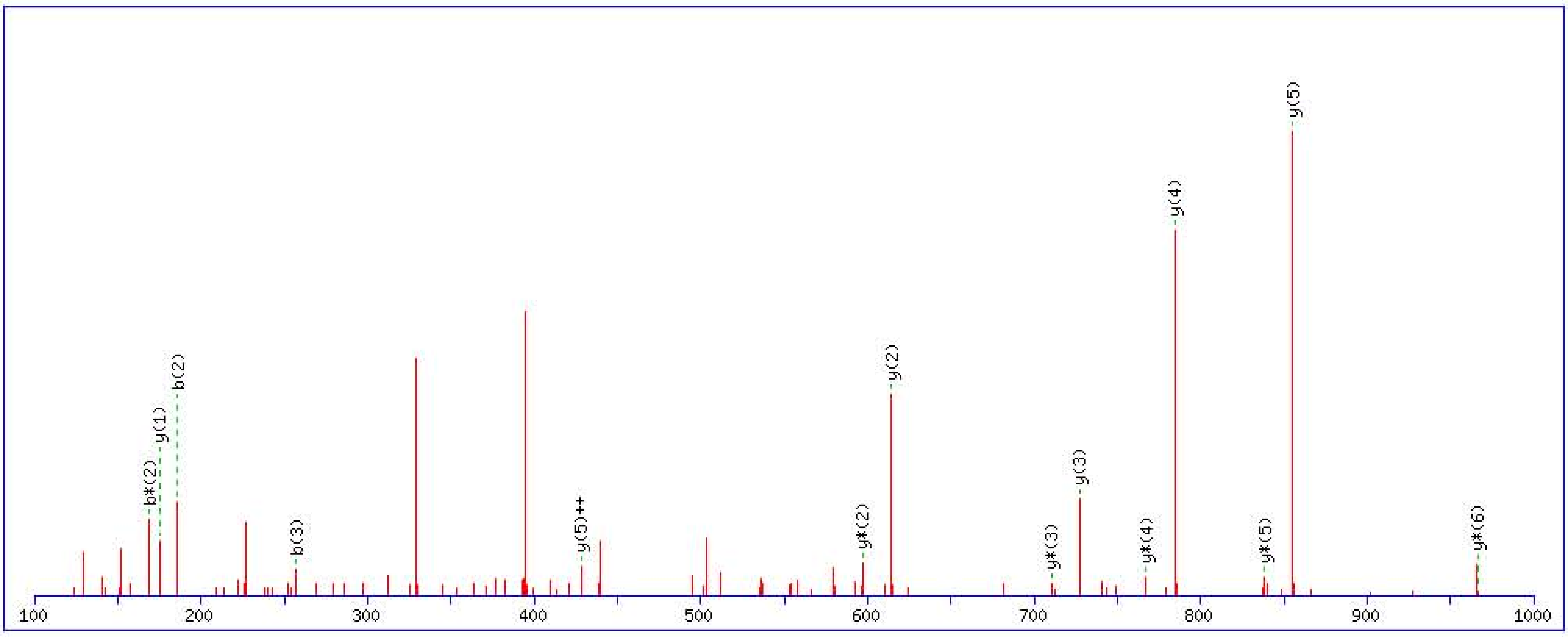
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQAGLQR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

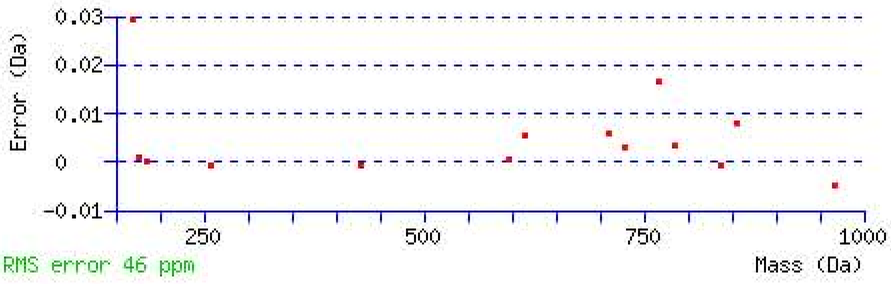
Match to Query 20649: 1039.558928 from(520.786740,2+) rtinseconds(1388) index(56120)
Title: Locus:1.1.1.2789.12 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

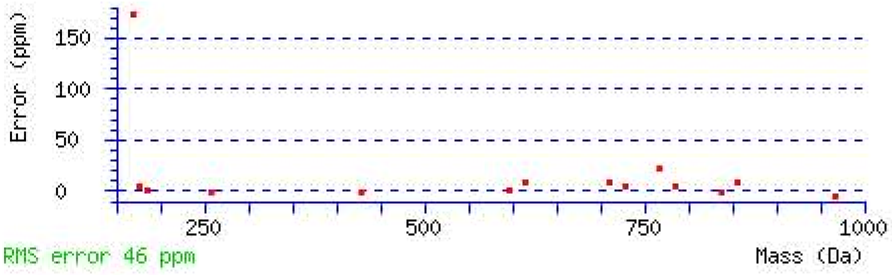
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1039.559677
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.034
Matches : 14/46 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	58.028740	29.518008			G					7
2	**186.087318**	93.547297	169.060769	85.034023	Q	983.545498	492.276387	966.518949	483.763113	6
3	**257.124432**	129.065854	240.097883	120.552580	A	***855.486920***	428.247098	838.460371	419.733824	5
4	314.145896	157.576586	297.119347	149.063312	G	***784.449806***	392.728541	767.423257	384.215267	4
5	427.229960	214.118618	410.203411	205.605344	L	***727.428342***	364.217809	710.401793	355.704535	3
6	866.455286	433.731281	849.428737	425.218007	Q	***614.344278***	307.675777	597.317729	299.162503	2
7					R	***175.118952***	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.0	1039.559677	-0.000749	GQAGLQR
10.6	1039.559677	-0.000749	GQQIQR
3.5	1039.559677	-0.000749	KGGPSQR
3.3	1039.552277	0.006651	QRAALDGGPR
3.2	1039.548431	0.010497	SPEIQR
2.9	1039.552277	0.006651	GQPQELGRR
2.0	1039.563492	-0.004564	AEGARARGPR
1.7	1039.548431	0.010497	LSPEQR

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

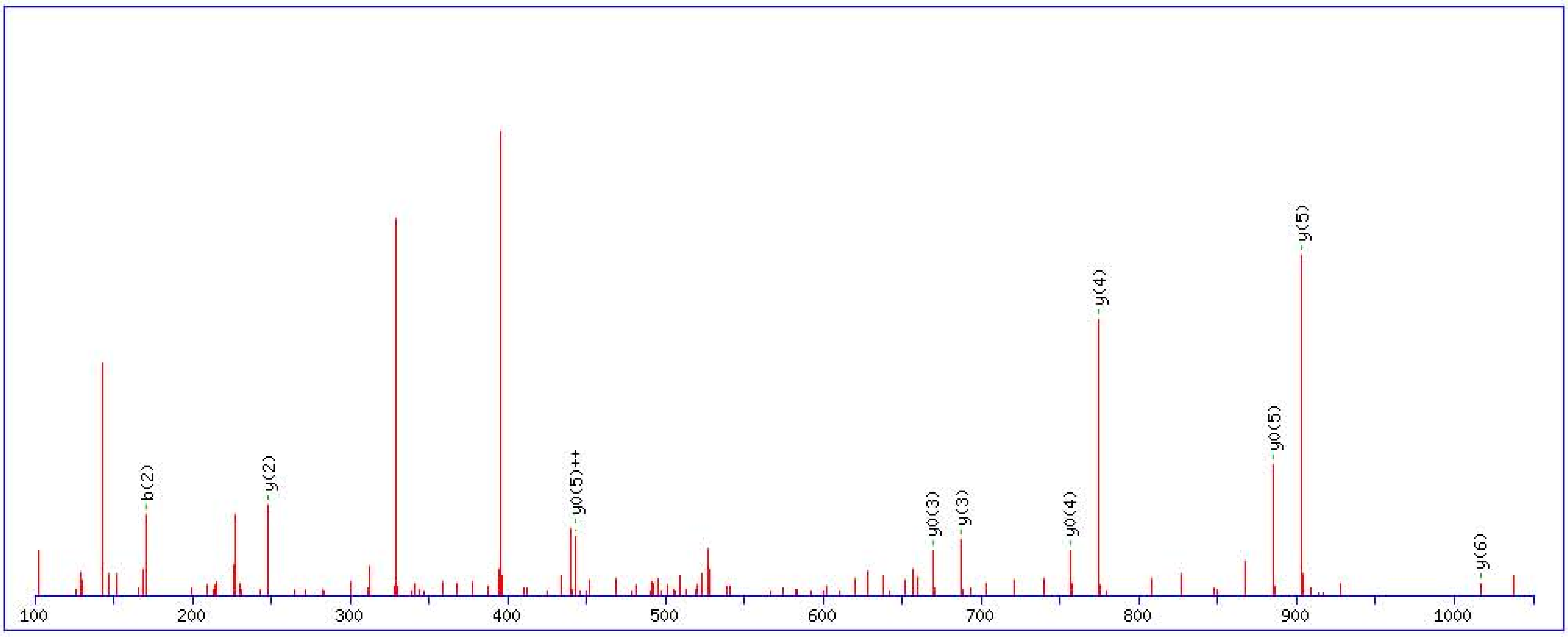
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLESQTK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

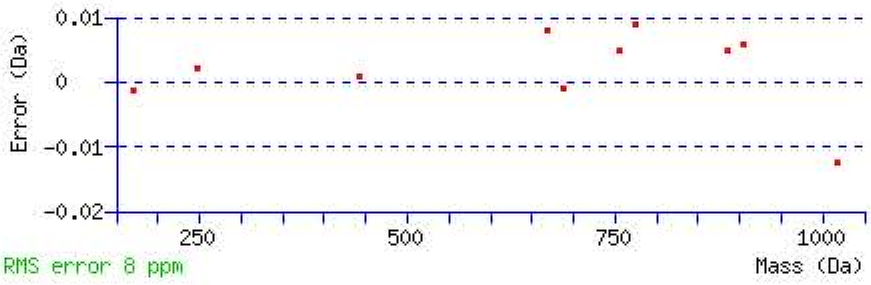
Match to Query 21733: 1072.563828 from(537.289190,2+) rtinseconds(1411) index(56302)
Title: Locus:1.1.1.2797.16 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

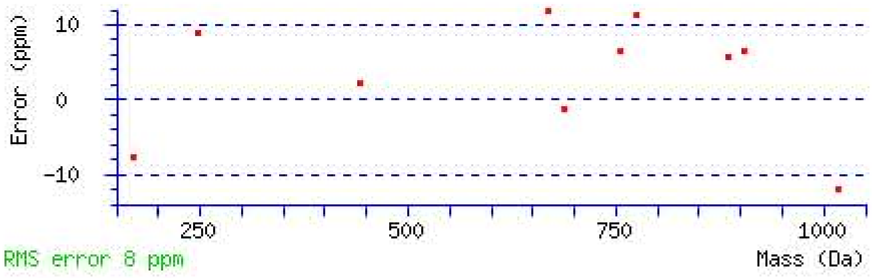
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1072.558670
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.039
Matches : 10/58 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							7
2	171.112804	86.060040					L	***1016.544494***	508.775885	999.517945	500.262611	998.533929	499.770603	6
3	300.155397	150.581336			282.144832	141.576054	E	***903.460430***	452.233853	886.433881	443.720579	885.449865	443.228571	5
4	387.187425	194.097351			369.176860	185.092068	S	***774.417837***	387.712557	757.391288	379.199282	756.407272	378.707274	4
5	826.412751	413.710014	809.386202	405.196739	808.402186	404.704731	Q	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
6	927.460430	464.233853	910.433881	455.720579	909.449865	455.228571	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
7							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.8	1072.558670	0.005158	GLESQTK
10.3	1072.558670	0.005158	LGECPAVLSK
6.1	1072.558670	0.005158	QSEGLTK
5.7	1072.551254	0.012574	KEAPRDETK
3.6	1072.576431	-0.012603	VAEGQTLDLK
3.3	1072.576447	-0.012619	LGGVLPDSTSK
3.1	1072.552155	0.011673	QSCVLR
2.6	1072.576462	-0.012634	TVVQEVVDGK
2.1	1072.551285	0.012543	GPRTTEPSTK

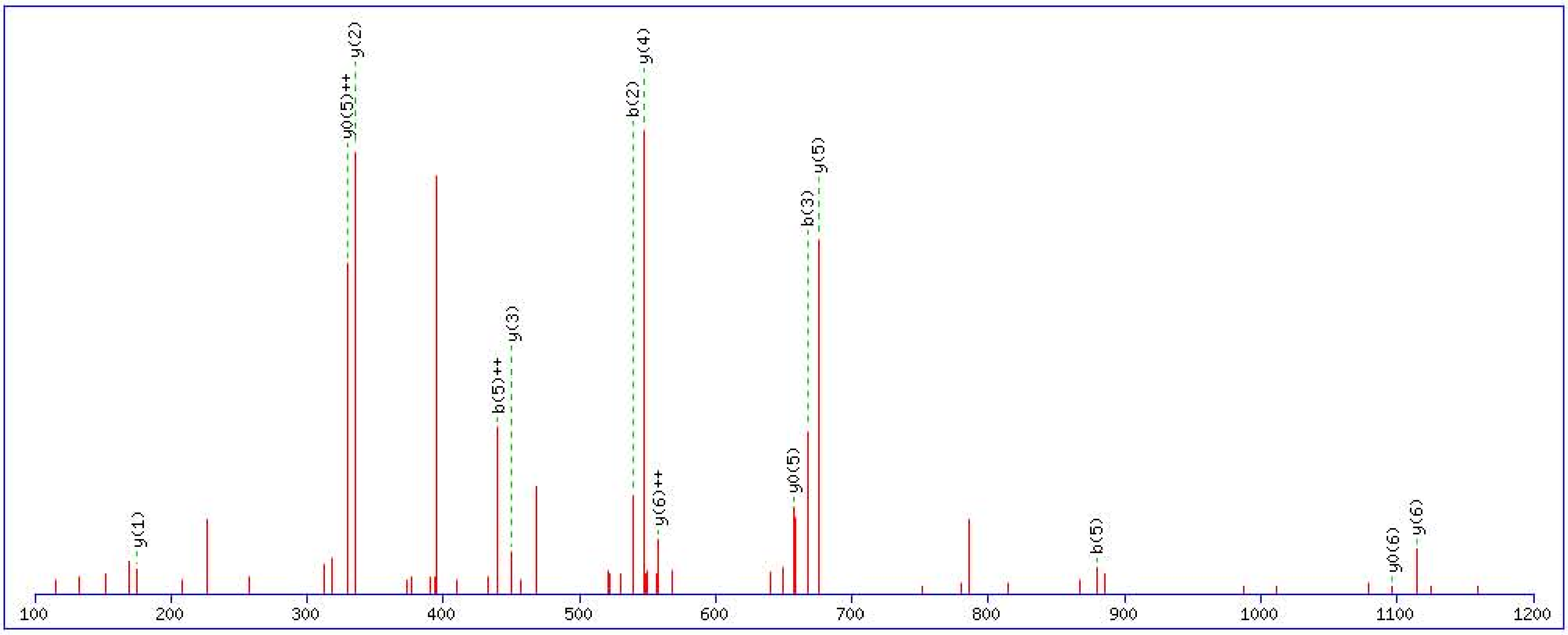
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQQPDCR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

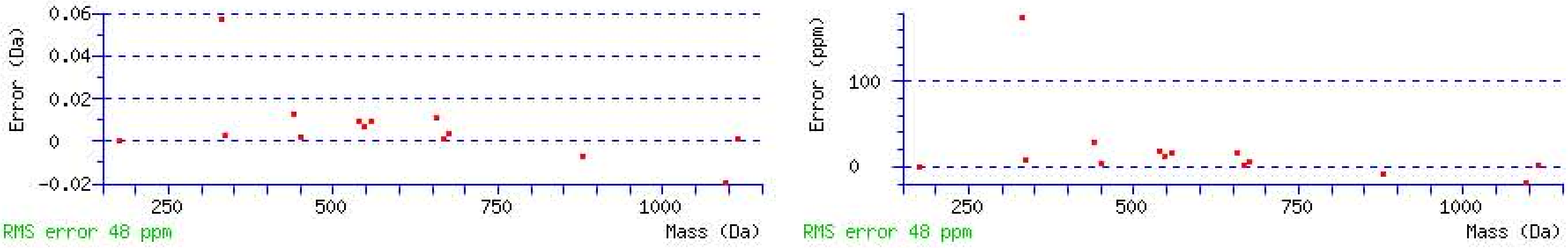
Match to Query 28041: 1212.578148 from(607.296350,2+) rtinseconds(1245) index(55163)
Title: Locus:1.1.1.2739.24 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1212.574356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.0087
Matches : 14/58 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							7
2	**539.301016**	270.154146	522.274467	261.640872			Q	***1114.513212***	557.760244	1097.486663	549.246970	1096.502647	548.754962	6
3	**667.359594**	334.183435	650.333045	325.670161			Q	***675.287886***	338.147581	658.261337	329.634307	657.277321	329.142299	5
4	764.412358	382.709817	747.385809	374.196543			P	***547.229308***	274.118292	530.202759	265.605018	529.218743	265.113010	4
5	**879.439301**	440.223289	862.412752	431.710014	861.428736	431.218006	D	***450.176544***	225.591910	433.149995	217.078635	432.165979	216.586627	3
6	1039.469950	520.238613	1022.443401	511.725339	1021.459385	511.233331	C	***335.149601***	168.078438	318.123052	159.565164			2
7							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.7	1212.574356	0.003792	VQQPDCR
13.3	1212.574356	0.003792	VQQPDCR
5.7	1212.596115	-0.017967	YFVEAGAMAVR

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

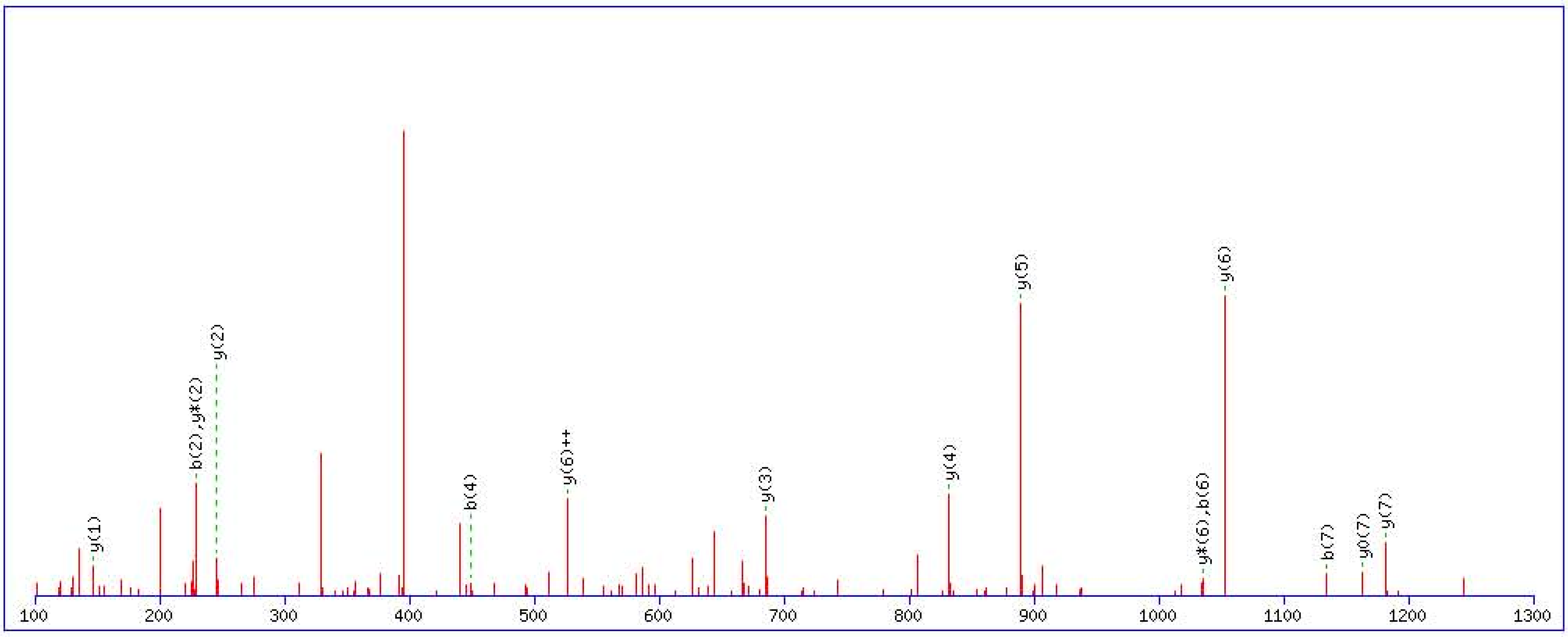
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEYGFQVK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

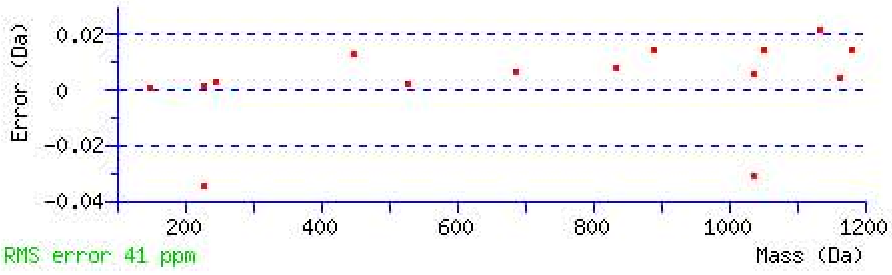
Match to Query 30241: 1279.673988 from(640.844270,2+) rtinseconds(1956) index(60240)
Title: Locus:1.1.1.2986.11 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

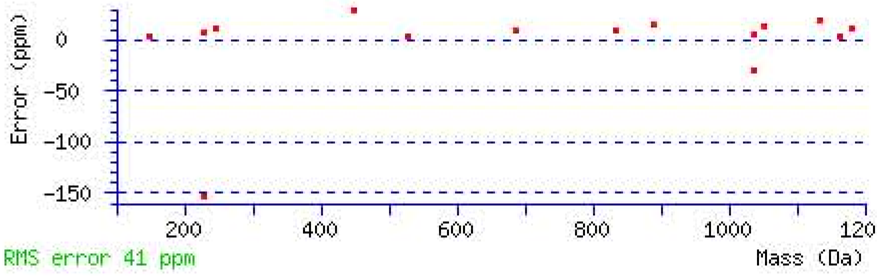
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1279.663483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0078
Matches : 15/60 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	**229.118283**	115.062780			211.107718	106.057497	E	***1181.602344***	591.304810	1164.575795	582.791536	1163.591779	582.299528	7
3	392.181612	196.594444			374.171047	187.589162	Y	***1052.559751***	526.783514	1035.533202	518.270239			6
4	**449.203076**	225.105176			431.192511	216.099894	G	***889.496422***	445.251849	872.469873	436.738575			5
5	596.271490	298.639383			578.260925	289.634101	F	***832.474958***	416.741117	815.448409	408.227843			4
6	**1035.496816**	518.252046	1018.470267	509.738772	1017.486251	509.246764	Q	***685.406544***	343.206910	668.379995	334.693636			3
7	**1134.565230**	567.786253	1117.538681	559.272979	1116.554665	558.780971	V	***246.181218***	123.594247	229.154669	115.080973			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.4	1279.663483	0.010505	VEYGFQVK
8.5	1279.684601	-0.010613	MSASAVFILDVK
7.6	1279.681229	-0.007241	EVTVKEWYVK
6.6	1279.677216	-0.003228	VFKTEDTQGKK
6.4	1279.663483	0.010505	QFVGYLDK
5.1	1279.659470	0.014518	VCSFGKQVVEK
4.9	1279.684601	-0.010613	TKPLMTEFSVK
1.3	1279.687958	-0.013970	LIKSMESVMVK
1.0	1279.666824	0.007164	VKEWSLMIMK

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

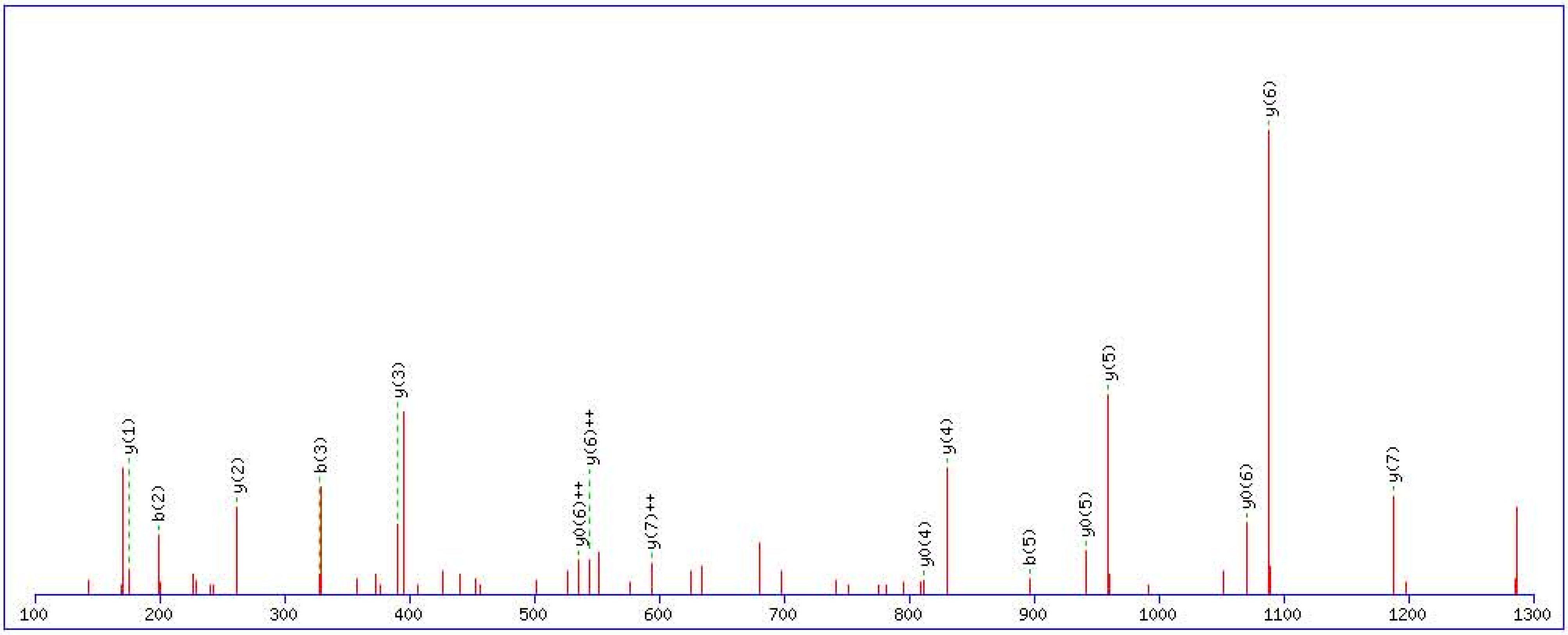
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVEEQESR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

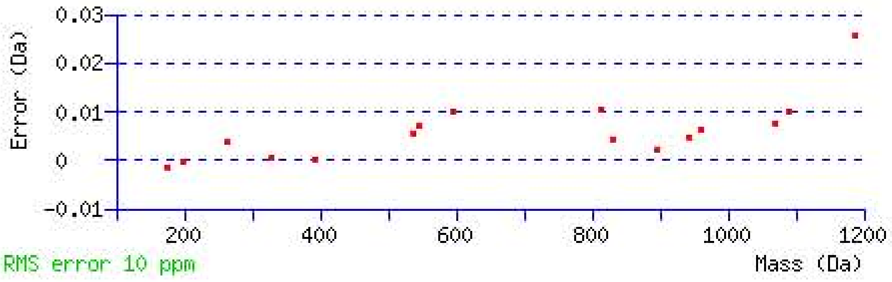
Match to Query 30578: 1285.641668 from(643.828110,2+) rtinseconds(1333) index(55718)
Title: Locus:1.1.1.2770.17 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

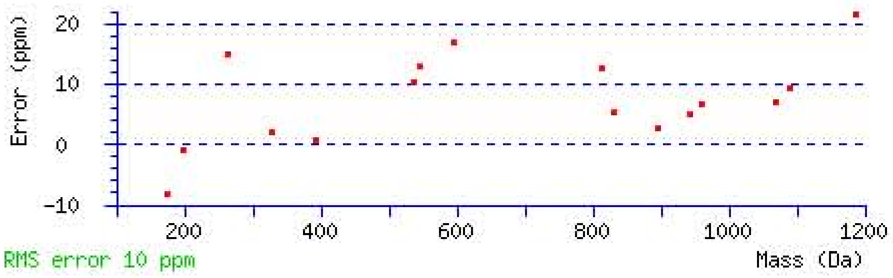
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1285.633621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0017
Matches : 16/70 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	**199.144104**	100.075690					V	***1187.572499***	594.289888	1170.545950	585.776613	1169.561934	585.284605	7
3	**328.186697**	164.596987			310.176132	155.591704	E	***1088.504085***	544.755681	1071.477536	536.242406	1070.493520	535.750398	6
4	457.229290	229.118283			439.218725	220.113001	E	***959.461492***	480.234384	942.434943	471.721110	941.450927	471.229102	5
5	**896.454616**	448.730946	879.428067	440.217672	878.444051	439.725664	Q	***830.418899***	415.713088	813.392350	407.199813	812.408334	406.707805	4
6	1025.497209	513.252243	1008.470660	504.738968	1007.486644	504.246960	E	***391.193573***	196.100425	374.167024	187.587150	373.183008	187.095142	3
7	1112.529237	556.768257	1095.502688	548.254982	1094.518672	547.762974	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	1285.633621	0.008047	VVEEQESR

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

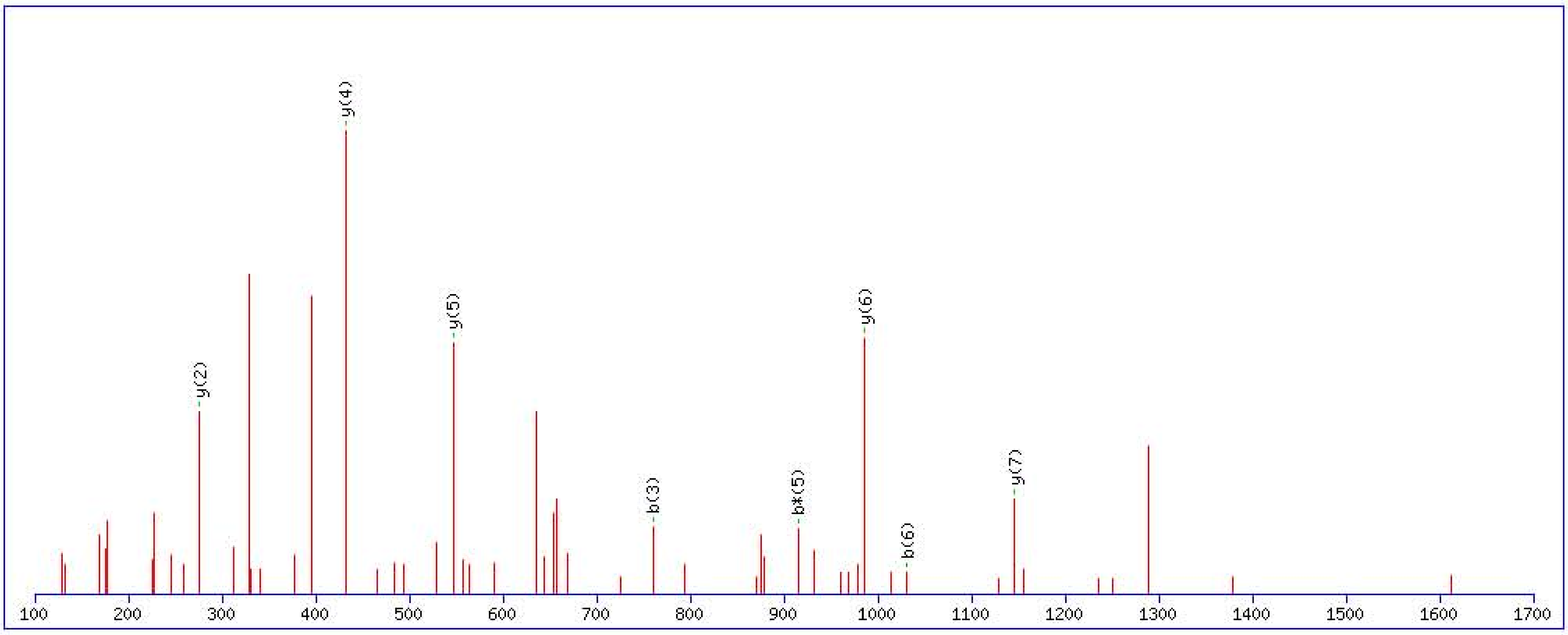
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CCQDGVTR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

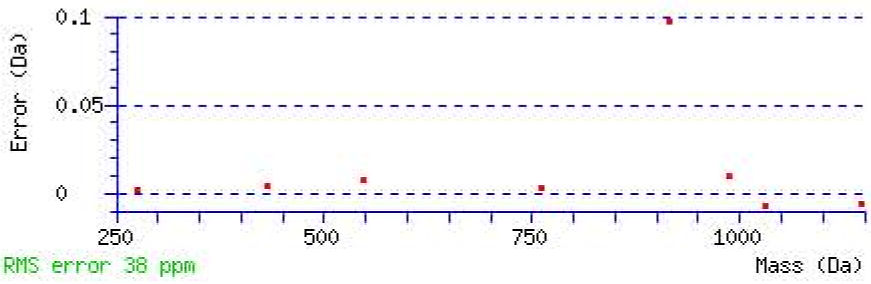
Match to Query 31054: 1305.572508 from(653.793530,2+) rtinseconds(1349) index(55787)
Title: Locus:1.1.1.2775.14 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

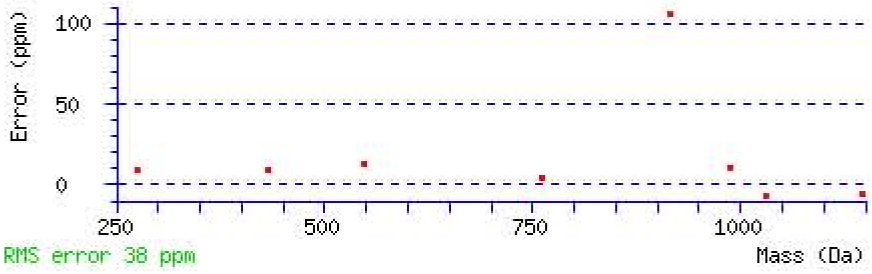
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1305.562820
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0012
Matches : 8/72 fragment ions using 12 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	161.037925	81.022600					C							8
2	321.068574	161.037925					C	*1146.539427*	573.773352	1129.512878	565.260077	1128.528862	564.768069	7
3	**760.293900**	380.650588	743.267351	372.137314			Q	*986.508778*	493.758027	969.482229	485.244753	968.498213	484.752745	6
4	875.320843	438.164060	858.294294	429.650785	857.310278	429.158777	D	*547.283452*	274.145364	530.256903	265.632090	529.272887	265.140082	5
5	932.342307	466.674792	915.315758	458.161517	914.331742	457.669509	G	*432.256509*	216.631893	415.229960	208.118618	414.245944	207.626610	4
6	**1031.410721**	516.208999	1014.384172	507.695724	1013.400156	507.203716	V	375.235045	188.121161	358.208496	179.607886	357.224480	179.115878	3
7	1132.458400	566.732838	1115.431851	558.219564	1114.447835	557.727556	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
8							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.1	1305.562820	0.009688	CCQDGVTR
8.8	1305.588409	-0.015901	CRSSTPADAWR
2.8	1305.577194	-0.004686	CDAGWLADGSVR

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

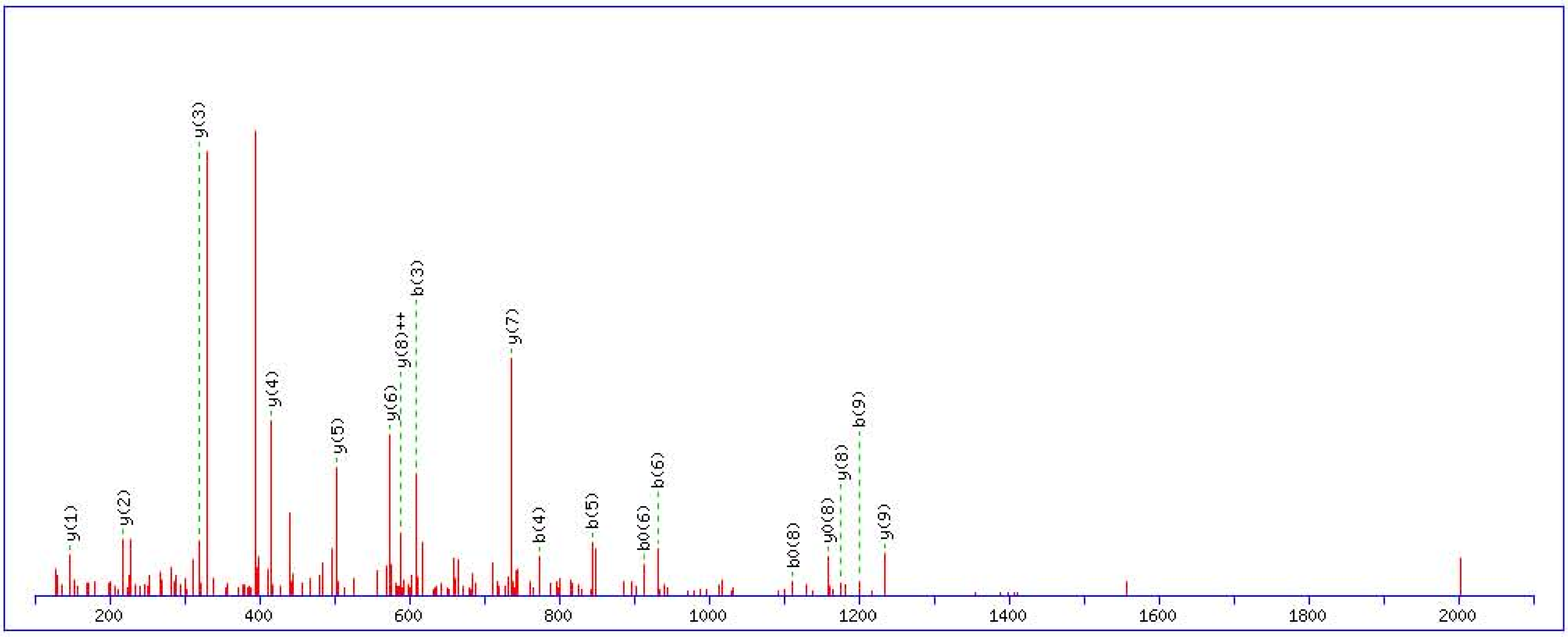
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGQYASPTAK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

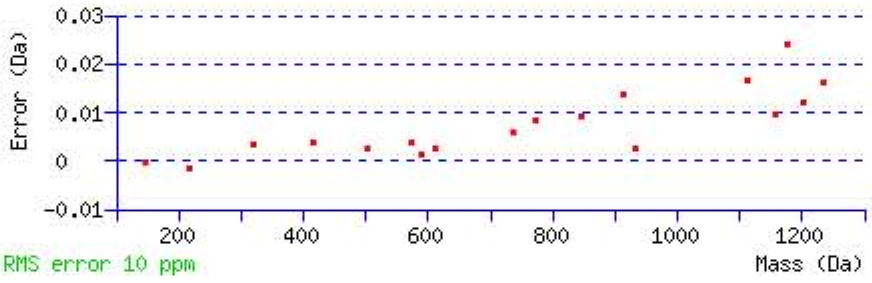
Match to Query 31920: 1345.714648 from(673.864600,2+) rtinseconds(1540) index(57248)
Title: Locus:1.1.1.2842.15 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

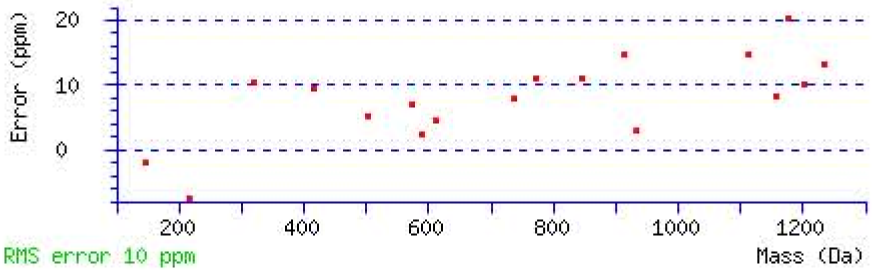
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1345.706390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 5.3e-005
Matches : 18/90 fragment ions using 35 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							10
2	171.112804	86.060040					G	***1233.629622***	617.318449	1216.603073	608.805175	1215.619057	608.313167	9
3	**610.338130**	305.672703	593.311581	297.159429			Q	***1176.608158***	588.807717	1159.581609	580.294443	1158.597593	579.802435	8
4	**773.401459**	387.204368	756.374910	378.691093			Y	***737.382832***	369.195054	720.356283	360.681780	719.372267	360.189772	7
5	**844.438573**	422.722925	827.412024	414.209650			A	***574.319503***	287.663389	557.292954	279.150115	556.308938	278.658107	6
6	**931.470601**	466.238939	914.444052	457.725664	913.460036	457.233656	S	***503.282389***	252.144832	486.255840	243.631558	485.271824	243.139550	5
7	1028.523365	514.765321	1011.496816	506.252046	1010.512800	505.760038	P	***416.250361***	208.628818	399.223812	200.115544	398.239796	199.623536	4
8	1129.571044	565.289160	1112.544495	556.775886	1111.560479	556.283878	T	***319.197597***	160.102436	302.171048	151.589162	301.187032	151.097154	3
9	**1200.608158**	600.807717	1183.581609	592.294443	1182.597593	591.802435	A	***218.149918***	109.578597	201.123369	101.065322			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.6	1345.706390	0.008258	LGQYASPTAK
9.5	1345.706390	0.008258	LGQYDQALK
9.2	1345.724182	-0.009534	LGAVPATSGPTTFK
8.3	1345.706406	0.008242	QGLYTPQTK
5.6	1345.727509	-0.012861	LGLMDNEIKVAK
2.0	1345.717636	-0.002988	QMPQPTFTLRK

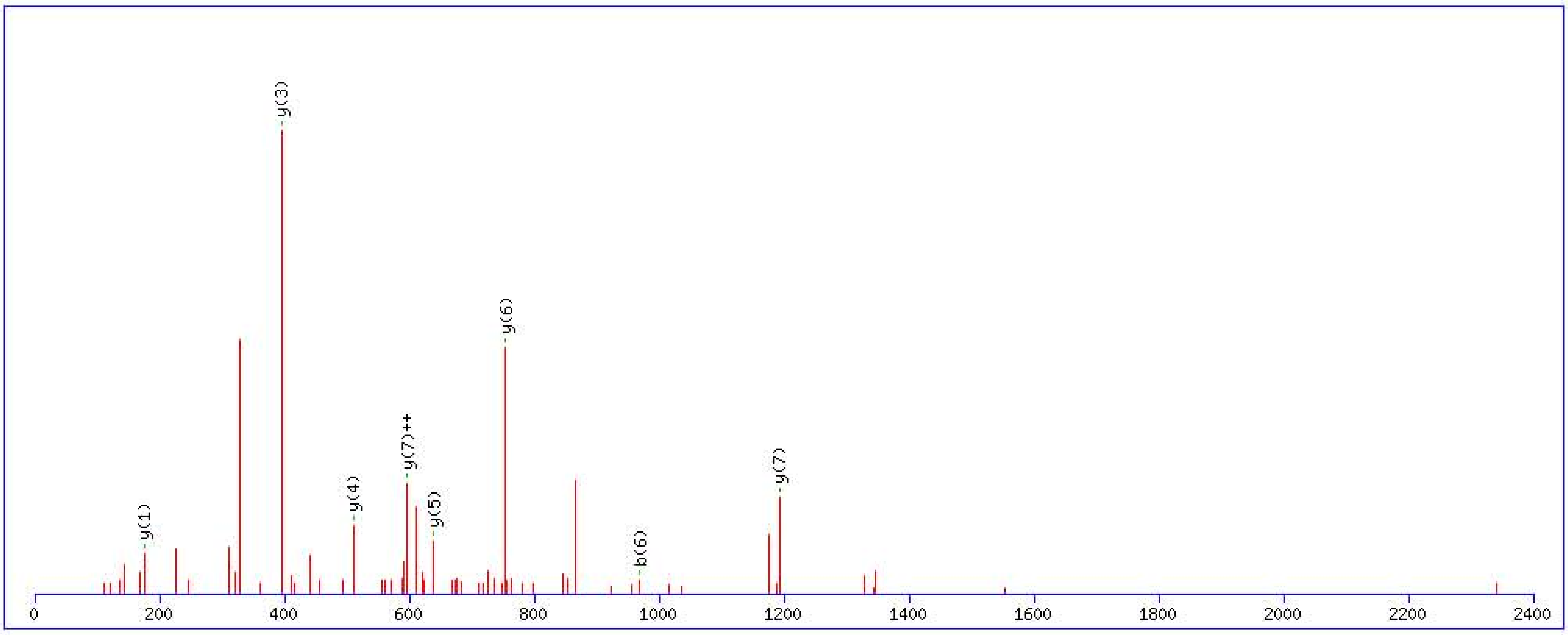
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLQDEDGYR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

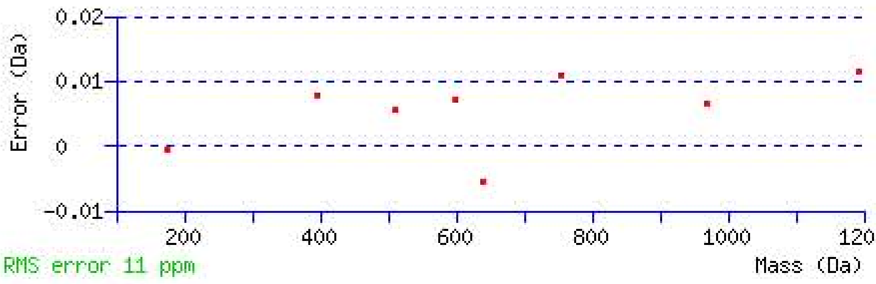
Match to Query 33236: 1362.630168 from(682.322360,2+) rtinseconds(1683) index(58185)
Title: Locus:1.1.1.2892.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

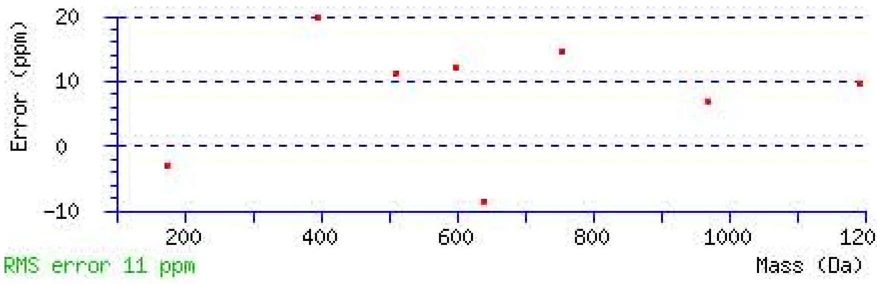
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1362.623795
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 7.7e-005
Matches : 8/80 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							9
2	171.112804	86.060040					L	1306.609614	653.808445	1289.583065	645.295171	1288.599049	644.803163	8
3	610.338130	305.672703	593.311581	297.159429			Q	***1193.525550***	597.266413	1176.499001	588.753139	1175.514985	588.261131	7
4	725.365073	363.186175	708.338524	354.672900	707.354508	354.180892	D	***754.300224***	377.653750	737.273675	369.140476	736.289659	368.648468	6
5	854.407666	427.707471	837.381117	419.194197	836.397101	418.702189	E	***639.273281***	320.140279	622.246732	311.627004	621.262716	311.134996	5
6	**969.434609**	485.220943	952.408060	476.707668	951.424044	476.215660	D	***510.230688***	255.618982	493.204139	247.105707	492.220123	246.613700	4
7	1026.456073	513.731675	1009.429524	505.218400	1008.445508	504.726392	G	***395.203745***	198.105511	378.177196	189.592236			3
8	1189.519402	595.263339	1172.492853	586.750065	1171.508837	586.258057	Y	338.182281	169.594778	321.155732	161.081504			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.6	1362.623795	0.006373	GLQDEDGYR
2.5	1362.623795	0.006373	TGFLEIDEHMR
0.1	1362.613251	0.016917	MGAGATGRAMDGPR

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

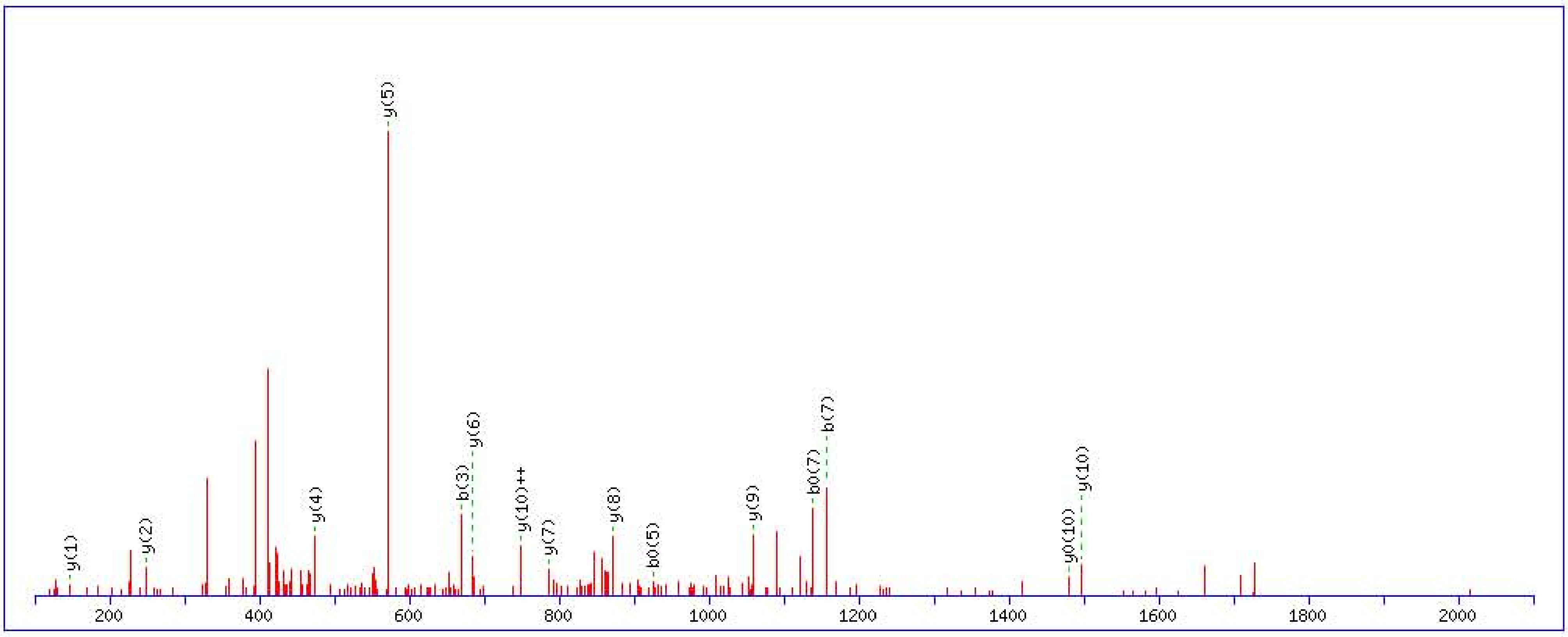
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEQWSTLPPETK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

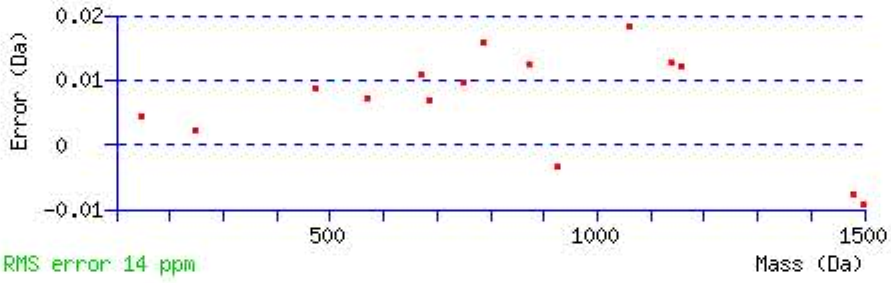
Match to Query 46460: 1726.877708 from(864.446130,2+) rtinseconds(2031) index(60756)
Title: Locus:1.1.1.3012.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

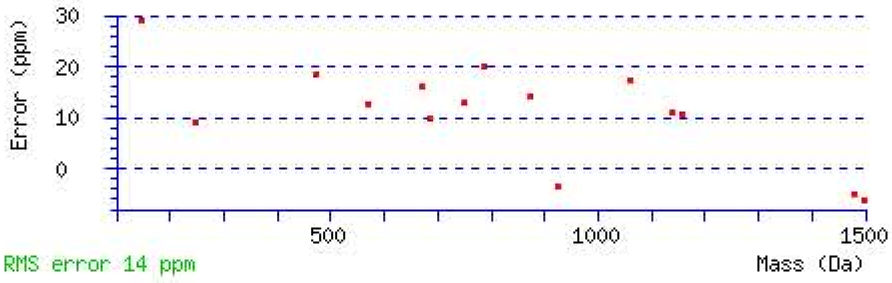
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1726.860001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 5.9e-005
Matches : 15/126 fragment ions using 33 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							12
2	231.097548	116.052412			213.086983	107.047130	E	1626.819607	813.913442	1609.793058	805.400167	1608.809042	804.908159	11
3	**670.322874**	335.665075	653.296325	327.151801	652.312309	326.659793	Q	***1497.777014***	749.392145	1480.750465	740.878871	1479.766449	740.386863	10
4	856.402187	428.704732	839.375638	420.191457	838.391622	419.699449	W	***1058.551688***	529.779482	1041.525139	521.266208	1040.541123	520.774200	9
5	943.434215	472.220746	926.407666	463.707471	925.423650	463.215463	S	***872.472375***	436.739826	855.445826	428.226551	854.461810	427.734543	8
6	1044.481894	522.744585	1027.455345	514.231311	1026.471329	513.739303	T	***785.440347***	393.223812	768.413798	384.710537	767.429782	384.218529	7
7	**1157.565958**	579.286617	1140.539409	570.773343	1139.555393	570.281334	L	***684.392668***	342.699972	667.366119	334.186698	666.382103	333.694690	6
8	1254.618722	627.812999	1237.592173	619.299725	1236.608157	618.807716	P	***571.308604***	286.157940	554.282055	277.644666	553.298039	277.152658	5
9	1351.671486	676.339381	1334.644937	667.826107	1333.660921	667.334098	P	***474.255840***	237.631558	457.229291	229.118284	456.245275	228.626276	4
10	1480.714079	740.860678	1463.687530	732.347403	1462.703514	731.855395	E	377.203076	189.105176	360.176527	180.591902	359.192511	180.099894	3
11	1581.761758	791.384517	1564.735209	782.871243	1563.751193	782.379235	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.3	1726.860001	0.017707	TEQWSTLPPETK
4.0	1726.867188	0.010520	KDHAEMQAVIDAKQK
0.6	1726.853485	0.024223	MASGHAFQPDLVK

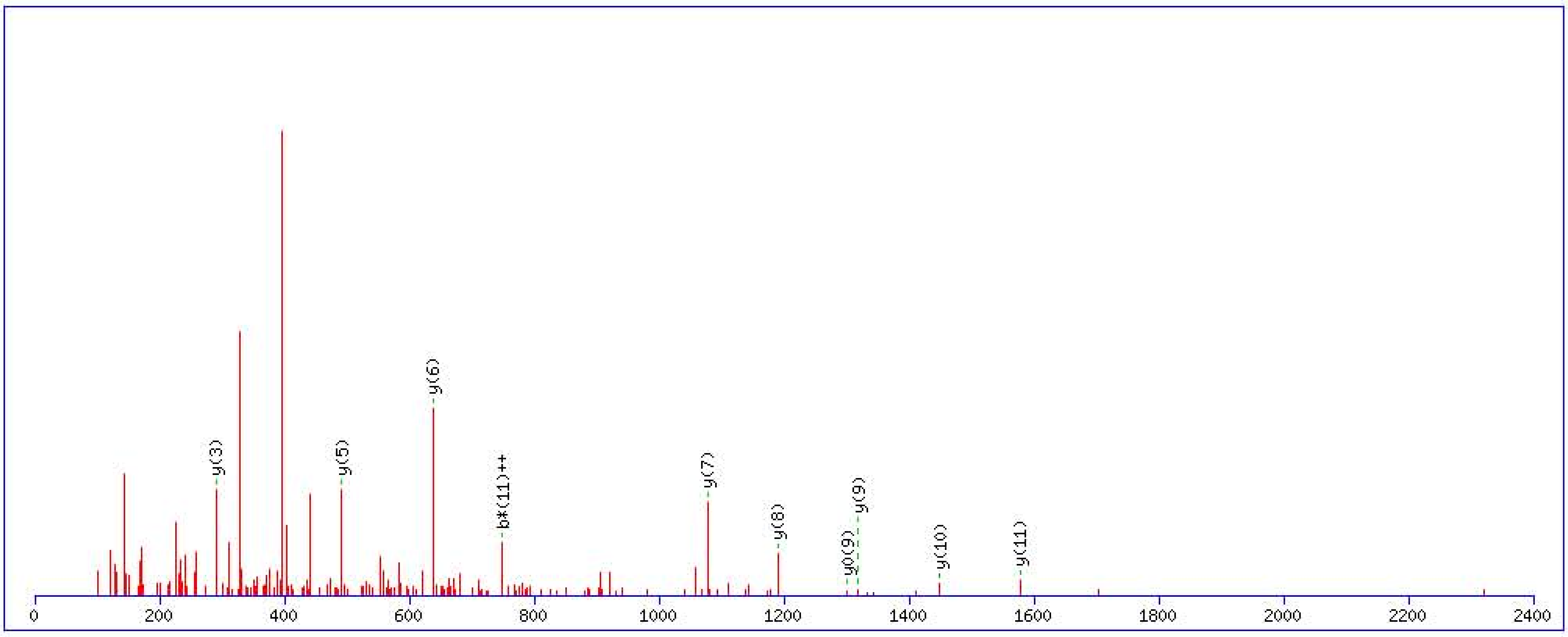
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLEEELQFSLGSK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

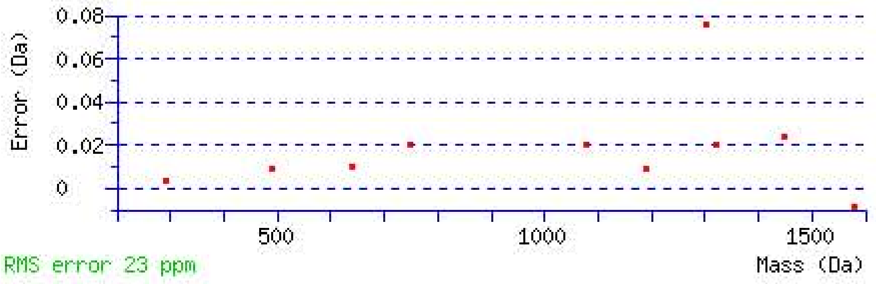
Match to Query 47083: 1746.907452 from(583.309760,3+) rtinseconds(2523) index(64206)
Title: Locus:1.1.1.3183.5 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

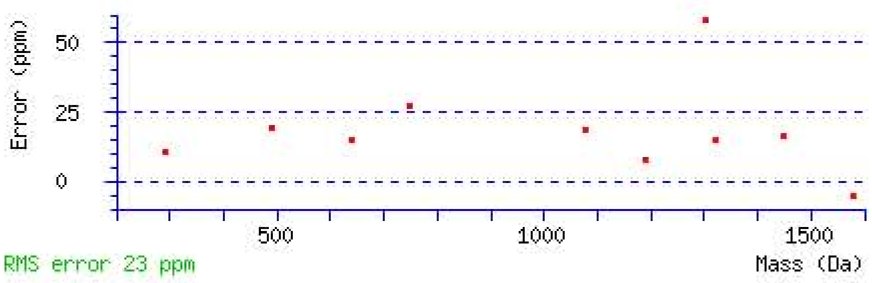
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1746.886200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 3.7e-005
Matches : 10/126 fragment ions using 16 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							13
2	171.112804	86.060040					L	1690.872035	845.939656	1673.845486	837.426381	1672.861470	836.934373	12
3	300.155397	150.581336			282.144832	141.576054	E	***1577.787971***	789.397624	1560.761422	780.884349	1559.777406	780.392341	11
4	429.197990	215.102633			411.187425	206.097351	E	***1448.745378***	724.876327	1431.718829	716.363053	1430.734813	715.871045	10
5	558.240583	279.623930			540.230018	270.618647	E	***1319.702785***	660.355031	1302.676236	651.841756	1301.692220	651.349748	9
6	671.324647	336.165962			653.314082	327.160679	L	***1190.660192***	595.833734	1173.633643	587.320460	1172.649627	586.828452	8
7	1110.549973	555.778624	1093.523424	547.265350	1092.539408	546.773342	Q	***1077.576128***	539.291702	1060.549579	530.778428	1059.565563	530.286419	7
8	1257.618387	629.312832	1240.591838	620.799557	1239.607822	620.307549	F	***638.350802***	319.679039	621.324253	311.165765	620.340237	310.673757	6
9	1344.650415	672.828846	1327.623866	664.315571	1326.639850	663.823563	S	***491.282388***	246.144832	474.255839	237.631557	473.271823	237.139549	5
10	1457.734479	729.370878	1440.707930	720.857603	1439.723914	720.365595	L	404.250360	202.628818	387.223811	194.115543	386.239795	193.623535	4
11	1514.755943	757.881609	1497.729394	749.368335	1496.745378	748.876327	G	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
12	1601.787971	801.397624	1584.761422	792.884349	1583.777406	792.392341	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.8	1746.886200	0.021252	GLEEELQFSLGSK
2.5	1746.891403	0.016049	HSSVLFRHQKLHSGD

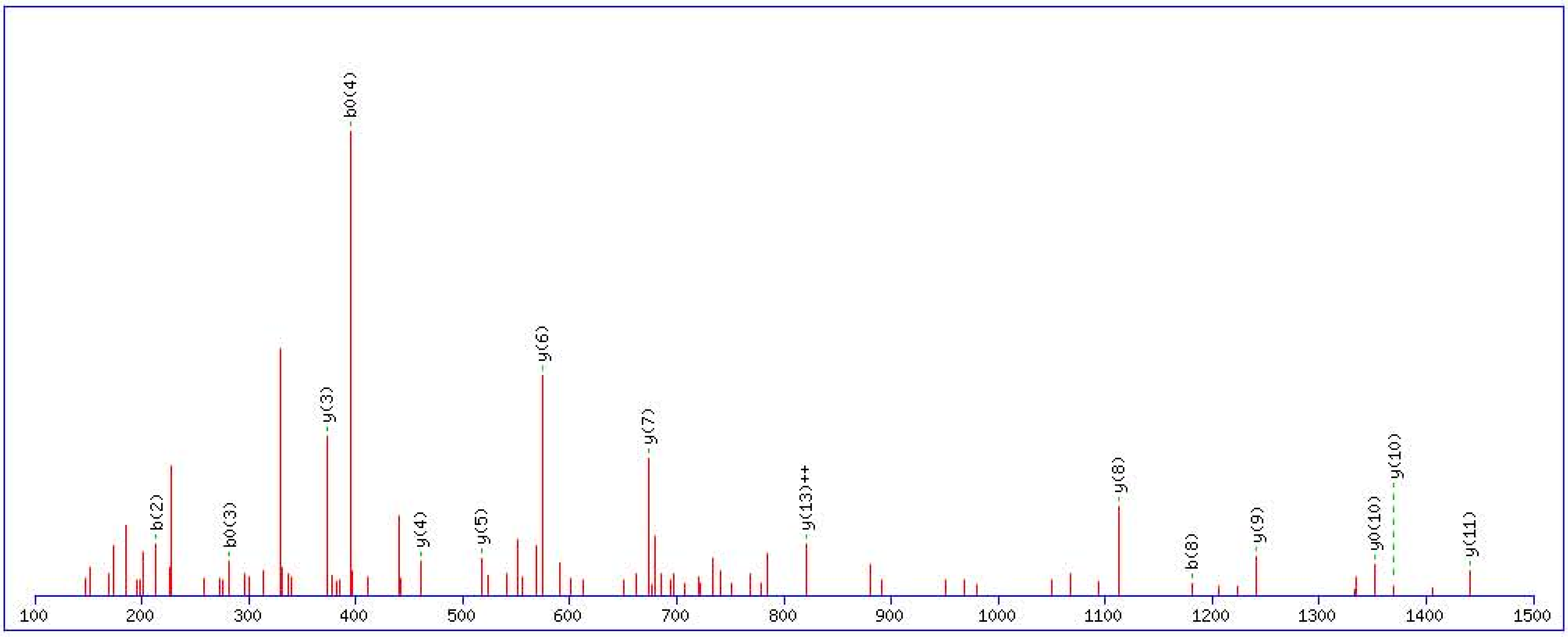
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSLAQEQVGGSPEK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

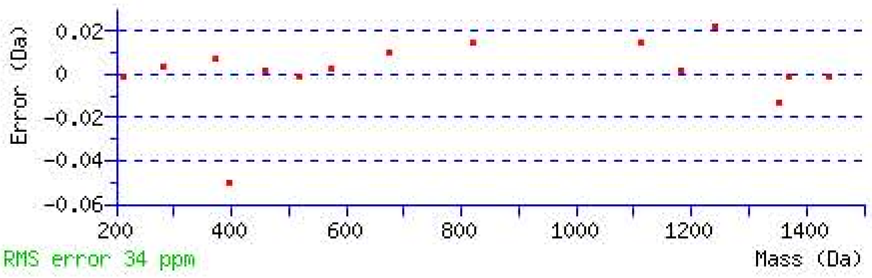
Match to Query 49516: 1851.991572 from(618.337800,3+) rtinseconds(1956) index(60239)
Title: Locus:1.1.1.2986.10 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

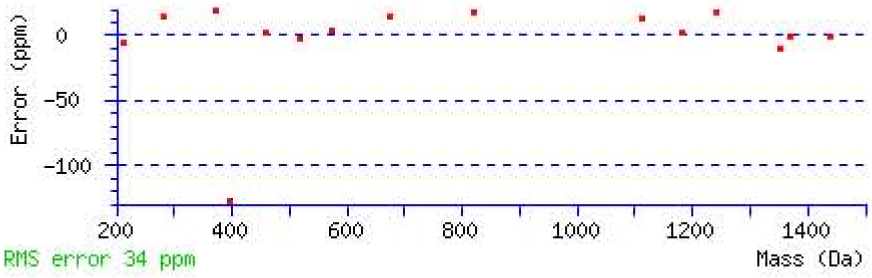
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1851.976425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.0022
Matches : 15/152 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							15
2	**213.159754**	107.083515					L	1753.915298	877.461287	1736.888749	868.948013	1735.904733	868.456004	14
3	300.191782	150.599529			282.181217	141.594247	S	1640.831234	820.919255	1623.804685	812.405981	1622.820669	811.913973	13
4	413.275846	207.141561			395.265281	198.136279	L	1553.799206	777.403241	1536.772657	768.889967	1535.788641	768.397958	12
5	484.312960	242.660118			466.302395	233.654836	A	***1440.715142***	720.861209	1423.688593	712.347935	1422.704577	711.855927	11
6	612.371538	306.689407	595.344989	298.176133	594.360973	297.684125	Q	***1369.678028***	685.342652	1352.651479	676.829378	1351.667463	676.337370	10
7	741.414131	371.210704	724.387582	362.697429	723.403566	362.205421	E	***1241.619450***	621.313363	1224.592901	612.800089	1223.608885	612.308080	9
8	**1180.639457**	590.823367	1163.612908	582.310092	1162.628892	581.818084	Q	***1112.576857***	556.792066	1095.550308	548.278792	1094.566292	547.786784	8
9	1279.707871	640.357574	1262.681322	631.844299	1261.697306	631.352291	V	***673.351531***	337.179404	656.324982	328.666129	655.340966	328.174121	7
10	1336.729335	668.868306	1319.702786	660.355031	1318.718770	659.863023	G	***574.283117***	287.645197	557.256568	279.131922	556.272552	278.639914	6
11	1393.750799	697.379037	1376.724250	688.865763	1375.740234	688.373755	G	***517.261653***	259.134465	500.235104	250.621190	499.251088	250.129182	5
12	1480.782827	740.895052	1463.756278	732.381777	1462.772262	731.889769	S	***460.240189***	230.623732	443.213640	222.110458	442.229624	221.618450	4
13	1577.835591	789.421434	1560.809042	780.908159	1559.825026	780.416151	P	***373.208161***	187.107718	356.181612	178.594444	355.197596	178.102436	3
14	1706.878184	853.942730	1689.851635	845.429456	1688.867619	844.937447	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.3	1851.976425	0.015147	VLSLAQEQVGGSPEK
23.7	1851.976425	0.015147	VLSLAQEQVGGSPEK

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

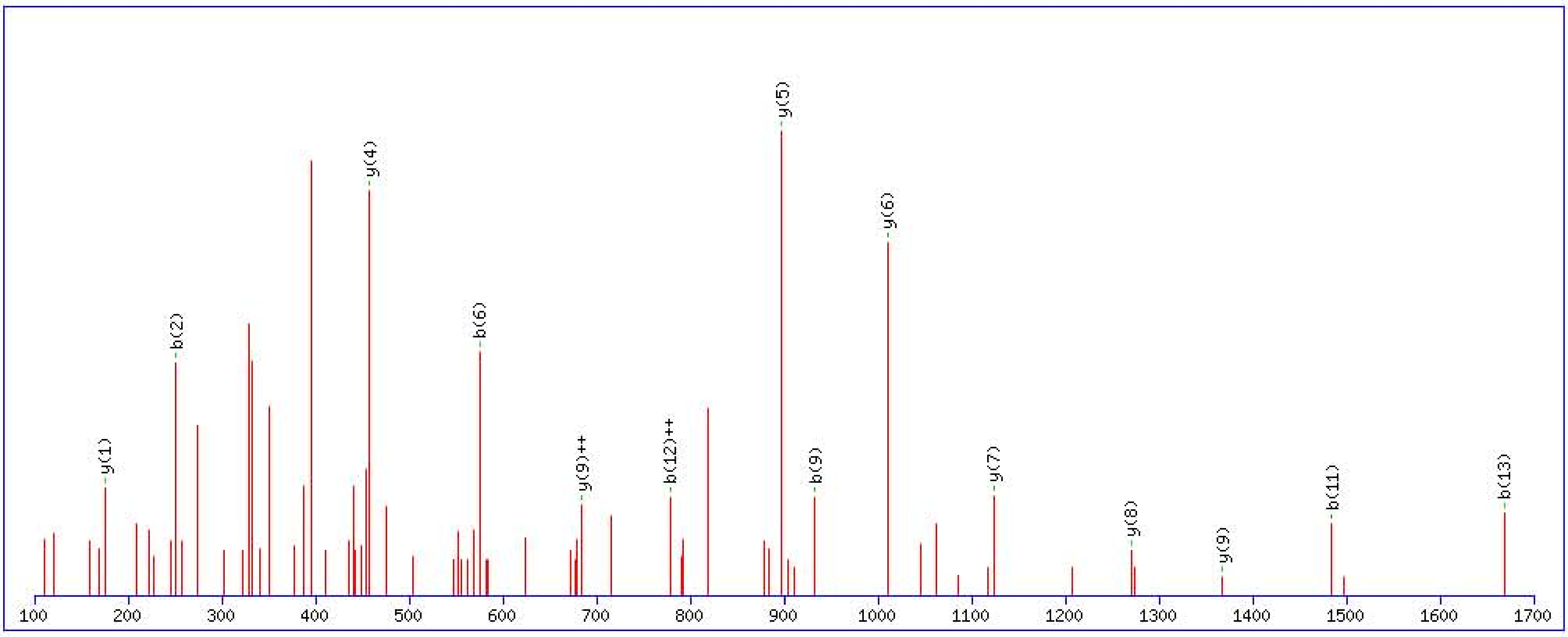
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLVPGAPFLLQALVR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

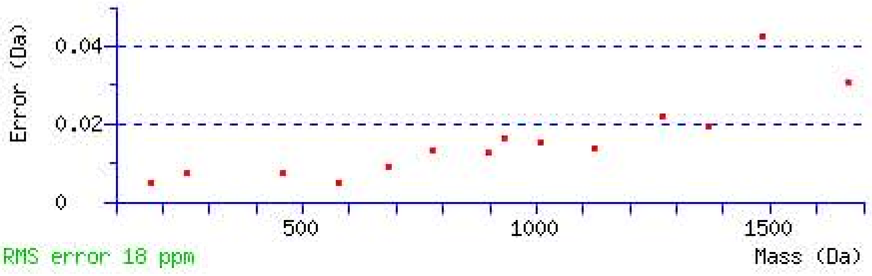
Match to Query 51553: 1941.164652 from(648.062160,3+) rtinseconds(2817) index(66281)
Title: Locus:1.1.1.3284.6 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

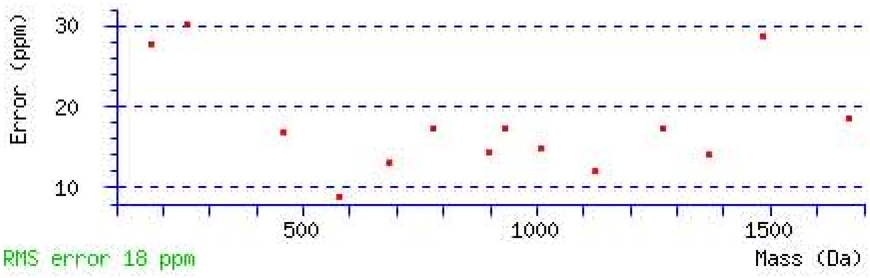
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1941.138626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 2.7e-006
Matches : 14/92 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	138.066188	69.536732			H					15
2	*251.150252*	126.078764			L	1805.086996	903.047136	1788.060447	894.533862	14
3	350.218666	175.612971			V	1692.002932	846.505104	1674.976383	837.991830	13
4	447.271430	224.139353			P	1592.934518	796.970897	1575.907969	788.457623	12
5	504.292894	252.650085			G	1495.881754	748.444515	1478.855205	739.931241	11
6	*575.330008*	288.168642			A	1438.860290	719.933783	1421.833741	711.420509	10
7	672.382772	336.695024			P	*1367.823176*	684.415226	1350.796627	675.901952	9
8	819.451186	410.229231			F	*1270.770412*	635.888844	1253.743863	627.375570	8
9	*932.535250*	466.771263			L	*1123.701998*	562.354637	1106.675449	553.841363	7
10	1045.619314	523.313295			L	*1010.617934*	505.812605	993.591385	497.299331	6
11	*1484.844640*	742.925958	1467.818091	734.412684	Q	*897.533870*	449.270573	880.507321	440.757298	5
12	1555.881754	778.444515	1538.855205	769.931241	A	*458.308544*	229.657910	441.281995	221.144635	4
13	*1668.965818*	834.986547	1651.939269	826.473273	L	387.271430	194.139353	370.244881	185.626078	3
14	1768.034232	884.520754	1751.007683	876.007480	V	274.187366	137.597321	257.160817	129.084047	2
15					R	*175.118952*	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.8	1941.138626	0.026026	HLVPGAPFLLQALVR

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

{MATRIX SCIENCE}

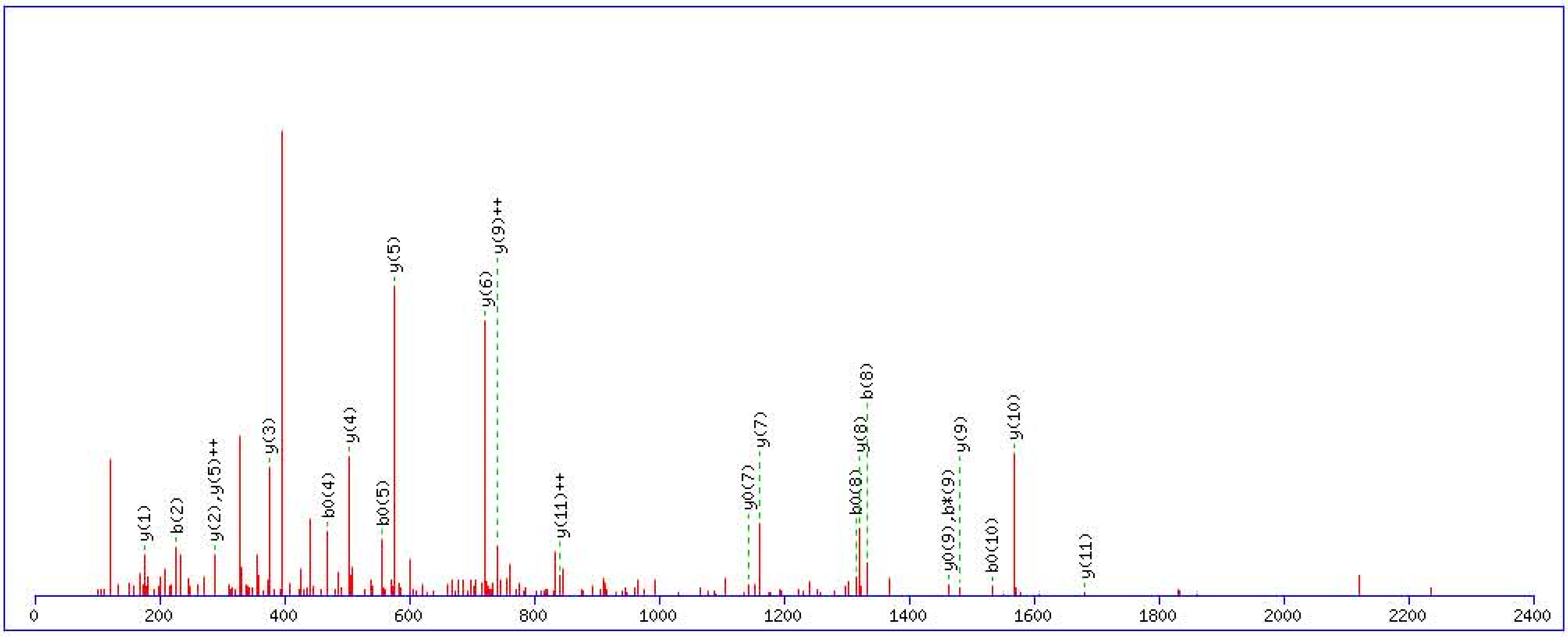
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPFLSCCQFAESLR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

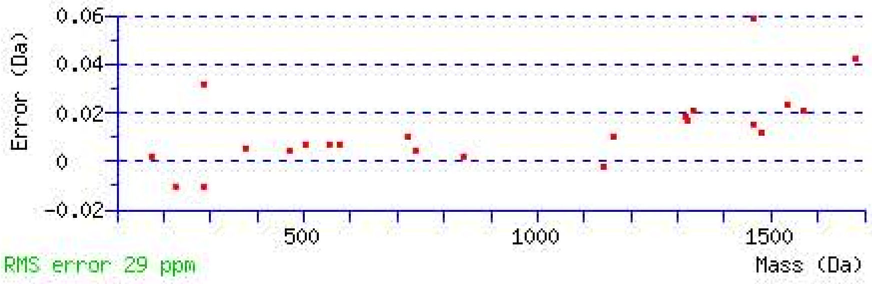
Match to Query 55066: 2053.967052 from(685.662960,3+) rtinseconds(2451) index(63695)
Title: Locus:1.1.1.3158.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

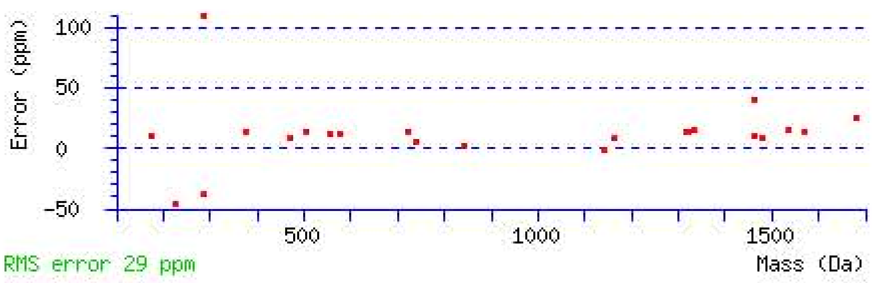
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2053.942368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 9.5e-006
Matches : 23/138 fragment ions using 49 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							14
2	**227.102633**	114.054954			209.092068	105.049672	P	1925.907059	963.457168	1908.880510	954.943893	1907.896494	954.451885	13
3	374.171047	187.589161			356.160482	178.583879	F	1828.854295	914.930786	1811.827746	906.417511	1810.843730	905.925503	12
4	487.255111	244.131193			469.244546	235.125911	L	***1681.785881***	841.396579	1664.759332	832.883304	1663.775316	832.391296	11
5	574.287139	287.647208			556.276574	278.641925	S	***1568.701817***	784.854547	1551.675268	776.341272	1550.691252	775.849264	10
6	734.317788	367.662532			716.307223	358.657250	C	***1481.669789***	741.338533	1464.643240	732.825258	1463.659224	732.333250	9
7	894.348437	447.677857			876.337872	438.672574	C	***1321.639140***	661.323208	1304.612591	652.809934	1303.628575	652.317926	8
8	**1333.573763**	667.290520	1316.547214	658.777245	1315.563198	658.285237	Q	***1161.608491***	581.307884	1144.581942	572.794609	1143.597926	572.302601	7
9	1480.642177	740.824727	1463.615628	732.311452	1462.631612	731.819444	F	***722.383165***	361.695221	705.356616	353.181946	704.372600	352.689938	6
10	1551.679291	776.343284	1534.652742	767.830009	1533.668726	767.338001	A	***575.314751***	288.161014	558.288202	279.647739	557.304186	279.155731	5
11	1680.721884	840.864580	1663.695335	832.351306	1662.711319	831.859298	E	***504.277637***	252.642457	487.251088	244.129182	486.267072	243.637174	4
12	1767.753912	884.380594	1750.727363	875.867320	1749.743347	875.375312	S	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
13	1880.837976	940.922626	1863.811427	932.409352	1862.827411	931.917344	L	***288.203016***	144.605146	271.176467	136.091871			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.7	2053.942368	0.024684	EPFLSCCQFAESLR
0.1	2053.985703	-0.018651	ENENERFAHYLEKTFK

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

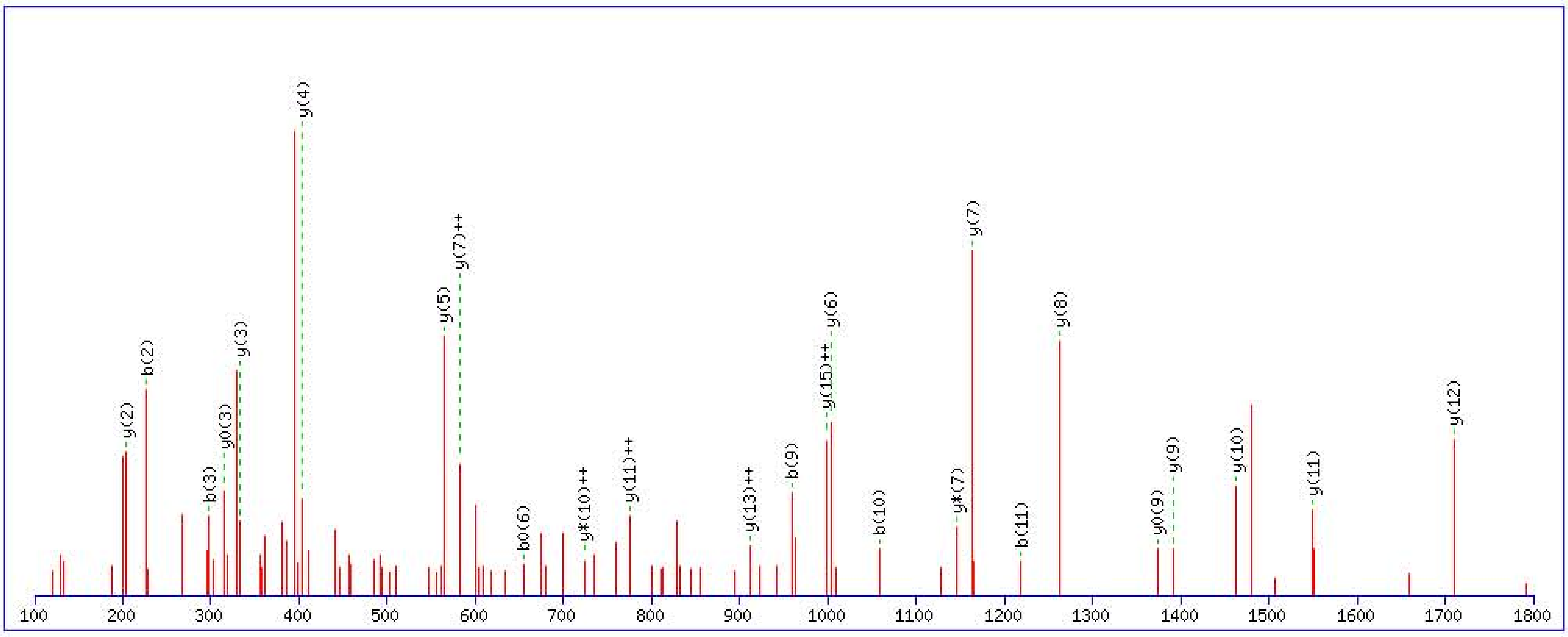
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLATLCSAEVCQCAEGK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

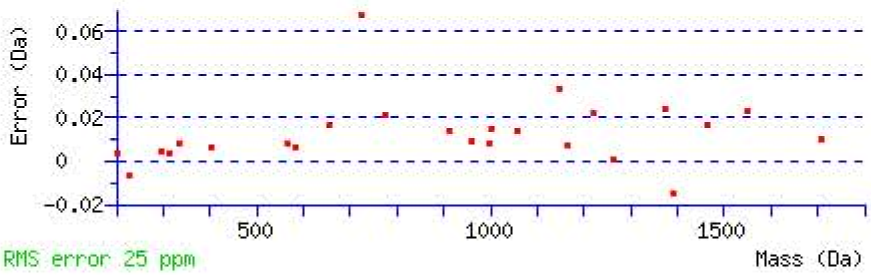
Match to Query 58701: 2220.062382 from(741.028070,3+) rtinseconds(2112) index(79267)
Title: Locus:1.1.1.2949.23 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

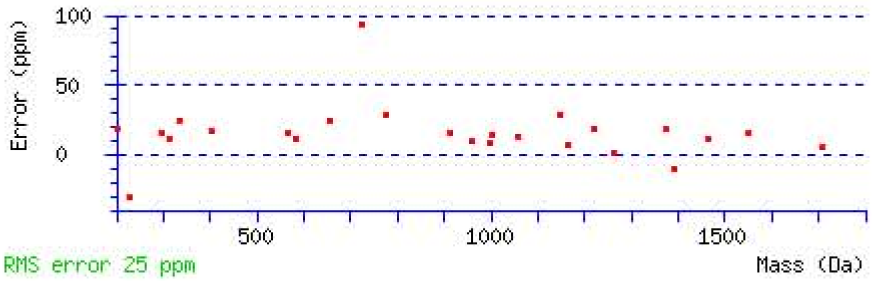
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2220.041092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00012
Matches : 25/160 fragment ions using 54 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							17
2	**227.175404**	114.091340					L	2107.964318	1054.485797	2090.937769	1045.972522	2089.953753	1045.480514	16
3	**298.212518**	149.609897					A	1994.880254	997.943765	1977.853705	989.430491	1976.869689	988.938483	15
4	399.260197	200.133737			381.249632	191.128454	T	1923.843140	962.425208	1906.816591	953.911934	1905.832575	953.419926	14
5	512.344261	256.675769			494.333696	247.670486	L	1822.795461	911.901369	1805.768912	903.388094	1804.784896	902.896086	13
6	672.374910	336.691093			654.364345	327.685811	C	***1709.711397***	855.359337	1692.684848	846.846062	1691.700832	846.354054	12
7	759.406938	380.207107			741.396373	371.201825	S	***1549.680748***	775.344012	1532.654199	766.830738	1531.670183	766.338730	11
8	830.444052	415.725664			812.433487	406.720382	A	***1462.648720***	731.827998	1445.622171	723.314724	1444.638155	722.822716	10
9	**959.486645**	480.246961			941.476080	471.241678	E	***1391.611606***	696.309441	1374.585057	687.796167	1373.601041	687.304159	9
10	**1058.555059**	529.781168			1040.544494	520.775885	V	***1262.569013***	631.788145	1245.542464	623.274870	1244.558448	622.782862	8
11	**1218.585708**	609.796492			1200.575143	600.791210	C	***1163.500599***	582.253938	1146.474050	573.740663	1145.490034	573.248655	7
12	1657.811034	829.409155	1640.784485	820.895881	1639.800469	820.403873	Q	***1003.469950***	502.238613	986.443401	493.725339	985.459385	493.233331	6
13	1817.841683	909.424480	1800.815134	900.911205	1799.831118	900.419197	C	***564.244624***	282.625950	547.218075	274.112676	546.234059	273.620668	5
14	1888.878797	944.943037	1871.852248	936.429762	1870.868232	935.937754	A	***404.213975***	202.610626	387.187426	194.097351	386.203410	193.605343	4
15	2017.921390	1009.464333	2000.894841	1000.951059	1999.910825	1000.459051	E	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	3
16	2074.942854	1037.975065	2057.916305	1029.461790	2056.932289	1028.969782	G	***204.134268***	102.570772	187.107719	94.057497			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.4	2220.041092	0.021290	LLATLCSAEVCQCAEGK

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

{MATRIX SCIENCE}

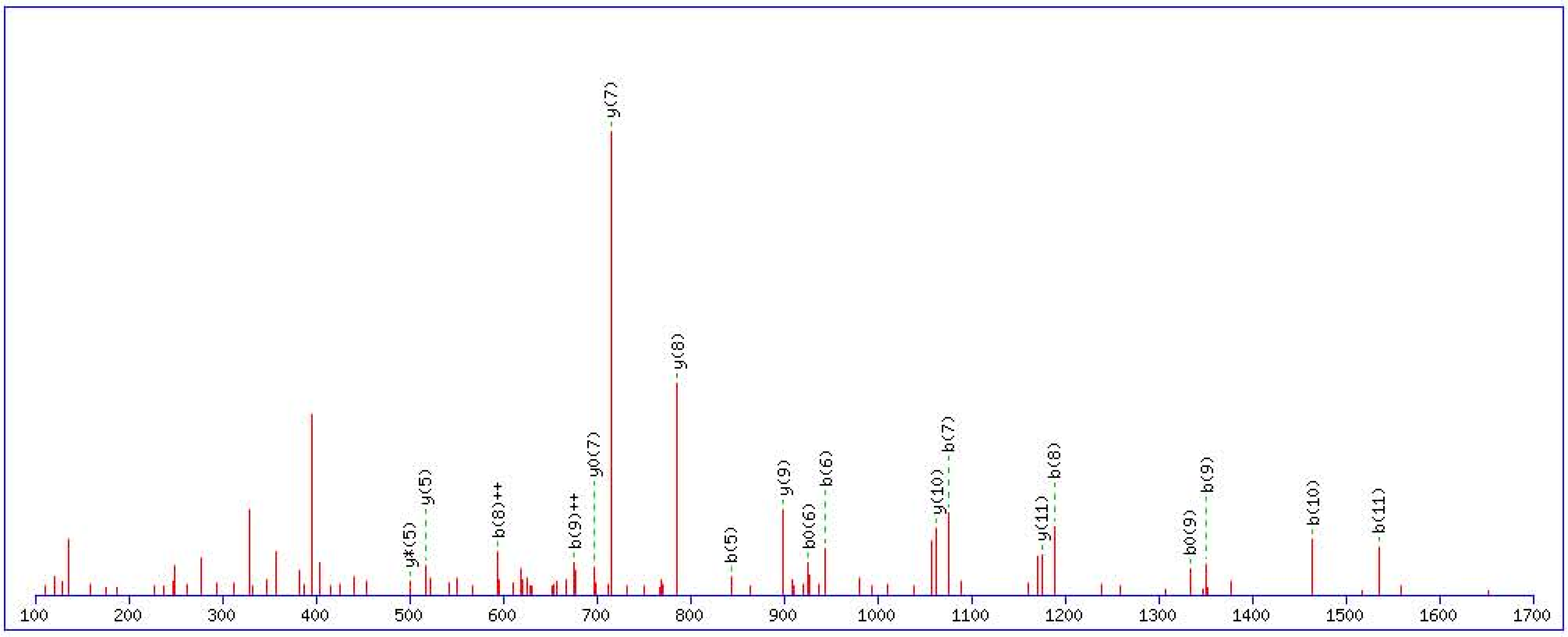
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GCGEQTMIYLAPTLAASR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

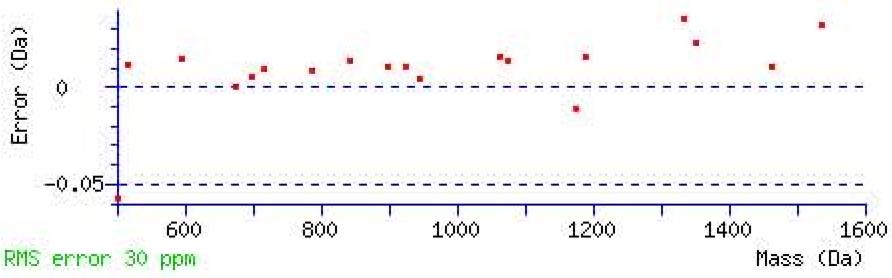
Match to Query 59329: 2249.133942 from(750.718590,3+) rtinseconds(2480) index(63895)
Title: Locus:1.1.1.3168.14 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

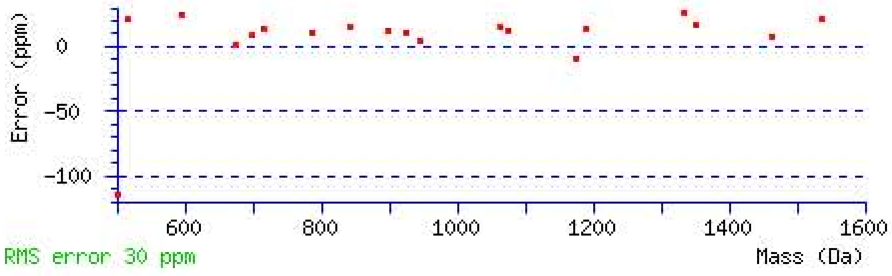
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2249.100647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0016
Matches : 19/188 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							18
2	218.059389	109.533333					C	2193.086482	1097.046879	2176.059933	1088.533604	2175.075917	1088.041596	17
3	275.080853	138.044064					G	2033.055833	1017.031555	2016.029284	1008.518280	2015.045268	1008.026272	16
4	404.123446	202.565361			386.112881	193.560079	E	1976.034369	988.520822	1959.007820	980.007548	1958.023804	979.515540	15
5	***843.348772***	422.178024	826.322223	413.664750	825.338207	413.172742	Q	1846.991776	923.999526	1829.965227	915.486251	1828.981211	914.994243	14
6	***944.396451***	472.701864	927.369902	464.188589	926.385886	463.696581	T	1407.766450	704.386863	1390.739901	695.873588	1389.755885	695.381580	13
7	***1075.436936***	538.222106	1058.410387	529.708832	1057.426371	529.216824	M	1306.718771	653.863023	1289.692222	645.349749	1288.708206	644.857741	12
8	***1188.521000***	**594.764138**	1171.494451	586.250864	1170.510435	585.758855	I	***1175.678286***	588.342781	1158.651737	579.829506	1157.667721	579.337498	11
9	***1351.584329***	**676.295803**	1334.557780	667.782528	1333.573764	667.290520	Y	***1062.594222***	531.800749	1045.567673	523.287475	1044.583657	522.795466	10
10	***1464.668393***	732.837834	1447.641844	724.324560	1446.657828	723.832552	L	***899.530893***	450.269084	882.504344	441.755810	881.520328	441.263802	9
11	***1535.705507***	768.356391	1518.678958	759.843117	1517.694942	759.351109	A	***786.446829***	393.727053	769.420280	385.213778	768.436264	384.721770	8
12	1632.758271	816.882773	1615.731722	808.369499	1614.747706	807.877491	P	***715.409715***	358.208496	698.383166	349.695221	697.399150	349.203213	7
13	1733.805950	867.406613	1716.779401	858.893339	1715.795385	858.401330	T	618.356951	309.682114	601.330402	301.168839	600.346386	300.676831	6
14	1846.890014	923.948645	1829.863465	915.435370	1828.879449	914.943362	L	***517.309272***	259.158274	500.282723	250.644999	499.298707	250.152991	5
15	1917.927128	959.467202	1900.900579	950.953927	1899.916563	950.461919	A	404.225208	202.616242	387.198659	194.102967	386.214643	193.610959	4
16	1988.964242	994.985759	1971.937693	986.472484	1970.953677	985.980476	A	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
17	2075.996270	1038.501773	2058.969721	1029.988498	2057.985705	1029.496490	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
18							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	2249.100647	0.033295	GCGEQTMIYLAPTLAASR
9.3	2249.115051	0.018891	YSTSLYASPSMVHEGVAVVPR
0.8	2249.137527	-0.003585	QKFERPICVSWSTDVKGGR
0.2	2249.143570	-0.009628	TPPPQPPLISSMDSISQK

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

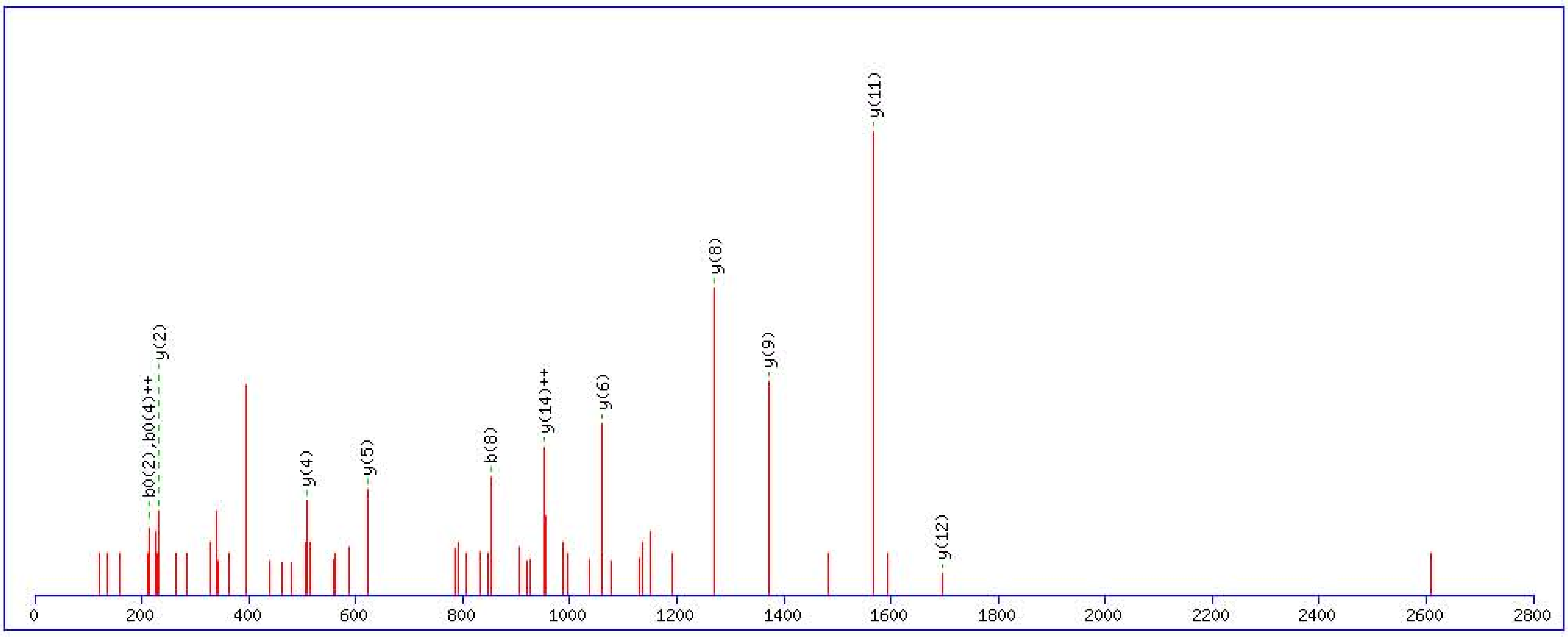
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DDPDAPLQPVTPLQLFEGR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

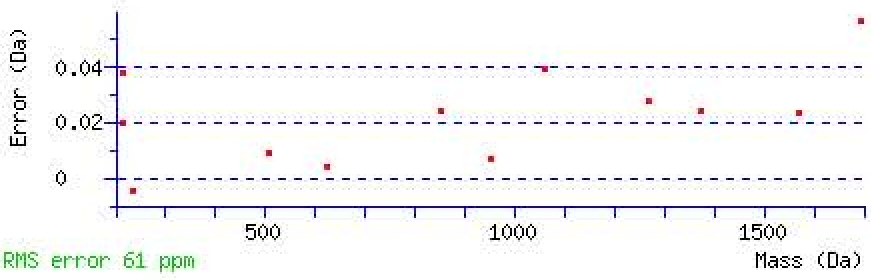
Match to Query 63019: 2418.258222 from(807.093350,3+) rtinseconds(2985) index(67691)
Title: Locus:1.1.1.3340.16 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

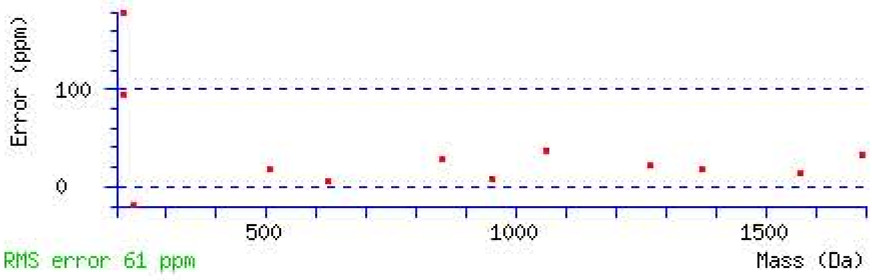
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2418.225342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00088
Matches : 12/198 fragment ions using 16 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							19
2	231.061162	116.034219			213.050597	107.028936	D	2304.205668	1152.606472	2287.179119	1144.093197	2286.195103	1143.601189	18
3	328.113926	164.560601			310.103361	155.555319	P	2189.178725	1095.093000	2172.152176	1086.579726	2171.168160	1086.087718	17
4	443.140869	222.074073			425.130304	213.068790	D	2092.125961	1046.566618	2075.099412	1038.053344	2074.115396	1037.561336	16
5	514.177983	257.592630			496.167418	248.587347	A	1977.099018	989.053147	1960.072469	980.539873	1959.088453	980.047865	15
6	611.230747	306.119012			593.220182	297.113729	P	1906.061904	953.534590	1889.035355	945.021316	1888.051339	944.529308	14
7	724.314811	362.661044			706.304246	353.655761	L	1809.009140	905.008208	1791.982591	896.494934	1790.998575	896.002926	13
8	852.373389	426.690333	835.346840	418.177058	834.362824	417.685050	Q	***1695.925076***	848.466176	1678.898527	839.952902	1677.914511	839.460894	12
9	949.426153	475.216715	932.399604	466.703440	931.415588	466.211432	P	***1567.866498***	784.436887	1550.839949	775.923613	1549.855933	775.431605	11
10	1048.494567	524.750922	1031.468018	516.237647	1030.484002	515.745639	V	1470.813734	735.910505	1453.787185	727.397231	1452.803169	726.905223	10
11	1149.542246	575.274761	1132.515697	566.761487	1131.531681	566.269479	T	***1371.745320***	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
12	1246.595010	623.801143	1229.568461	615.287869	1228.584445	614.795861	P	***1270.697641***	635.852459	1253.671092	627.339184	1252.687076	626.847176	8
13	1359.679074	680.343175	1342.652525	671.829901	1341.668509	671.337893	L	1173.644877	587.326077	1156.618328	578.812802	1155.634312	578.320794	7
14	1798.904400	899.955838	1781.877851	891.442564	1780.893835	890.950556	Q	***1060.560813***	530.784045	1043.534264	522.270770	1042.550248	521.778762	6
15	1911.988464	956.497870	1894.961915	947.984596	1893.977899	947.492588	L	***621.335487***	311.171382	604.308938	302.658107	603.324922	302.166099	5
16	2059.056878	1030.032077	2042.030329	1021.518803	2041.046313	1021.026794	F	***508.251423***	254.629350	491.224874	246.116075	490.240858	245.624067	4
17	2188.099471	1094.553373	2171.072922	1086.040099	2170.088906	1085.548091	E	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
18	2245.120935	1123.064105	2228.094386	1114.550831	2227.110370	1114.058823	G	***232.140416***	116.573846	215.113867	108.060571			2
19							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.4	2418.225342	0.032880	DDPDAPLQPVTPLQLFEGR
11.6	2418.225342	0.032880	DDPDAPLQPVTPLQLFEGR

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

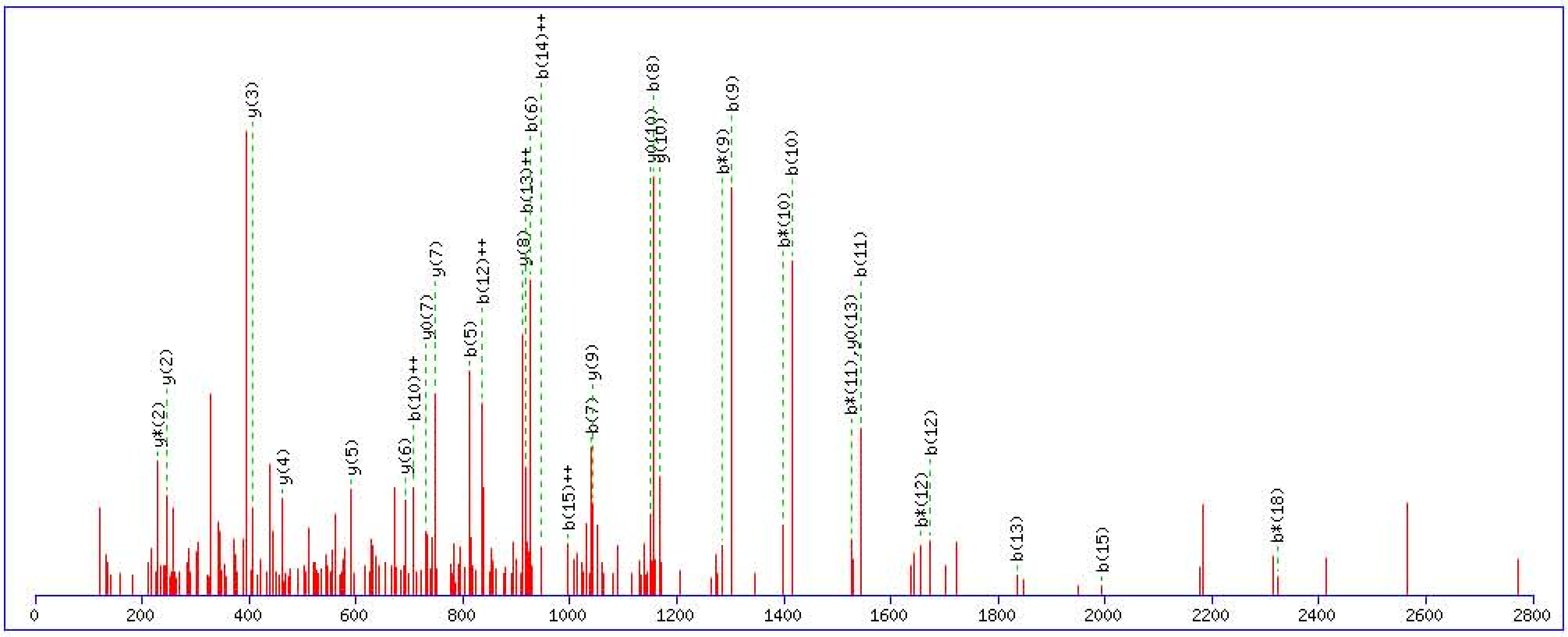
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AACAQLNDFLQEYGTQGCQV**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

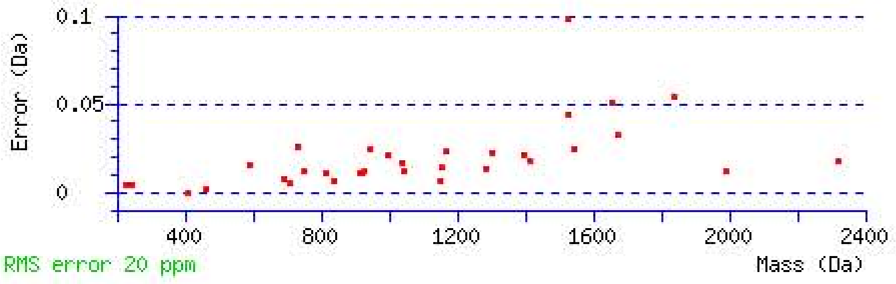
Match to Query 66392: 2583.193812 from(862.071880,3+) rtinseconds(2713) index(65399)
Title: Locus:1.1.1.3248.23 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

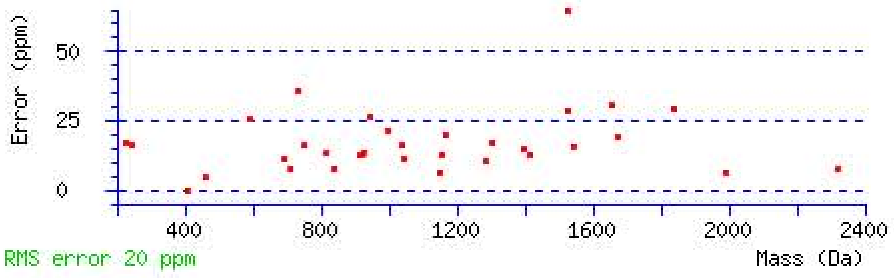
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2583.155624
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 1.8e-005
Matches : 33/194 fragment ions using 58 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							20
2	143.081504	72.044390					A	2513.125782	1257.066529	2496.099233	1248.553254	2495.115217	1248.061246	19
3	303.112153	152.059714					C	2442.088668	1221.547972	2425.062119	1213.034697	2424.078103	1212.542689	18
4	374.149267	187.578271					A	2282.058019	1141.532647	2265.031470	1133.019373	2264.047454	1132.527365	17
5	***813.374593***	407.190935	796.348044	398.677660			Q	2211.020905	1106.014090	2193.994356	1097.500816	2193.010340	1097.008808	16
6	***926.458657***	463.732967	909.432108	455.219692			L	1771.795579	886.401428	1754.769030	877.888153	1753.785014	877.396145	15
7	***1040.501584***	520.754430	1023.475035	512.241155			N	1658.711515	829.859396	1641.684966	821.346121	1640.700950	820.854113	14
8	***1155.528527***	578.267902	1138.501978	569.754627	1137.517962	569.262619	D	1544.668588	772.837932	1527.642039	764.324658	1526.658023	763.832650	13
9	***1302.596941***	651.802109	1285.570392	643.288834	1284.586376	642.796826	F	1429.641645	715.324460	1412.615096	706.811186	1411.631080	706.319178	12
10	***1415.681005***	**708.344141**	1398.654456	699.830866	1397.670440	699.338858	L	1282.573231	641.790253	1265.546682	633.276979	1264.562666	632.784971	11
11	***1543.739583***	772.373430	1526.713034	763.860155	1525.729018	763.368147	Q	***1169.489167***	585.248222	1152.462618	576.734947	1151.478602	576.242939	10
12	***1672.782176***	**836.894726**	1655.755627	828.381452	1654.771611	827.889444	E	***1041.430589***	521.218932	1024.404040	512.705658	1023.420024	512.213650	9
13	***1835.845505***	**918.426391**	1818.818956	909.913116	1817.834940	909.421108	Y	***912.387996***	456.697636	895.361447	448.184361	894.377431	447.692353	8
14	1892.866969	**946.937123**	1875.840420	938.423848	1874.856404	937.931840	G	***749.324667***	375.165971	732.298118	366.652697	731.314102	366.160689	7
15	***1993.914648***	**997.460962**	1976.888099	988.947688	1975.904083	988.455680	T	***692.303203***	346.655239	675.276654	338.141965	674.292638	337.649957	6
16	2121.973226	1061.490251	2104.946677	1052.976976	2103.962661	1052.484968	Q	***591.255524***	296.131400	574.228975	287.618125			5
17	2178.994690	1090.000983	2161.968141	1081.487708	2160.984125	1080.995700	G	***463.196946***	232.102111	446.170397	223.588836			4
18	2339.025339	1170.016307	2321.998790	1161.503033	2321.014774	1161.011025	C	***406.175482***	203.591379	389.148933	195.078104			3
19	2467.083917	1234.045596	2450.057368	1225.532322	2449.073352	1225.040314	Q	***246.144833***	123.576054	229.118284	115.062780			2
20							V	118.086255	59.546765					1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	2583.155624	0.038188	AACAQLNDFLQEYGTQGCQV
19.8	2583.155624	0.038188	AACAQLNDFLQEYGTQGCQV

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

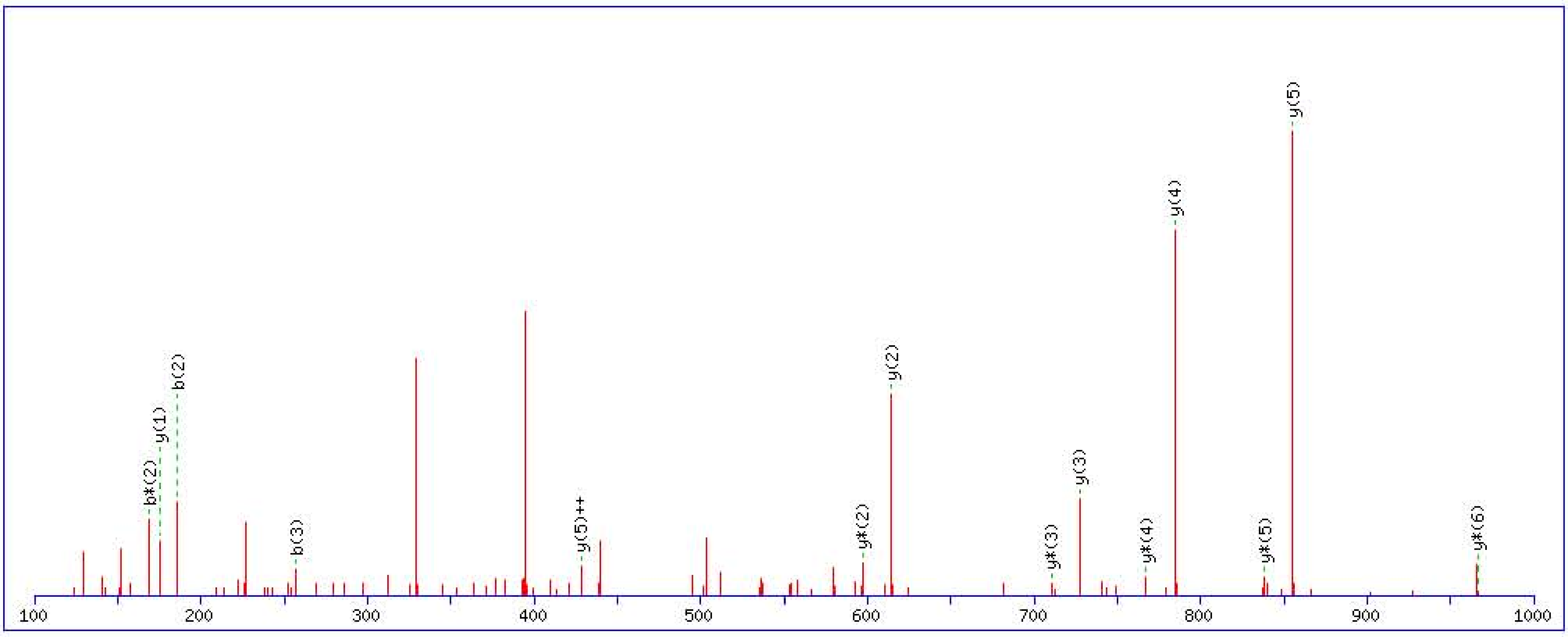
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQAGLQR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

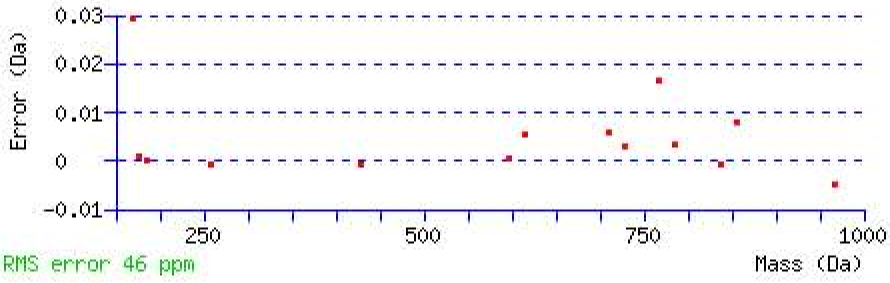
Match to Query 20649: 1039.558928 from(520.786740,2+) rtinseconds(1388) index(56120)
Title: Locus:1.1.1.2789.12 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

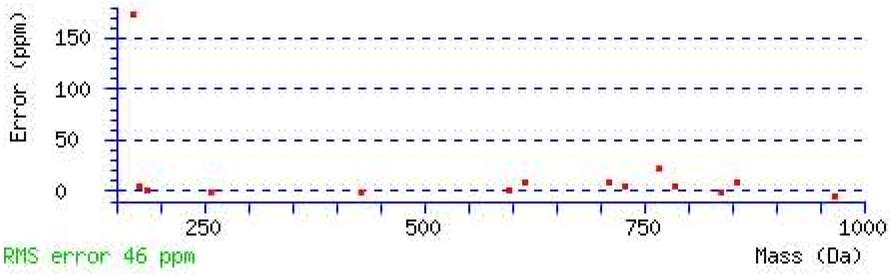
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1039.559677
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.034
Matches : 14/46 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	58.028740	29.518008			G					7
2	**186.087318**	93.547297	169.060769	85.034023	Q	983.545498	492.276387	966.518949	483.763113	6
3	**257.124432**	129.065854	240.097883	120.552580	A	***855.486920***	428.247098	838.460371	419.733824	5
4	314.145896	157.576586	297.119347	149.063312	G	***784.449806***	392.728541	767.423257	384.215267	4
5	427.229960	214.118618	410.203411	205.605344	L	***727.428342***	364.217809	710.401793	355.704535	3
6	866.455286	433.731281	849.428737	425.218007	Q	***614.344278***	307.675777	597.317729	299.162503	2
7					R	***175.118952***	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.0	1039.559677	-0.000749	GQAGLQR
10.6	1039.559677	-0.000749	GQQIQR
3.5	1039.559677	-0.000749	KGGPSQR
3.3	1039.552277	0.006651	QRAALDGGPR
3.2	1039.548431	0.010497	SPEIQR
2.9	1039.552277	0.006651	GQPQELGRR
2.0	1039.563492	-0.004564	AEGARARGPR
1.7	1039.548431	0.010497	LSPEQR

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

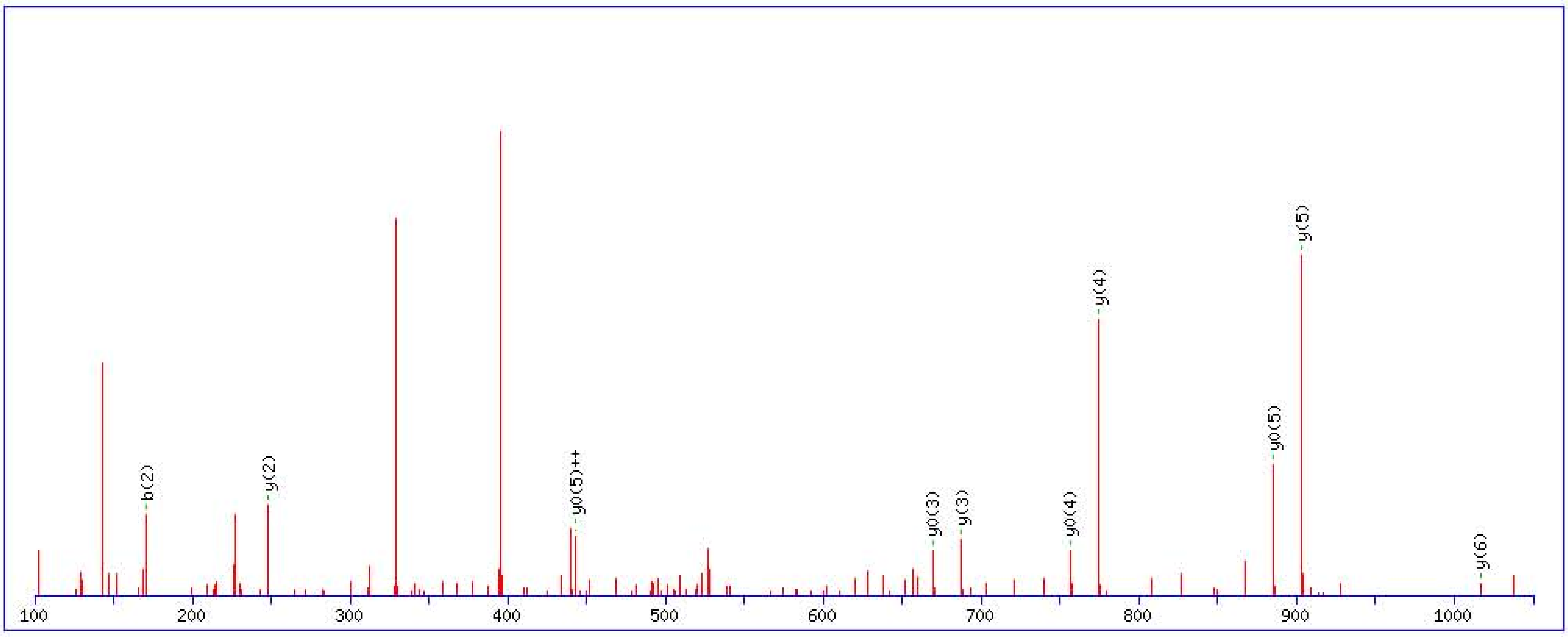
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLESQTK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

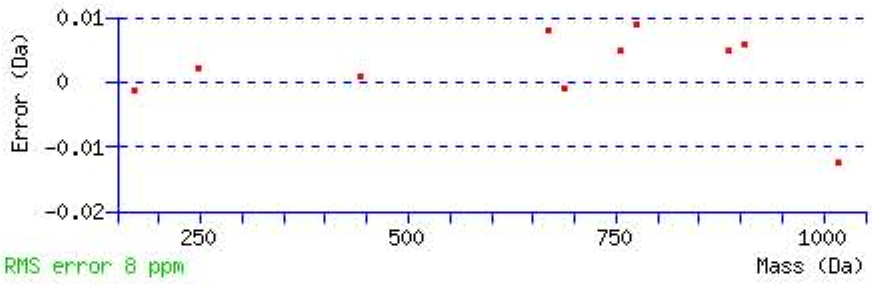
Match to Query 21733: 1072.563828 from(537.289190,2+) rtinseconds(1411) index(56302)
Title: Locus:1.1.1.2797.16 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

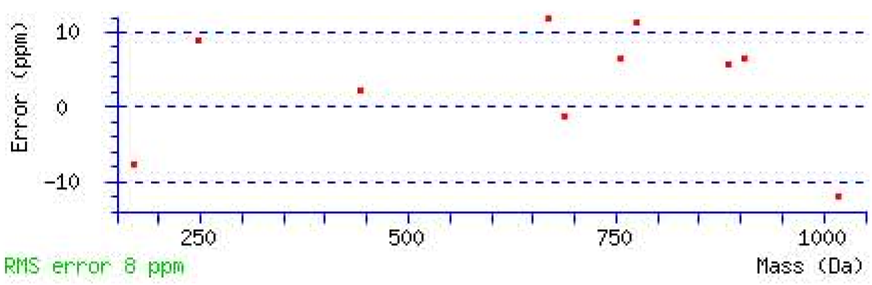
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1072.558670
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.039
Matches : 10/58 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							7
2	171.112804	86.060040					L	***1016.544494***	508.775885	999.517945	500.262611	998.533929	499.770603	6
3	300.155397	150.581336			282.144832	141.576054	E	***903.460430***	452.233853	886.433881	443.720579	885.449865	443.228571	5
4	387.187425	194.097351			369.176860	185.092068	S	***774.417837***	387.712557	757.391288	379.199282	756.407272	378.707274	4
5	826.412751	413.710014	809.386202	405.196739	808.402186	404.704731	Q	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
6	927.460430	464.233853	910.433881	455.720579	909.449865	455.228571	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
7							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.8	1072.558670	0.005158	GLESQTK
10.3	1072.558670	0.005158	LGECPAVLSK
6.1	1072.558670	0.005158	QSEGLTK
5.7	1072.551254	0.012574	KEAPRDETK
3.6	1072.576431	-0.012603	VAEGQTLDLK
3.3	1072.576447	-0.012619	LGGVLPDSTSK
3.1	1072.552155	0.011673	QSCVLR
2.6	1072.576462	-0.012634	TVVQEVVDGK
2.1	1072.551285	0.012543	GPRTTEPSTK

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

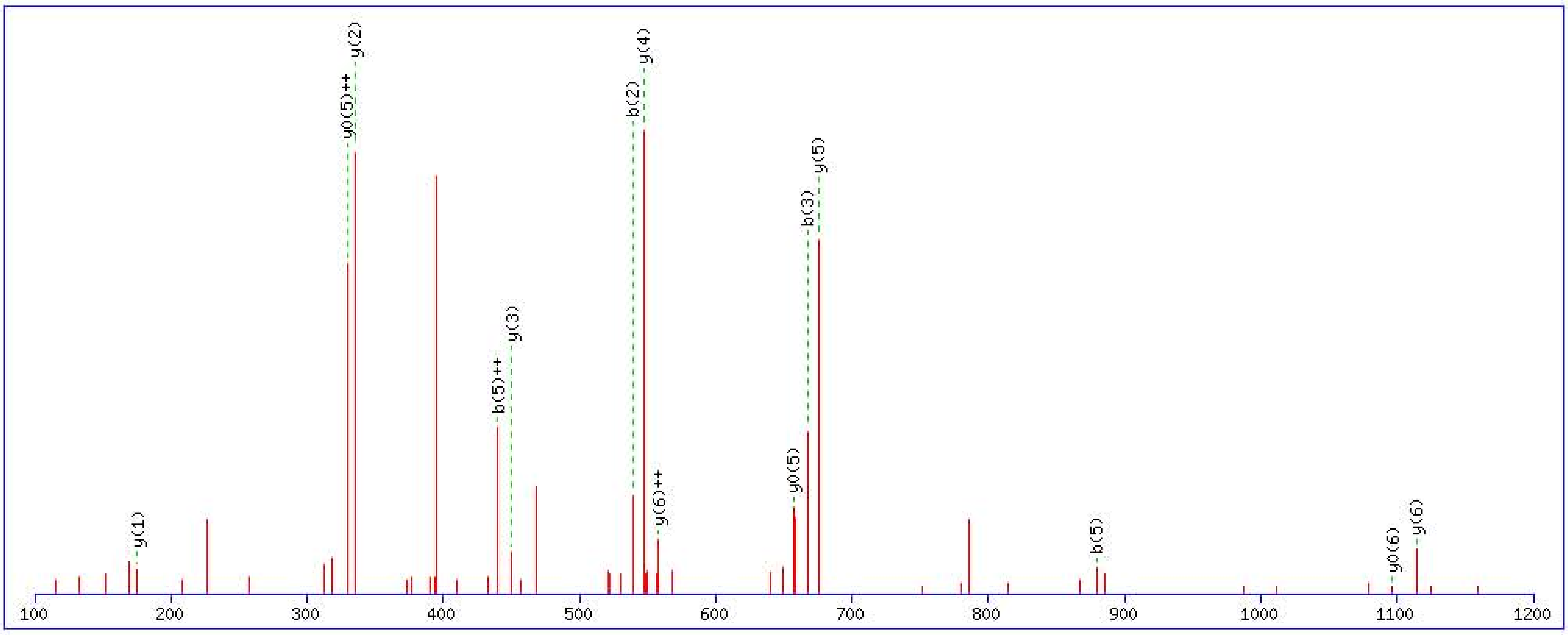
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQQPDCR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

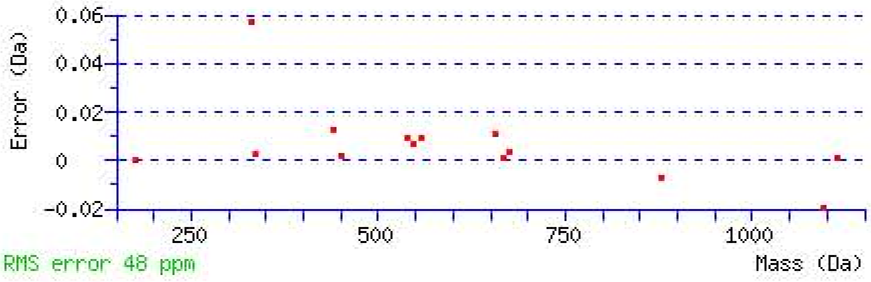
Match to Query 28041: 1212.578148 from(607.296350,2+) rtinseconds(1245) index(55163)
Title: Locus:1.1.1.2739.24 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

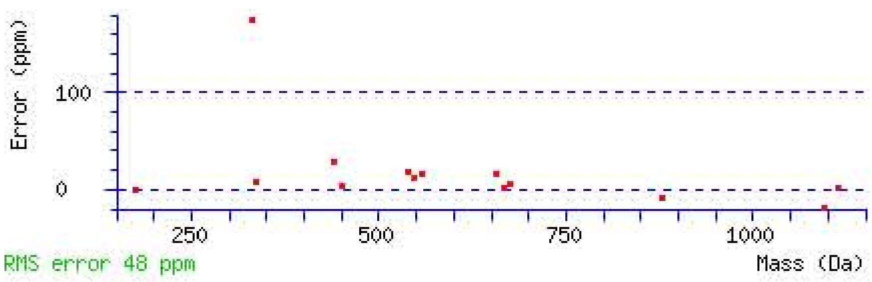
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1212.574356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0087
Matches : 14/58 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							7
2	**539.301016**	270.154146	522.274467	261.640872			Q	***1114.513212***	557.760244	1097.486663	549.246970	1096.502647	548.754962	6
3	**667.359594**	334.183435	650.333045	325.670161			Q	***675.287886***	338.147581	658.261337	329.634307	657.277321	329.142299	5
4	764.412358	382.709817	747.385809	374.196543			P	***547.229308***	274.118292	530.202759	265.605018	529.218743	265.113010	4
5	**879.439301**	440.223289	862.412752	431.710014	861.428736	431.218006	D	***450.176544***	225.591910	433.149995	217.078635	432.165979	216.586627	3
6	1039.469950	520.238613	1022.443401	511.725339	1021.459385	511.233331	C	***335.149601***	168.078438	318.123052	159.565164			2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.7	1212.574356	0.003792	VQQPDCR
13.3	1212.574356	0.003792	VQQPDCR
5.7	1212.596115	-0.017967	YFVEAGAMAVR

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

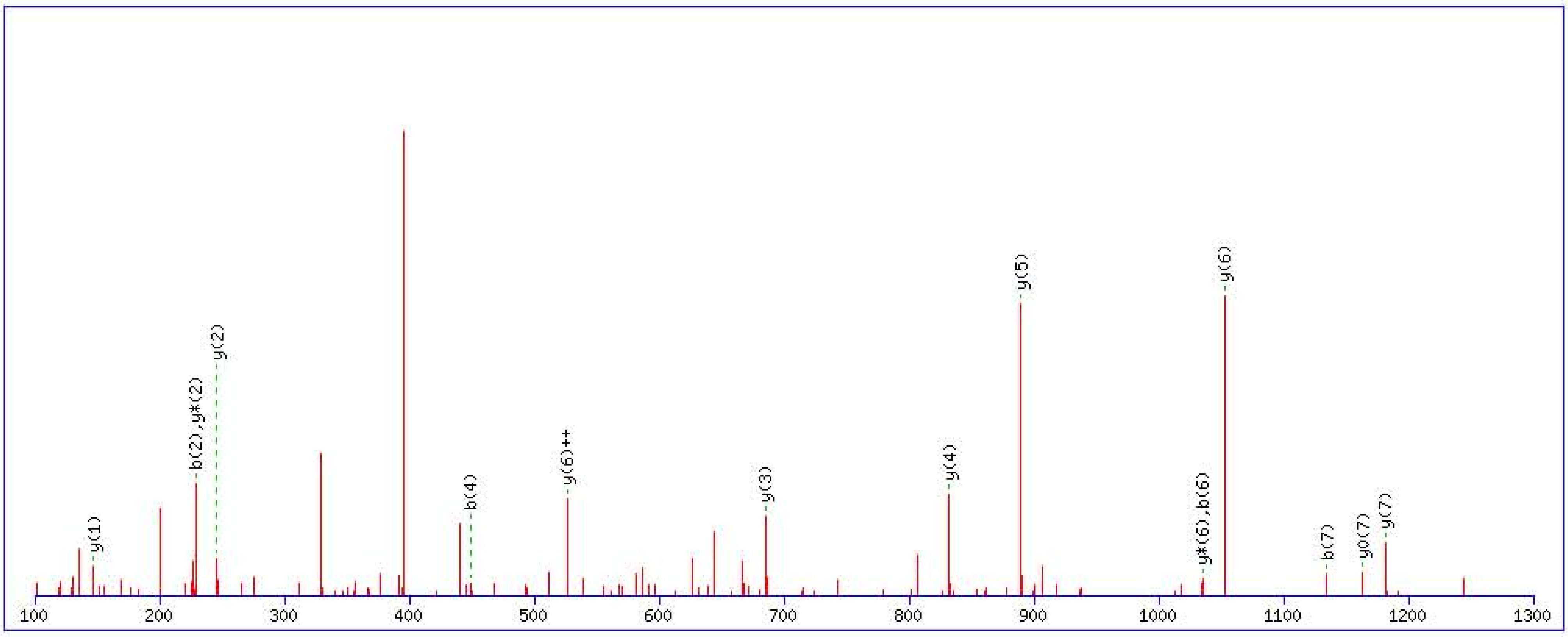
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEYGFQVK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

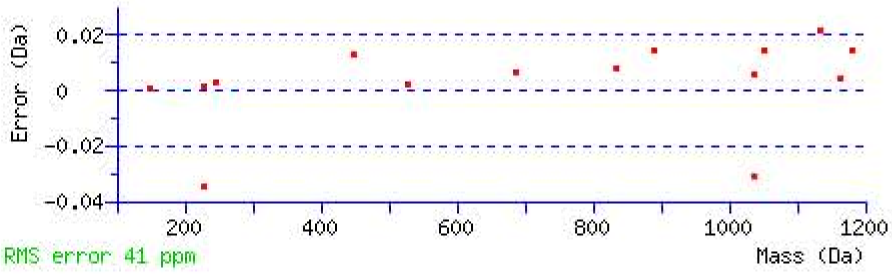
Match to Query 30241: 1279.673988 from(640.844270,2+) rtinseconds(1956) index(60240)
Title: Locus:1.1.1.2986.11 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

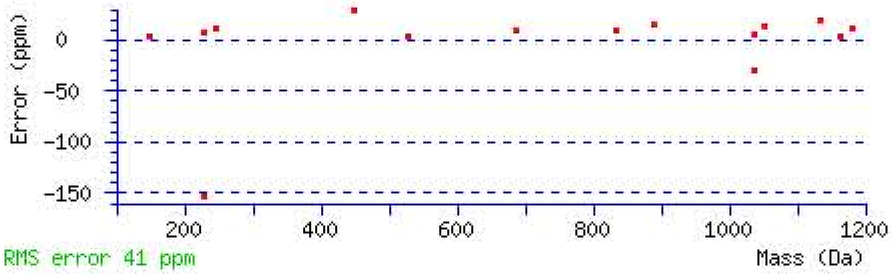
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1279.663483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0078
Matches : 15/60 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							8
2	**229.118283**	115.062780			211.107718	106.057497	E	***1181.602344***	591.304810	1164.575795	582.791536	1163.591779	582.299528	7
3	392.181612	196.594444			374.171047	187.589162	Y	***1052.559751***	526.783514	1035.533202	518.270239			6
4	**449.203076**	225.105176			431.192511	216.099894	G	***889.496422***	445.251849	872.469873	436.738575			5
5	596.271490	298.639383			578.260925	289.634101	F	***832.474958***	416.741117	815.448409	408.227843			4
6	**1035.496816**	518.252046	1018.470267	509.738772	1017.486251	509.246764	Q	***685.406544***	343.206910	668.379995	334.693636			3
7	**1134.565230**	567.786253	1117.538681	559.272979	1116.554665	558.780971	V	***246.181218***	123.594247	229.154669	115.080973			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.4	1279.663483	0.010505	VEYGFQVK
8.5	1279.684601	-0.010613	MSASAVFILDVK
7.6	1279.681229	-0.007241	EVTVKEWYVK
6.6	1279.677216	-0.003228	VFKTEDTQGKK
6.4	1279.663483	0.010505	QFVGYLDK
5.1	1279.659470	0.014518	VCSFGKQVVEK
4.9	1279.684601	-0.010613	TKPLMTEFSVK
1.3	1279.687958	-0.013970	LIKSMESVMVK
1.0	1279.666824	0.007164	VKEWSLMIMK

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

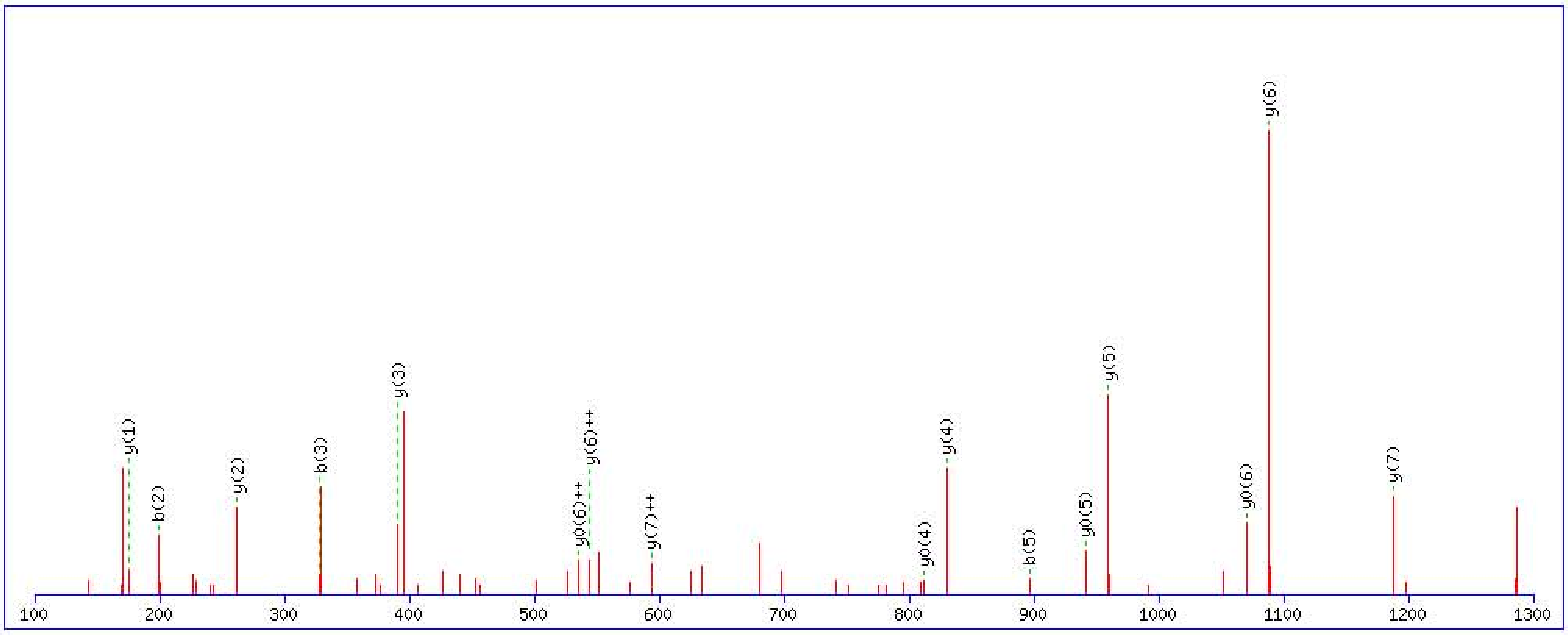
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVEEQESR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

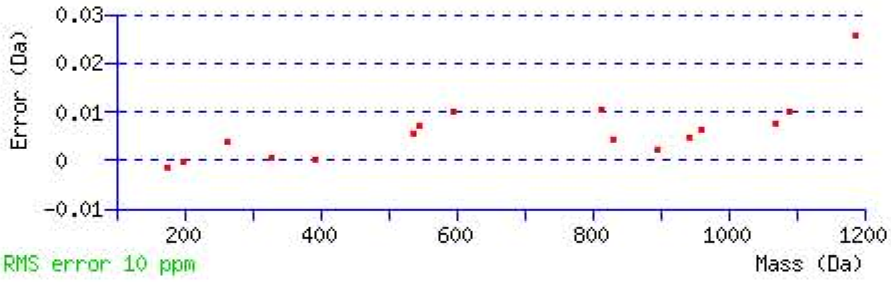
Match to Query 30578: 1285.641668 from(643.828110,2+) rtinseconds(1333) index(55718)
Title: Locus:1.1.1.2770.17 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

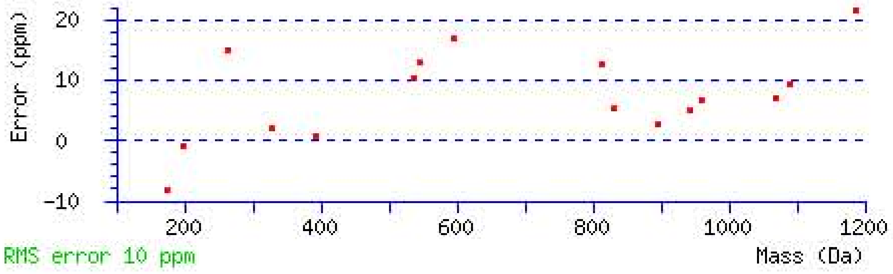
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1285.633621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0017
Matches : 16/70 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	**199.144104**	100.075690					V	***1187.572499***	594.289888	1170.545950	585.776613	1169.561934	585.284605	7
3	**328.186697**	164.596987			310.176132	155.591704	E	***1088.504085***	544.755681	1071.477536	536.242406	1070.493520	535.750398	6
4	457.229290	229.118283			439.218725	220.113001	E	***959.461492***	480.234384	942.434943	471.721110	941.450927	471.229102	5
5	**896.454616**	448.730946	879.428067	440.217672	878.444051	439.725664	Q	***830.418899***	415.713088	813.392350	407.199813	812.408334	406.707805	4
6	1025.497209	513.252243	1008.470660	504.738968	1007.486644	504.246960	E	***391.193573***	196.100425	374.167024	187.587150	373.183008	187.095142	3
7	1112.529237	556.768257	1095.502688	548.254982	1094.518672	547.762974	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	1285.633621	0.008047	VVEEQESR

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

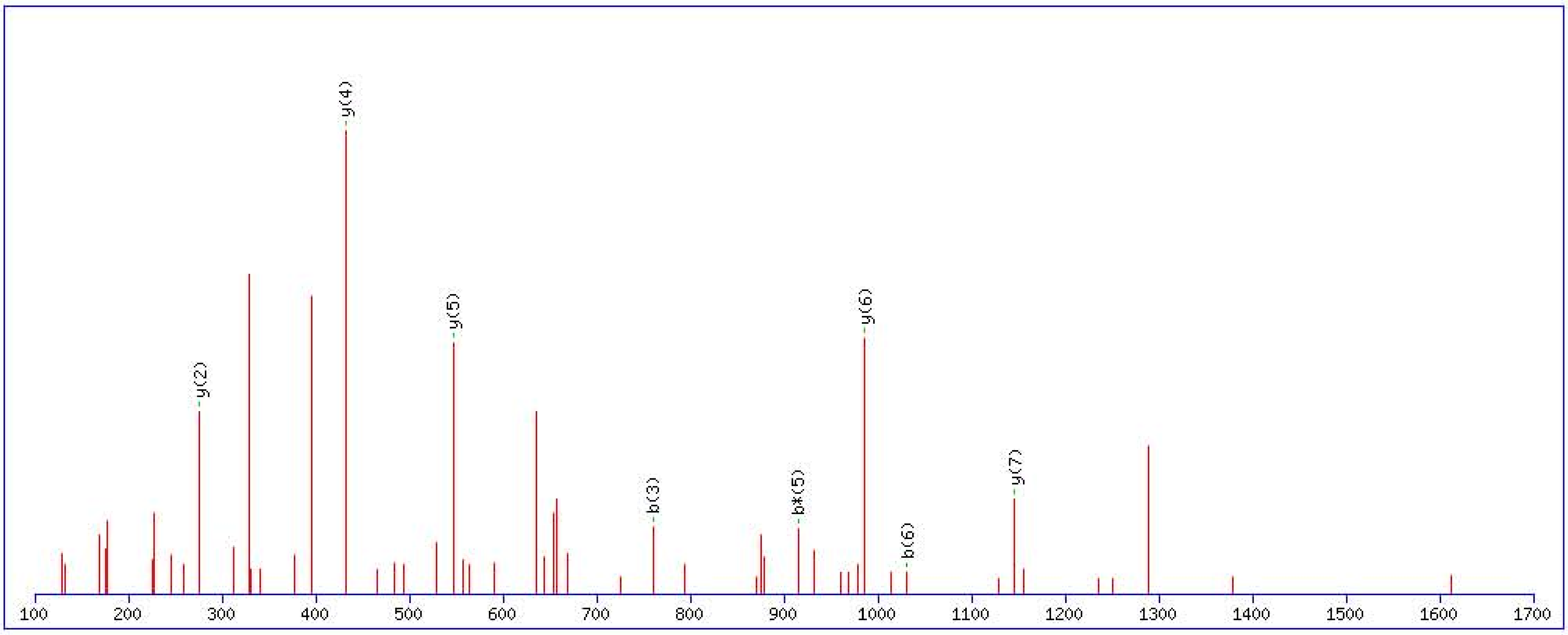
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CCQDGVTR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

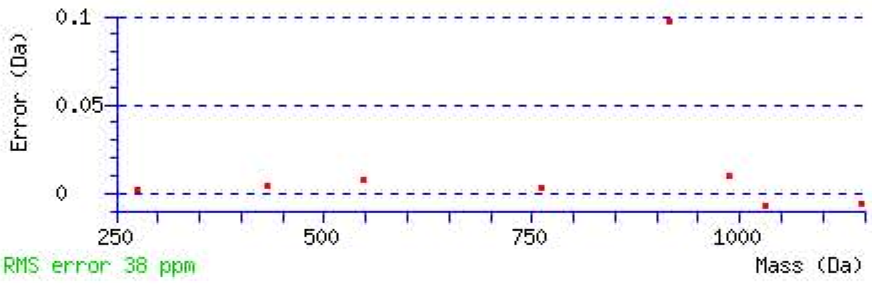
Match to Query 31054: 1305.572508 from(653.793530,2+) rtinseconds(1349) index(55787)
Title: Locus:1.1.1.2775.14 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

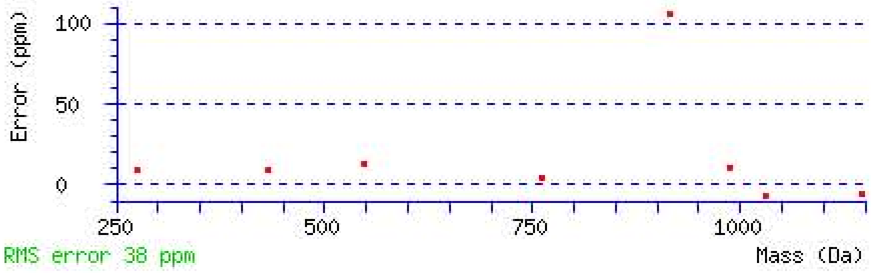
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1305.562820
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.0012
Matches : 8/72 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600					C							8
2	321.068574	161.037925					C	***1146.539427***	573.773352	1129.512878	565.260077	1128.528862	564.768069	7
3	**760.293900**	380.650588	743.267351	372.137314			Q	***986.508778***	493.758027	969.482229	485.244753	968.498213	484.752745	6
4	875.320843	438.164060	858.294294	429.650785	857.310278	429.158777	D	***547.283452***	274.145364	530.256903	265.632090	529.272887	265.140082	5
5	932.342307	466.674792	915.315758	458.161517	914.331742	457.669509	G	***432.256509***	216.631893	415.229960	208.118618	414.245944	207.626610	4
6	**1031.410721**	516.208999	1014.384172	507.695724	1013.400156	507.203716	V	375.235045	188.121161	358.208496	179.607886	357.224480	179.115878	3
7	1132.458400	566.732838	1115.431851	558.219564	1114.447835	557.727556	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
8							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.1	1305.562820	0.009688	CCQDGVTR
8.8	1305.588409	-0.015901	CRSSTPADAWR
2.8	1305.577194	-0.004686	CDAGWLADGSVR

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

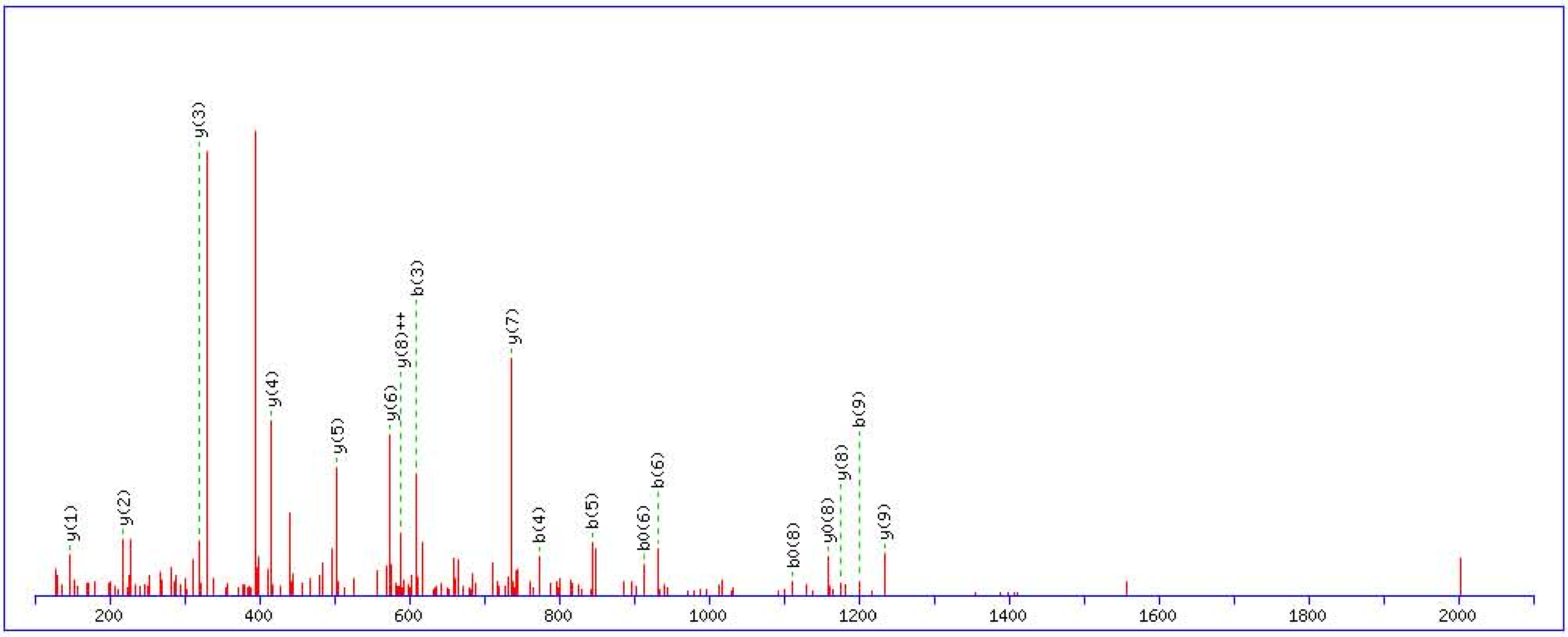
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGQYASPTAK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

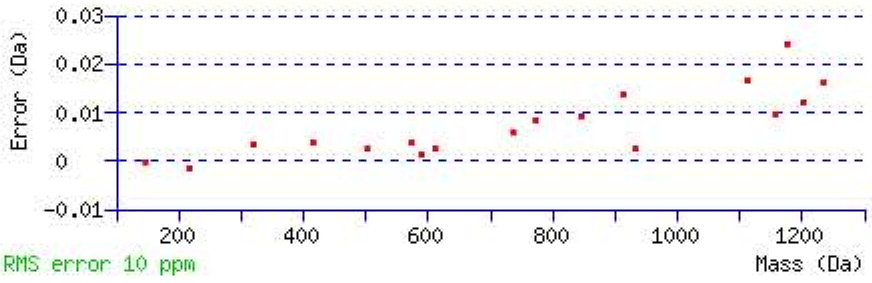
Match to Query 31920: 1345.714648 from(673.864600,2+) rtinseconds(1540) index(57248)
Title: Locus:1.1.1.2842.15 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

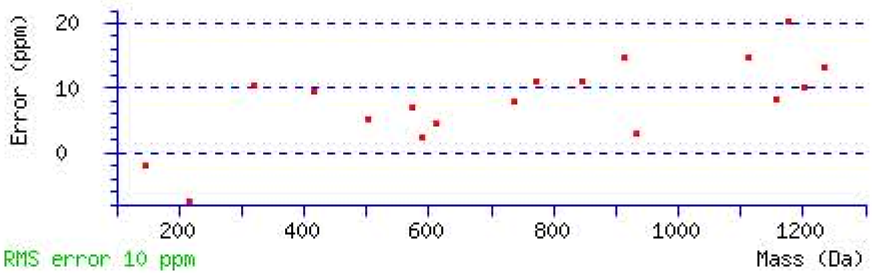
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1345.706390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 5.3e-005
Matches : 18/90 fragment ions using 35 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							10
2	171.112804	86.060040					G	*1233.629622*	617.318449	1216.603073	608.805175	1215.619057	608.313167	9
3	**610.338130**	305.672703	593.311581	297.159429			Q	*1176.608158*	588.807717	1159.581609	580.294443	1158.597593	579.802435	8
4	**773.401459**	387.204368	756.374910	378.691093			Y	*737.382832*	369.195054	720.356283	360.681780	719.372267	360.189772	7
5	**844.438573**	422.722925	827.412024	414.209650			A	*574.319503*	287.663389	557.292954	279.150115	556.308938	278.658107	6
6	**931.470601**	466.238939	914.444052	457.725664	913.460036	457.233656	S	*503.282389*	252.144832	486.255840	243.631558	485.271824	243.139550	5
7	1028.523365	514.765321	1011.496816	506.252046	1010.512800	505.760038	P	*416.250361*	208.628818	399.223812	200.115544	398.239796	199.623536	4
8	1129.571044	565.289160	1112.544495	556.775886	1111.560479	556.283878	T	*319.197597*	160.102436	302.171048	151.589162	301.187032	151.097154	3
9	**1200.608158**	600.807717	1183.581609	592.294443	1182.597593	591.802435	A	*218.149918*	109.578597	201.123369	101.065322			2
10							K	*147.112804*	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.6	1345.706390	0.008258	LGQYASPTAK
9.5	1345.706390	0.008258	LGQYDQALK
9.2	1345.724182	-0.009534	LGAVPATSGPTTFK
8.3	1345.706406	0.008242	QGLYTPQTK
5.6	1345.727509	-0.012861	LGLMDNEIKVAK
2.0	1345.717636	-0.002988	QMPQPTFTLRK

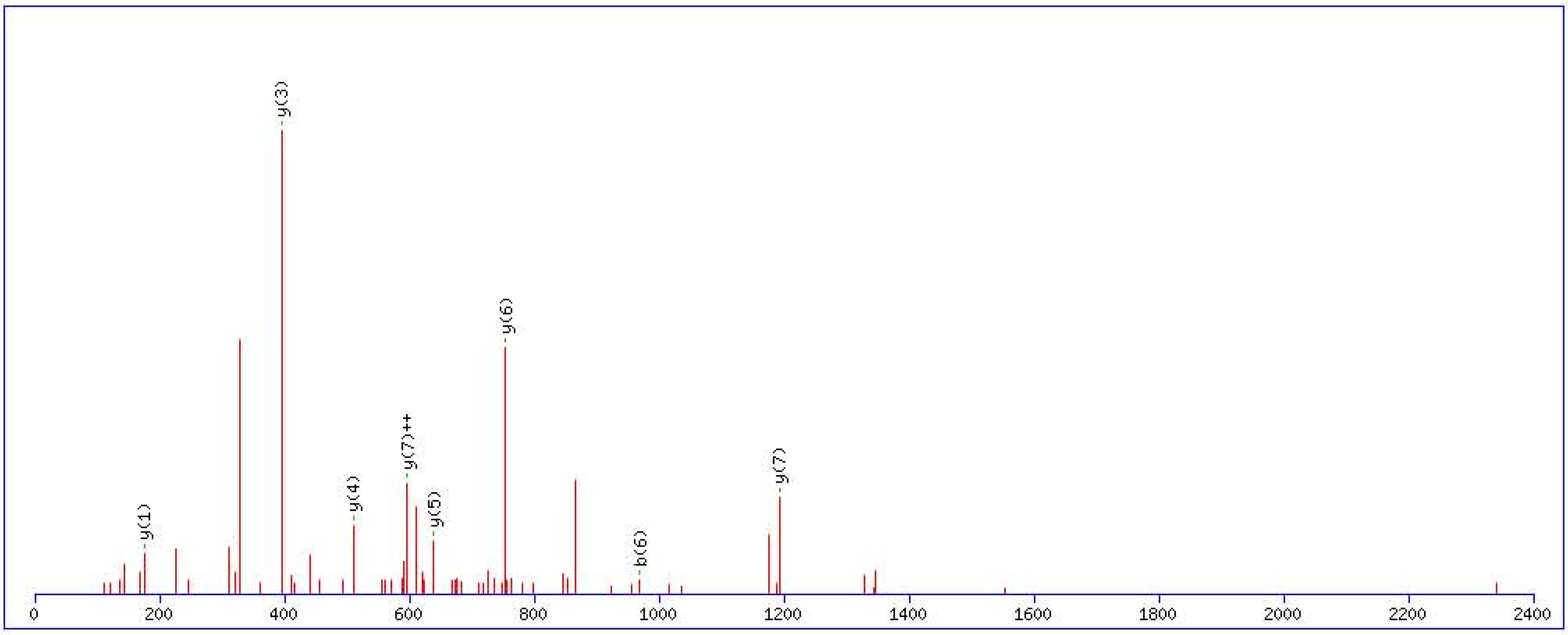
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLQDEDGYR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

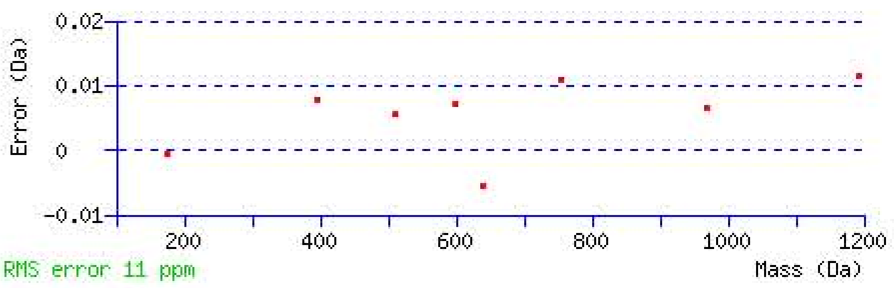
Match to Query 33236: 1362.630168 from(682.322360,2+) rtinseconds(1683) index(58185)
Title: Locus:1.1.1.2892.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

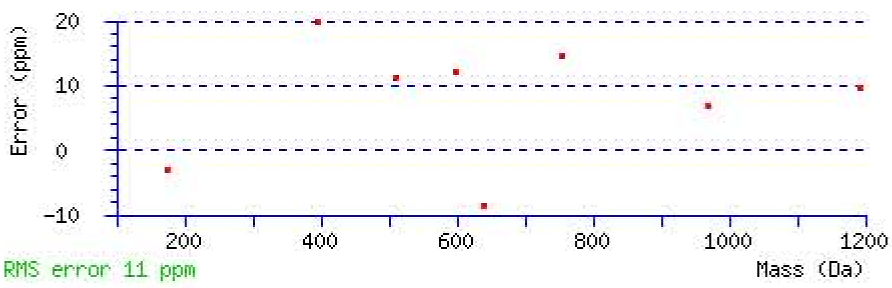
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1362.623795
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 47 **Expect:** 7.7e-005
Matches : 8/80 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							9
2	171.112804	86.060040					L	1306.609614	653.808445	1289.583065	645.295171	1288.599049	644.803163	8
3	610.338130	305.672703	593.311581	297.159429			Q	***1193.525550***	597.266413	1176.499001	588.753139	1175.514985	588.261131	7
4	725.365073	363.186175	708.338524	354.672900	707.354508	354.180892	D	***754.300224***	377.653750	737.273675	369.140476	736.289659	368.648468	6
5	854.407666	427.707471	837.381117	419.194197	836.397101	418.702189	E	***639.273281***	320.140279	622.246732	311.627004	621.262716	311.134996	5
6	**969.434609**	485.220943	952.408060	476.707668	951.424044	476.215660	D	***510.230688***	255.618982	493.204139	247.105707	492.220123	246.613700	4
7	1026.456073	513.731675	1009.429524	505.218400	1008.445508	504.726392	G	***395.203745***	198.105511	378.177196	189.592236			3
8	1189.519402	595.263339	1172.492853	586.750065	1171.508837	586.258057	Y	338.182281	169.594778	321.155732	161.081504			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.6	1362.623795	0.006373	GLQDEDGYR
2.5	1362.623795	0.006373	TGFLEIDEHMR
0.1	1362.613251	0.016917	MGAGATGRAMDGPR

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

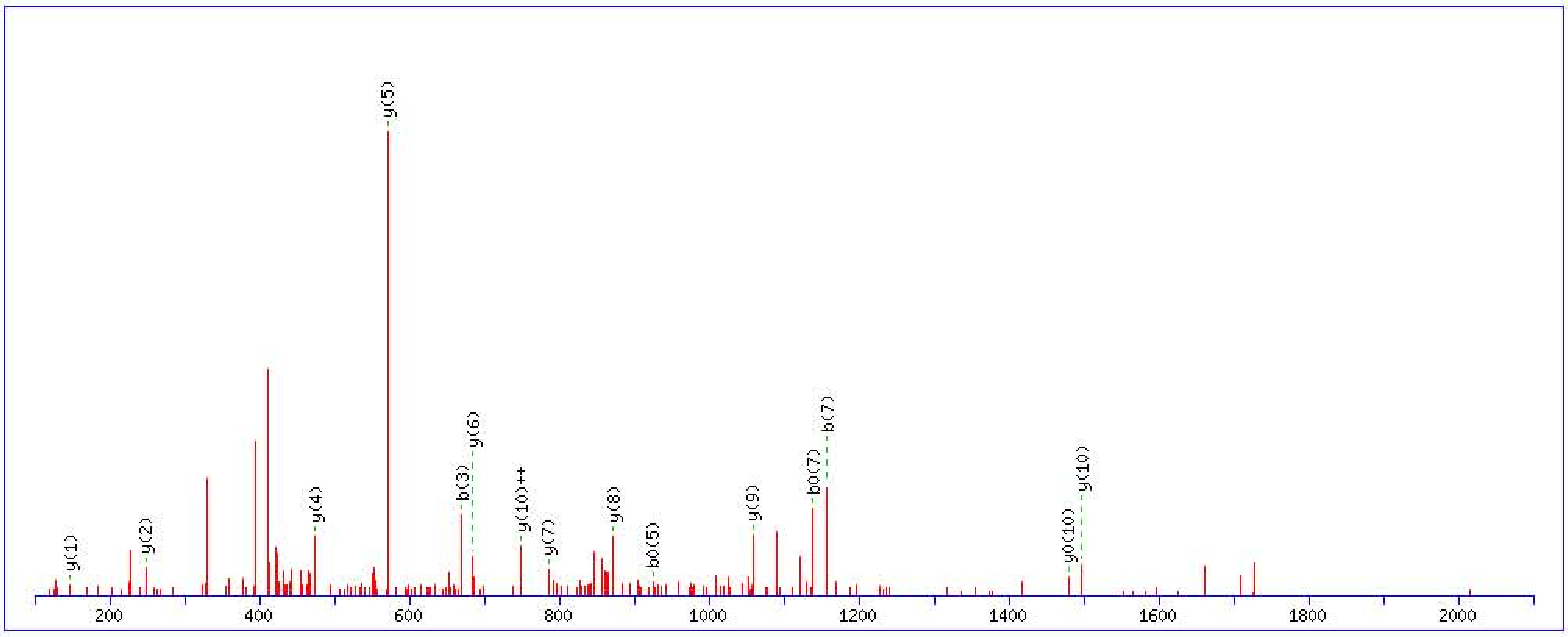
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEQWSTLPPETK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

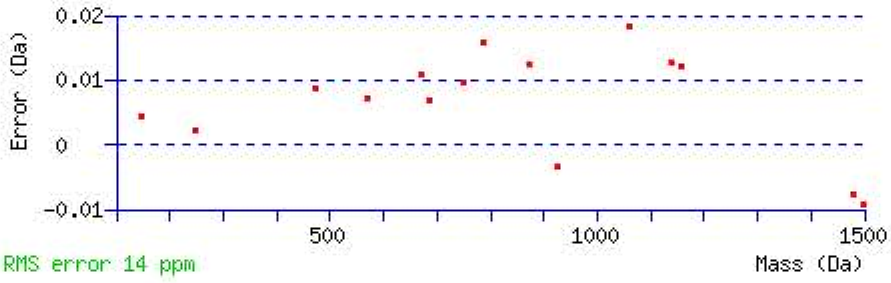
Match to Query 46460: 1726.877708 from(864.446130,2+) rtinseconds(2031) index(60756)
Title: Locus:1.1.1.3012.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

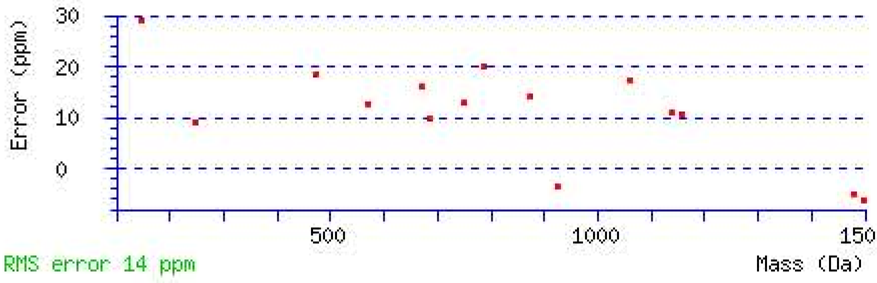
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1726.860001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 5.9e-005
Matches : 15/126 fragment ions using 33 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.054955	51.531116			84.044390	42.525833	T							12
2	231.097548	116.052412			213.086983	107.047130	E	1626.819607	813.913442	1609.793058	805.400167	1608.809042	804.908159	11
3	**670.322874**	335.665075	653.296325	327.151801	652.312309	326.659793	Q	***1497.777014***	749.392145	1480.750465	740.878871	1479.766449	740.386863	10
4	856.402187	428.704732	839.375638	420.191457	838.391622	419.699449	W	***1058.551688***	529.779482	1041.525139	521.266208	1040.541123	520.774200	9
5	943.434215	472.220746	926.407666	463.707471	925.423650	463.215463	S	***872.472375***	436.739826	855.445826	428.226551	854.461810	427.734543	8
6	1044.481894	522.744585	1027.455345	514.231311	1026.471329	513.739303	T	***785.440347***	393.223812	768.413798	384.710537	767.429782	384.218529	7
7	**1157.565958**	579.286617	1140.539409	570.773343	1139.555393	570.281334	L	***684.392668***	342.699972	667.366119	334.186698	666.382103	333.694690	6
8	1254.618722	627.812999	1237.592173	619.299725	1236.608157	618.807716	P	***571.308604***	286.157940	554.282055	277.644666	553.298039	277.152658	5
9	1351.671486	676.339381	1334.644937	667.826107	1333.660921	667.334098	P	***474.255840***	237.631558	457.229291	229.118284	456.245275	228.626276	4
10	1480.714079	740.860678	1463.687530	732.347403	1462.703514	731.855395	E	377.203076	189.105176	360.176527	180.591902	359.192511	180.099894	3
11	1581.761758	791.384517	1564.735209	782.871243	1563.751193	782.379235	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.3	1726.860001	0.017707	TEQWSTLPPETK
4.0	1726.867188	0.010520	KDHAEMQAVIDAKQK
0.6	1726.853485	0.024223	MASGHAFQPDLVK

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

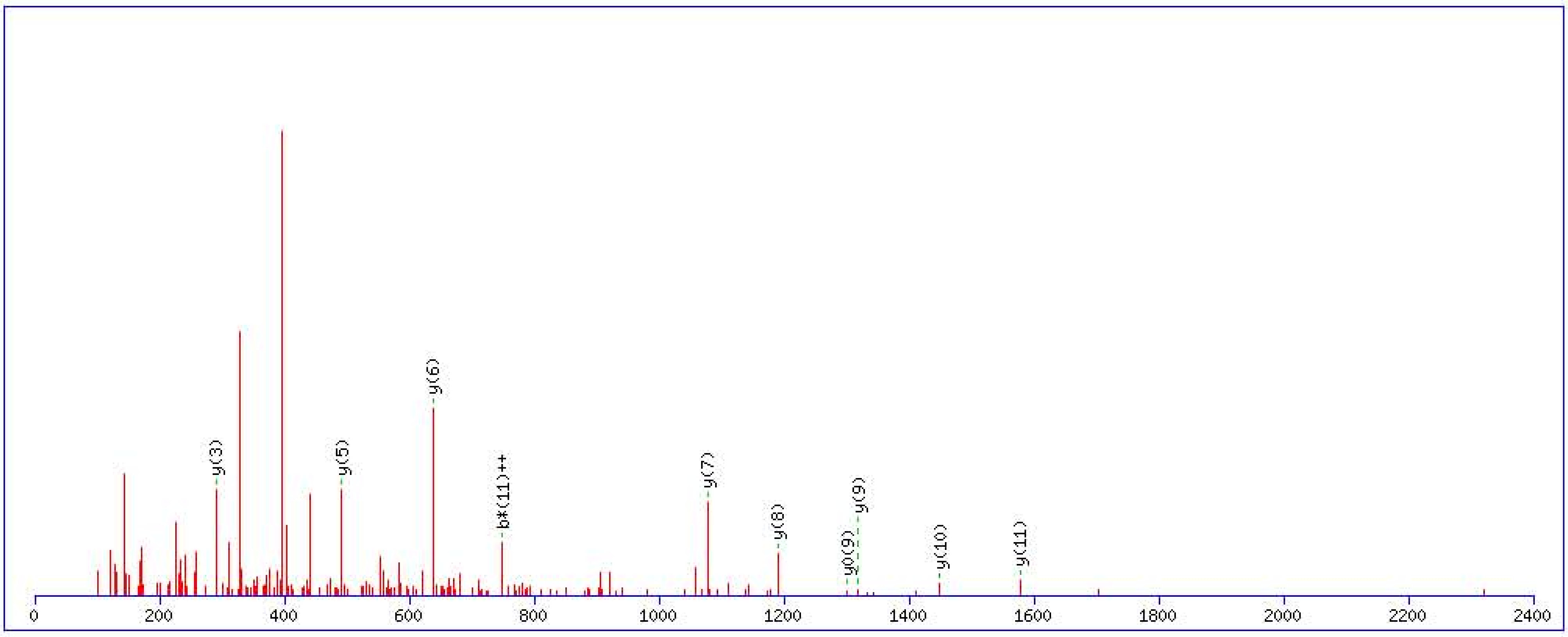
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLEEELQFSLGSK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

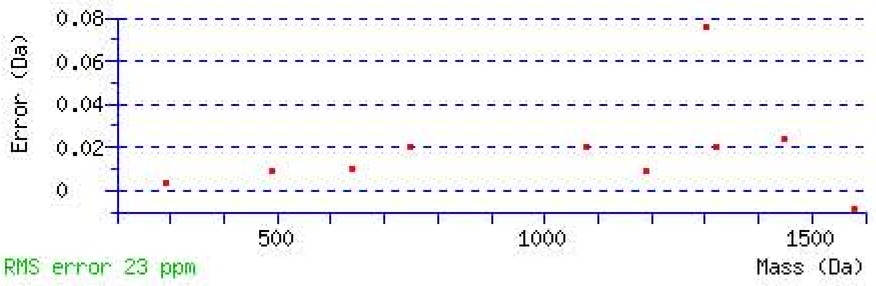
Match to Query 47083: 1746.907452 from(583.309760,3+) rtinseconds(2523) index(64206)
Title: Locus:1.1.1.3183.5 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

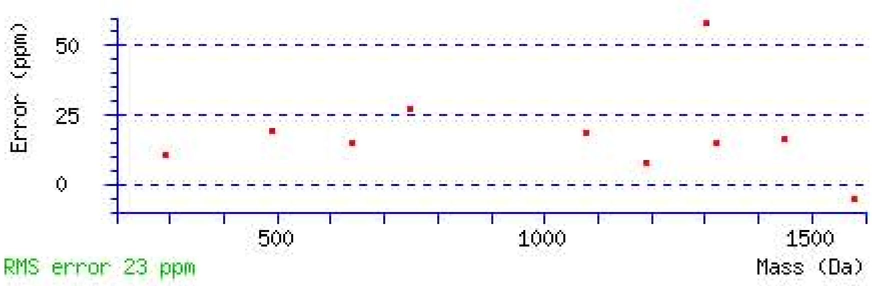
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1746.886200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 3.7e-005
Matches : 10/126 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							13
2	171.112804	86.060040					L	1690.872035	845.939656	1673.845486	837.426381	1672.861470	836.934373	12
3	300.155397	150.581336			282.144832	141.576054	E	***1577.787971***	789.397624	1560.761422	780.884349	1559.777406	780.392341	11
4	429.197990	215.102633			411.187425	206.097351	E	***1448.745378***	724.876327	1431.718829	716.363053	1430.734813	715.871045	10
5	558.240583	279.623930			540.230018	270.618647	E	***1319.702785***	660.355031	1302.676236	651.841756	1301.692220	651.349748	9
6	671.324647	336.165962			653.314082	327.160679	L	***1190.660192***	595.833734	1173.633643	587.320460	1172.649627	586.828452	8
7	1110.549973	555.778624	1093.523424	547.265350	1092.539408	546.773342	Q	***1077.576128***	539.291702	1060.549579	530.778428	1059.565563	530.286419	7
8	1257.618387	629.312832	1240.591838	620.799557	1239.607822	620.307549	F	***638.350802***	319.679039	621.324253	311.165765	620.340237	310.673757	6
9	1344.650415	672.828846	1327.623866	664.315571	1326.639850	663.823563	S	***491.282388***	246.144832	474.255839	237.631557	473.271823	237.139549	5
10	1457.734479	729.370878	1440.707930	720.857603	1439.723914	720.365595	L	404.250360	202.628818	387.223811	194.115543	386.239795	193.623535	4
11	1514.755943	757.881609	1497.729394	749.368335	1496.745378	748.876327	G	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
12	1601.787971	801.397624	1584.761422	792.884349	1583.777406	792.392341	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.8	1746.886200	0.021252	GLEEELQFSLGSK
2.5	1746.891403	0.016049	HSSVLFRHQKLHSGD

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

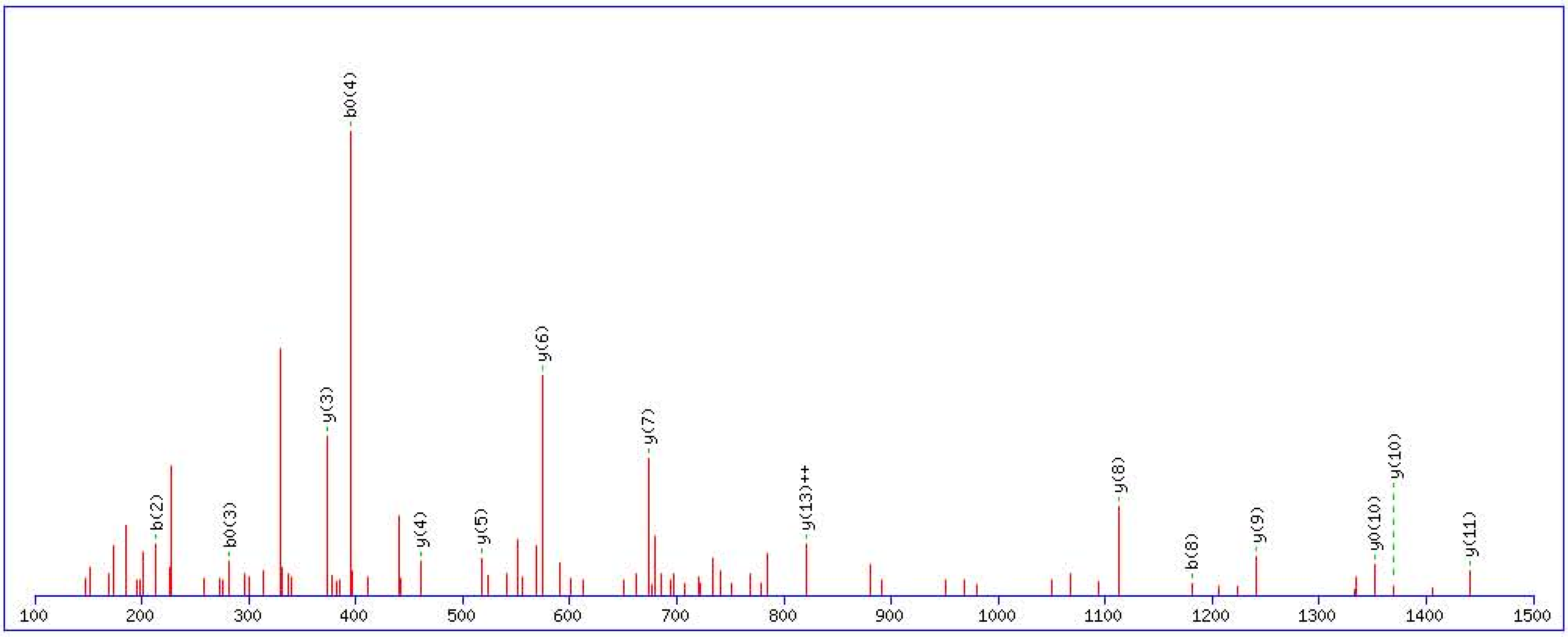
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSLAQEQVGGSPEK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

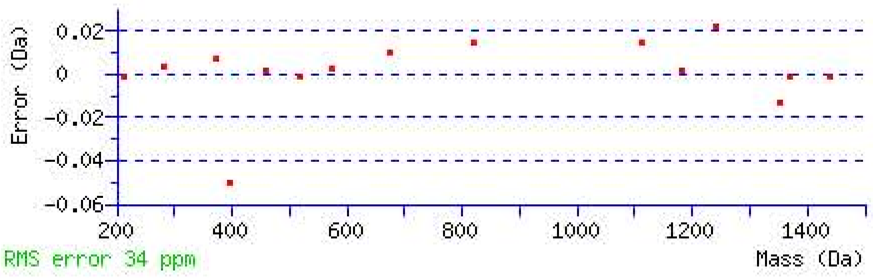
Match to Query 49516: 1851.991572 from(618.337800,3+) rtinseconds(1956) index(60239)
Title: Locus:1.1.1.2986.10 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

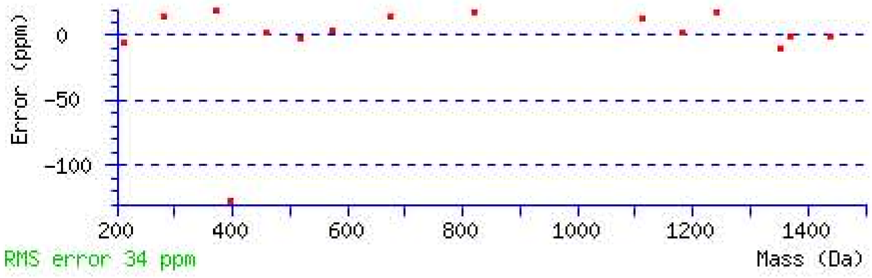
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1851.976425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0022
Matches : 15/152 fragment ions using 37 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							15
2	**213.159754**	107.083515					L	1753.915298	877.461287	1736.888749	868.948013	1735.904733	868.456004	14
3	300.191782	150.599529			282.181217	141.594247	S	1640.831234	820.919255	1623.804685	812.405981	1622.820669	811.913973	13
4	413.275846	207.141561			395.265281	198.136279	L	1553.799206	777.403241	1536.772657	768.889967	1535.788641	768.397958	12
5	484.312960	242.660118			466.302395	233.654836	A	*1440.715142*	720.861209	1423.688593	712.347935	1422.704577	711.855927	11
6	612.371538	306.689407	595.344989	298.176133	594.360973	297.684125	Q	*1369.678028*	685.342652	1352.651479	676.829378	1351.667463	676.337370	10
7	741.414131	371.210704	724.387582	362.697429	723.403566	362.205421	E	*1241.619450*	621.313363	1224.592901	612.800089	1223.608885	612.308080	9
8	**1180.639457**	590.823367	1163.612908	582.310092	1162.628892	581.818084	Q	*1112.576857*	556.792066	1095.550308	548.278792	1094.566292	547.786784	8
9	1279.707871	640.357574	1262.681322	631.844299	1261.697306	631.352291	V	*673.351531*	337.179404	656.324982	328.666129	655.340966	328.174121	7
10	1336.729335	668.868306	1319.702786	660.355031	1318.718770	659.863023	G	*574.283117*	287.645197	557.256568	279.131922	556.272552	278.639914	6
11	1393.750799	697.379037	1376.724250	688.865763	1375.740234	688.373755	G	*517.261653*	259.134465	500.235104	250.621190	499.251088	250.129182	5
12	1480.782827	740.895052	1463.756278	732.381777	1462.772262	731.889769	S	*460.240189*	230.623732	443.213640	222.110458	442.229624	221.618450	4
13	1577.835591	789.421434	1560.809042	780.908159	1559.825026	780.416151	P	*373.208161*	187.107718	356.181612	178.594444	355.197596	178.102436	3
14	1706.878184	853.942730	1689.851635	845.429456	1688.867619	844.937447	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.3	1851.976425	0.015147	VLSLAQEQVGGSPEK
23.7	1851.976425	0.015147	VLSLAQEQVGGSPEK

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

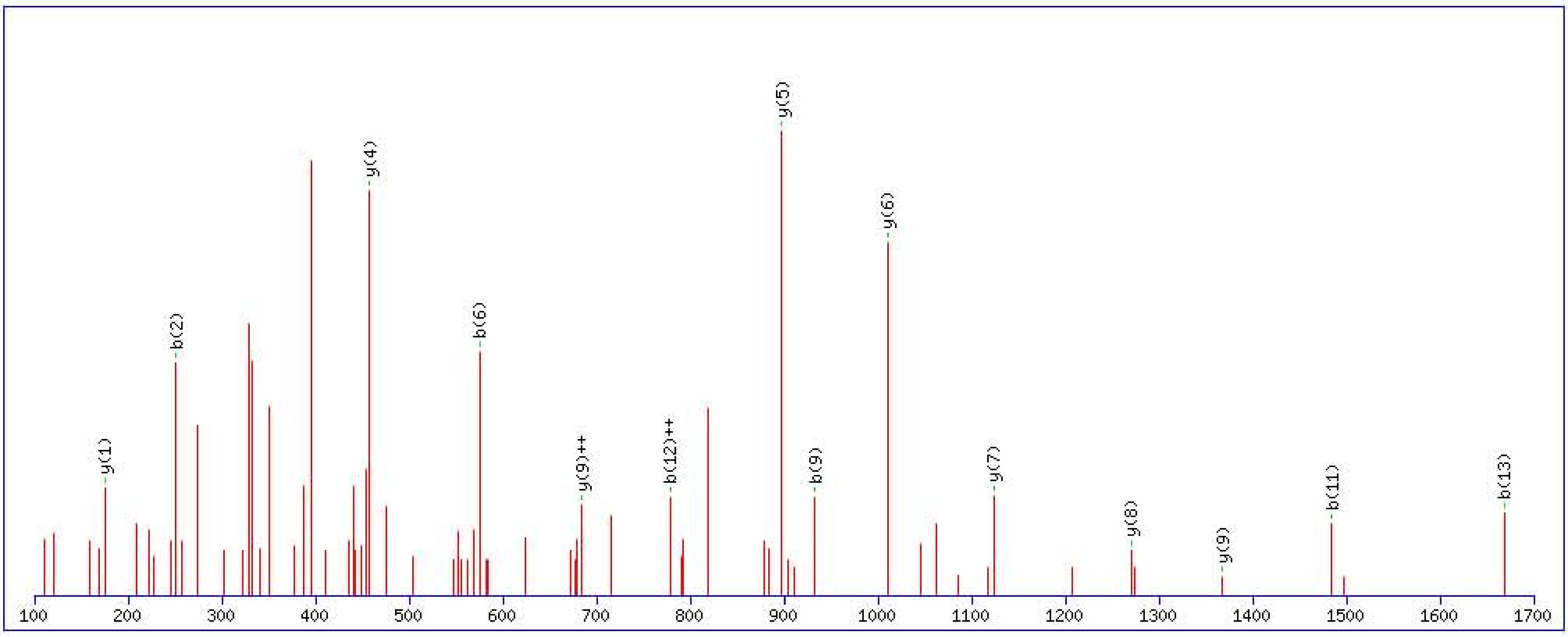
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLVPGAPFLLQALVR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

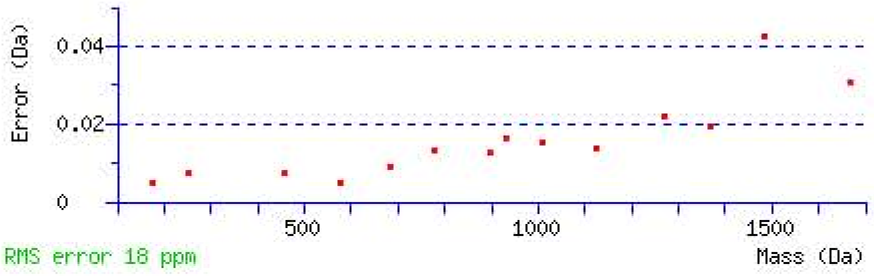
Match to Query 51553: 1941.164652 from(648.062160,3+) rtinseconds(2817) index(66281)
Title: Locus:1.1.1.3284.6 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

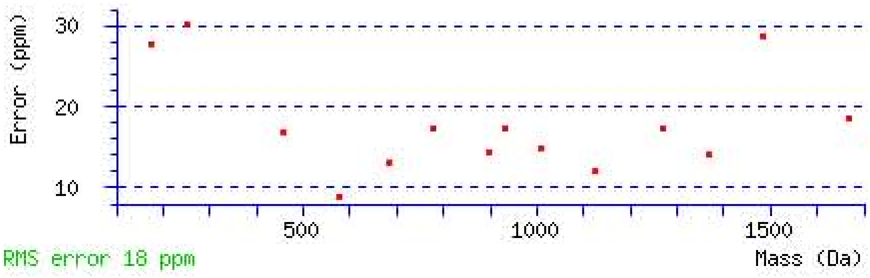


```
Monoisotopic mass of neutral peptide Mr(calc): 1941.138626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 2.7e-006
Matches : 14/92 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	138.066188	69.536732			H					15
2	***251.150252***	126.078764			L	1805.086996	903.047136	1788.060447	894.533862	14
3	350.218666	175.612971			V	1692.002932	846.505104	1674.976383	837.991830	13
4	447.271430	224.139353			P	1592.934518	796.970897	1575.907969	788.457623	12
5	504.292894	252.650085			G	1495.881754	748.444515	1478.855205	739.931241	11
6	***575.330008***	288.168642			A	1438.860290	719.933783	1421.833741	711.420509	10
7	672.382772	336.695024			P	***1367.823176***	684.415226	1350.796627	675.901952	9
8	819.451186	410.229231			F	***1270.770412***	635.888844	1253.743863	627.375570	8
9	***932.535250***	466.771263			L	***1123.701998***	562.354637	1106.675449	553.841363	7
10	1045.619314	523.313295			L	***1010.617934***	505.812605	993.591385	497.299331	6
11	***1484.844640***	742.925958	1467.818091	734.412684	Q	***897.533870***	449.270573	880.507321	440.757298	5
12	1555.881754	778.444515	1538.855205	769.931241	A	***458.308544***	229.657910	441.281995	221.144635	4
13	***1668.965818***	834.986547	1651.939269	826.473273	L	387.271430	194.139353	370.244881	185.626078	3
14	1768.034232	884.520754	1751.007683	876.007480	V	274.187366	137.597321	257.160817	129.084047	2
15					R	***175.118952***	88.063114	158.092403	79.549839	1



RMS error 18 ppm



RMS error 18 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.8	1941.138626	0.026026	HLVPGAPFLLQALVR

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

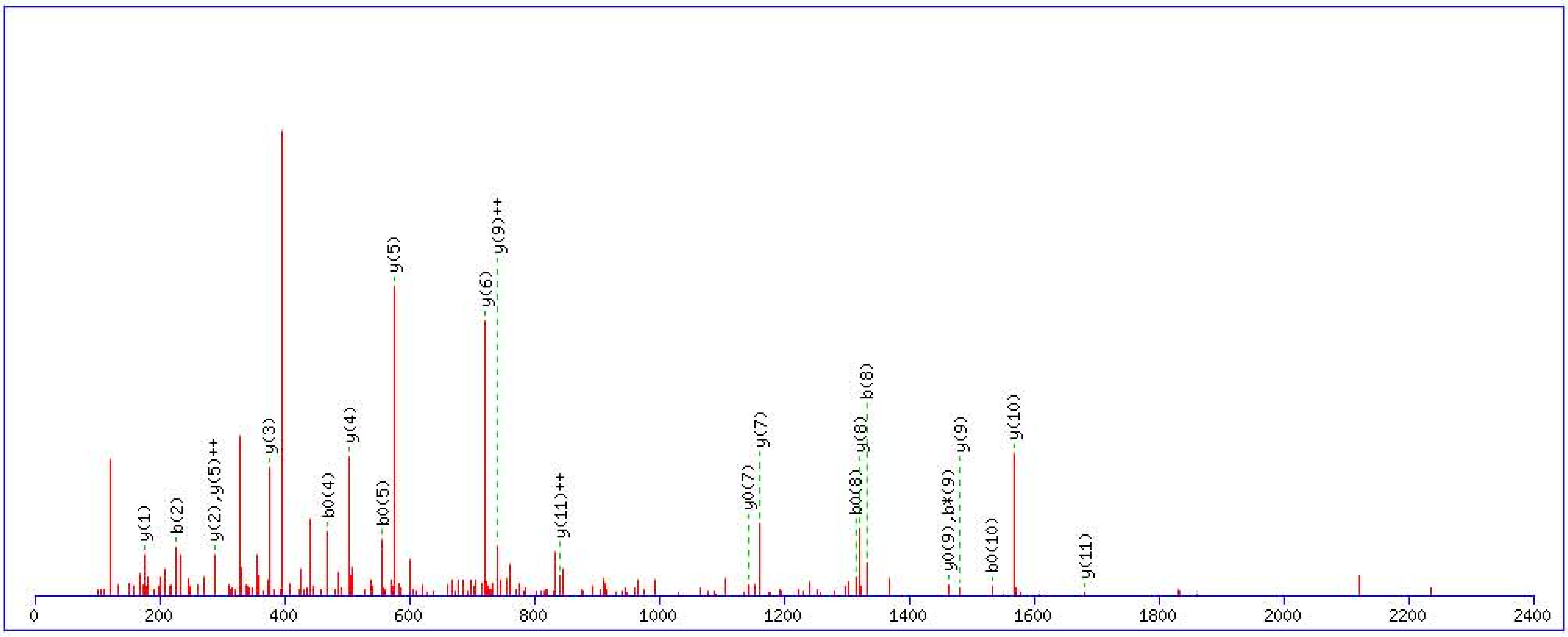
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPFLSCCQFAESLR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

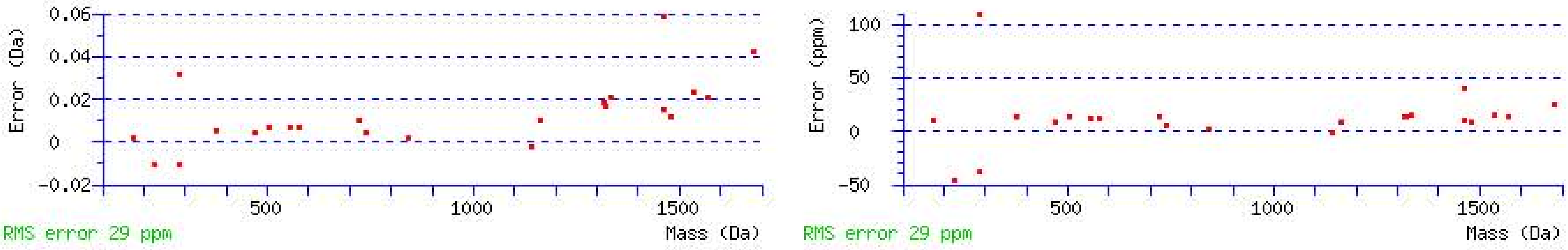
Match to Query 55066: 2053.967052 from(685.662960,3+) rtinseconds(2451) index(63695)
Title: Locus:1.1.1.3158.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2053.942368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 9.5e-006
Matches : 23/138 fragment ions using 49 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							14
2	**227.102633**	114.054954			209.092068	105.049672	P	1925.907059	963.457168	1908.880510	954.943893	1907.896494	954.451885	13
3	374.171047	187.589161			356.160482	178.583879	F	1828.854295	914.930786	1811.827746	906.417511	1810.843730	905.925503	12
4	487.255111	244.131193			469.244546	235.125911	L	***1681.785881***	841.396579	1664.759332	832.883304	1663.775316	832.391296	11
5	574.287139	287.647208			556.276574	278.641925	S	***1568.701817***	784.854547	1551.675268	776.341272	1550.691252	775.849264	10
6	734.317788	367.662532			716.307223	358.657250	C	***1481.669789***	741.338533	1464.643240	732.825258	1463.659224	732.333250	9
7	894.348437	447.677857			876.337872	438.672574	C	***1321.639140***	661.323208	1304.612591	652.809934	1303.628575	652.317926	8
8	**1333.573763**	667.290520	1316.547214	658.777245	1315.563198	658.285237	Q	***1161.608491***	581.307884	1144.581942	572.794609	1143.597926	572.302601	7
9	1480.642177	740.824727	1463.615628	732.311452	1462.631612	731.819444	F	***722.383165***	361.695221	705.356616	353.181946	704.372600	352.689938	6
10	1551.679291	776.343284	1534.652742	767.830009	1533.668726	767.338001	A	***575.314751***	288.161014	558.288202	279.647739	557.304186	279.155731	5
11	1680.721884	840.864580	1663.695335	832.351306	1662.711319	831.859298	E	***504.277637***	252.642457	487.251088	244.129182	486.267072	243.637174	4
12	1767.753912	884.380594	1750.727363	875.867320	1749.743347	875.375312	S	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
13	1880.837976	940.922626	1863.811427	932.409352	1862.827411	931.917344	L	***288.203016***	144.605146	271.176467	136.091871			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.7	2053.942368	0.024684	EPFLSCCQFAESLR
0.1	2053.985703	-0.018651	ENENERFAHYLEKTFK

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

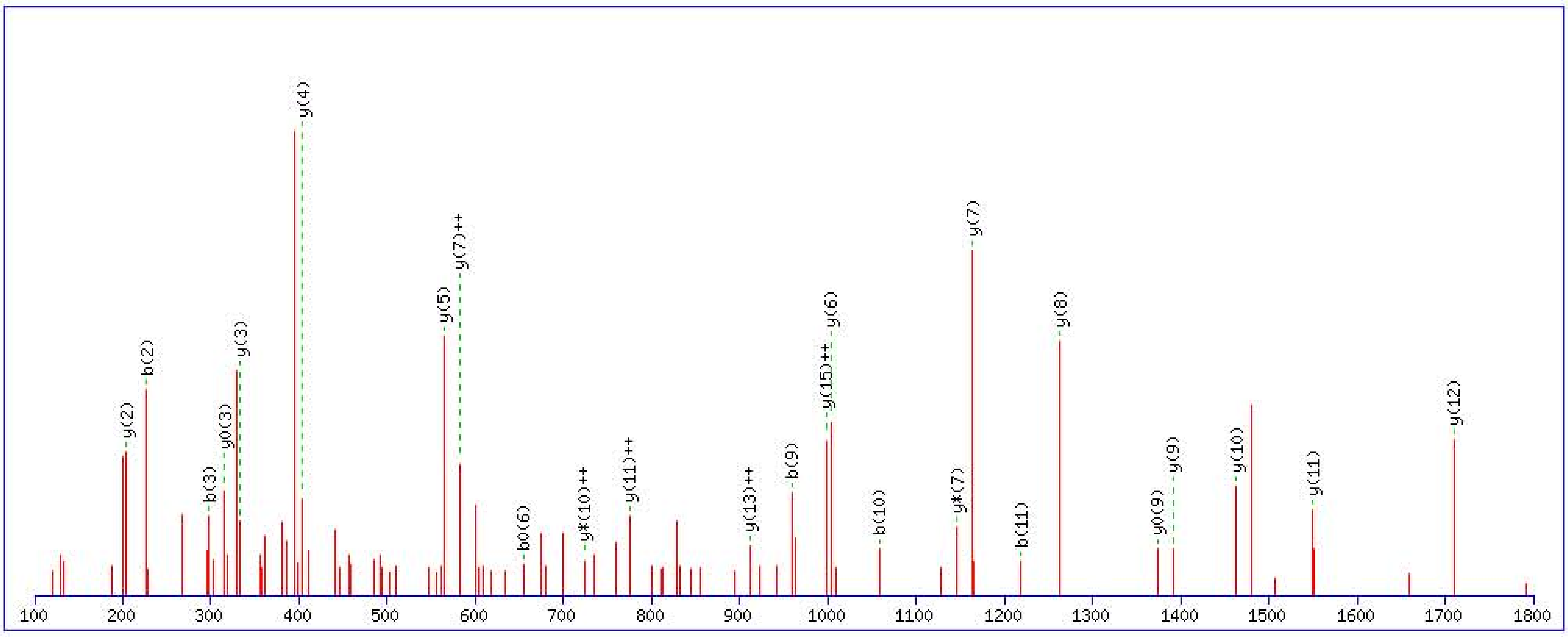
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLATLCSAEVCQCAEGK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

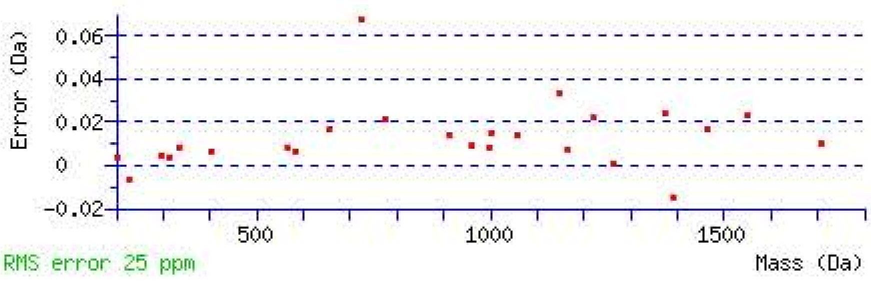
Match to Query 58701: 2220.062382 from(741.028070,3+) rtinseconds(2112) index(79267)
Title: Locus:1.1.1.2949.23 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

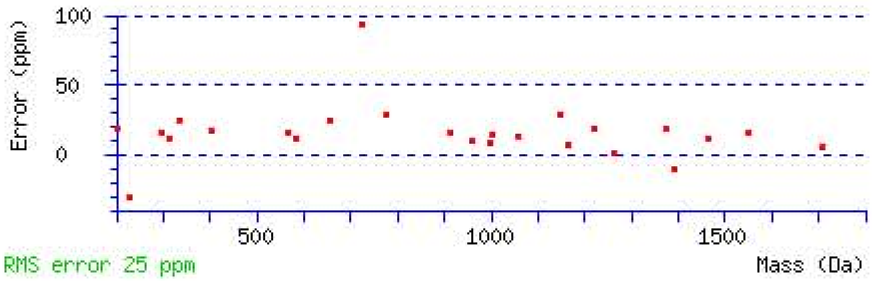
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2220.041092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00012
Matches : 25/160 fragment ions using 54 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							17
2	**227.175404**	114.091340					L	2107.964318	1054.485797	2090.937769	1045.972522	2089.953753	1045.480514	16
3	**298.212518**	149.609897					A	1994.880254	997.943765	1977.853705	989.430491	1976.869689	988.938483	15
4	399.260197	200.133737			381.249632	191.128454	T	1923.843140	962.425208	1906.816591	953.911934	1905.832575	953.419926	14
5	512.344261	256.675769			494.333696	247.670486	L	1822.795461	911.901369	1805.768912	903.388094	1804.784896	902.896086	13
6	672.374910	336.691093			654.364345	327.685811	C	***1709.711397***	855.359337	1692.684848	846.846062	1691.700832	846.354054	12
7	759.406938	380.207107			741.396373	371.201825	S	***1549.680748***	775.344012	1532.654199	766.830738	1531.670183	766.338730	11
8	830.444052	415.725664			812.433487	406.720382	A	***1462.648720***	731.827998	1445.622171	723.314724	1444.638155	722.822716	10
9	**959.486645**	480.246961			941.476080	471.241678	E	***1391.611606***	696.309441	1374.585057	687.796167	1373.601041	687.304159	9
10	**1058.555059**	529.781168			1040.544494	520.775885	V	***1262.569013***	631.788145	1245.542464	623.274870	1244.558448	622.782862	8
11	**1218.585708**	609.796492			1200.575143	600.791210	C	***1163.500599***	582.253938	1146.474050	573.740663	1145.490034	573.248655	7
12	1657.811034	829.409155	1640.784485	820.895881	1639.800469	820.403873	Q	***1003.469950***	502.238613	986.443401	493.725339	985.459385	493.233331	6
13	1817.841683	909.424480	1800.815134	900.911205	1799.831118	900.419197	C	***564.244624***	282.625950	547.218075	274.112676	546.234059	273.620668	5
14	1888.878797	944.943037	1871.852248	936.429762	1870.868232	935.937754	A	***404.213975***	202.610626	387.187426	194.097351	386.203410	193.605343	4
15	2017.921390	1009.464333	2000.894841	1000.951059	1999.910825	1000.459051	E	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	3
16	2074.942854	1037.975065	2057.916305	1029.461790	2056.932289	1028.969782	G	***204.134268***	102.570772	187.107719	94.057497			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.4	2220.041092	0.021290	LLATLCSAEVCQCAEGK

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

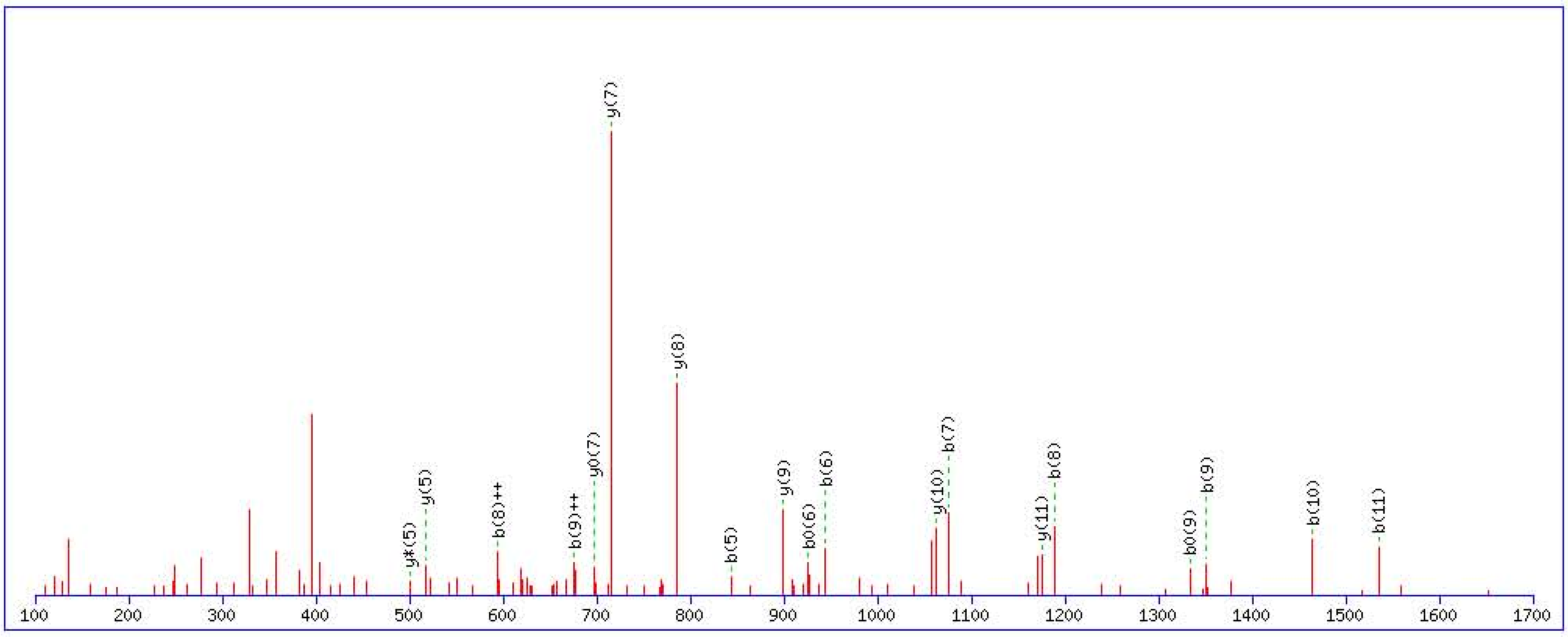
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GCGEQTMIYLAPTLAASR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

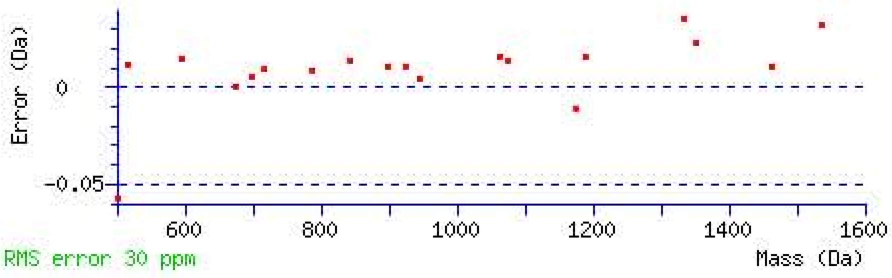
Match to Query 59329: 2249.133942 from(750.718590,3+) rtinseconds(2480) index(63895)
Title: Locus:1.1.1.3168.14 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

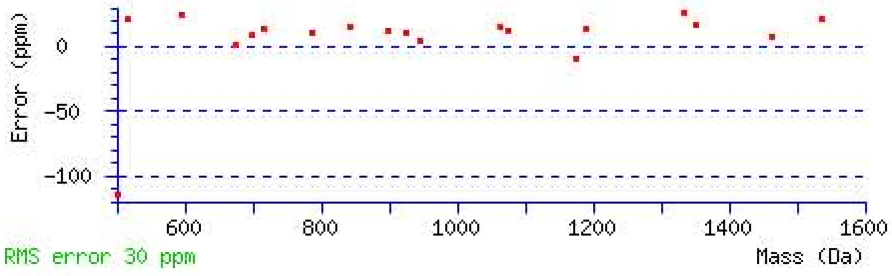
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2249.100647
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0016
Matches : 19/188 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							18
2	218.059389	109.533333					C	2193.086482	1097.046879	2176.059933	1088.533604	2175.075917	1088.041596	17
3	275.080853	138.044064					G	2033.055833	1017.031555	2016.029284	1008.518280	2015.045268	1008.026272	16
4	404.123446	202.565361			386.112881	193.560079	E	1976.034369	988.520822	1959.007820	980.007548	1958.023804	979.515540	15
5	***843.348772***	422.178024	826.322223	413.664750	825.338207	413.172742	Q	1846.991776	923.999526	1829.965227	915.486251	1828.981211	914.994243	14
6	***944.396451***	472.701864	927.369902	464.188589	926.385886	463.696581	T	1407.766450	704.386863	1390.739901	695.873588	1389.755885	695.381580	13
7	***1075.436936***	538.222106	1058.410387	529.708832	1057.426371	529.216824	M	1306.718771	653.863023	1289.692222	645.349749	1288.708206	644.857741	12
8	***1188.521000***	**594.764138**	1171.494451	586.250864	1170.510435	585.758855	I	***1175.678286***	588.342781	1158.651737	579.829506	1157.667721	579.337498	11
9	***1351.584329***	**676.295803**	1334.557780	667.782528	1333.573764	667.290520	Y	***1062.594222***	531.800749	1045.567673	523.287475	1044.583657	522.795466	10
10	***1464.668393***	732.837834	1447.641844	724.324560	1446.657828	723.832552	L	***899.530893***	450.269084	882.504344	441.755810	881.520328	441.263802	9
11	***1535.705507***	768.356391	1518.678958	759.843117	1517.694942	759.351109	A	***786.446829***	393.727053	769.420280	385.213778	768.436264	384.721770	8
12	1632.758271	816.882773	1615.731722	808.369499	1614.747706	807.877491	P	***715.409715***	358.208496	698.383166	349.695221	697.399150	349.203213	7
13	1733.805950	867.406613	1716.779401	858.893339	1715.795385	858.401330	T	618.356951	309.682114	601.330402	301.168839	600.346386	300.676831	6
14	1846.890014	923.948645	1829.863465	915.435370	1828.879449	914.943362	L	***517.309272***	259.158274	500.282723	250.644999	499.298707	250.152991	5
15	1917.927128	959.467202	1900.900579	950.953927	1899.916563	950.461919	A	404.225208	202.616242	387.198659	194.102967	386.214643	193.610959	4
16	1988.964242	994.985759	1971.937693	986.472484	1970.953677	985.980476	A	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
17	2075.996270	1038.501773	2058.969721	1029.988498	2057.985705	1029.496490	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
18							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	2249.100647	0.033295	GCGEQTMIYLAPTLAASR
9.3	2249.115051	0.018891	YSTSLYASPSMVHEGVAVVPR
0.8	2249.137527	-0.003585	QKFERPICVSWSTDVKGGR
0.2	2249.143570	-0.009628	TPPPQPPLISSMDSISQK

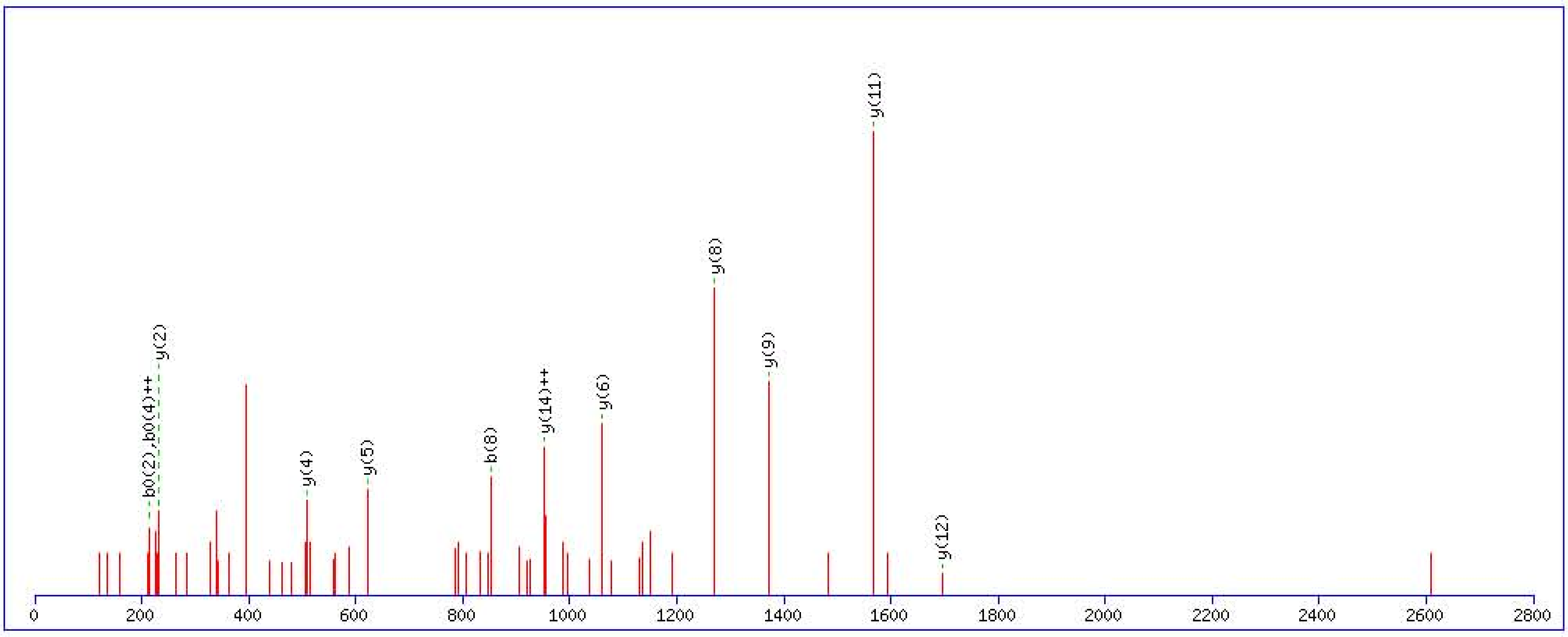
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DDPDAPLQPVTPLQLFEGR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

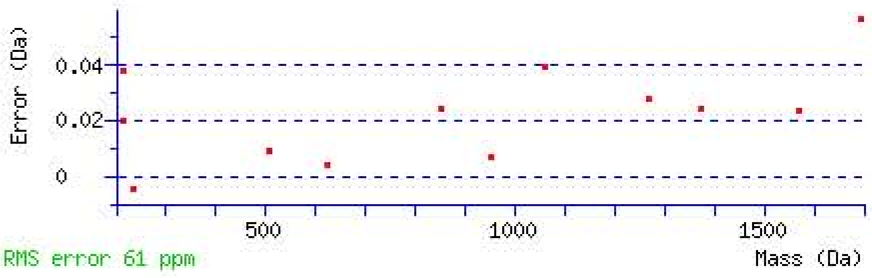
Match to Query 63019: 2418.258222 from(807.093350,3+) rtinseconds(2985) index(67691)
Title: Locus:1.1.1.3340.16 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

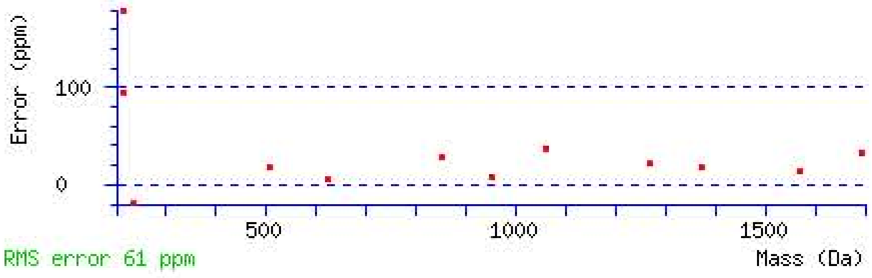
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2418.225342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 44 **Expect:** 0.00088
Matches : 12/198 fragment ions using 16 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**							**19**
2	231.061162	116.034219			213.050597	107.028936	**D**	2304.205668	1152.606472	2287.179119	1144.093197	2286.195103	1143.601189	**18**
3	328.113926	164.560601			310.103361	155.555319	**P**	2189.178725	1095.093000	2172.152176	1086.579726	2171.168160	1086.087718	**17**
4	443.140869	222.074073			425.130304	213.068790	**D**	2092.125961	1046.566618	2075.099412	1038.053344	2074.115396	1037.561336	**16**
5	514.177983	257.592630			496.167418	248.587347	**A**	1977.099018	989.053147	1960.072469	980.539873	1959.088453	980.047865	**15**
6	611.230747	306.119012			593.220182	297.113729	**P**	1906.061904	953.534590	1889.035355	945.021316	1888.051339	944.529308	**14**
7	724.314811	362.661044			706.304246	353.655761	**L**	1809.009140	905.008208	1791.982591	896.494934	1790.998575	896.002926	**13**
8	852.373389	426.690333	835.346840	418.177058	834.362824	417.685050	**Q**	***1695.925076***	848.466176	1678.898527	839.952902	1677.914511	839.460894	**12**
9	949.426153	475.216715	932.399604	466.703440	931.415588	466.211432	**P**	***1567.866498***	784.436887	1550.839949	775.923613	1549.855933	775.431605	**11**
10	1048.494567	524.750922	1031.468018	516.237647	1030.484002	515.745639	**V**	1470.813734	735.910505	1453.787185	727.397231	1452.803169	726.905223	**10**
11	1149.542246	575.274761	1132.515697	566.761487	1131.531681	566.269479	**T**	***1371.745320***	686.376298	1354.718771	677.863024	1353.734755	677.371016	**9**
12	1246.595010	623.801143	1229.568461	615.287869	1228.584445	614.795861	**P**	***1270.697641***	635.852459	1253.671092	627.339184	1252.687076	626.847176	**8**
13	1359.679074	680.343175	1342.652525	671.829901	1341.668509	671.337893	**L**	1173.644877	587.326077	1156.618328	578.812802	1155.634312	578.320794	**7**
14	1798.904400	899.955838	1781.877851	891.442564	1780.893835	890.950556	**Q**	***1060.560813***	530.784045	1043.534264	522.270770	1042.550248	521.778762	**6**
15	1911.988464	956.497870	1894.961915	947.984596	1893.977899	947.492588	**L**	***621.335487***	311.171382	604.308938	302.658107	603.324922	302.166099	**5**
16	2059.056878	1030.032077	2042.030329	1021.518803	2041.046313	1021.026794	**F**	***508.251423***	254.629350	491.224874	246.116075	490.240858	245.624067	**4**
17	2188.099471	1094.553373	2171.072922	1086.040099	2170.088906	1085.548091	**E**	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	**3**
18	2245.120935	1123.064105	2228.094386	1114.550831	2227.110370	1114.058823	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
19							**R**	175.118952	88.063114	158.092403	79.549839			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.4	2418.225342	0.032880	DDPDAPLQPVTPLQLFEGR
11.6	2418.225342	0.032880	DDPDAPLQPVTPLQLFEGR

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

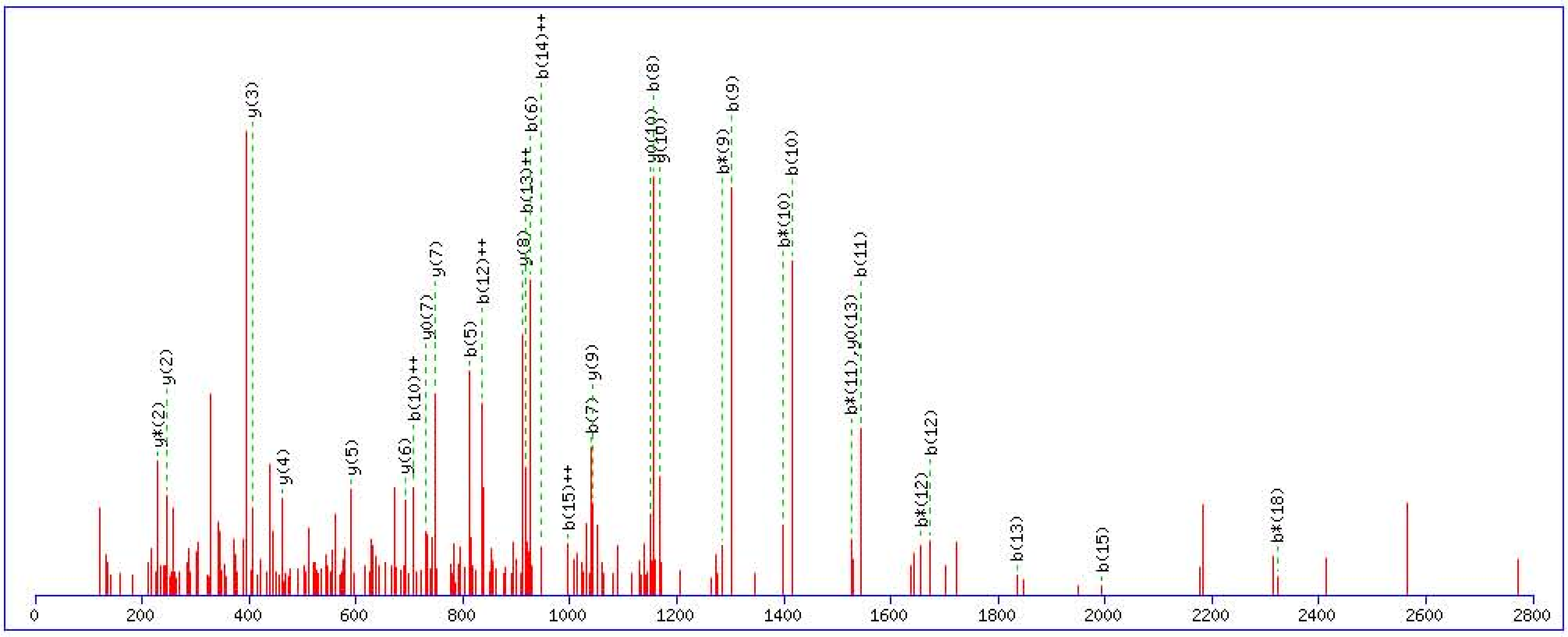
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AACAQLNDFLQEYGTQGCQV**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

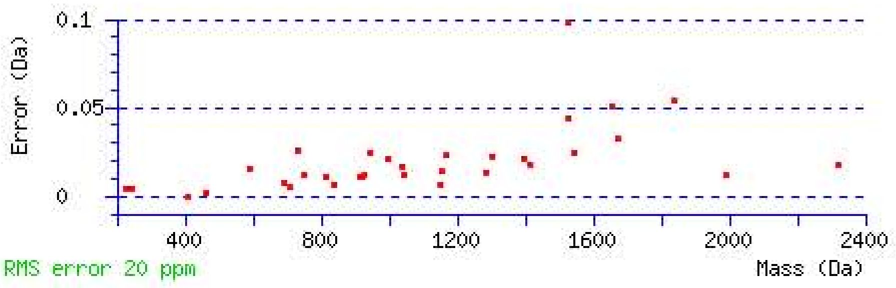
Match to Query 66392: 2583.193812 from(862.071880,3+) rtinseconds(2713) index(65399)
Title: Locus:1.1.1.3248.23 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

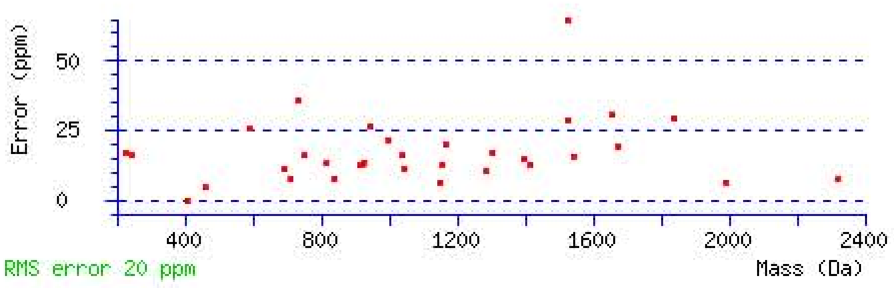
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2583.155624
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 1.8e-005
Matches : 33/194 fragment ions using 58 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							20
2	143.081504	72.044390					A	2513.125782	1257.066529	2496.099233	1248.553254	2495.115217	1248.061246	19
3	303.112153	152.059714					C	2442.088668	1221.547972	2425.062119	1213.034697	2424.078103	1212.542689	18
4	374.149267	187.578271					A	2282.058019	1141.532647	2265.031470	1133.019373	2264.047454	1132.527365	17
5	***813.374593***	407.190935	796.348044	398.677660			Q	2211.020905	1106.014090	2193.994356	1097.500816	2193.010340	1097.008808	16
6	***926.458657***	463.732967	909.432108	455.219692			L	1771.795579	886.401428	1754.769030	877.888153	1753.785014	877.396145	15
7	***1040.501584***	520.754430	1023.475035	512.241155			N	1658.711515	829.859396	1641.684966	821.346121	1640.700950	820.854113	14
8	***1155.528527***	578.267902	1138.501978	569.754627	1137.517962	569.262619	D	1544.668588	772.837932	1527.642039	764.324658	1526.658023	763.832650	13
9	***1302.596941***	651.802109	1285.570392	643.288834	1284.586376	642.796826	F	1429.641645	715.324460	1412.615096	706.811186	1411.631080	706.319178	12
10	***1415.681005***	**708.344141**	1398.654456	699.830866	1397.670440	699.338858	L	1282.573231	641.790253	1265.546682	633.276979	1264.562666	632.784971	11
11	***1543.739583***	772.373430	1526.713034	763.860155	1525.729018	763.368147	Q	***1169.489167***	585.248222	1152.462618	576.734947	1151.478602	576.242939	10
12	***1672.782176***	**836.894726**	1655.755627	828.381452	1654.771611	827.889444	E	***1041.430589***	521.218932	1024.404040	512.705658	1023.420024	512.213650	9
13	***1835.845505***	**918.426391**	1818.818956	909.913116	1817.834940	909.421108	Y	***912.387996***	456.697636	895.361447	448.184361	894.377431	447.692353	8
14	1892.866969	**946.937123**	1875.840420	938.423848	1874.856404	937.931840	G	***749.324667***	375.165971	732.298118	366.652697	731.314102	366.160689	7
15	***1993.914648***	**997.460962**	1976.888099	988.947688	1975.904083	988.455680	T	***692.303203***	346.655239	675.276654	338.141965	674.292638	337.649957	6
16	2121.973226	1061.490251	2104.946677	1052.976976	2103.962661	1052.484968	Q	***591.255524***	296.131400	574.228975	287.618125			5
17	2178.994690	1090.000983	2161.968141	1081.487708	2160.984125	1080.995700	G	***463.196946***	232.102111	446.170397	223.588836			4
18	2339.025339	1170.016307	2321.998790	1161.503033	2321.014774	1161.011025	C	***406.175482***	203.591379	389.148933	195.078104			3
19	2467.083917	1234.045596	2450.057368	1225.532322	2449.073352	1225.040314	Q	***246.144833***	123.576054	229.118284	115.062780			2
20							V	118.086255	59.546765					1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	2583.155624	0.038188	AACAQLNDFLQEYGTQGCQV
19.8	2583.155624	0.038188	AACAQLNDFLQEYGTQGCQV

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

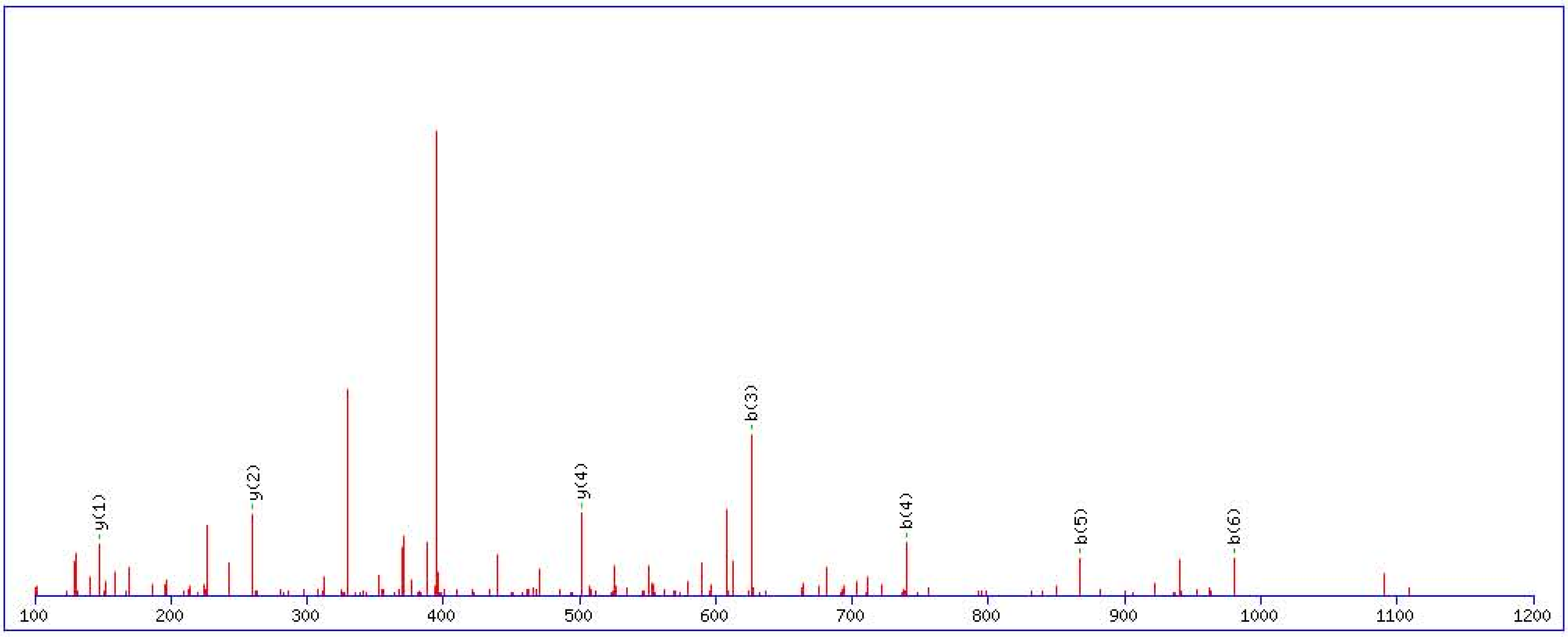
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEQIQLK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

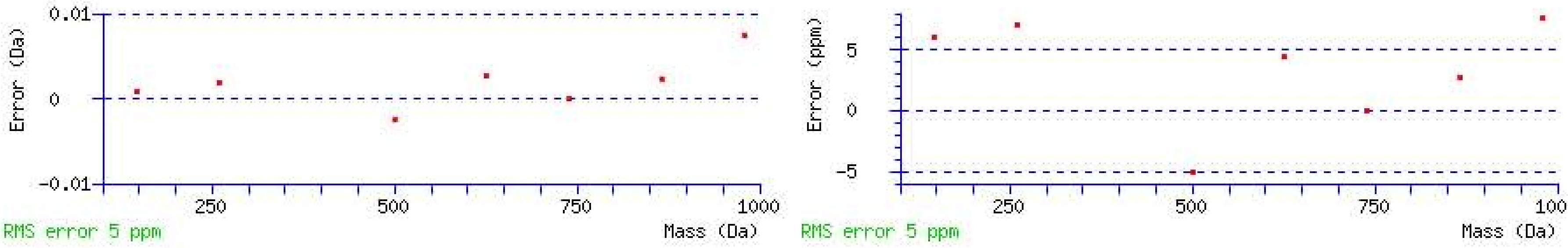
Match to Query 23949: 1125.623328 from(563.818940,2+) rtinseconds(1718) index(40221)
Title: Locus:1.1.1.2882.13 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1125.621597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.05
Matches : 7/56 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	58.028740	29.518008					G							7
2	187.071333	94.039305			169.060768	85.034022	E	1069.607429	535.307353	1052.580880	526.794078	1051.596864	526.302070	6
3	***626.296659***	313.651968	609.270110	305.138693	608.286094	304.646685	Q	940.564836	470.786056	923.538287	462.272782			5
4	***739.380723***	370.194000	722.354174	361.680725	721.370158	361.188717	I	**501.339510**	251.173393	484.312961	242.660119			4
5	***867.439301***	434.223289	850.412752	425.710014	849.428736	425.218006	Q	388.255446	194.631361	371.228897	186.118087			3
6	***980.523365***	490.765321	963.496816	482.252046	962.512800	481.760038	L	**260.196868**	130.602072	243.170319	122.088798			2
7							K	**147.112804**	74.060040	130.086255	65.546766			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.4	1125.621597	0.001731	GEQIQLK
18.7	1125.607666	0.015662	QMDRHAKIK
13.0	1125.632828	-0.009500	KLCLSHLQK
11.4	1125.621597	0.001731	GQELIQK
11.4	1125.639359	-0.016031	LDLLGNLPGSK
11.2	1125.621597	0.001731	EQVAQLK
10.8	1125.632813	-0.009485	EQAARLK
9.6	1125.621582	0.001746	QNLEALK
9.6	1125.621613	0.001715	QVDVNIK
8.4	1125.636856	-0.013528	WAAQVIK

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

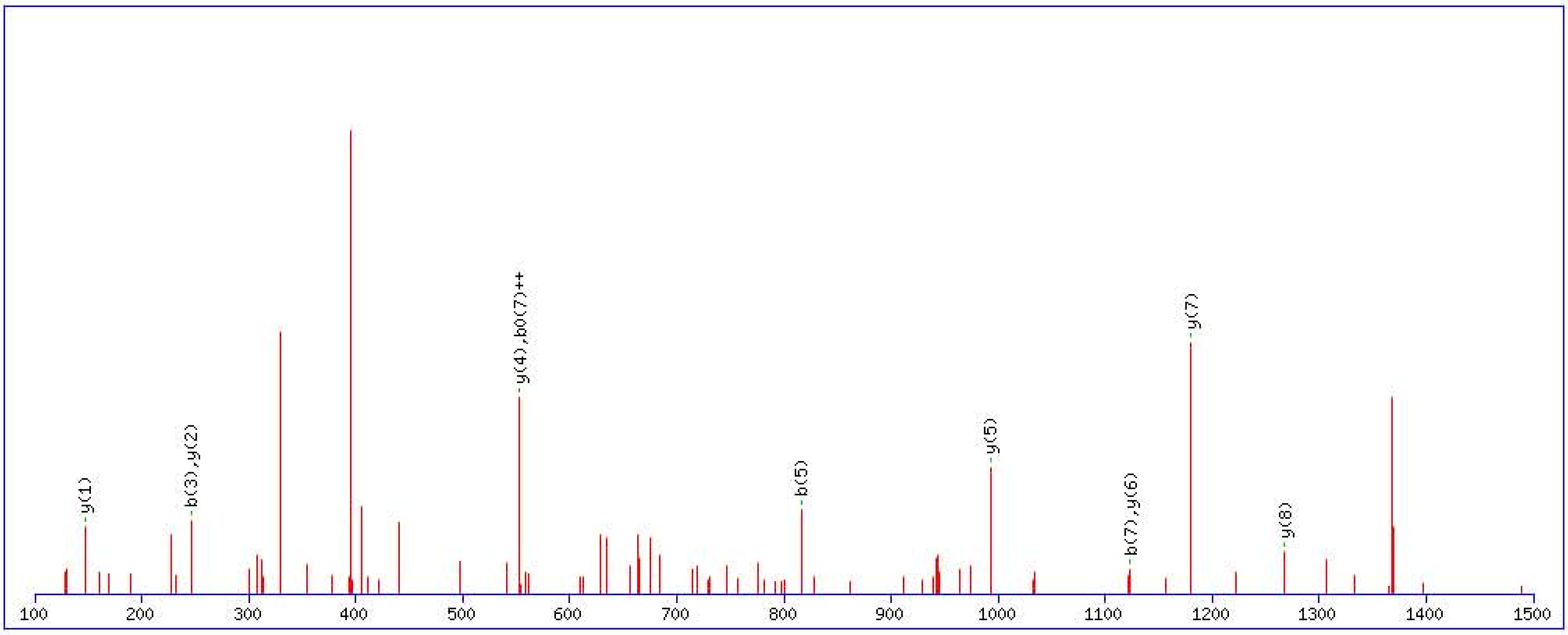
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSGMQFCVK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

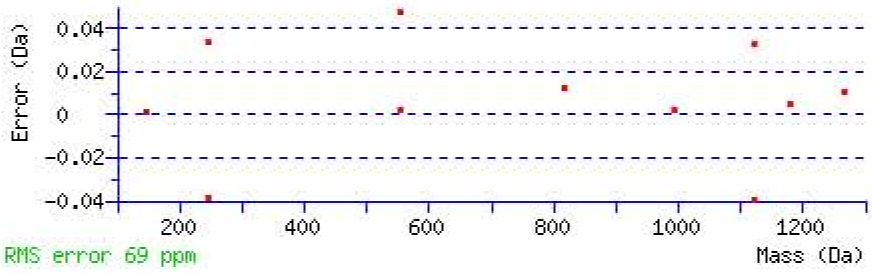
Match to Query 33478: 1367.645968 from(684.830260,2+) rtinseconds(1905) index(41458)
Title: Locus:1.1.1.2947.17 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

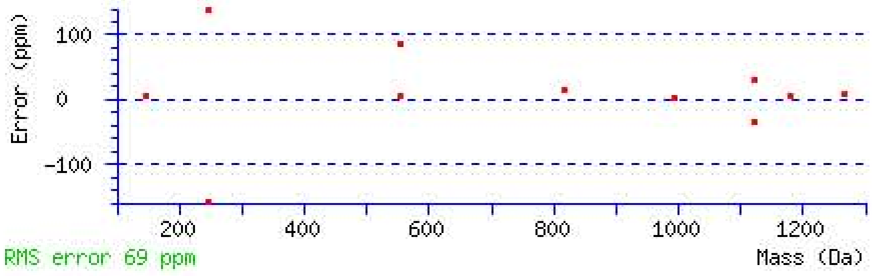
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1367.639999
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 3.2e-005
Matches : 11/74 fragment ions using 13 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							9
2	189.086983	95.047129			171.076418	86.041847	S	***1267.599584***	634.303430	1250.573035	625.790156	1249.589019	625.298148	8
3	**246.108447**	123.557861			228.097882	114.552579	G	***1180.567556***	590.787416	1163.541007	582.274142			7
4	377.148932	189.078104			359.138367	180.072822	M	***1123.546092***	562.276684	1106.519543	553.763410			6
5	**816.374258**	408.690767	799.347709	400.177493	798.363693	399.685485	Q	***992.505607***	496.756442	975.479058	488.243167			5
6	963.442672	482.224974	946.416123	473.711700	945.432107	473.219692	F	***553.280281***	277.143779	536.253732	268.630504			4
7	**1123.473321**	562.240298	1106.446772	553.727024	1105.462756	553.235016	C	406.211867	203.609571	389.185318	195.096297			3
8	1222.541735	611.774506	1205.515186	603.261231	1204.531170	602.769223	V	***246.181218***	123.594247	229.154669	115.080973			2
9							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.4	1367.639999	0.005969	TSGMQFCVK
4.3	1367.650314	-0.004346	TLQGERMENYK
1.4	1367.646484	-0.000516	QIMEETYK

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

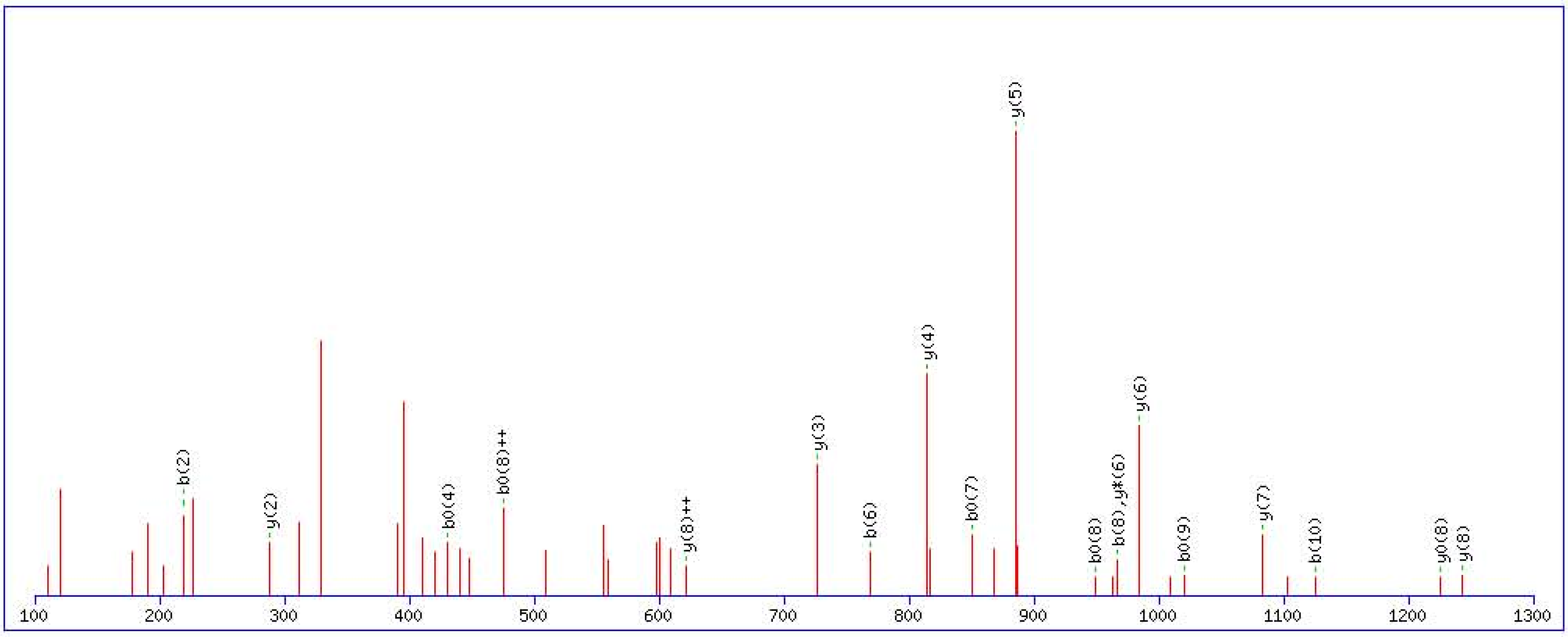
Mascot Search Results

Peptide View

MS/MS Fragmentation of AFTECCVVASQLR
Found in CO5_HUMAN, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

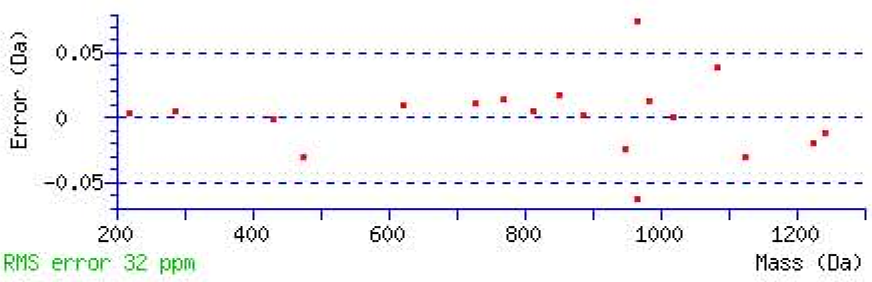
Match to Query 49501: 1850.895012 from(617.972280,3+) rtinseconds(2161) index(43164)
Title: Locus:1.1.1.3036.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

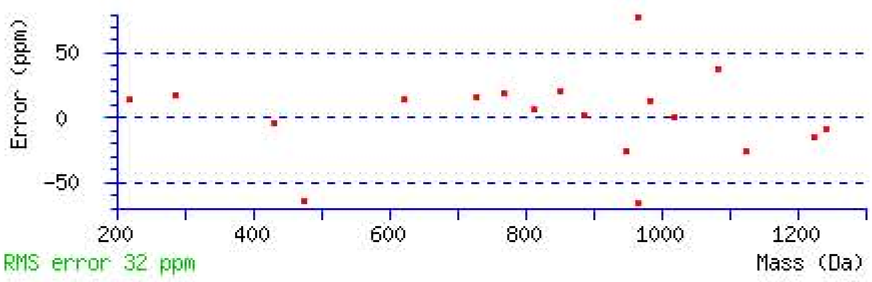
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1850.884140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.00039
Matches : 19/114 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							13
2	**219.112804**	110.060040					F	1780.854296	890.930786	1763.827747	882.417512	1762.843731	881.925504	12
3	320.160483	160.583879			302.149918	151.578597	T	1633.785882	817.396579	1616.759333	808.883305	1615.775317	808.391297	11
4	449.203076	225.105176			431.192511	216.099894	E	1532.738203	766.872740	1515.711654	758.359465	1514.727638	757.867457	10
5	609.233725	305.120501			591.223160	296.115218	C	1403.695610	702.351443	1386.669061	693.838169	1385.685045	693.346161	9
6	**769.264374**	385.135825			751.253809	376.130543	C	***1243.664961***	622.336119	1226.638412	613.822844	1225.654396	613.330836	8
7	868.332788	434.670032			850.322223	425.664750	V	***1083.634312***	542.320794	1066.607763	533.807520	1065.623747	533.315512	7
8	**967.401202**	484.204239			949.390637	475.198957	V	***984.565898***	492.786587	967.539349	484.273313	966.555333	483.781305	6
9	1038.438316	519.722796			1020.427751	510.717514	A	***885.497484***	443.252380	868.470935	434.739106	867.486919	434.247098	5
10	**1125.470344**	563.238810			1107.459779	554.233528	S	***814.460370***	407.733823	797.433821	399.220549	796.449805	398.728541	4
11	1564.695670	782.851473	1547.669121	774.338199	1546.685105	773.846191	Q	***727.428342***	364.217809	710.401793	355.704535			3
12	1677.779734	839.393505	1660.753185	830.880231	1659.769169	830.388223	L	***288.203016***	144.605146	271.176467	136.091871			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.8	1850.884140	0.010872	AFTECCVVASQLR
0.5	1850.893127	0.001885	AMESTATAAVAAELVSADK
0.3	1850.901901	-0.006889	KSVEGRPMFVSPCVDK

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

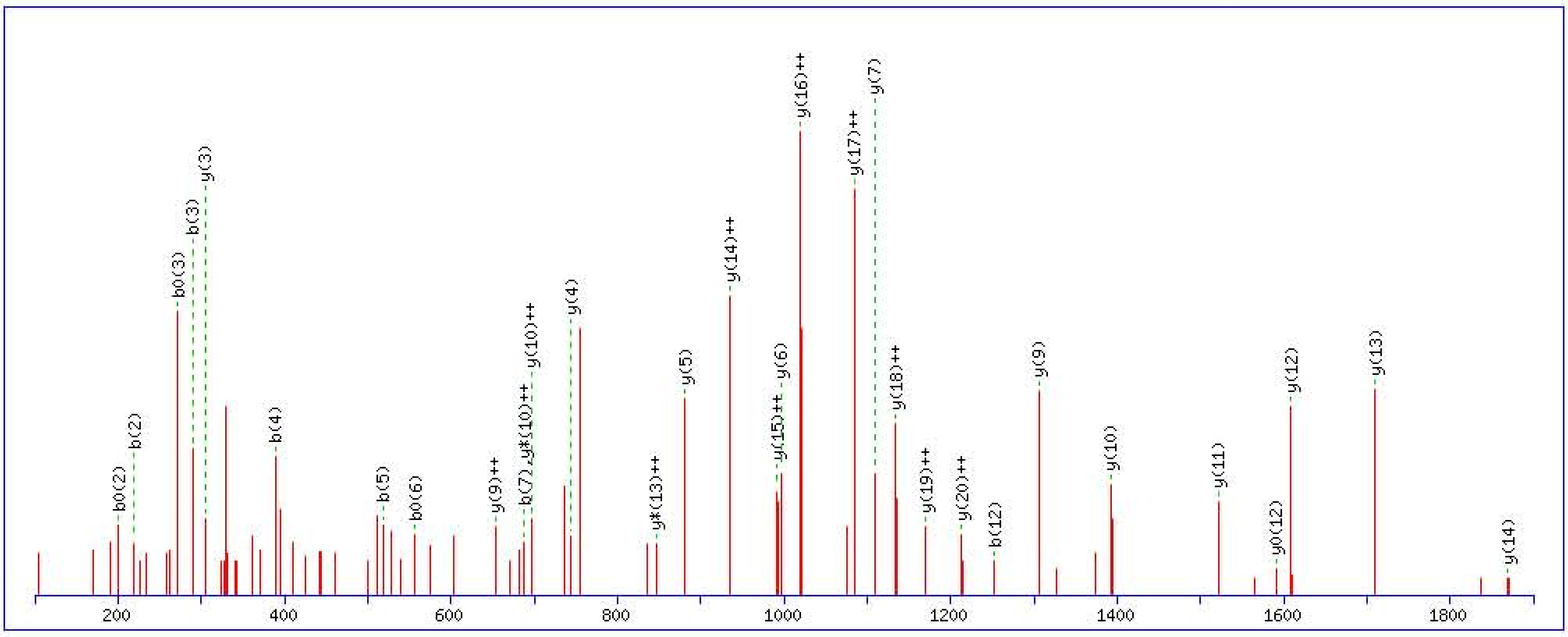
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSAVEGICTSESPVIDHQGTK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

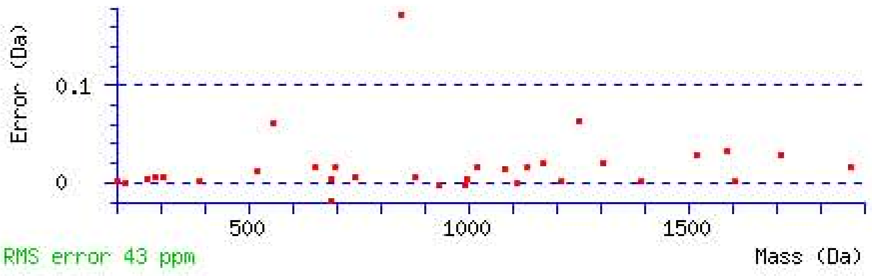
Match to Query 66127: 2556.220602 from(853.080810,3+) rtinseconds(1920) index(41582)
Title: Locus:1.1.1.2952.24 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

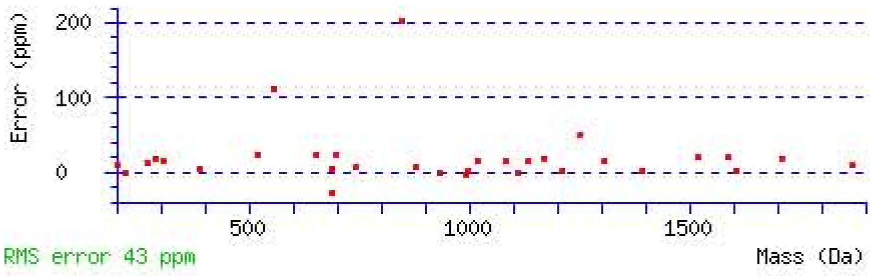
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2556.202240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 70  Expect: 2.4e-006
Matches : 32/202 fragment ions using 60 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	132.047761	66.527518					M							21
2	**219.079789**	110.043532			201.069224	101.038250	S	2426.169024	1213.588150	2409.142475	1205.074875	2408.158459	1204.582867	20
3	**290.116903**	145.562089			272.106338	136.556807	A	2339.136996	1170.072136	2322.110447	1161.558861	2321.126431	1161.066853	19
4	**389.185317**	195.096296			371.174752	186.091014	V	2268.099882	1134.553579	2251.073333	1126.040304	2250.089317	1125.548296	18
5	**518.227910**	259.617593			500.217345	250.612311	E	2169.031468	1085.019372	2152.004919	1076.506097	2151.020903	1076.014089	17
6	575.249374	288.128325			557.238809	279.123043	G	2039.988875	1020.498076	2022.962326	1011.984801	2021.978310	1011.492793	16
7	**688.333438**	344.670357			670.322873	335.665075	I	1982.967411	991.987343	1965.940862	983.474069	1964.956846	982.982061	15
8	848.364087	424.685682			830.353522	415.680399	C	***1869.883347***	935.445312	1852.856798	926.932037	1851.872782	926.440029	14
9	949.411766	475.209521			931.401201	466.204239	T	***1709.852698***	855.429987	1692.826149	846.916713	1691.842133	846.424704	13
10	1036.443794	518.725535			1018.433229	509.720253	S	***1608.805019***	804.906147	1591.778470	796.392873	1590.794454	795.900865	12
11	1165.486387	583.246832			1147.475822	574.241549	E	***1521.772991***	761.390133	1504.746442	752.876859	1503.762426	752.384851	11
12	**1252.518415**	626.762846			1234.507850	617.757563	S	***1392.730398***	696.868837	1375.703849	688.355563	1374.719833	687.863554	10
13	1349.571179	675.289228			1331.560614	666.283945	P	***1305.698370***	653.352823	1288.671821	644.839548	1287.687805	644.347540	9
14	1448.639593	724.823435			1430.629028	715.818152	V	1208.645606	604.826441	1191.619057	596.313166	1190.635041	595.821158	8
15	1561.723657	781.365467			1543.713092	772.360184	I	***1109.577192***	555.292234	1092.550643	546.778959	1091.566627	546.286951	7
16	1676.750600	838.878938			1658.740035	829.873656	D	***996.493128***	498.750202	979.466579	490.236927	978.482563	489.744919	6
17	1813.809512	907.408394			1795.798947	898.403112	H	***881.466185***	441.236730	864.439636	432.723456	863.455620	432.231448	5
18	2253.034838	1127.021057	2236.008289	1118.507782	2235.024273	1118.015774	Q	***744.407273***	372.707274	727.380724	364.194000	726.396708	363.701992	4
19	2310.056302	1155.531789	2293.029753	1147.018514	2292.045737	1146.526506	G	***305.181947***	153.094611	288.155398	144.581337	287.171382	144.089329	3
20	2411.103981	1206.055628	2394.077432	1197.542354	2393.093416	1197.050346	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
21							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.7	2556.202240	0.018362	MSAVEGICTSESPVIDHQGTK

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

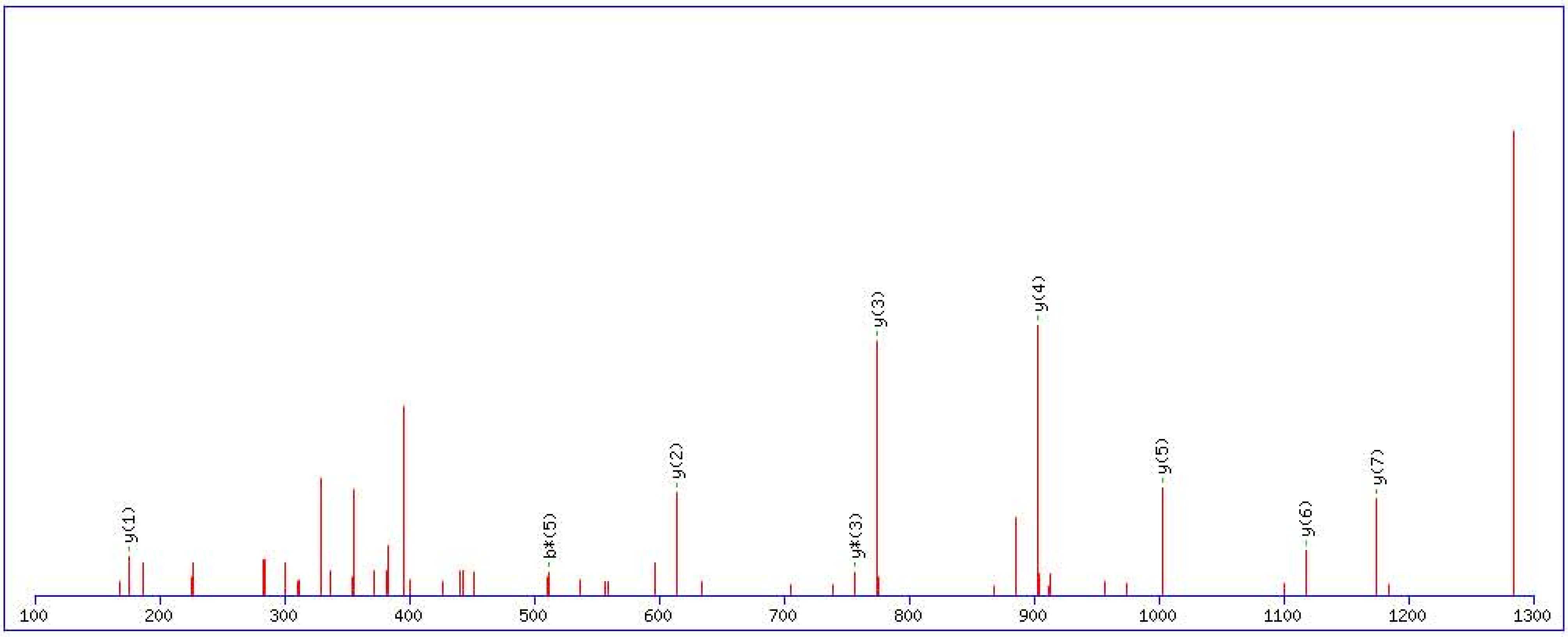
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGDVECQR**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

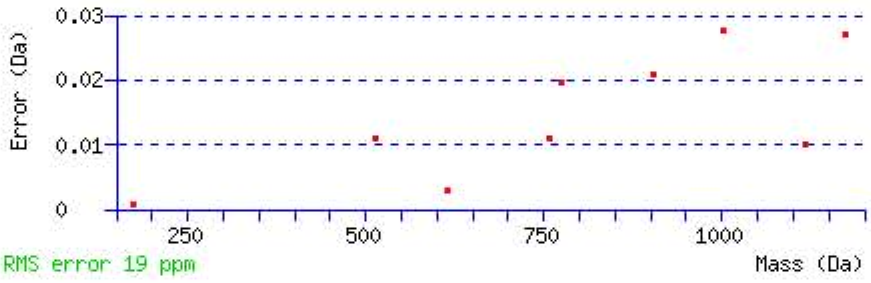
Match to Query 30982: 1301.603068 from(651.808810,2+) rtinseconds(1326) index(19874)
Title: Locus:1.1.1.2416.18 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

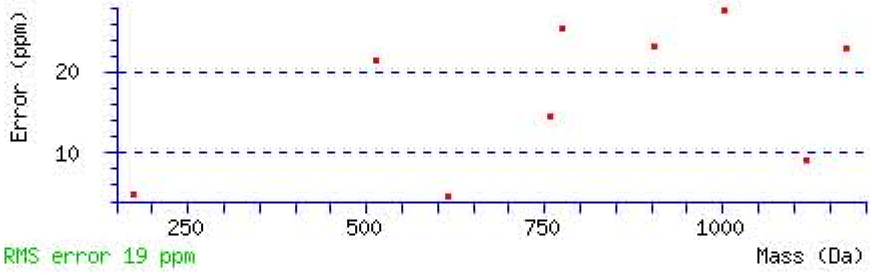
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1301.585648
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 8.8e-006
Matches : 9/74 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							8
2	186.087318	93.547297	169.060769	85.034023			G	*1174.534341*	587.770809	1157.507792	579.257534	1156.523776	578.765526	7
3	301.114261	151.060768	284.087712	142.547494	283.103696	142.055486	D	*1117.512877*	559.260077	1100.486328	550.746802	1099.502312	550.254794	6
4	400.182675	200.594976	383.156126	192.081701	382.172110	191.589693	V	*1002.485934*	501.746605	985.459385	493.233331	984.475369	492.741323	5
5	529.225268	265.116272	512.198719	256.602998	511.214703	256.110990	E	*903.417520*	452.212398	886.390971	443.699124	885.406955	443.207116	4
6	689.255917	345.131597	672.229368	336.618322	671.245352	336.126314	C	*774.374927*	387.691102	757.348378	379.177827			3
7	1128.481243	564.744260	1111.454694	556.230985	1110.470678	555.738977	Q	*614.344278*	307.675777	597.317729	299.162503			2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.1	1301.585648	0.017420	QGDVECQR
15.8	1301.584763	0.018305	KATEDAEGGDGPR
13.3	1301.621994	-0.018926	AEKEACQR
11.7	1301.584747	0.018321	QESPSQENIDR
2.0	1301.604263	-0.001195	CPAAMTVMHLR
1.6	1301.604263	-0.001195	CPAAMTVMHLR
0.2	1301.603378	-0.000310	KPEGTCPAAESR
0.1	1301.603378	-0.000310	TTENNEQR
0.0	1301.584763	0.018305	ASPESAQSTDPGR
0.0	1301.584778	0.018290	GGSDSSLSEPGPGR

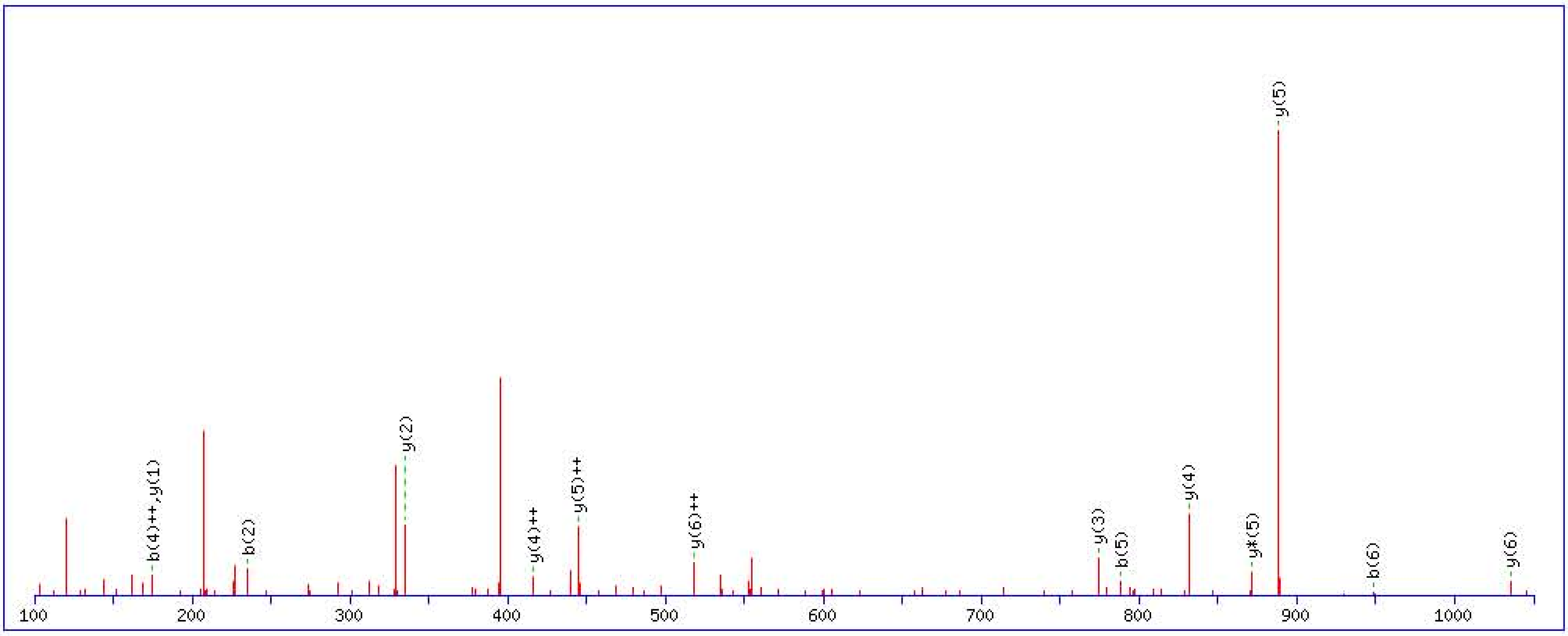
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFGGQCR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

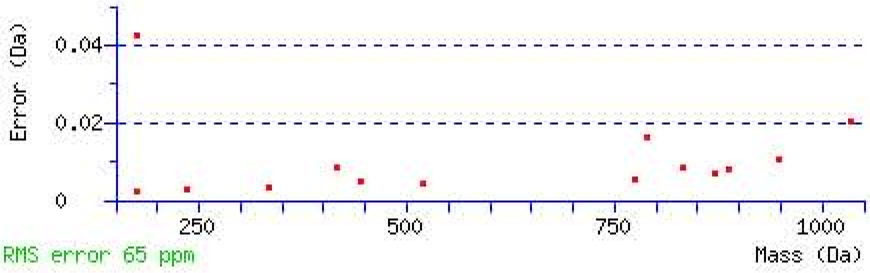
Match to Query 23858: 1121.517208 from(561.765880,2+) rtinseconds(1477) index(3592)
Title: Locus:1.1.1.2646.14 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

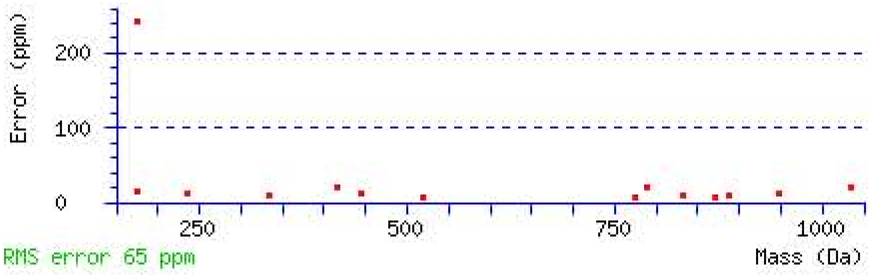
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1121.511032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.0029
Matches : 14/52 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					7
2	**235.107718**	118.057497			217.097153	109.052214	F	***1035.486269***	518.246773	1018.459720	509.733498	6
3	292.129182	146.568229			274.118617	137.562946	G	***888.417855***	444.712566	871.391306	436.199291	5
4	349.150646	175.078961			331.140081	166.073678	G	***831.396391***	416.201834	814.369842	407.688559	4
5	**788.375972**	394.691624	771.349423	386.178350	770.365407	385.686342	Q	***774.374927***	387.691102	757.348378	379.177827	3
6	**948.406621**	474.706949	931.380072	466.193674	930.396056	465.701666	C	***335.149601***	168.078438	318.123052	159.565164	2
7							R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.4	1121.511032	0.006176	SFGGQCR
2.3	1121.502274	0.014934	MSVEEQIDR

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

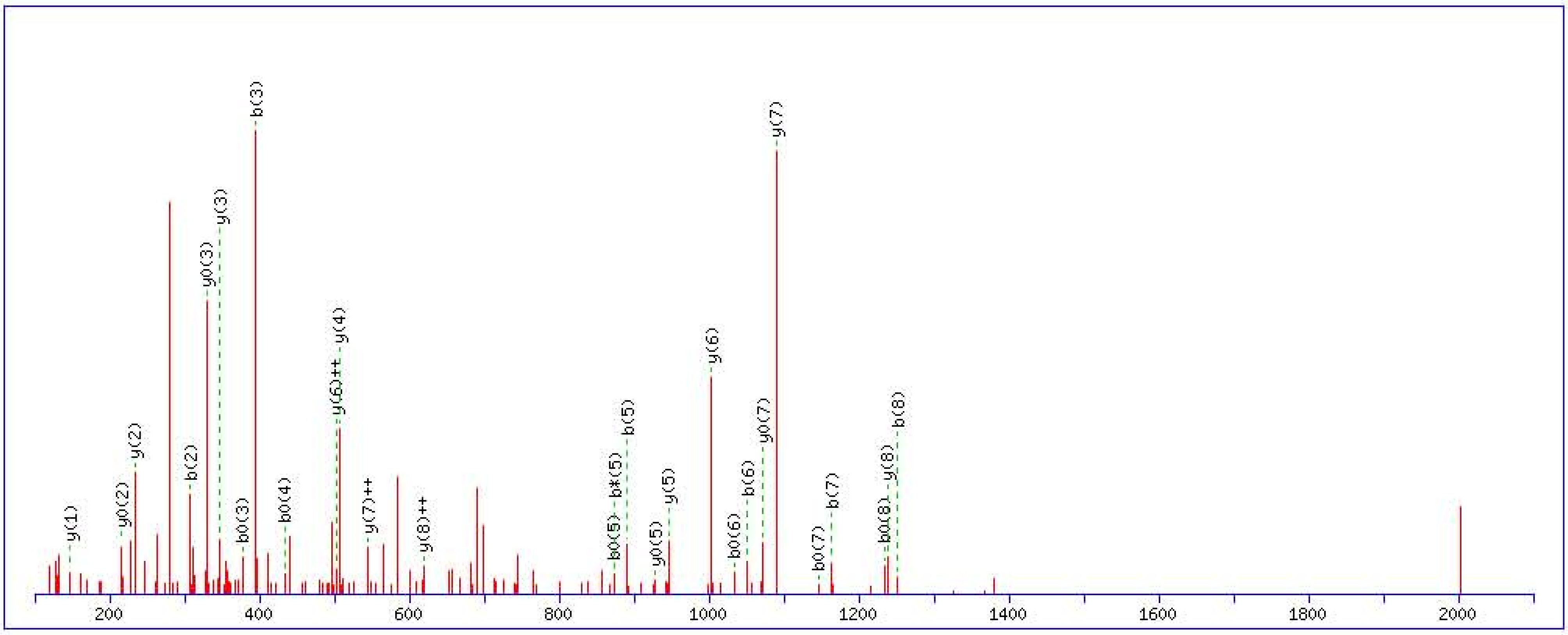
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CFSGQCISK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

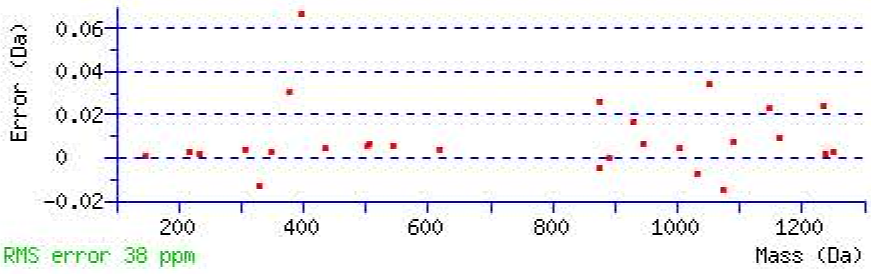
Match to Query 34496: 1396.637728 from(699.326140,2+) rtinseconds(1626) index(4536)
Title: Locus:1.1.1.2698.13 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

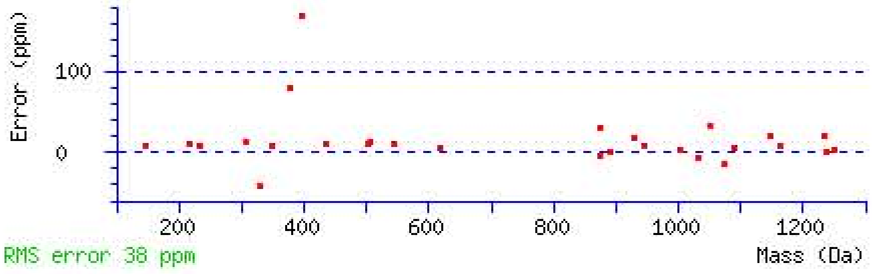
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1396.630157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.00069
Matches : 28/82 fragment ions using 61 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600					C							9
2	**308.106339**	154.556807					F	***1237.606777***	619.307027	1220.580228	610.793752	1219.596212	610.301744	8
3	**395.138367**	198.072821			377.127802	189.067539	S	***1090.538363***	545.772819	1073.511814	537.259545	1072.527798	536.767537	7
4	452.159831	226.583553			434.149266	217.578271	G	***1003.506335***	502.256806	986.479786	493.743531	985.495770	493.251523	6
5	**891.385157**	446.196217	874.358608	437.682942	873.374592	437.190934	Q	***946.484871***	473.746074	929.458322	465.232799	928.474306	464.740791	5
6	**1051.415806**	526.211541	1034.389257	517.698267	1033.405241	517.206258	C	***507.259545***	254.133410	490.232996	245.620136	489.248980	245.128128	4
7	**1164.499870**	582.753573	1147.473321	574.240298	1146.489305	573.748290	I	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	3
8	**1251.531898**	626.269587	1234.505349	617.756313	1233.521333	617.264304	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
9							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.2	1396.630157	0.007571	CFSGQCISK
15.1	1396.629272	0.008456	QLSQAEATDFCK

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

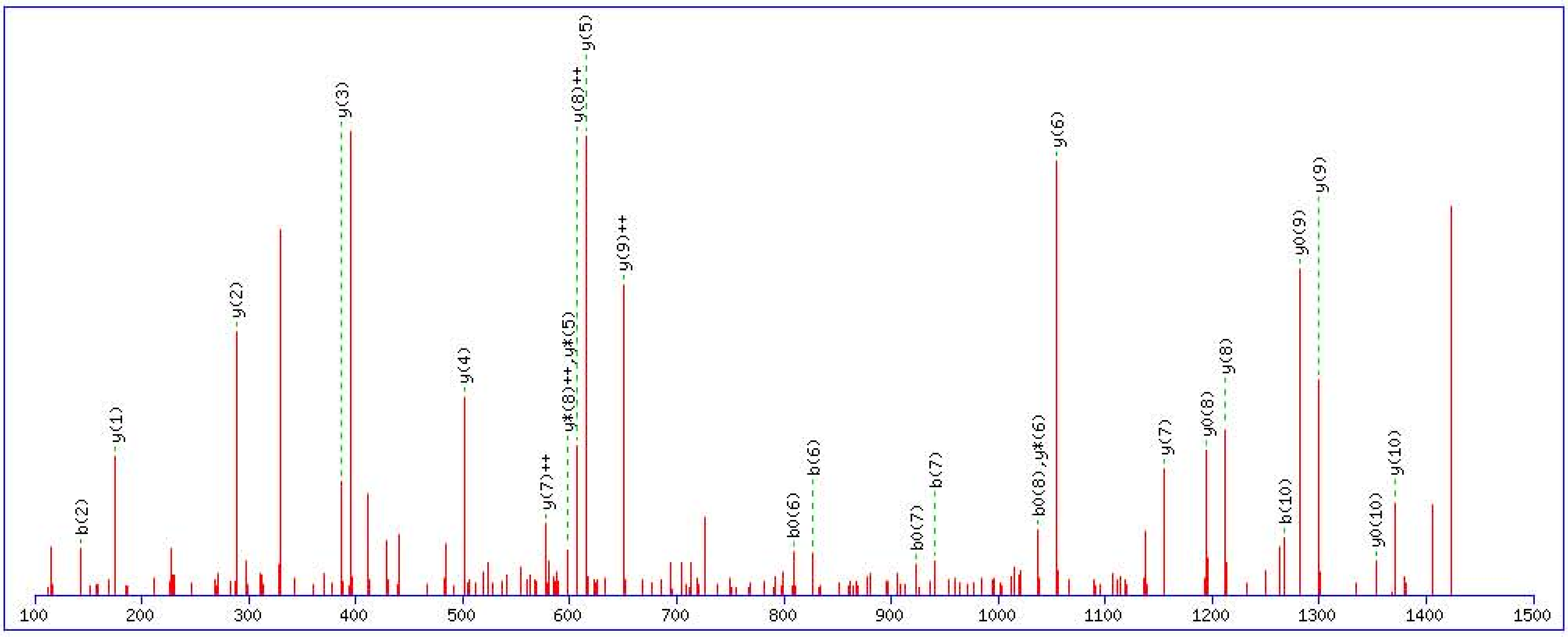
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AASGTQNNVLR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

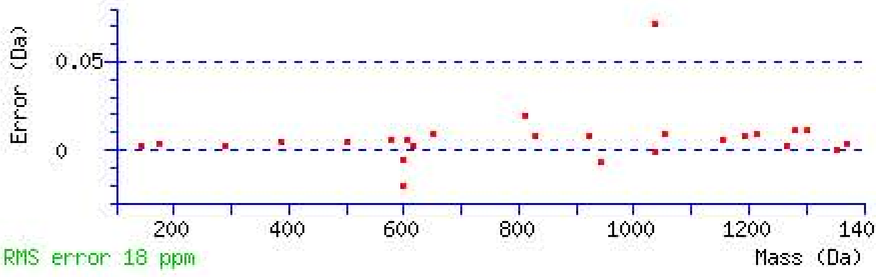
Match to Query 36727: 1440.758568 from(721.386560,2+) rtinseconds(1535) index(3982)
Title: Locus:1.1.1.2666.21 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

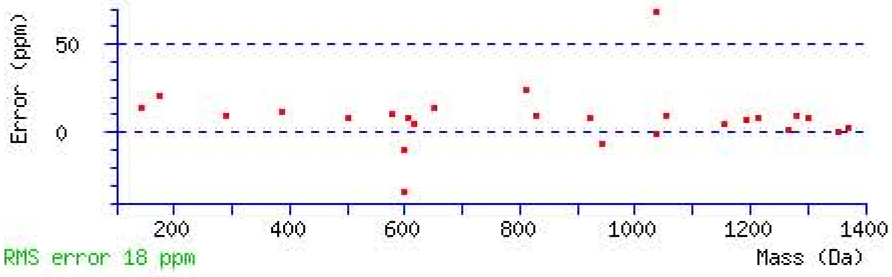
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1440.750717
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 77 **Expect:** 2.7e-007
Matches : 26/94 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							11
2	**143.081504**	72.044390					A	***1370.720895***	685.864086	1353.694346	677.350811	1352.710330	676.858803	10
3	230.113532	115.560404			212.102967	106.555121	S	***1299.683781***	650.345529	1282.657232	641.832254	1281.673216	641.340246	9
4	287.134996	144.071136			269.124431	135.065854	G	***1212.651753***	606.829515	1195.625204	598.316240	1194.641188	597.824232	8
5	388.182675	194.594976			370.172110	185.589693	T	***1155.630289***	578.318783	1138.603740	569.805508	1137.619724	569.313500	7
6	**827.408001**	414.207639	810.381452	405.694364	809.397436	405.202356	Q	***1054.582610***	527.794943	1037.556061	519.281669			6
7	**941.450928**	471.229102	924.424379	462.715828	923.440363	462.223820	N	***615.357284***	308.182280	598.330735	299.669006			5
8	1055.493855	528.250566	1038.467306	519.737291	1037.483290	519.245283	N	***501.314357***	251.160816	484.287808	242.647542			4
9	1154.562269	577.784773	1137.535720	569.271498	1136.551704	568.779490	V	***387.271430***	194.139353	370.244881	185.626078			3
10	**1267.646333**	634.326805	1250.619784	625.813530	1249.635768	625.321522	L	***288.203016***	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.5	1440.750717	0.007851	AASGTQNNVLR
6.1	1440.757202	0.001366	NNLLQAELEELR
5.5	1440.739487	0.019081	AAVTGQDEAIR
5.0	1440.779709	-0.021141	AAAGVGGSLRAQVER
4.5	1440.743317	0.015251	TQHLSAARSSDLR
4.5	1440.743515	0.015053	FIQLLTEFQMR
4.1	1440.764618	-0.006050	LEEEIQTLR
1.3	1440.773163	-0.014595	KRALEAGAGCRPR
1.3	1440.775864	-0.017296	ADILEMTVKHLR
1.2	1440.754745	0.003823	WEATQQVLR

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

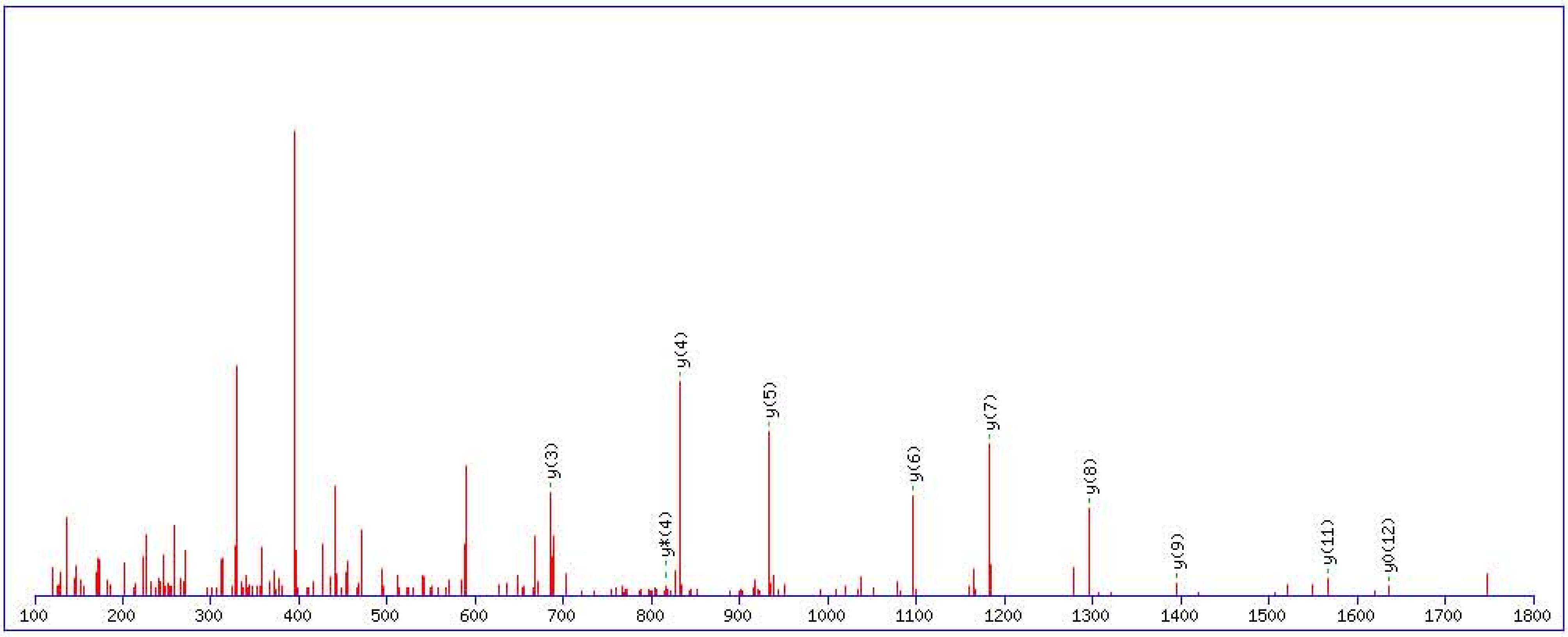
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSGNVLSYTFQVK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

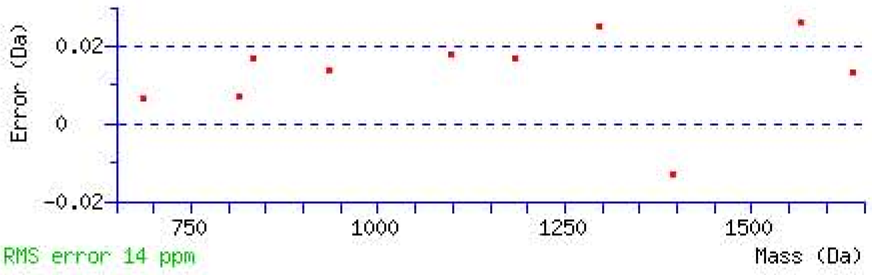
Match to Query 47597: 1765.963332 from(589.661720,3+) rtinseconds(2444) index(9916)
Title: Locus:1.1.1.2983.9 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

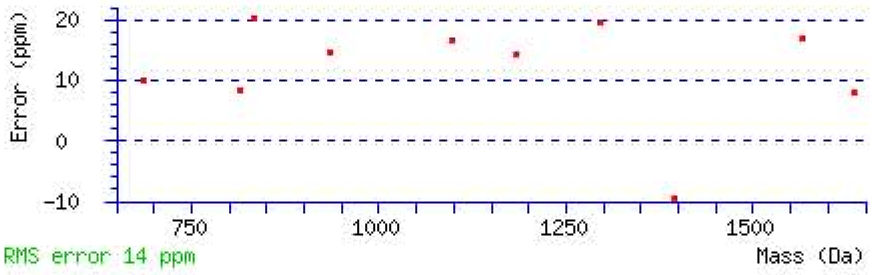
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1765.943680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 2.2e-005
Matches : 10/128 fragment ions using 17 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							13
2	201.123368	101.065322			183.112803	92.060039	S	1653.866891	827.437084	1636.840342	818.923809	1635.856326	818.431801	12
3	258.144832	129.576054			240.134267	120.570771	G	***1566.834863***	783.921070	1549.808314	775.407795	1548.824298	774.915787	11
4	372.187759	186.597517	355.161210	178.084243	354.177194	177.592235	N	1509.813399	755.410338	1492.786850	746.897063	1491.802834	746.405055	10
5	471.256173	236.131724	454.229624	227.618450	453.245608	227.126442	V	***1395.770472***	698.388874	1378.743923	689.875600	1377.759907	689.383592	9
6	584.340237	292.673757	567.313688	284.160482	566.329672	283.668474	L	***1296.702058***	648.854667	1279.675509	640.341393	1278.691493	639.849385	8
7	671.372265	336.189771	654.345716	327.676496	653.361700	327.184488	S	***1183.617994***	592.312635	1166.591445	583.799361	1165.607429	583.307353	7
8	834.435594	417.721435	817.409045	409.208161	816.425029	408.716153	Y	***1096.585966***	548.796621	1079.559417	540.283347	1078.575401	539.791339	6
9	935.483273	468.245275	918.456724	459.732000	917.472708	459.239992	T	***933.522637***	467.264957	916.496088	458.751682	915.512072	458.259674	5
10	1082.551687	541.779482	1065.525138	533.266207	1064.541122	532.774199	F	***832.474958***	416.741117	815.448409	408.227843			4
11	1521.777013	761.392145	1504.750464	752.878870	1503.766448	752.386862	Q	***685.406544***	343.206910	668.379995	334.693636			3
12	1620.845427	810.926352	1603.818878	802.413077	1602.834862	801.921069	V	246.181218	123.594247	229.154669	115.080973			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.0	1765.943680	0.019652	LSGNVLSYTFQVK
1.3	1765.982544	-0.019212	SLQLDIIPASIPGSEVK
0.4	1765.940262	0.023070	EAKLYLFQAQEWLK
0.1	1765.950882	0.012450	VTGNVSKKTNYLVMGR

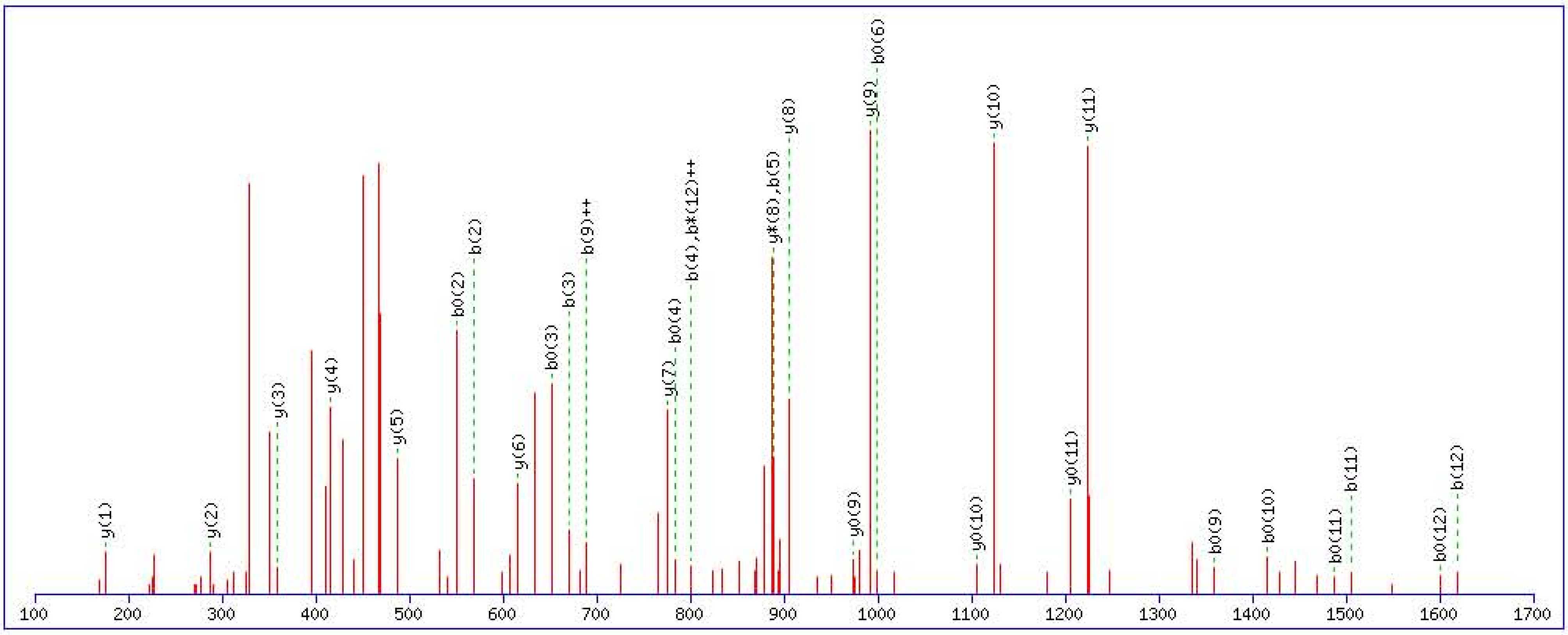
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQTMSECEAGALR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

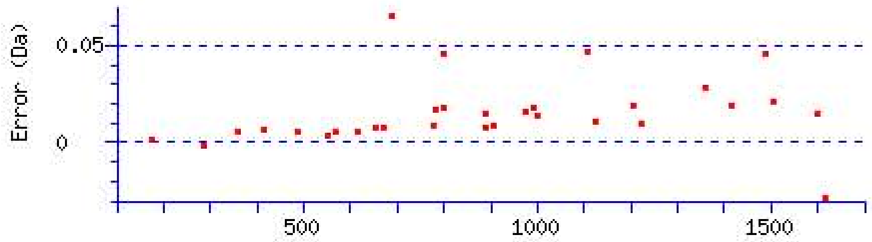
Match to Query 48236: 1791.806528 from(896.910540,2+) rtinseconds(1715) index(5147)
Title: Locus:1.1.1.2729.21 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

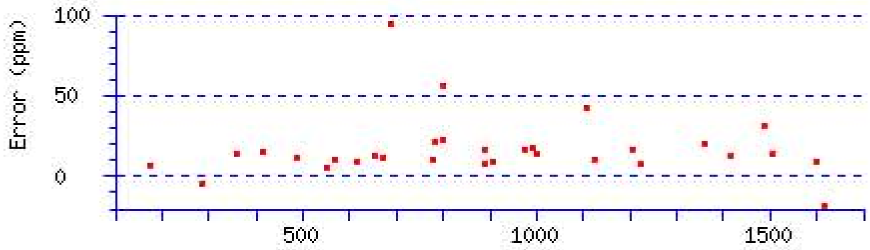


```
Monoisotopic mass of neutral peptide Mr(calc): 1791.795349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 5.6e-006
Matches : 31/132 fragment ions using 55 most intense peaks   (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							13
2	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1663.760061	832.383668	1646.733512	823.870394	1645.749496	823.378386	12
3	**670.322874**	335.665075	653.296325	327.151801	652.312309	326.659793	T	***1224.534735***	612.771005	1207.508186	604.257731	1206.524170	603.765723	11
4	**801.363359**	401.185318	784.336810	392.672043	783.352794	392.180035	M	***1123.487056***	562.247166	1106.460507	553.733891	1105.476491	553.241883	10
5	**888.395387**	444.701332	871.368838	436.188057	870.384822	435.696049	S	***992.446571***	496.726923	975.420022	488.213649	974.436006	487.721641	9
6	1017.437980	509.222628	1000.411431	500.709354	999.427415	500.217346	E	***905.414543***	453.210909	888.387994	444.697635	887.403978	444.205627	8
7	1177.468629	589.237953	1160.442080	580.724678	1159.458064	580.232670	C	***776.371950***	388.689613	759.345401	380.176338	758.361385	379.684330	7
8	1306.511222	653.759249	1289.484673	645.245974	1288.500657	644.753966	E	***616.341301***	308.674288	599.314752	300.161014	598.330736	299.669006	6
9	1377.548336	689.277806	1360.521787	680.764531	1359.537771	680.272523	A	***487.298708***	244.152992	470.272159	235.639717			5
10	1434.569800	717.788538	1417.543251	709.275263	1416.559235	708.783255	G	***416.261594***	208.634435	399.235045	200.121160			4
11	**1505.606914**	753.307095	1488.580365	744.793820	1487.596349	744.301812	A	***359.240130***	180.123703	342.213581	171.610428			3
12	**1618.690978**	809.849127	1601.664429	801.335852	1600.680413	800.843844	L	***288.203016***	144.605146	271.176467	136.091871			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 25 ppm



RMS error 25 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.3	1791.795349	0.011179	EQTMSECEAGALR

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

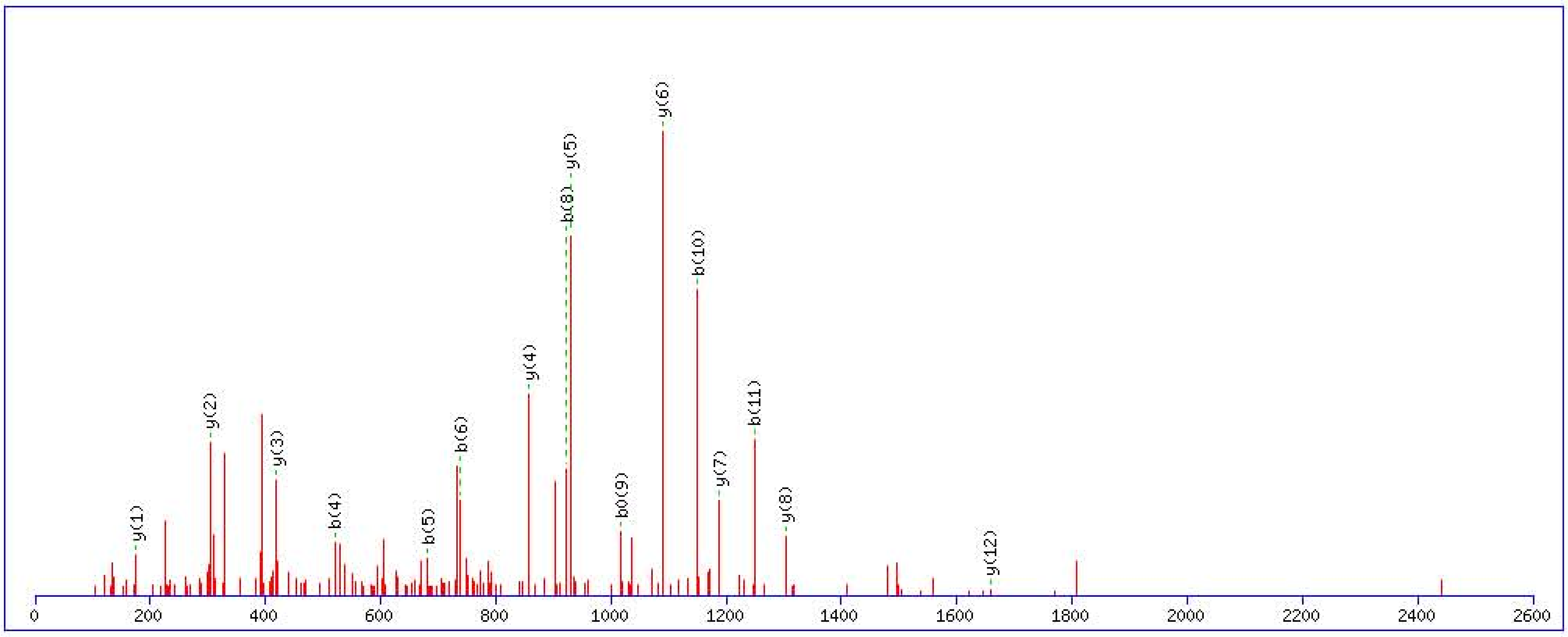
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPYECGPSLDVCAQDER**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

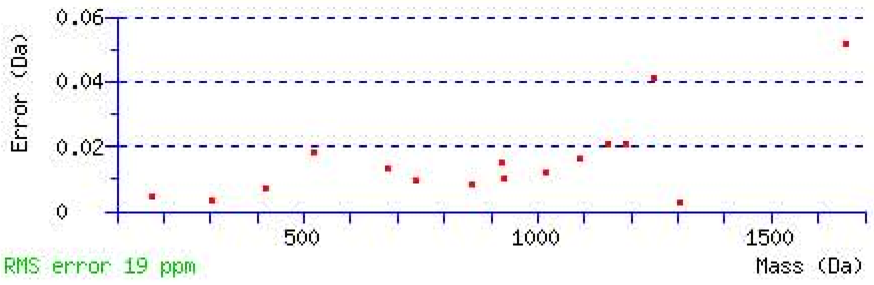
Match to Query 61496: 2337.019302 from(780.013710,3+) rtinseconds(2083) index(7552)
Title: Locus:1.1.1.2857.19 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

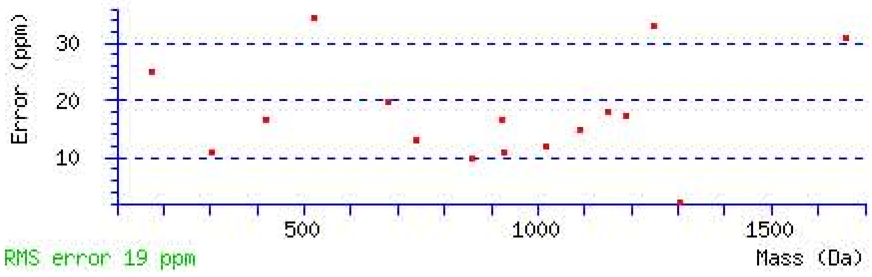
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2336.989792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00011
Matches : 16/158 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							17
2	229.100525	115.053900					P	2206.956589	1103.981932	2189.930040	1095.468658	2188.946024	1094.976650	16
3	392.163854	196.585565					Y	2109.903825	1055.455550	2092.877276	1046.942276	2091.893260	1046.450268	15
4	***521.206447***	261.106862			503.195882	252.101579	E	1946.840496	973.923886	1929.813947	965.410612	1928.829931	964.918604	14
5	***681.237096***	341.122186			663.226531	332.116904	C	1817.797903	909.402590	1800.771354	900.889315	1799.787338	900.397307	13
6	***738.258560***	369.632918			720.247995	360.627636	G	***1657.767254***	829.387265	1640.740705	820.873991	1639.756689	820.381983	12
7	835.311324	418.159300			817.300759	409.154018	P	1600.745790	800.876533	1583.719241	792.363259	1582.735225	791.871251	11
8	***922.343352***	461.675314			904.332787	452.670032	S	1503.693026	752.350151	1486.666477	743.836877	1485.682461	743.344869	10
9	1035.427416	518.217346			1017.416851	509.212064	L	1416.660998	708.834137	1399.634449	700.320863	1398.650433	699.828855	9
10	***1150.454359***	575.730818			1132.443794	566.725535	D	***1303.576934***	652.292105	1286.550385	643.778831	1285.566369	643.286823	8
11	***1249.522773***	625.265025			1231.512208	616.259742	V	***1188.549991***	594.778634	1171.523442	586.265359	1170.539426	585.773351	7
12	1409.553422	705.280349			1391.542857	696.275067	C	***1089.481577***	545.244427	1072.455028	536.731152	1071.471012	536.239144	6
13	1480.590536	740.798906			1462.579971	731.793624	A	***929.450928***	465.229102	912.424379	456.715827	911.440363	456.223819	5
14	1919.815862	960.411569	1902.789313	951.898295	1901.805297	951.406287	Q	***858.413814***	429.710545	841.387265	421.197271	840.403249	420.705263	4
15	2034.842805	1017.925041	2017.816256	1009.411766	2016.832240	1008.919758	D	***419.188488***	210.097882	402.161939	201.584607	401.177923	201.092599	3
16	2163.885398	1082.446337	2146.858849	1073.933062	2145.874833	1073.441054	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
17							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.3	2336.989792	0.029510	MPYECGPSLDVCAQDER

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

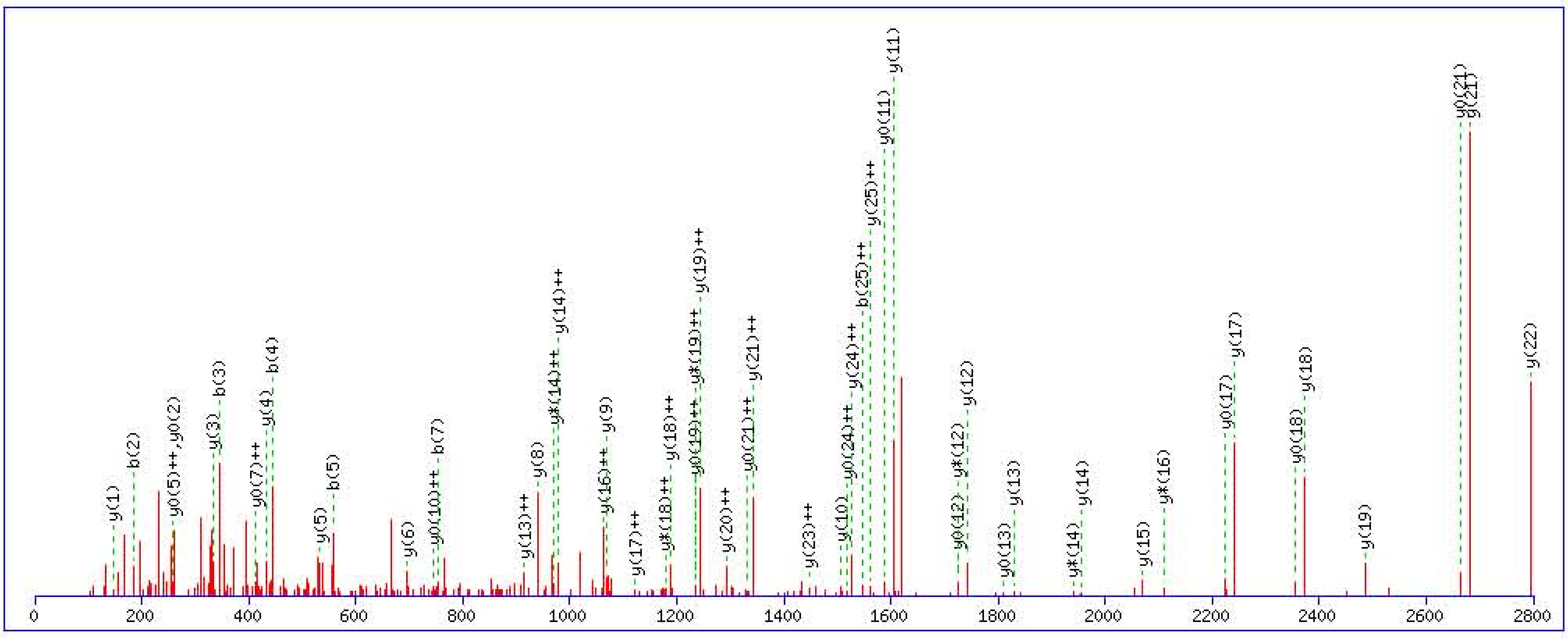
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IACVLPVLMDGIQSHPQKPFYTVGEK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

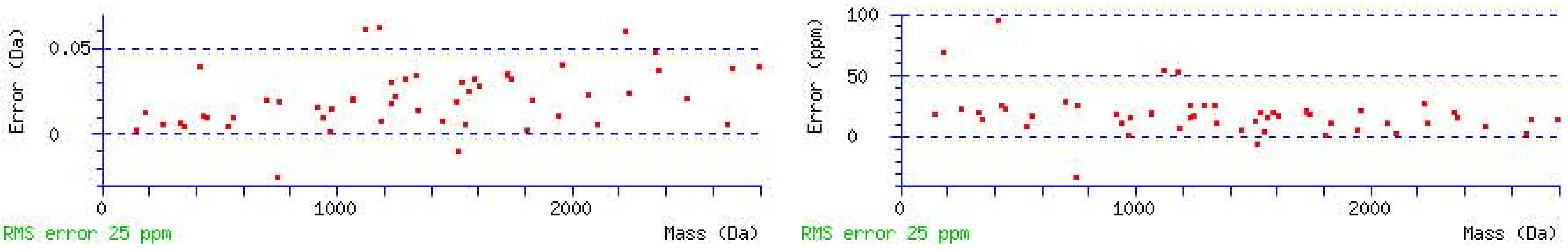
Match to Query 74705: 3237.719496 from(810.437150,4+) rtinseconds(2545) index(10452)
Title: Locus:1.1.1.3018.11 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3237.675262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17    : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 1.5e-005
Matches : 54/256 fragment ions using 160 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							26
2	**185.128454**	93.067865					A	3125.598471	1563.302873	3108.571922	1554.789599	3107.587906	1554.297591	25
3	**345.159103**	173.083190					C	3054.561357	1527.784316	3037.534808	1519.271042	3036.550792	1518.779034	24
4	**444.227517**	222.617397					V	2894.530708	1447.768992	2877.504159	1439.255717	2876.520143	1438.763709	23
5	**557.311581**	279.159429					L	***2795.462294***	1398.234785	2778.435745	1389.721510	2777.451729	1389.229502	22
6	654.364345	327.685811					P	***2682.378230***	1341.692753	2665.351681	1333.179478	2664.367665	1332.687470	21
7	**753.432759**	377.220018					V	2585.325466	1293.166371	2568.298917	1284.653096	2567.314901	1284.161088	20
8	866.516823	433.762050					L	***2486.257052***	1243.632164	2469.230503	1235.118889	2468.246487	1234.626881	19
9	997.557308	499.282292					M	***2373.172988***	1187.090132	2356.146439	1178.576857	2355.162423	1178.084849	18
10	1112.584251	556.795764			1094.573686	547.790481	D	***2242.132503***	1121.569889	2225.105954	1113.056615	2224.121938	1112.564607	17
11	1169.605715	585.306495			1151.595150	576.301213	G	2127.105560	1064.056418	2110.079011	1055.543143	2109.094995	1055.051135	16
12	1282.689779	641.848527			1264.679214	632.843245	I	***2070.084096***	1035.545686	2053.057547	1027.032411	2052.073531	1026.540403	15
13	1410.748357	705.877816	1393.721808	697.364542	1392.737792	696.872534	Q	***1957.000032***	979.003654	1939.973483	970.490380	1938.989467	969.998371	14
14	1497.780385	749.393830	1480.753836	740.880556	1479.769820	740.388548	S	***1828.941454***	914.974365	1811.914905	906.461091	1810.930889	905.969083	13
15	1634.839297	817.923286	1617.812748	809.410012	1616.828732	808.918004	H	***1741.909426***	871.458351	1724.882877	862.945077	1723.898861	862.453068	12
16	1731.892061	866.449668	1714.865512	857.936394	1713.881496	857.444386	P	***1604.850514***	802.928895	1587.823965	794.415621	1586.839949	793.923612	11
17	2171.117387	1086.062331	2154.090838	1077.549057	2153.106822	1077.057049	Q	***1507.797750***	754.402513	1490.771201	745.889239	1489.787185	745.397230	10
18	2299.212350	1150.109813	2282.185801	1141.596538	2281.201785	1141.104530	K	***1068.572424***	534.789850	1051.545875	526.276575	1050.561859	525.784567	9
19	2396.265114	1198.636195	2379.238565	1190.122920	2378.254549	1189.630912	P	***940.477461***	470.742368	923.450912	462.229094	922.466896	461.737086	8
20	2543.333528	1272.170402	2526.306979	1263.657127	2525.322963	1263.165119	F	843.424697	422.215986	826.398148	413.702712	825.414132	413.210704	7
21	2706.396857	1353.702066	2689.370308	1345.188792	2688.386292	1344.696784	Y	***696.356283***	348.681779	679.329734	340.168505	678.345718	339.676497	6
22	2807.444536	1404.225906	2790.417987	1395.712631	2789.433971	1395.220623	T	***533.292954***	267.150115	516.266405	258.636840	515.282389	258.144832	5
23	2906.512950	1453.760113	2889.486401	1445.246838	2888.502385	1444.754830	V	***432.245275***	216.626275	415.218726	208.113001	414.234710	207.620993	4
24	2963.534414	1482.270845	2946.507865	1473.757570	2945.523849	1473.265562	G	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	3
25	3092.577007	1546.792141	3075.550458	1538.278867	3074.566442	1537.786859	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
26							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.2	3237.675262	0.044234	IACVLPVLMDGIQSHPQKPFYTVGEK
40.0	3237.675262	0.044234	IACVLPVLMDGIQSHPQKPFYTVGEK

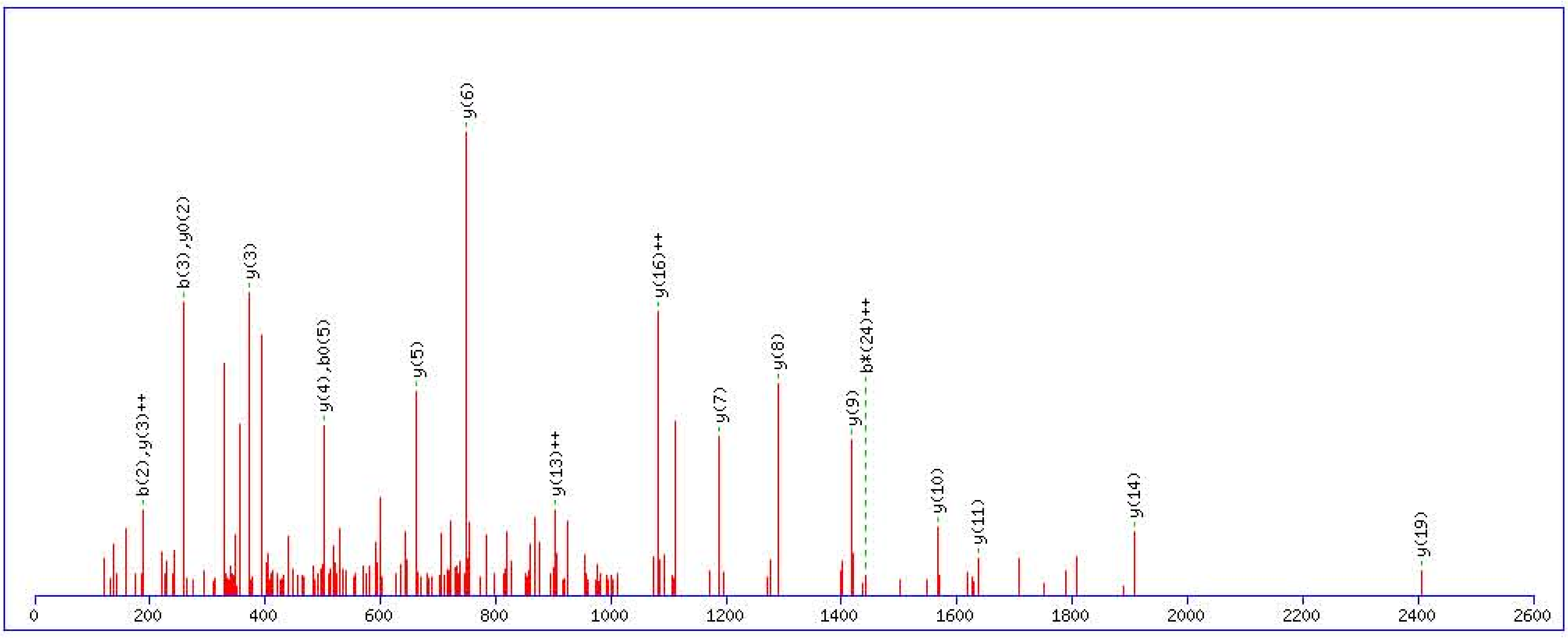
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVAVYGQYGGQPCVGNAFETQSCEPTR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

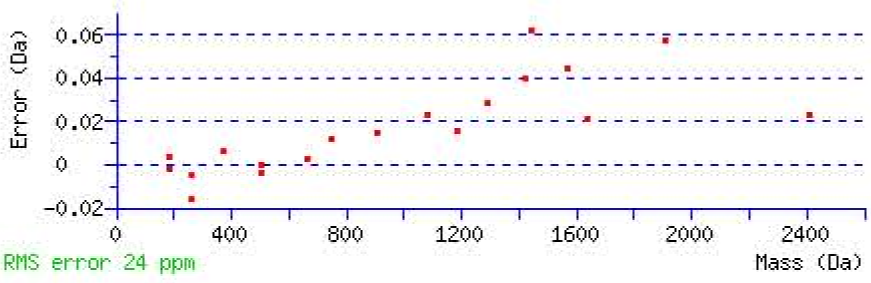
Match to Query 75774: 3272.507136 from(819.134060,4+) rtinseconds(2152) index(8050)
Title: Locus:1.1.1.2881.24 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

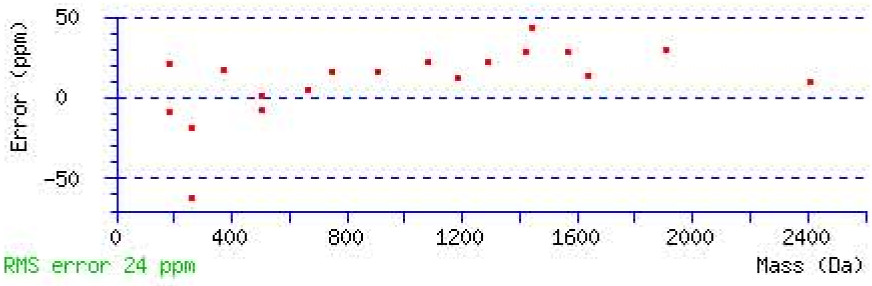
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3272.468933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21    : Biotin:Thermo-21345 (Q)
Ions Score: 86  Expect: 3.4e-008
Matches : 19/298 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							27
2	**187.107718**	94.057497			169.097153	85.052214	V	3186.444157	1593.725716	3169.417608	1585.212442	3168.433592	1584.720434	26
3	**258.144832**	129.576054			240.134267	120.570772	A	3087.375743	1544.191509	3070.349194	1535.678235	3069.365178	1535.186227	25
4	357.213246	179.110261			339.202681	170.104979	V	3016.338629	1508.672952	2999.312080	1500.159678	2998.328064	1499.667670	24
5	520.276575	260.641926			502.266010	251.636643	Y	2917.270215	1459.138745	2900.243666	1450.625471	2899.259650	1450.133463	23
6	577.298039	289.152658			559.287474	280.147375	G	2754.206886	1377.607081	2737.180337	1369.093806	2736.196321	1368.601798	22
7	705.356617	353.181947	688.330068	344.668672	687.346052	344.176664	Q	2697.185422	1349.096349	2680.158873	1340.583074	2679.174857	1340.091066	21
8	868.419946	434.713611	851.393397	426.200337	850.409381	425.708329	Y	2569.126844	1285.067060	2552.100295	1276.553785	2551.116279	1276.061777	20
9	925.441410	463.224343	908.414861	454.711069	907.430845	454.219061	G	***2406.063515***	1203.535395	2389.036966	1195.022121	2388.052950	1194.530113	19
10	982.462874	491.735075	965.436325	483.221801	964.452309	482.729793	G	2349.042051	1175.024663	2332.015502	1166.511389	2331.031486	1166.019381	18
11	1110.521452	555.764364	1093.494903	547.251090	1092.510887	546.759082	Q	2292.020587	1146.513931	2274.994038	1138.000657	2274.010022	1137.508649	17
12	1207.574216	604.290746	1190.547667	595.777472	1189.563651	595.285464	P	2163.962009	1082.484642	2146.935460	1073.971368	2145.951444	1073.479360	16
13	1367.604865	684.306071	1350.578316	675.792796	1349.594300	675.300788	C	2066.909245	1033.958260	2049.882696	1025.444986	2048.898680	1024.952978	15
14	1466.673279	733.840278	1449.646730	725.327003	1448.662714	724.834995	V	***1906.878596***	953.942936	1889.852047	945.429662	1888.868031	944.937654	14
15	1523.694743	762.351010	1506.668194	753.837735	1505.684178	753.345727	G	1807.810182	904.408729	1790.783633	895.895455	1789.799617	895.403446	13
16	1637.737670	819.372473	1620.711121	810.859199	1619.727105	810.367191	N	1750.788718	875.897997	1733.762169	867.384723	1732.778153	866.892715	12
17	1708.774784	854.891030	1691.748235	846.377756	1690.764219	845.885748	A	***1636.745791***	818.876534	1619.719242	810.363259	1618.735226	809.871251	11
18	1855.843198	928.425237	1838.816649	919.911963	1837.832633	919.419955	F	***1565.708677***	783.357977	1548.682128	774.844702	1547.698112	774.352694	10
19	1984.885791	992.946534	1967.859242	984.433259	1966.875226	983.941251	E	***1418.640263***	709.823770	1401.613714	701.310495	1400.629698	700.818487	9
20	2085.933470	1043.470373	2068.906921	1034.957098	2067.922905	1034.465090	T	***1289.597670***	645.302473	1272.571121	636.789199	1271.587105	636.297190	8
21	2525.158796	1263.083036	2508.132247	1254.569761	2507.148231	1254.077754	Q	***1188.549991***	594.778634	1171.523442	586.265359	1170.539426	585.773351	7
22	2612.190824	1306.599050	2595.164275	1298.085776	2594.180259	1297.593768	S	***749.324665***	375.165970	732.298116	366.652696	731.314100	366.160688	6
23	2772.221473	1386.614374	2755.194924	1378.101100	2754.210908	1377.609092	C	***662.292637***	331.649956	645.266088	323.136682	644.282072	322.644674	5
24	2901.264066	1451.135671	2884.237517	1442.622396	2883.253501	1442.130389	E	***502.261988***	251.634632	485.235439	243.121357	484.251423	242.629349	4
25	2998.316830	1499.662053	2981.290281	1491.148778	2980.306265	1490.656771	P	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
26	3099.364509	1550.185892	3082.337960	1541.672618	3081.353944	1541.180610	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
27							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
85.8	3272.468933	0.038203	SVAVYGQYGGQPCVGNAFETQSCEPTR
13.1	3272.468933	0.038203	SVAVYGQYGGQPCVGNAFETQSCEPTR
6.8	3272.468933	0.038203	SVAVYGQYGGQPCVGNAFETQSCEPTR

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

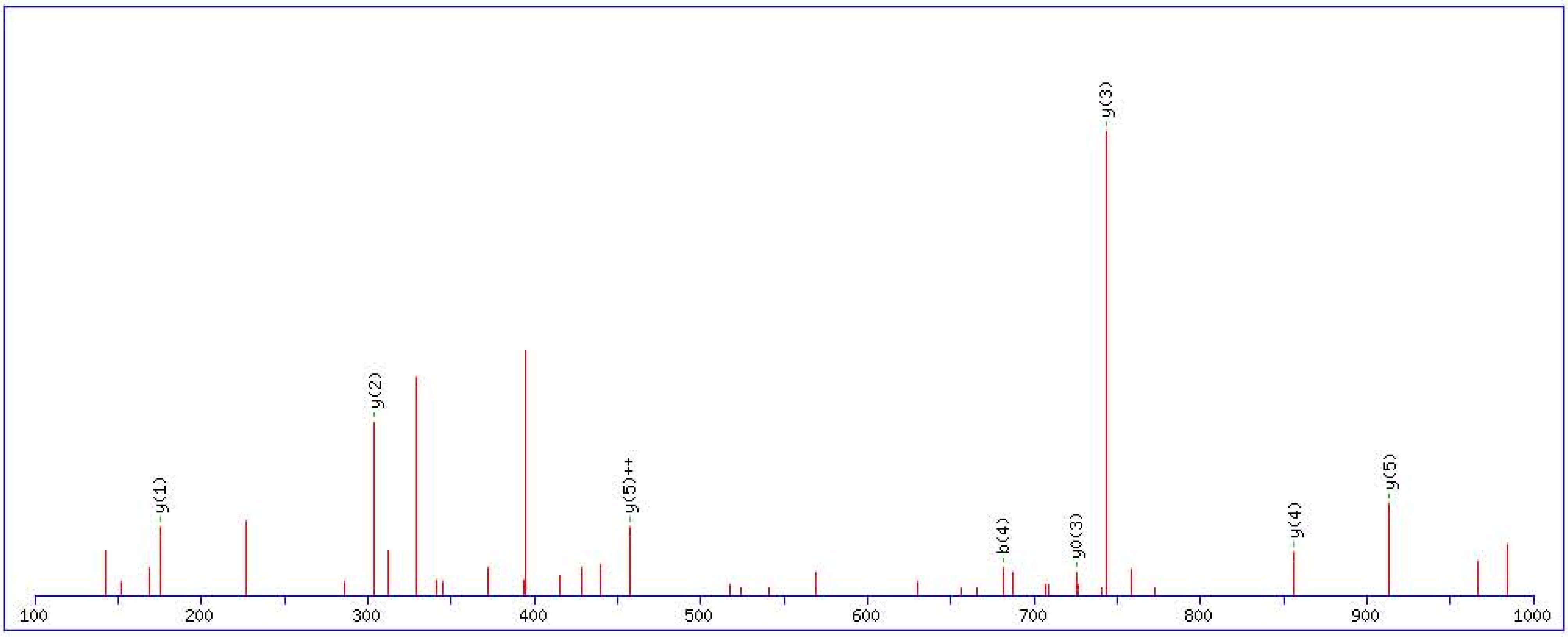
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGIQER**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

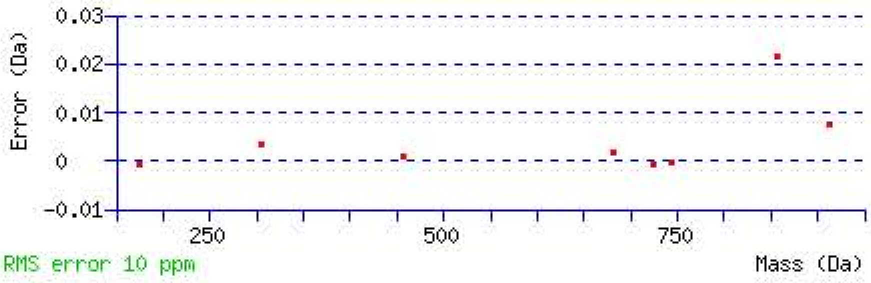
Match to Query 18479: 983.520568 from(492.767560,2+) rtinseconds(1386) index(37988)
Title: Locus:1.1.1.2766.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

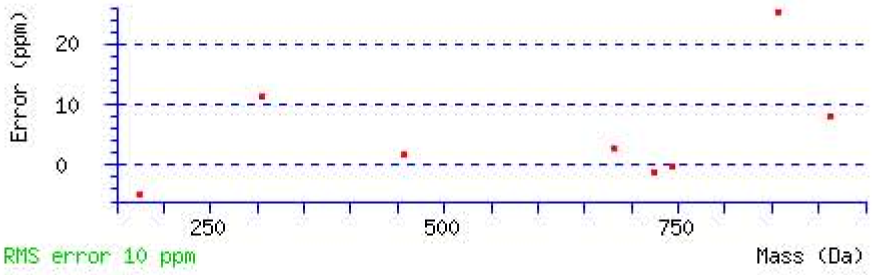
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 983.522217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.043
Matches : 8/44 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							6
2	129.065854	65.036565					G	***913.492399***	457.249838	896.465850	448.736563	895.481834	448.244555	5
3	242.149918	121.578597					I	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
4	681.375244	341.191260	664.348695	332.677986			Q	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
5	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
6							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.7	983.522217	-0.001649	AGIQER
15.9	983.522217	-0.001649	QIQER
15.9	983.522217	-0.001649	QLQER
15.7	983.522217	-0.001649	AGLQER
11.1	983.530090	-0.009522	QLLNHFGR
7.9	983.522217	-0.001649	IQQER
7.9	983.522217	-0.001649	LQQER
7.5	983.514832	0.005736	QSVEKTHR
6.9	983.522202	-0.001634	KLMENPPR
6.9	983.522217	-0.001649	QLEQR

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

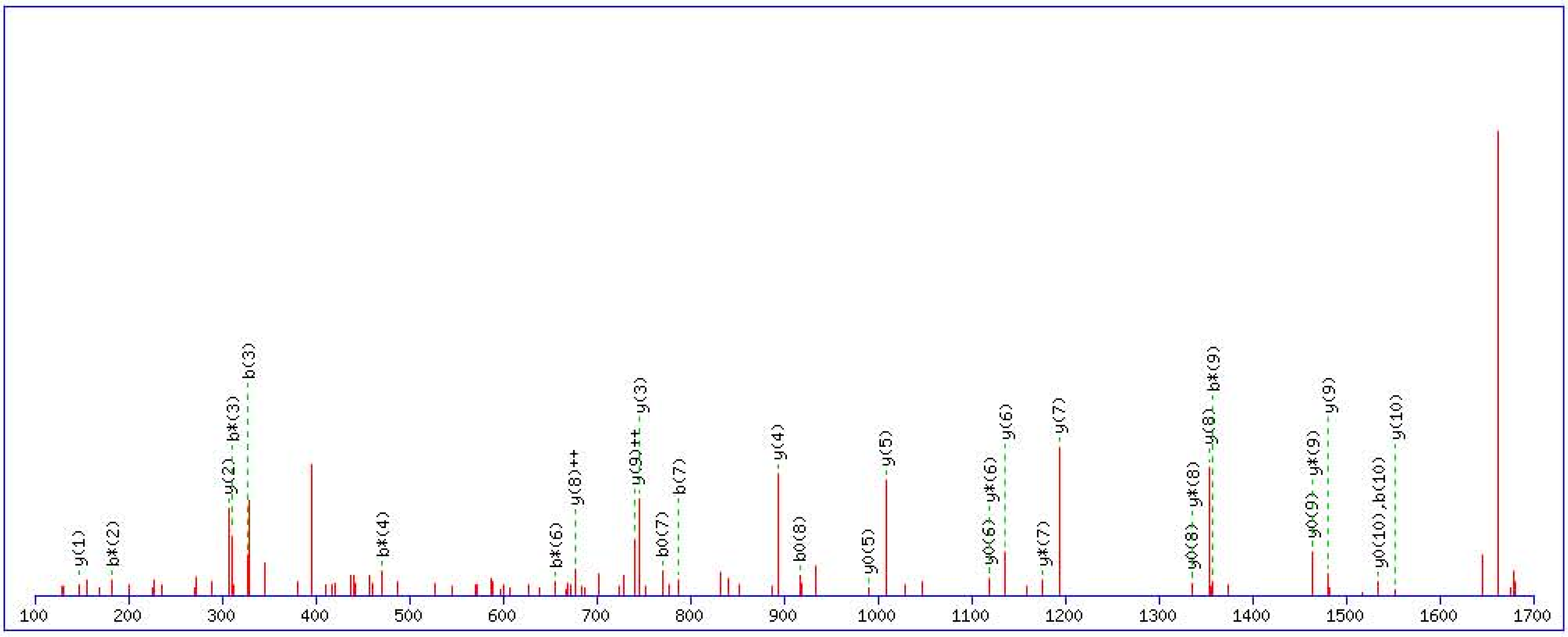
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QAQCGQDFQCK**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

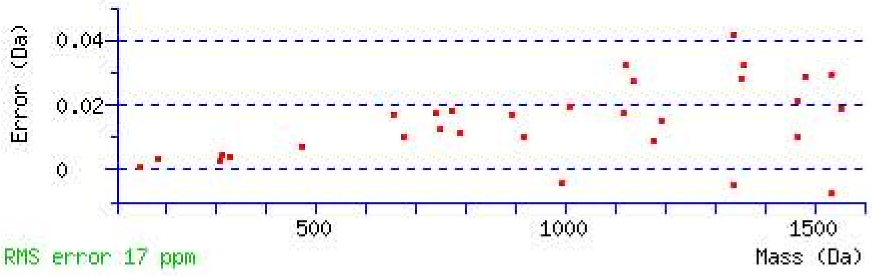
Match to Query 45335: 1679.738508 from(840.876530,2+) rtinseconds(1508) index(21253)
Title: Locus:1.1.1.2479.18 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

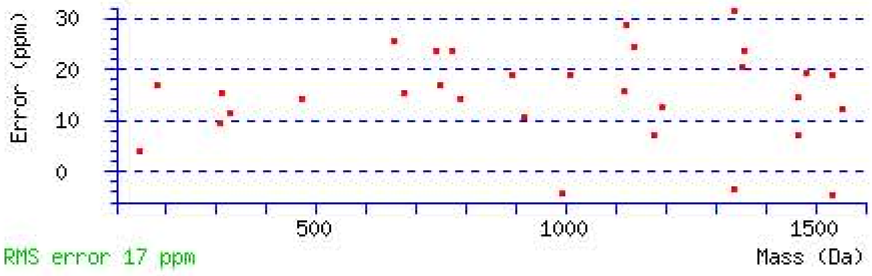
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1679.721832
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 60 **Expect:** 6.1e-006
Matches : 31/100 fragment ions using 57 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							11
2	200.102968	100.555122	183.076419	92.041848			A	***1552.670519***	776.838898	1535.643970	768.325623	1534.659954	767.833615	10
3	**328.161546**	164.584411	311.134997	156.071136			Q	***1481.633405***	741.320341	1464.606856	732.807066	1463.622840	732.315058	9
4	488.192195	244.599736	471.165646	236.086461			C	***1353.574827***	677.291052	1336.548278	668.777777	1335.564262	668.285769	8
5	545.213659	273.110468	528.187110	264.597193			G	***1193.544178***	597.275727	1176.517629	588.762453	1175.533613	588.270445	7
6	673.272237	337.139757	656.245688	328.626482			Q	***1136.522714***	568.764995	1119.496165	560.251721	1118.512149	559.759713	6
7	**788.299180**	394.653228	771.272631	386.139954	770.288615	385.647946	D	***1008.464136***	504.735706	991.437587	496.222432	990.453571	495.730424	5
8	935.367594	468.187435	918.341045	459.674161	917.357029	459.182153	F	***893.437193***	447.222235	876.410644	438.708960			4
9	1374.592920	687.800098	1357.566371	679.286824	1356.582355	678.794816	Q	***746.368779***	373.688028	729.342230	365.174753			3
10	**1534.623569**	767.815423	1517.597020	759.302148	1516.613004	758.810140	C	***307.143453***	154.075365	290.116904	145.562090			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.0	1679.721832	0.016676	QAQCGQDFQCK
25.1	1679.721832	0.016676	QAQCGQDFQCK
5.0	1679.760681	-0.022173	CGQAGDASLMELEKR
0.5	1679.740250	-0.001742	RGGGNEMNCCRTLR

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

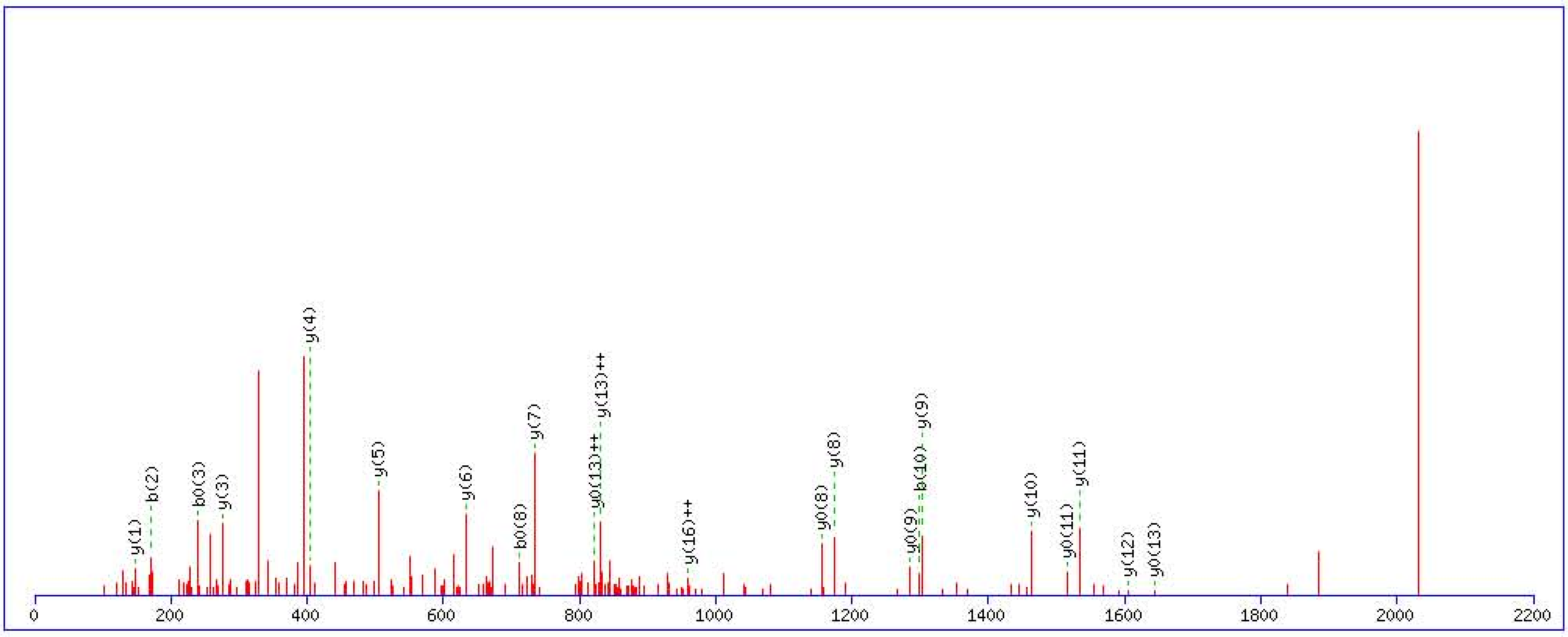
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGSLGAACEQTQTEGAK**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

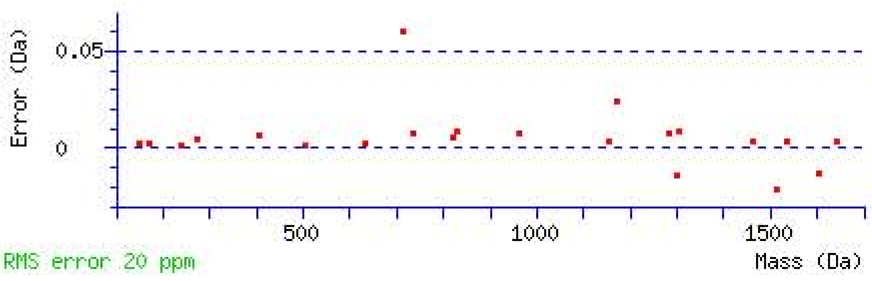
Match to Query 54503: 2030.982522 from(678.001450,3+) rtinseconds(1702) index(40093)
Title: Locus:1.1.1.2876.20 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

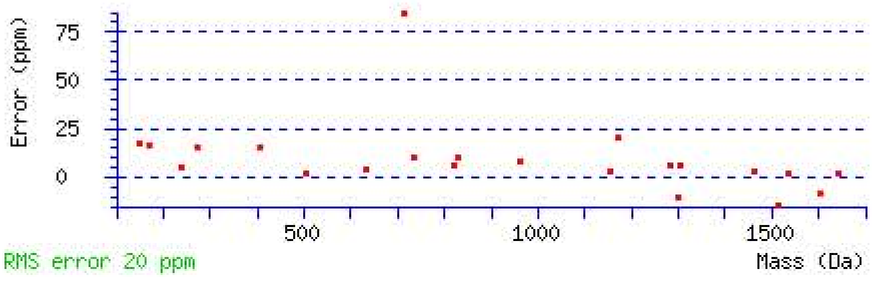
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2030.976501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 76 **Expect:** 1e-007
Matches : 22/164 fragment ions using 34 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							17
2	**171.112804**	86.060040					G	1918.899727	959.953502	1901.873178	951.440227	1900.889162	950.948219	16
3	258.144832	129.576054			240.134267	120.570772	S	1861.878263	931.442770	1844.851714	922.929495	1843.867698	922.437487	15
4	371.228896	186.118086			353.218331	177.112804	L	1774.846235	887.926756	1757.819686	879.413481	1756.835670	878.921473	14
5	428.250360	214.628818			410.239795	205.623536	G	1661.762171	831.384724	1644.735622	822.871449	1643.751606	822.379441	13
6	499.287474	250.147375			481.276909	241.142093	A	***1604.740707***	802.873992	1587.714158	794.360717	1586.730142	793.868709	12
7	570.324588	285.665932			552.314023	276.660650	A	***1533.703593***	767.355435	1516.677044	758.842160	1515.693028	758.350152	11
8	730.355237	365.681257			712.344672	356.675974	C	***1462.666479***	731.836878	1445.639930	723.323603	1444.655914	722.831595	10
9	859.397830	430.202553			841.387265	421.197271	E	***1302.635830***	651.821553	1285.609281	643.308279	1284.625265	642.816270	9
10	**1298.623156**	649.815216	1281.596607	641.301942	1280.612591	640.809934	Q	***1173.593237***	587.300257	1156.566688	578.786982	1155.582672	578.294974	8
11	1399.670835	700.339056	1382.644286	691.825781	1381.660270	691.333773	T	***734.367911***	367.687594	717.341362	359.174319	716.357346	358.682311	7
12	1527.729413	764.368345	1510.702864	755.855070	1509.718848	755.363062	Q	***633.320232***	317.163754	616.293683	308.650480	615.309667	308.158472	6
13	1628.777092	814.892184	1611.750543	806.378910	1610.766527	805.886902	T	***505.261654***	253.134465	488.235105	244.621190	487.251089	244.129182	5
14	1757.819685	879.413481	1740.793136	870.900206	1739.809120	870.408198	E	***404.213975***	202.610625	387.187426	194.097351	386.203410	193.605343	4
15	1814.841149	907.924213	1797.814600	899.410938	1796.830584	898.918930	G	***275.171382***	138.089329	258.144833	129.576054			3
16	1885.878263	943.442770	1868.851714	934.929495	1867.867698	934.437487	A	218.149918	109.578597	201.123369	101.065322			2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.8	2030.976501	0.006021	LGSLGAACEQTQTEGAK
42.9	2030.976501	0.006021	LGSLGAACEQTQTEGAK
1.2	2030.958710	0.023812	QPMNAASGAAMSLAGAEK

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

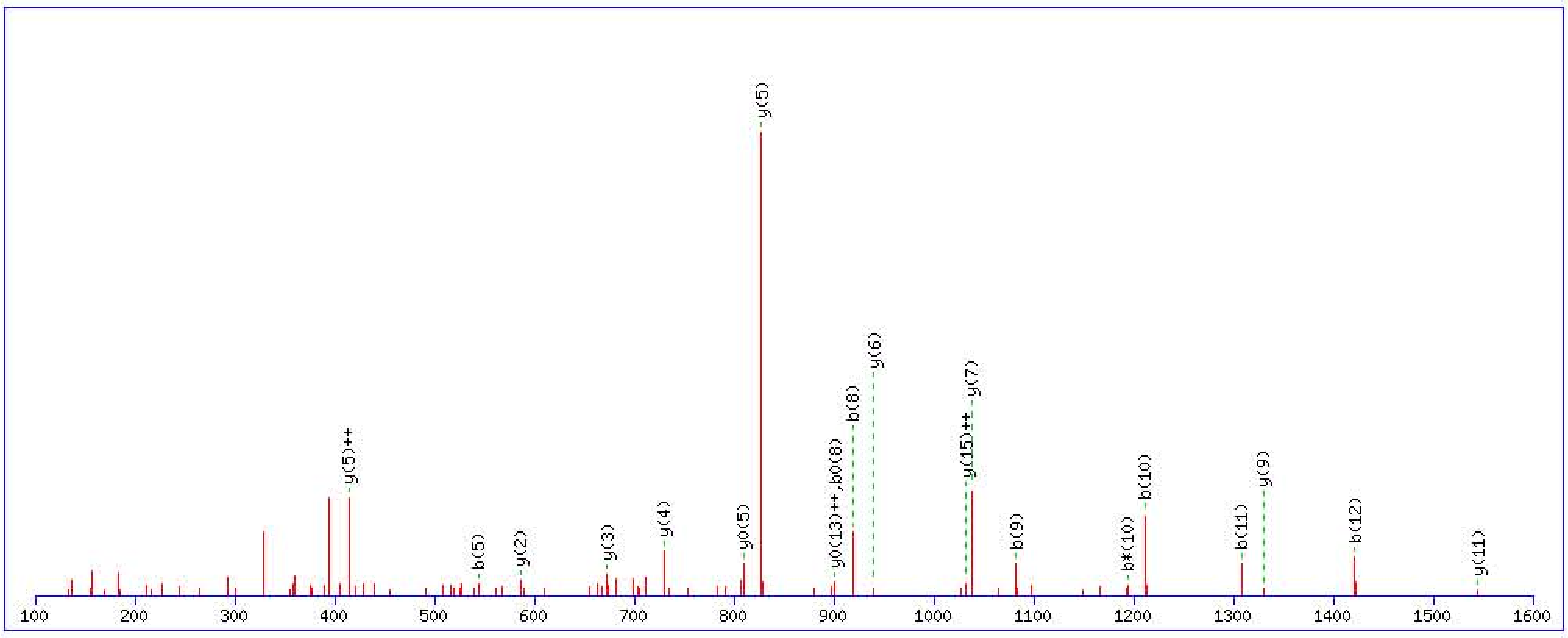
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIDEDCSQYEPIPGSQK**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

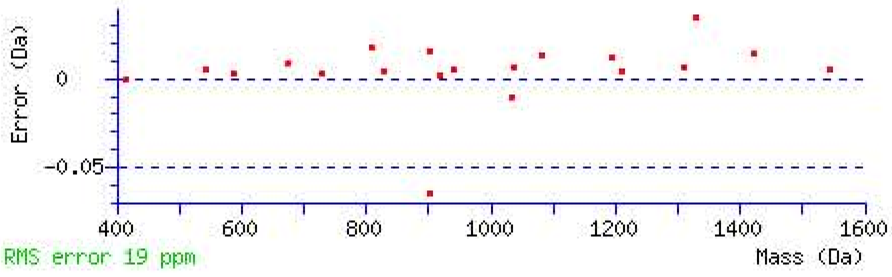
Match to Query 59288: 2247.034242 from(750.018690,3+) rtinseconds(1885) index(41289)
Title: Locus:1.1.1.2940.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

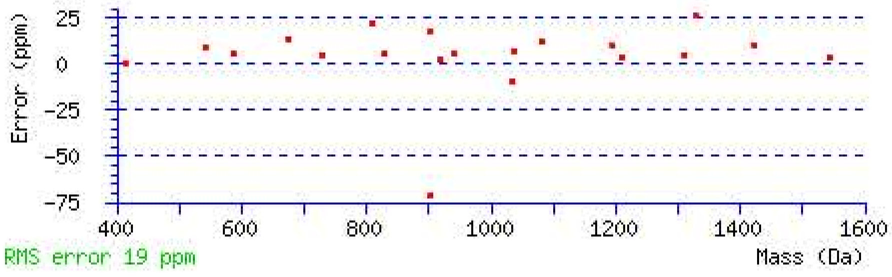
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2247.018753
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 1.4e-005
Matches : 20/170 fragment ions using 27 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							17
2	185.128454	93.067865					I	2176.988934	1088.998105	2159.962385	1080.484830	2158.978369	1079.992822	16
3	300.155397	150.581336			282.144832	141.576054	D	2063.904870	1032.456073	2046.878321	1023.942798	2045.894305	1023.450790	15
4	429.197990	215.102633			411.187425	206.097351	E	1948.877927	974.942602	1931.851378	966.429327	1930.867362	965.937319	14
5	***544.224933***	272.616105			526.214368	263.610822	D	1819.835334	910.421305	1802.808785	901.908031	1801.824769	901.416022	13
6	704.255582	352.631429			686.245017	343.626147	C	1704.808391	852.907833	1687.781842	844.394559	1686.797826	843.902551	12
7	791.287610	396.147443			773.277045	387.142161	S	***1544.777742***	772.892509	1527.751193	764.379235	1526.767177	763.887227	11
8	***919.346188***	460.176732	902.319639	451.663458	901.335623	451.171450	Q	1457.745714	729.376495	1440.719165	720.863221	1439.735149	720.371212	10
9	***1082.409517***	541.708397	1065.382968	533.195122	1064.398952	532.703114	Y	***1329.687136***	665.347206	1312.660587	656.833931	1311.676571	656.341923	9
10	***1211.452110***	606.229693	1194.425561	597.716419	1193.441545	597.224410	E	1166.623807	583.815541	1149.597258	575.302267	1148.613242	574.810259	8
11	***1308.504874***	654.756075	1291.478325	646.242801	1290.494309	645.750792	P	***1037.581214***	519.294245	1020.554665	510.780971	1019.570649	510.288963	7
12	***1421.588938***	711.298107	1404.562389	702.784832	1403.578373	702.292824	I	***940.528450***	470.767863	923.501901	462.254589	922.517885	461.762581	6
13	1518.641702	759.824489	1501.615153	751.311215	1500.631137	750.819206	P	***827.444386***	414.225831	810.417837	405.712557	809.433821	405.220549	5
14	1575.663166	788.335221	1558.636617	779.821946	1557.652601	779.329938	G	***730.391622***	365.699449	713.365073	357.186175	712.381057	356.694167	4
15	1662.695194	831.851235	1645.668645	823.337961	1644.684629	822.845952	S	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
16	2101.920520	1051.463898	2084.893971	1042.950623	2083.909955	1042.458615	Q	***586.338130***	293.672703	569.311581	285.159429			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.1	2247.018753	0.015489	AIDEDCSQYEPIPGSQK
3.1	2247.063034	-0.028792	VTDANDNPPVFSQDVYR
1.2	2247.033356	0.000886	RTVLELDRMEMSMDAFQK
1.2	2247.005737	0.028505	SDGAQGGVYACPQCR
0.8	2247.047760	-0.013518	FDPSAVPLPDTDMDSLREAR
0.8	2247.033813	0.000429	QEEERQDGGQNESFKR
0.8	2247.062378	-0.028136	QGTVALQEAQDTMQGTSR
0.8	2247.062378	-0.028136	QGTVALQEAQDTMQGTSR
0.6	2247.054901	-0.020659	QASAAEDRIRELEEAMAGER
0.2	2247.026825	0.007417	SDMICGYACLKGTAAMRNTK

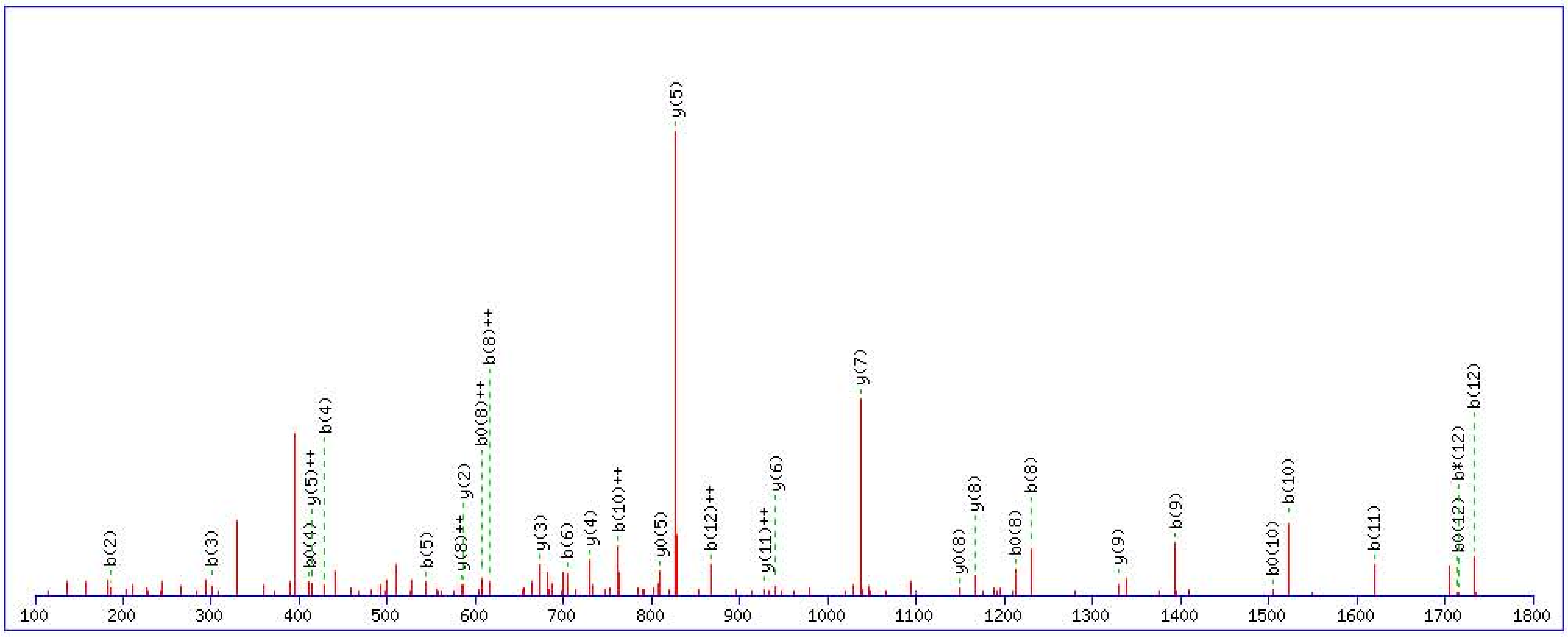
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIDEDCSQYEPIPGSQK**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

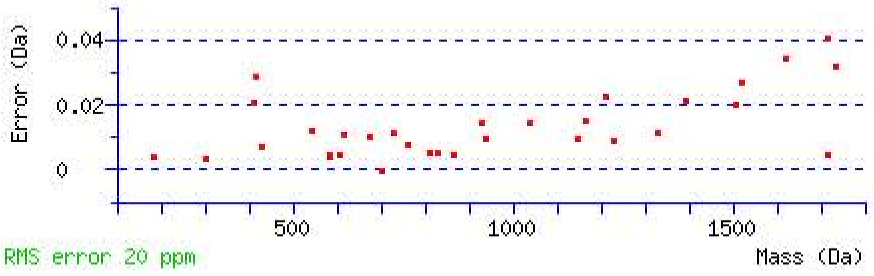
Match to Query 66151: 2558.208942 from(853.743590,3+) rtinseconds(2130) index(42915)
Title: Locus:1.1.1.3025.16 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

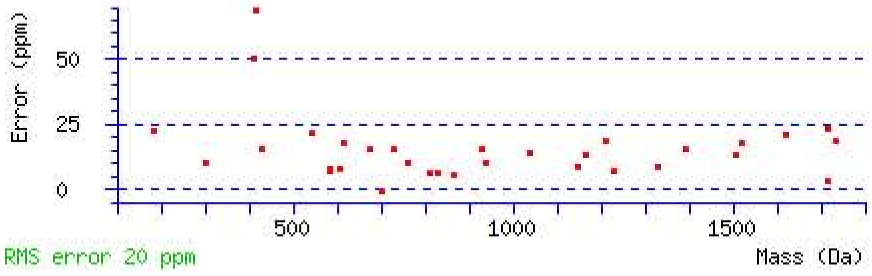
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2558.185501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00022
Matches : 32/170 fragment ions using 73 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							17
2	***185.128454***	93.067865					I	2488.155682	1244.581479	2471.129133	1236.068204	2470.145117	1235.576196	16
3	***300.155397***	150.581336			282.144832	141.576054	D	2375.071618	1188.039447	2358.045069	1179.526172	2357.061053	1179.034164	15
4	***429.197990***	215.102633			411.187425	206.097351	E	2260.044675	1130.525975	2243.018126	1122.012701	2242.034110	1121.520693	14
5	***544.224933***	272.616105			526.214368	263.610822	D	2131.002082	1066.004679	2113.975533	1057.491404	2112.991517	1056.999396	13
6	***704.255582***	352.631429			686.245017	343.626147	C	2015.975139	1008.491208	1998.948590	999.977933	1997.964574	999.485925	12
7	791.287610	396.147443			773.277045	387.142161	S	1855.944490	928.475883	1838.917941	919.962609	1837.933925	919.470601	11
8	***1230.512936***	**615.760106**	1213.486387	607.246832	1212.502371	606.754824	Q	1768.912462	884.959869	1751.885913	876.446595	1750.901897	875.954587	10
9	***1393.576265***	697.291771	1376.549716	688.778496	1375.565700	688.286488	Y	***1329.687136***	665.347206	1312.660587	656.833932	1311.676571	656.341924	9
10	***1522.618858***	**761.813067**	1505.592309	753.299793	1504.608293	752.807785	E	***1166.623807***	583.815541	1149.597258	575.302267	1148.613242	574.810259	8
11	***1619.671622***	810.339449	1602.645073	801.826175	1601.661057	801.334167	P	***1037.581214***	519.294245	1020.554665	510.780971	1019.570649	510.288963	7
12	***1732.755686***	**866.881481**	1715.729137	858.368207	1714.745121	857.876198	I	***940.528450***	470.767863	923.501901	462.254589	922.517885	461.762581	6
13	1829.808450	915.407863	1812.781901	906.894589	1811.797885	906.402581	P	***827.444386***	414.225831	810.417837	405.712557	809.433821	405.220549	5
14	1886.829914	943.918595	1869.803365	935.405321	1868.819349	934.913312	G	***730.391622***	365.699449	713.365073	357.186175	712.381057	356.694167	4
15	1973.861942	987.434609	1956.835393	978.921335	1955.851377	978.429327	S	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
16	2413.087268	1207.047272	2396.060719	1198.533997	2395.076703	1198.041989	Q	***586.338130***	293.672703	569.311581	285.159429			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.5	2558.185501	0.023441	AIDEDCSQYEPIPGSQK
1.5	2558.171906	0.037036	QGSGSGQSPGHGQRGSGSRQSPSYGR

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

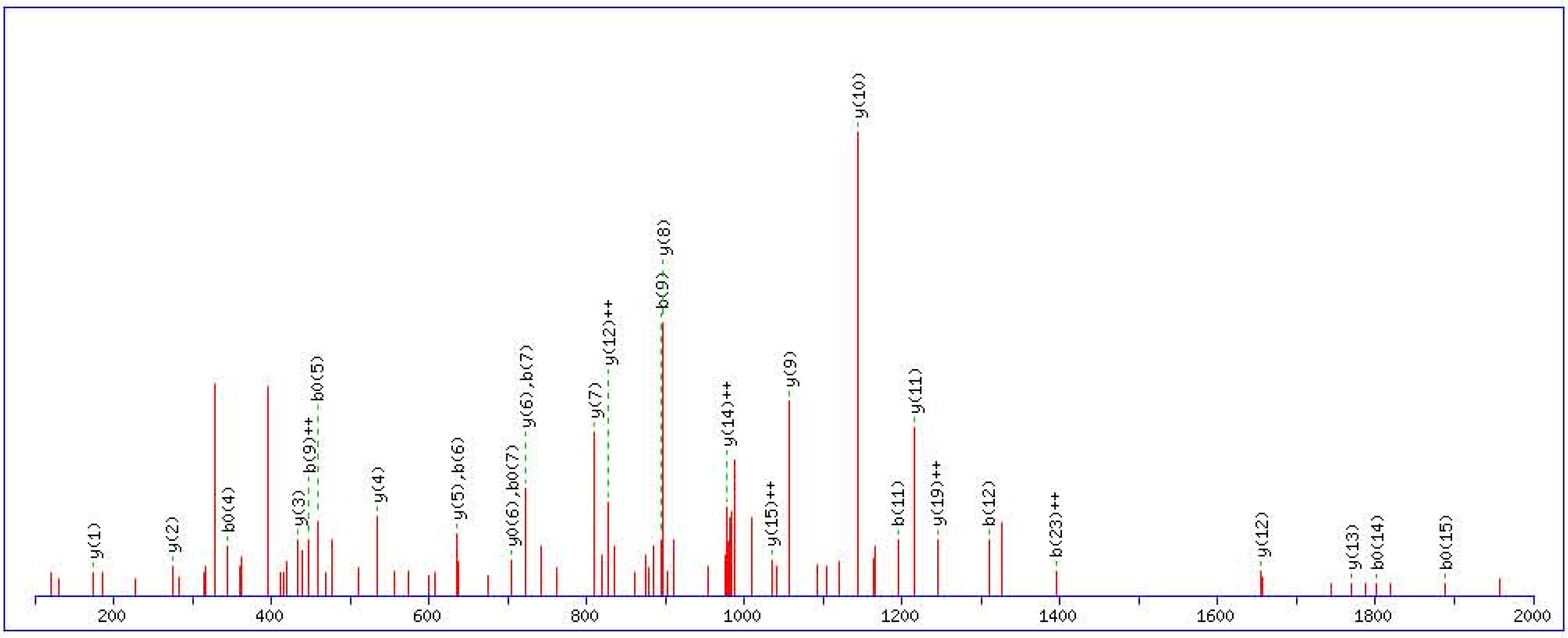
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGGTICSGDIWDQASCSSSTTCVR**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

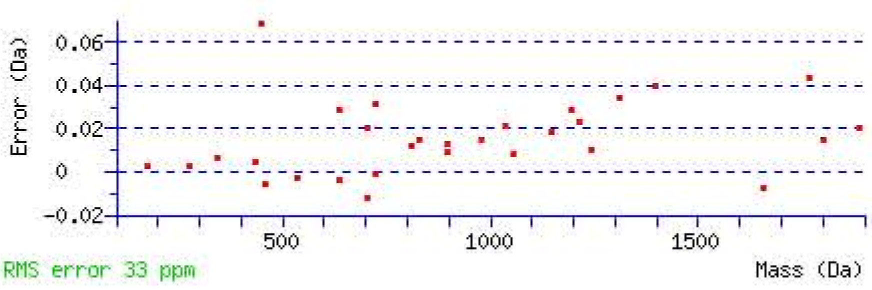
Match to Query 71330: 2962.312392 from(988.444740,3+) rtinseconds(2360) index(44487)
Title: Locus:1.1.1.3105.25 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

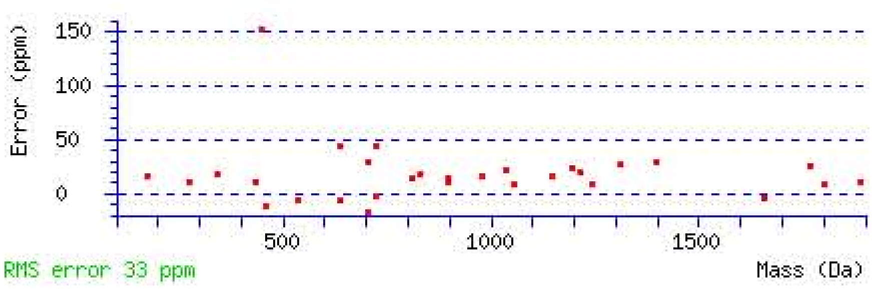
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2962.271835
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 78 **Expect:** 1.2e-007
Matches : 30/240 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							24
2	205.097154	103.052215					G	2816.210649	1408.608962	2799.184100	1400.095688	2798.200084	1399.603680	23
3	262.118618	131.562947					G	2759.189185	1380.098230	2742.162636	1371.584956	2741.178620	1371.092948	22
4	363.166297	182.086786			345.155732	173.081504	T	2702.167721	1351.587498	2685.141172	1343.074224	2684.157156	1342.582216	21
5	476.250361	238.628818			458.239796	229.623536	I	2601.120042	1301.063659	2584.093493	1292.550384	2583.109477	1292.058376	20
6	**636.281010**	318.644143			618.270445	309.638861	C	2488.035978	1244.521627	2471.009429	1236.008352	2470.025413	1235.516344	19
7	**723.313038**	362.160157			705.302473	353.154875	S	2328.005329	1164.506302	2310.978780	1155.993028	2309.994764	1155.501020	18
8	780.334502	390.670889			762.323937	381.665607	G	2240.973301	1120.990288	2223.946752	1112.477014	2222.962736	1111.985006	17
9	**895.361445**	**448.184361**			877.350880	439.179078	D	2183.951837	1092.479556	2166.925288	1083.966282	2165.941272	1083.474274	16
10	1008.445509	504.726393			990.434944	495.721110	I	2068.924894	1034.966085	2051.898345	1026.452810	2050.914329	1025.960802	15
11	**1194.524822**	597.766049			1176.514257	588.760767	W	1955.840830	978.424053	1938.814281	969.910778	1937.830265	969.418770	14
12	**1309.551765**	655.279521			1291.541200	646.274238	D	***1769.761517***	885.384396	1752.734968	876.871122	1751.750952	876.379114	13
13	1748.777091	874.892184	1731.750542	866.378909	1730.766526	865.886901	Q	***1654.734574***	827.870925	1637.708025	819.357650	1636.724009	818.865642	12
14	1819.814205	910.410741	1802.787656	901.897466	1801.803640	901.405458	A	***1215.509248***	608.258262	1198.482699	599.744987	1197.498683	599.252979	11
15	1906.846233	953.926755	1889.819684	945.413480	1888.835668	944.921472	S	***1144.472134***	572.739705	1127.445585	564.226430	1126.461569	563.734422	10
16	2066.876882	1033.942079	2049.850333	1025.428804	2048.866317	1024.936796	C	***1057.440106***	529.223691	1040.413557	520.710416	1039.429541	520.218408	9
17	2153.908910	1077.458093	2136.882361	1068.944818	2135.898345	1068.452810	S	***897.409457***	449.208366	880.382908	440.695092	879.398892	440.203084	8
18	2240.940938	1120.974107	2223.914389	1112.460832	2222.930373	1111.968825	S	***810.377429***	405.692352	793.350880	397.179078	792.366864	396.687070	7
19	2327.972966	1164.490121	2310.946417	1155.976847	2309.962401	1155.484839	S	***723.345401***	362.176338	706.318852	353.663064	705.334836	353.171056	6
20	2429.020645	1215.013960	2411.994096	1206.500686	2411.010080	1206.008678	T	***636.313373***	318.660324	619.286824	310.147050	618.302808	309.655042	5
21	2530.068324	1265.537800	2513.041775	1257.024525	2512.057759	1256.532517	T	***535.265694***	268.136485	518.239145	259.623210	517.255129	259.131202	4
22	2690.098973	1345.553124	2673.072424	1337.039850	2672.088408	1336.547842	C	***434.218015***	217.612645	417.191466	209.099371			3
23	2789.167387	**1395.087331**	2772.140838	1386.574057	2771.156822	1386.082049	V	***274.187366***	137.597321	257.160817	129.084046			2
24							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.1	2962.271835	0.040557	FGGTICSGDIWDQASCSSSTTCVR

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

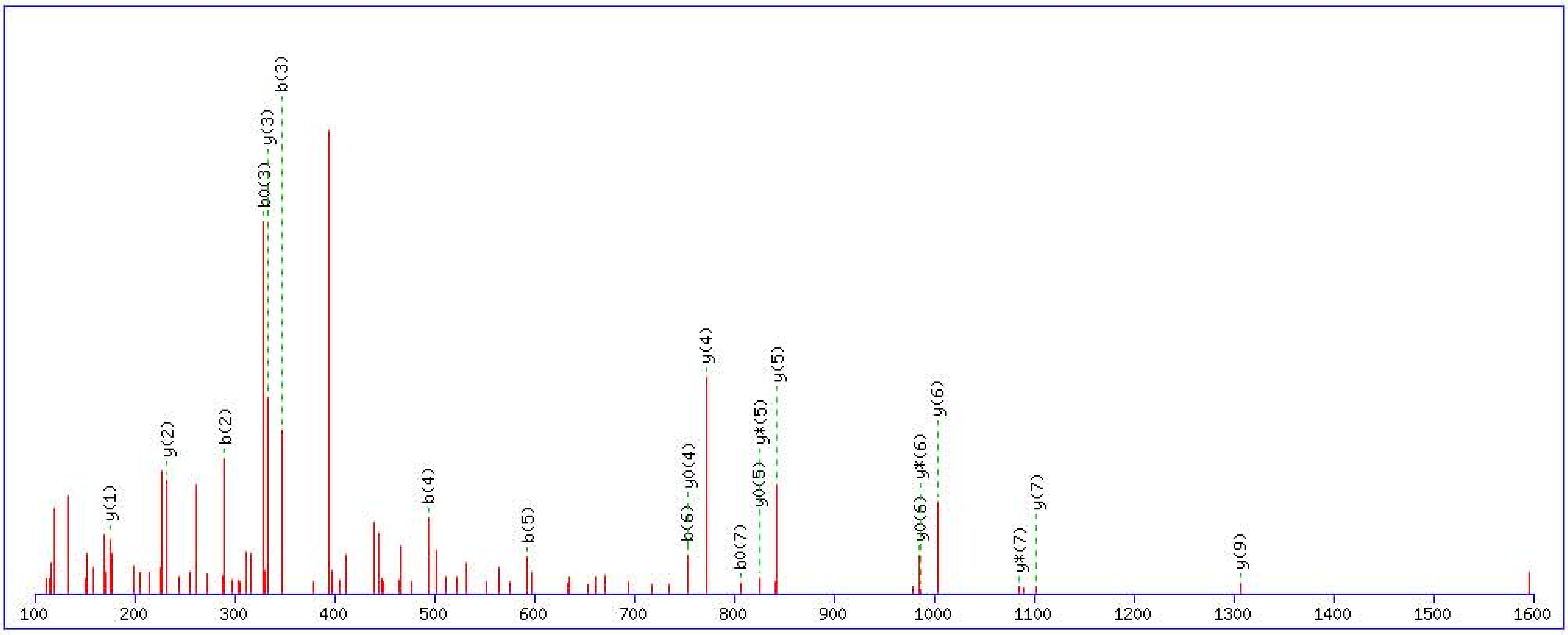
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CEGFVCAQTGR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

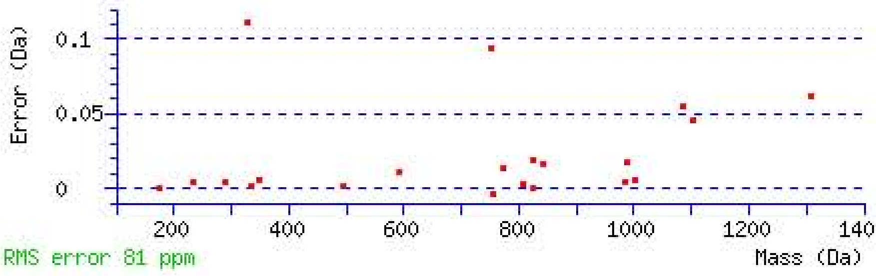
Match to Query 41890: 1594.723092 from(532.581640,3+) rtinseconds(1768) index(23133)
Title: Locus:1.1.1.2570.5 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

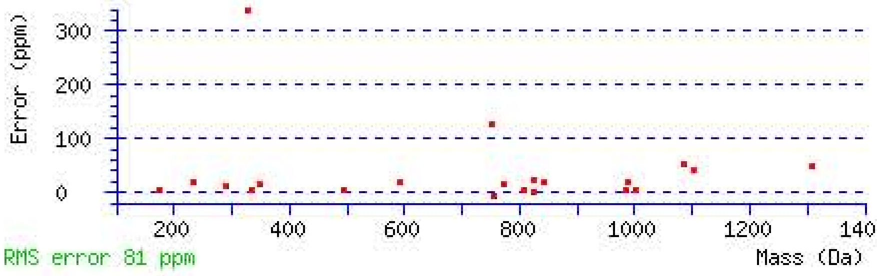
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1594.705460
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 42 **Expect:** 0.00047
Matches : 21/100 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.037925	81.022600					C							11
2	**290.080518**	145.543897			272.069953	136.538615	E	1435.682069	718.344673	1418.655520	709.831398	1417.671504	709.339390	10
3	**347.101982**	174.054629			329.091417	165.049347	G	***1306.639476***	653.823376	1289.612927	645.310102	1288.628911	644.818094	9
4	**494.170396**	247.588836			476.159831	238.583554	F	1249.618012	625.312644	1232.591463	616.799370	1231.607447	616.307361	8
5	**593.238810**	297.123043			575.228245	288.117761	V	***1102.549598***	551.778437	1085.523049	543.265162	1084.539033	542.773154	7
6	**753.269459**	377.138368			735.258894	368.133085	C	***1003.481184***	502.244230	986.454635	493.730955	985.470619	493.238947	6
7	824.306573	412.656925			806.296008	403.651642	A	***843.450535***	422.228906	826.423986	413.715631	825.439970	413.223623	5
8	1263.531899	632.269588	1246.505350	623.756313	1245.521334	623.264305	Q	***772.413421***	386.710349	755.386872	378.197074	754.402856	377.705066	4
9	1364.579578	682.793427	1347.553029	674.280153	1346.569013	673.788145	T	***333.188095***	167.097685	316.161546	158.584411	315.177530	158.092403	3
10	1421.601042	711.304159	1404.574493	702.790885	1403.590477	702.298877	G	***232.140416***	116.573846	215.113867	108.060571			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.4	1594.705460	0.017632	CEGFVCAQTGR

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

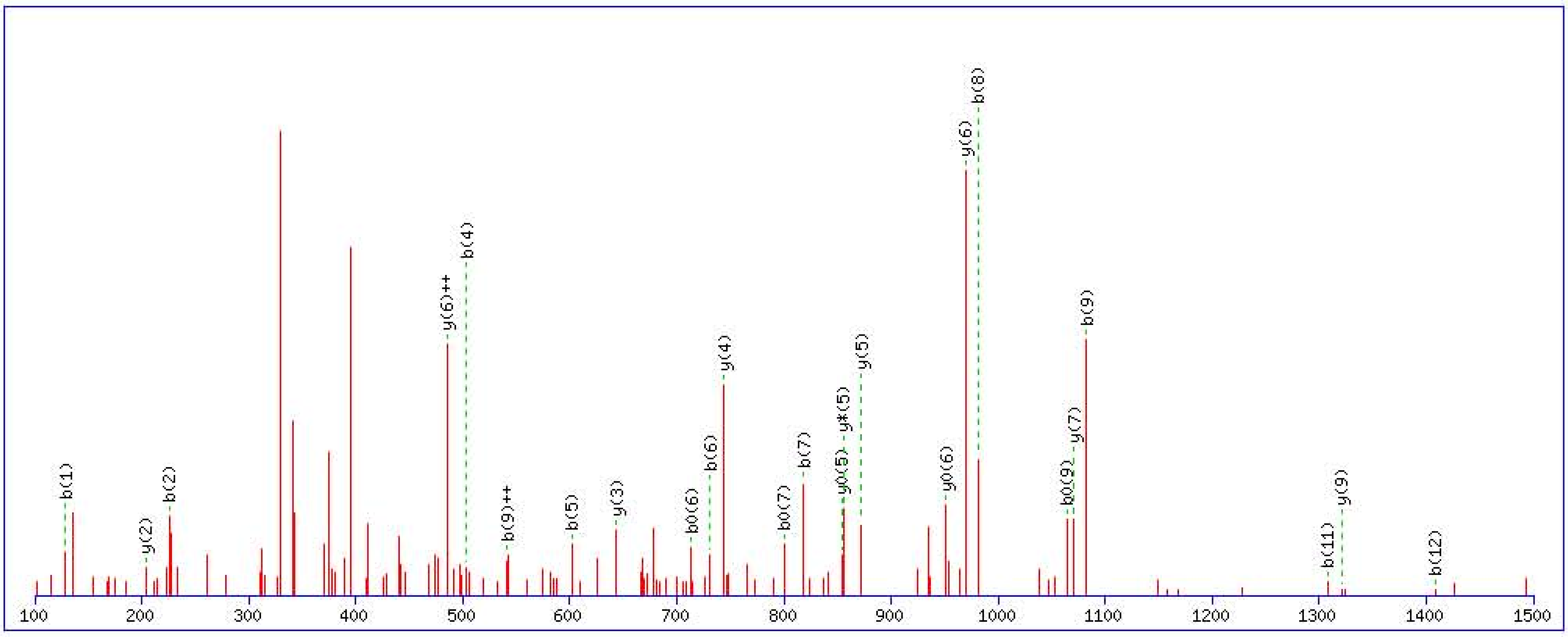
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPYNVESYTPQTQGK**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

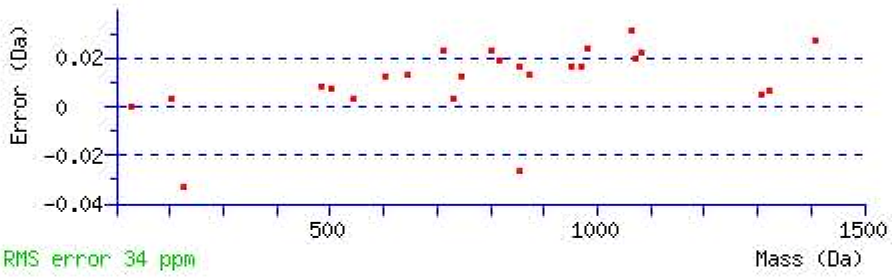
Match to Query 55008: 2050.045812 from(684.355880,3+) rtinseconds(1590) index(21823)
Title: Locus:1.1.1.2508.9 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

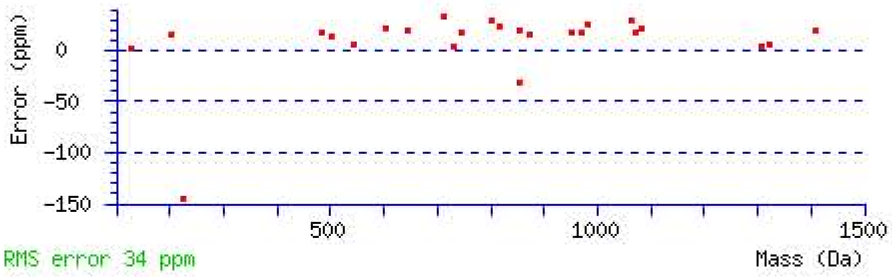
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2050.019348
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 47 **Expect:** 4.6e-005
Matches : 25/152 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							15
2	***226.155003***	113.581139	209.128454	105.067865			P	1922.931678	961.969477	1905.905129	953.456203	1904.921113	952.964195	14
3	389.218332	195.112804	372.191783	186.599529			Y	1825.878914	913.443095	1808.852365	904.929821	1807.868349	904.437813	13
4	***503.261259***	252.134267	486.234710	243.620993			N	1662.815585	831.911431	1645.789036	823.398156	1644.805020	822.906148	12
5	***602.329673***	301.668475	585.303124	293.155200			V	1548.772658	774.889967	1531.746109	766.376693	1530.762093	765.884685	11
6	***731.372266***	366.189771	714.345717	357.676497	713.361701	357.184489	E	1449.704244	725.355760	1432.677695	716.842486	1431.693679	716.350478	10
7	***818.404294***	409.705785	801.377745	401.192511	800.393729	400.700503	S	**1320.661651**	660.834464	1303.635102	652.321189	1302.651086	651.829181	9
8	***981.467623***	491.237450	964.441074	482.724175	963.457058	482.232167	Y	1233.629623	617.318450	1216.603074	608.805175	1215.619058	608.313167	8
9	***1082.515302***	541.761289	1065.488753	533.248015	1064.504737	532.756007	T	**1070.566294**	535.786785	1053.539745	527.273511	1052.555729	526.781503	7
10	1179.568066	590.287671	1162.541517	581.774397	1161.557501	581.282389	P	**969.518615**	485.262946	952.492066	476.749671	951.508050	476.257663	6
11	***1307.626644***	654.316960	1290.600095	645.803686	1289.616079	645.311678	Q	**872.465851**	436.736564	855.439302	428.223289	854.455286	427.731281	5
12	***1408.674323***	704.840800	1391.647774	696.327525	1390.663758	695.835517	T	**744.407273**	372.707275	727.380724	364.194000	726.396708	363.701992	4
13	1847.899649	924.453463	1830.873100	915.940188	1829.889084	915.448180	Q	**643.359594**	322.183435	626.333045	313.670161			3
14	1904.921113	952.964195	1887.894564	944.450920	1886.910548	943.958912	G	**204.134268**	102.570772	187.107719	94.057497			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.1	2050.019348	0.026464	KPYNVESYTPQTQGK
26.6	2050.019348	0.026464	KPYNVESYTPQTQGK
0.9	2050.025192	0.020620	LKISNDGLQMEKDESSLK

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

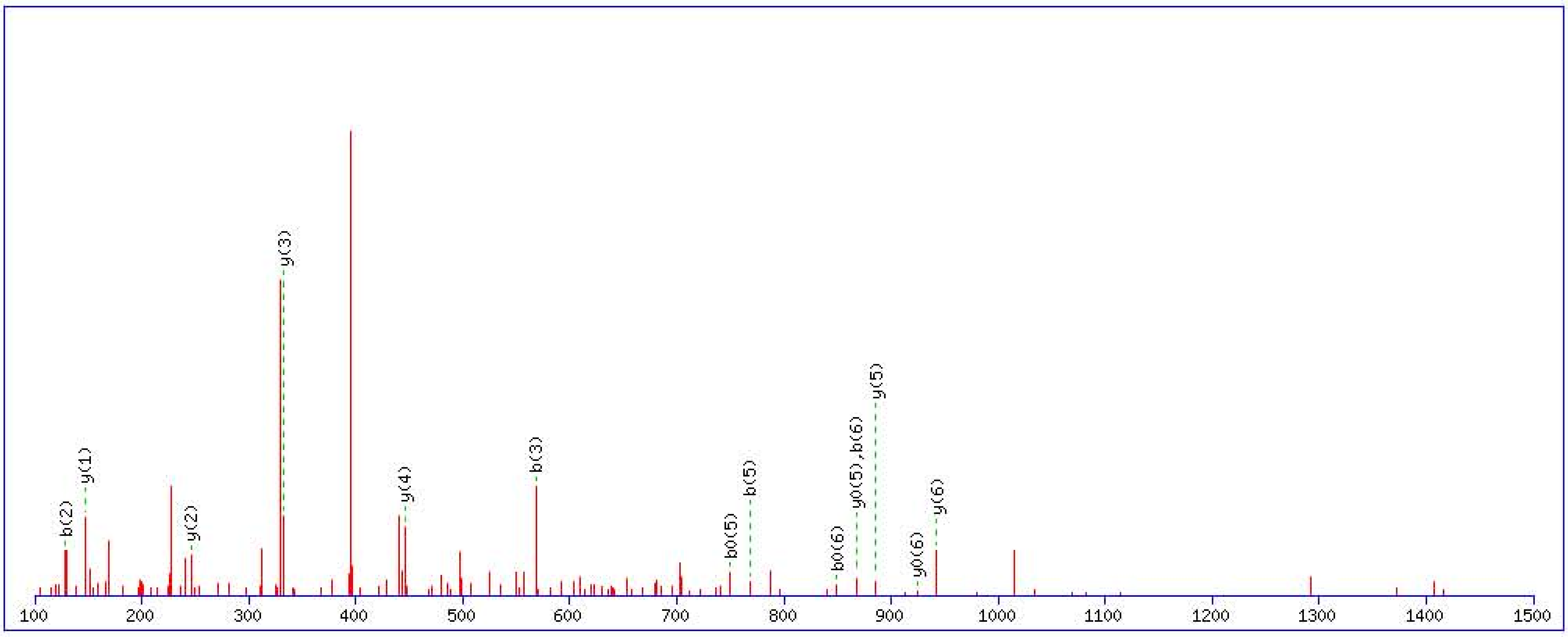
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGQLSVK**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

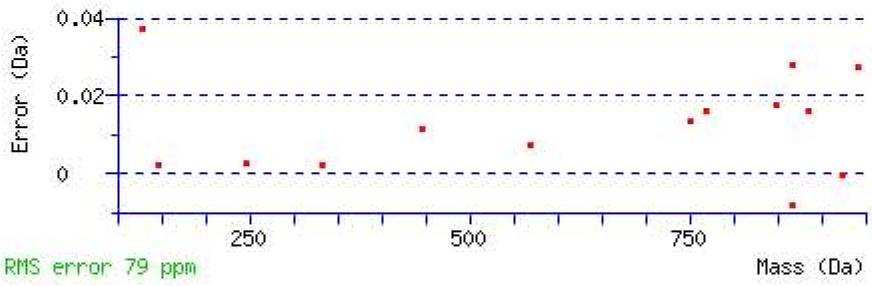
Match to Query 19349: 1012.582528 from(507.298540,2+) rtinseconds(1536) index(21474)
Title: Locus:1.1.1.2489.14 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

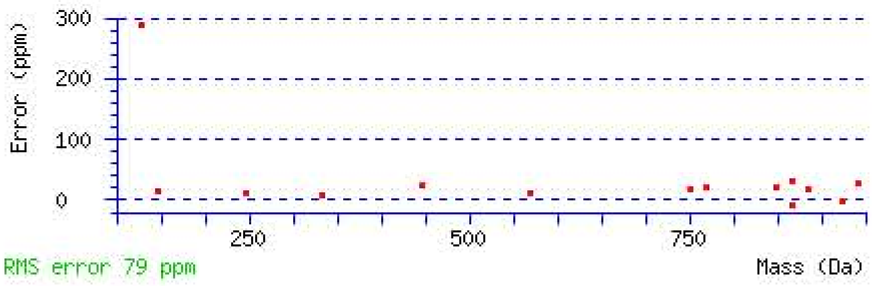
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1012.573929
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.017
Matches : 14/56 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	72.044390	36.525833					A							7
2	**129.065854**	65.036565					G	***942.544100***	471.775688	925.517551	463.262414	924.533535	462.770406	6
3	**568.291180**	284.649228	551.264631	276.135954			Q	***885.522636***	443.264956	868.496087	434.751682	867.512071	434.259674	5
4	681.375244	341.191260	664.348695	332.677986			L	***446.297310***	223.652293	429.270761	215.139018	428.286745	214.647010	4
5	**768.407272**	384.707274	751.380723	376.194000	750.396707	375.701992	S	***333.213246***	167.110261	316.186697	158.596986	315.202681	158.104978	3
6	**867.475686**	434.241481	850.449137	425.728207	849.465121	425.236199	V	***246.181218***	123.594247	229.154669	115.080972			2
7							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.8	1012.573929	0.008599	AGQLSVK
10.4	1012.573914	0.008614	KEAQVK
7.9	1012.591675	-0.009147	GAEAKTVLPK
7.5	1012.573929	0.008599	QAGLVSK
7.5	1012.573914	0.008614	QKADIK
7.5	1012.573914	0.008614	QKADLK
7.5	1012.573914	0.008614	QKEGIK
7.5	1012.573914	0.008614	QKLEGK
7.5	1012.585144	-0.002616	QKNGKK
7.5	1012.589172	-0.006644	QKWLK

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

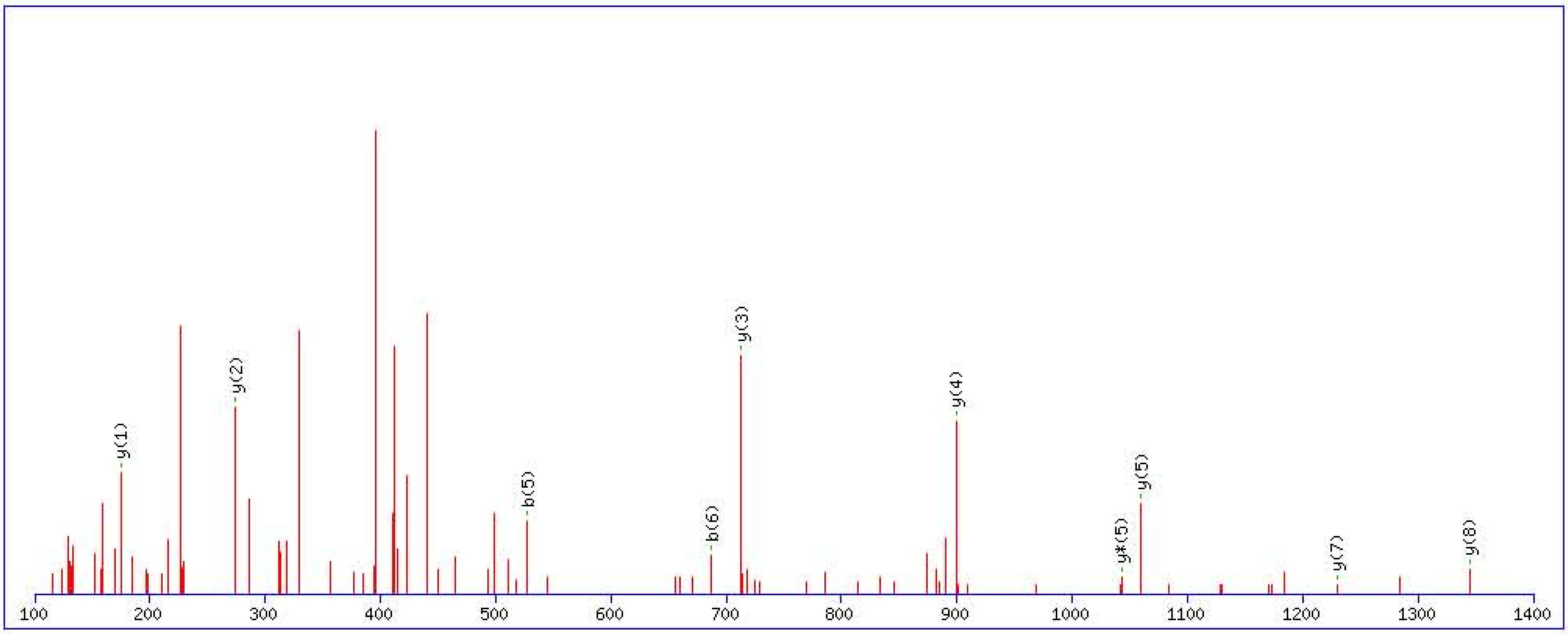
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLDGICWQVR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

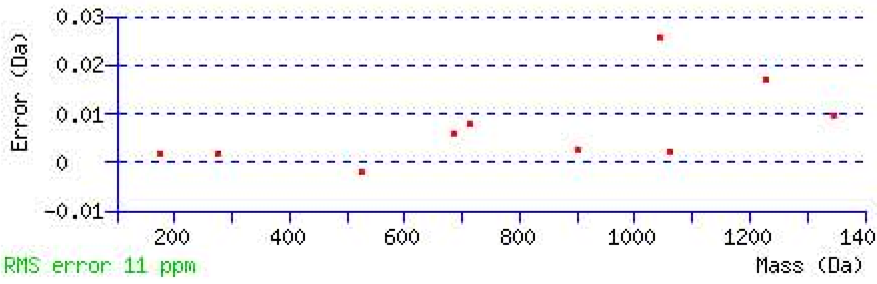
Match to Query 41445: 1584.832962 from(529.284930,3+) rtinseconds(2045) index(42403)
Title: Locus:1.1.1.2996.6 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

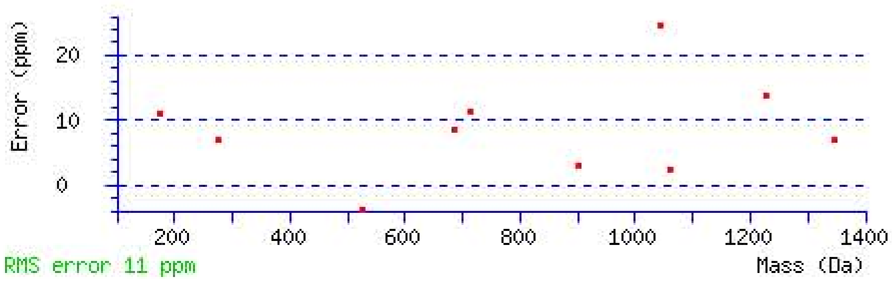
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1584.826874
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0038
Matches : 10/90 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			K							10
2	242.186303	121.596790	225.159754	113.083515			L	1457.739189	729.373233	1440.712640	720.859958	1439.728624	720.367950	9
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	D	***1344.655125***	672.831201	1327.628576	664.317926	1326.644560	663.825918	8
4	414.234710	207.620993	397.208161	199.107719	396.224145	198.615711	G	***1229.628182***	615.317729	1212.601633	606.804455			7
5	**527.318774**	264.163025	510.292225	255.649751	509.308209	255.157743	I	1172.606718	586.806997	1155.580169	578.293723			6
6	**687.349423**	344.178350	670.322874	335.665075	669.338858	335.173067	C	***1059.522654***	530.264965	1042.496105	521.751691			5
7	873.428736	437.218006	856.402187	428.704732	855.418171	428.212724	W	***899.492005***	450.249641	882.465456	441.736366			4
8	1312.654062	656.830669	1295.627513	648.317395	1294.643497	647.825387	Q	***713.412692***	357.209984	696.386143	348.696710			3
9	1411.722476	706.364876	1394.695927	697.851602	1393.711911	697.359594	V	***274.187366***	137.597321	257.160817	129.084047			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.6	1584.826874	0.006088	KLDGICWQVR
4.7	1584.810730	0.022232	KVSPDPQKSSEDIR
4.6	1584.829346	0.003616	QAESQINKQTK

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

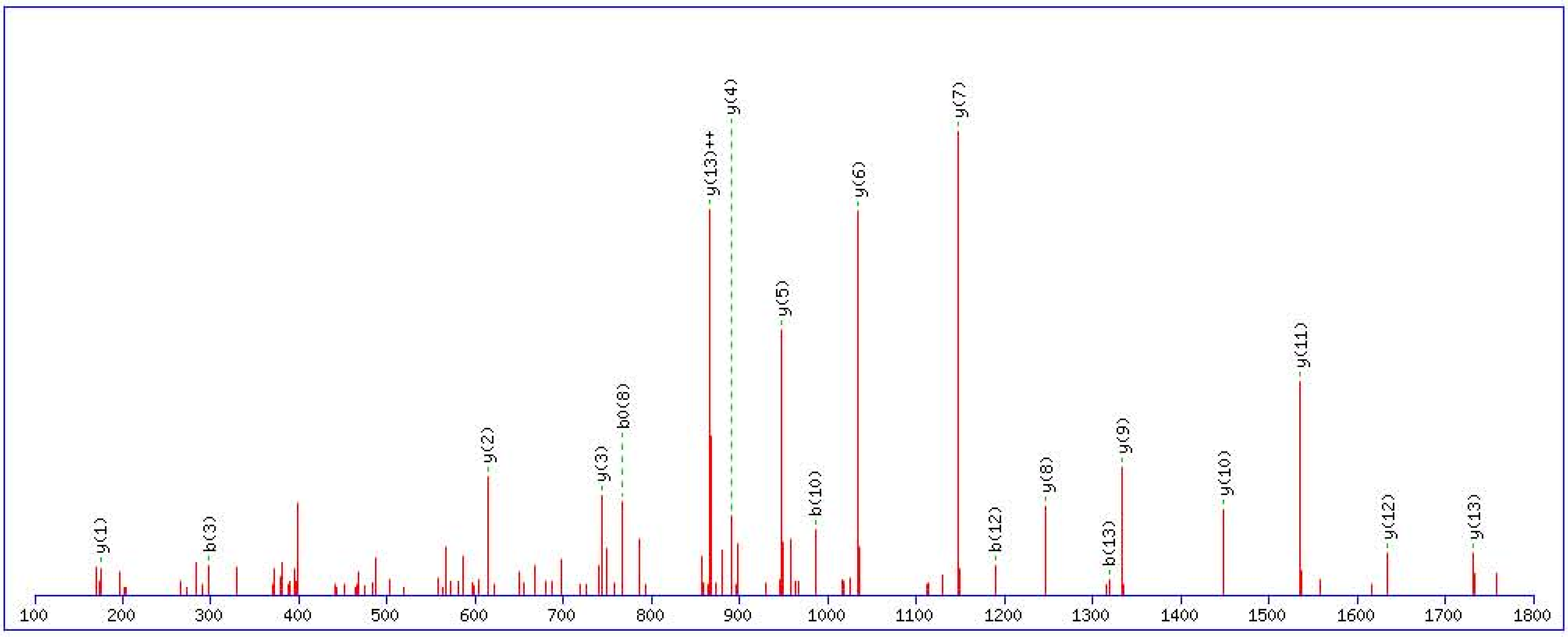
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLPVSDSVLSGFEQR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

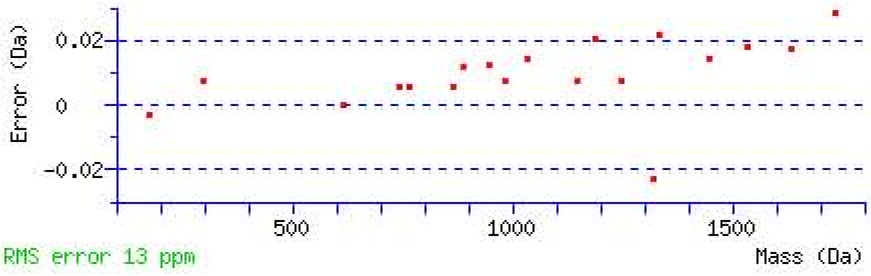
Match to Query 51252: 1931.004208 from(966.509380,2+) rtinseconds(2495) index(45280)
Title: Locus:1.1.1.3152.26 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

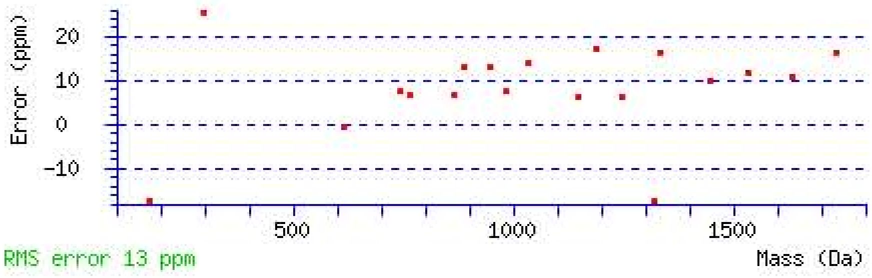


```
Monoisotopic mass of neutral peptide Mr(calc): 1930.982254
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 99  Expect: 1.5e-009
Matches : 19/138 fragment ions using 31 most intense peaks   (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							15
2	201.123368	101.065322			183.112803	92.060039	L	1844.957496	922.982386	1827.930947	914.469112	1826.946931	913.977104	14
3	**298.176132**	149.591704			280.165567	140.586422	P	***1731.873432***	866.440354	1714.846883	857.927080	1713.862867	857.435072	13
4	397.244546	199.125911			379.233981	190.120629	V	***1634.820668***	817.913972	1617.794119	809.400698	1616.810103	808.908690	12
5	484.276574	242.641925			466.266009	233.636643	S	***1535.752254***	768.379765	1518.725705	759.866491	1517.741689	759.374483	11
6	599.303517	300.155397			581.292952	291.150114	D	***1448.720226***	724.863751	1431.693677	716.350477	1430.709661	715.858469	10
7	686.335545	343.671411			668.324980	334.666128	S	***1333.693283***	667.350280	1316.666734	658.837005	1315.682718	658.344997	9
8	785.403959	393.205618			767.393394	384.200335	V	***1246.661255***	623.834266	1229.634706	615.320991	1228.650690	614.828983	8
9	898.488023	449.747650			880.477458	440.742367	L	***1147.592841***	574.300059	1130.566292	565.786784	1129.582276	565.294776	7
10	**985.520051**	493.263664			967.509486	484.258381	S	***1034.508777***	517.758027	1017.482228	509.244752	1016.498212	508.752744	6
11	1042.541515	521.774395			1024.530950	512.769113	G	***947.476749***	474.242013	930.450200	465.728738	929.466184	465.236730	5
12	**1189.609929**	595.308603			1171.599364	586.303320	F	***890.455285***	445.731281	873.428736	437.218006	872.444720	436.725998	4
13	**1318.652522**	659.829899			1300.641957	650.824617	E	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
14	1757.877848	879.442562	1740.851299	870.929288	1739.867283	870.437280	Q	***614.344278***	307.675777	597.317729	299.162503			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 13 ppm



RMS error 13 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
99.1	1930.982254	0.021954	SLPVSDSVLSGFEQR
4.8	1930.989410	0.014798	EAQSQLIKSDEMQRLR
4.4	1931.000885	0.003323	LSPVTACAGQTLQFK
3.6	1931.026505	-0.022297	VPSPFGPREQSTYVLVR
0.1	1930.978195	0.026013	VALSNISKDGNLMETAPR

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

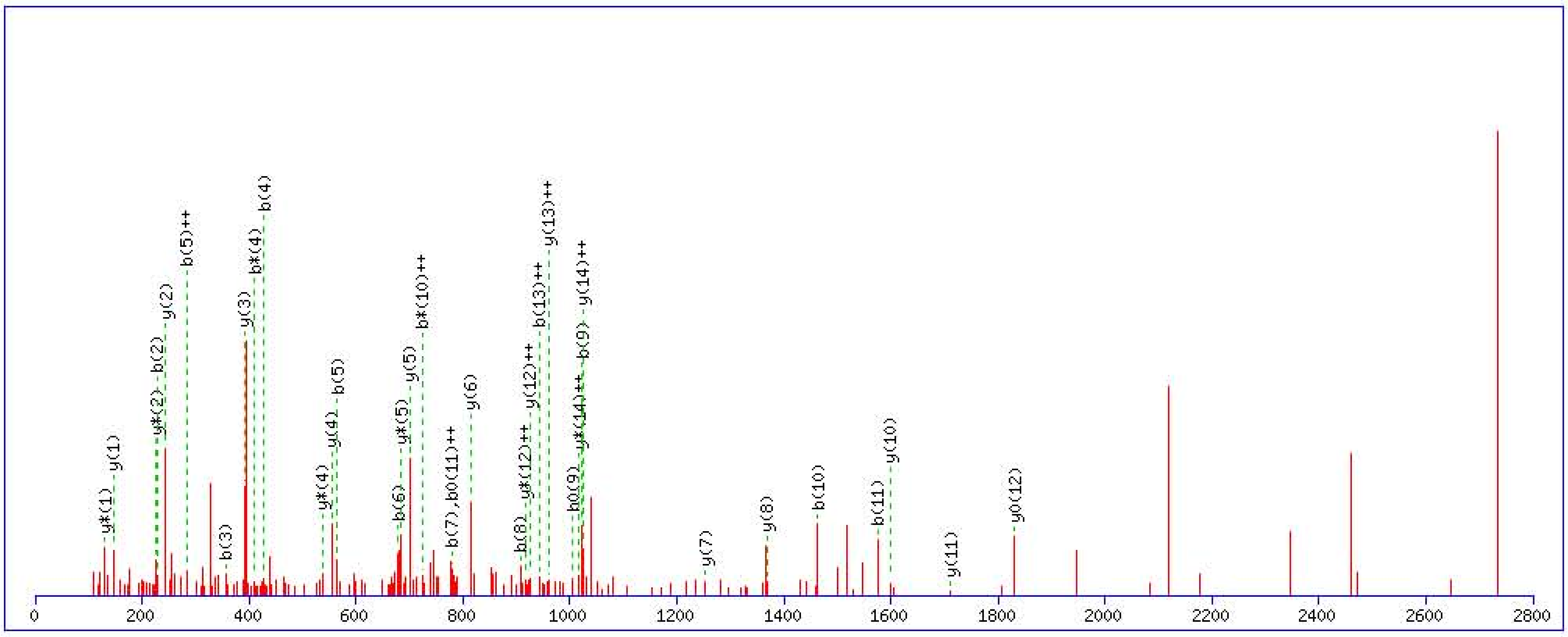
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQEAHLTEDQIFYFPK**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

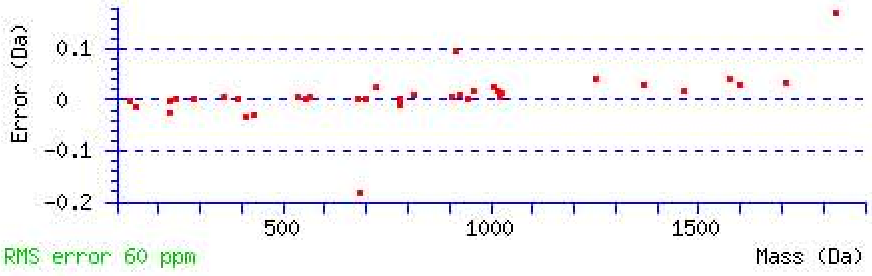
Match to Query 60101: 2275.156812 from(759.392880,3+) rtinseconds(2366) index(44521)
Title: Locus:1.1.1.3107.14 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

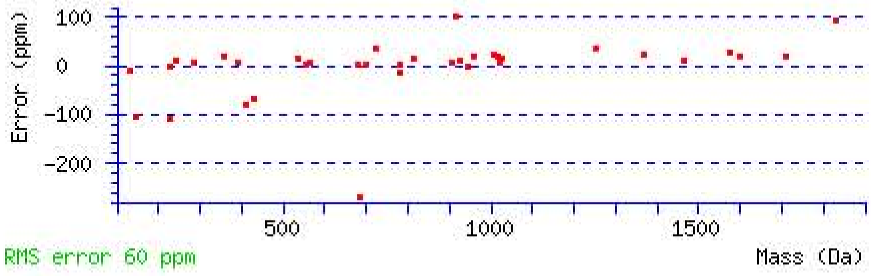
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from [0] to [2800] Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2275.134720
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.012
Matches : 36/160 fragment ions using 105 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							16
2	***228.134268***	114.570772	211.107719	106.057498			Q	2177.073591	1089.040433	2160.047042	1080.527159	2159.063026	1080.035151	15
3	***357.176861***	179.092069	340.150312	170.578794	339.166296	170.086786	E	2049.015013	1025.011144	2031.988464	1016.497870	2031.004448	1016.005862	14
4	***428.213975***	214.610626	411.187426	206.097351	410.203410	205.605343	A	1919.972420	960.489848	1902.945871	951.976573	1901.961855	951.484565	13
5	***565.272887***	**283.140082**	548.246338	274.626807	547.262322	274.134799	H	1848.935306	924.971291	1831.908757	916.458016	1830.924741	915.966008	12
6	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	L	***1711.876394***	856.441835	1694.849845	847.928561	1693.865829	847.436552	11
7	***779.404630***	390.205953	762.378081	381.692679	761.394065	381.200671	T	***1598.792330***	799.899803	1581.765781	791.386529	1580.781765	790.894521	10
8	***908.447223***	454.727250	891.420674	446.213975	890.436658	445.721967	E	1497.744651	749.375963	1480.718102	740.862689	1479.734086	740.370681	9
9	***1023.474166***	512.240721	1006.447617	503.727447	1005.463601	503.235439	D	***1368.702058***	684.854667	1351.675509	676.341392	1350.691493	675.849384	8
10	***1462.699492***	731.853384	1445.672943	723.340110	1444.688927	722.848101	Q	***1253.675115***	627.341195	1236.648566	618.827921			7
11	***1575.783556***	788.395416	1558.757007	779.882141	1557.772991	779.390133	I	***814.449789***	407.728533	797.423240	399.215258			6
12	1722.851970	861.929623	1705.825421	853.416349	1704.841405	852.924340	F	***701.365725***	351.186501	684.339176	342.673226			5
13	1885.915299	**943.461288**	1868.888750	934.948013	1867.904734	934.456005	Y	***554.297311***	277.652294	537.270762	269.139019			4
14	2032.983713	1016.995495	2015.957164	1008.482220	2014.973148	1007.990212	F	***391.233982***	196.120629	374.207433	187.607354			3
15	2130.036477	1065.521876	2113.009928	1057.008602	2112.025912	1056.516594	P	***244.165568***	122.586422	227.139019	114.073147			2
16							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.2	2275.134720	0.022092	VQEAHLTEDQIFYFPK
1.8	2275.134720	0.022092	VQEAHLTEDQIFYFPK

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

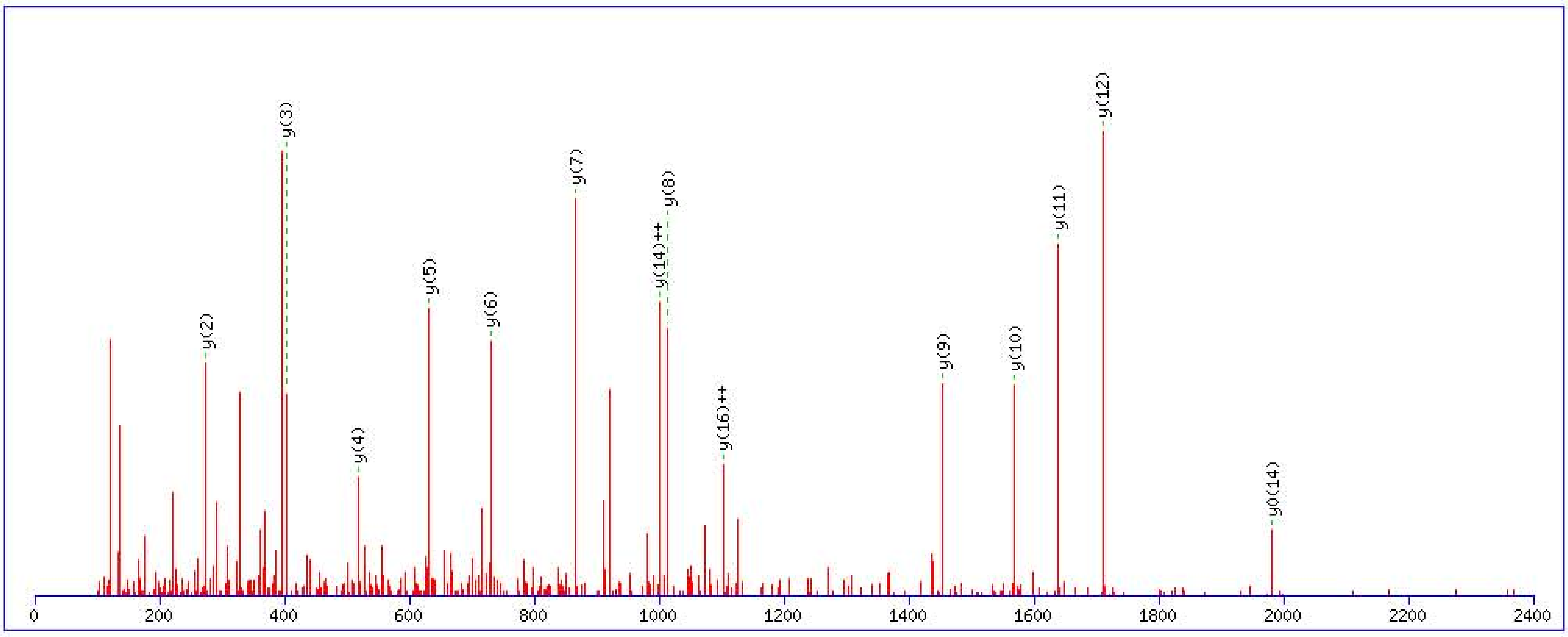
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGFCEAADQFHVLDEVR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

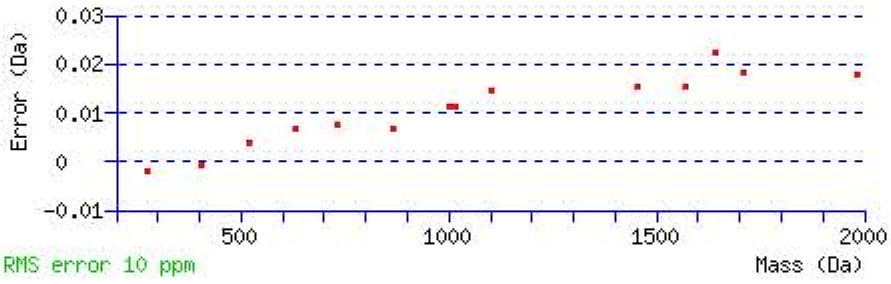
Match to Query 61882: 2366.109222 from(789.710350,3+) rtinseconds(2531) index(45531)
Title: Locus:1.1.1.3165.5 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

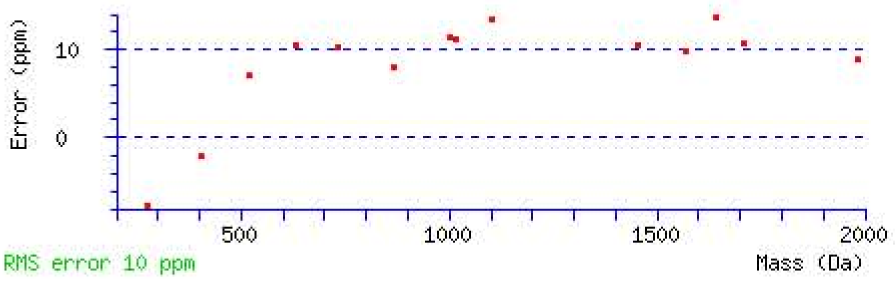
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2366.082382
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 77  Expect: 3.3e-007
Matches : 14/164 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	164.070605	82.538940					Y							17
2	221.092069	111.049673					G	2204.026323	1102.516799	2186.999774	1094.003525	2186.015758	1093.511517	16
3	368.160483	184.583879					F	2147.004859	1074.006067	2129.978310	1065.492793	2128.994294	1065.000785	15
4	528.191132	264.599204					C	1999.936445	1000.471860	1982.909896	991.958586	1981.925880	991.466578	14
5	657.233725	329.120501			639.223160	320.115218	E	1839.905796	920.456536	1822.879247	911.943261	1821.895231	911.451253	13
6	728.270839	364.639058			710.260274	355.633775	A	***1710.863203***	855.935239	1693.836654	847.421965	1692.852638	846.929957	12
7	799.307953	400.157615			781.297388	391.152332	A	***1639.826089***	820.416682	1622.799540	811.903408	1621.815524	811.411400	11
8	914.334896	457.671086			896.324331	448.665803	D	***1568.788975***	784.898125	1551.762426	776.384851	1550.778410	775.892843	10
9	1353.560222	677.283749	1336.533673	668.770474	1335.549657	668.278466	Q	***1453.762032***	727.384654	1436.735483	718.871379	1435.751467	718.379371	9
10	1500.628636	750.817956	1483.602087	742.304682	1482.618071	741.812673	F	***1014.536706***	507.771991	997.510157	499.258717	996.526141	498.766709	8
11	1637.687548	819.347412	1620.660999	810.834138	1619.676983	810.342129	H	***867.468292***	434.237784	850.441743	425.724510	849.457727	425.232502	7
12	1736.755962	868.881619	1719.729413	860.368345	1718.745397	859.876336	V	***730.409380***	365.708328	713.382831	357.195054	712.398815	356.703046	6
13	1849.840026	925.423651	1832.813477	916.910376	1831.829461	916.418368	L	***631.340966***	316.174121	614.314417	307.660846	613.330401	307.168838	5
14	1964.866969	982.937122	1947.840420	974.423848	1946.856404	973.931840	D	***518.256902***	259.632089	501.230353	251.118815	500.246337	250.626807	4
15	2093.909562	1047.458419	2076.883013	1038.945144	2075.898997	1038.453136	E	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
16	2192.977976	1096.992626	2175.951427	1088.479351	2174.967411	1087.987343	V	***274.187366***	137.597321	257.160817	129.084046			2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.5	2366.082382	0.026840	YGFCEAADQFHVLDEVR

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

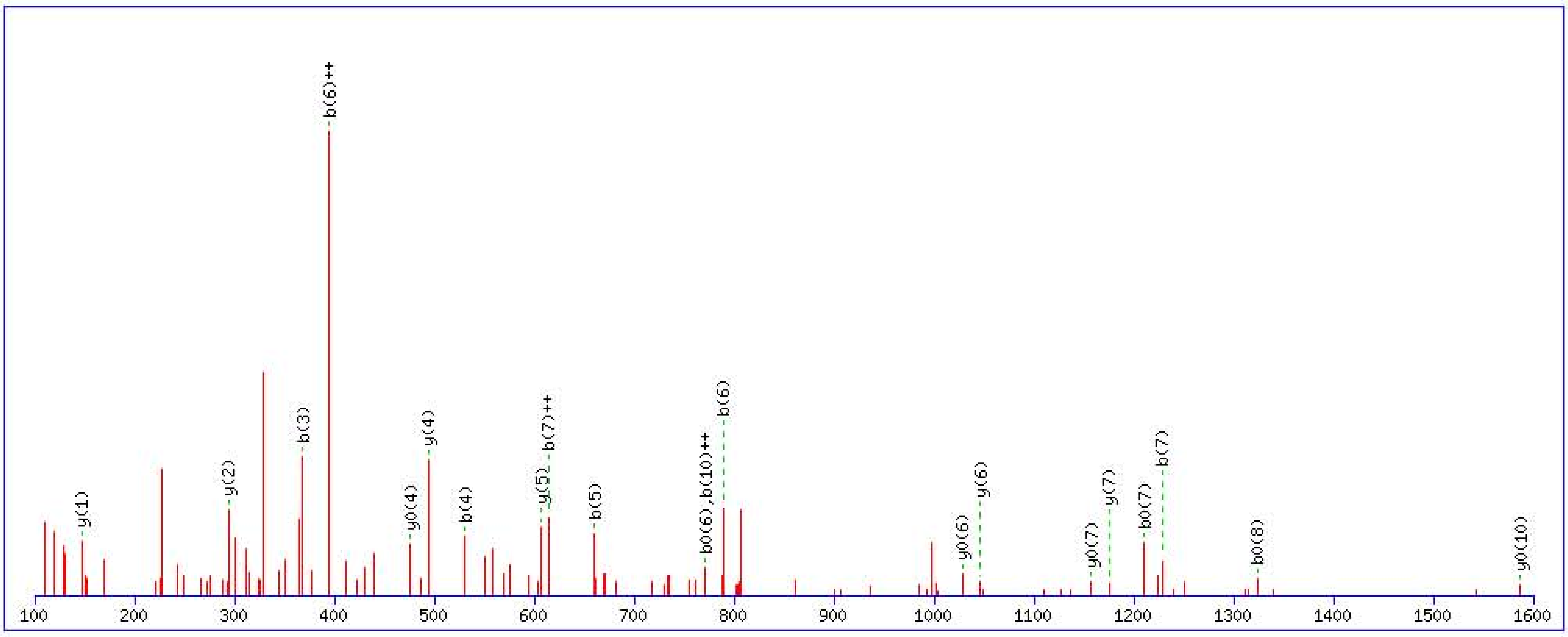
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEHYEEQIEAFK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

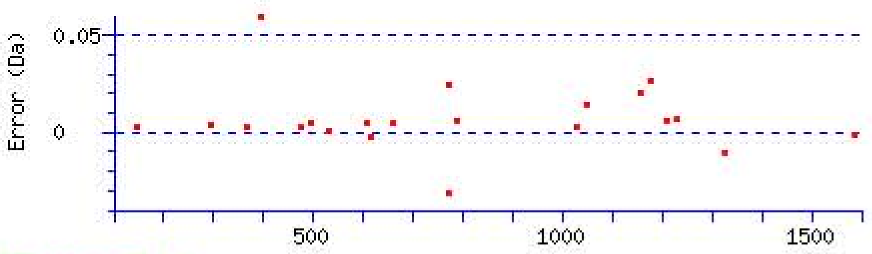
Match to Query 49148: 1833.869742 from(612.297190,3+) rtinseconds(1954) index(41850)
Title: Locus:1.1.1.2964.16 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

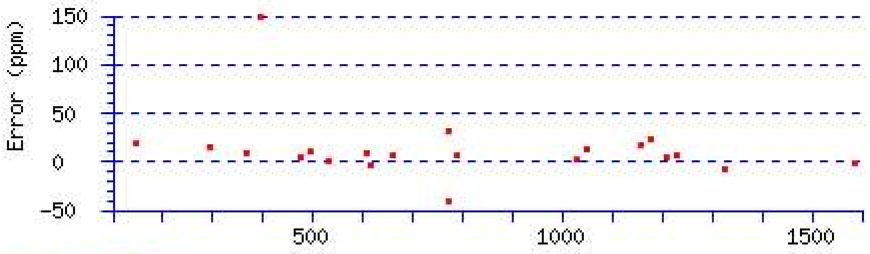


```
Monoisotopic mass of neutral peptide Mr(calc): 1833.860703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.0082
Matches : 21/114 fragment ions using 41 most intense peaks   (help)
```

#	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							12
2	231.097548	116.052412			213.086983	107.047130	E	1733.820335	867.413805	1716.793786	858.900531	1715.809770	858.408523	11
3	***368.156460***	184.581868			350.145895	175.576585	H	1604.777742	802.892509	1587.751193	794.379235	1586.767177	793.887227	10
4	***531.219789***	266.113533			513.209224	257.108250	Y	1467.718830	734.363053	1450.692281	725.849779	1449.708265	725.357771	9
5	***660.262382***	330.634829			642.251817	321.629547	E	1304.655501	652.831389	1287.628952	644.318114	1286.644936	643.826106	8
6	***789.304975***	**395.156126**			771.294410	386.150843	E	***1175.612908***	588.310092	1158.586359	579.796817	1157.602343	579.304809	7
7	***1228.530301***	**614.768789**	1211.503752	606.255514	1210.519736	605.763506	Q	***1046.570315***	523.788795	1029.543766	515.275521	1028.559750	514.783513	6
8	1341.614365	671.310820	1324.587816	662.797546	1323.603800	662.305538	I	***607.344989***	304.176132	590.318440	295.662858	589.334424	295.170850	5
9	1470.656958	735.832117	1453.630409	727.318842	1452.646393	726.826834	E	***494.260925***	247.634100	477.234376	239.120826	476.250360	238.628818	4
10	1541.694072	**771.350674**	1524.667523	762.837399	1523.683507	762.345391	A	365.218332	183.112804	348.191783	174.599530			3
11	1688.762486	844.884881	1671.735937	836.371606	1670.751921	835.879598	F	***294.181218***	147.594247	277.154669	139.080973			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 35 ppm



RMS error 35 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.1	1833.860703	0.009039	TEHYEEQIEAFK
3.6	1833.877808	-0.008066	ALSKGQNVTEEECLEK
0.5	1833.896942	-0.027200	STVNGVSWTNETQRQK

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

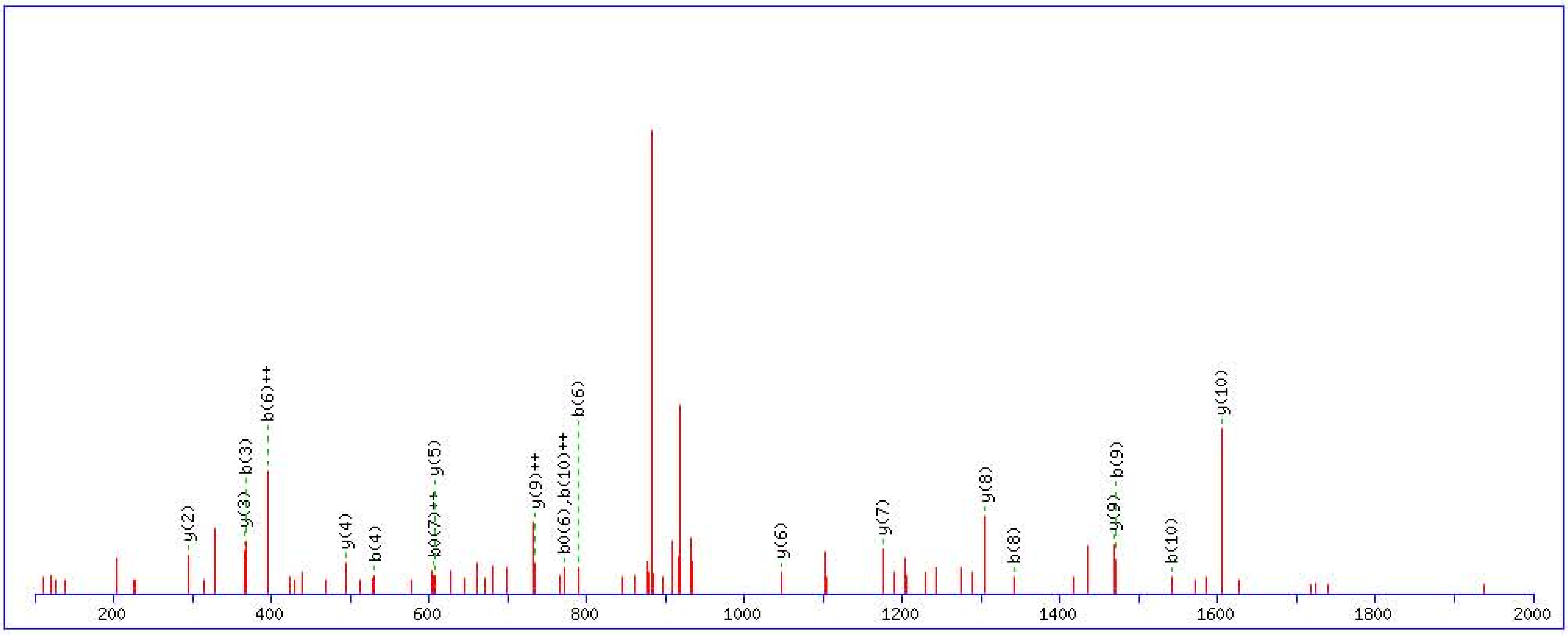
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEHYEEQIEAFK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

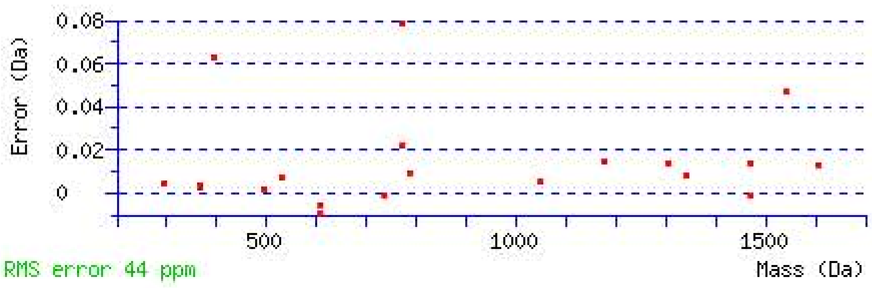
Match to Query 49152: 1833.877628 from(917.946090,2+) rtinseconds(1952) index(41832)
Title: Locus:1.1.1.2963.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

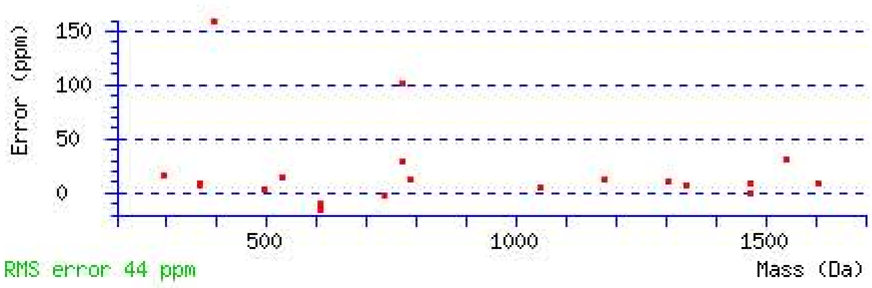
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1833.860703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.031
Matches : 20/114 fragment ions using 59 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							12
2	231.097548	116.052412			213.086983	107.047130	E	1733.820335	867.413805	1716.793786	858.900531	1715.809770	858.408523	11
3	**368.156460**	184.581868			350.145895	175.576585	H	***1604.777742***	802.892509	1587.751193	794.379235	1586.767177	793.887227	10
4	**531.219789**	266.113533			513.209224	257.108250	Y	***1467.718830***	734.363053	1450.692281	725.849779	1449.708265	725.357771	9
5	660.262382	330.634829			642.251817	321.629547	E	***1304.655501***	652.831389	1287.628952	644.318114	1286.644936	643.826106	8
6	**789.304975**	**395.156126**			771.294410	386.150843	E	***1175.612908***	588.310092	1158.586359	579.796817	1157.602343	579.304809	7
7	1228.530301	614.768789	1211.503752	606.255514	1210.519736	605.763506	Q	***1046.570315***	523.788795	1029.543766	515.275521	1028.559750	514.783513	6
8	**1341.614365**	671.310820	1324.587816	662.797546	1323.603800	662.305538	I	***607.344989***	304.176132	590.318440	295.662858	589.334424	295.170850	5
9	**1470.656958**	735.832117	1453.630409	727.318842	1452.646393	726.826834	E	***494.260925***	247.634100	477.234376	239.120826	476.250360	238.628818	4
10	**1541.694072**	**771.350674**	1524.667523	762.837399	1523.683507	762.345391	A	***365.218332***	183.112804	348.191783	174.599530			3
11	1688.762486	844.884881	1671.735937	836.371606	1670.751921	835.879598	F	***294.181218***	147.594247	277.154669	139.080973			2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.7	1833.860703	0.016925	TEHYEEQIEAFK

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

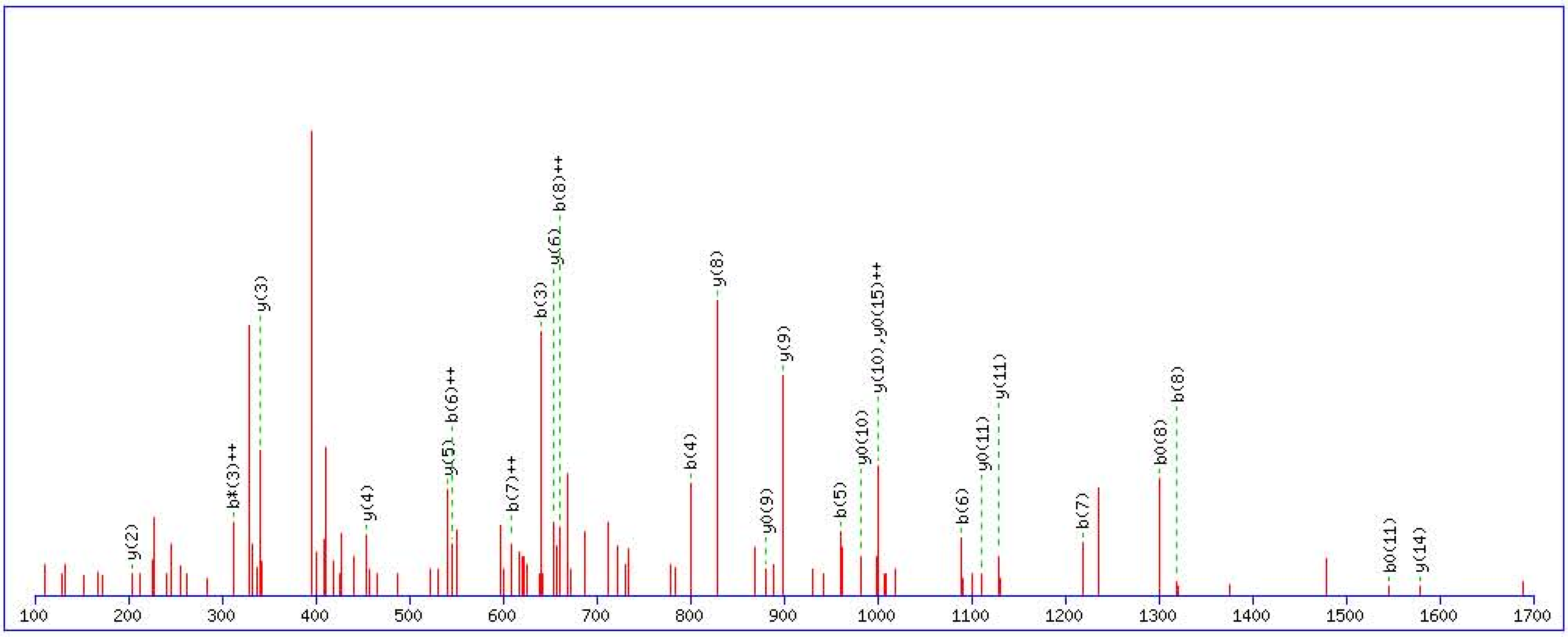
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEQCCEETASSISLHGK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

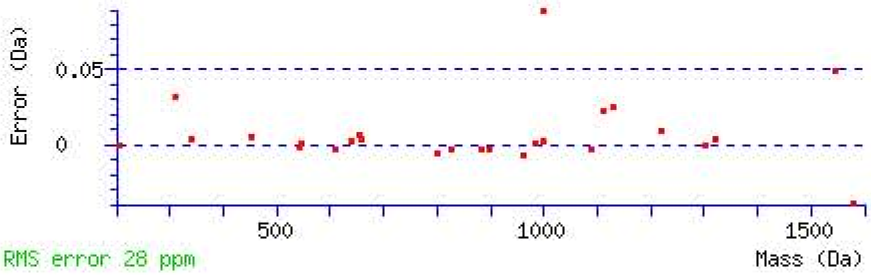
Match to Query 58586: 2216.993862 from(740.005230,3+) rtinseconds(1533) index(39106)
Title: Locus:1.1.1.2817.17 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

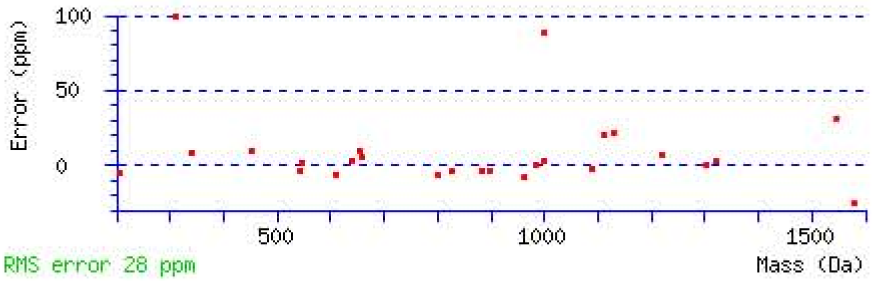
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2216.986404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0017
Matches : 26/178 fragment ions using 63 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							17
2	201.086983	101.047130			183.076418	92.041847	E	2146.956588	1073.981932	2129.930039	1065.468657	2128.946023	1064.976649	16
3	**640.312309**	320.659793	623.285760	312.146518	622.301744	311.654510	Q	2017.913995	1009.460636	2000.887446	1000.947361	1999.903430	1000.455353	15
4	**800.342958**	400.675117	783.316409	392.161843	782.332393	391.669835	C	***1578.688669***	789.847972	1561.662120	781.334698	1560.678104	780.842690	14
5	**960.373607**	480.690442	943.347058	472.177167	942.363042	471.685159	C	1418.658020	709.832648	1401.631471	701.319374	1400.647455	700.827366	13
6	**1089.416200**	**545.211738**	1072.389651	536.698464	1071.405635	536.206456	E	1258.627371	629.817323	1241.600822	621.304049	1240.616806	620.812041	12
7	**1218.458793**	**609.733035**	1201.432244	601.219760	1200.448228	600.727752	E	***1129.584778***	565.296027	1112.558229	556.782753	1111.574213	556.290744	11
8	**1319.506472**	**660.256874**	1302.479923	651.743600	1301.495907	651.251592	T	***1000.542185***	500.774731	983.515636	492.261456	982.531620	491.769448	10
9	1390.543586	695.775431	1373.517037	687.262157	1372.533021	686.770149	A	***899.494506***	450.250891	882.467957	441.737617	881.483941	441.245609	9
10	1477.575614	739.291445	1460.549065	730.778171	1459.565049	730.286163	S	***828.457392***	414.732334	811.430843	406.219060	810.446827	405.727052	8
11	1564.607642	782.807459	1547.581093	774.294185	1546.597077	773.802177	S	741.425364	371.216320	724.398815	362.703045	723.414799	362.211037	7
12	1677.691706	839.349491	1660.665157	830.836217	1659.681141	830.344209	I	***654.393336***	327.700306	637.366787	319.187031	636.382771	318.695023	6
13	1764.723734	882.865505	1747.697185	874.352231	1746.713169	873.860223	S	***541.309272***	271.158274	524.282723	262.644999	523.298707	262.152991	5
14	1877.807798	939.407537	1860.781249	930.894263	1859.797233	930.402255	L	***454.277244***	227.642260	437.250695	219.128985			4
15	2014.866710	1007.936993	1997.840161	999.423719	1996.856145	998.931711	H	***341.193180***	171.100228	324.166631	162.586953			3
16	2071.888174	1036.447725	2054.861625	1027.934450	2053.877609	1027.442442	G	***204.134268***	102.570772	187.107719	94.057497			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.6	2216.986404	0.007458	AEQCCEETASSISLHGK

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

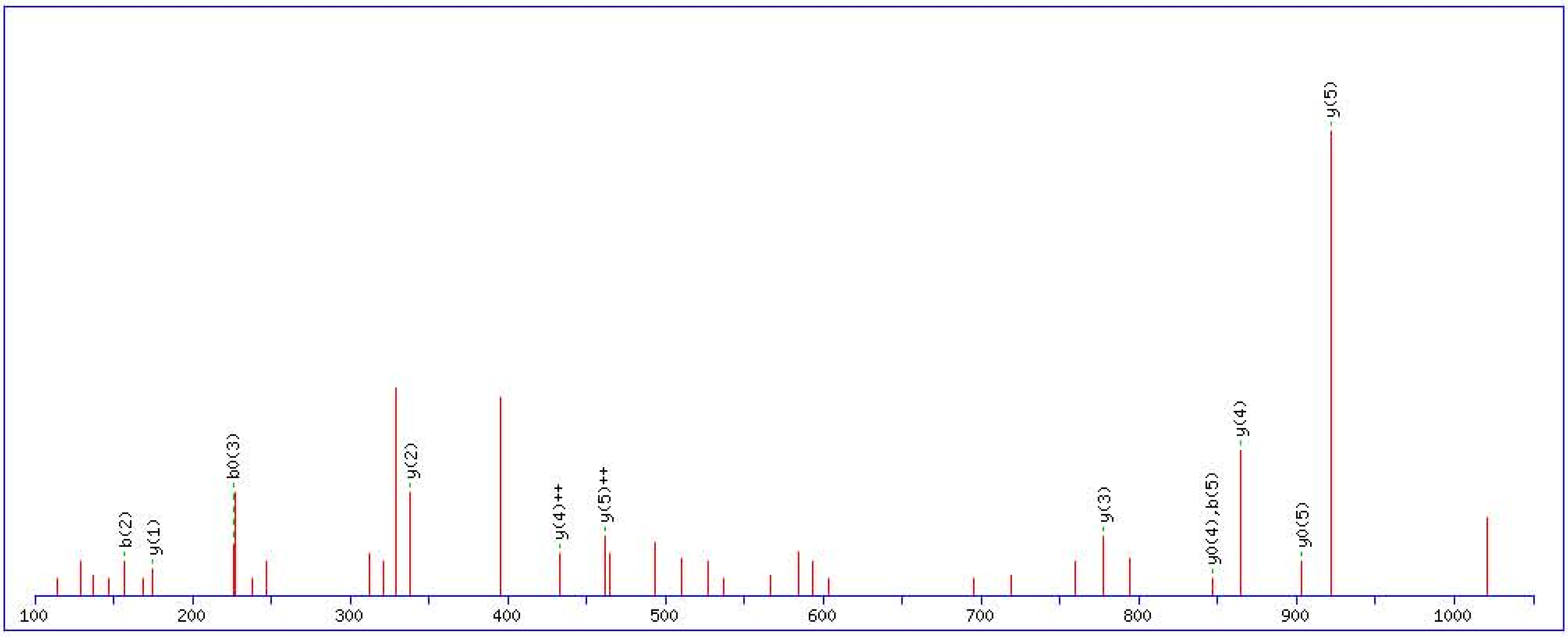
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGSQYR**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

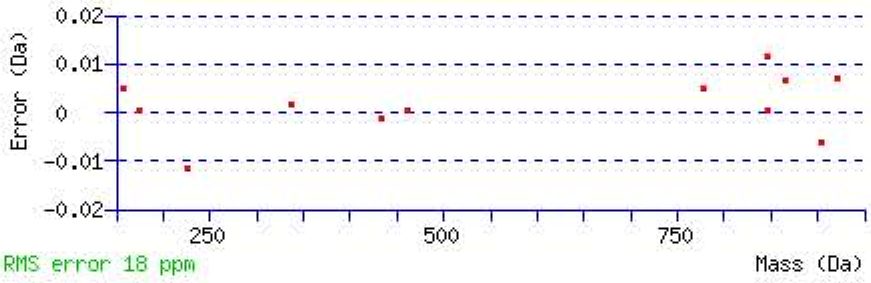
Match to Query 19817: 1019.525268 from(510.769910,2+) rtinseconds(1372) index(74227)
Title: Locus:1.1.1.2692.16 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

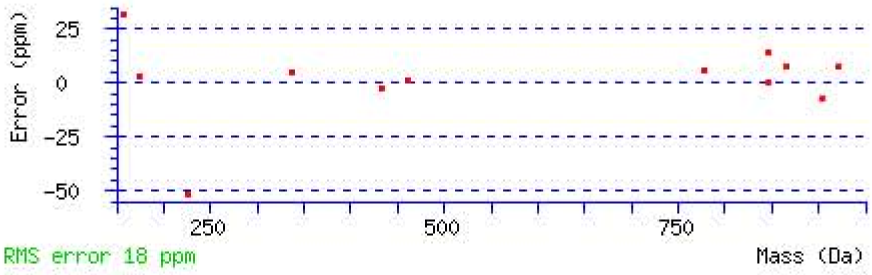
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1050] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1019.522232
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.045
Matches : 12/44 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	100.075690	50.541483					V							6
2	**157.097154**	79.052215					G	***921.461099***	461.234188	904.434550	452.720913	903.450534	452.228905	5
3	244.129182	122.568229			226.118617	113.562946	S	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
4	683.354508	342.180892	666.327959	333.667618	665.343943	333.175610	Q	***777.407607***	389.207442	760.381058	380.694167			3
5	**846.417837**	423.712557	829.391288	415.199282	828.407272	414.707274	Y	***338.182281***	169.594778	321.155732	161.081504			2
6							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.0	1019.522232	0.003036	VGSQYR
12.8	1019.533447	-0.008179	RSQYR
8.9	1019.539993	-0.014725	VGEAFALTGR
7.0	1019.510818	0.014450	RSSVSSGGAGR
6.1	1019.512146	0.013122	RSRGHHDR
3.8	1019.529419	-0.004151	REGLMRSR
3.2	1019.526062	-0.000794	KPHTAHSSR
2.6	1019.533447	-0.008179	RQSYR
1.8	1019.510803	0.014465	RDTTRESR
1.8	1019.529419	-0.004151	RMRESVSR

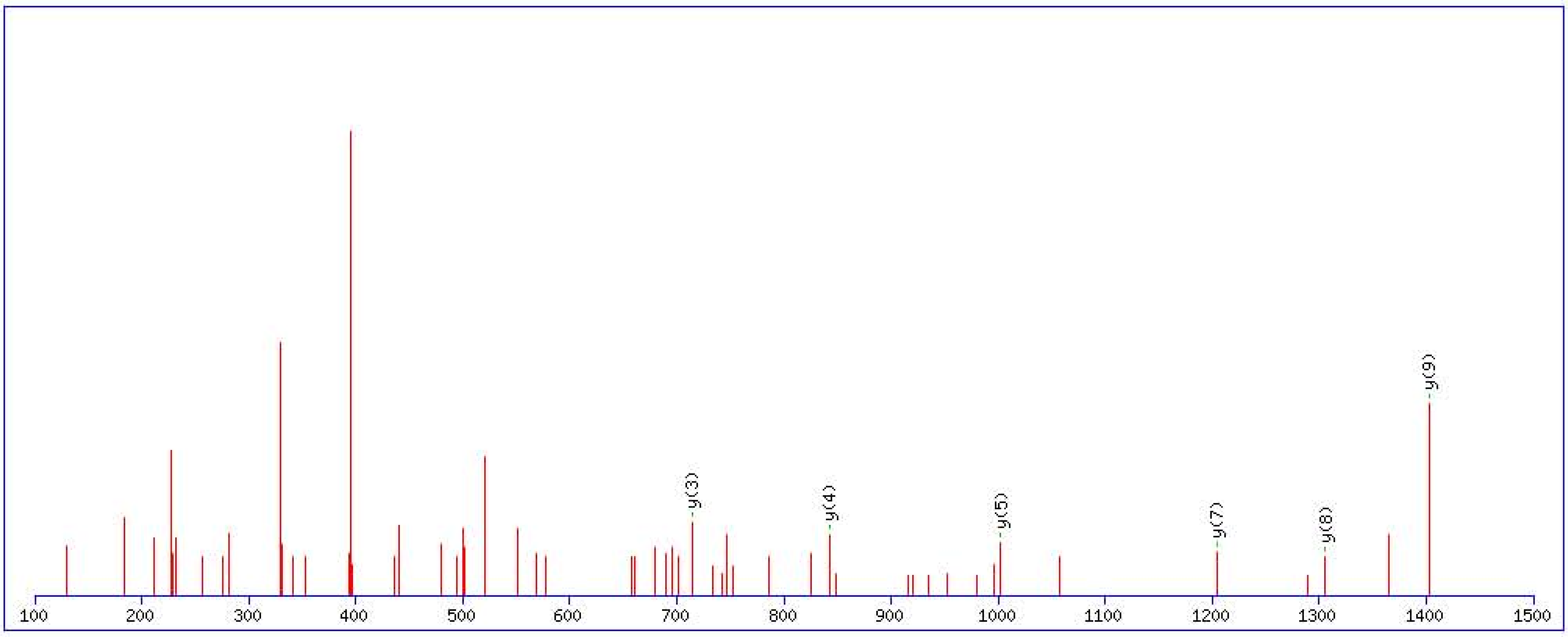
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPPTTTCQQQK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

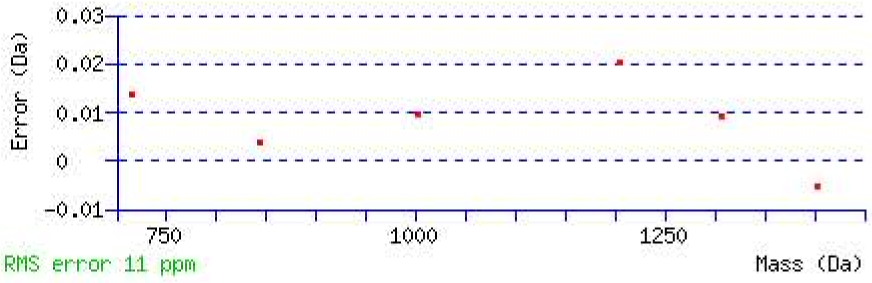
Match to Query 42700: 1611.815982 from(538.279270,3+) rtinseconds(1436) index(74767)
Title: Locus:1.1.1.2714.19 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

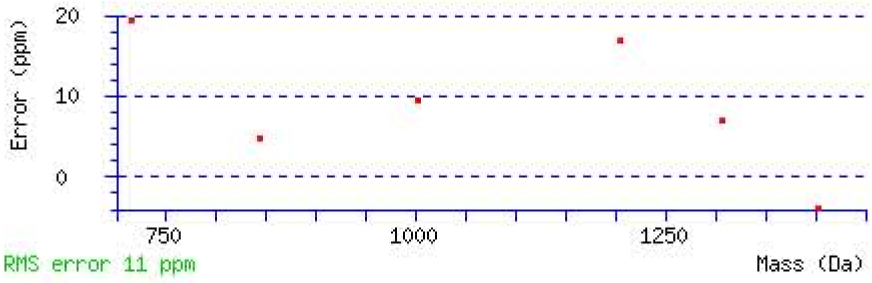
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1611.811295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.0027
Matches : 6/90 fragment ions using 13 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							11
2	211.144104	106.075690					P	1499.734500	750.370888	1482.707951	741.857614	1481.723935	741.365606	10
3	308.196868	154.602072					P	*1402.681736*	701.844506	1385.655187	693.331232	1384.671171	692.839224	9
4	409.244547	205.125911			391.233982	196.120629	T	*1305.628972*	653.318124	1288.602423	644.804850	1287.618407	644.312842	8
5	510.292226	255.649751			492.281661	246.644468	T	*1204.581293*	602.794285	1187.554744	594.281010	1186.570728	593.789002	7
6	611.339905	306.173591			593.329340	297.168308	T	1103.533614	552.270445	1086.507065	543.757171	1085.523049	543.265163	6
7	771.370554	386.188915			753.359989	377.183633	C	*1002.485935*	501.746606	985.459386	493.233331			5
8	899.429132	450.218204	882.402583	441.704930	881.418567	441.212922	Q	*842.455286*	421.731281	825.428737	413.218007			4
9	1027.487710	514.247493	1010.461161	505.734219	1009.477145	505.242211	Q	*714.396708*	357.701992	697.370159	349.188718			3
10	1466.713036	733.860156	1449.686487	725.346882	1448.702471	724.854874	Q	586.338130	293.672703	569.311581	285.159429			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.6	1611.811295	0.004687	LPPTTTCQQQK
27.6	1611.811295	0.004687	LPPTTTCQQQK
16.1	1611.811295	0.004687	LPPTTTCQQQK
0.1	1611.815094	0.000888	NDVEGAKMHLRQAK

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

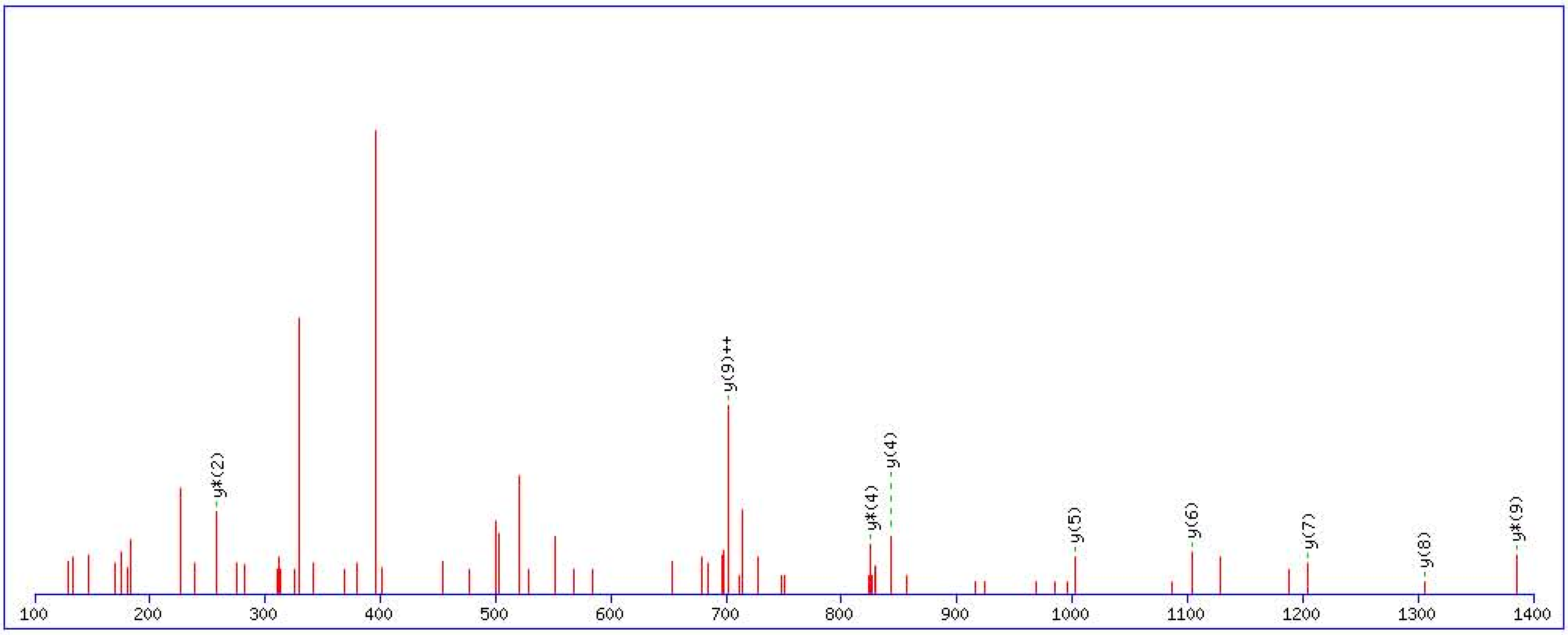
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPPTTTCQQQK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

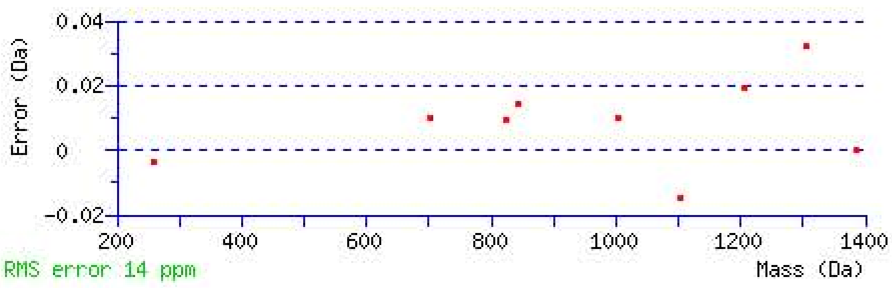
Match to Query 42701: 1611.815982 from(538.279270,3+) rtinseconds(1427) index(74691)
Title: Locus:1.1.1.2711.18 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

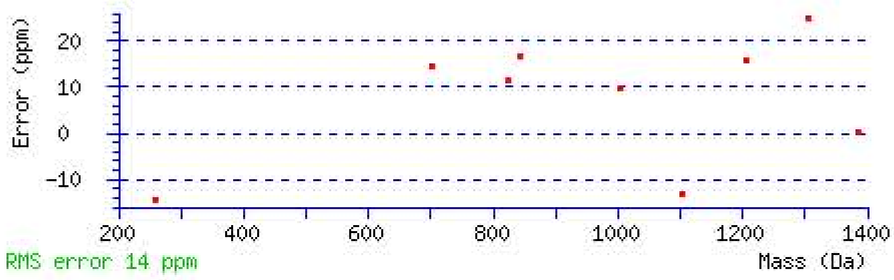
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1611.811295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.045
Matches : 9/90 fragment ions using 13 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							11
2	211.144104	106.075690					P	1499.734500	750.370888	1482.707951	741.857614	1481.723935	741.365606	10
3	308.196868	154.602072					P	1402.681736	701.844506	1385.655187	693.331232	1384.671171	692.839224	9
4	409.244547	205.125911			391.233982	196.120629	T	***1305.628972***	653.318124	1288.602423	644.804850	1287.618407	644.312842	8
5	510.292226	255.649751			492.281661	246.644468	T	***1204.581293***	602.794285	1187.554744	594.281010	1186.570728	593.789002	7
6	611.339905	306.173591			593.329340	297.168308	T	***1103.533614***	552.270445	1086.507065	543.757171	1085.523049	543.265163	6
7	771.370554	386.188915			753.359989	377.183633	C	***1002.485935***	501.746606	985.459386	493.233331			5
8	899.429132	450.218204	882.402583	441.704930	881.418567	441.212922	Q	***842.455286***	421.731281	825.428737	413.218007			4
9	1338.654458	669.830867	1321.627909	661.317593	1320.643893	660.825585	Q	714.396708	357.701992	697.370159	349.188718			3
10	1466.713036	733.860156	1449.686487	725.346882	1448.702471	724.854874	Q	275.171382	138.089329	258.144833	129.576055			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.6	1611.811295	0.004687	LPPTTTCQQQK
27.6	1611.811295	0.004687	LPPTTTCQQQK
24.4	1611.811295	0.004687	LPPTTTCQQQK

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

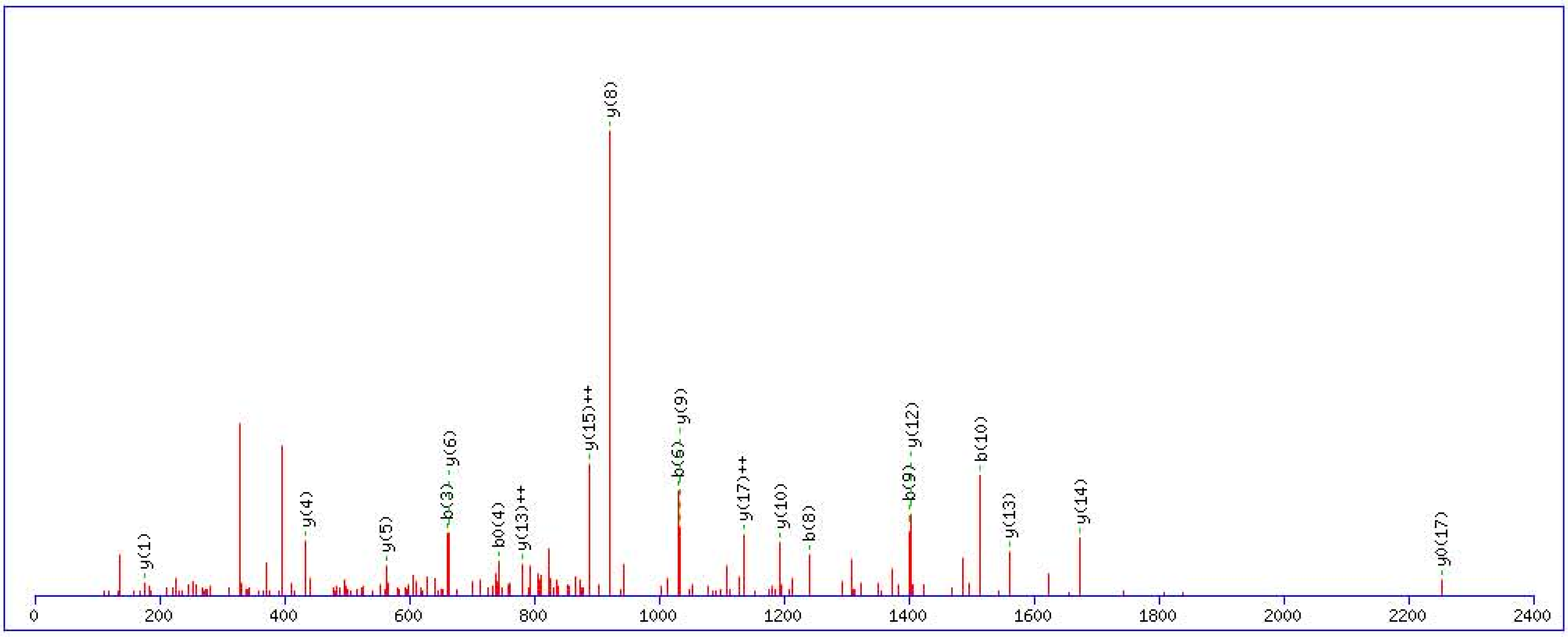
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGQTIRPICLPCTEGTTR**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

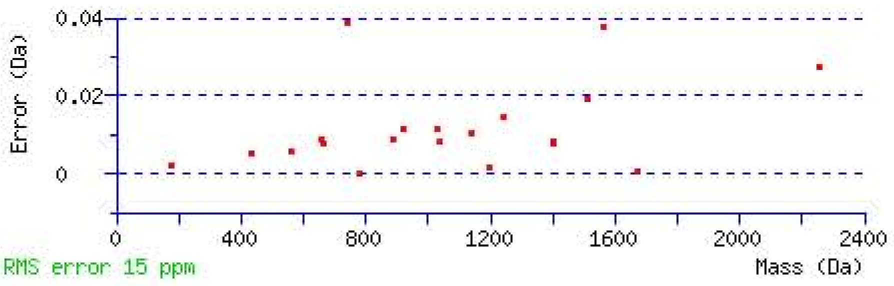
Match to Query 63516: 2433.215322 from(812.079050,3+) rtinseconds(2060) index(78927)
Title: Locus:1.1.1.2931.22 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

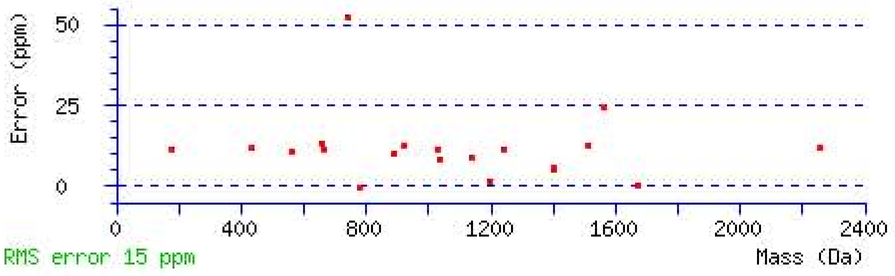
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2433.196701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 55 **Expect:** 8.5e-005
Matches : 20/192 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							18
2	221.092069	111.049673					G	2271.140644	1136.073960	2254.114095	1127.560685	2253.130079	1127.068677	17
3	**660.317395**	330.662336	643.290846	322.149061			Q	2214.119180	1107.563228	2197.092631	1099.049953	2196.108615	1098.557945	16
4	761.365074	381.186175	744.338525	372.672901	743.354509	372.180893	T	1774.893854	887.950565	1757.867305	879.437290	1756.883289	878.945282	15
5	874.449138	437.728207	857.422589	429.214933	856.438573	428.722925	I	***1673.846175***	837.426725	1656.819626	828.913451	1655.835610	828.421443	14
6	**1030.550249**	515.778763	1013.523700	507.265488	1012.539684	506.773480	R	***1560.762111***	780.884693	1543.735562	772.371419	1542.751546	771.879411	13
7	1127.603013	564.305145	1110.576464	555.791870	1109.592448	555.299862	P	***1404.661000***	702.834138	1387.634451	694.320863	1386.650435	693.828855	12
8	**1240.687077**	620.847177	1223.660528	612.333902	1222.676512	611.841894	I	1307.608236	654.307756	1290.581687	645.794481	1289.597671	645.302473	11
9	**1400.717726**	700.862501	1383.691177	692.349227	1382.707161	691.857219	C	***1194.524172***	597.765724	1177.497623	589.252449	1176.513607	588.760441	10
10	**1513.801790**	757.404533	1496.775241	748.891259	1495.791225	748.399250	L	***1034.493523***	517.750399	1017.466974	509.237125	1016.482958	508.745117	9
11	1610.854554	805.930915	1593.828005	797.417641	1592.843989	796.925633	P	***921.409459***	461.208367	904.382910	452.695093	903.398894	452.203085	8
12	1770.885203	885.946240	1753.858654	877.432965	1752.874638	876.940957	C	824.356695	412.681985	807.330146	404.168711	806.346130	403.676703	7
13	1871.932882	936.470079	1854.906333	927.956805	1853.922317	927.464797	T	***664.326046***	332.666661	647.299497	324.153386	646.315481	323.661378	6
14	2000.975475	1000.991376	1983.948926	992.478101	1982.964910	991.986093	E	***563.278367***	282.142821	546.251818	273.629547	545.267802	273.137539	5
15	2057.996939	1029.502107	2040.970390	1020.988833	2039.986374	1020.496825	G	***434.235774***	217.621525	417.209225	209.108250	416.225209	208.616242	4
16	2159.044618	1080.025947	2142.018069	1071.512672	2141.034053	1071.020664	T	377.214310	189.110793	360.187761	180.597518	359.203745	180.105510	3
17	2260.092297	1130.549786	2243.065748	1122.036512	2242.081732	1121.544504	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.5	2433.196701	0.018621	YGQTIRPICLPCTEGTTR

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

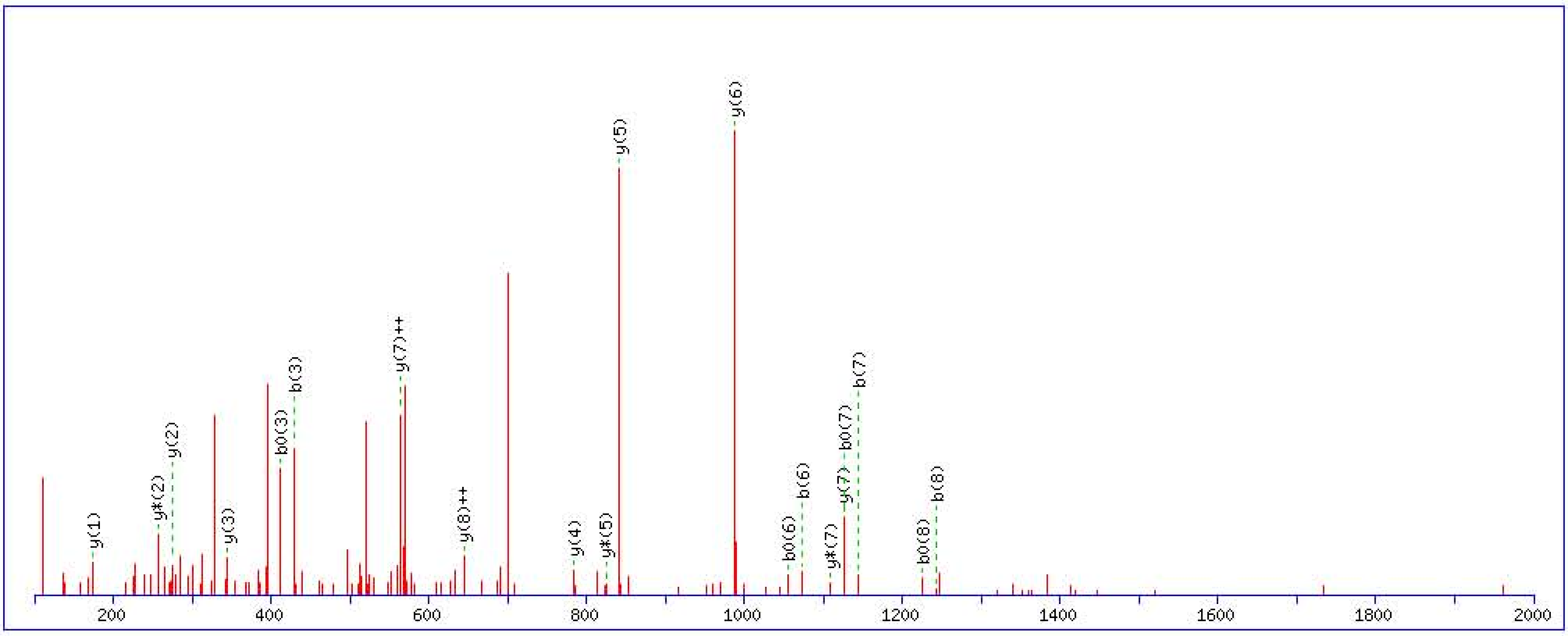
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYHFGQAVR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

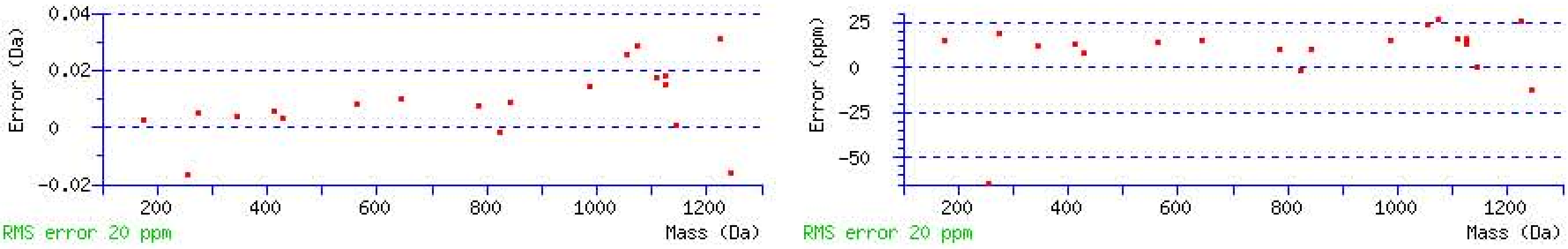
Match to Query 35645: 1416.715408 from(709.364980,2+) rtinseconds(1676) index(22423)
Title: Locus:1.1.1.2538.10 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1416.697235
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0039
Matches : 20/70 fragment ions using 49 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	130.049869	65.528572			112.039304	56.523290	E					9
2	293.113198	147.060237			275.102633	138.054955	Y	1288.661925	644.834601	1271.635376	636.321326	8
3	**430.172110**	215.589693			412.161545	206.584411	H	***1125.598596***	563.302936	1108.572047	554.789662	7
4	577.240524	289.123900			559.229959	280.118618	F	***988.539684***	494.773480	971.513135	486.260206	6
5	634.261988	317.634632			616.251423	308.629350	G	***841.471270***	421.239273	824.444721	412.725999	5
6	**1073.487314**	537.247295	1056.460765	528.734021	1055.476749	528.242013	Q	***784.449806***	392.728541	767.423257	384.215267	4
7	**1144.524428**	572.765852	1127.497879	564.252578	1126.513863	563.760570	A	***345.224480***	173.115878	328.197931	164.602603	3
8	**1243.592842**	622.300059	1226.566293	613.786785	1225.582277	613.294777	V	***274.187366***	137.597321	257.160817	129.084047	2
9							R	***175.118952***	88.063114	158.092403	79.549839	1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.7	1416.697235	0.018173	EYHFGQAVR
5.6	1416.704453	0.010955	YCATVRVQQHR
0.3	1416.736130	-0.020722	GLAPGQEYQVTVR
0.2	1416.732086	-0.016678	EAVSQVRAEATTR

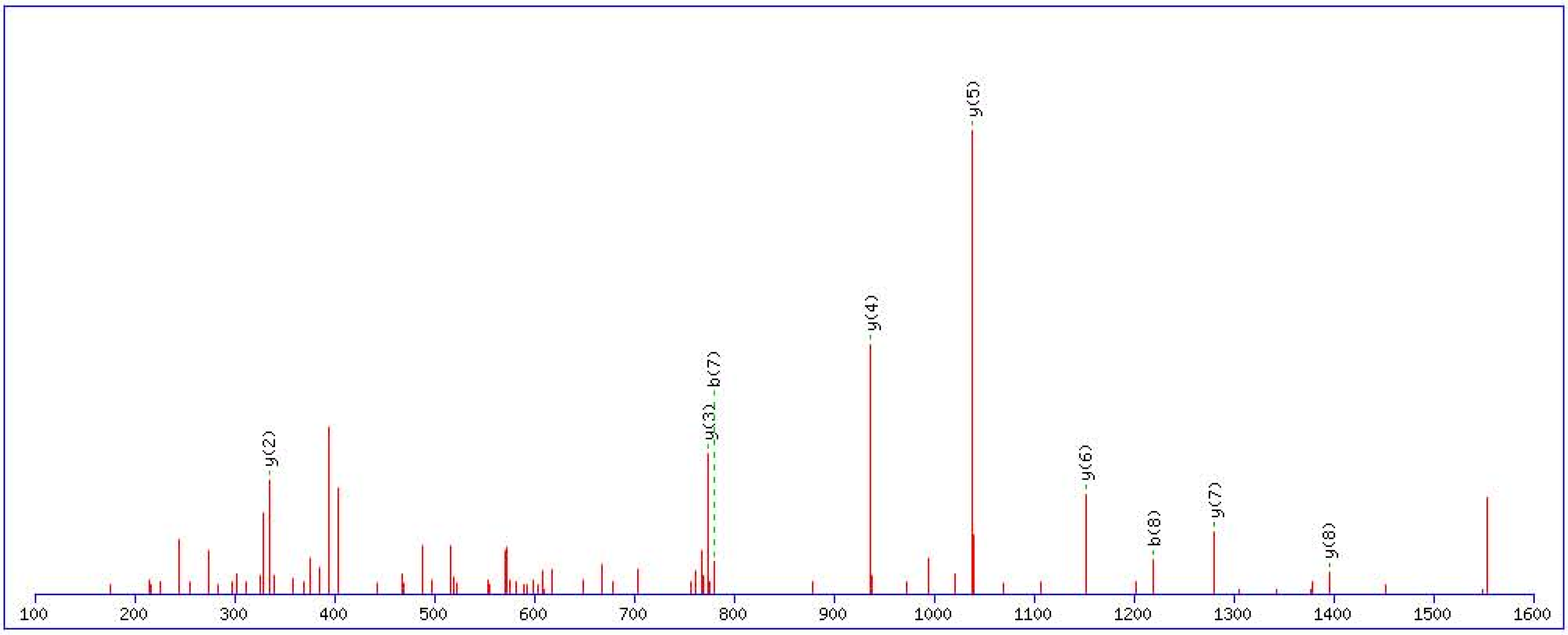
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGDEITYQCR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

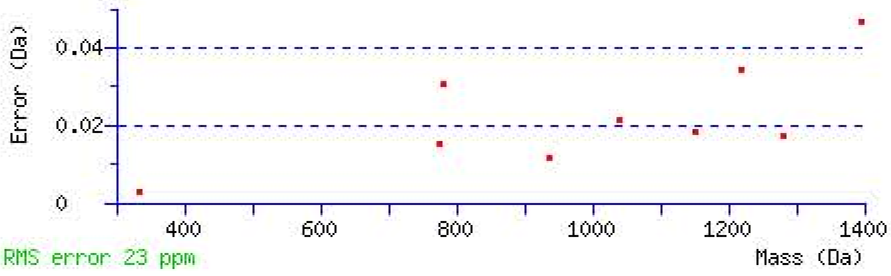
Match to Query 39985: 1552.718348 from(777.366450,2+) rtinseconds(1670) index(22372)
Title: Locus:1.1.1.2536.7 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

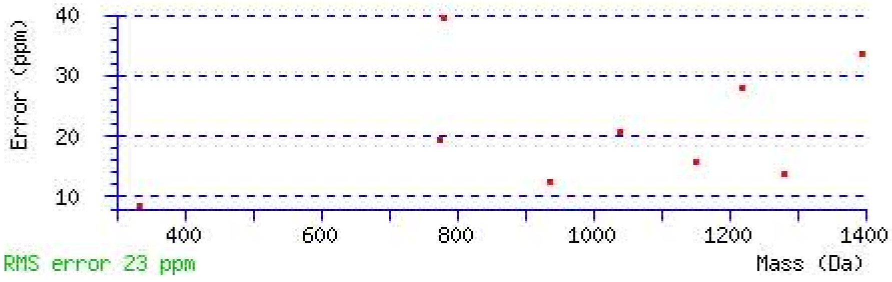
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1552.701401
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 8.3e-005
Matches : 9/86 fragment ions using 14 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							10
2	159.076419	80.041847			141.065854	71.036565	G	1452.660999	726.834138	1435.634450	718.320863	1434.650434	717.828855	9
3	274.103362	137.555319			256.092797	128.550037	D	***1395.639535***	698.323406	1378.612986	689.810131	1377.628970	689.318123	8
4	403.145955	202.076616			385.135390	193.071333	E	***1280.612592***	640.809934	1263.586043	632.296660	1262.602027	631.804652	7
5	516.230019	258.618648			498.219454	249.613365	I	***1151.569999***	576.288638	1134.543450	567.775363	1133.559434	567.283355	6
6	617.277698	309.142487			599.267133	300.137205	T	***1038.485935***	519.746606	1021.459386	511.233331	1020.475370	510.741323	5
7	**780.341027**	390.674152			762.330462	381.668869	Y	***937.438256***	469.222766	920.411707	460.709492			4
8	**1219.566353**	610.286815	1202.539804	601.773540	1201.555788	601.281532	Q	***774.374927***	387.691102	757.348378	379.177827			3
9	1379.597002	690.302139	1362.570453	681.788865	1361.586437	681.296857	C	***335.149601***	168.078438	318.123052	159.565164			2
10							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.4	1552.701401	0.016947	TGDEITYQCR
6.5	1552.715149	0.003199	LTNGSSSCSGTVEVR
3.7	1552.716629	0.001719	NEQPYLYCR

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

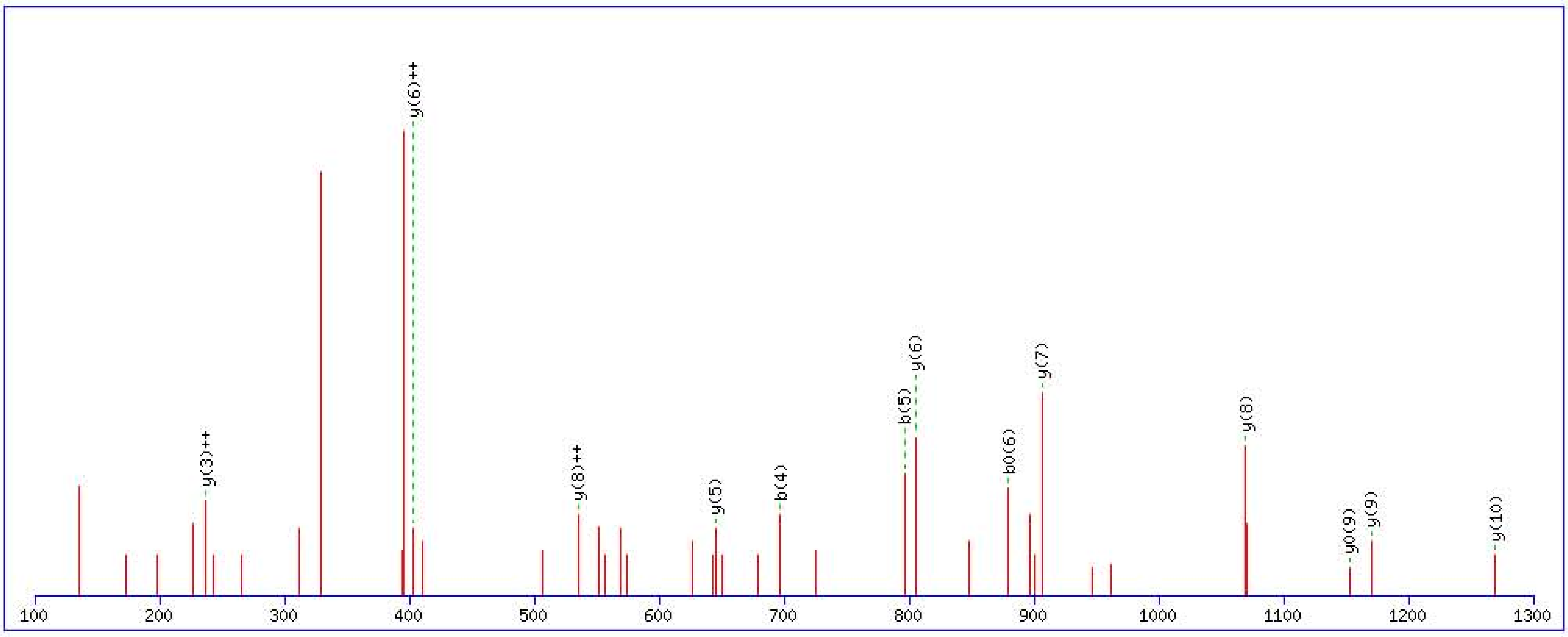
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGEQVTYTCATYYK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

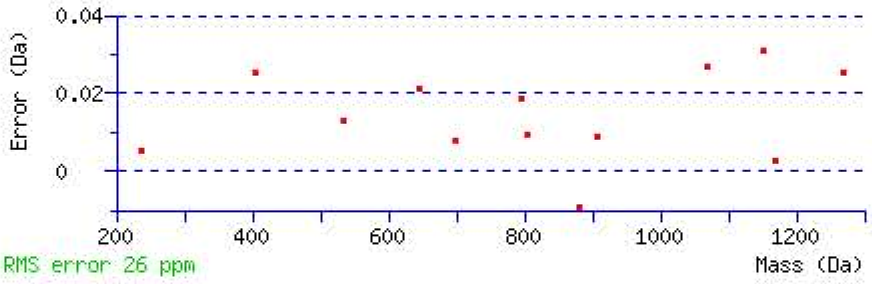
Match to Query 52124: 1964.914332 from(655.978720,3+) rtinseconds(1844) index(5926)
Title: Locus:1.1.1.2774.18 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

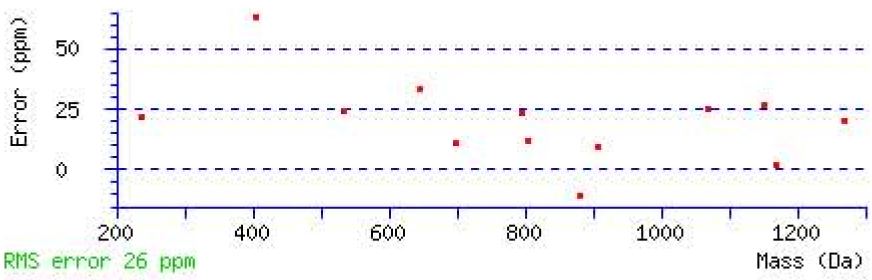
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1964.901215
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.018
Matches : 13/140 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							14
2	129.065854	65.036565					G	1894.871388	947.939332	1877.844839	939.426058	1876.860823	938.934050	13
3	258.108447	129.557862			240.097882	120.552579	E	1837.849924	919.428600	1820.823375	910.915326	1819.839359	910.423318	12
4	**697.333773**	349.170525	680.307224	340.657250	679.323208	340.165242	Q	1708.807331	854.907304	1691.780782	846.394029	1690.796766	845.902021	11
5	**796.402187**	398.704732	779.375638	390.191457	778.391622	389.699449	V	***1269.582005***	635.294641	1252.555456	626.781366	1251.571440	626.289358	10
6	897.449866	449.228571	880.423317	440.715297	879.439301	440.223289	T	***1170.513591***	585.760434	1153.487042	577.247159	1152.503026	576.755151	9
7	1060.513195	530.760236	1043.486646	522.246961	1042.502630	521.754953	Y	***1069.465912***	535.236594	1052.439363	526.723320	1051.455347	526.231312	8
8	1161.560874	581.284075	1144.534325	572.770801	1143.550309	572.278793	T	***906.402583***	453.704930	889.376034	445.191655	888.392018	444.699647	7
9	1321.591523	661.299400	1304.564974	652.786125	1303.580958	652.294117	C	***805.354904***	403.181090	788.328355	394.667816	787.344339	394.175808	6
10	1392.628637	696.817957	1375.602088	688.304682	1374.618072	687.812674	A	***645.324255***	323.165766	628.297706	314.652491	627.313690	314.160483	5
11	1493.676316	747.341796	1476.649767	738.828522	1475.665751	738.336514	T	574.287141	287.647209	557.260592	279.133934	556.276576	278.641926	4
12	1656.739645	828.873461	1639.713096	820.360186	1638.729080	819.868178	Y	473.239462	237.123369	456.212913	228.610095			3
13	1819.802974	910.405125	1802.776425	901.891851	1801.792409	901.399843	Y	310.176133	155.591705	293.149584	147.078430			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.8	1964.901215	0.013117	AGEQVTYTCATYYK

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

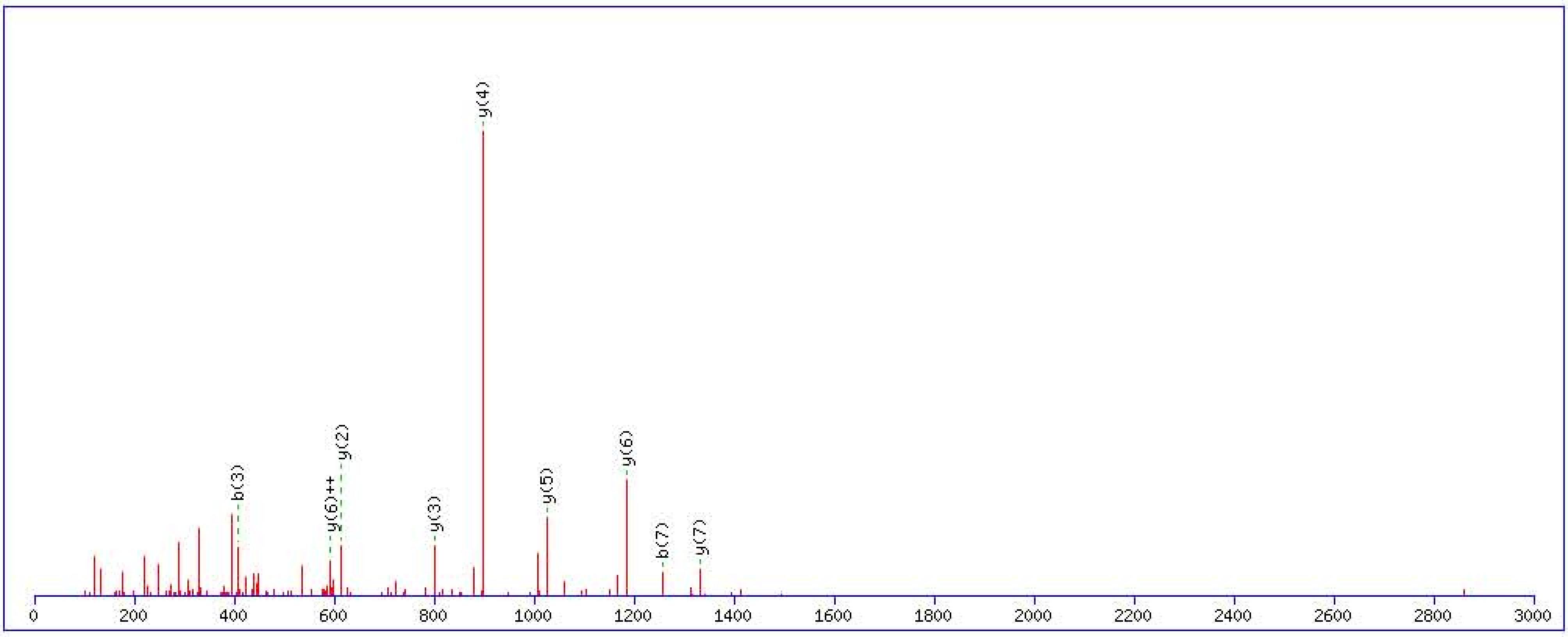
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFCQPWQR**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

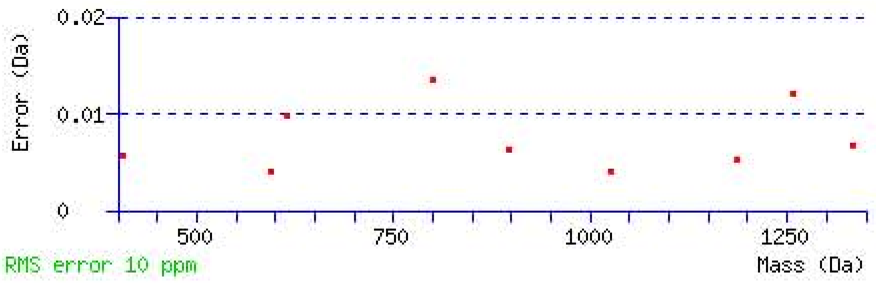
Match to Query 36370: 1430.706048 from(716.360300,2+) rtinseconds(2030) index(78702)
Title: Locus:1.1.1.2921.10 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

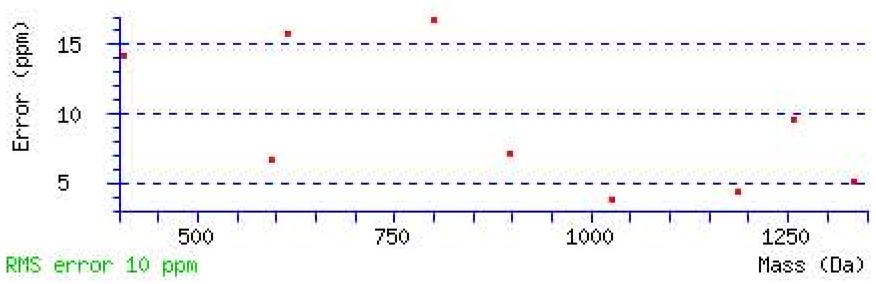
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1430.695145
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00013
Matches : 9/50 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	100.075690	50.541483			V					8
2	247.144104	124.075690			F	1332.633996	666.820636	1315.607447	658.307362	7
3	407.174753	204.091014			C	1185.565582	593.286429	1168.539033	584.773155	6
4	535.233331	268.120304	518.206782	259.607029	Q	1025.534933	513.271105	1008.508384	504.757830	5
5	632.286095	316.646686	615.259546	308.133411	P	897.476355	449.241816	880.449806	440.728541	4
6	818.365408	409.686342	801.338859	401.173068	W	800.423591	400.715434	783.397042	392.202159	3
7	1257.590734	629.299005	1240.564185	620.785731	Q	614.344278	307.675777	597.317729	299.162503	2
8					R	175.118952	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	1430.695145	0.010903	VFCQPWQR
8.1	1430.695145	0.010903	VFCQPWQR
2.6	1430.693619	0.012429	QLQTLSMPGGGGNR
1.6	1430.700989	0.005059	DMGLMNAIGLQPR
0.9	1430.726822	-0.020774	VFDVYLCFLQK
0.5	1430.711319	-0.005271	RAKAEDENETLR
0.2	1430.722565	-0.016517	REAGEAGAATSKQR

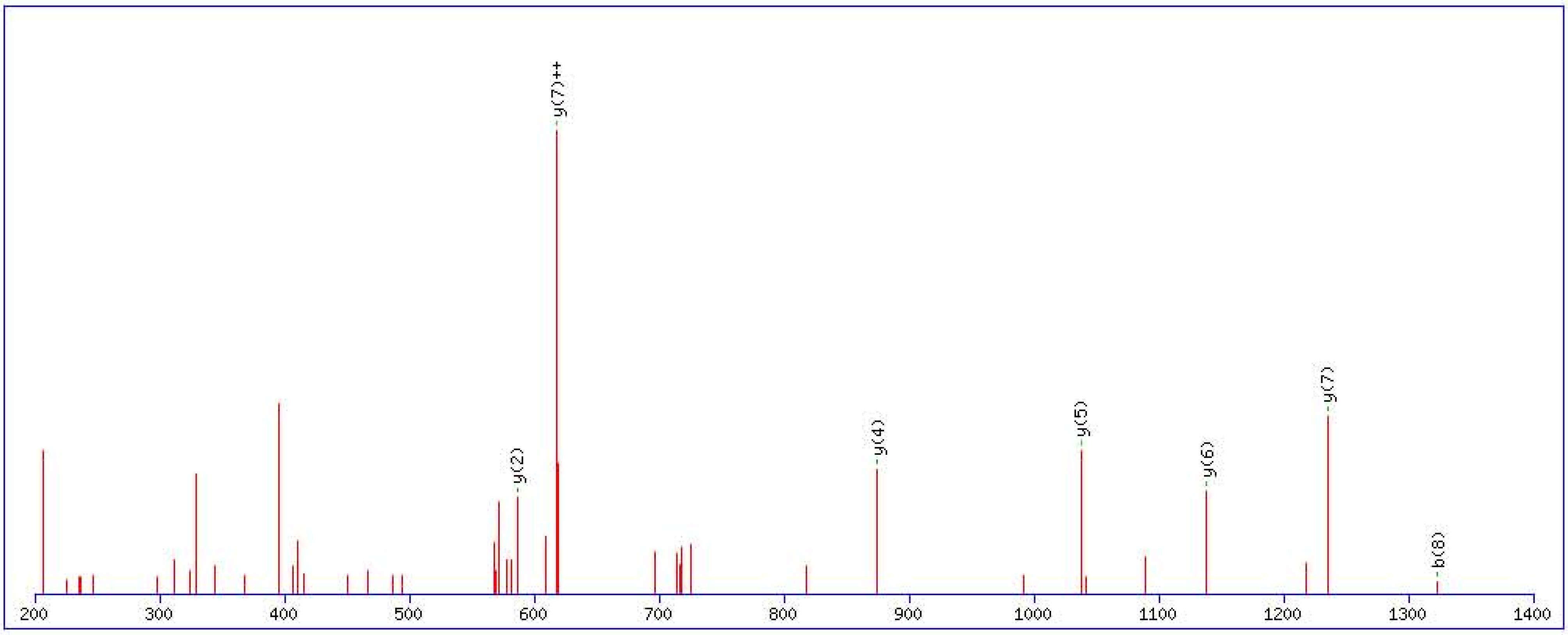
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFPTYCQQK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

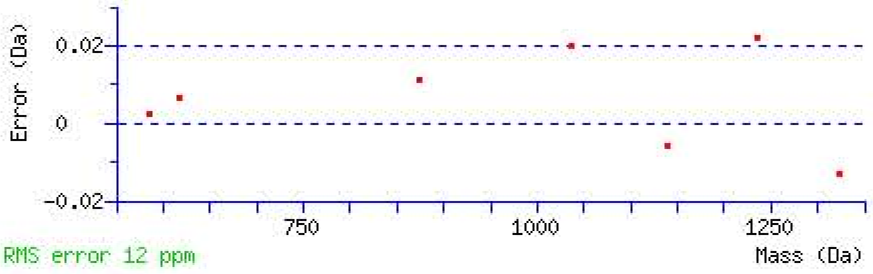
Match to Query 37604: 1468.680468 from(735.347510,2+) rtinseconds(1754) index(76856)
Title: Locus:1.1.1.2825.18 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

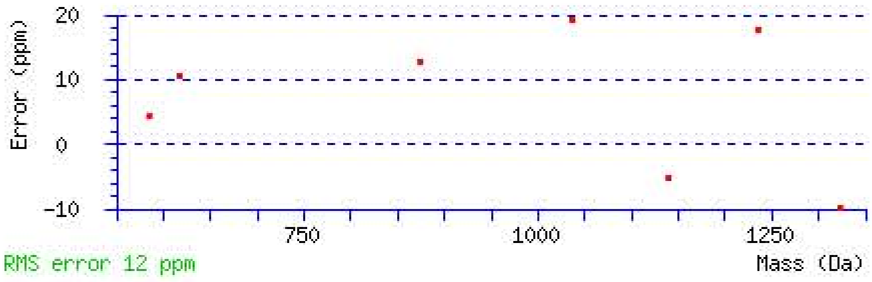
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1468.684296
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.0023
Matches : 7/74 fragment ions using 12 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							9
2	235.107718	118.057497			217.097153	109.052214	F	1382.659543	691.833410	1365.632994	683.320135	1364.648978	682.828127	8
3	332.160482	166.583879			314.149917	157.578596	P	***1235.591129***	618.299203	1218.564580	609.785928	1217.580564	609.293920	7
4	433.208161	217.107718			415.197596	208.102436	T	***1138.538365***	569.772821	1121.511816	561.259546	1120.527800	560.767538	6
5	596.271490	298.639383			578.260925	289.634101	Y	***1037.490686***	519.248981	1020.464137	510.735707			5
6	756.302139	378.654708			738.291574	369.649425	C	***874.427357***	437.717317	857.400808	429.204042			4
7	884.360717	442.683997	867.334168	434.170722	866.350152	433.678714	Q	714.396708	357.701992	697.370159	349.188718			3
8	**1323.586043**	662.296660	1306.559494	653.783385	1305.575478	653.291377	Q	***586.338130***	293.672703	569.311581	285.159428			2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.0	1468.684296	-0.003828	SFPTYCQQK
18.0	1468.684296	-0.003828	SFPTYCQQK
0.9	1468.671524	0.008944	MEAETGSSVETGKK

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

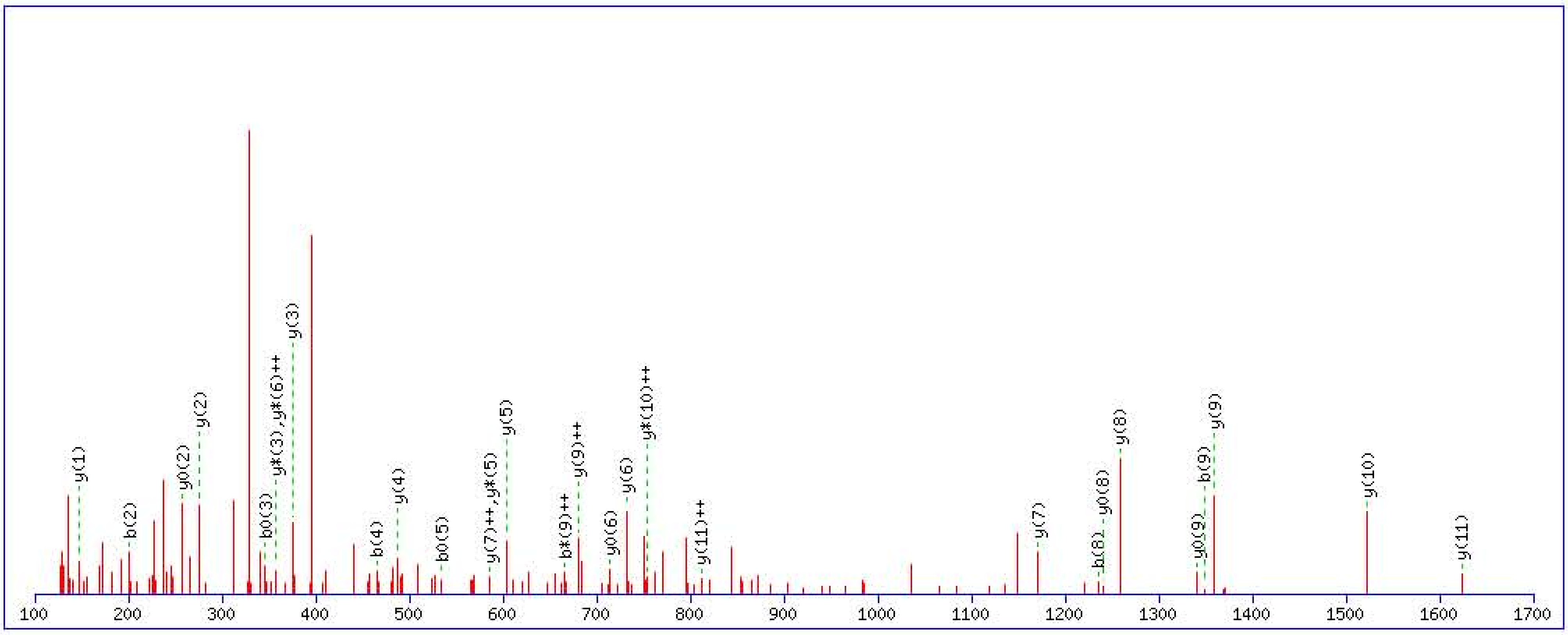
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTYTSQEDLVEK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

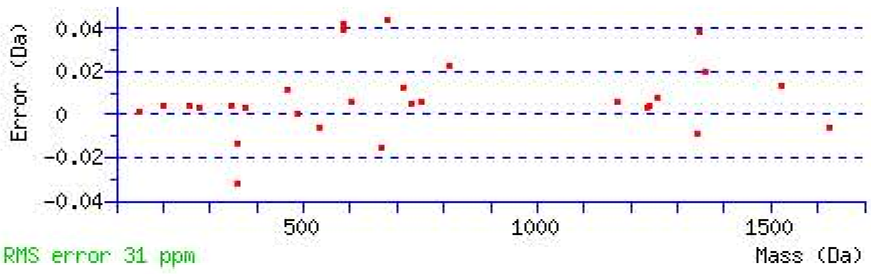
Match to Query 46341: 1721.857152 from(574.959660,3+) rtinseconds(1883) index(77562)
Title: Locus:1.1.1.2870.19 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

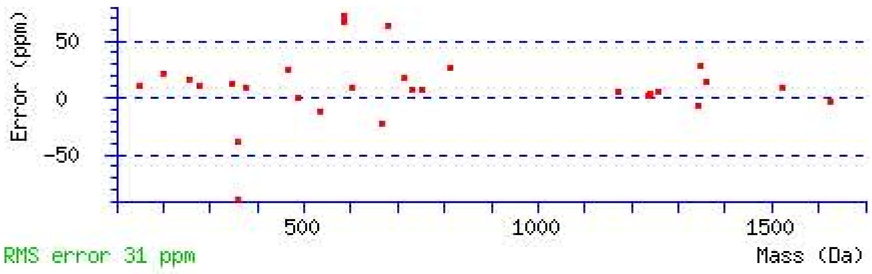
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1721.854584
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.0018
Matches : 29/118 fragment ions using 81 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							12
2	**201.123369**	101.065322			183.112804	92.060040	T	***1623.793452***	812.400364	1606.766903	803.887090	1605.782887	803.395081	11
3	364.186698	182.596987			346.176133	173.591705	Y	***1522.745773***	761.876524	1505.719224	753.363250	1504.735208	752.871242	10
4	**465.234377**	233.120827			447.223812	224.115544	T	***1359.682444***	680.344860	1342.655895	671.831585	1341.671879	671.339577	9
5	552.266405	276.636841			534.255840	267.631558	S	***1258.634765***	629.821021	1241.608216	621.307746	1240.624200	620.815738	8
6	991.491731	496.249504	974.465182	487.736229	973.481166	487.244221	Q	***1171.602737***	586.305006	1154.576188	577.791732	1153.592172	577.299724	7
7	1120.534324	560.770800	1103.507775	552.257526	1102.523759	551.765517	E	***732.377411***	366.692343	715.350862	358.179069	714.366846	357.687061	6
8	**1235.561267**	618.284272	1218.534718	609.770997	1217.550702	609.278989	D	***603.334818***	302.171047	586.308269	293.657773	585.324253	293.165765	5
9	**1348.645331**	674.826303	1331.618782	666.313029	1330.634766	665.821021	L	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.652293	4
10	1447.713745	724.360511	1430.687196	715.847236	1429.703180	715.355228	V	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
11	1576.756338	788.881807	1559.729789	780.368533	1558.745773	779.876524	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.3	1721.854584	0.002568	VTYTSQEDLVEK

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

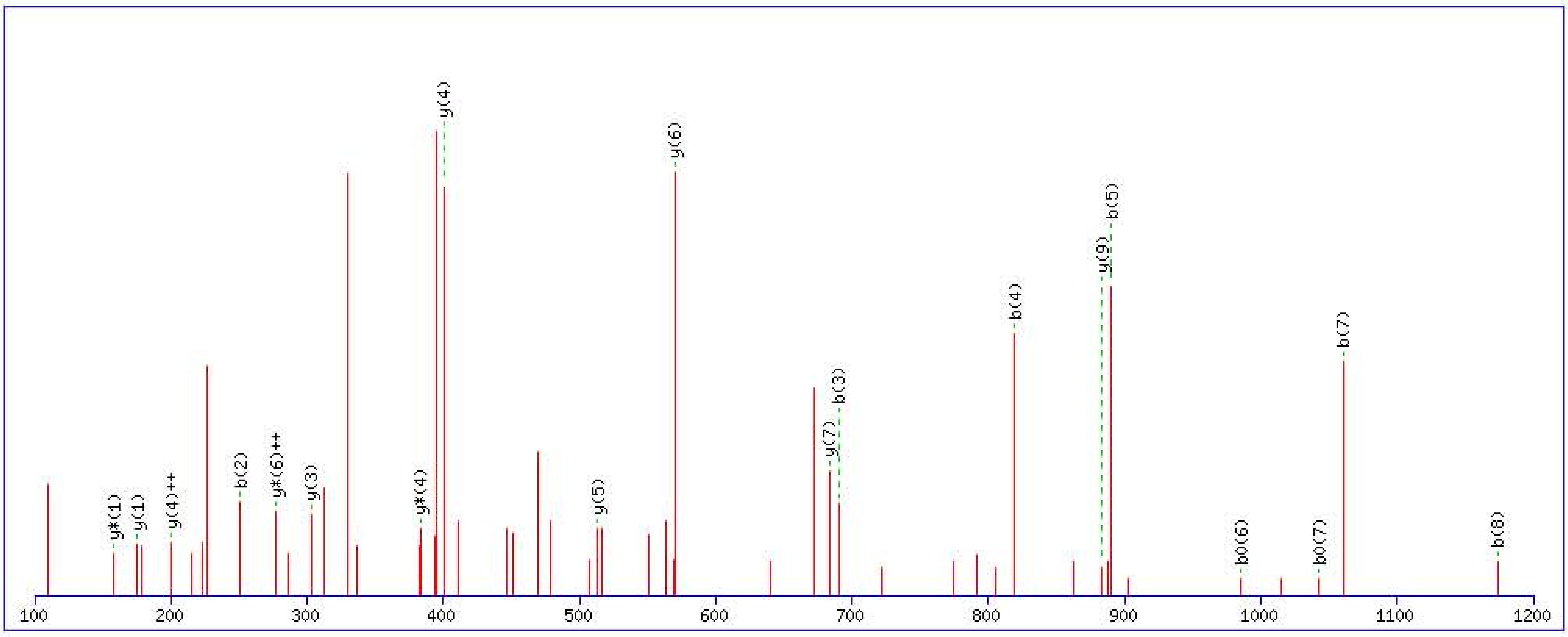
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLQEALGLPAGR**
Found in **CLC11_HUMAN**, C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1

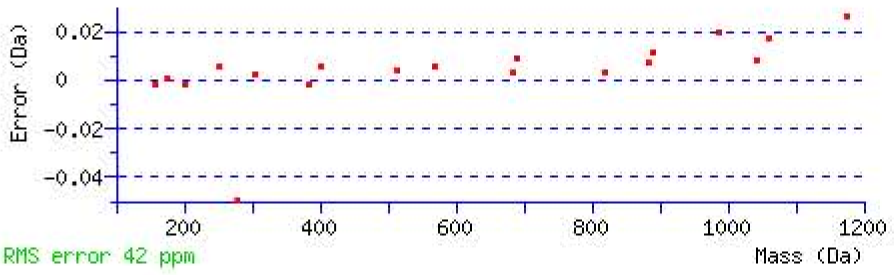
Match to Query 40644: 1571.868792 from(524.963540,3+) rtinseconds(1903) index(59793)
Title: Locus:1.1.1.2968.14 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

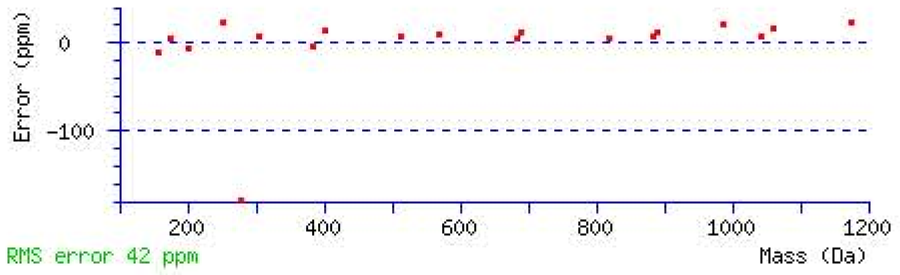
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1571.860596
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0056
Matches : 19/106 fragment ions using 43 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							12
2	***251.150252***	126.078764					L	1435.808983	718.408129	1418.782434	709.894855	1417.798418	709.402847	11
3	***690.375578***	345.691427	673.349029	337.178153			Q	1322.724919	661.866098	1305.698370	653.352823	1304.714354	652.860815	10
4	***819.418171***	410.212724	802.391622	401.699449	801.407606	401.207441	E	***883.499593***	442.253434	866.473044	433.740160	865.489028	433.248152	9
5	***890.455285***	445.731281	873.428736	437.218006	872.444720	436.725998	A	754.457000	377.732138	737.430451	369.218863			8
6	1003.539349	502.273313	986.512800	493.760038	985.528784	493.268030	L	***683.419886***	342.213581	666.393337	333.700306			7
7	***1060.560813***	530.784045	1043.534264	522.270770	1042.550248	521.778762	G	***570.335822***	285.671549	553.309273	277.158274			6
8	***1173.644877***	587.326077	1156.618328	578.812802	1155.634312	578.320794	L	***513.314358***	257.160817	496.287809	248.647542			5
9	1270.697641	635.852459	1253.671092	627.339184	1252.687076	626.847176	P	***400.230294***	200.618785	383.203745	192.105510			4
10	1341.734755	671.371016	1324.708206	662.857741	1323.724190	662.365733	A	***303.177530***	152.092403	286.150981	143.579128			3
11	1398.756219	699.881747	1381.729670	691.368473	1380.745654	690.876465	G	232.140416	116.573846	215.113867	108.060571			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.8	1571.860596	0.008196	HLQEALGLPAGR
7.4	1571.856567	0.012225	QVRELQMRLDIR
3.4	1571.878372	-0.009580	LTGRVLALSFDAPGR
1.8	1571.871826	-0.003034	THREPQLRPK

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

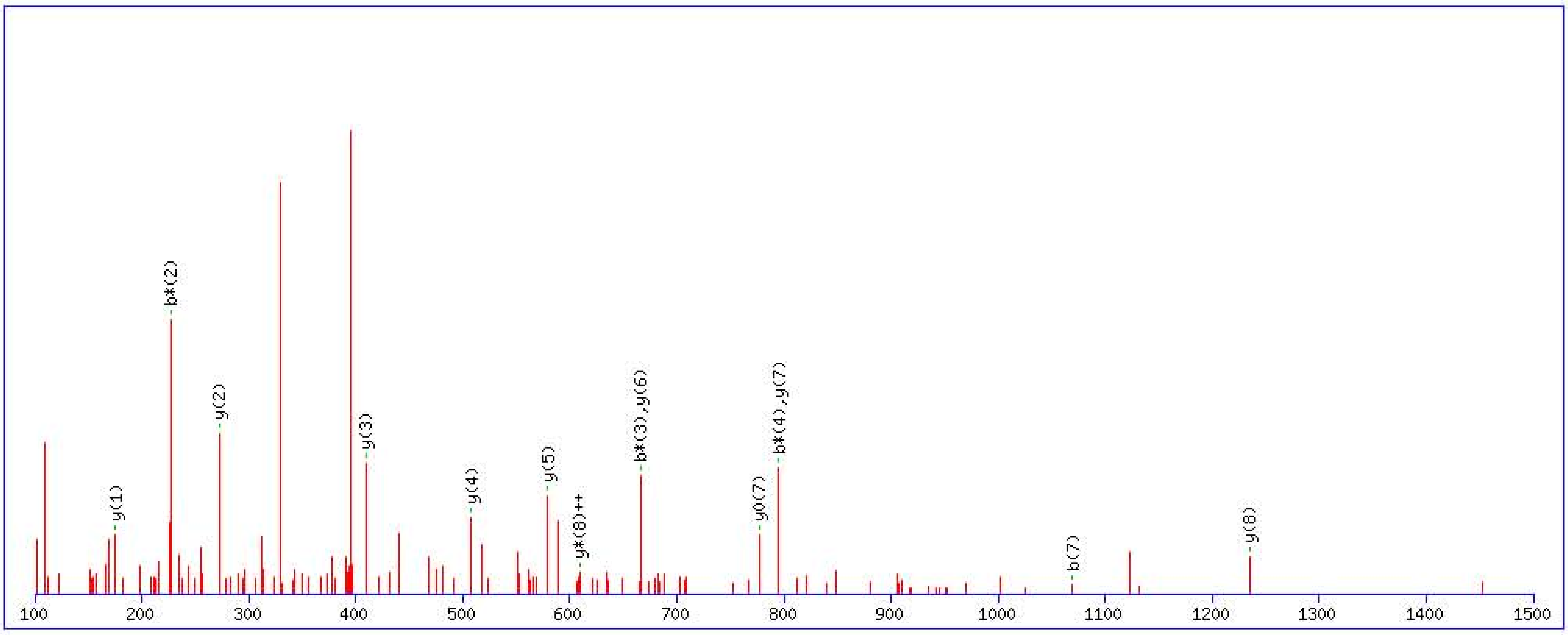
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NEQESAVHPR**
Found in **DBNL_HUMAN**, Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1

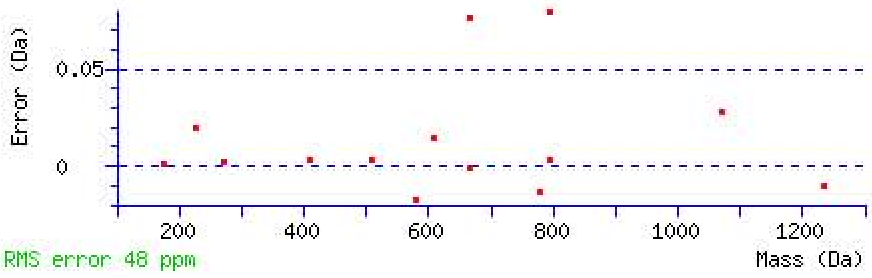
Match to Query 37885: 1476.724482 from(493.248770,3+) rtinseconds(1250) index(55194)
Title: Locus:1.1.1.2741.7 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

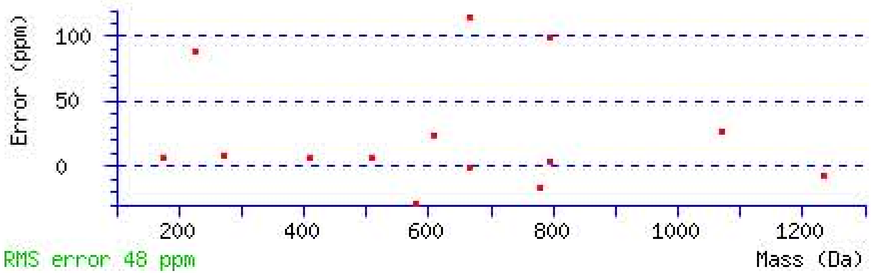
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1476.714325
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 42 **Expect:** 0.0002
Matches : 14/96 fragment ions using 24 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							10
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	E	1363.678696	682.342986	1346.652147	673.829712	1345.668131	673.337704	9
3	683.318122	342.162699	666.291573	333.649425	665.307557	333.157417	Q	***1234.636103***	617.821690	1217.609554	609.308415	1216.625538	608.816407	8
4	812.360715	406.683996	795.334166	398.170721	794.350150	397.678713	E	***795.410777***	398.209027	778.384228	389.695752	777.400212	389.203744	7
5	899.392743	450.200010	882.366194	441.686735	881.382178	441.194727	S	***666.368184***	333.687730	649.341635	325.174456	648.357619	324.682448	6
6	970.429857	485.718567	953.403308	477.205292	952.419292	476.713284	A	***579.336156***	290.171716	562.309607	281.658442			5
7	1069.498271	535.252774	1052.471722	526.739499	1051.487706	526.247491	V	***508.299042***	254.653159	491.272493	246.139884			4
8	1206.557183	603.782230	1189.530634	595.268955	1188.546618	594.776947	H	***409.230628***	205.118952	392.204079	196.605677			3
9	1303.609947	652.308612	1286.583398	643.795337	1285.599382	643.303329	P	***272.171716***	136.589496	255.145167	128.076221			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.8	1476.714325	0.010157	NEQESAVHPR
2.3	1476.745987	-0.021505	LVKEVPEEYSER

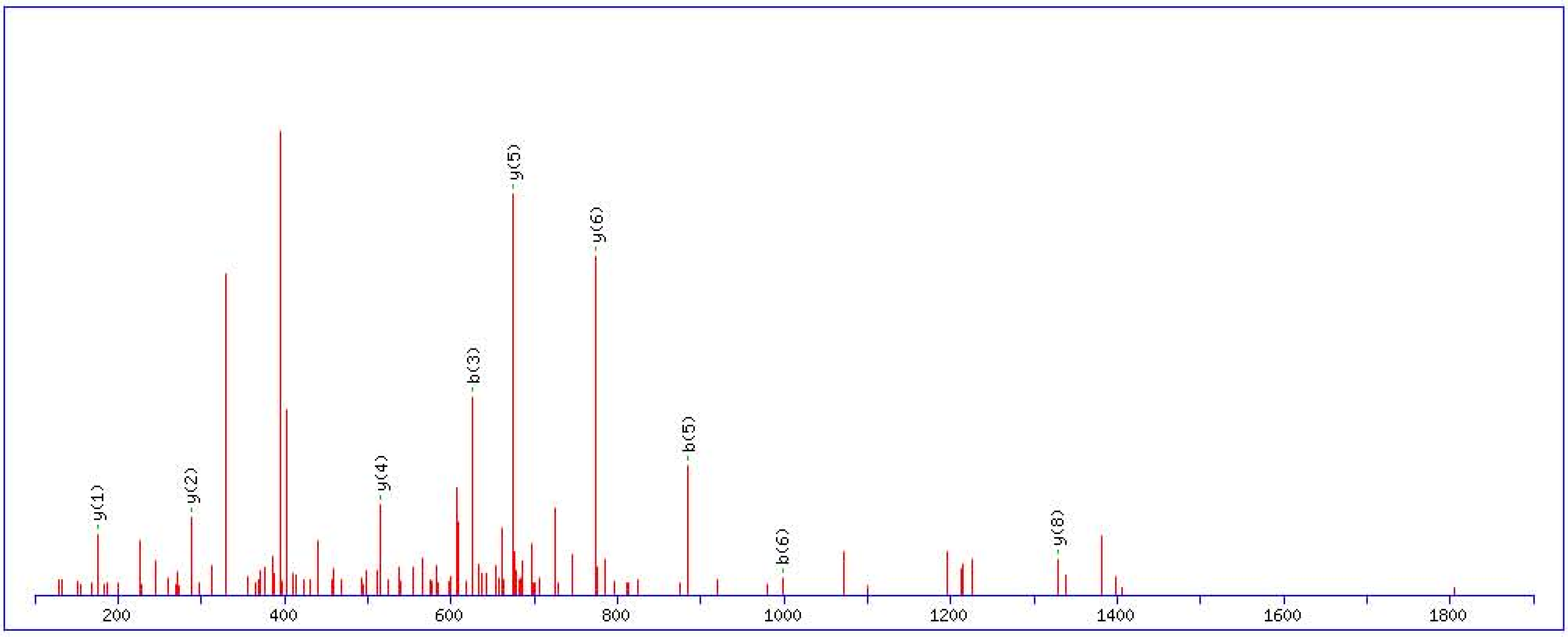
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADQVCINLR**
Found in **FBLN3_HUMAN**, EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2

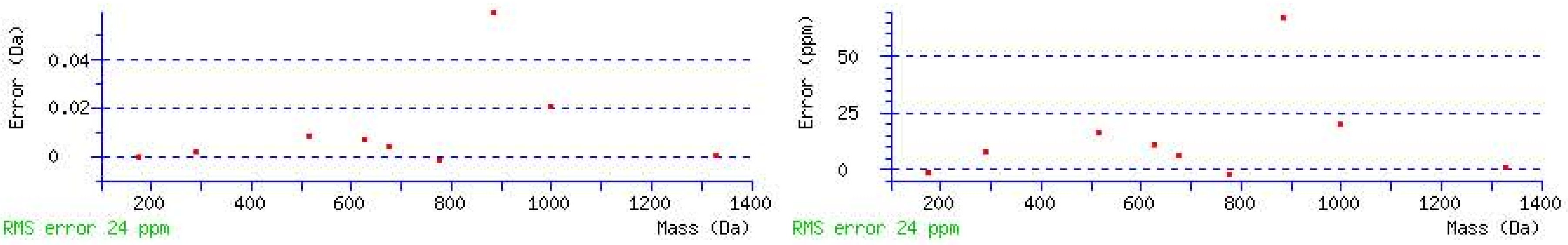
Match to Query 34542: 1398.726948 from(700.370750,2+) rtinseconds(1996) index(60515)
Title: Locus:1.1.1.3000.11 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1398.711166
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.0002
Matches : 9/76 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							9
2	187.071333	94.039304			169.060768	85.034022	D	***1328.681339***	664.844308	1311.654790	656.331033	1310.670774	655.839025	8
3	**626.296659**	313.651968	609.270110	305.138693	608.286094	304.646685	Q	1213.654396	607.330836	1196.627847	598.817562			7
4	725.365073	363.186175	708.338524	354.672900	707.354508	354.180892	V	***774.429070***	387.718173	757.402521	379.204898			6
5	**885.395722**	443.201499	868.369173	434.688225	867.385157	434.196217	C	***675.360656***	338.183966	658.334107	329.670691			5
6	**998.479786**	499.743531	981.453237	491.230257	980.469221	490.738249	I	***515.330007***	258.168641	498.303458	249.655367			4
7	1112.522713	556.764995	1095.496164	548.251720	1094.512148	547.759712	N	402.245943	201.626609	385.219394	193.113335			3
8	1225.606777	613.307027	1208.580228	604.793752	1207.596212	604.301744	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 ADQVCINLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.4	1398.711166	0.015782	ADQVCINLR
5.6	1398.740143	-0.013195	QITAREGASR
4.8	1398.723038	0.003910	ILACAPLYHWR
3.3	1398.746643	-0.019695	EEIEREVNILR
3.0	1398.721497	0.005451	QGRLAAEEAADLR
2.1	1398.740814	-0.013866	QPFQSWLQIPR
1.1	1398.721527	0.005421	AATASAGAGGIDGKPR
1.1	1398.729584	-0.002636	WLAPDGLIFPDR
0.7	1398.710251	0.016697	IAAEIAQAEEQAR
0.3	1398.726227	0.000721	APGRASGRVCAAAR

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

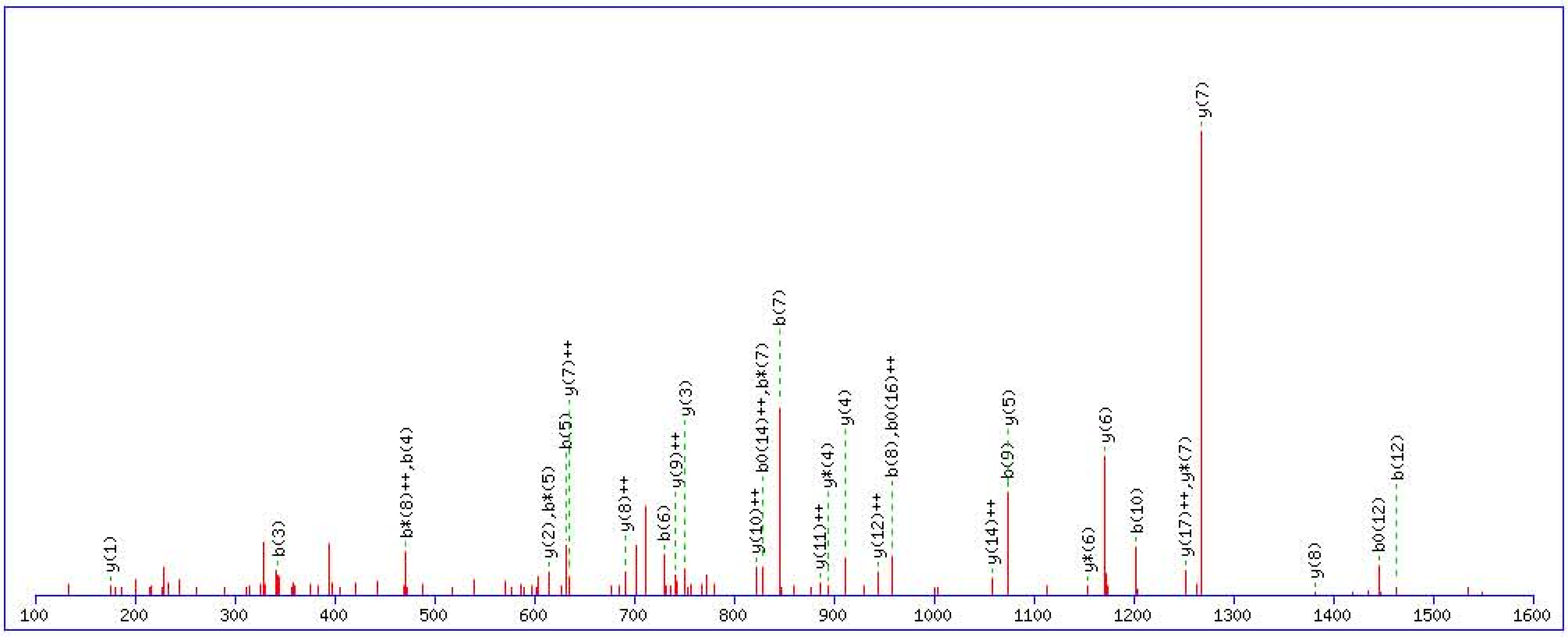
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RGEQCVDIDECTIPPYCHQR**
Found in **FBLN3_HUMAN**, EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2

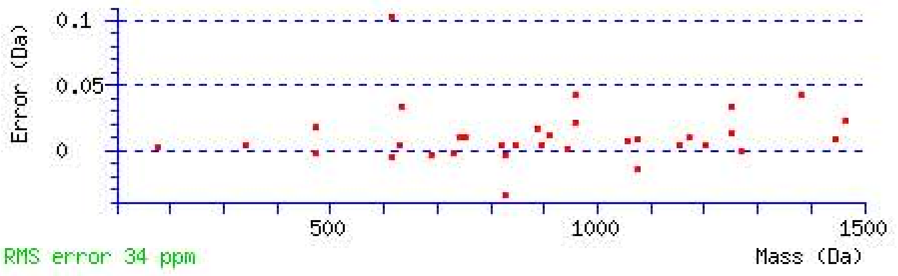
Match to Query 69466: 2843.279816 from(711.827230,4+) rtinseconds(1742) index(40391)
Title: Locus:1.1.1.2890.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

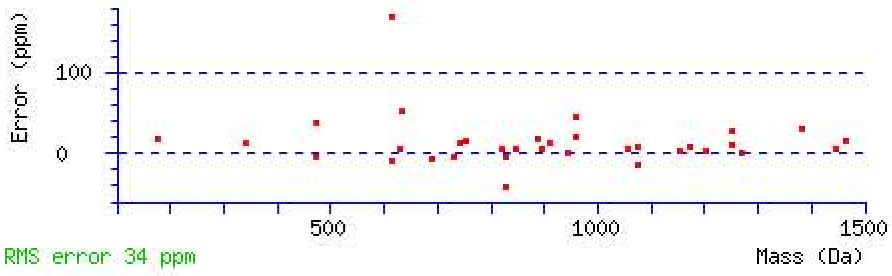


```
Monoisotopic mass of neutral peptide Mr(calc): 2843.261169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 9e-005
Matches : 34/208 fragment ions using 65 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	157.108387	79.057831	140.081838	70.544557			R							20
2	214.129851	107.568564	197.103302	99.055289			G	2688.167329	1344.587302	2671.140780	1336.074028	2670.156764	1335.582020	19
3	***343.172444***	172.089860	326.145895	163.576585	325.161879	163.084577	E	2631.145865	1316.076570	2614.119316	1307.563296	2613.135300	1307.071288	18
4	***471.231022***	236.119149	454.204473	227.605875	453.220457	227.113867	Q	2502.103272	1251.555274	2485.076723	1243.041999	2484.092707	1242.549991	17
5	***631.261671***	316.134474	614.235122	307.621199	613.251106	307.129191	C	2374.044694	1187.525985	2357.018145	1179.012710	2356.034129	1178.520702	16
6	***730.330085***	365.668681	713.303536	357.155406	712.319520	356.663398	V	2214.014045	1107.510660	2196.987496	1098.997386	2196.003480	1098.505378	15
7	***845.357028***	423.182152	828.330479	414.668878	827.346463	414.176870	D	2114.945631	1057.976453	2097.919082	1049.463179	2096.935066	1048.971171	14
8	***958.441092***	479.724184	941.414543	471.210910	940.430527	470.718902	I	1999.918688	1000.462982	1982.892139	991.949708	1981.908123	991.457700	13
9	***1073.468035***	537.237656	1056.441486	528.724381	1055.457470	528.232373	D	1886.834624	943.920950	1869.808075	935.407676	1868.824059	934.915668	12
10	***1202.510628***	601.758952	1185.484079	593.245678	1184.500063	592.753670	E	1771.807681	886.407479	1754.781132	877.894204	1753.797116	877.402196	11
11	1362.541277	681.774277	1345.514728	673.261002	1344.530712	672.768994	C	1642.765088	821.886182	1625.738539	813.372908	1624.754523	812.880900	10
12	***1463.588956***	732.298116	1446.562407	723.784842	1445.578391	723.292834	T	1482.734439	741.870858	1465.707890	733.357583	1464.723874	732.865575	9
13	1576.673020	788.840148	1559.646471	780.326874	1558.662455	779.834866	I	***1381.686760***	691.347018	1364.660211	682.833744			8
14	1673.725784	837.366530	1656.699235	828.853256	1655.715219	828.361248	P	***1268.602696***	634.804986	1251.576147	626.291712			7
15	1770.778548	885.892912	1753.751999	877.379638	1752.767983	876.887630	P	***1171.549932***	586.278604	1154.523383	577.765330			6
16	1933.841877	967.424577	1916.815328	958.911302	1915.831312	958.419294	Y	***1074.497168***	537.752222	1057.470619	529.238948			5
17	2093.872526	1047.439901	2076.845977	1038.926626	2075.861961	1038.434618	C	***911.433839***	456.220558	894.407290	447.707283			4
18	2230.931438	1115.969357	2213.904889	1107.456082	2212.920873	1106.964074	H	***751.403190***	376.205233	734.376641	367.691959			3
19	2670.156764	1335.582020	2653.130215	1327.068746	2652.146199	1326.576738	Q	***614.344278***	307.675777	597.317729	299.162503			2
20							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 34 ppm



RMS error 34 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.5	2843.261169	0.018647	RGEQCVDIDECTIPPYCHQR

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

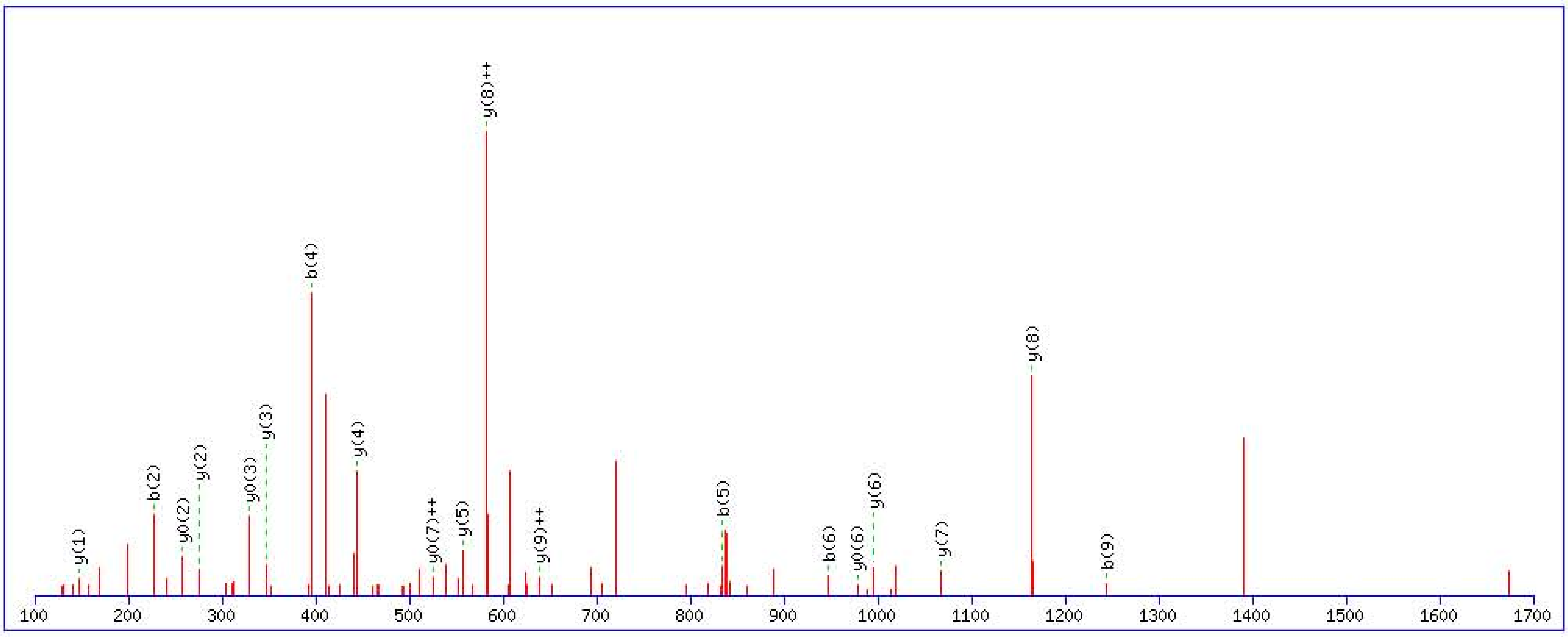
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPAQLPAEK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

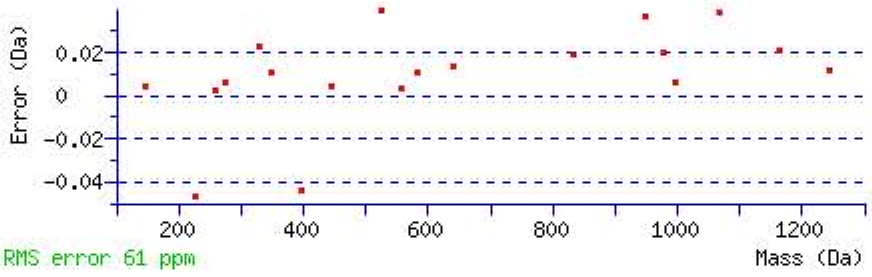
Match to Query 34167: 1389.818748 from(695.916650,2+) rtinseconds(1996) index(6974)
Title: Locus:1.1.1.2827.16 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

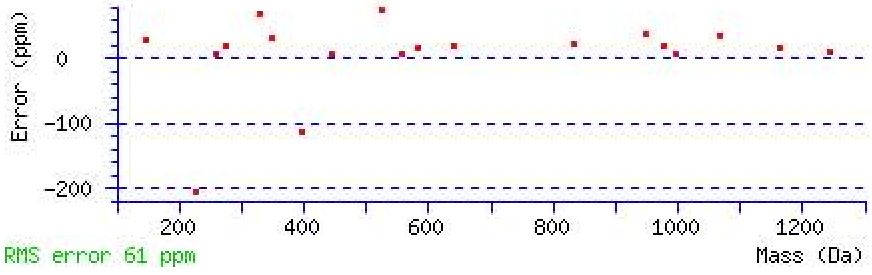
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1389.805359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 7e-005
Matches : 19/82 fragment ions using 38 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							10
2	**227.175404**	114.091340					L	1277.728607	639.367942	1260.702058	630.854667	1259.718042	630.362659	9
3	324.228168	162.617722					P	***1164.644543***	582.825909	1147.617994	574.312635	1146.633978	573.820627	8
4	**395.265282**	198.136279					A	***1067.591779***	534.299527	1050.565230	525.786253	1049.581214	525.294245	7
5	**834.490608**	417.748942	817.464059	409.235668			Q	***996.554665***	498.780970	979.528116	490.267696	978.544100	489.775688	6
6	**947.574672**	474.290974	930.548123	465.777700			L	***557.329339***	279.168307	540.302790	270.655033	539.318774	270.163025	5
7	1044.627436	522.817356	1027.600887	514.304082			P	***444.245275***	222.626275	427.218726	214.113001	426.234710	213.620993	4
8	1115.664550	558.335913	1098.638001	549.822639			A	***347.192511***	174.099893	330.165962	165.586619	329.181946	165.094611	3
9	**1244.707143**	622.857209	1227.680594	614.343935	1226.696578	613.851927	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.3	1389.805359	0.013389	LLPAQLPAEK
1.0	1389.823135	-0.004387	ILIVITDGQKYK
0.5	1389.816605	0.002143	ILGPLPKHMIQK
0.5	1389.805359	0.013389	LLSSYLQKK
0.4	1389.834366	-0.015618	ILQKSPLPPGNVK

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

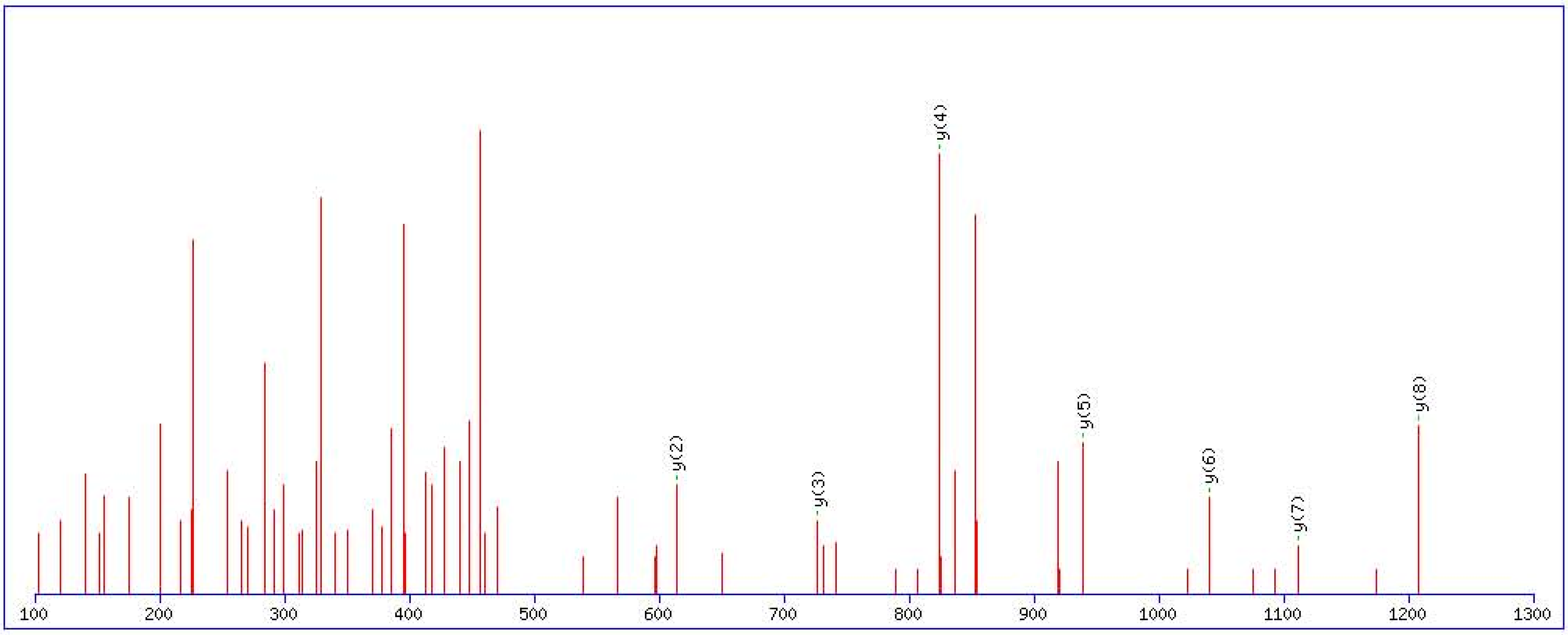
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLPATDPLQR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

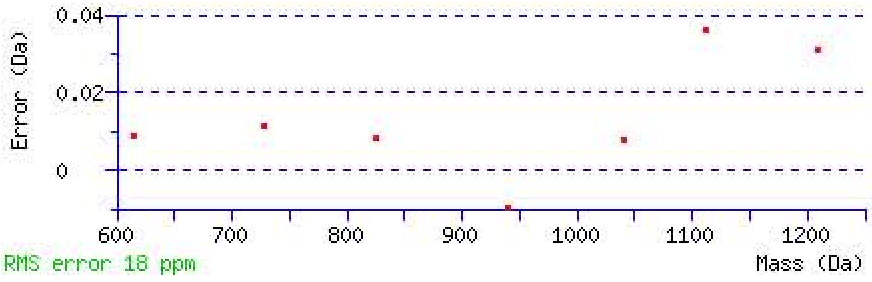
Match to Query 36572: 1434.768102 from(479.263310,3+) rtinseconds(1964) index(6806)
Title: Locus:1.1.1.2816.8 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

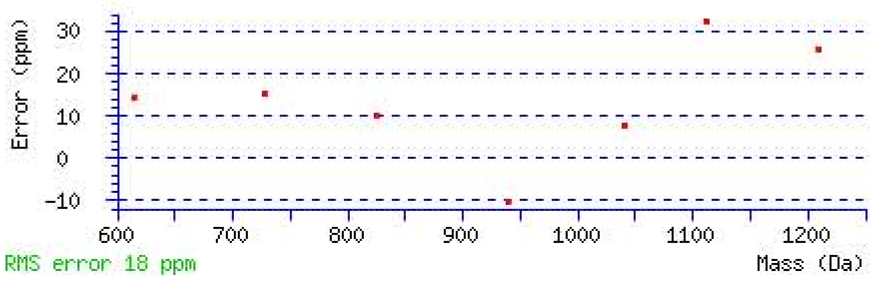
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1434.765305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00062
Matches : 7/92 fragment ions using 12 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							10
2	228.134267	114.570771	211.107718	106.057497			L	1321.729670	661.368473	1304.703121	652.855199	1303.719105	652.363190	9
3	325.187031	163.097153	308.160482	154.583879			P	***1208.645606***	604.826441	1191.619057	596.313166	1190.635041	595.821158	8
4	396.224145	198.615710	379.197596	190.102436			A	***1111.592842***	556.300059	1094.566293	547.786784	1093.582277	547.294776	7
5	497.271824	249.139550	480.245275	240.626275	479.261259	240.134267	T	***1040.555728***	520.781502	1023.529179	512.268227	1022.545163	511.776220	6
6	612.298767	306.653022	595.272218	298.139747	594.288202	297.647739	D	***939.508049***	470.257662	922.481500	461.744388	921.497484	461.252380	5
7	709.351531	355.179404	692.324982	346.666129	691.340966	346.174121	P	***824.481106***	412.744191	807.454557	404.230916			4
8	822.435595	411.721436	805.409046	403.208161	804.425030	402.716153	L	***727.428342***	364.217809	710.401793	355.704534			3
9	1261.660921	631.334098	1244.634372	622.820824	1243.650356	622.328816	Q	***614.344278***	307.675777	597.317729	299.162502			2
10							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.7	1434.765305	0.002797	NLPATDPLQR

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

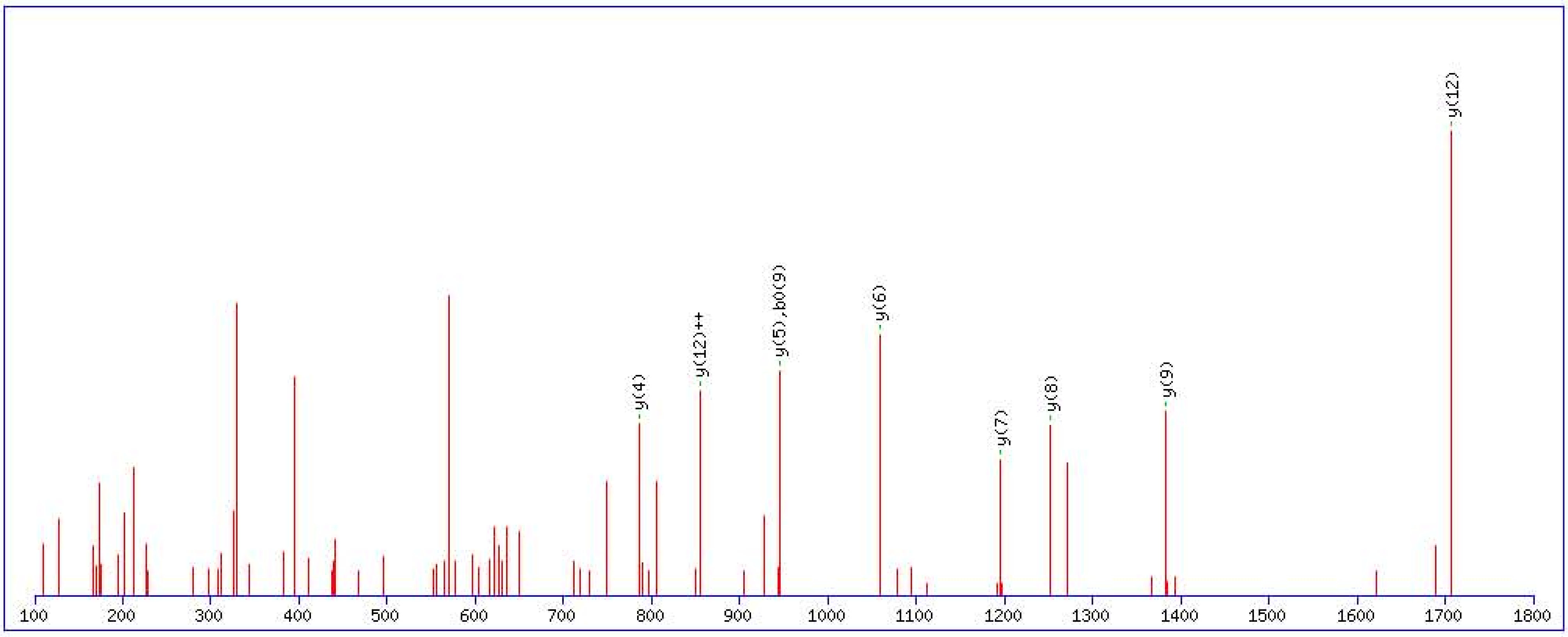
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTPNLMGHLCGNQR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

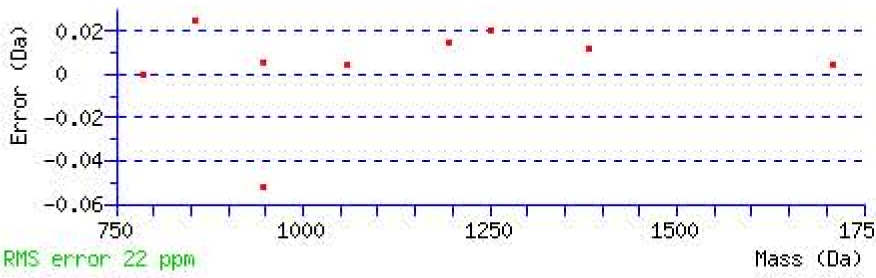
Match to Query 50719: 1906.940472 from(636.654100,3+) rtinseconds(1870) index(41159)
Title: Locus:1.1.1.2935.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

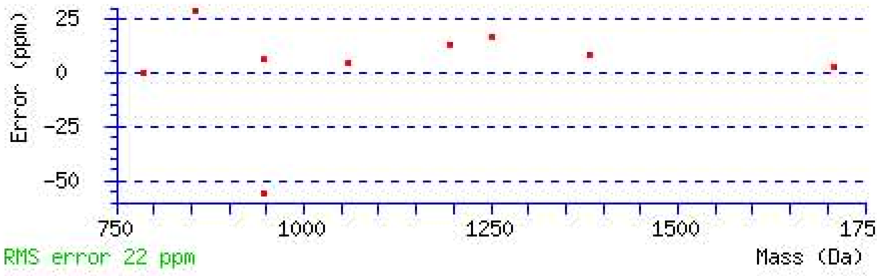
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1906.932816
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0016
Matches : 9/124 fragment ions using 14 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							14
2	201.123369	101.065322			183.112804	92.060040	T	1808.871677	904.939477	1791.845128	896.426202	1790.861112	895.934194	13
3	298.176133	149.591704			280.165568	140.586422	P	***1707.823998***	854.415637	1690.797449	845.902363			12
4	412.219060	206.613168	395.192511	198.099894	394.208495	197.607886	N	1610.771234	805.889255	1593.744685	797.375981			11
5	525.303124	263.155200	508.276575	254.641926	507.292559	254.149918	L	1496.728307	748.867792	1479.701758	740.354517			10
6	656.343609	328.675443	639.317060	320.162168	638.333044	319.670160	M	***1383.644243***	692.325760	1366.617694	683.812485			9
7	713.365073	357.186175	696.338524	348.672900	695.354508	348.180892	G	***1252.603758***	626.805517	1235.577209	618.292243			8
8	850.423985	425.715631	833.397436	417.202356	832.413420	416.710348	H	***1195.582294***	598.294785	1178.555745	589.781511			7
9	963.508049	482.257663	946.481500	473.744388	945.497484	473.252380	L	***1058.523382***	529.765329	1041.496833	521.252055			6
10	1123.538698	562.272987	1106.512149	553.759713	1105.528133	553.267705	C	***945.439318***	473.223297	928.412769	464.710023			5
11	1180.560162	590.783719	1163.533613	582.270445	1162.549597	581.778437	G	***785.408669***	393.207973	768.382120	384.694698			4
12	1294.603089	647.805183	1277.576540	639.291908	1276.592524	638.799900	N	728.387205	364.697241	711.360656	356.183966			3
13	1733.828415	867.417846	1716.801866	858.904571	1715.817850	858.412563	Q	614.344278	307.675777	597.317729	299.162503			2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.9	1906.932816	0.007656	VTPNLMGHLCGNQR

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

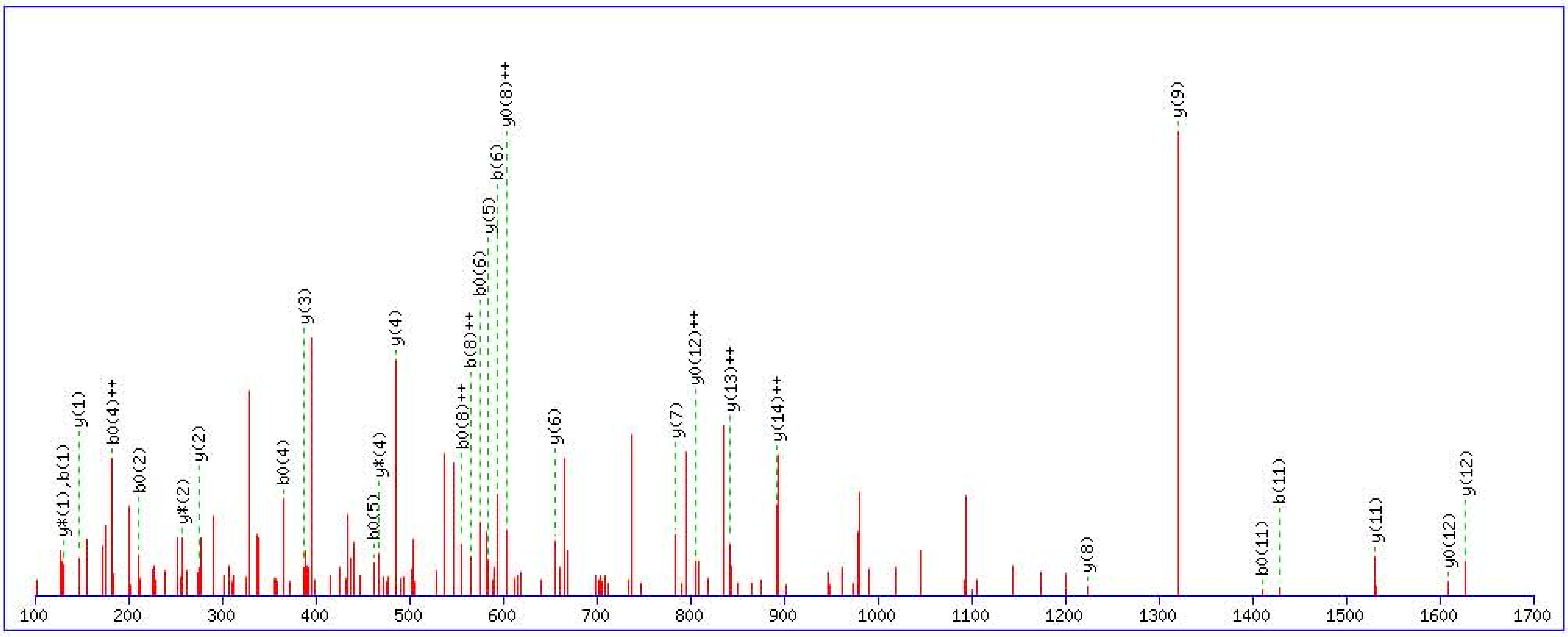
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVGPPLPQEAVPLQK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

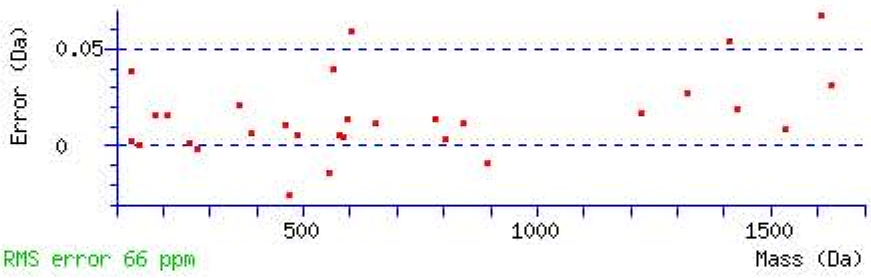
Match to Query 50931: 1912.067742 from(638.363190,3+) rtinseconds(2197) index(8377)
Title: Locus:1.1.1.2897.11 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

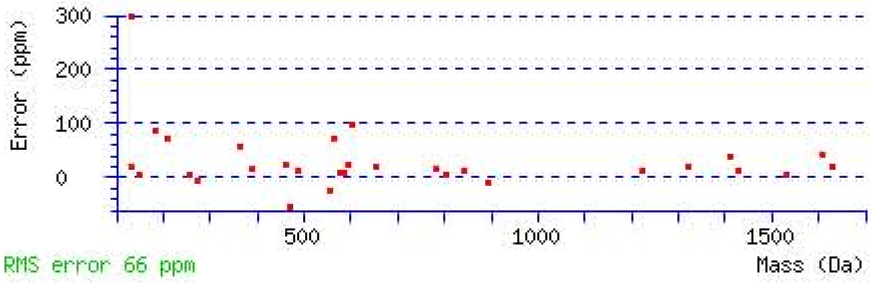
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1912.049194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 31 **Expect:** 0.011
Matches : 30/142 fragment ions using 99 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							15
2	229.118283	115.062780			211.107718	106.057497	V	1784.013891	892.510583	1766.987342	883.997309	1766.003326	883.505301	14
3	286.139747	143.573512			268.129182	134.568229	G	1684.945477	842.976377	1667.918928	834.463102	1666.934912	833.971094	13
4	383.192511	192.099894			365.181946	183.094611	P	***1627.924013***	814.465645	1610.897464	805.952370	1609.913448	805.460362	12
5	480.245275	240.626276			462.234710	231.620993	P	***1530.871249***	765.939263	1513.844700	757.425988	1512.860684	756.933980	11
6	**593.329339**	297.168308			575.318774	288.163025	L	1433.818485	717.412881	1416.791936	708.899606	1415.807920	708.407598	10
7	690.382103	345.694690			672.371538	336.689407	P	***1320.734421***	660.870848	1303.707872	652.357574	1302.723856	651.865566	9
8	1129.607429	565.307353	1112.580880	556.794078	1111.596864	556.302070	Q	***1223.681657***	612.344466	1206.655108	603.831192	1205.671092	603.339184	8
9	1258.650022	629.828649	1241.623473	621.315375	1240.639457	620.823367	E	***784.456331***	392.731803	767.429782	384.218529	766.445766	383.726521	7
10	1329.687136	665.347206	1312.660587	656.833932	1311.676571	656.341924	A	***655.413738***	328.210507	638.387189	319.697232			6
11	**1428.755550**	714.881413	1411.729001	706.368139	1410.744985	705.876131	V	***584.376624***	292.691950	567.350075	284.178676			5
12	1525.808314	763.407795	1508.781765	754.894521	1507.797749	754.402513	P	***485.308210***	243.157743	468.281661	234.644468			4
13	1638.892378	819.949827	1621.865829	811.436553	1620.881813	810.944545	L	***388.255446***	194.631361	371.228897	186.118086			3
14	1766.950956	883.979116	1749.924407	875.465842	1748.940391	874.973833	Q	***275.171382***	138.089329	258.144833	129.576054			2
15							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.8	1912.049194	0.018548	EVGPPLPQEAVPLQK
6.7	1912.049194	0.018548	EVGPPLPQEAVPLQK

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

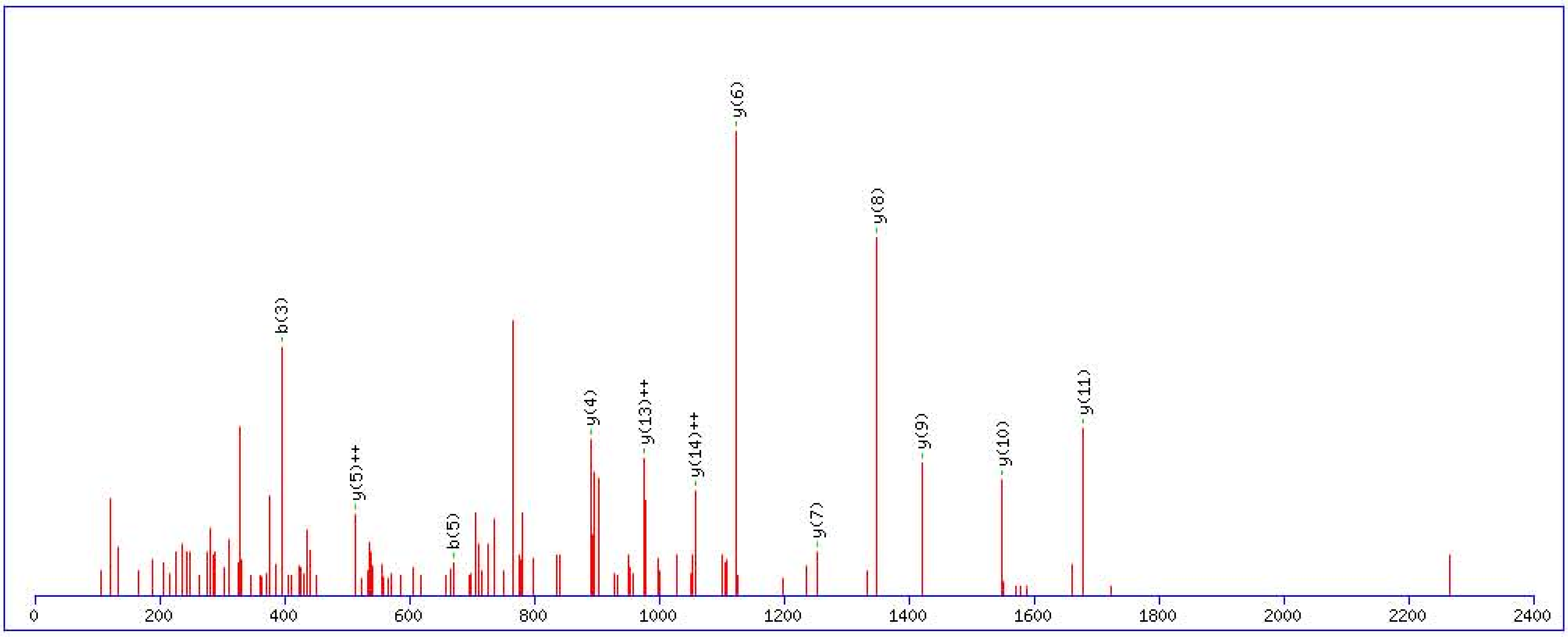
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSCFQEEAPQPHYQLR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

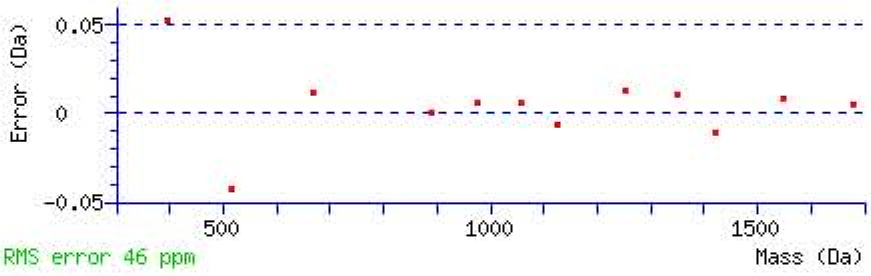
Match to Query 61609: 2347.101882 from(783.374570,3+) rtinseconds(1911) index(41510)
Title: Locus:1.1.1.2949.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

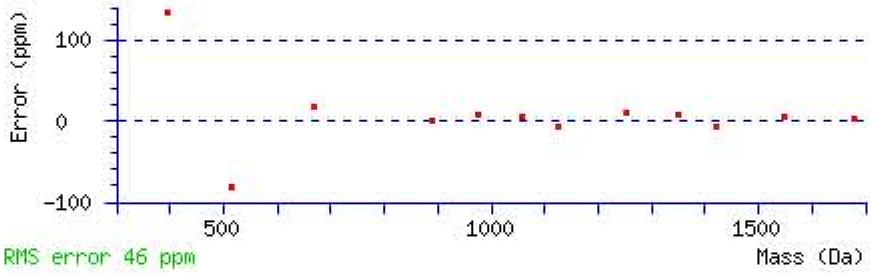
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2347.087784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0011
Matches : 12/152 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							16
2	235.107718	118.057497			217.097153	109.052214	S	2201.026658	1101.016967	2184.000109	1092.503692	2183.016093	1092.011684	15
3	**395.138367**	198.072821			377.127802	189.067539	C	2113.994630	1057.500953	2096.968081	1048.987678	2095.984065	1048.495670	14
4	542.206781	271.607029			524.196216	262.601746	F	1953.963981	977.485629	1936.937432	968.972354	1935.953416	968.480346	13
5	**670.265359**	335.636318	653.238810	327.123043	652.254794	326.631035	Q	1806.895567	903.951422	1789.869018	895.438147	1788.885002	894.946139	12
6	799.307952	400.157614	782.281403	391.644340	781.297387	391.152332	E	***1678.836989***	839.922133	1661.810440	831.408858	1660.826424	830.916850	11
7	928.350545	464.678911	911.323996	456.165636	910.339980	455.673628	E	***1549.794396***	775.400836	1532.767847	766.887562	1531.783831	766.395554	10
8	999.387659	500.197468	982.361110	491.684193	981.377094	491.192185	A	***1420.751803***	710.879540	1403.725254	702.366265			9
9	1096.440423	548.723850	1079.413874	540.210575	1078.429858	539.718567	P	***1349.714689***	675.360983	1332.688140	666.847708			8
10	1224.499001	612.753138	1207.472452	604.239864	1206.488436	603.747856	Q	***1252.661925***	626.834601	1235.635376	618.321326			7
11	1321.551765	661.279520	1304.525216	652.766246	1303.541200	652.274238	P	***1124.603347***	562.805312	1107.576798	554.292037			6
12	1458.610677	729.808976	1441.584128	721.295702	1440.600112	720.803694	H	1027.550583	514.278930	1010.524034	505.765655			5
13	1621.674006	811.340641	1604.647457	802.827367	1603.663441	802.335358	Y	***890.491671***	445.749474	873.465122	437.236199			4
14	2060.899332	1030.953304	2043.872783	1022.440030	2042.888767	1021.948022	Q	727.428342	364.217809	710.401793	355.704535			3
15	2173.983396	1087.495336	2156.956847	1078.982061	2155.972831	1078.490053	L	288.203016	144.605146	271.176467	136.091872			2
16							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.9	2347.087784	0.014098	FSCFQEEAPQPHYQLR
17.3	2347.087784	0.014098	FSCFQEEAPQPHYQLR

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

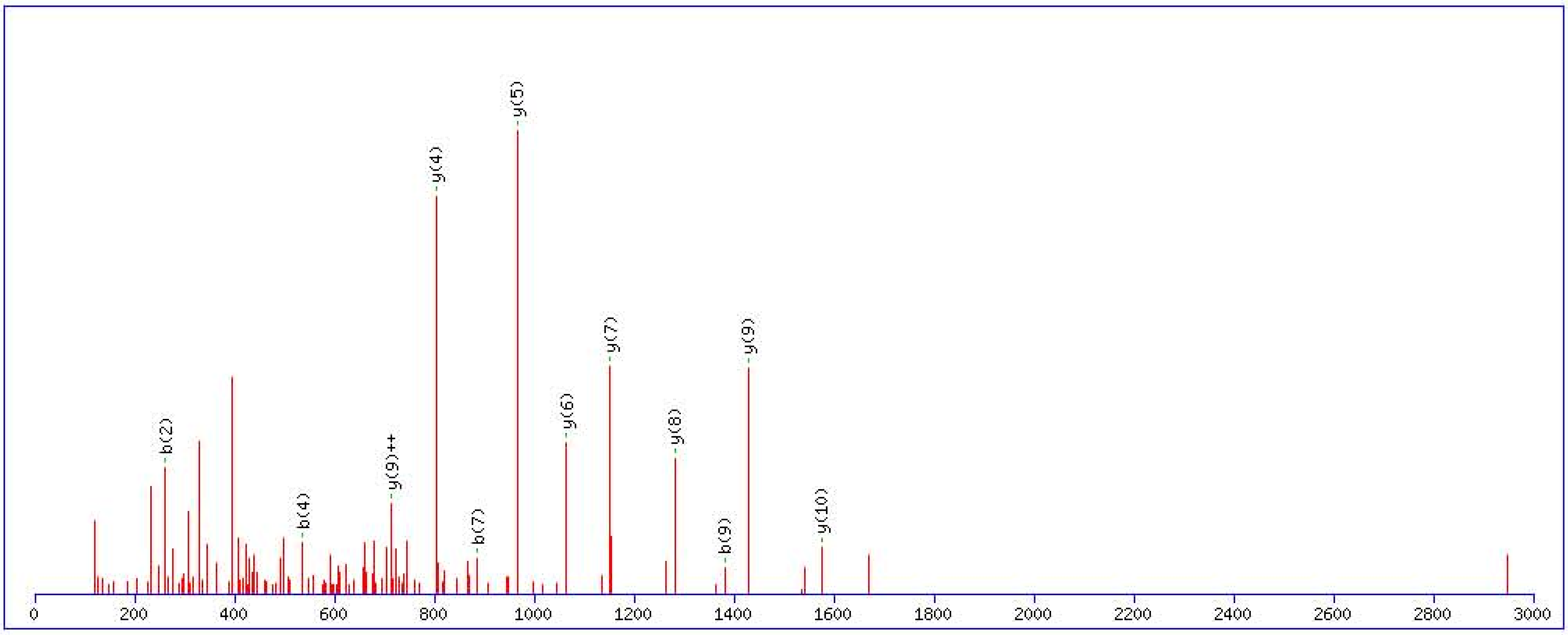
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFFESVYGQCK**
Found in **FETUB_HUMAN**, Fetuin-B OS=Homo sapiens GN=FETUB PE=1 SV=2

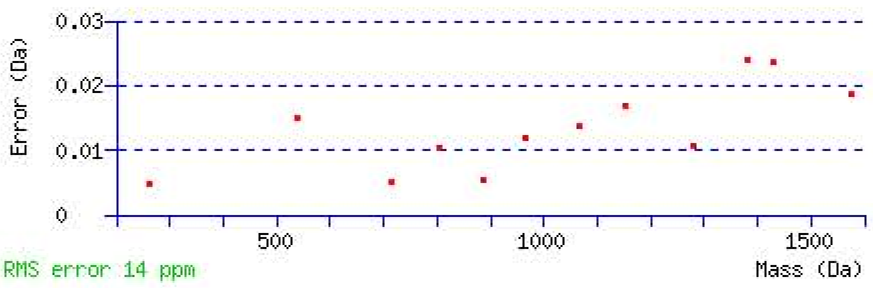
Match to Query 45518: 1687.827808 from(844.921180,2+) rtinseconds(2324) index(80738)
Title: Locus:1.1.1.3023.14 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

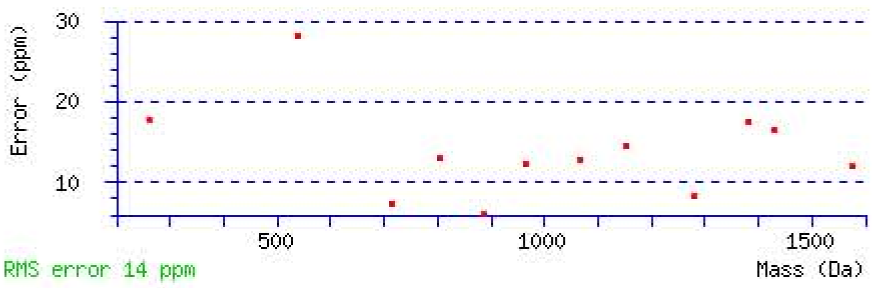
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1687.810226
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00014
Matches : 12/86 fragment ions using 16 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							11
2	**261.159754**	131.083515					F	***1575.733435***	788.370356	1558.706886	779.857081	1557.722870	779.365073	10
3	408.228168	204.617722					F	***1428.665021***	714.836149	1411.638472	706.322874	1410.654456	705.830866	9
4	**537.270761**	269.139019			519.260196	260.133736	E	***1281.596607***	641.301942	1264.570058	632.788667	1263.586042	632.296659	8
5	624.302789	312.655033			606.292224	303.649750	S	***1152.554014***	576.780645	1135.527465	568.267371	1134.543449	567.775363	7
6	723.371203	362.189239			705.360638	353.183957	V	***1065.521986***	533.264631	1048.495437	524.751357			6
7	**886.434532**	443.720904			868.423967	434.715622	Y	***966.453572***	483.730424	949.427023	475.217150			5
8	943.455996	472.231636			925.445431	463.226354	G	***803.390243***	402.198760	786.363694	393.685485			4
9	**1382.681322**	691.844299	1365.654773	683.331025	1364.670757	682.839017	Q	746.368779	373.688028	729.342230	365.174753			3
10	1542.711971	771.859624	1525.685422	763.346349	1524.701406	762.854341	C	307.143453	154.075365	290.116904	145.562090			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.1	1687.810226	0.017582	IFFESVYGQCK

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

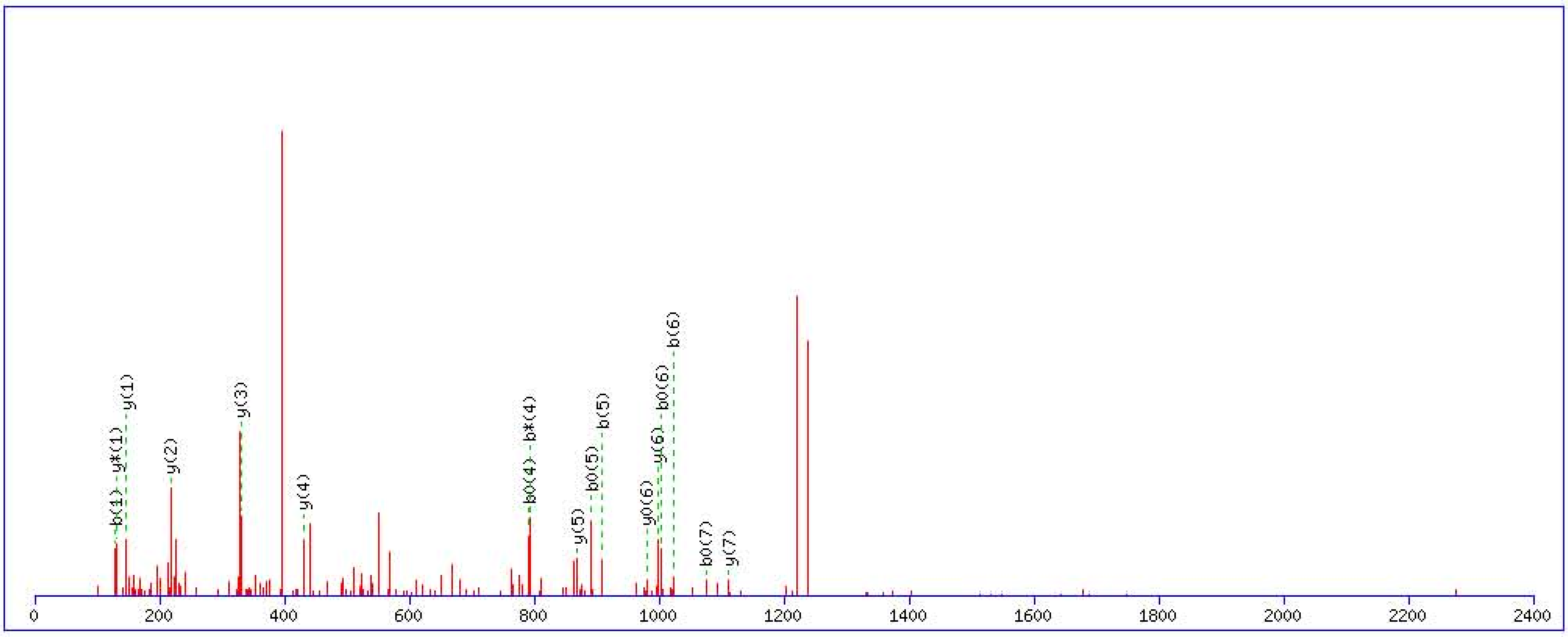
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLEQVIAK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

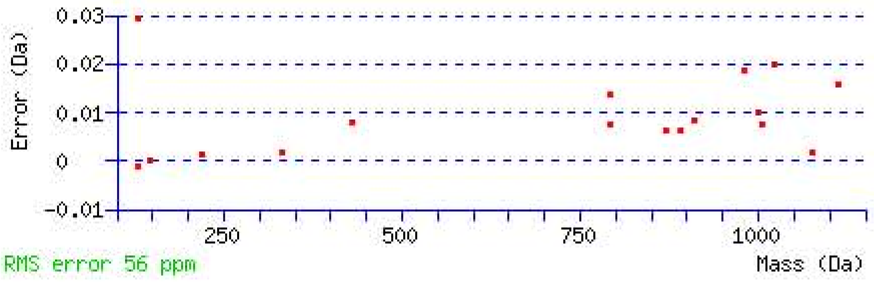
Match to Query 28837: 1238.714648 from(620.364600,2+) rtinseconds(1744) index(58681)
Title: Locus:1.1.1.2913.8 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

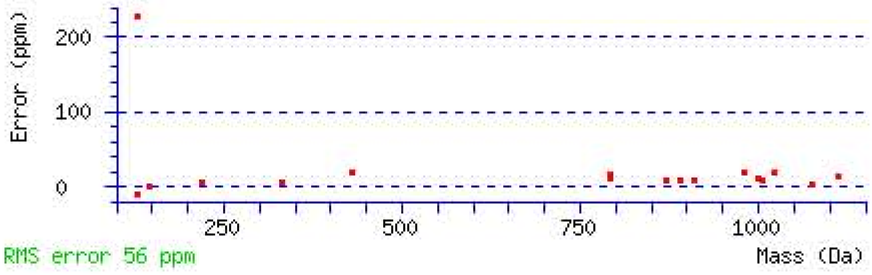
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1238.705658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0023
Matches : 17/70 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.065854**	65.036565	112.039305	56.523291			Q							8
2	242.149918	121.578597	225.123369	113.065323			L	***1111.654379***	556.330828	1094.627830	547.817553	1093.643814	547.325545	7
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	***998.570315***	499.788796	981.543766	491.275521	980.559750	490.783513	6
4	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	Q	***869.527722***	435.267499	852.501173	426.754225			5
5	**909.486251**	455.246764	892.459702	446.733489	891.475686	446.241481	V	***430.302396***	215.654836	413.275847	207.141562			4
6	**1022.570315**	511.788796	1005.543766	503.275521	1004.559750	502.783513	I	***331.233982***	166.120629	314.207433	157.607355			3
7	1093.607429	547.307353	1076.580880	538.794078	1075.596864	538.302070	A	***218.149918***	109.578597	201.123369	101.065323			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.8	1238.705658	0.008990	QLEQVIAK
14.9	1238.705658	0.008990	QLEQVIAK
9.3	1238.698257	0.016391	IHADASSKVLAK
8.1	1238.716904	-0.002256	DRVQVAIK
6.0	1238.702301	0.012347	DVFKKGFSIAK
5.8	1238.698273	0.016375	GHVTQLKESLK
5.1	1238.728119	-0.013471	QEVRRLK
4.5	1238.705658	0.008990	QIAQEIVK
3.7	1238.720917	-0.006269	QLWLQLK
2.8	1238.709473	0.005175	NDLRPANKLAK

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

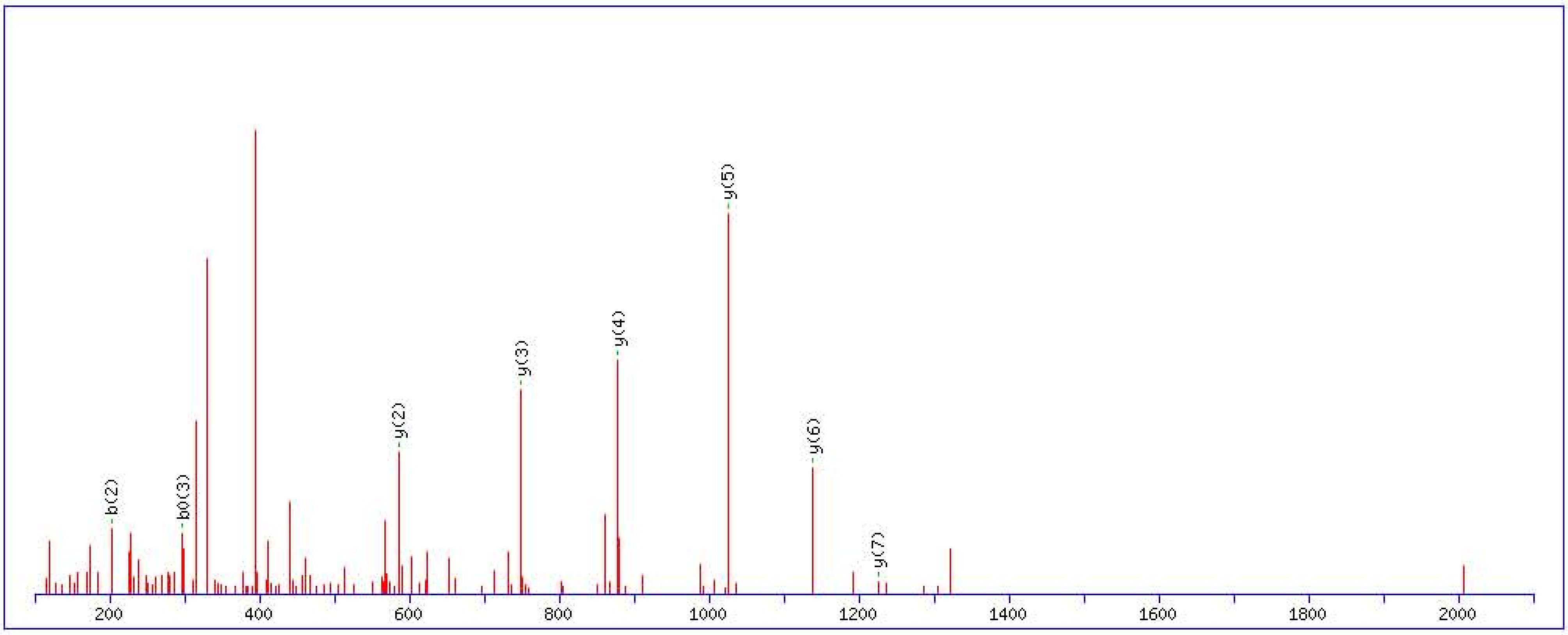
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSLFEYQK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

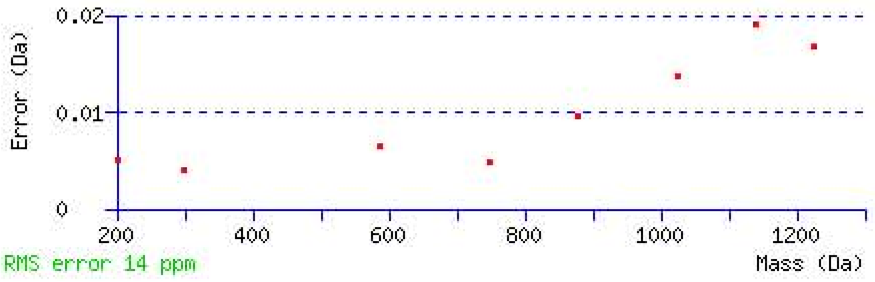
Match to Query 31759: 1338.677028 from(670.345790,2+) rtinseconds(2045) index(7316)
Title: Locus:1.1.1.2844.14 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

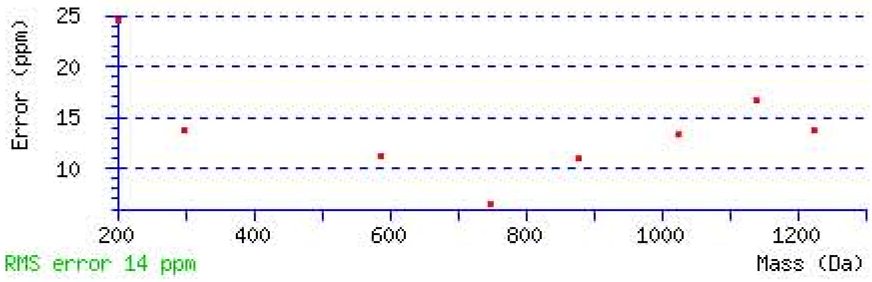
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1338.664185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 42 **Expect:** 0.0012
Matches : 8/76 fragment ions using 13 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							8
2	**202.082231**	101.544753	185.055682	93.031479	184.071666	92.539471	S	***1225.628558***	613.317917	1208.602009	604.804643	1207.617993	604.312635	7
3	315.166295	158.086785	298.139746	149.573511	297.155730	149.081503	L	***1138.596530***	569.801903	1121.569981	561.288629	1120.585965	560.796621	6
4	462.234709	231.620993	445.208160	223.107718	444.224144	222.615710	F	***1025.512466***	513.259871	1008.485917	504.746597	1007.501901	504.254589	5
5	591.277302	296.142289	574.250753	287.629015	573.266737	287.137007	E	***878.444052***	439.725664	861.417503	431.212390	860.433487	430.720382	4
6	754.340631	377.673954	737.314082	369.160679	736.330066	368.668671	Y	***749.401459***	375.204368	732.374910	366.691093			3
7	1193.565957	597.286617	1176.539408	588.773342	1175.555392	588.281334	Q	***586.338130***	293.672703	569.311581	285.159429			2
8							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.1	1338.664185	0.012843	NSLFEYQK
13.7	1338.660172	0.016856	NSMFTAGKGVAEK
5.2	1338.660172	0.016856	BTVYLQMBSLR
2.7	1338.666672	0.010356	ESIKDLADYASK
2.0	1338.682632	-0.005604	NLSRMQSRFGK
1.3	1338.686188	-0.009160	TVKMMYQK

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

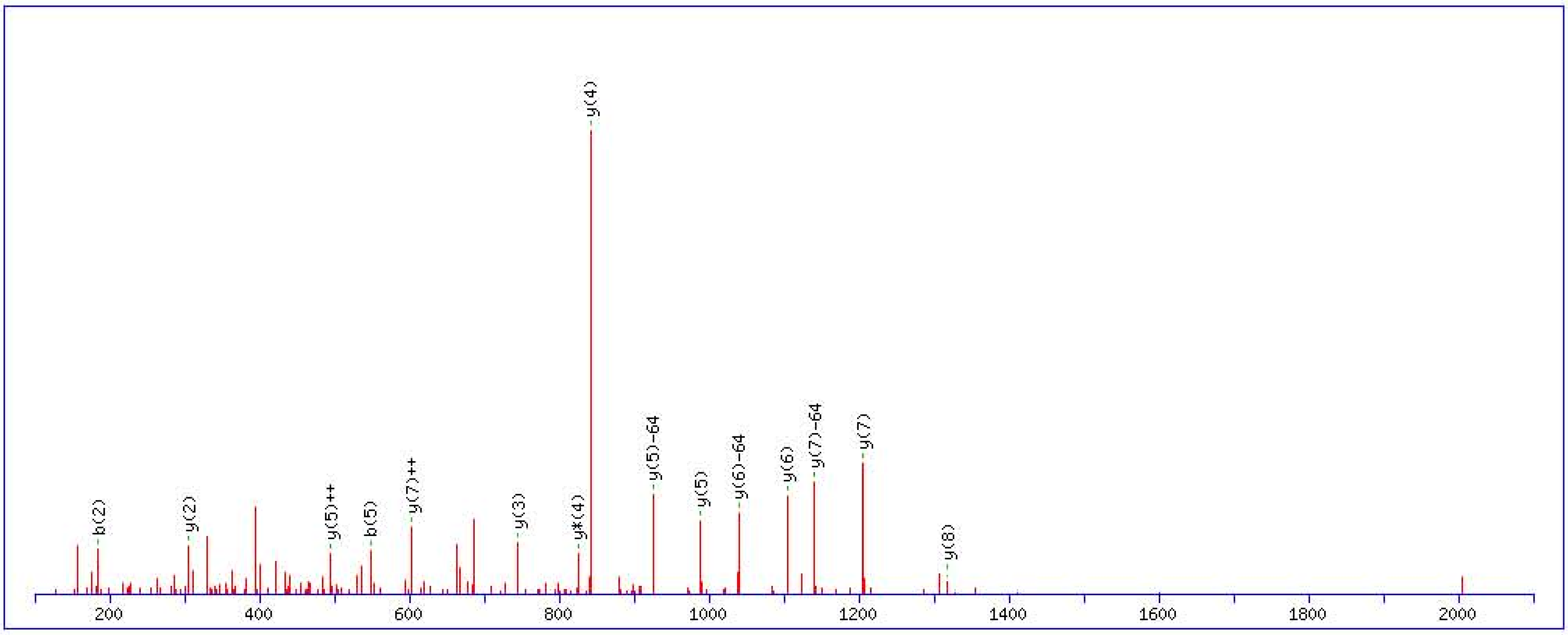
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALTDMPQMR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

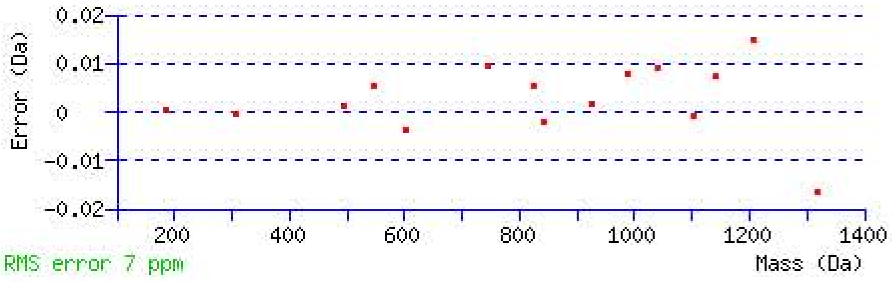
Match to Query 34007: 1388.664508 from(695.339530,2+) rtinseconds(1642) index(39721)
Title: Locus:1.1.1.2855.9 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

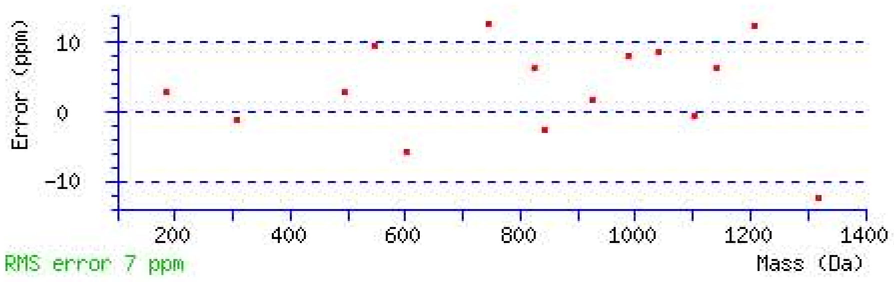
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1388.661438
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 2.1e-005
Matches : 15/112 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							9
2	**185.128454**	93.067865					L	***1318.631613***	659.819445	1301.605064	651.306170	1300.621048	650.814162	8
3	286.176133	143.591704			268.165568	134.586422	T	***1205.547549***	603.277413	1188.521000	594.764138	1187.536984	594.272130	7
4	401.203076	201.105176			383.192511	192.099894	D	***1104.499870***	552.753573	1087.473321	544.240298	1086.489305	543.748290	6
5	**548.238476**	274.622876			530.227911	265.617594	M	***989.472927***	495.240102	972.446378	486.726827			5
6	645.291240	323.149258			627.280675	314.143976	P	***842.437527***	421.722402	825.410978	413.209127			4
7	1084.516566	542.761921	1067.490017	534.248647	1066.506001	533.756639	Q	***745.384763***	373.196020	728.358214	364.682745			3
8	1215.557051	608.282164	1198.530502	599.768889	1197.546486	599.276881	M	***306.159437***	153.583356	289.132888	145.070082			2
9							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.7	1388.661438	0.003070	ALTDMPQMR
17.4	1388.661438	0.003070	ALTDMPQMR
3.7	1388.669296	-0.004788	DREPFQMR
3.0	1388.660568	0.003940	SEMTASPLVGPER

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

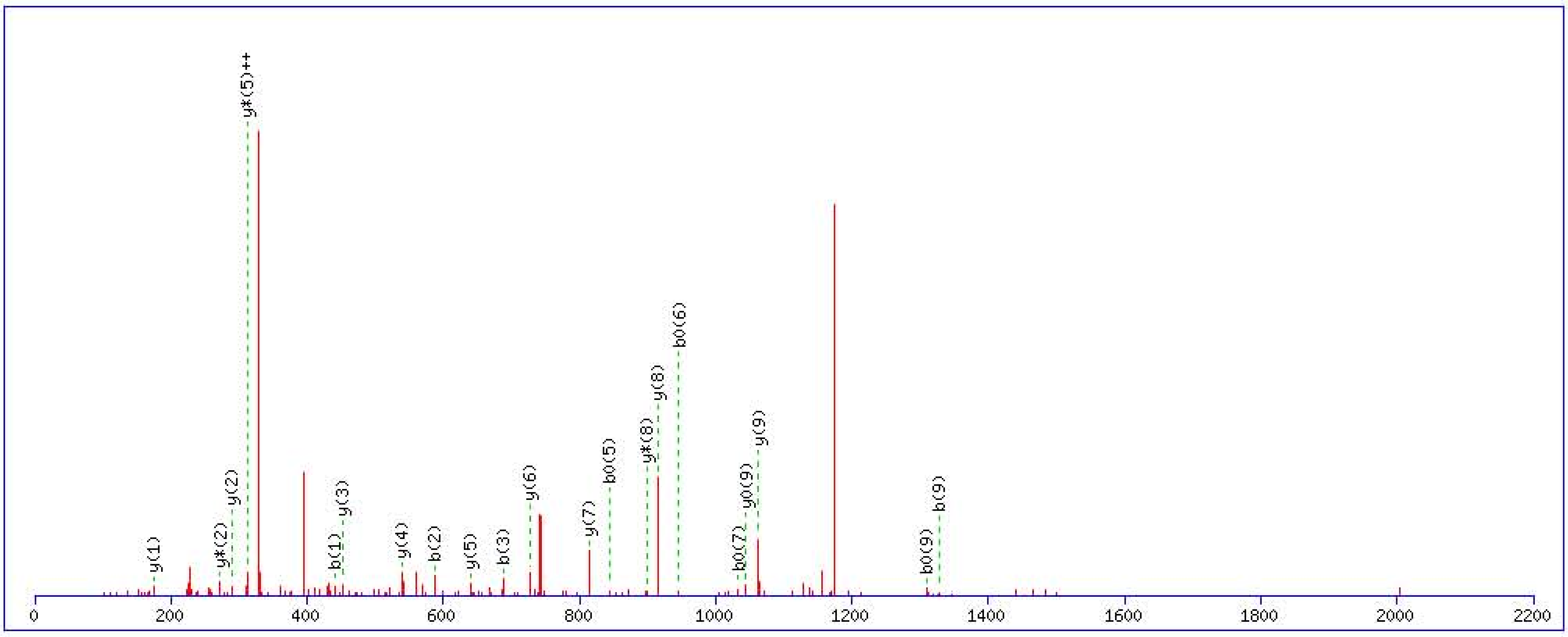
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QFTSSTSYNR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

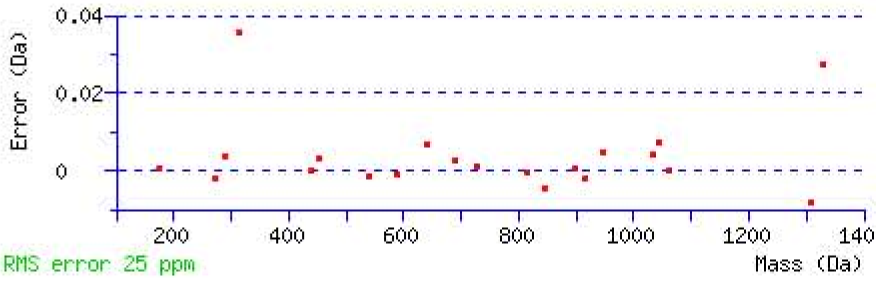
Match to Query 38553: 1500.708008 from(751.361280,2+) rtinseconds(1535) index(39124)
Title: Locus:1.1.1.2818.17 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

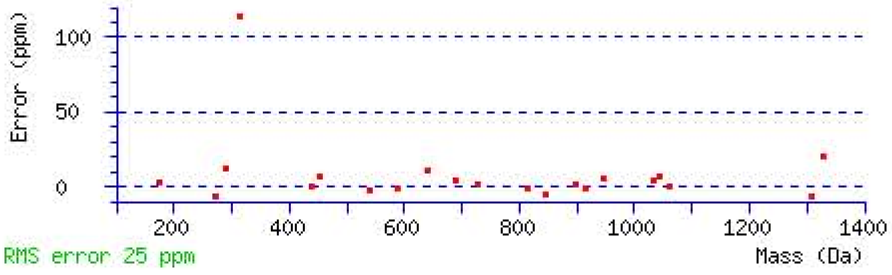
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1500.703110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00029
Matches : 21/98 fragment ions using 52 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**440.232602**	220.619939	423.206053	212.106664			Q							10
2	**587.301016**	294.154146	570.274467	285.640872			F	***1062.485064***	531.746170	1045.458515	523.232896	1044.474499	522.740887	9
3	**688.348695**	344.677986	671.322146	336.164711	670.338130	335.672703	T	***915.416650***	458.211963	898.390101	449.698689	897.406085	449.206681	8
4	775.380723	388.194000	758.354174	379.680725	757.370158	379.188717	S	***814.368971***	407.688124	797.342422	399.174849	796.358406	398.682841	7
5	862.412751	431.710014	845.386202	423.196739	844.402186	422.704731	S	***727.336943***	364.172110	710.310394	355.658835	709.326378	355.166827	6
6	963.460430	482.233853	946.433881	473.720578	945.449865	473.228570	T	***640.304915***	320.656096	623.278366	312.142821	622.294350	311.650813	5
7	1050.492458	525.749867	1033.465909	517.236593	1032.481893	516.744584	S	***539.257236***	270.132256	522.230687	261.618982	521.246671	261.126974	4
8	1213.555787	607.281532	1196.529238	598.768257	1195.545222	598.276249	Y	***452.225208***	226.616242	435.198659	218.102967			3
9	**1327.598714**	664.302995	1310.572165	655.789721	1309.588149	655.297712	N	***289.161879***	145.084577	272.135330	136.571303			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.0	1500.703110	0.004898	QFTSSTSYNR
6.8	1500.725571	-0.017563	HQSHTAEAGPR
5.8	1500.728043	-0.020035	EEARTTPGREEAR
3.5	1500.699768	0.008240	AEAGSGGPGFTFTFR
3.2	1500.702927	0.005081	REAPTGRDQGSGDR
2.1	1500.724869	-0.016861	SKIEDYFPEFAR
0.8	1500.724228	-0.016220	EQLSSSDTAPR
0.5	1500.725586	-0.017578	IGQICKNDFGGHR

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

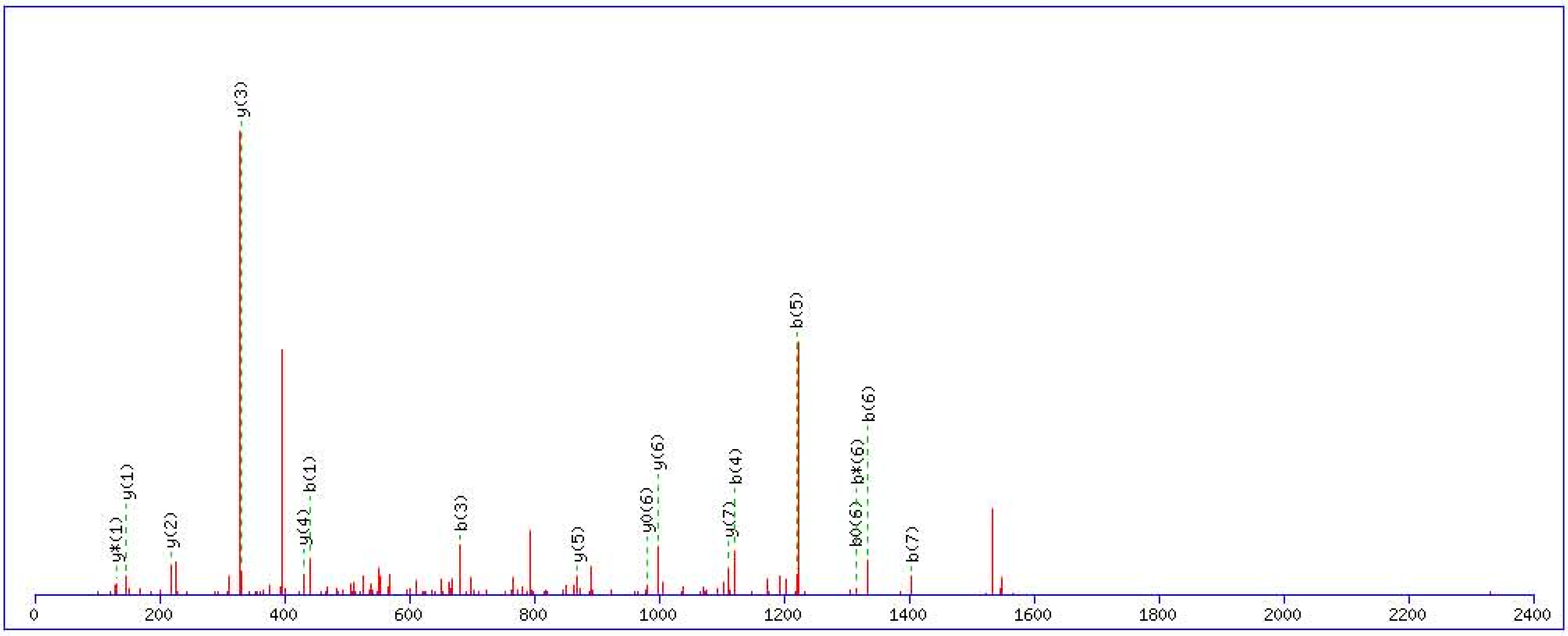
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLEQVIAK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

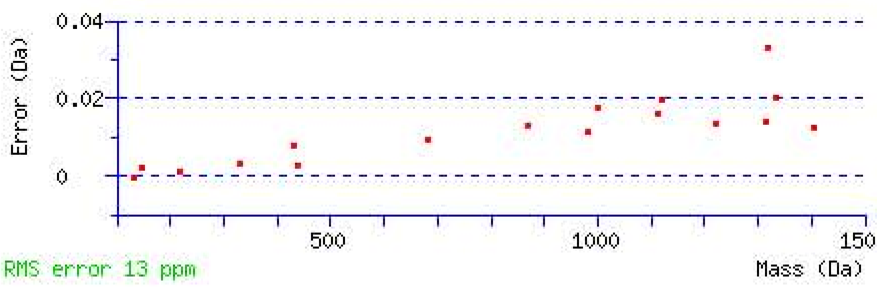
Match to Query 39946: 1549.894228 from(775.954390,2+) rtinseconds(2095) index(61199)
Title: Locus:1.1.1.3034.19 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

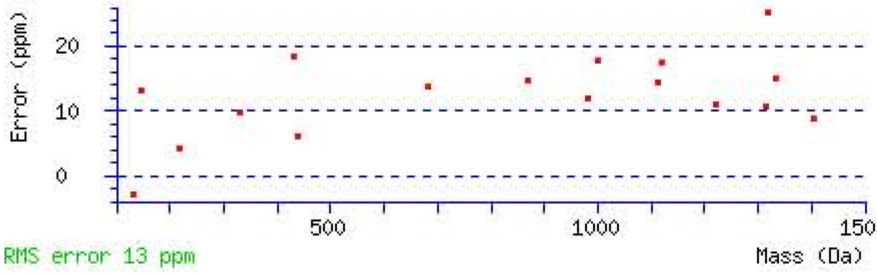
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1549.872406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.017
Matches : 17/70 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**440.232602**	220.619939	423.206053	212.106664			**Q**							8
2	553.316666	277.161971	536.290117	268.648697			**L**	***1111.654379***	556.330828	1094.627830	547.817553	1093.643814	547.325545	7
3	**682.359259**	341.683268	665.332710	333.169993	664.348694	332.677985	**E**	***998.570315***	499.788796	981.543766	491.275521	980.559750	490.783513	6
4	**1121.584585**	561.295931	1104.558036	552.782656	1103.574020	552.290648	**Q**	***869.527722***	435.267499	852.501173	426.754225			5
5	**1220.652999**	610.830138	1203.626450	602.316863	1202.642434	601.824855	**V**	***430.302396***	215.654836	413.275847	207.141561			4
6	**1333.737063**	667.372170	1316.710514	658.858895	1315.726498	658.366887	**I**	***331.233982***	166.120629	314.207433	157.607354			3
7	**1404.774177**	702.890727	1387.747628	694.377452	1386.763612	693.885444	**A**	***218.149918***	109.578597	201.123369	101.065322			2
8							**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.9	1549.872406	0.021822	QLEQVIAK
8.5	1549.907944	-0.013716	VKTTGIIETKFSVK
6.4	1549.876251	0.017977	LVDINLVRCHALK
6.3	1549.893967	0.000261	LIRENHELKSAIK
5.9	1549.886810	0.007418	YVIGIGVGAGAYVLAK
5.1	1549.886795	0.007433	KGNLVYIIDFGLAK
4.2	1549.887665	0.006563	QLWLQLK
4.1	1549.890152	0.004076	AQEILSQLPIK
3.5	1549.872406	0.021822	QIAQEIVK
1.4	1549.907944	-0.013716	EVVKPVPITSPAVSK

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

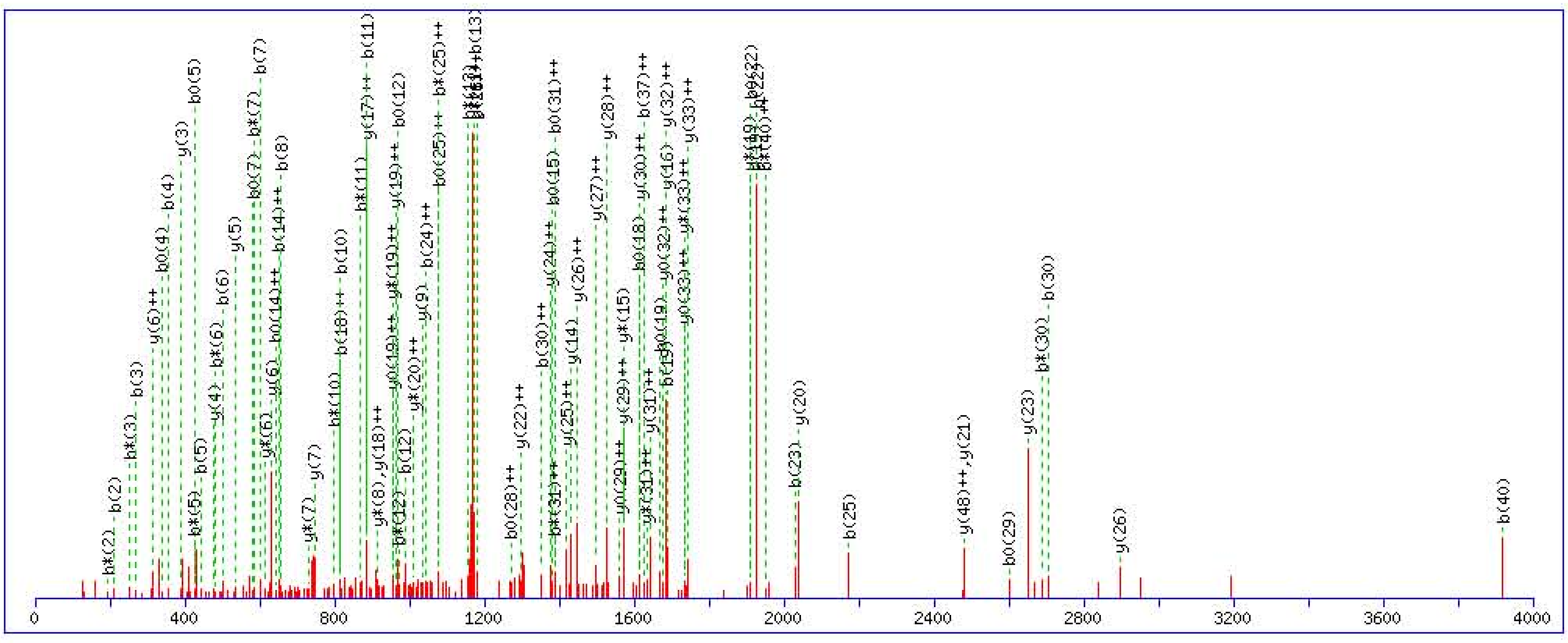
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

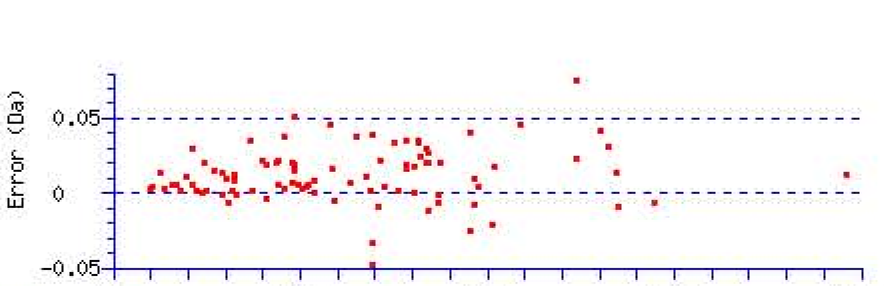
Match to Query 88601: 5844.691920 from(1169.945660,5+) rtinseconds(1719) index(5175)
Title: Locus:1.1.1.2730.24 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

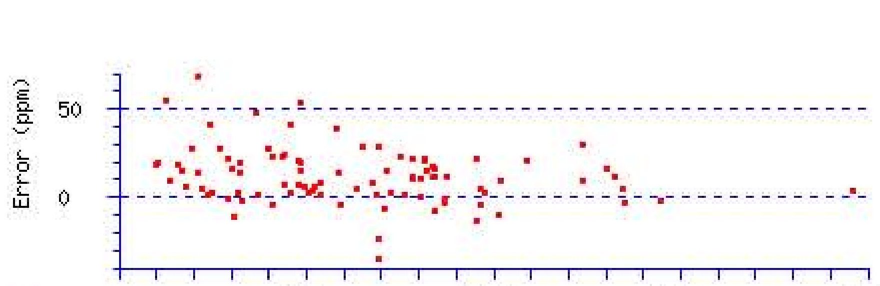
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 5844.608032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q39    : Biotin:Thermo-21345 (Q)
Ions Score: 82  Expect: 4.7e-008
Matches : 92/688 fragment ions using 190 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							59
2	***212.102967***	106.555121	195.076418	98.041847			P	5731.572302	2866.289789	5714.545753	2857.776515	5713.561737	2857.284507	58
3	***269.124431***	135.065853	252.097882	126.552579			G	5634.519538	2817.763407	5617.492989	2809.250133	5616.508973	2808.758125	57
4	***356.156459***	178.581867	339.129910	170.068593	338.145894	169.576585	S	5577.498074	2789.252675	5560.471525	2780.739401	5559.487509	2780.247393	56
5	***443.188487***	222.097881	426.161938	213.584607	425.177922	213.092599	S	5490.466046	2745.736661	5473.439497	2737.223387	5472.455481	2736.731379	55
6	***500.209951***	250.608613	483.183402	242.095339	482.199386	241.603331	G	5403.434018	2702.220647	5386.407469	2693.707373	5385.423453	2693.215365	54
7	***601.257630***	301.132453	584.231081	292.619178	583.247065	292.127170	T	5346.412554	2673.709915	5329.386005	2665.196641	5328.401989	2664.704633	53
8	***658.279094***	329.643185	641.252545	321.129910	640.268529	320.637903	G	5245.364875	2623.186076	5228.338326	2614.672801	5227.354310	2614.180793	52
9	715.300558	358.153917	698.274009	349.640643	697.289993	349.148635	G	5188.343411	2594.675344	5171.316862	2586.162069	5170.332846	2585.670061	51
10	***816.348237***	408.677757	799.321688	400.164482	798.337672	399.672474	T	5131.321947	2566.164612	5114.295398	2557.651337	5113.311382	2557.159329	50
11	***887.385351***	444.196314	870.358802	435.683039	869.374786	435.191031	A	5030.274268	2515.640772	5013.247719	2507.127498	5012.263703	2506.635490	49
12	***988.433030***	494.720153	971.406481	486.206879	970.422465	485.714871	T	4959.237154	2480.122215	4942.210605	2471.608941	4941.226589	2471.116933	48
13	***1174.512343***	587.759810	1157.485794	579.246535	1156.501778	578.754527	W	4858.189475	2429.598376	4841.162926	2421.085101	4840.178910	2420.593093	47
14	1302.607306	**651.807291**	1285.580757	643.294017	1284.596741	642.802009	K	4672.110162	2336.558719	4655.083613	2328.045445	4654.099597	2327.553437	46
15	1399.660070	700.333673	1382.633521	691.820399	1381.649505	691.328391	P	4544.015199	2272.511238	4526.988650	2263.997963	4526.004634	2263.505955	45
16	1456.681534	728.844405	1439.654985	720.331131	1438.670969	719.839123	G	4446.962435	2223.984856	4429.935886	2215.471581	4428.951870	2214.979573	44
17	1543.713562	772.360419	1526.687013	763.847145	1525.702997	763.355137	S	4389.940971	2195.474124	4372.914422	2186.960849	4371.930406	2186.468841	43
18	1630.745590	**815.876433**	1613.719041	807.363159	1612.735025	806.871151	S	4302.908943	2151.958110	4285.882394	2143.444835	4284.898378	2142.952827	42
19	***1687.767054***	844.387165	1670.740505	835.873891	1669.756489	835.381883	G	4215.876915	2108.442096	4198.850366	2099.928821	4197.866350	2099.436813	41
20	1784.819818	892.913547	1767.793269	884.400273	1766.809253	883.908265	P	4158.855451	2079.931364	4141.828902	2071.418089	4140.844886	2070.926081	40
21	1841.841282	921.424279	1824.814733	912.911005	1823.830717	912.418997	G	4061.802687	2031.404982	4044.776138	2022.891707	4043.792122	2022.399699	39
22	***1928.873310***	964.940293	1911.846761	956.427019	1910.862745	955.935011	S	4004.781223	2002.894250	3987.754674	1994.380975	3986.770658	1993.888967	38
23	***2029.920989***	1015.464133	2012.894440	1006.950858	2011.910424	1006.458850	T	3917.749195	1959.378236	3900.722646	1950.864961	3899.738630	1950.372953	37
24	2086.942453	**1043.974865**	2069.915904	1035.461590	2068.931888	1034.969582	G	3816.701516	1908.854396	3799.674967	1900.341122	3798.690951	1899.849114	36
25	***2173.974481***	1087.490879	2156.947932	1078.977604	2155.963916	1078.485596	S	3759.680052	1880.343664	3742.653503	1871.830389	3741.669487	1871.338382	35
26	2360.053794	**1180.530535**	2343.027245	1172.017261	2342.043229	1171.525253	W	3672.648024	1836.827650	3655.621475	1828.314375	3654.637459	1827.822367	34
27	2474.096721	1237.551999	2457.070172	1229.038724	2456.086156	1228.546716	N	3486.568711	1743.787993	3469.542162	1735.274719	3468.558146	1734.782711	33
28	2561.128749	1281.068013	2544.102200	1272.554738	2543.118184	1272.062730	S	3372.525784	1686.766530	3355.499235	1678.253255	3354.515219	1677.761247	32
29	2618.150213	1309.578745	2601.123664	1301.065470	2600.139648	1300.573462	G	3285.493756	1643.250516	3268.467207	1634.737241	3267.483191	1634.245233	31
30	***2705.182241***	**1353.094759**	2688.155692	1344.581484	2687.171676	1344.089476	S	3228.472292	1614.739784	3211.445743	1606.226509	3210.461727	1605.734501	30
31	2792.214269	1396.610773	2775.187720	1388.097498	2774.203704	1387.605490	S	3141.440264	1571.223770	3124.413715	1562.710495	3123.429699	1562.218487	29
32	2849.235733	1425.121505	2832.209184	1416.608230	2831.225168	1416.116222	G	3054.408236	1527.707756	3037.381687	1519.194481	3036.397671	1518.702473	28
33	2950.283412	1475.645344	2933.256863	1467.132069	2932.272847	1466.640062	T	2997.386772	1499.197024	2980.360223	1490.683749	2979.376207	1490.191741	27
34	3007.304876	1504.156076	2990.278327	1495.642801	2989.294311	1495.150794	G	***2896.339093***	1448.673184	2879.312544	1440.159910	2878.328528	1439.667902	26
35	3094.336904	1547.672090	3077.310355	1539.158815	3076.326339	1538.666808	S	2839.317629	1420.162453	2822.291080	1411.649178	2821.307064	1411.157170	25
36	3195.384583	1598.195929	3178.358034	1589.682655	3177.374018	1589.190647	T	2752.285601	1376.646438	2735.259052	1368.133164	2734.275036	1367.641156	24
37	3252.406047	**1626.706661**	3235.379498	1618.193387	3234.395482	1617.701379	G	***2651.237922***	1326.122599	2634.211373	1317.609325	2633.227357	1317.117317	23
38	3366.448974	1683.728125	3349.422425	1675.214850	3348.438409	1674.722842	N	2594.216458	1297.611867	2577.189909	1289.098593	2576.205893	1288.606585	22
39	3805.674300	1903.340788	3788.647751	1894.827513	3787.663735	1894.335506	Q	***2480.173531***	1240.590404	2463.146982	1232.077129	2462.162966	1231.585121	21
40	***3919.717227***	1960.362252	3902.690678	1951.848977	3901.706662	1951.356969	N	***2040.948205***	1020.977741	2023.921656	1012.464466	2022.937640	1011.972458	20
41	4016.769991	2008.888634	3999.743442	2000.375359	3998.759426	1999.883351	P	***1926.905278***	963.956277	1909.878729	955.443003	1908.894713	954.950995	19
42	4073.791455	2037.399365	4056.764906	2028.886091	4055.780890	2028.394083	G	1829.852514	915.429895	1812.825965	906.916621	1811.841949	906.424613	18
43	4160.823483	2080.915380	4143.796934	2072.402105	4142.812918	2071.910097	S	1772.831050	886.919163	1755.804501	878.405889	1754.820485	877.913881	17
44	4257.876247	2129.441762	4240.849698	2120.928487	4239.865682	2120.436479	P	***1685.799022***	843.403149	1668.772473	834.889875	1667.788457	834.397867	16
45	4413.977358	2207.492317	4396.950809	2198.979043	4395.966793	2198.487035	R	1588.746258	794.876767	1571.719709	786.363493	1570.735693	785.871485	15
46	4511.030122	2256.018699	4494.003573	2247.505425	4493.019557	2247.013417	P	***1432.645147***	716.826212	1415.618598	708.312937	1414.634582	707.820929	14
47	4568.051586	2284.529431	4551.025037	2276.016157	4550.041021	2275.524149	G	1335.592383	668.299830	1318.565834	659.786555	1317.581818	659.294547	13
48	4655.083614	2328.045445	4638.057065	2319.532171	4637.073049	2319.040163	S	1278.570919	639.789098	1261.544370	631.275823	1260.560354	630.783815	12
49	4756.131293	2378.569285	4739.104744	2370.056010	4738.120728	2369.564002	T	1191.538891	596.273084	1174.512342	587.759809	1173.528326	587.267801	11
50	4813.152757	2407.080017	4796.126208	2398.566742	4795.142192	2398.074734	G	1090.491212	545.749244	1073.464663	537.235970	1072.480647	536.743962	10
51	4914.200436	2457.603856	4897.173887	2449.090582	4896.189871	2448.598574	T	***1033.469748***	517.238512	1016.443199	508.725238	1015.459183	508.233230	9
52	5100.279749	2550.643513	5083.253200	2542.130238	5082.269184	2541.638230	W	932.422069	466.714673	915.395520	458.201398	914.411504	457.709390	8
53	5214.322676	2607.664976	5197.296127	2599.151702	5196.312111	2598.659694	N	***746.342756***	373.675016	729.316207	365.161742	728.332191	364.669734	7
54	5311.375440	2656.191358	5294.348891	2647.678084	5293.364875	2647.186076	P	***632.299829***	316.653552	615.273280	308.140278	614.289264	307.648270	6
55	5368.396904	2684.702090	5351.370355	2676.188816	5350.386339	2675.696808	G	***535.247065***	268.127170	518.220516	259.613896	517.236500	259.121888	5
56	5455.428932	2728.218104	5438.402383	2719.704830	5437.418367	2719.212822	S	***478.225601***	239.616438	461.199052	231.103164	460.215036	230.611156	4
57	5542.460960	2771.734118	5525.434411	2763.220844	5524.450395	2762.728836	S	***391.193573***	196.100424	374.167024	187.587150	373.183008	187.095142	3
58	5671.503553	2836.255415	5654.477004	2827.742140	5653.492988	2827.250132	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
59							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.8	5844.608032	0.083888	NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER

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

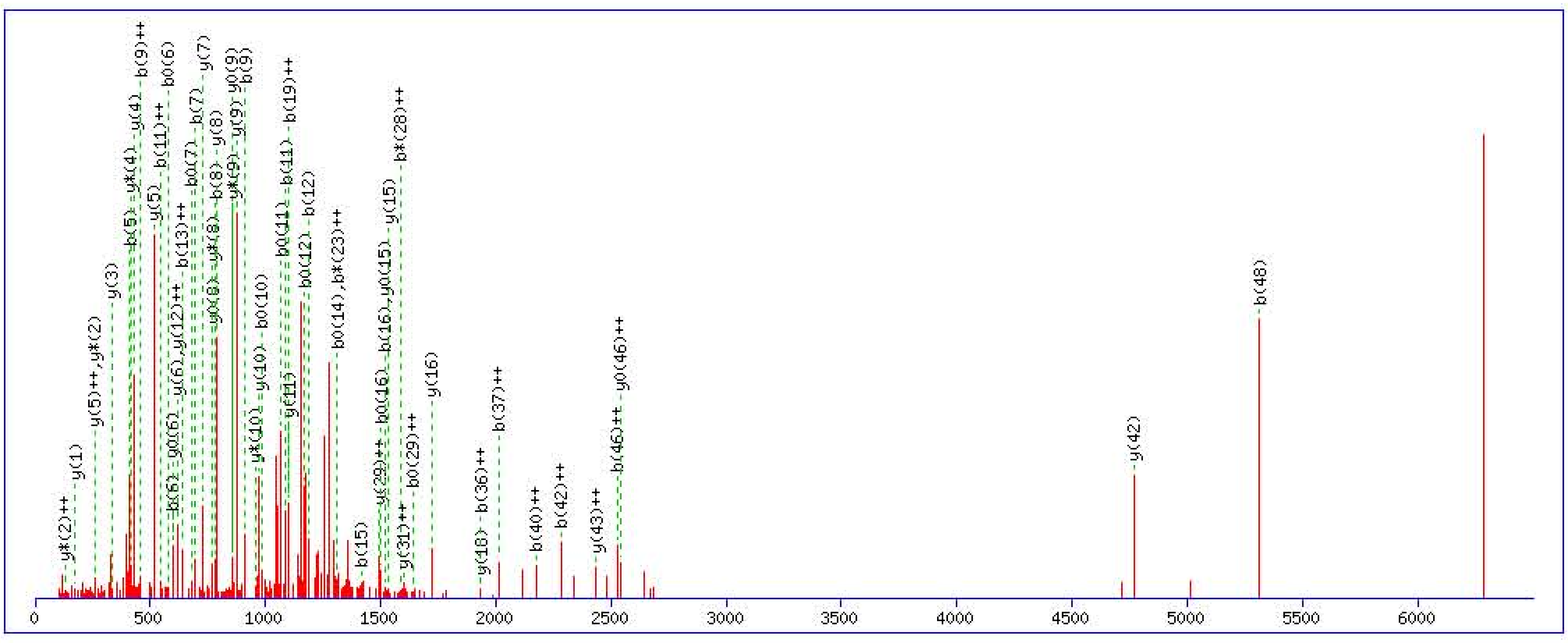
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

Match to Query 89008: 6284.865264 from(1048.484820,6+) rtinseconds(2024) index(42279)
Title: Locus:1.1.1.2988.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [6500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



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Monoisotopic mass of neutral peptide Mr(calc): 6284.792847
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00023
Matches : 59/646 fragment ions using 119 most intense peaks   (help)
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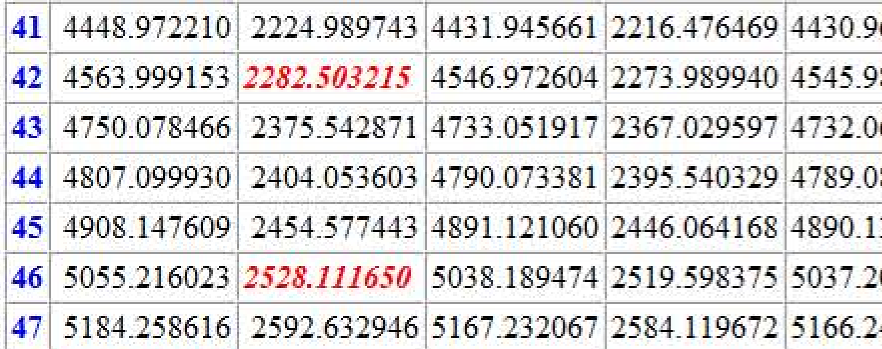
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							58
2	145.060768	73.034022			127.050203	64.028740	S	6228.778603	3114.892940	6211.752054	3106.379665	6210.768038	3105.887657	57
3	216.097882	108.552579			198.087317	99.547296	A	6141.746575	3071.376926	6124.720026	3062.863651	6123.736010	3062.371643	56
4	273.119346	137.063311			255.108781	128.058029	G	6070.709461	3035.858369	6053.682912	3027.345094	6052.698896	3026.853086	55
5	***410.178258***	205.592767			392.167693	196.587484	H	6013.687997	3007.347637	5996.661448	2998.834362	5995.677432	2998.342354	54
6	***596.257571***	298.632424			578.247006	289.627141	W	5876.629085	2938.818181	5859.602536	2930.304906	5858.618520	2929.812898	53
7	***697.305250***	349.156263			679.294685	340.150981	T	5690.549772	2845.778524	5673.523223	2837.265250	5672.539207	2836.773242	52
8	***784.337278***	392.672277			766.326713	383.666995	S	5589.502093	2795.254685	5572.475544	2786.741410	5571.491528	2786.249402	51
9	***913.379871***	***457.193574***			895.369306	448.188291	E	5502.470065	2751.738671	5485.443516	2743.225396	5484.459500	2742.733388	50
10	1000.411899	500.709588			982.401334	491.704305	S	5373.427472	2687.217374	5356.400923	2678.704100	5355.416907	2678.212092	49
11	***1087.443927***	***544.225602***			1069.433362	535.220319	S	5286.395444	2643.701360	5269.368895	2635.188086	5268.384879	2634.696078	48
12	***1186.512341***	593.759809			1168.501776	584.754526	V	5199.363416	2600.185346	5182.336867	2591.672072	5181.352851	2591.180064	47
13	1273.544369	***637.275823***			1255.533804	628.270540	S	5100.295002	2550.651139	5083.268453	2542.137865	5082.284437	2541.645857	46
14	1330.565833	665.786555			1312.555268	656.781272	G	5013.262974	2507.135125	4996.236425	2498.621851	4995.252409	2498.129843	45
15	***1417.597861***	709.302569			1399.587296	700.297286	S	4956.241510	2478.624393	4939.214961	2470.111119	4938.230945	2469.619111	44
16	***1518.645540***	759.826408			1500.634975	750.821126	T	4869.209482	2435.108379	4852.182933	2426.595105	4851.198917	2426.103097	43
17	1575.667004	788.337140			1557.656439	779.331858	G	***4768.161803***	2384.584540	4751.135254	2376.071265	4750.151238	2375.579257	42
18	2014.892330	1007.949803	1997.865781	999.436529	1996.881765	998.944521	Q	4711.140339	2356.073808	4694.113790	2347.560533	4693.129774	2347.068525	41
19	2200.971643	***1100.989460***	2183.945094	1092.476185	2182.961078	1091.984177	W	4271.915013	2136.461145	4254.888464	2127.947870	4253.904448	2127.455862	40
20	2338.030555	1169.518916	2321.004006	1161.005641	2320.019990	1160.513633	H	4085.835700	2043.421488	4068.809151	2034.908214	4067.825135	2034.416206	39
21	2425.062583	1213.034930	2408.036034	1204.521655	2407.052018	1204.029647	S	3948.776788	1974.892032	3931.750239	1966.378758	3930.766223	1965.886750	38
22	2554.105176	1277.556226	2537.078627	1269.042952	2536.094611	1268.550944	E	3861.744760	1931.376018	3844.718211	1922.862744	3843.734195	1922.370736	37
23	2641.137204	1321.072240	2624.110655	1312.558966	2623.126639	1312.066958	S	3732.702167	1866.854722	3715.675618	1858.341447	3714.691602	1857.849439	36
24	2698.158668	1349.582972	2681.132119	1341.069698	2680.148103	1340.577690	G	3645.670139	1823.338708	3628.643590	1814.825433	3627.659574	1814.333425	35
25	2785.190696	1393.098986	2768.164147	1384.585712	2767.180131	1384.093704	S	3588.648675	1794.827976	3571.622126	1786.314701	3570.638110	1785.822693	34
26	2932.259110	1466.633193	2915.232561	1458.119919	2914.248545	1457.627911	F	3501.616647	1751.311962	3484.590098	1742.798687	3483.606082	1742.306679	33
27	3088.360221	1544.683749	3071.333672	1536.170474	3070.349656	1535.678466	R	3354.548233	1677.777755	3337.521684	1669.264480	3336.537668	1668.772472	32
28	3185.412985	1593.210131	3168.386436	1584.696856	3167.402420	1584.204848	P	3198.447122	1599.727199	3181.420573	1591.213925	3180.436557	1590.721917	31
29	3300.439928	1650.723602	3283.413379	1642.210327	3282.429363	1641.718320	D	3101.394358	1551.200817	3084.367809	1542.687543	3083.383793	1542.195535	30
30	3387.471956	1694.239616	3370.445407	1685.726342	3369.461391	1685.234334	S	2986.367415	1493.687346	2969.340866	1485.174071	2968.356850	1484.682063	29
31	3484.524720	1742.765998	3467.498171	1734.252724	3466.514155	1733.760716	P	2899.335387	1450.171332	2882.308838	1441.658057	2881.324822	1441.166049	28
32	3541.546184	1771.276730	3524.519635	1762.763456	3523.535619	1762.271448	G	2802.282623	1401.644950	2785.256074	1393.131675	2784.272058	1392.639667	27
33	3628.578212	1814.792744	3611.551663	1806.279470	3610.567647	1805.787462	S	2745.261159	1373.134218	2728.234610	1364.620943	2727.250594	1364.128935	26
34	3685.599676	1843.303476	3668.573127	1834.790202	3667.589111	1834.298194	G	2658.229131	1329.618204	2641.202582	1321.104929	2640.218566	1320.612921	25
35	3799.642603	1900.324940	3782.616054	1891.811665	3781.632038	1891.319657	N	2601.207667	1301.107472	2584.181118	1292.594197	2583.197102	1292.102189	24
36	3870.679717	***1935.843497***	3853.653168	1927.330222	3852.669152	1926.838214	A	2487.164740	1244.086008	2470.138191	1235.572734	2469.154175	1235.080726	23
37	4026.780828	***2013.894052***	4009.754279	2005.380778	4008.770263	2004.888770	R	2416.127626	1208.567451	2399.101077	1200.054177	2398.117061	1199.562169	22
38	4123.833592	2062.420434	4106.807043	2053.907160	4105.823027	2053.415152	P	2260.026515	1130.516896	2242.999966	1122.003621	2242.015950	1121.511613	21
39	4237.876519	2119.441898	4220.849970	2110.928623	4219.865954	2110.436615	N	2162.973751	1081.990514	2145.947202	1073.477239	2144.963186	1072.985231	20
40	4351.919446	***2176.463361***	4334.892897	2167.950087	4333.908881	2167.458079	N	2048.930824	1024.969050	2031.904275	1016.455776	2030.920259	1015.963768	19
41	4448.972210	2224.989743	4431.945661	2216.476469	4430.961645	2215.984461	P	***1934.887897***	967.947587	1917.861348	959.434312	1916.877332	958.942304	18
42	4563.999153	***2282.503215***	4546.972604	2273.989940	4545.988588	2273.497932	D	1837.835133	919.421205	1820.808584	910.907930	1819.824568	910.415922	17
43	4750.078466	2375.542871	4733.051917	2367.029597	4732.067901	2366.537589	W	***1722.808190***	861.907733	1705.781641	853.394459	1704.797625	852.902451	16
44	4807.099930	2404.053603	4790.073381	2395.540329	4789.089365	2395.048321	G	***1536.728877***	768.868077	1519.702328	760.354802	1518.718312	759.862794	15
45	4908.147609	2454.577443	4891.121060	2446.064168	4890.137044	2445.572160	T	1479.707413	740.357345	1462.680864	731.844070	1461.696848	731.352062	14
46	5055.216023	***2528.111650***	5038.189474	2519.598375	5037.205458	2519.106367	F	1378.659734	689.833505	1361.633185	681.320231	1360.649169	680.828223	13
47	5184.258616	2592.632946	5167.232067	2584.119672	5166.248051	2583.627664	E	1231.591320	616.299298	1214.564771	607.786024	1213.580755	607.294016	12
48	***5313.301209***	2657.154243	5296.274660	2648.640968	5295.290644	2648.148960	E	***1102.548727***	551.778002	1085.522178	543.264727	1084.538162	542.772719	11
49	5412.369623	2706.688450	5395.343074	2698.175175	5394.359058	2697.683167	V	***973.506134***	487.256705	956.479585	478.743431	955.495569	478.251423	10
50	5499.401651	2750.204464	5482.375102	2741.691189	5481.391086	2741.199181	S	***874.437720***	437.722498	857.411171	429.209224	856.427155	428.717216	9
51	5556.423115	2778.715196	5539.396566	2770.201921	5538.412550	2769.709913	G	***787.405692***	394.206484	770.379143	385.693210	769.395127	385.201202	8
52	5670.466042	2835.736659	5653.439493	2827.223385	5652.455477	2826.731377	N	***730.384228***	365.695752	713.357679	357.182478	712.373663	356.690470	7
53	5769.534456	2885.270866	5752.507907	2876.757592	5751.523891	2876.265584	V	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	6
54	5856.566484	2928.786880	5839.539935	2920.273606	5838.555919	2919.781598	S	***517.272887***	259.140082	500.246338	250.626807	499.262322	250.134799	5
55	5953.619248	2977.313262	5936.592699	2968.799988	5935.608683	2968.307980	P	***430.240859***	215.624068	413.214310	207.110793	412.230294	206.618785	4
56	6010.640712	3005.823994	5993.614163	2997.310720	5992.630147	2996.818712	G	***333.188095***	167.097686	316.161546	158.584411	315.177530	158.092403	3
57	6111.688391	3056.347834	6094.661842	3047.834559	6093.677826	3047.342551	T	276.166631	138.586954	259.140082	130.073679	258.156066	129.581671	2
58							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.1	6284.792847	0.072417	GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTR

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

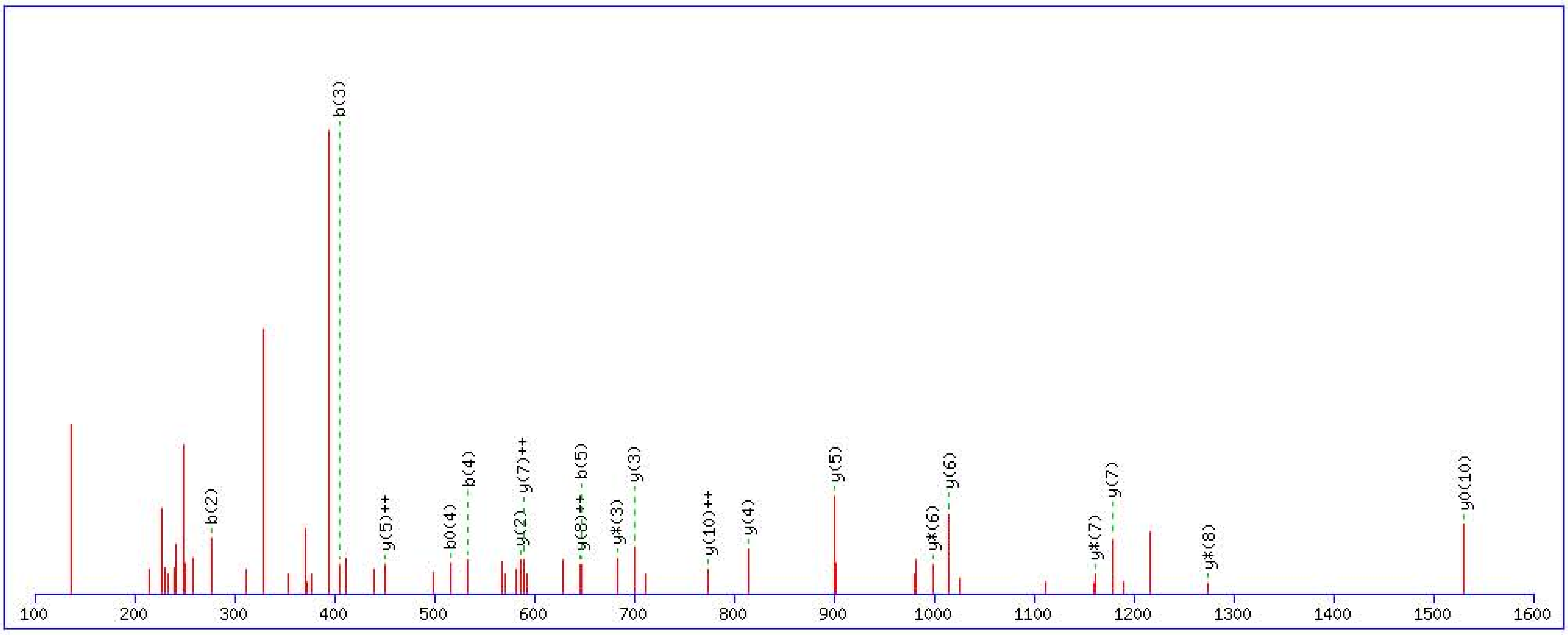
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLQEIYNSNNQK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

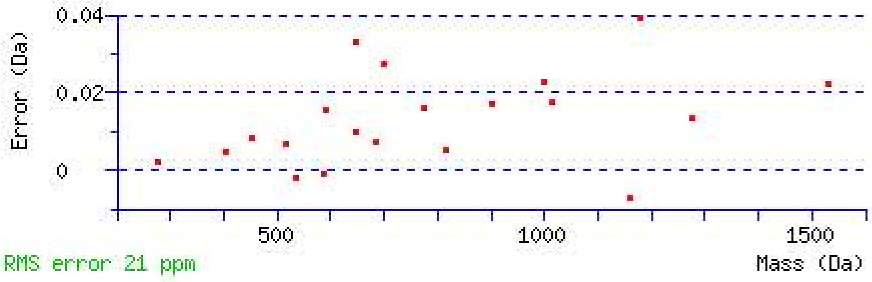
Match to Query 48989: 1823.914572 from(608.978800,3+) rtinseconds(1825) index(23526)
Title: Locus:1.1.1.2590.5 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

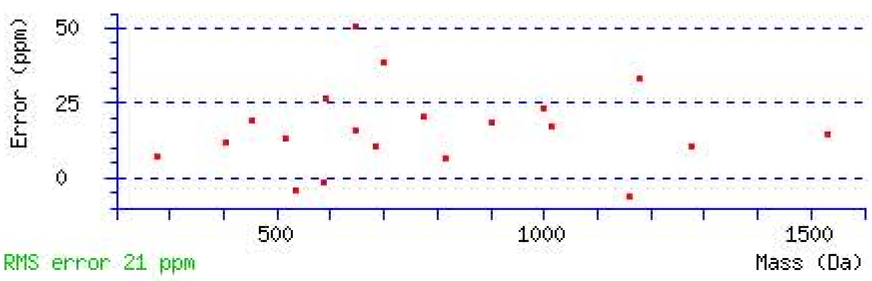
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1823.887573
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.052
Matches : 20/114 fragment ions using 39 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							12
2	***277.154669***	139.080973					L	1661.831567	831.419422	1644.805018	822.906147	1643.821002	822.414139	11
3	***405.213247***	203.110262	388.186698	194.596987			Q	1548.747503	774.877390	1531.720954	766.364115	1530.736938	765.872107	10
4	***534.255840***	267.631558	517.229291	259.118284	516.245275	258.626276	E	1420.688925	710.848100	1403.662376	702.334826	1402.678360	701.842818	9
5	***647.339904***	324.173590	630.313355	315.660316	629.329339	315.168308	I	1291.646332	646.326804	1274.619783	637.813530	1273.635767	637.321522	8
6	810.403233	405.705255	793.376684	397.191980	792.392668	396.699972	Y	***1178.562268***	589.784772	1161.535719	581.271498	1160.551703	580.779489	7
7	924.446160	462.726718	907.419611	454.213443	906.435595	453.721435	N	***1015.498939***	508.253108	998.472390	499.739833	997.488374	499.247825	6
8	1011.478188	506.242732	994.451639	497.729457	993.467623	497.237449	S	***901.456012***	451.231644	884.429463	442.718370	883.445447	442.226362	5
9	1125.521115	563.264196	1108.494566	554.750921	1107.510550	554.258913	N	***814.423984***	407.715630	797.397435	399.202356			4
10	1239.564042	620.285659	1222.537493	611.772385	1221.553477	611.280376	N	***700.381057***	350.694167	683.354508	342.180892			3
11	1678.789368	839.898322	1661.762819	831.385048	1660.778803	830.893039	Q	***586.338130***	293.672703	569.311581	285.159429			2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.0	1823.887573	0.026999	YLQEIYNSNNQK

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

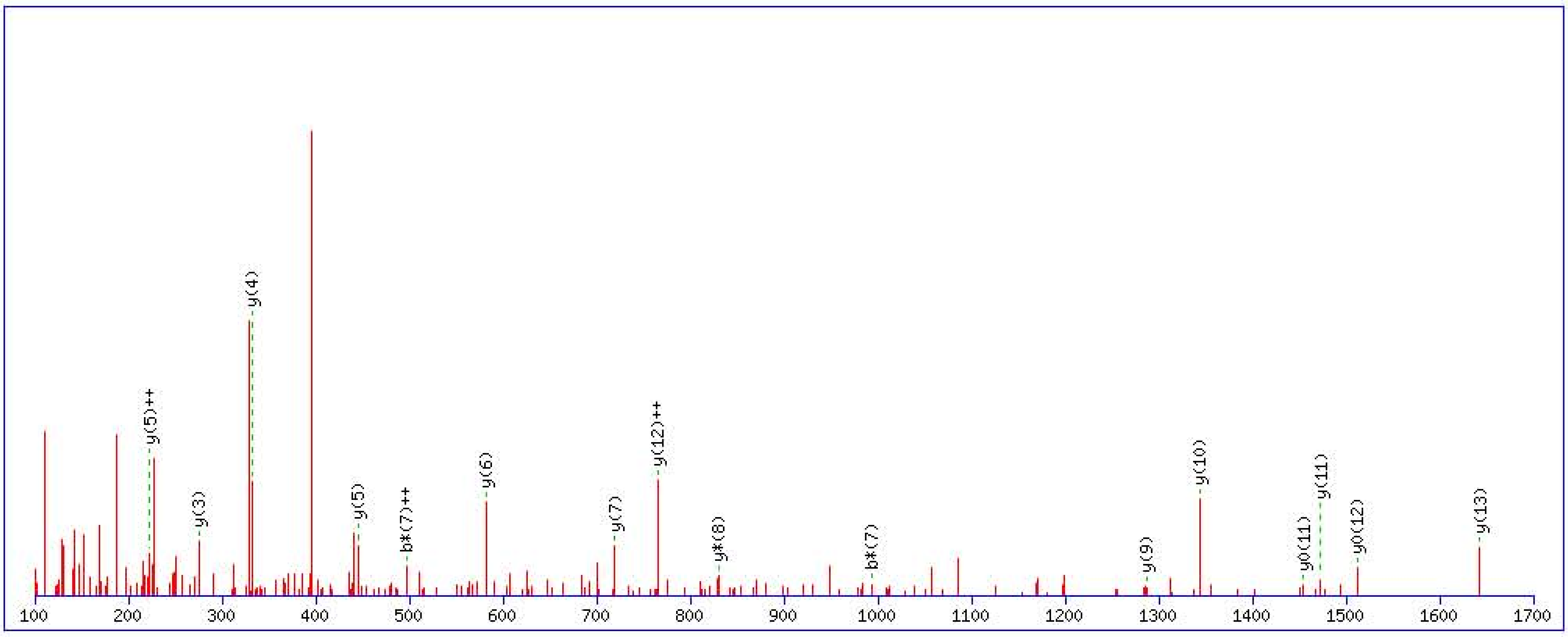
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

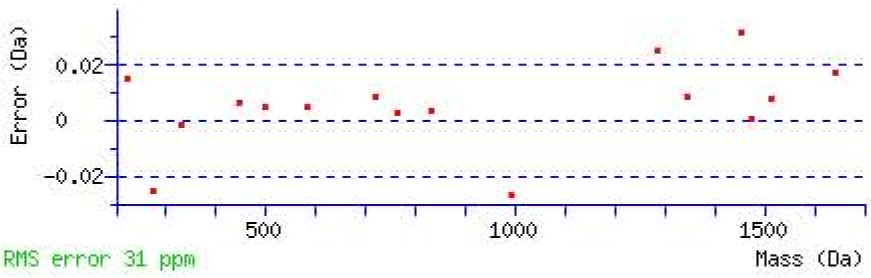
Match to Query 49846: 1855.977096 from(465.001550,4+) rtinseconds(1468) index(56687)
Title: Locus:1.1.1.2817.8 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

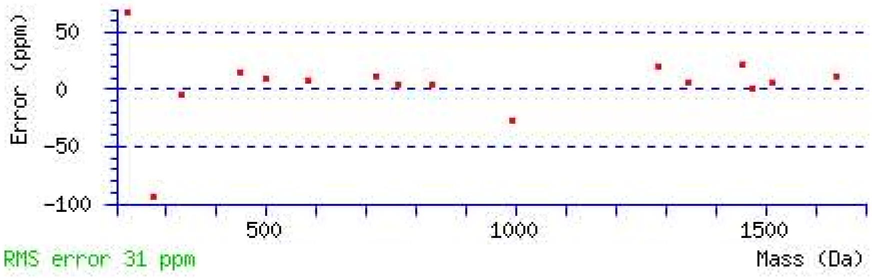
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1855.972687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.002
Matches : 16/134 fragment ions using 44 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							15
2	215.139019	108.073147			197.128454	99.067865	T	1743.895902	872.451589	1726.869353	863.938314	1725.885337	863.446306	14
3	328.223083	164.615179			310.212518	155.609897	I	***1642.848223***	821.927749	1625.821674	813.414475	1624.837658	812.922467	13
4	385.244547	193.125911			367.233982	184.120629	G	1529.764159	765.385717	1512.737610	756.872443	1511.753594	756.380435	12
5	514.287140	257.647208			496.276575	248.641926	E	***1472.742695***	736.874985	1455.716146	728.361711	1454.732130	727.869703	11
6	571.308604	286.157940			553.298039	277.152658	G	***1343.700102***	672.353689	1326.673553	663.840414			10
7	1010.533930	505.770603	993.507381	497.257329	992.523365	496.765321	Q	***1286.678638***	643.842957	1269.652089	635.329682			9
8	1138.592508	569.799892	1121.565959	561.286618	1120.581943	560.794609	Q	847.453312	424.230294	830.426763	415.717019			8
9	1275.651420	638.329348	1258.624871	629.816074	1257.640855	629.324065	H	***719.394734***	360.201005	702.368185	351.687730			7
10	1412.710332	706.858804	1395.683783	698.345530	1394.699767	697.853521	H	***582.335822***	291.671549	565.309273	283.158274			6
11	1525.794396	763.400836	1508.767847	754.887561	1507.783831	754.395553	L	***445.276910***	223.142093	428.250361	214.628818			5
12	1582.815860	791.911568	1565.789311	783.398293	1564.805295	782.906285	G	***332.192846***	166.600061	315.166297	158.086786			4
13	1639.837324	820.422300	1622.810775	811.909025	1621.826759	811.417017	G	***275.171382***	138.089329	258.144833	129.576054			3
14	1710.874438	855.940857	1693.847889	847.427582	1692.863873	846.935574	A	218.149918	109.578597	201.123369	101.065322			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.6	1855.972687	0.004409	LTIGEGQQHHLGGAK
28.6	1855.972687	0.004409	LTIGEGQQHHLGGAK
1.9	1855.967957	0.009139	EDKEAFAIVPVSPAEVR

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

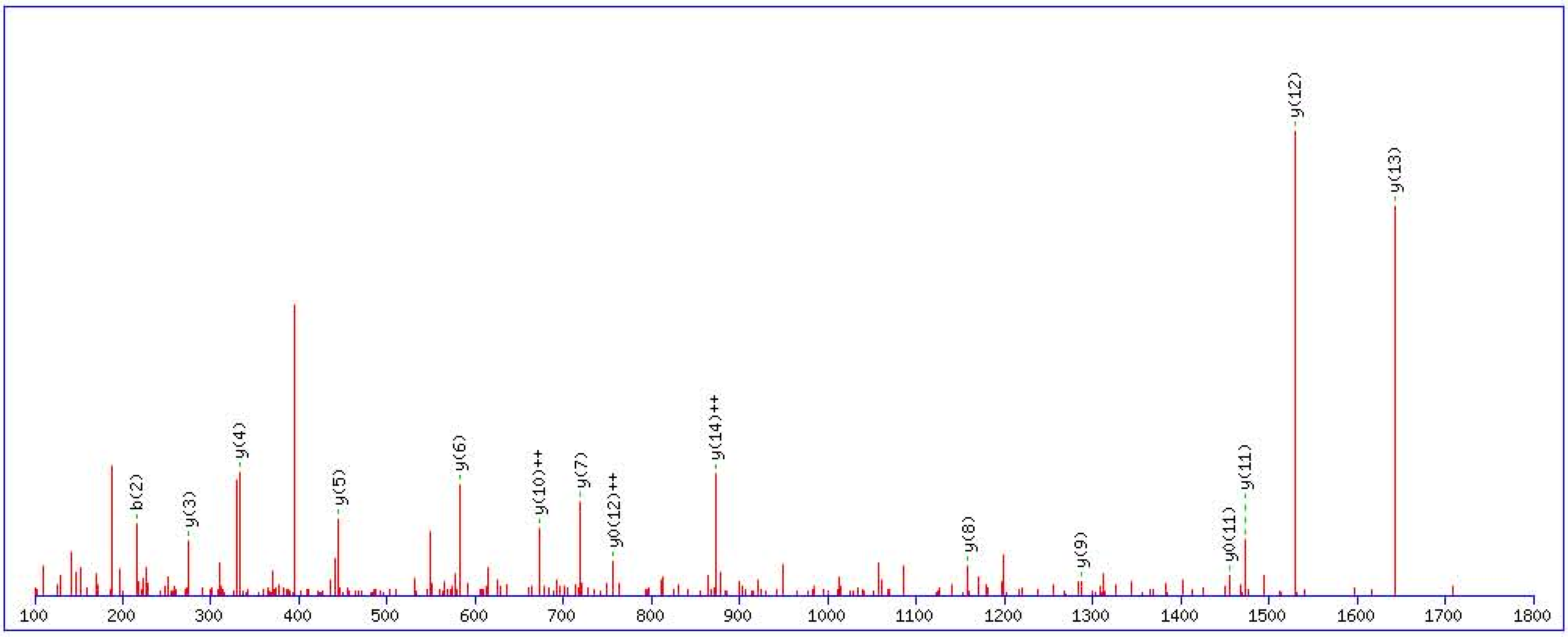
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

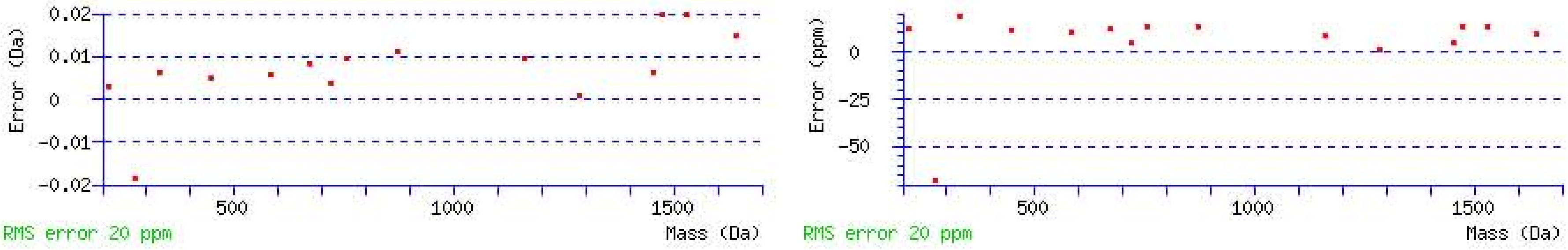
Match to Query 49869: 1855.994952 from(619.672260,3+) rtinseconds(1471) index(21009)
Title: Locus:1.1.1.2466.20 File:"2013-07-02 CLN FXIII 60 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1855.972687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 6.2e-006
Matches : 15/134 fragment ions using 33 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							15
2	215.139019	108.073147			197.128454	99.067865	T	1743.895902	872.451589	1726.869353	863.938314	1725.885337	863.446306	14
3	328.223083	164.615179			310.212518	155.609897	I	***1642.848223***	821.927749	1625.821674	813.414475	1624.837658	812.922467	13
4	385.244547	193.125911			367.233982	184.120629	G	***1529.764159***	765.385717	1512.737610	756.872443	1511.753594	756.380435	12
5	514.287140	257.647208			496.276575	248.641926	E	***1472.742695***	736.874985	1455.716146	728.361711	1454.732130	727.869703	11
6	571.308604	286.157940			553.298039	277.152658	G	1343.700102	672.353689	1326.673553	663.840414			10
7	699.367182	350.187229	682.340633	341.673955	681.356617	341.181947	Q	***1286.678638***	643.842957	1269.652089	635.329682			9
8	1138.592508	569.799892	1121.565959	561.286618	1120.581943	560.794609	Q	***1158.620060***	579.813668	1141.593511	571.300393			8
9	1275.651420	638.329348	1258.624871	629.816074	1257.640855	629.324065	H	***719.394734***	360.201005	702.368185	351.687730			7
10	1412.710332	706.858804	1395.683783	698.345530	1394.699767	697.853521	H	***582.335822***	291.671549	565.309273	283.158274			6
11	1525.794396	763.400836	1508.767847	754.887561	1507.783831	754.395553	L	***445.276910***	223.142093	428.250361	214.628818			5
12	1582.815860	791.911568	1565.789311	783.398293	1564.805295	782.906285	G	***332.192846***	166.600061	315.166297	158.086786			4
13	1639.837324	820.422300	1622.810775	811.909025	1621.826759	811.417017	G	***275.171382***	138.089329	258.144833	129.576054			3
14	1710.874438	855.940857	1693.847889	847.427582	1692.863873	846.935574	A	218.149918	109.578597	201.123369	101.065322			2
15							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.0	1855.972687	0.022265	LTIGEGQQHHLGGAK
44.8	1855.972687	0.022265	LTIGEGQQHHLGGAK
0.5	1855.979202	0.015750	ITIVENVGSVEGLAYHR

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

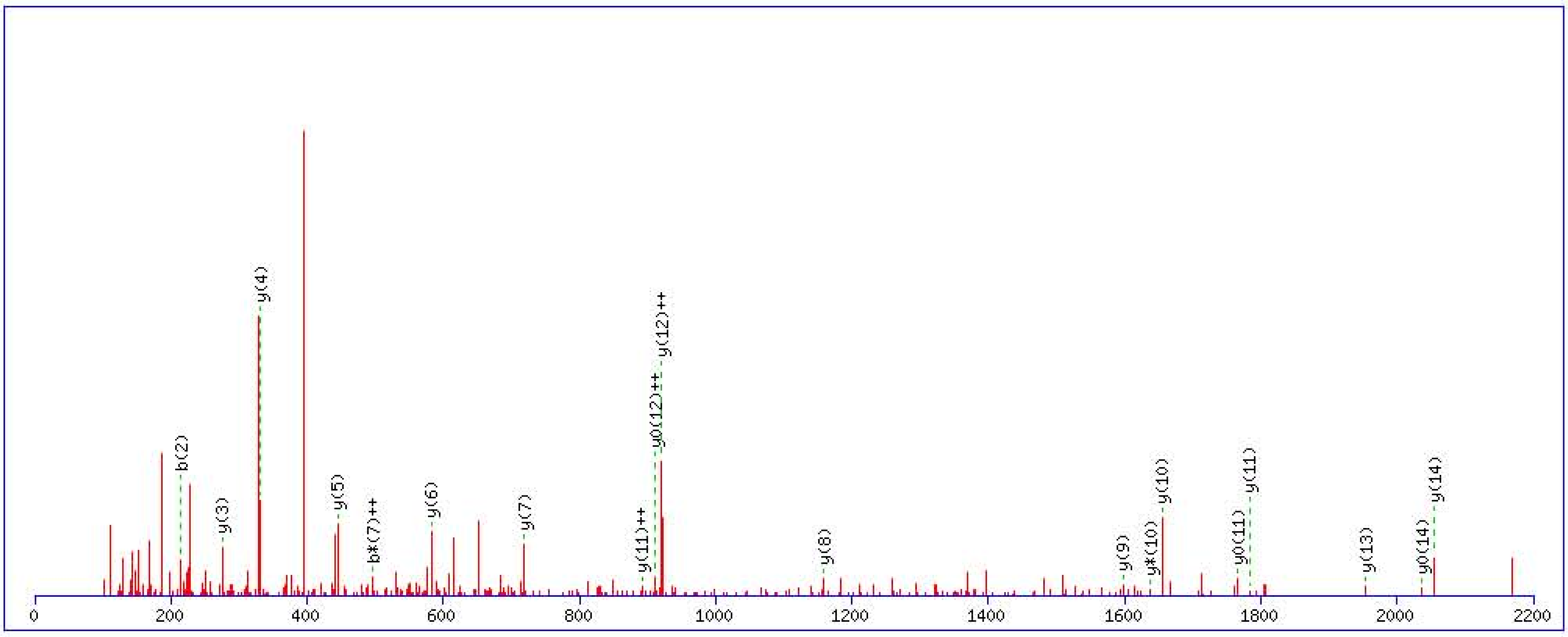
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

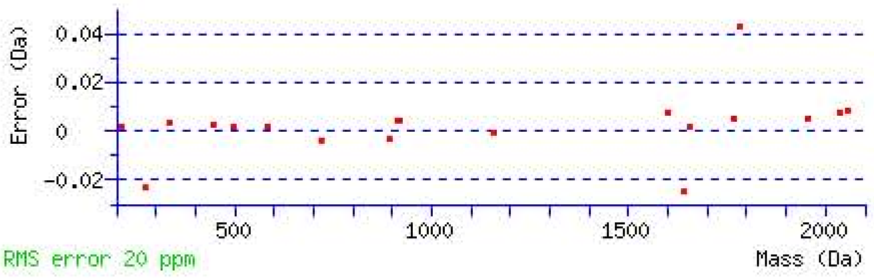
Match to Query 57421: 2167.145216 from(542.793580,4+) rtinseconds(1753) index(40451)
Title: Locus:1.1.1.2894.8 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

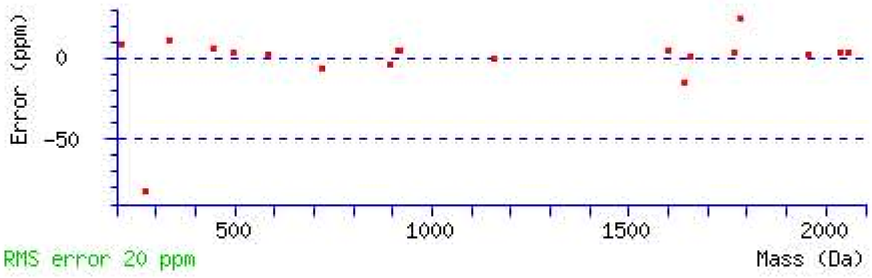
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2167.139435
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.05
Matches : 19/134 fragment ions using 73 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							15
2	215.139019	108.073147			197.128454	99.067865	T	***2055.062650***	1028.034963	2038.036101	1019.521688	2037.052085	1019.029680	14
3	328.223083	164.615179			310.212518	155.609897	I	***1954.014971***	977.511123	1936.988422	968.997849	1936.004406	968.505841	13
4	385.244547	193.125911			367.233982	184.120629	G	1840.930907	920.969091	1823.904358	912.455817	1822.920342	911.963809	12
5	514.287140	257.647208			496.276575	248.641926	E	***1783.909443***	892.458359	1766.882894	883.945085	1765.898878	883.453077	11
6	571.308604	286.157940			553.298039	277.152658	G	***1654.866850***	827.937063	1637.840301	819.423788			10
7	1010.533930	505.770603	993.507381	497.257329	992.523365	496.765321	Q	***1597.845386***	799.426331	1580.818837	790.913056			9
8	1449.759256	725.383266	1432.732707	716.869992	1431.748691	716.377984	Q	***1158.620060***	579.813668	1141.593511	571.300393			8
9	1586.818168	793.912722	1569.791619	785.399448	1568.807603	784.907440	H	***719.394734***	360.201005	702.368185	351.687730			7
10	1723.877080	862.442178	1706.850531	853.928904	1705.866515	853.436895	H	***582.335822***	291.671549	565.309273	283.158274			6
11	1836.961144	918.984210	1819.934595	910.470936	1818.950579	909.978927	L	***445.276910***	223.142093	428.250361	214.628818			5
12	1893.982608	947.494942	1876.956059	938.981667	1875.972043	938.489659	G	***332.192846***	166.600061	315.166297	158.086786			4
13	1951.004072	976.005674	1933.977523	967.492399	1932.993507	967.000391	G	***275.171382***	138.089329	258.144833	129.576054			3
14	2022.041186	1011.524231	2005.014637	1003.010956	2004.030621	1002.518948	A	218.149918	109.578597	201.123369	101.065322			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.9	2167.139435	0.005781	LTIGEGQQHHLGGAK

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

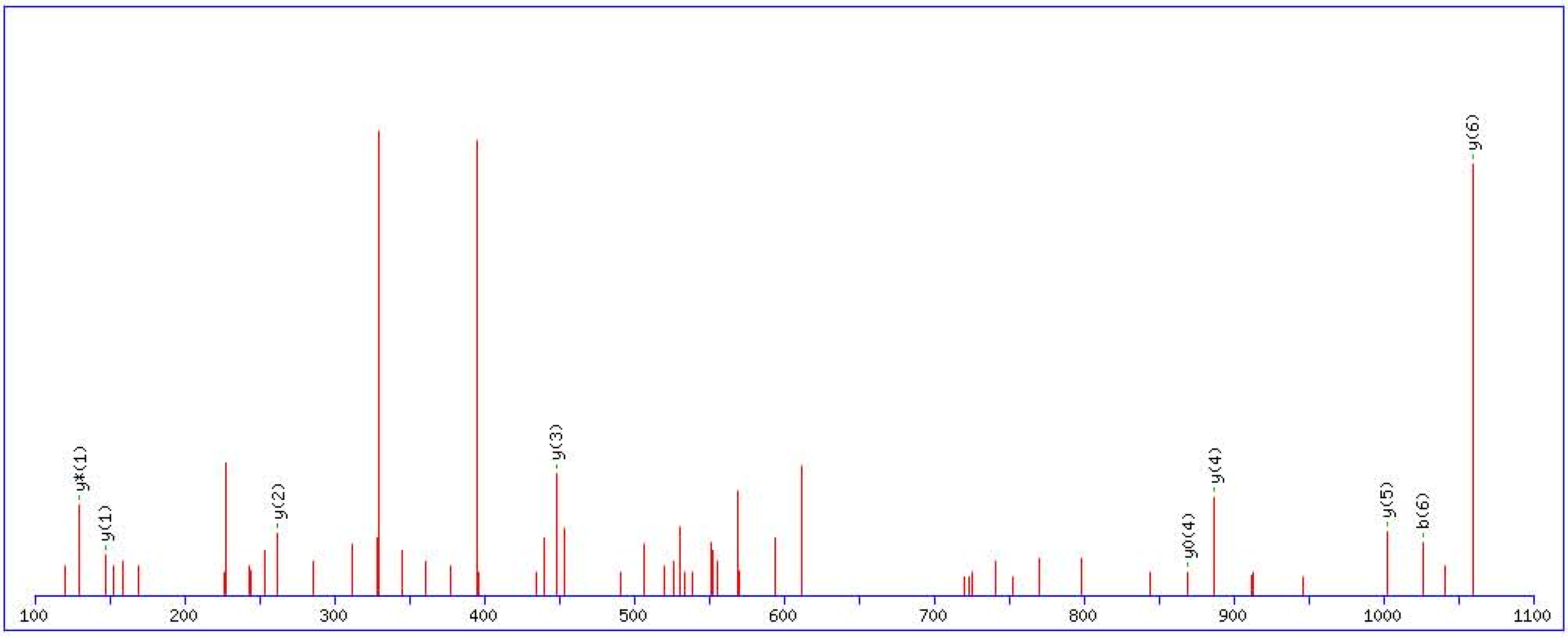
{MATRIX SCIENCE} **Mascot Search Results**

Peptide View

MS/MS Fragmentation of **IGDQWDK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

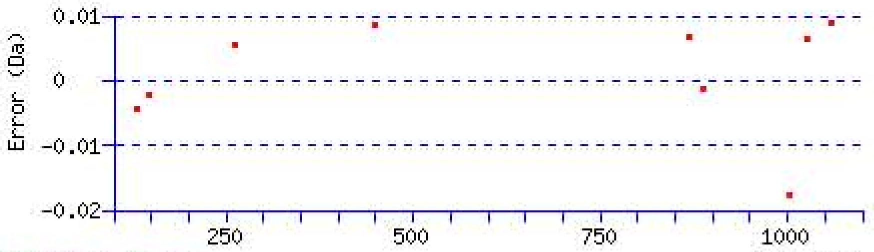
Match to Query 26556: 1171.574528 from(586.794540,2+) rtinseconds(1784) index(40661)
Title: Locus:1.1.1.2905.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

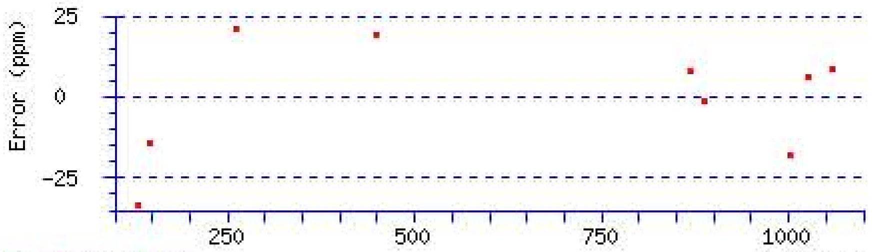


```
Monoisotopic mass of neutral peptide Mr(calc): 1171.569580
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0093
Matches : 9/60 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							7
2	171.112804	86.060040					G	***1059.492793***	530.250035	1042.466244	521.736760	1041.482228	521.244752	6
3	286.139747	143.573512			268.129182	134.568229	D	***1002.471329***	501.739303	985.444780	493.226028	984.460764	492.734020	5
4	725.365073	363.186175	708.338524	354.672900	707.354508	354.180892	Q	***887.444386***	444.225831	870.417837	435.712557	869.433821	435.220549	4
5	911.444386	456.225831	894.417837	447.712557	893.433821	447.220549	W	***448.219060***	224.613168	431.192511	216.099894	430.208495	215.607886	3
6	1026.471329	513.739303	1009.444780	505.226028	1008.460764	504.734020	D	***262.139747***	131.573512	245.113198	123.060237	244.129182	122.568229	2
7							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 17 ppm



RMS error 17 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.7	1171.569580	0.004948	IGDQWDK
9.4	1171.590714	-0.016186	GEVQVSDK
9.1	1171.569565	0.004963	LGPEWSQPMK
6.8	1171.576096	-0.001568	LYFSDATLDK
6.4	1171.590698	-0.016170	LPALSGQDMPK
4.6	1171.590683	-0.016155	ELCADNPILK
3.5	1171.590668	-0.016140	EKAEQEK
3.5	1171.590668	-0.016140	EKAQEEK
2.6	1171.583328	-0.008800	GEVGDPGQKGTK
2.4	1171.583298	-0.008770	EPGVERSSPSK

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

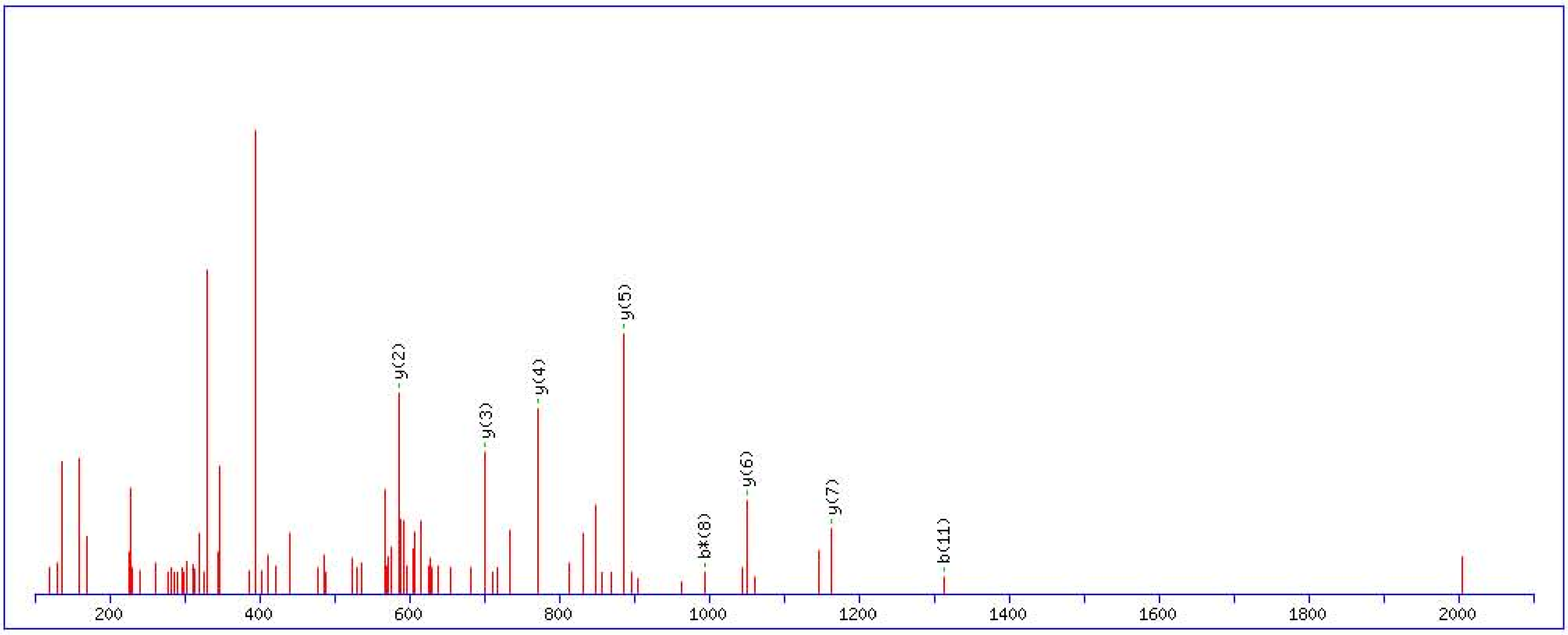
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WCGTTQNYDADQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

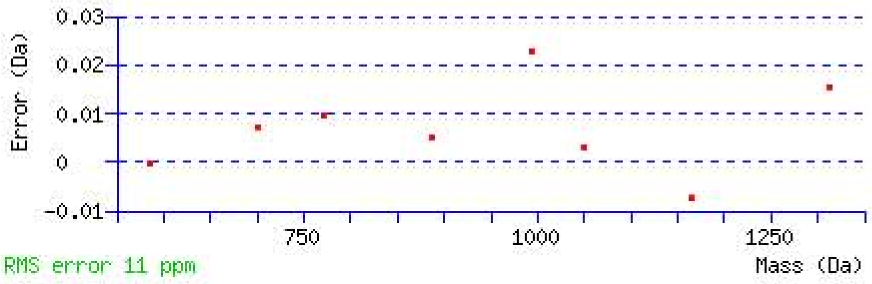
Match to Query 50504: 1896.816522 from(633.279450,3+) rtinseconds(1650) index(39769)
Title: Locus:1.1.1.2858.16 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

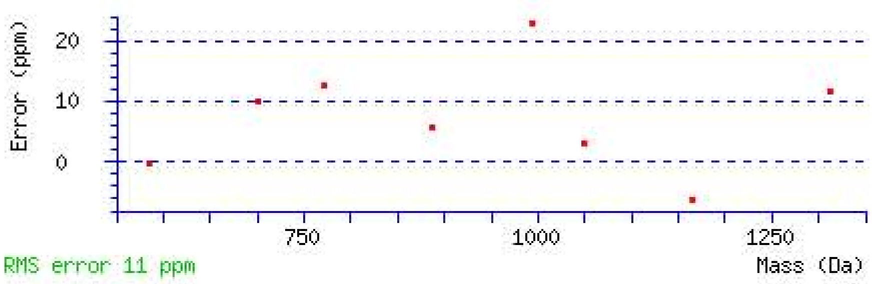
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1896.813477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.0012
Matches : 8/124 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932					W							13
2	347.117238	174.062257					C	1711.741435	856.374356	1694.714886	847.861081	1693.730870	847.369073	12
3	404.138702	202.572989					G	1551.710786	776.359031	1534.684237	767.845757	1533.700221	767.353749	11
4	505.186381	253.096828			487.175816	244.091546	T	1494.689322	747.848299	1477.662773	739.335025	1476.678757	738.843017	10
5	606.234060	303.620668			588.223495	294.615386	T	1393.641643	697.324460	1376.615094	688.811185	1375.631078	688.319177	9
6	734.292638	367.649957	717.266089	359.136683	716.282073	358.644675	Q	1292.593964	646.800620	1275.567415	638.287346	1274.583399	637.795338	8
7	848.335565	424.671421	831.309016	416.158146	830.325000	415.666138	N	***1164.535386***	582.771331	1147.508837	574.258057	1146.524821	573.766049	7
8	1011.398894	506.203085	994.372345	497.689810	993.388329	497.197802	Y	***1050.492459***	525.749868	1033.465910	517.236593	1032.481894	516.744585	6
9	1126.425837	563.716557	1109.399288	555.203282	1108.415272	554.711274	D	***887.429130***	444.218203	870.402581	435.704929	869.418565	435.212921	5
10	1197.462951	599.235114	1180.436402	590.721839	1179.452386	590.229831	A	***772.402187***	386.704732	755.375638	378.191457	754.391622	377.699449	4
11	**1312.489894**	656.748585	1295.463345	648.235311	1294.479329	647.743303	D	***701.365073***	351.186175	684.338524	342.672900	683.354508	342.180892	3
12	1751.715220	876.361248	1734.688671	867.847974	1733.704655	867.355966	Q	***586.338130***	293.672703	569.311581	285.159429			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.8	1896.813477	0.003045	WCGTTQNYDADQK

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

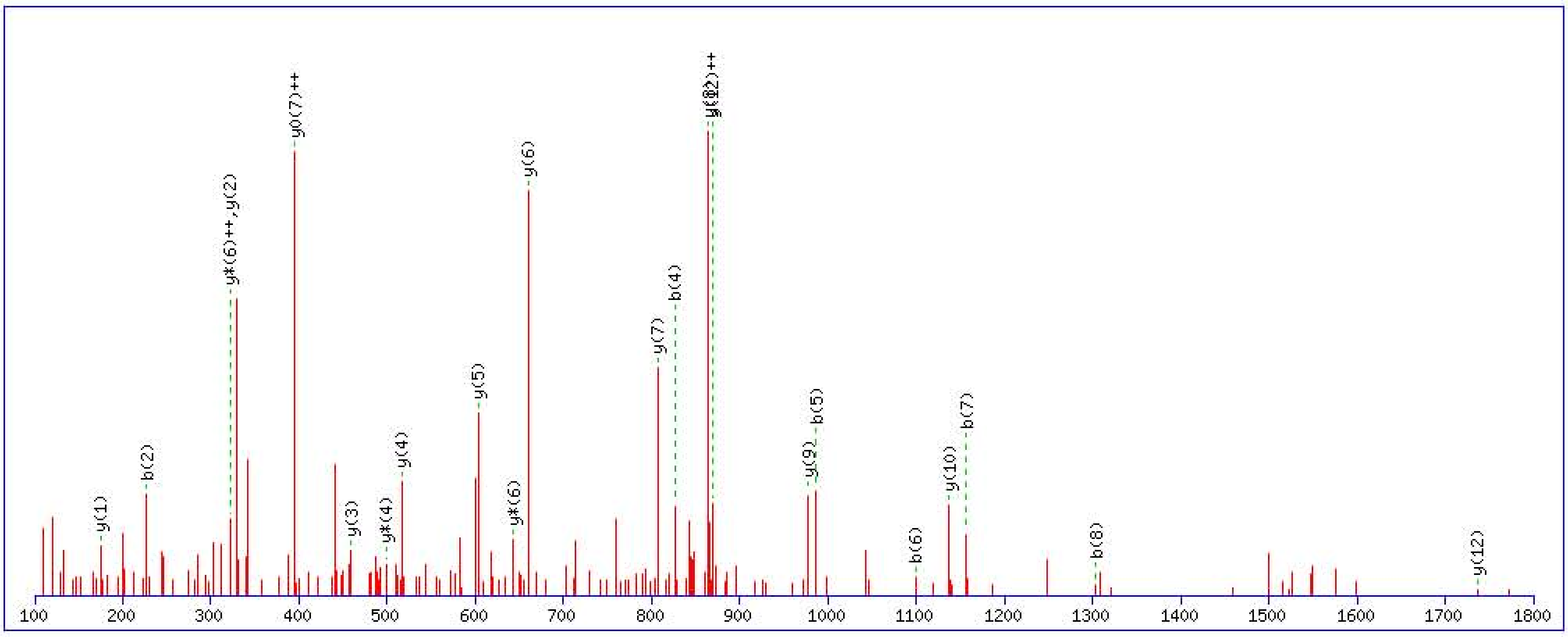
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLCQCLGFGSGHFR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

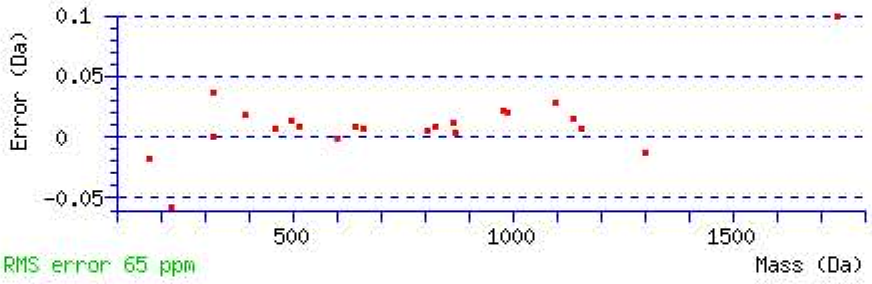
Match to Query 52001: 1961.955102 from(654.992310,3+) rtinseconds(2150) index(43069)
Title: Locus:1.1.1.3032.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

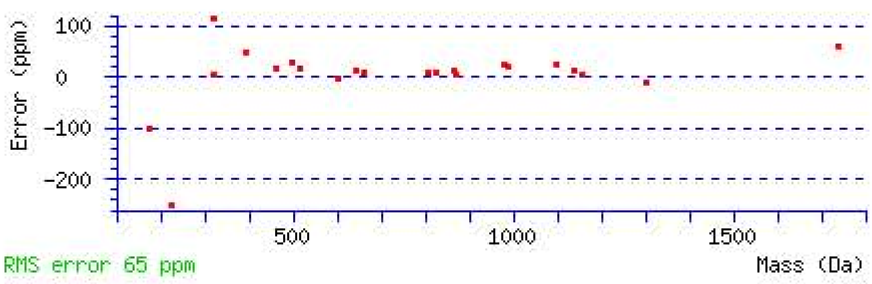
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1961.942673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00034
Matches : 22/124 fragment ions using 55 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							14
2	**227.175404**	114.091340					L	1849.865864	925.436570	1832.839315	916.923296	1831.855299	916.431288	13
3	387.206053	194.106664					C	***1736.781800***	868.894538	1719.755251	860.381264	1718.771235	859.889255	12
4	**826.431379**	413.719328	809.404830	405.206053			Q	1576.751151	788.879213	1559.724602	780.365939	1558.740586	779.873931	11
5	**986.462028**	493.734652	969.435479	485.221378			C	***1137.525825***	569.266550	1120.499276	560.753276	1119.515260	560.261268	10
6	**1099.546092**	550.276684	1082.519543	541.763410			L	***977.495176***	489.251226	960.468627	480.737952	959.484611	480.245944	9
7	**1156.567556**	578.787416	1139.541007	570.274142			G	***864.411112***	432.709194	847.384563	424.195920	846.400547	423.703912	8
8	**1303.635970**	652.321623	1286.609421	643.808349			F	***807.389648***	404.198462	790.363099	395.685188	789.379083	395.193180	7
9	1360.657434	680.832355	1343.630885	672.319081			G	***660.321234***	330.664255	643.294685	322.150981	642.310669	321.658973	6
10	1447.689462	724.348369	1430.662913	715.835095	1429.678897	715.343087	S	***603.299770***	302.153523	586.273221	293.640249	585.289205	293.148241	5
11	1504.710926	752.859101	1487.684377	744.345827	1486.700361	743.853818	G	***516.267742***	258.637509	499.241193	250.124235			4
12	1641.769838	821.388557	1624.743289	812.875283	1623.759273	812.383274	H	***459.246278***	230.126777	442.219729	221.613502			3
13	1788.838252	894.922764	1771.811703	886.409490	1770.827687	885.917482	F	***322.187366***	161.597321	305.160817	153.084047			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.5	1961.942673	0.012429	LLCQCLGFGSGHFR

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

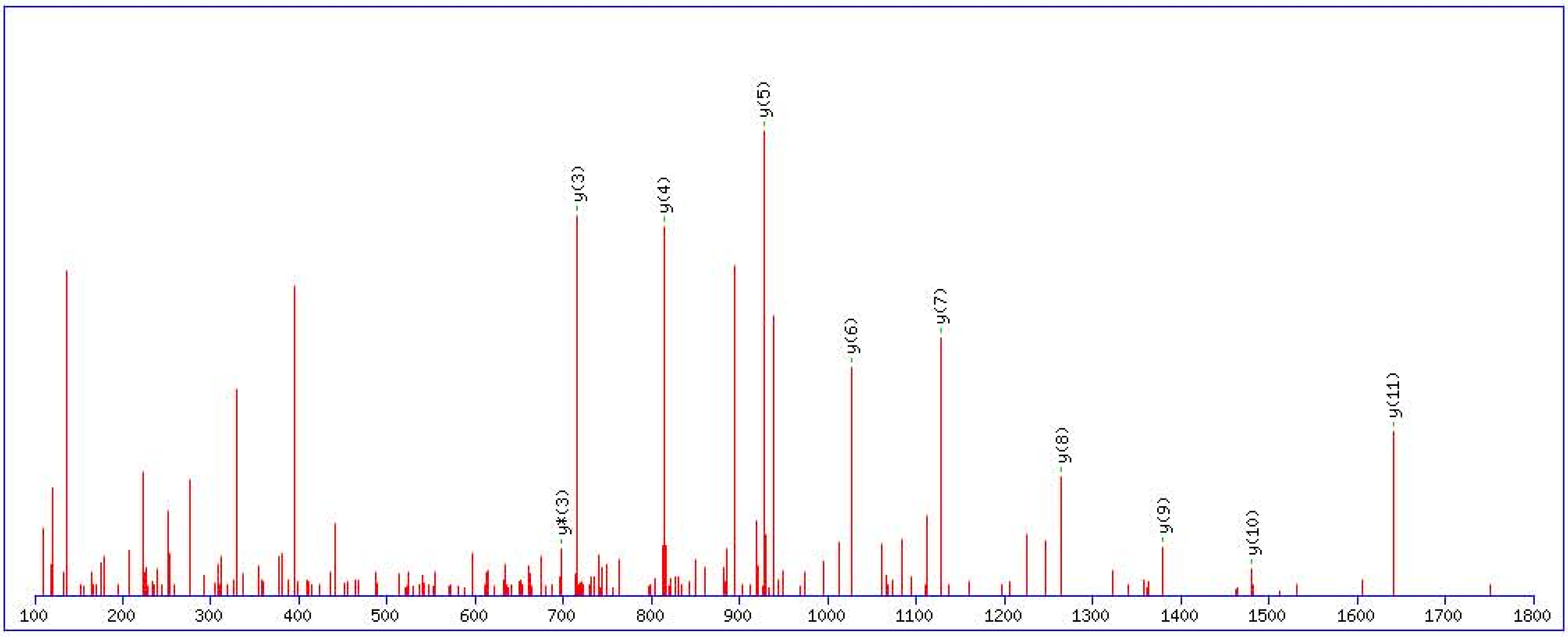
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSFCTDHTVLVQTR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

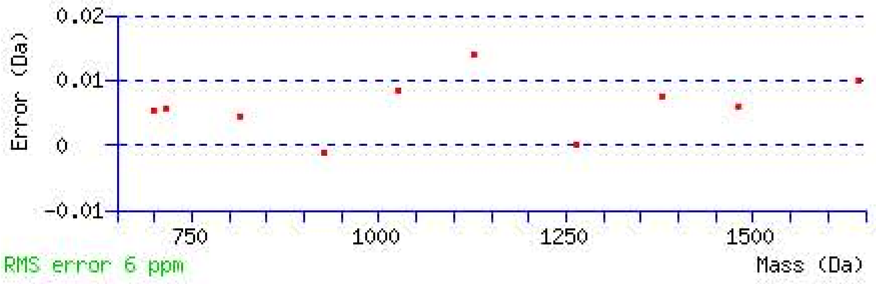
Match to Query 54619: 2036.993952 from(680.005260,3+) rtinseconds(1983) index(42014)
Title: Locus:1.1.1.2974.7 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

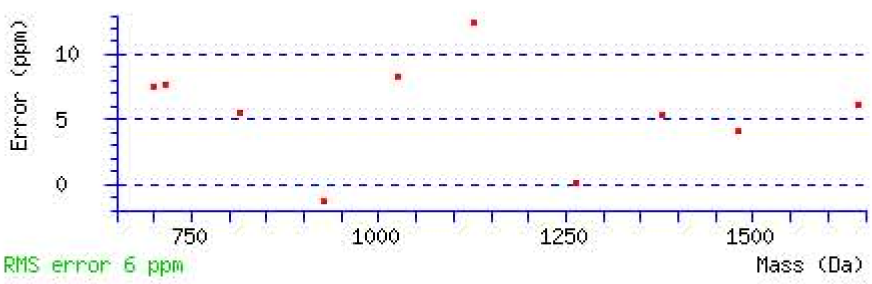
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2036.981232
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 2.7e-005
Matches : 10/130 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							14
2	251.102633	126.054954			233.092068	117.049672	S	1874.925153	937.966215	1857.898604	929.452940	1856.914588	928.960932	13
3	398.171047	199.589161			380.160482	190.583879	F	1787.893125	894.450201	1770.866576	885.936926	1769.882560	885.444918	12
4	558.201696	279.604486			540.191131	270.599204	C	***1640.824711***	820.915994	1623.798162	812.402719	1622.814146	811.910711	11
5	659.249375	330.128326			641.238810	321.123043	T	***1480.794062***	740.900669	1463.767513	732.387395	1462.783497	731.895387	10
6	774.276318	387.641797			756.265753	378.636515	D	***1379.746383***	690.376830	1362.719834	681.863555	1361.735818	681.371547	9
7	911.335230	456.171253			893.324665	447.165971	H	***1264.719440***	632.863358	1247.692891	624.350084	1246.708875	623.858076	8
8	1012.382909	506.695093			994.372344	497.689810	T	***1127.660528***	564.333902	1110.633979	555.820628	1109.649963	555.328620	7
9	1111.451323	556.229300			1093.440758	547.224017	V	***1026.612849***	513.810063	1009.586300	505.296788	1008.602284	504.804780	6
10	1224.535387	612.771331			1206.524822	603.766049	L	***927.544435***	464.275856	910.517886	455.762581	909.533870	455.270573	5
11	1323.603801	662.305539			1305.593236	653.300256	V	***814.460371***	407.733824	797.433822	399.220549	796.449806	398.728541	4
12	1762.829127	881.918202	1745.802578	873.404927	1744.818562	872.912919	Q	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
13	1863.876806	932.442041	1846.850257	923.928767	1845.866241	923.436759	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.0	2036.981232	0.012720	YSFCTDHTVLVQTR

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

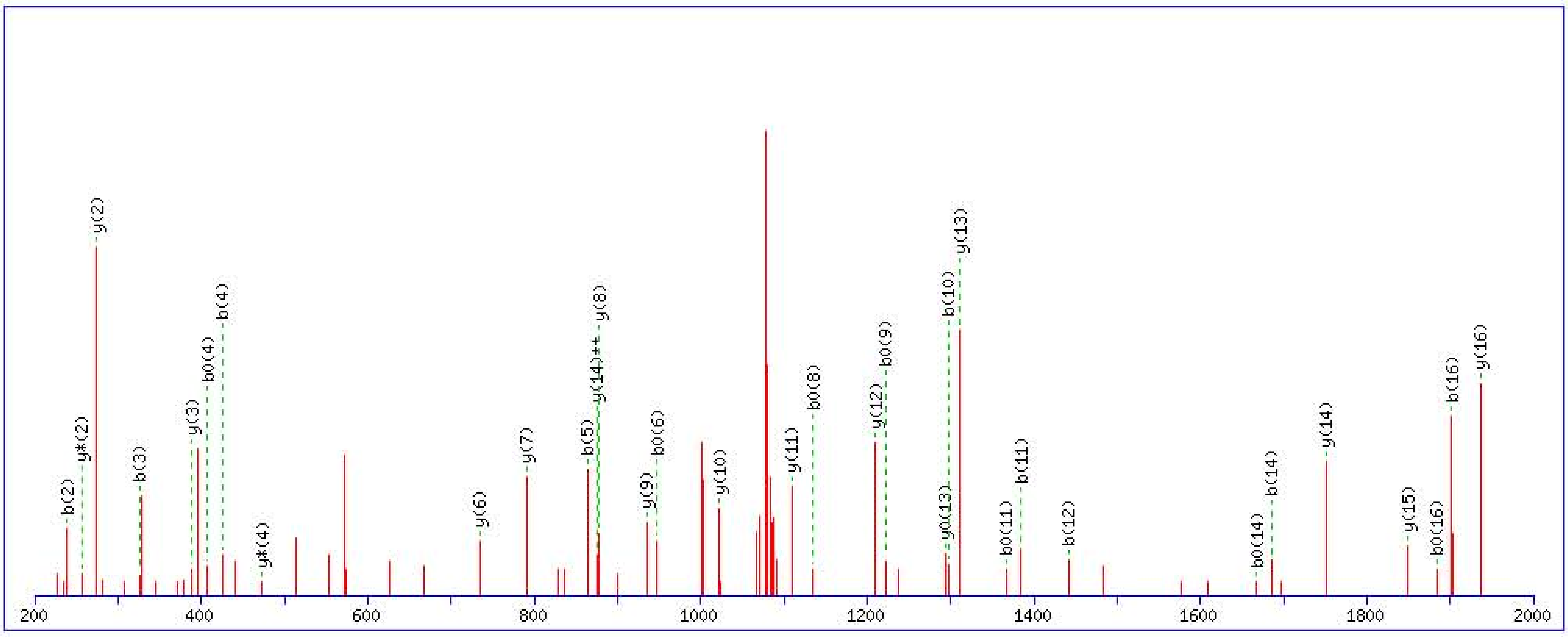
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HTSVQTTSSGSGPFTDVR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

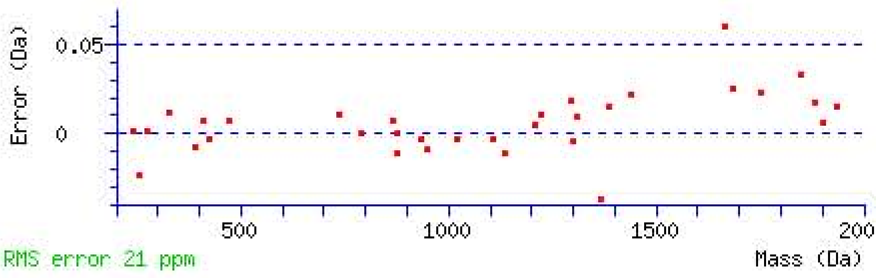
Match to Query 57604: 2174.060408 from(1088.037480,2+) rtinseconds(1651) index(39773)
Title: Locus:1.1.1.2858.20 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

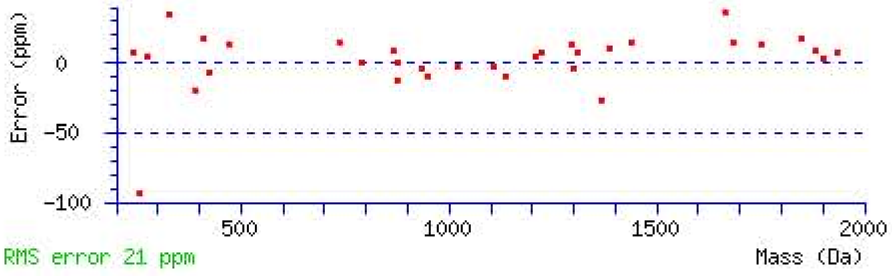
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2174.042664
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 84  Expect: 9.2e-008
Matches : 33/190 fragment ions using 59 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							18
2	**239.113867**	120.060571			221.103302	111.055289	T	2037.990983	1019.499130	2020.964434	1010.985855	2019.980418	1010.493847	17
3	**326.145895**	163.576585			308.135330	154.571303	S	***1936.943304***	968.975290	1919.916755	960.462016	1918.932739	959.970008	16
4	**425.214309**	213.110792			407.203744	204.105510	V	***1849.911276***	925.459276	1832.884727	916.946002	1831.900711	916.453994	15
5	**864.439635**	432.723456	847.413086	424.210181	846.429070	423.718173	Q	***1750.842862***	875.925069	1733.816313	867.411795	1732.832297	866.919787	14
6	965.487314	483.247295	948.460765	474.734021	947.476749	474.242013	T	***1311.617536***	656.312406	1294.590987	647.799132	1293.606971	647.307124	13
7	1066.534993	533.771135	1049.508444	525.257860	1048.524428	524.765852	T	***1210.569857***	605.788567	1193.543308	597.275292	1192.559292	596.783284	12
8	1153.567021	577.287149	1136.540472	568.773874	1135.556456	568.281866	S	***1109.522178***	555.264727	1092.495629	546.751453	1091.511613	546.259445	11
9	1240.599049	620.803163	1223.572500	612.289888	1222.588484	611.797880	S	***1022.490150***	511.748713	1005.463601	503.235439	1004.479585	502.743431	10
10	**1297.620513**	649.313895	1280.593964	640.800620	1279.609948	640.308612	G	***935.458122***	468.232699	918.431573	459.719425	917.447557	459.227417	9
11	**1384.652541**	692.829909	1367.625992	684.316634	1366.641976	683.824626	S	***878.436658***	439.721967	861.410109	431.208693	860.426093	430.716685	8
12	**1441.674005**	721.340641	1424.647456	712.827366	1423.663440	712.335358	G	***791.404630***	396.205953	774.378081	387.692679	773.394065	387.200671	7
13	1538.726769	769.867023	1521.700220	761.353748	1520.716204	760.861740	P	***734.383166***	367.695221	717.356617	359.181947	716.372601	358.689939	6
14	**1685.795183**	843.401230	1668.768634	834.887955	1667.784618	834.395947	F	637.330402	319.168839	620.303853	310.655565	619.319837	310.163557	5
15	1786.842862	893.925069	1769.816313	885.411795	1768.832297	884.919787	T	490.261988	245.634632	473.235439	237.121358	472.251423	236.629350	4
16	**1901.869805**	951.438541	1884.843256	942.925266	1883.859240	942.433258	D	***389.214309***	195.110793	372.187760	186.597518	371.203744	186.105510	3
17	2000.938219	1000.972748	1983.911670	992.459473	1982.927654	991.967465	V	***274.187366***	137.597321	257.160817	129.084047			2
18							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.3	2174.042664	0.017744	HTSVQTTSSGSGPFTDVR

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

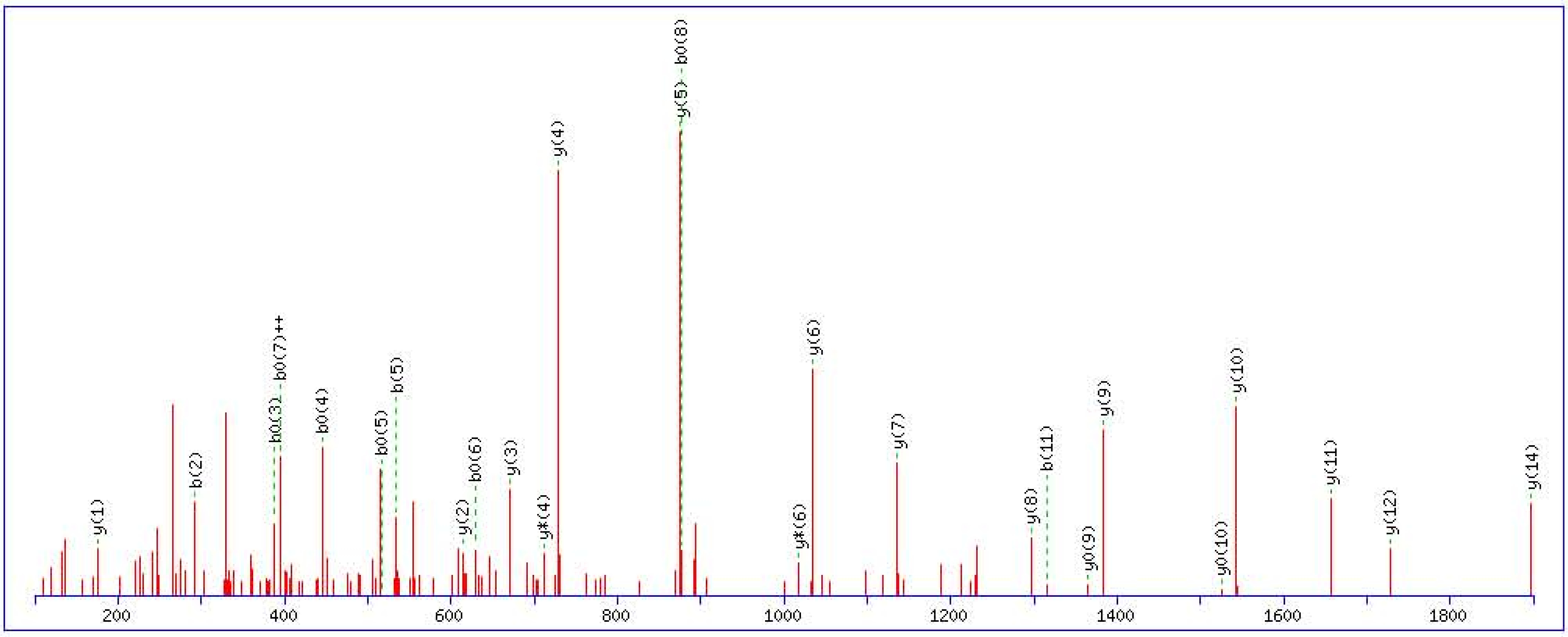
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYLGAICSCTCFGGQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

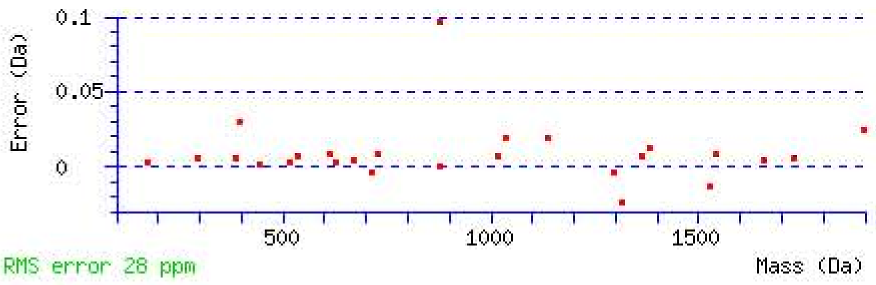
Match to Query 57930: 2188.968582 from(730.663470,3+) rtinseconds(2159) index(43148)
Title: Locus:1.1.1.3035.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

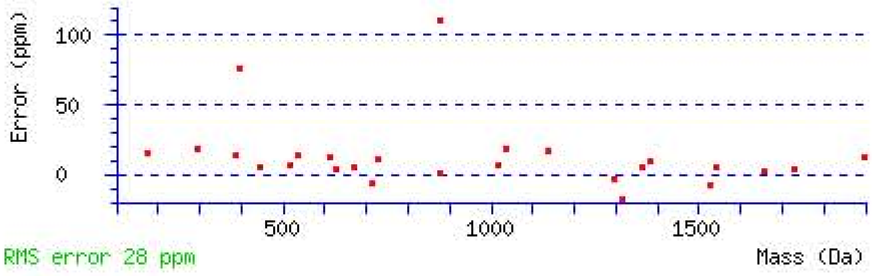
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2188.952637
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 91  Expect: 7.1e-009
Matches : 26/140 fragment ions using 43 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.049869	65.528572			112.039304	56.523290	E							16
2	**293.113198**	147.060237			275.102633	138.054955	Y	2060.917309	1030.962292	2043.890760	1022.449018	2042.906744	1021.957010	15
3	406.197262	203.602269			388.186697	194.596987	L	***1897.853980***	949.430628	1880.827431	940.917354	1879.843415	940.425346	14
4	463.218726	232.113001			445.208161	223.107719	G	1784.769916	892.888596	1767.743367	884.375322	1766.759351	883.883314	13
5	**534.255840**	267.631558			516.245275	258.626276	A	***1727.748452***	864.377864	1710.721903	855.864590	1709.737887	855.372582	12
6	647.339904	324.173590			629.329339	315.168308	I	***1656.711338***	828.859307	1639.684789	820.346033	1638.700773	819.854025	11
7	807.370553	404.188915			789.359988	395.183632	C	***1543.627274***	772.317275	1526.600725	763.804001	1525.616709	763.311993	10
8	894.402581	447.704929			876.392016	438.699646	S	***1383.596625***	692.301951	1366.570076	683.788676	1365.586060	683.296668	9
9	1054.433230	527.720253			1036.422665	518.714971	C	***1296.564597***	648.785937	1279.538048	640.272662	1278.554032	639.780654	8
10	1155.480909	578.244093			1137.470344	569.238810	T	***1136.533948***	568.770612	1119.507399	560.257338	1118.523383	559.765330	7
11	**1315.511558**	658.259417			1297.500993	649.254135	C	***1035.486269***	518.246773	1018.459720	509.733498			6
12	1462.579972	731.793624			1444.569407	722.788342	F	***875.455620***	438.231448	858.429071	429.718174			5
13	1519.601436	760.304356			1501.590871	751.299074	G	***728.387206***	364.697241	711.360657	356.183967			4
14	1576.622900	788.815088			1558.612335	779.809806	G	***671.365742***	336.186509	654.339193	327.673235			3
15	2015.848226	1008.427751	1998.821677	999.914477	1997.837661	999.422469	Q	***614.344278***	307.675777	597.317729	299.162503			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
90.5	2188.952637	0.015945	EYLGAICSCTCFGGQR

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

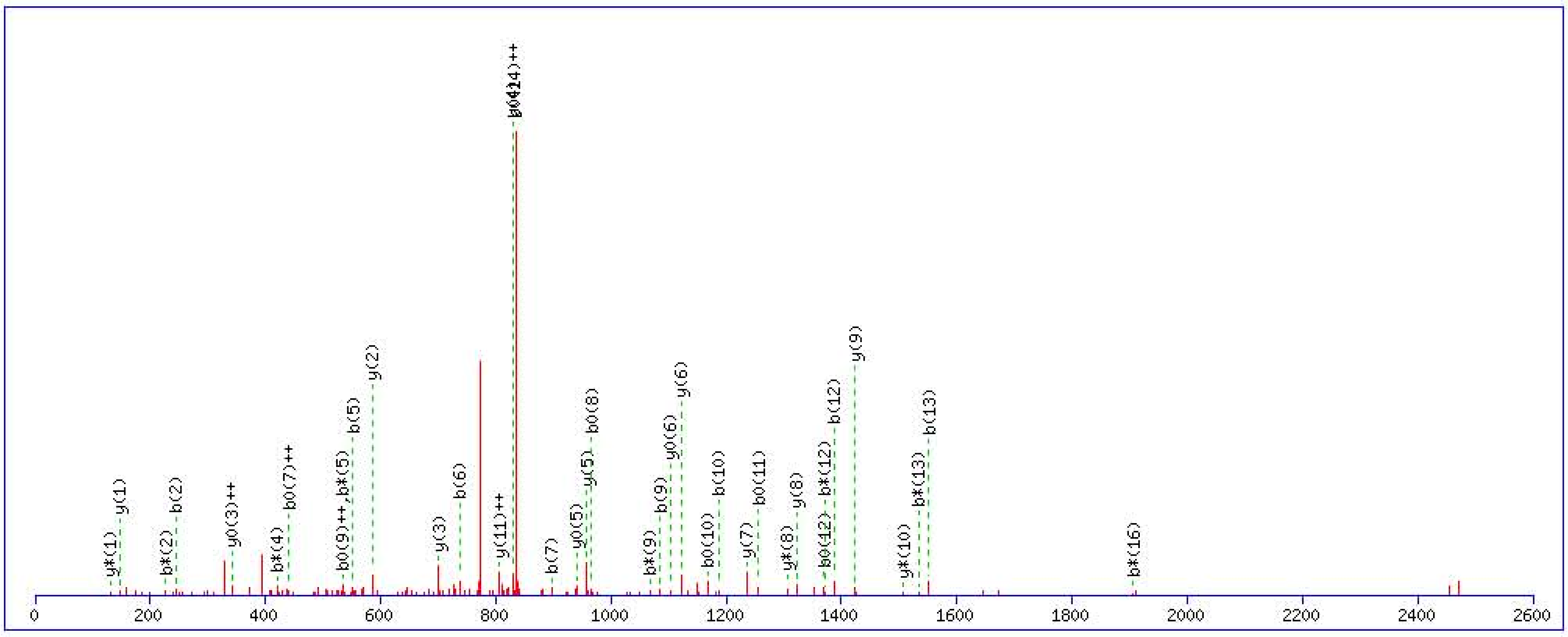
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDGHLWCSTTSNYEQDQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

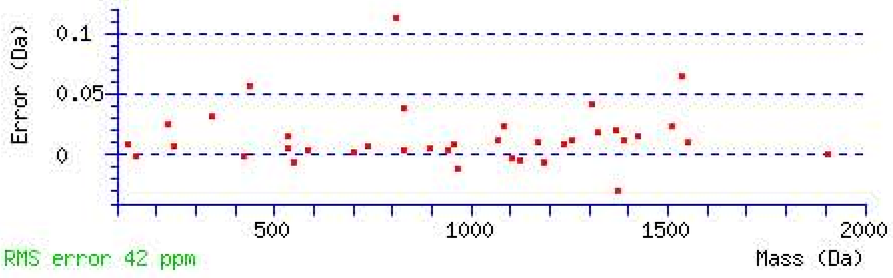
Match to Query 65572: 2507.100792 from(836.707540,3+) rtinseconds(1751) index(40443)
Title: Locus:1.1.1.2893.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

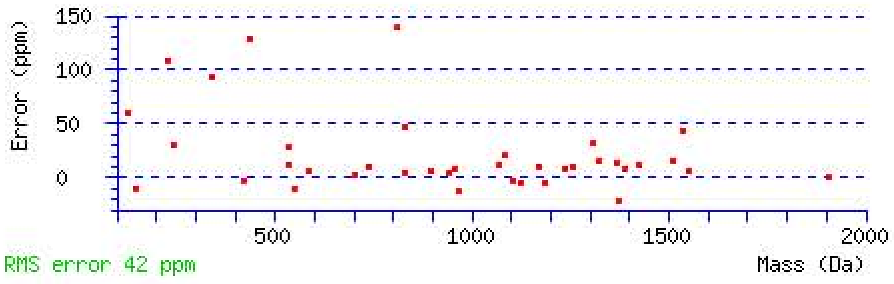
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2507.084564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17     : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0007
Matches : 38/198 fragment ions using 75 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.065854	65.036565	112.039305	56.523291			Q							18
2	***244.092797***	122.550037	227.066248	114.036762	226.082232	113.544754	D	2380.033259	1190.520267	2363.006710	1182.006993	2362.022694	1181.514985	17
3	301.114261	151.060768	284.087712	142.547494	283.103696	142.055486	G	2265.006316	1133.006796	2247.979767	1124.493521	2246.995751	1124.001513	16
4	438.173173	219.590224	421.146624	211.076950	420.162608	210.584942	H	2207.984852	1104.496064	2190.958303	1095.982789	2189.974287	1095.490781	15
5	***551.257237***	276.132257	534.230688	267.618982	533.246672	267.126974	L	2070.925940	1035.966608	2053.899391	1027.453333	2052.915375	1026.961325	14
6	***737.336550***	369.171913	720.310001	360.658639	719.325985	360.166631	W	1957.841876	979.424576	1940.815327	970.911302	1939.831311	970.419294	13
7	***897.367199***	449.187238	880.340650	440.673963	879.356634	440.181955	C	1771.762563	886.384920	1754.736014	877.871645	1753.751998	877.379637	12
8	984.399227	492.703252	967.372678	484.189977	966.388662	483.697969	S	1611.731914	806.369595	1594.705365	797.856321	1593.721349	797.364313	11
9	***1085.446906***	543.227091	1068.420357	534.713817	1067.436341	534.221808	T	1524.699886	762.853581	1507.673337	754.340307	1506.689321	753.848299	10
10	***1186.494585***	593.750930	1169.468036	585.237656	1168.484020	584.745648	T	***1423.652207***	712.329742	1406.625658	703.816467	1405.641642	703.324459	9
11	1273.526613	637.266945	1256.500064	628.753670	1255.516048	628.261662	S	***1322.604528***	661.805902	1305.577979	653.292628	1304.593963	652.800620	8
12	***1387.569540***	694.288408	1370.542991	685.775134	1369.558975	685.283125	N	***1235.572500***	618.289888	1218.545951	609.776614	1217.561935	609.284606	7
13	***1550.632869***	775.820073	1533.606320	767.306798	1532.622304	766.814790	Y	***1121.529573***	561.268425	1104.503024	552.755150	1103.519008	552.263142	6
14	1679.675462	840.341369	1662.648913	831.828095	1661.664897	831.336086	E	***958.466244***	479.736760	941.439695	471.223486	940.455679	470.731478	5
15	1807.734040	904.370658	1790.707491	895.857384	1789.723475	895.365376	Q	***829.423651***	415.215464	812.397102	406.702189	811.413086	406.210181	4
16	1922.760983	961.884130	1905.734434	953.370855	1904.750418	952.878847	D	***701.365073***	351.186175	684.338524	342.672900	683.354508	342.180892	3
17	2361.986309	1181.496792	2344.959760	1172.983518	2343.975744	1172.491510	Q	***586.338130***	293.672703	569.311581	285.159429			2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.1	2507.084564	0.016228	QDGHLWCSTTSNYEQDQK
25.2	2507.084564	0.016228	QDGHLWCSTTSNYEQDQK

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

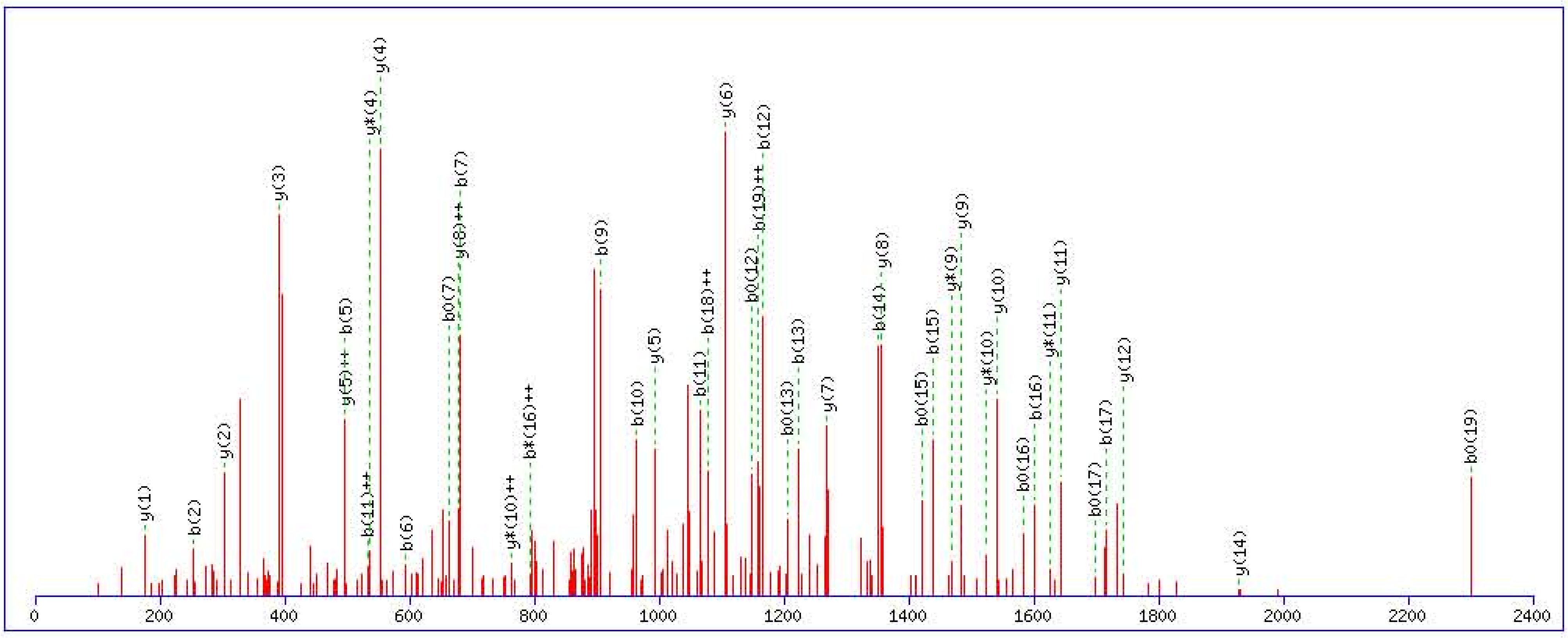
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

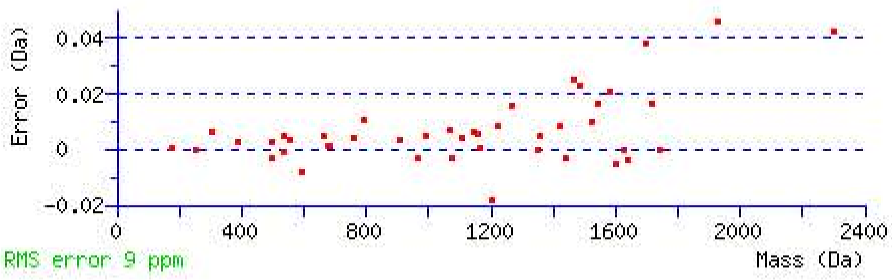
Match to Query 67538: 2706.253482 from(903.091770,3+) rtinseconds(1453) index(38549)
Title: Locus:1.1.1.2789.26 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

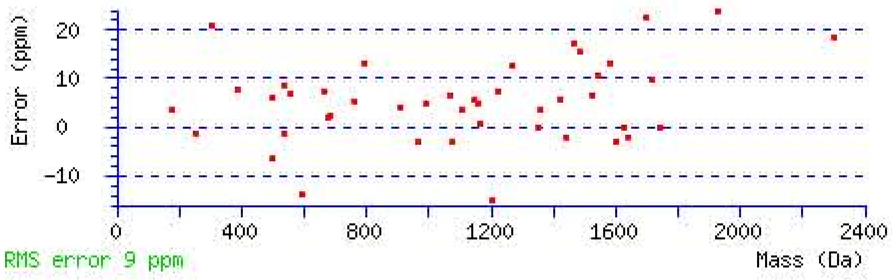
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2706.245621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18 : Biotin:Thermo-21345 (Q)
Ions Score: 90 **Expect:** 1.3e-008
Matches : 44/240 fragment ions using 74 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							22
2	***254.161151***	127.584213	237.134602	119.070939			P	2551.151795	1276.079535	2534.125246	1267.566261	2533.141230	1267.074253	21
3	311.182615	156.094945	294.156066	147.581671			G	2454.099031	1227.553153	2437.072482	1219.039879	2436.088466	1218.547871	20
4	368.204079	184.605677	351.177530	176.092403			G	2397.077567	1199.042421	2380.051018	1190.529147	2379.067002	1190.037139	19
5	***497.246672***	249.126974	480.220123	240.613700	479.236107	240.121692	E	2340.056103	1170.531689	2323.029554	1162.018415	2322.045538	1161.526407	18
6	***594.299436***	297.653356	577.272887	289.140082	576.288871	288.648074	P	2211.013510	1106.010393	2193.986961	1097.497118	2193.002945	1097.005110	17
7	***681.331464***	341.169370	664.304915	332.656095	663.320899	332.164087	S	2113.960746	1057.484011	2096.934197	1048.970736	2095.950181	1048.478728	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	2026.928718	1013.967997	2009.902169	1005.454723	2008.918153	1004.962715	15
9	***907.426821***	454.217049	890.400272	445.703774	889.416256	445.211766	E	***1929.875954***	965.441615	1912.849405	956.928341	1911.865389	956.436333	14
10	***964.448285***	482.727781	947.421736	474.214506	946.437720	473.722498	G	1800.833361	900.920319	1783.806812	892.407044	1782.822796	891.915036	13
11	***1065.495964***	**533.251620**	1048.469415	524.738346	1047.485399	524.246337	T	***1743.811897***	872.409587	1726.785348	863.896312	1725.801332	863.404304	12
12	***1166.543643***	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	***1642.764218***	821.885747	1625.737669	813.372473	1624.753653	812.880465	11
13	***1223.565107***	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	***1541.716539***	771.361908	1524.689990	762.848633	1523.705974	762.356625	10
14	***1351.623685***	676.315480	1334.597136	667.802206	1333.613120	667.310198	Q	***1484.695075***	742.851176	1467.668526	734.337901	1466.684510	733.845893	9
15	***1438.655713***	719.831494	1421.629164	711.318220	1420.645148	710.826212	S	***1356.636497***	678.821887	1339.609948	670.308612	1338.625932	669.816604	8
16	***1601.719042***	801.363159	1584.692493	792.849885	1583.708477	792.357876	Y	***1269.604469***	635.305873	1252.577920	626.792598	1251.593904	626.300590	7
17	***1715.761969***	858.384622	1698.735420	849.871348	1697.751404	849.379340	N	***1106.541140***	553.774208	1089.514591	545.260934	1088.530575	544.768926	6
18	2154.987295	**1077.997285**	2137.960746	1069.484011	2136.976730	1068.992003	Q	***992.498213***	496.752745	975.471664	488.239470	974.487648	487.747462	5
19	2318.050624	**1159.528950**	2301.024075	1151.015675	2300.040059	1150.523667	Y	***553.272887***	277.140082	536.246338	268.626807	535.262322	268.134799	4
20	2405.082652	1203.044964	2388.056103	1194.531689	2387.072087	1194.039681	S	***390.209558***	195.608417	373.183009	187.095143	372.198993	186.603135	3
21	2533.141230	1267.074253	2516.114681	1258.560978	2515.130665	1258.068971	Q	***303.177530***	152.092403	286.150981	143.579129			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
90.5	2706.245621	0.007861	RPGGEPSPEGTTGQSYNQYSQR
70.9	2706.245621	0.007861	RPGGEPSPEGTTGQSYNQYSQR
41.1	2706.245621	0.007861	RPGGEPSPEGTTGQSYNQYSQR

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

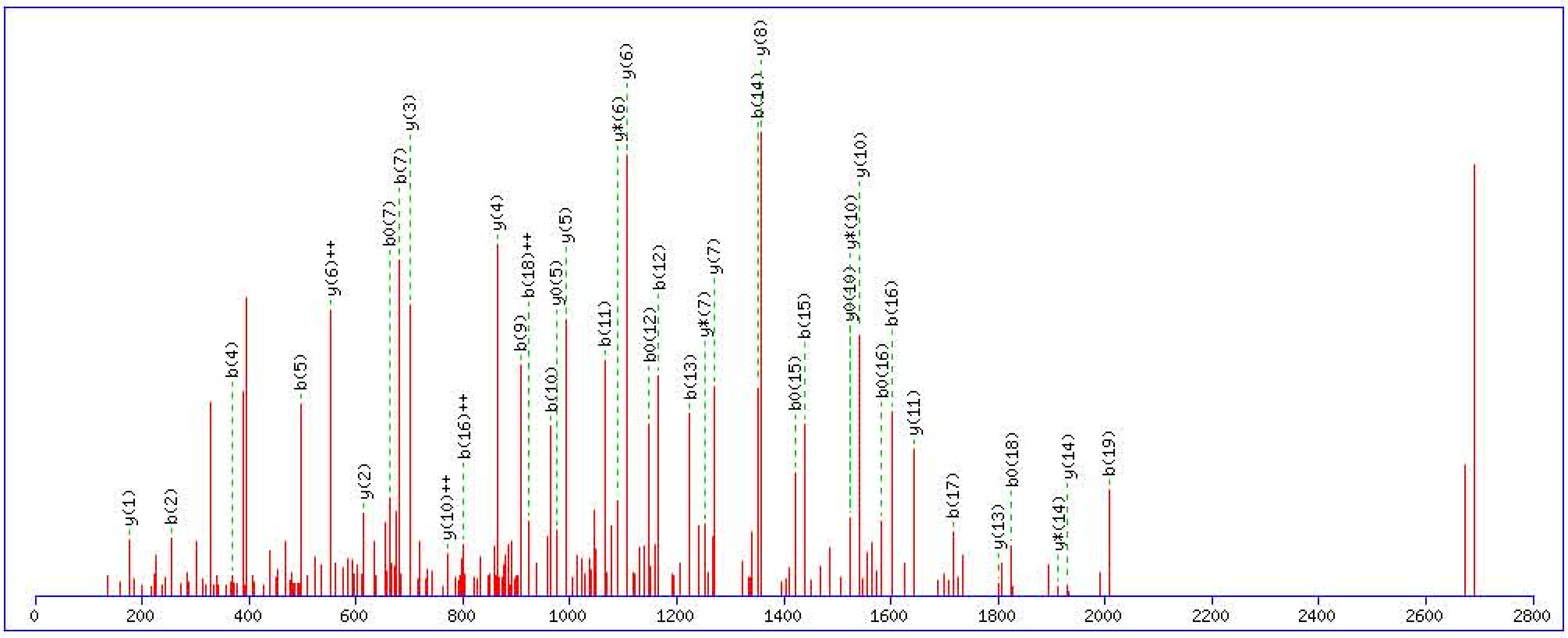
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

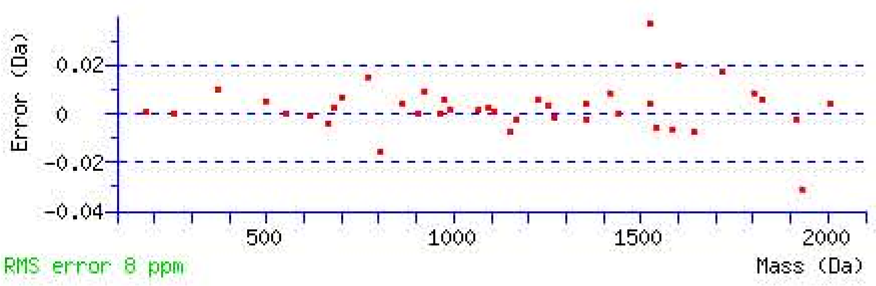
Match to Query 67539: 2706.253482 from(903.091770,3+) rtinseconds(1462) index(38613)
Title: Locus:1.1.1.2792.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

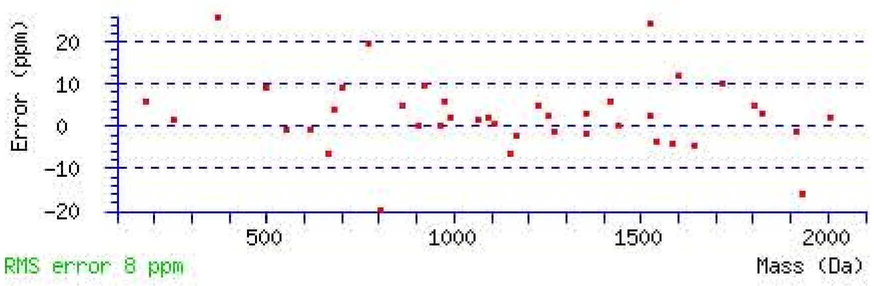
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2706.245621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21    : Biotin:Thermo-21345 (Q)
Ions Score: 114  Expect: 4.8e-011
Matches : 41/240 fragment ions using 58 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							22
2	***254.161151***	127.584213	237.134602	119.070939			P	2551.151795	1276.079535	2534.125246	1267.566261	2533.141230	1267.074253	21
3	311.182615	156.094945	294.156066	147.581671			G	2454.099031	1227.553153	2437.072482	1219.039879	2436.088466	1218.547871	20
4	***368.204079***	184.605677	351.177530	176.092403			G	2397.077567	1199.042421	2380.051018	1190.529147	2379.067002	1190.037139	19
5	***497.246672***	249.126974	480.220123	240.613700	479.236107	240.121692	E	2340.056103	1170.531689	2323.029554	1162.018415	2322.045538	1161.526407	18
6	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	P	2211.013510	1106.010393	2193.986961	1097.497118	2193.002945	1097.005110	17
7	***681.331464***	341.169370	664.304915	332.656095	663.320899	332.164087	S	2113.960746	1057.484011	2096.934197	1048.970736	2095.950181	1048.478728	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	2026.928718	1013.967997	2009.902169	1005.454723	2008.918153	1004.962715	15
9	***907.426821***	454.217049	890.400272	445.703774	889.416256	445.211766	E	***1929.875954***	965.441615	1912.849405	956.928341	1911.865389	956.436333	14
10	***964.448285***	482.727781	947.421736	474.214506	946.437720	473.722498	G	***1800.833361***	900.920319	1783.806812	892.407044	1782.822796	891.915036	13
11	***1065.495964***	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	1743.811897	872.409587	1726.785348	863.896312	1725.801332	863.404304	12
12	***1166.543643***	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	***1642.764218***	821.885747	1625.737669	813.372473	1624.753653	812.880465	11
13	***1223.565107***	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	***1541.716539***	771.361908	1524.689990	762.848633	1523.705974	762.356625	10
14	***1351.623685***	676.315480	1334.597136	667.802206	1333.613120	667.310198	Q	1484.695075	742.851176	1467.668526	734.337901	1466.684510	733.845893	9
15	***1438.655713***	719.831494	1421.629164	711.318220	1420.645148	710.826212	S	***1356.636497***	678.821887	1339.609948	670.308612	1338.625932	669.816604	8
16	***1601.719042***	**801.363159**	1584.692493	792.849885	1583.708477	792.357876	Y	***1269.604469***	635.305873	1252.577920	626.792598	1251.593904	626.300590	7
17	***1715.761969***	858.384622	1698.735420	849.871348	1697.751404	849.379340	N	***1106.541140***	553.774208	1089.514591	545.260934	1088.530575	544.768926	6
18	1843.820547	**922.413912**	1826.793998	913.900637	1825.809982	913.408629	Q	***992.498213***	496.752745	975.471664	488.239470	974.487648	487.747462	5
19	***2006.883876***	1003.945576	1989.857327	995.432302	1988.873311	994.940294	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
20	2093.915904	1047.461590	2076.889355	1038.948315	2075.905339	1038.456307	S	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
21	2533.141230	1267.074253	2516.114681	1258.560978	2515.130665	1258.068971	Q	***614.344278***	307.675777	597.317729	299.162503			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
114.1	2706.245621	0.007861	RPGGEPSPEGTTGQSYNQYSQR
102.4	2706.245621	0.007861	RPGGEPSPEGTTGQSYNQYSQR
49.4	2706.245621	0.007861	RPGGEPSPEGTTGQSYNQYSQR
4.0	2706.262695	-0.009213	ALRQLKPGQNSCRDSDSESASGESK

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

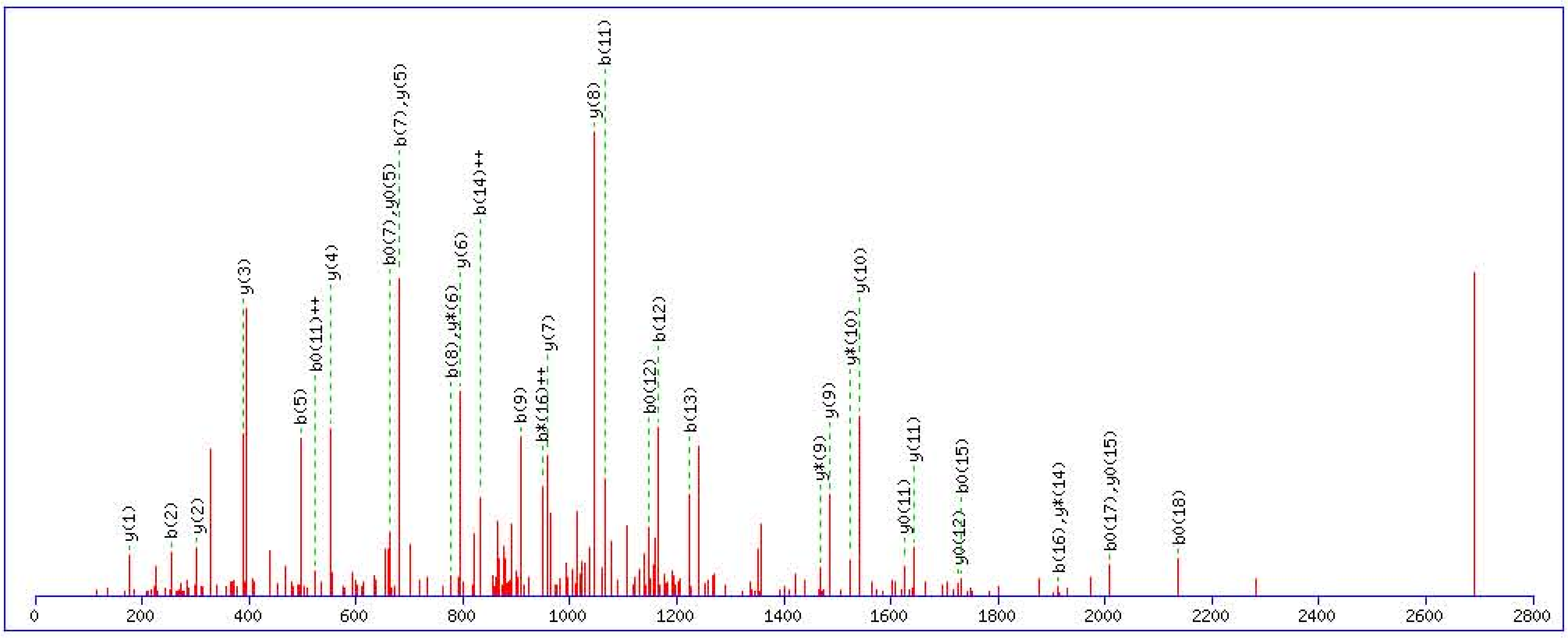
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

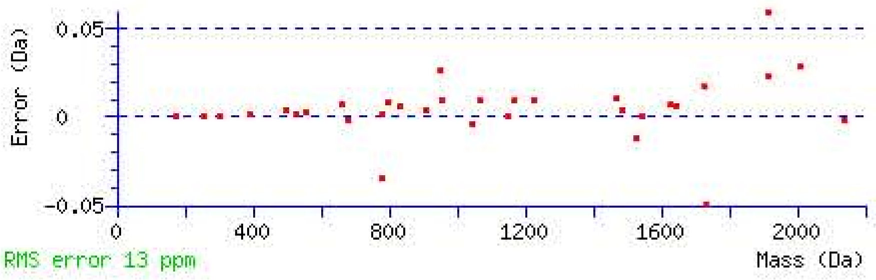
Match to Query 67541: 2706.259092 from(903.093640,3+) rtinseconds(1470) index(38665)
Title: Locus:1.1.1.2795.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

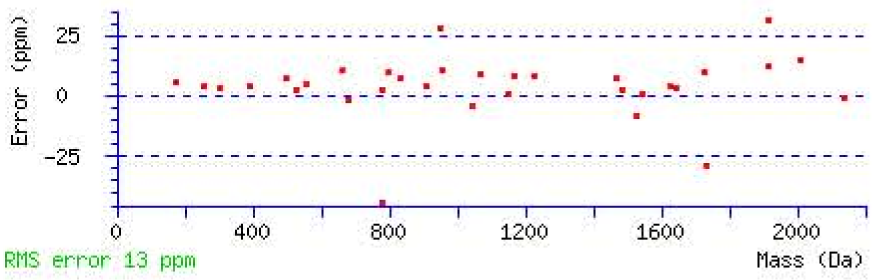
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2706.245621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 88 **Expect:** 8e-009
Matches : 36/240 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							22
2	***254.161151***	127.584213	237.134602	119.070939			P	2551.151795	1276.079535	2534.125246	1267.566261	2533.141230	1267.074253	21
3	311.182615	156.094945	294.156066	147.581671			G	2454.099031	1227.553153	2437.072482	1219.039879	2436.088466	1218.547871	20
4	368.204079	184.605677	351.177530	176.092403			G	2397.077567	1199.042421	2380.051018	1190.529147	2379.067002	1190.037139	19
5	***497.246672***	249.126974	480.220123	240.613700	479.236107	240.121692	E	2340.056103	1170.531689	2323.029554	1162.018415	2322.045538	1161.526407	18
6	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	P	2211.013510	1106.010393	2193.986961	1097.497118	2193.002945	1097.005110	17
7	***681.331464***	341.169370	664.304915	332.656095	663.320899	332.164087	S	2113.960746	1057.484011	2096.934197	1048.970736	2095.950181	1048.478728	16
8	***778.384228***	389.695752	761.357679	381.182478	760.373663	380.690470	P	2026.928718	1013.967997	2009.902169	1005.454723	2008.918153	1004.962715	15
9	***907.426821***	454.217049	890.400272	445.703774	889.416256	445.211766	E	1929.875954	965.441615	1912.849405	956.928341	1911.865389	956.436333	14
10	964.448285	482.727781	947.421736	474.214506	946.437720	473.722498	G	1800.833361	900.920319	1783.806812	892.407044	1782.822796	891.915036	13
11	***1065.495964***	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	1743.811897	872.409587	1726.785348	863.896312	1725.801332	863.404304	12
12	***1166.543643***	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	***1642.764218***	821.885747	1625.737669	813.372473	1624.753653	812.880465	11
13	***1223.565107***	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	***1541.716539***	771.361908	1524.689990	762.848633	1523.705974	762.356625	10
14	1662.790433	831.898854	1645.763884	823.385580	1644.779868	822.893572	Q	***1484.695075***	742.851176	1467.668526	734.337901	1466.684510	733.845893	9
15	1749.822461	875.414869	1732.795912	866.901594	1731.811896	866.409586	S	***1045.469749***	523.238513	1028.443200	514.725238	1027.459184	514.233230	8
16	***1912.885790***	956.946533	1895.859241	948.433259	1894.875225	947.941251	Y	***958.437721***	479.722499	941.411172	471.209224	940.427156	470.717216	7
17	2026.928717	1013.967997	2009.902168	1005.454722	2008.918152	1004.962714	N	***795.374392***	398.190834	778.347843	389.677560	777.363827	389.185552	6
18	2154.987295	1077.997285	2137.960746	1069.484011	2136.976730	1068.992003	Q	***681.331465***	341.169371	664.304916	332.656096	663.320900	332.164088	5
19	2318.050624	1159.528950	2301.024075	1151.015675	2300.040059	1150.523667	Y	***553.272887***	277.140082	536.246338	268.626807	535.262322	268.134799	4
20	2405.082652	1203.044964	2388.056103	1194.531689	2387.072087	1194.039681	S	***390.209558***	195.608417	373.183009	187.095143	372.198993	186.603135	3
21	2533.141230	1267.074253	2516.114681	1258.560978	2515.130665	1258.068971	Q	***303.177530***	152.092403	286.150981	143.579129			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.3	2706.245621	0.013471	RPGGEPSPEGTTGQSYNQYSQR
71.8	2706.245621	0.013471	RPGGEPSPEGTTGQSYNQYSQR
61.4	2706.245621	0.013471	RPGGEPSPEGTTGQSYNQYSQR
2.0	2706.246658	0.012434	MAQKMSFGFYKYSNMEFVR

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **HRPRPYPPNVGEEIQIGHIPR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

Match to Query 68428: 2772.493416 from(694.130630,4+) rtinseconds(1736) index(40345)
Title: Locus:1.1.1.2888.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2772.475815
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00058
Matches : 31/200 fragment ions using 70 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	138.066188	69.536732					H							21
2	***294.167299***	147.587288	277.140750	139.074013			R	2636.424208	1318.715742	2619.397659	1310.202467	2618.413643	1309.710459	20
3	391.220063	196.113670	374.193514	187.600395			P	2480.323097	1240.665186	2463.296548	1232.151912	2462.312532	1231.659904	19
4	***547.321174***	274.164225	530.294625	265.650951			R	2383.270333	1192.138804	2366.243784	1183.625530	2365.259768	1183.133522	18
5	644.373938	322.690607	627.347389	314.177333			P	2227.169222	1114.088249	2210.142673	1105.574974	2209.158657	1105.082966	17
6	***807.437267***	404.222272	790.410718	395.708997			Y	2130.116458	1065.561867	2113.089909	1057.048592	2112.105893	1056.556584	16
7	904.490031	452.748654	887.463482	444.235379			P	***1967.053129***	984.030203	1950.026580	975.516928	1949.042564	975.024920	15
8	1001.542795	501.275036	984.516246	492.761761			P	1870.000365	935.503821	1852.973816	926.990546	1851.989800	926.498538	14
9	***1115.585722***	558.296499	1098.559173	549.783225			N	1772.947601	886.977439	1755.921052	878.464164	1754.937036	877.972156	13
10	1214.654136	607.830706	1197.627587	599.317432			V	1658.904674	829.955975	1641.878125	821.442701	1640.894109	820.950693	12
11	***1271.675600***	636.341438	1254.649051	627.828164			G	***1559.836260***	780.421768	1542.809711	771.908494	1541.825695	771.416486	11
12	***1400.718193***	700.862735	1383.691644	692.349460	1382.707628	691.857452	E	1502.814796	751.911036	1485.788247	743.397762	1484.804231	742.905754	10
13	***1529.760786***	**765.384031**	1512.734237	756.870757	1511.750221	756.378749	E	1373.772203	687.389740	1356.745654	678.876465	1355.761638	678.384457	9
14	***1642.844850***	821.926063	1625.818301	813.412789	1624.834285	812.920781	I	1244.729610	622.868443	1227.703061	614.355169			8
15	2082.070176	**1041.538726**	2065.043627	1033.025451	2064.059611	1032.533444	Q	***1131.645546***	566.326411	1114.618997	557.813137			7
16	2195.154240	1098.080758	2178.127691	1089.567484	2177.143675	1089.075476	I	***692.420220***	346.713748	675.393671	338.200474			6
17	***2252.175704***	1126.591490	2235.149155	1118.078215	2234.165139	1117.586208	G	***579.336156***	290.171716	562.309607	281.658442			5
18	2389.234616	1195.120946	2372.208067	1186.607671	2371.224051	1186.115664	H	***522.314692***	261.660984	505.288143	253.147710			4
19	2502.318680	1251.662978	2485.292131	1243.149704	2484.308115	1242.657696	I	***385.255780***	193.131528	368.229231	184.618254			3
20	2599.371444	1300.189360	2582.344895	1291.676086	2581.360879	1291.184078	P	***272.171716***	136.589496	255.145167	128.076221			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	2772.475815	0.017601	HRPRPYPPNVGEEIQIGHIPR

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

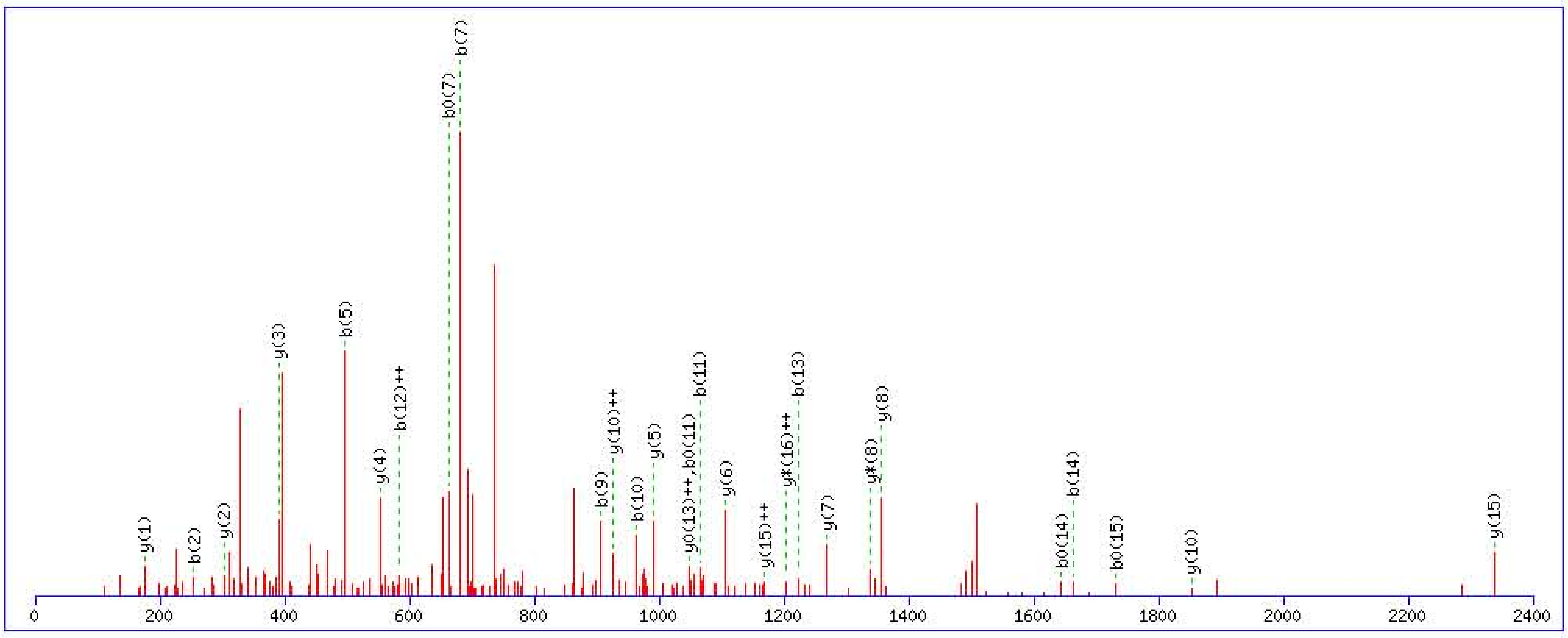
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

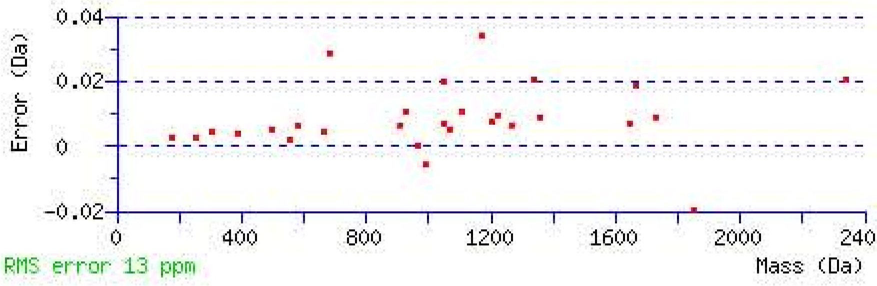
Match to Query 71781: 3017.431816 from(755.365230,4+) rtinseconds(1777) index(40604)
Title: Locus:1.1.1.2902.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

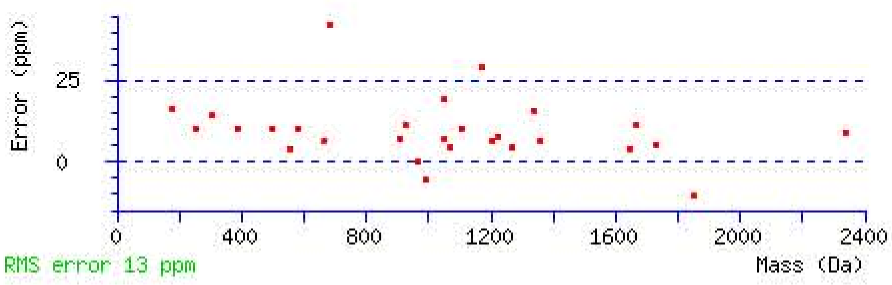
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3017.412369
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 3.1e-005
Matches : 28/240 fragment ions using 54 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							22
2	***254.161151***	127.584213	237.134602	119.070939			P	2862.318543	1431.662909	2845.291994	1423.149635	2844.307978	1422.657627	21
3	311.182615	156.094945	294.156066	147.581671			G	2765.265779	1383.136527	2748.239230	1374.623253	2747.255214	1374.131245	20
4	368.204079	184.605677	351.177530	176.092403			G	2708.244315	1354.625795	2691.217766	1346.112521	2690.233750	1345.620513	19
5	***497.246672***	249.126974	480.220123	240.613700	479.236107	240.121692	E	2651.222851	1326.115063	2634.196302	1317.601789	2633.212286	1317.109781	18
6	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	P	2522.180258	1261.593767	2505.153709	1253.080492	2504.169693	1252.588484	17
7	***681.331464***	341.169370	664.304915	332.656095	663.320899	332.164087	S	2425.127494	1213.067385	2408.100945	1204.554110	2407.116929	1204.062102	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	***2338.095466***	1169.551371	2321.068917	1161.038096	2320.084901	1160.546088	15
9	***907.426821***	454.217049	890.400272	445.703774	889.416256	445.211766	E	2241.042702	1121.024989	2224.016153	1112.511714	2223.032137	1112.019706	14
10	***964.448285***	482.727781	947.421736	474.214506	946.437720	473.722498	G	2112.000109	1056.503692	2094.973560	1047.990418	2093.989544	1047.498410	13
11	***1065.495964***	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	2054.978645	1027.992960	2037.952096	1019.479686	2036.968080	1018.987678	12
12	1166.543643	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	1953.930966	977.469121	1936.904417	968.955847	1935.920401	968.463839	11
13	***1223.565107***	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	***1852.883287***	926.945282	1835.856738	918.432007	1834.872722	917.939999	10
14	***1662.790433***	831.898854	1645.763884	823.385580	1644.779868	822.893572	Q	1795.861823	898.434550	1778.835274	889.921275	1777.851258	889.429267	9
15	1749.822461	875.414869	1732.795912	866.901594	1731.811896	866.409586	S	***1356.636497***	678.821887	1339.609948	670.308612	1338.625932	669.816604	8
16	1912.885790	956.946533	1895.859241	948.433259	1894.875225	947.941251	Y	***1269.604469***	635.305873	1252.577920	626.792598	1251.593904	626.300590	7
17	2026.928717	1013.967997	2009.902168	1005.454722	2008.918152	1004.962714	N	***1106.541140***	553.774208	1089.514591	545.260934	1088.530575	544.768926	6
18	2466.154043	1233.580659	2449.127494	1225.067385	2448.143478	1224.575377	Q	***992.498213***	496.752745	975.471664	488.239470	974.487648	487.747462	5
19	2629.217372	1315.112324	2612.190823	1306.599049	2611.206807	1306.107041	Y	***553.272887***	277.140082	536.246338	268.626807	535.262322	268.134799	4
20	2716.249400	1358.628338	2699.222851	1350.115063	2698.238835	1349.623056	S	***390.209558***	195.608417	373.183009	187.095143	372.198993	186.603135	3
21	2844.307978	1422.657627	2827.281429	1414.144353	2826.297413	1413.652345	Q	***303.177530***	152.092403	286.150981	143.579129			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.2	3017.412369	0.019447	RPGGEPSPEGTTGQSYNQYSQR
47.0	3017.412369	0.019447	RPGGEPSPEGTTGQSYNQYSQR
26.6	3017.412369	0.019447	RPGGEPSPEGTTGQSYNQYSQR

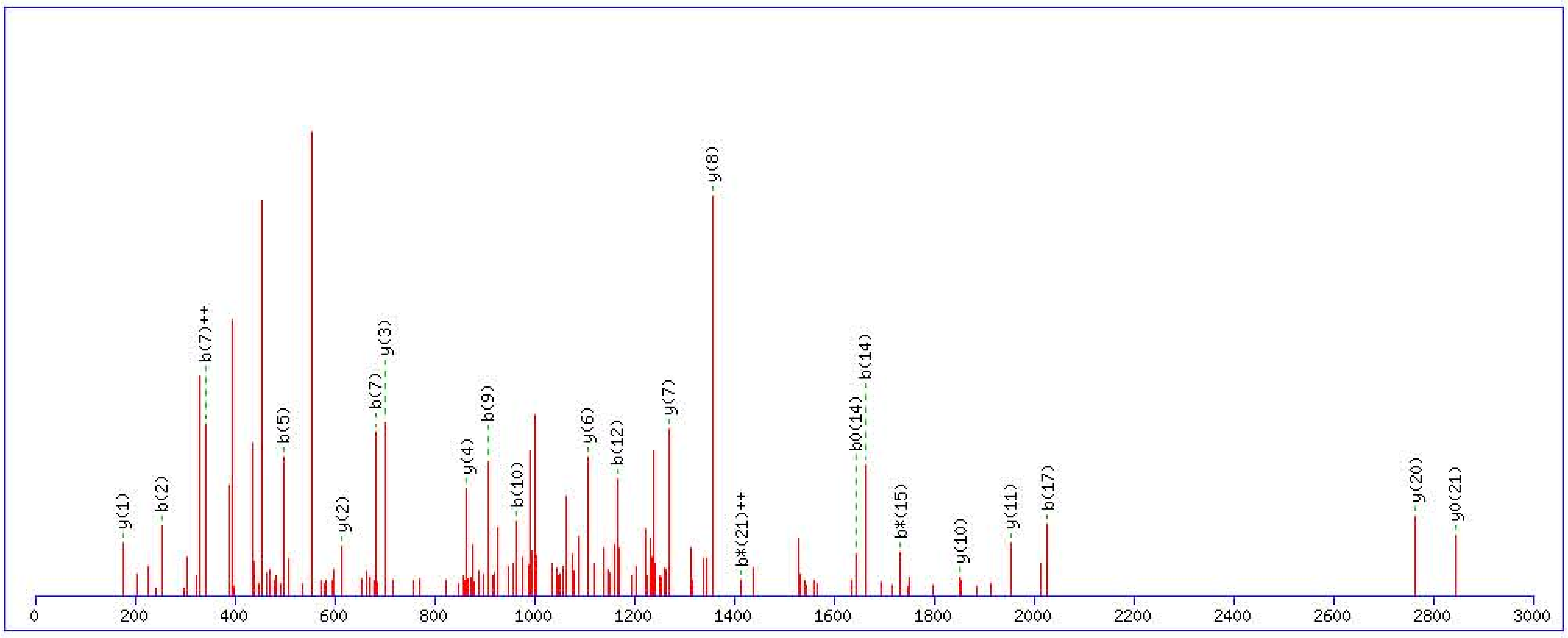
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

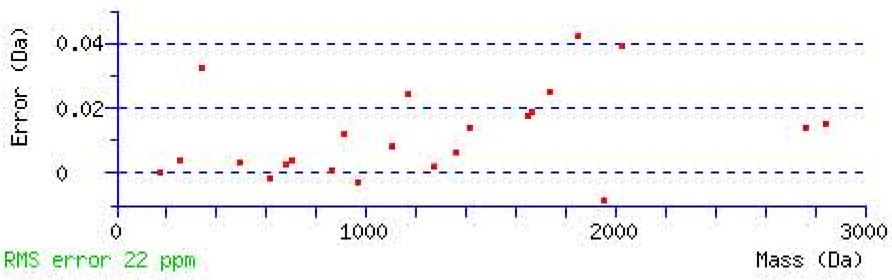
Match to Query 71782: 3017.439852 from(1006.820560,3+) rtinseconds(1779) index(40621)
Title: Locus:1.1.1.2903.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

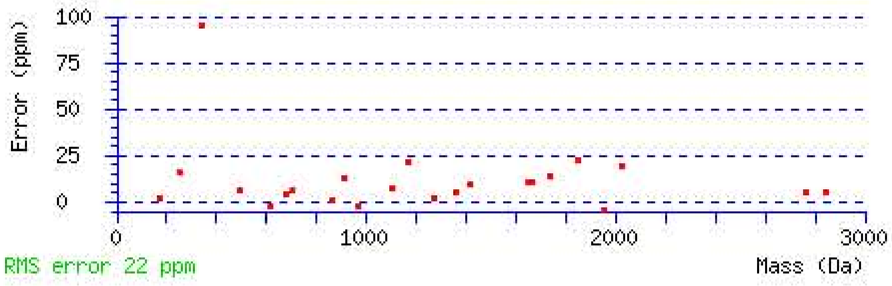
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3017.412369
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 1.1e-005
Matches : 24/240 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							22
2	***254.161151***	127.584213	237.134602	119.070939			P	2862.318543	1431.662909	2845.291994	1423.149635	2844.307978	1422.657627	21
3	311.182615	156.094945	294.156066	147.581671			G	***2765.265779***	1383.136527	2748.239230	1374.623253	2747.255214	1374.131245	20
4	368.204079	184.605677	351.177530	176.092403			G	2708.244315	1354.625795	2691.217766	1346.112521	2690.233750	1345.620513	19
5	***497.246672***	249.126974	480.220123	240.613700	479.236107	240.121692	E	2651.222851	1326.115063	2634.196302	1317.601789	2633.212286	1317.109781	18
6	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	P	2522.180258	1261.593767	2505.153709	1253.080492	2504.169693	1252.588484	17
7	***681.331464***	341.169370	664.304915	332.656095	663.320899	332.164087	S	2425.127494	1213.067385	2408.100945	1204.554110	2407.116929	1204.062102	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	2338.095466	1169.551371	2321.068917	1161.038096	2320.084901	1160.546088	15
9	***907.426821***	454.217049	890.400272	445.703774	889.416256	445.211766	E	2241.042702	1121.024989	2224.016153	1112.511714	2223.032137	1112.019706	14
10	***964.448285***	482.727781	947.421736	474.214506	946.437720	473.722498	G	2112.000109	1056.503692	2094.973560	1047.990418	2093.989544	1047.498410	13
11	1065.495964	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	2054.978645	1027.992960	2037.952096	1019.479686	2036.968080	1018.987678	12
12	***1166.543643***	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	***1953.930966***	977.469121	1936.904417	968.955847	1935.920401	968.463839	11
13	1223.565107	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	***1852.883287***	926.945282	1835.856738	918.432007	1834.872722	917.939999	10
14	***1662.790433***	831.898854	1645.763884	823.385580	1644.779868	822.893572	Q	1795.861823	898.434550	1778.835274	889.921275	1777.851258	889.429267	9
15	1749.822461	875.414869	1732.795912	866.901594	1731.811896	866.409586	S	***1356.636497***	678.821887	1339.609948	670.308612	1338.625932	669.816604	8
16	1912.885790	956.946533	1895.859241	948.433259	1894.875225	947.941251	Y	***1269.604469***	635.305873	1252.577920	626.792598	1251.593904	626.300590	7
17	***2026.928717***	1013.967997	2009.902168	1005.454722	2008.918152	1004.962714	N	***1106.541140***	553.774208	1089.514591	545.260934	1088.530575	544.768926	6
18	2154.987295	1077.997285	2137.960746	1069.484011	2136.976730	1068.992003	Q	992.498213	496.752745	975.471664	488.239470	974.487648	487.747462	5
19	2318.050624	1159.528950	2301.024075	1151.015675	2300.040059	1150.523667	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
20	2405.082652	1203.044964	2388.056103	1194.531689	2387.072087	1194.039681	S	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
21	***2844.307978***	1422.657627	2827.281429	1414.144353	2826.297413	1413.652345	Q	***614.344278***	307.675777	597.317729	299.162503			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.7	3017.412369	0.027483	RPGGEPSPEGTTGQSYNQYSQR
48.4	3017.412369	0.027483	RPGGEPSPEGTTGQSYNQYSQR
30.9	3017.412369	0.027483	RPGGEPSPEGTTGQSYNQYSQR

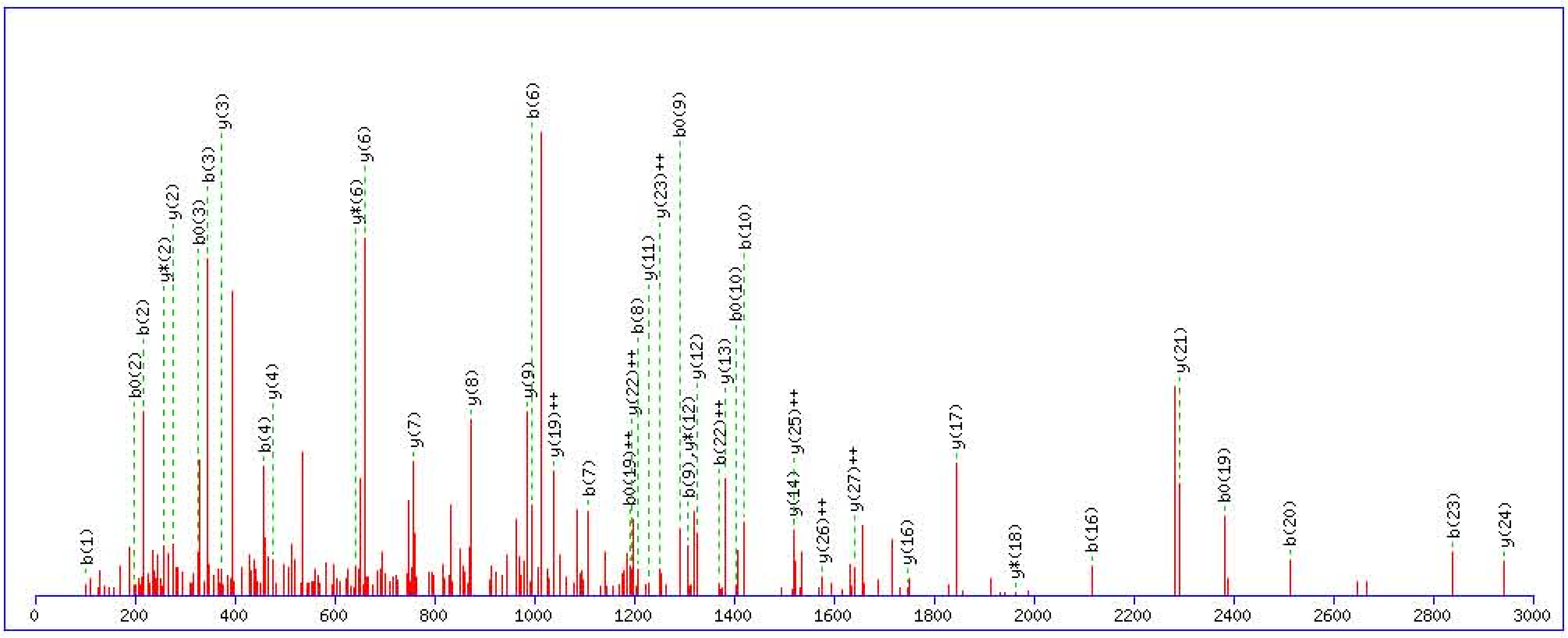
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDELPQLVTLPHPNLHGPEILDVPSTVQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

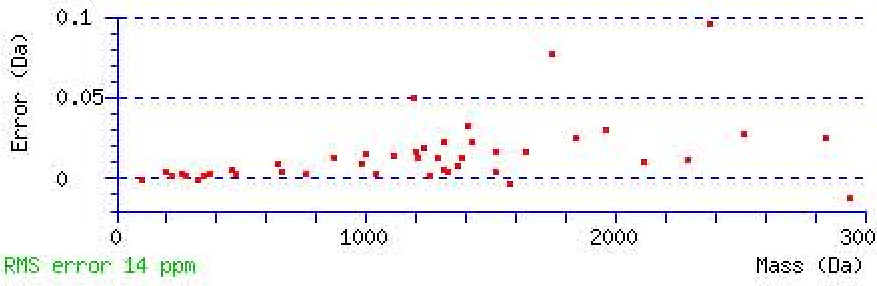
Match to Query 77879: 3497.906736 from(875.483960,4+) rtinseconds(2569) index(45668)
Title: Locus:1.1.1.3178.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

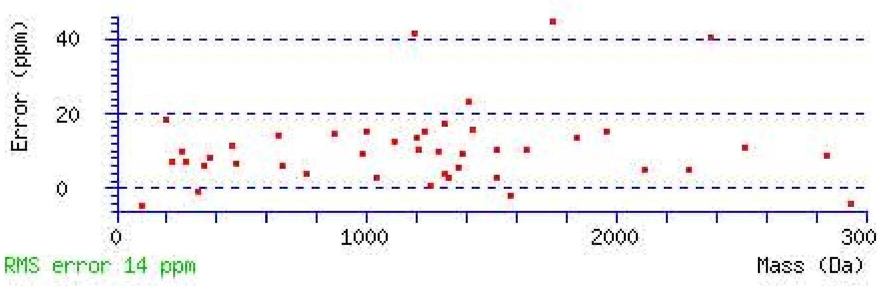
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3497.859238
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 6.4e-006
Matches : 44/320 fragment ions using 121 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							29
2	***217.081898***	109.044587			199.071333	100.039304	D	3397.818827	1699.413051	3380.792278	1690.899777	3379.808262	1690.407769	28
3	***346.124491***	173.565883			328.113926	164.560601	E	3282.791884	1641.899580	3265.765335	1633.386305	3264.781319	1632.894297	27
4	***459.208555***	230.107915			441.197990	221.102633	L	3153.749291	1577.378283	3136.722742	1568.865009	3135.738726	1568.373001	26
5	556.261319	278.634298			538.250754	269.629015	P	3040.665227	1520.836251	3023.638678	1512.322977	3022.654662	1511.830969	25
6	***995.486645***	498.246961	978.460096	489.733686	977.476080	489.241678	Q	***2943.612463***	1472.309869	2926.585914	1463.796595	2925.601898	1463.304587	24
7	***1108.570709***	554.788993	1091.544160	546.275718	1090.560144	545.783710	L	2504.387137	1252.697206	2487.360588	1244.183932	2486.376572	1243.691924	23
8	***1207.639123***	604.323200	1190.612574	595.809925	1189.628558	595.317917	V	2391.303073	1196.155174	2374.276524	1187.641900	2373.292508	1187.149892	22
9	***1308.686802***	654.847039	1291.660253	646.333765	1290.676237	645.841757	T	***2292.234659***	1146.620967	2275.208110	1138.107693	2274.224094	1137.615685	21
10	***1421.770866***	711.389071	1404.744317	702.875797	1403.760301	702.383789	L	2191.186980	1096.097128	2174.160431	1087.583853	2173.176415	1087.091845	20
11	1518.823630	759.915453	1501.797081	751.402179	1500.813065	750.910171	P	2078.102916	1039.555096	2061.076367	1031.041821	2060.092351	1030.549813	19
12	1655.882542	828.444909	1638.855993	819.931635	1637.871977	819.439627	H	1981.050152	991.028714	1964.023603	982.515440	1963.039587	982.023432	18
13	1752.935306	876.971291	1735.908757	868.458017	1734.924741	867.966009	P	***1843.991240***	922.499258	1826.964691	913.985984	1825.980675	913.493976	17
14	1866.978233	933.992755	1849.951684	925.479480	1848.967668	924.987472	N	***1746.938476***	873.972876	1729.911927	865.459602	1728.927911	864.967594	16
15	1980.062297	990.534787	1963.035748	982.021512	1962.051732	981.529504	L	1632.895549	816.951413	1615.869000	808.438138	1614.884984	807.946130	15
16	***2117.121209***	1059.064242	2100.094660	1050.550968	2099.110644	1050.058960	H	***1519.811485***	760.409381	1502.784936	751.896106	1501.800920	751.404098	14
17	2174.142673	1087.574974	2157.116124	1079.061700	2156.132108	1078.569692	G	***1382.752573***	691.879925	1365.726024	683.366650	1364.742008	682.874642	13
18	2271.195437	1136.101356	2254.168888	1127.588082	2253.184872	1127.096074	P	***1325.731109***	663.369193	1308.704560	654.855918	1307.720544	654.363910	12
19	2400.238030	1200.622653	2383.211481	1192.109378	2382.227465	1191.617370	E	***1228.678345***	614.842811	1211.651796	606.329536	1210.667780	605.837528	11
20	***2513.322094***	1257.164685	2496.295545	1248.651410	2495.311529	1248.159402	I	1099.635752	550.321514	1082.609203	541.808240	1081.625187	541.316231	10
21	2626.406158	1313.706717	2609.379609	1305.193442	2608.395593	1304.701435	L	***986.551688***	493.779482	969.525139	485.266207	968.541123	484.774199	9
22	2741.433101	1371.220188	2724.406552	1362.706914	2723.422536	1362.214906	D	***873.467624***	437.237450	856.441075	428.724175	855.457059	428.232167	8
23	***2840.501515***	1420.754395	2823.474966	1412.241121	2822.490950	1411.749113	V	***758.440681***	379.723978	741.414132	371.210704	740.430116	370.718696	7
24	2937.554279	1469.280777	2920.527730	1460.767503	2919.543714	1460.275495	P	***659.372267***	330.189772	642.345718	321.676497	641.361702	321.184489	6
25	3024.586307	1512.796791	3007.559758	1504.283517	3006.575742	1503.791509	S	562.319503	281.663389	545.292954	273.150115	544.308938	272.658107	5
26	3125.633986	1563.320631	3108.607437	1554.807356	3107.623421	1554.315348	T	***475.287475***	238.147375	458.260926	229.634101	457.276910	229.142093	4
27	3224.702400	1612.854838	3207.675851	1604.341563	3206.691835	1603.849555	V	***374.239796***	187.623536	357.213247	179.110261			3
28	3352.760978	1676.884127	3335.734429	1668.370852	3334.750413	1667.878844	Q	***275.171382***	138.089329	258.144833	129.576055			2
29							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.2	3497.859238	0.047498	TDELPQLVTLPHPNLHGPEILDVPSTVQK

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

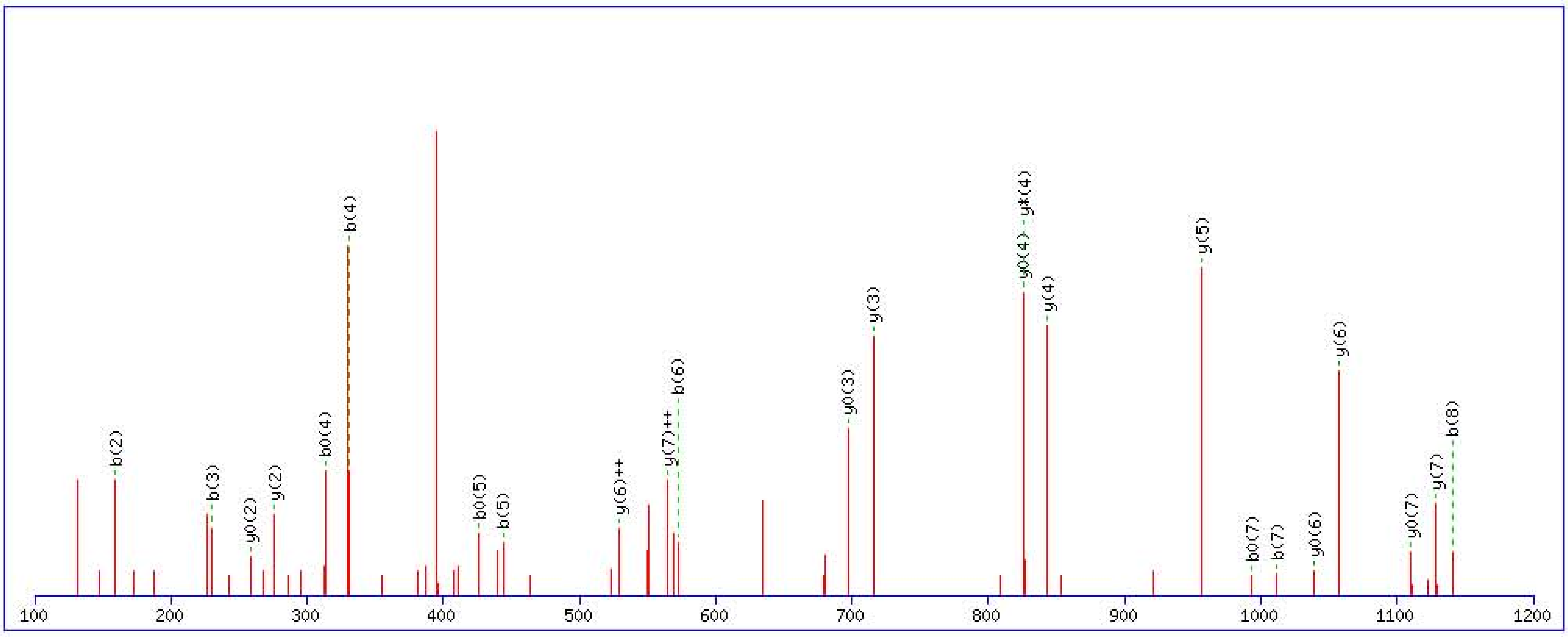
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAATLQQEK**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

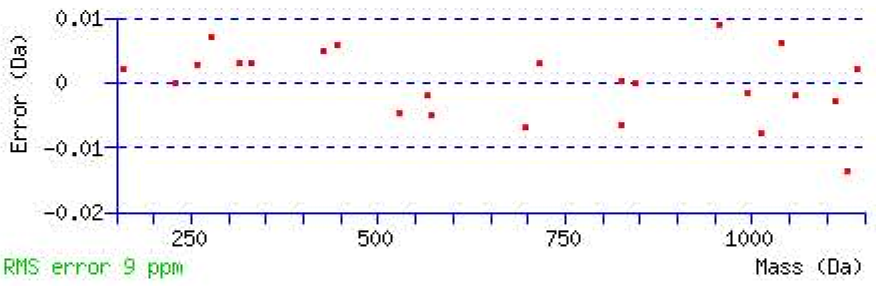
Match to Query 30580: 1285.673088 from(643.843820,2+) rtinseconds(1456) index(38571)
Title: Locus:1.1.1.2790.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

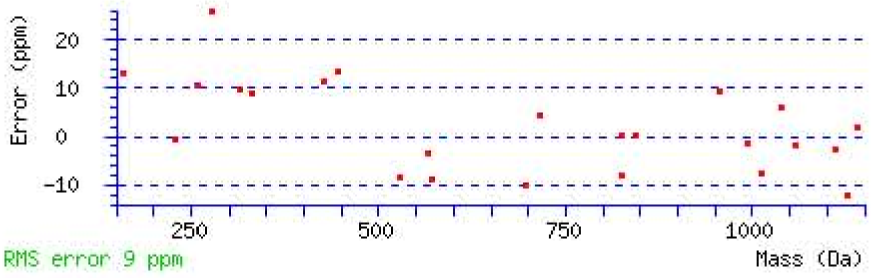
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1285.669998
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00055
Matches : 24/84 fragment ions using 39 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							9
2	***159.076418***	80.041847			141.065853	71.036564	A	1199.645272	600.326274	1182.618723	591.813000	1181.634707	591.320991	8
3	***230.113532***	115.560404			212.102967	106.555121	A	**1128.608158**	564.807717	1111.581609	556.294443	1110.597593	555.802435	7
4	***331.161211***	166.084243			313.150646	157.078961	T	**1057.571044**	529.289160	1040.544495	520.775886	1039.560479	520.283878	6
5	***444.245275***	222.626275			426.234710	213.620993	L	**956.523365**	478.765321	939.496816	470.252046	938.512800	469.760038	5
6	***572.303853***	286.655565	555.277304	278.142290	554.293288	277.650282	Q	**843.439301**	422.223289	826.412752	413.710014	825.428736	413.218006	4
7	***1011.529179***	506.268228	994.502630	497.754953	993.518614	497.262945	Q	**715.380723**	358.194000	698.354174	349.680725	697.370158	349.188717	3
8	***1140.571772***	570.789524	1123.545223	562.276250	1122.561207	561.784242	E	**276.155397**	138.581336	259.128848	130.068062	258.144832	129.576054	2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	1285.669998	0.003090	SAATLQQEK
31.5	1285.669998	0.003090	SAATLQQEK
9.4	1285.669998	0.003090	ASLDQGKEK
8.9	1285.673859	-0.000771	NDVGGQRSLVNK
7.0	1285.688614	-0.015526	SMANQLLAK
4.2	1285.685074	-0.011986	RGVSETAPASRR
2.6	1285.662598	0.010490	EARSDQVKPEK
0.5	1285.685074	-0.011986	TRNLSGEPRTR
0.3	1285.671326	0.001762	MRRLANTAPAW

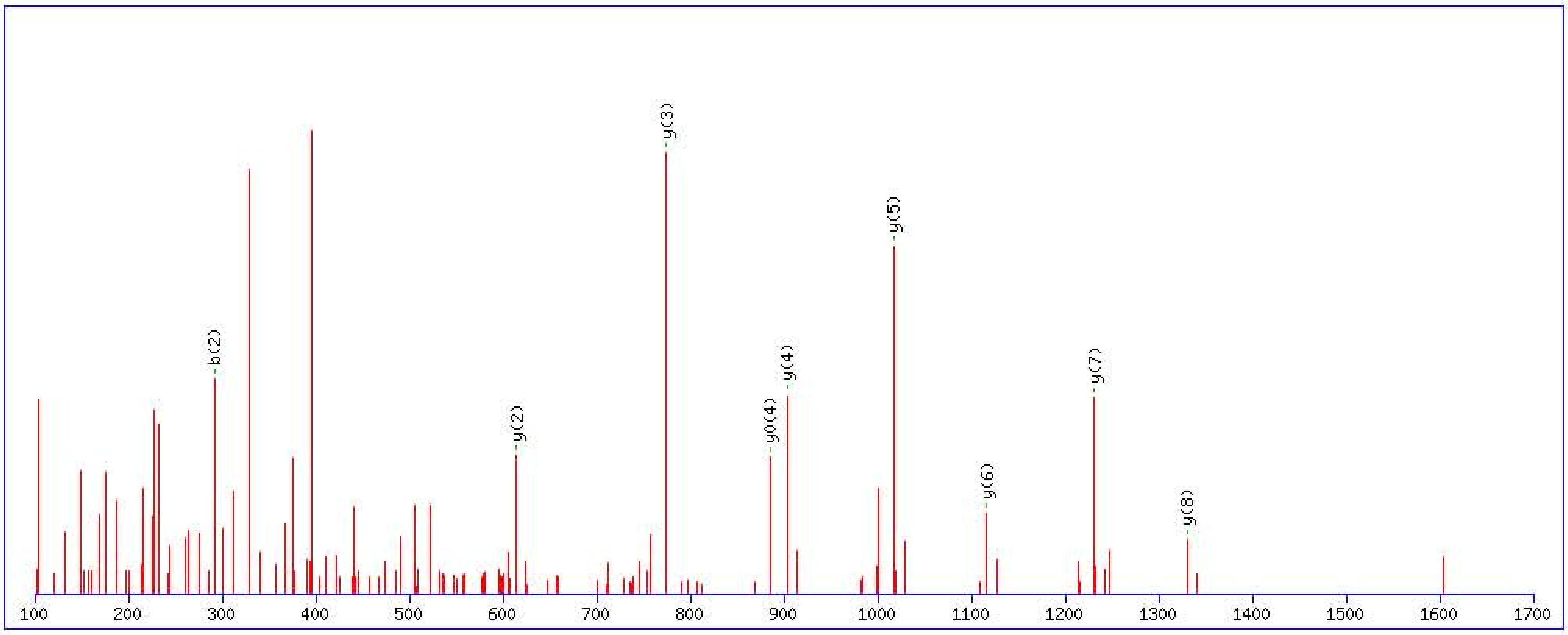
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCVDVNECQR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

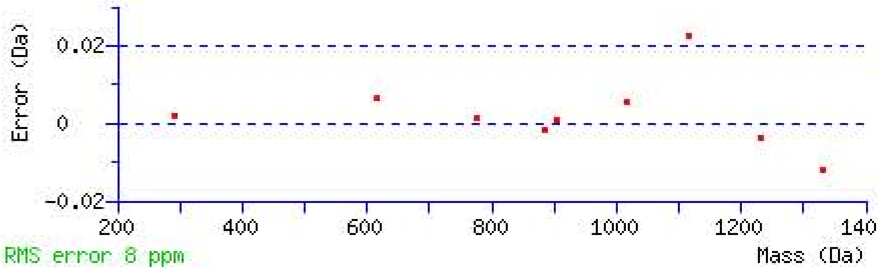
Match to Query 43031: 1620.692052 from(541.237960,3+) rtinseconds(1695) index(40048)
Title: Locus:1.1.1.2874.8 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

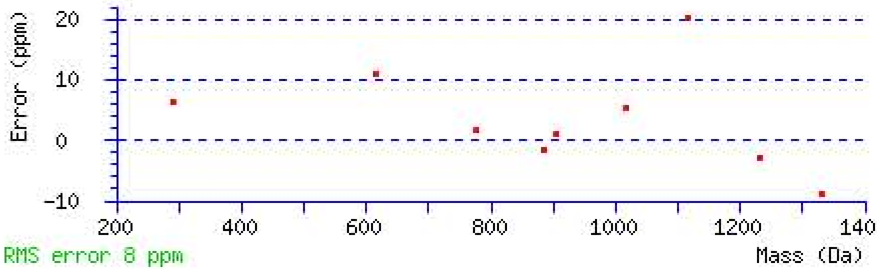
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1620.688080
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 3.8e-005
Matches : 9/86 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							10
2	**292.078410**	146.542843					C	1490.654867	745.831072	1473.628318	737.317797	1472.644302	736.825789	9
3	391.146824	196.077050					V	***1330.624218***	665.815747	1313.597669	657.302473	1312.613653	656.810464	8
4	506.173767	253.590522			488.163202	244.585239	D	***1231.555804***	616.281540	1214.529255	607.768265	1213.545239	607.276257	7
5	605.242181	303.124729			587.231616	294.119446	V	***1116.528861***	558.768069	1099.502312	550.254794	1098.518296	549.762786	6
6	719.285108	360.146192	702.258559	351.632918	701.274543	351.140910	N	***1017.460447***	509.233861	1000.433898	500.720587	999.449882	500.228579	5
7	848.327701	424.667489	831.301152	416.154214	830.317136	415.662206	E	***903.417520***	452.212398	886.390971	443.699123	885.406955	443.207115	4
8	1008.358350	504.682813	991.331801	496.169539	990.347785	495.677531	C	***774.374927***	387.691102	757.348378	379.177827			3
9	1447.583676	724.295476	1430.557127	715.782202	1429.573111	715.290193	Q	***614.344278***	307.675777	597.317729	299.162502			2
10							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.5	1620.688080	0.003972	MCVDVNECQR
2.8	1620.678024	0.014028	QSGRPGCCGGRCGGR

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

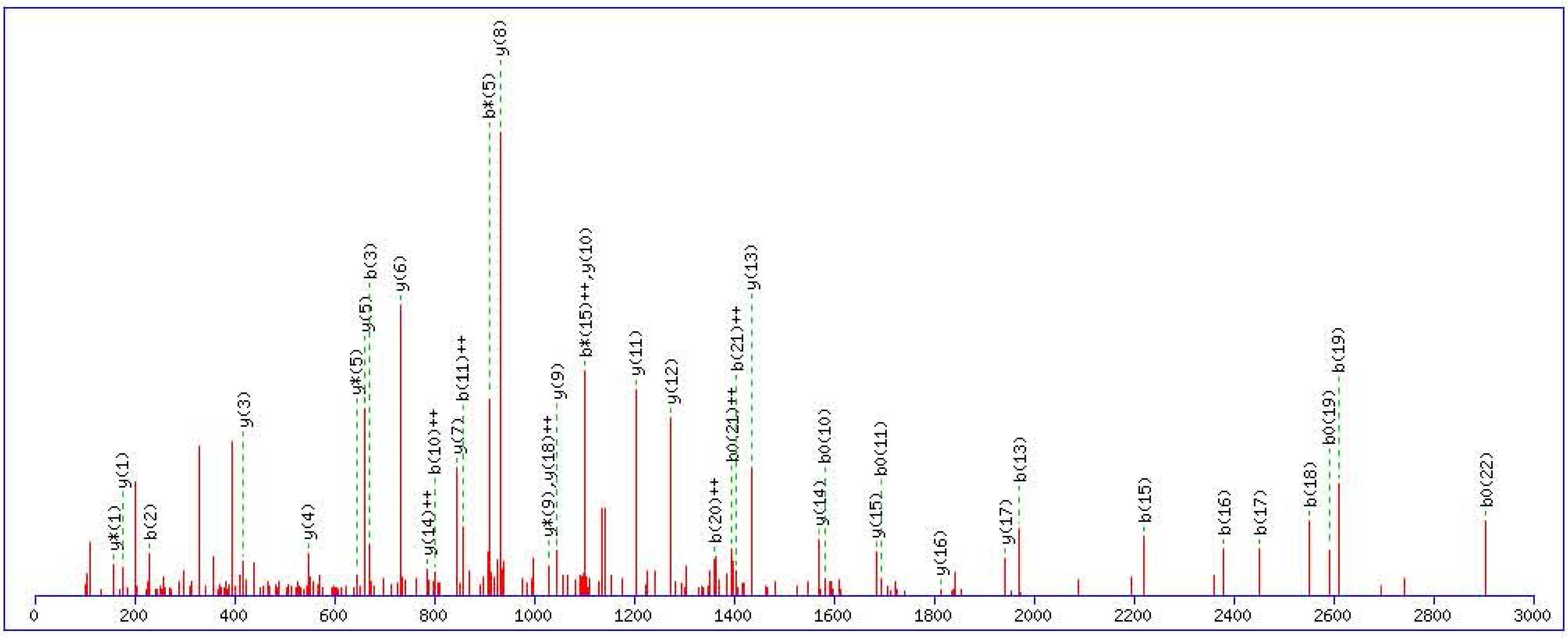
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

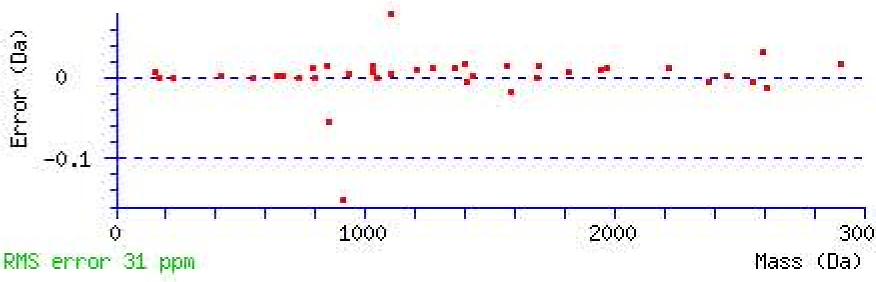
Match to Query 79328: 3653.647016 from(914.419030,4+) rtinseconds(1952) index(41831)
Title: Locus:1.1.1.2963.22 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

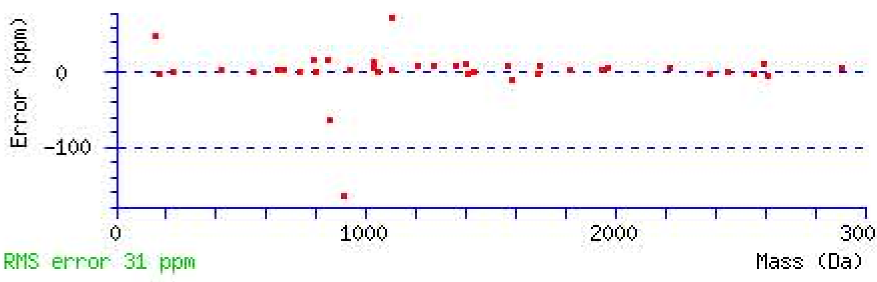
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 84  Expect: 1.8e-008
Matches : 40/312 fragment ions using 70 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							28
2	**231.116175**	116.061725					V	3523.582122	1762.294699	3506.555573	1753.781424	3505.571557	1753.289416	27
3	**670.341501**	335.674389	653.314952	327.161114			Q	3424.513708	1712.760492	3407.487159	1704.247217	3406.503143	1703.755209	26
4	799.384094	400.195685	782.357545	391.682411	781.373529	391.190403	E	2985.288382	1493.147829	2968.261833	1484.634554	2967.277817	1484.142546	25
5	927.442672	464.224974	910.416123	455.711700	909.432107	455.219692	Q	2856.245789	1428.626532	2839.219240	1420.113258	2838.235224	1419.621250	24
6	1087.473321	544.240299	1070.446772	535.727024	1069.462756	535.235016	C	2728.187211	1364.597243	2711.160662	1356.083969	2710.176646	1355.591961	23
7	1247.503970	624.255623	1230.477421	615.742349	1229.493405	615.250341	C	2568.156562	1284.581919	2551.130013	1276.068644	2550.145997	1275.576636	22
8	1384.562882	692.785079	1367.536333	684.271805	1366.552317	683.779797	H	2408.125913	1204.566594	2391.099364	1196.053320	2390.115348	1195.561312	21
9	1471.594910	736.301093	1454.568361	727.787819	1453.584345	727.295811	S	2271.067001	1136.037138	2254.040452	1127.523864	2253.056436	1127.031856	20
10	1599.653488	**800.330382**	1582.626939	791.817108	1581.642923	791.325100	Q	2184.034973	1092.521124	2167.008424	1084.007850	2166.024408	1083.515842	19
11	1712.737552	**856.872414**	1695.711003	848.359140	1694.726987	847.867132	L	2055.976395	1028.491835	2038.949846	1019.978561	2037.965830	1019.486553	18
12	1841.780145	921.393711	1824.753596	912.880436	1823.769580	912.388428	E	***1942.892331***	971.949804	1925.865782	963.436529	1924.881766	962.944521	17
13	**1970.822738**	985.915007	1953.796189	977.401733	1952.812173	976.909725	E	***1813.849738***	907.428507	1796.823189	898.915233	1795.839173	898.423225	16
14	2083.906802	1042.457039	2066.880253	1033.943764	2065.896237	1033.451756	L	***1684.807145***	842.907211	1667.780596	834.393936	1666.796580	833.901928	15
15	**2220.965714**	1110.986495	2203.939165	1102.473220	2202.955149	1101.981212	H	***1571.723081***	786.365179	1554.696532	777.851904	1553.712516	777.359896	14
16	**2380.996363**	1191.001819	2363.969814	1182.488545	2362.985798	1181.996537	C	***1434.664169***	717.835723	1417.637620	709.322448	1416.653604	708.830440	13
17	**2452.033477**	1226.520376	2435.006928	1218.007102	2434.022912	1217.515094	A	***1274.633520***	637.820398	1257.606971	629.307124	1256.622955	628.815116	12
18	**2553.081156**	1277.044216	2536.054607	1268.530941	2535.070591	1268.038933	T	***1203.596406***	602.301841	1186.569857	593.788567	1185.585841	593.296559	11
19	**2610.102620**	1305.554948	2593.076071	1297.041673	2592.092055	1296.549665	G	***1102.548727***	551.778002	1085.522178	543.264727	1084.538162	542.772719	10
20	2723.186684	**1362.096980**	2706.160135	1353.583705	2705.176119	1353.091697	I	***1045.527263***	523.267270	1028.500714	514.753995	1027.516698	514.261987	9
21	2810.218712	**1405.612994**	2793.192163	1397.099719	2792.208147	1396.607711	S	***932.443199***	466.725238	915.416650	458.211963	914.432634	457.719955	8
22	2923.302776	1462.155026	2906.276227	1453.641751	2905.292211	1453.149743	L	***845.411171***	423.209224	828.384622	414.695949	827.400606	414.203941	7
23	2994.339890	1497.673583	2977.313341	1489.160308	2976.329325	1488.668301	A	***732.327107***	366.667192	715.300558	358.153917	714.316542	357.661909	6
24	3108.382817	1554.695047	3091.356268	1546.181772	3090.372252	1545.689764	N	***661.289993***	331.148635	644.263444	322.635360	643.279428	322.143352	5
25	3237.425410	1619.216343	3220.398861	1610.703069	3219.414845	1610.211061	E	***547.247066***	274.127171	530.220517	265.613897	529.236501	265.121889	4
26	3365.483988	1683.245632	3348.457439	1674.732358	3347.473423	1674.240350	Q	***418.204473***	209.605874	401.177924	201.092600	400.193908	200.600592	3
27	3480.510931	1740.759104	3463.484382	1732.245829	3462.500366	1731.753821	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
28							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.0	3653.615311	0.031705	MVQEQCCHSQLEELHCATGISLANEQDR
84.0	3653.615311	0.031705	MVQEQCCHSQLEELHCATGISLANEQDR
83.9	3653.615311	0.031705	MVQEQCCHSQLEELHCATGISLANEQDR
1.4	3653.684525	-0.037509	FTDRETEAAAGTLAHMGFAPPTSFSHFTDQELR

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

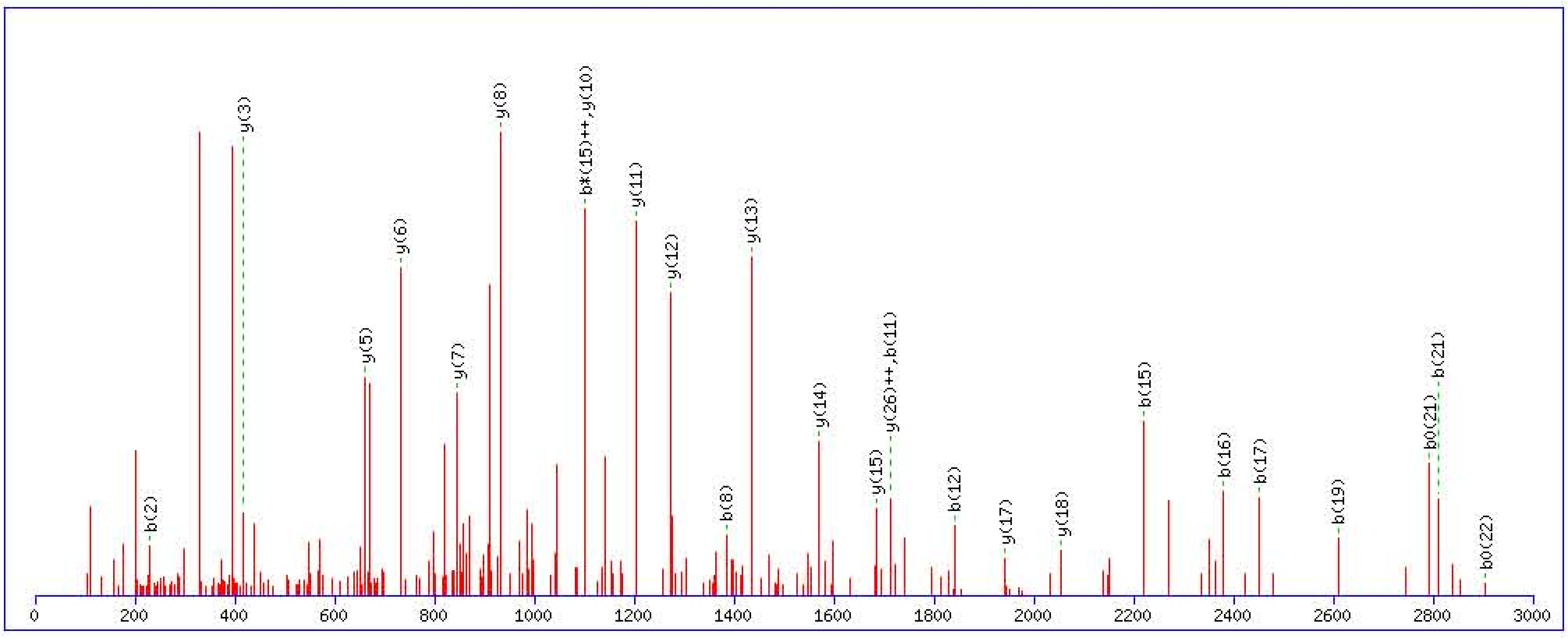
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

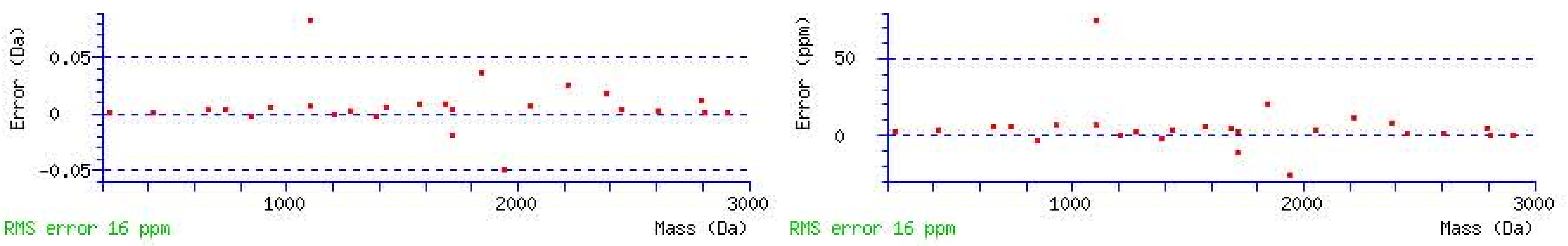
Match to Query 79329: 3653.647016 from(914.419030,4+) rtinseconds(1961) index(41905)
Title: Locus:1.1.1.2966.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 112  Expect: 6.5e-011
Matches : 26/312 fragment ions using 28 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.047761	66.527518					M							28
2	***231.116175***	116.061725					V	3523.582122	1762.294699	3506.555573	1753.781424	3505.571557	1753.289416	27
3	359.174753	180.091015	342.148204	171.577740			Q	3424.513708	1712.760492	3407.487159	1704.247217	3406.503143	1703.755209	26
4	488.217346	244.612311	471.190797	236.099037	470.206781	235.607029	E	3296.455130	1648.731203	3279.428581	1640.217928	3278.444565	1639.725920	25
5	927.442672	464.224974	910.416123	455.711700	909.432107	455.219692	Q	3167.412537	1584.209906	3150.385988	1575.696632	3149.401972	1575.204624	24
6	1087.473321	544.240298	1070.446772	535.727024	1069.462756	535.235016	C	2728.187211	1364.597243	2711.160662	1356.083969	2710.176646	1355.591961	23
7	1247.503970	624.255623	1230.477421	615.742349	1229.493405	615.250340	C	2568.156562	1284.581919	2551.130013	1276.068644	2550.145997	1275.576636	22
8	***1384.562882***	692.785079	1367.536333	684.271805	1366.552317	683.779796	H	2408.125913	1204.566594	2391.099364	1196.053320	2390.115348	1195.561312	21
9	1471.594910	736.301093	1454.568361	727.787819	1453.584345	727.295811	S	2271.067001	1136.037138	2254.040452	1127.523864	2253.056436	1127.031856	20
10	1599.653488	800.330382	1582.626939	791.817108	1581.642923	791.325100	Q	2184.034973	1092.521124	2167.008424	1084.007850	2166.024408	1083.515842	19
11	***1712.737552***	856.872414	1695.711003	848.359140	1694.726987	847.867132	L	***2055.976395***	1028.491835	2038.949846	1019.978561	2037.965830	1019.486553	18
12	***1841.780145***	921.393711	1824.753596	912.880436	1823.769580	912.388428	E	***1942.892331***	971.949804	1925.865782	963.436529	1924.881766	962.944521	17
13	1970.822738	985.915007	1953.796189	977.401733	1952.812173	976.909725	E	1813.849738	907.428507	1796.823189	898.915233	1795.839173	898.423225	16
14	2083.906802	1042.457039	2066.880253	1033.943764	2065.896237	1033.451756	L	***1684.807145***	842.907211	1667.780596	834.393936	1666.796580	833.901928	15
15	***2220.965714***	1110.986495	2203.939165	1102.473220	2202.955149	1101.981212	H	***1571.723081***	786.365179	1554.696532	777.851904	1553.712516	777.359896	14
16	***2380.996363***	1191.001819	2363.969814	1182.488545	2362.985798	1181.996537	C	***1434.664169***	717.835723	1417.637620	709.322448	1416.653604	708.830440	13
17	***2452.033477***	1226.520376	2435.006928	1218.007102	2434.022912	1217.515094	A	***1274.633520***	637.820398	1257.606971	629.307124	1256.622955	628.815116	12
18	2553.081156	1277.044216	2536.054607	1268.530941	2535.070591	1268.038933	T	***1203.596406***	602.301841	1186.569857	593.788567	1185.585841	593.296559	11
19	***2610.102620***	1305.554948	2593.076071	1297.041673	2592.092055	1296.549665	G	***1102.548727***	551.778002	1085.522178	543.264727	1084.538162	542.772719	10
20	2723.186684	1362.096980	2706.160135	1353.583705	2705.176119	1353.091697	I	1045.527263	523.267270	1028.500714	514.753995	1027.516698	514.261987	9
21	***2810.218712***	1405.612994	2793.192163	1397.099719	2792.208147	1396.607711	S	***932.443199***	466.725238	915.416650	458.211963	914.432634	457.719955	8
22	2923.302776	1462.155026	2906.276227	1453.641751	2905.292211	1453.149743	L	***845.411171***	423.209224	828.384622	414.695949	827.400606	414.203941	7
23	2994.339890	1497.673583	2977.313341	1489.160308	2976.329325	1488.668301	A	***732.327107***	366.667192	715.300558	358.153917	714.316542	357.661909	6
24	3108.382817	1554.695047	3091.356268	1546.181772	3090.372252	1545.689764	N	***661.289993***	331.148635	644.263444	322.635360	643.279428	322.143352	5
25	3237.425410	1619.216343	3220.398861	1610.703069	3219.414845	1610.211061	E	547.247066	274.127171	530.220517	265.613897	529.236501	265.121889	4
26	3365.483988	1683.245632	3348.457439	1674.732358	3347.473423	1674.240350	Q	***418.204473***	209.605874	401.177924	201.092600	400.193908	200.600592	3
27	3480.510931	1740.759104	3463.484382	1732.245829	3462.500366	1731.753821	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
28							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
112.0	3653.615311	0.031705	MVQEQCCHSQLEELHCATGISLANEQDR
112.0	3653.615311	0.031705	MVQEQCCHSQLEELHCATGISLANEQDR
100.1	3653.615311	0.031705	MVQEQCCHSQLEELHCATGISLANEQDR

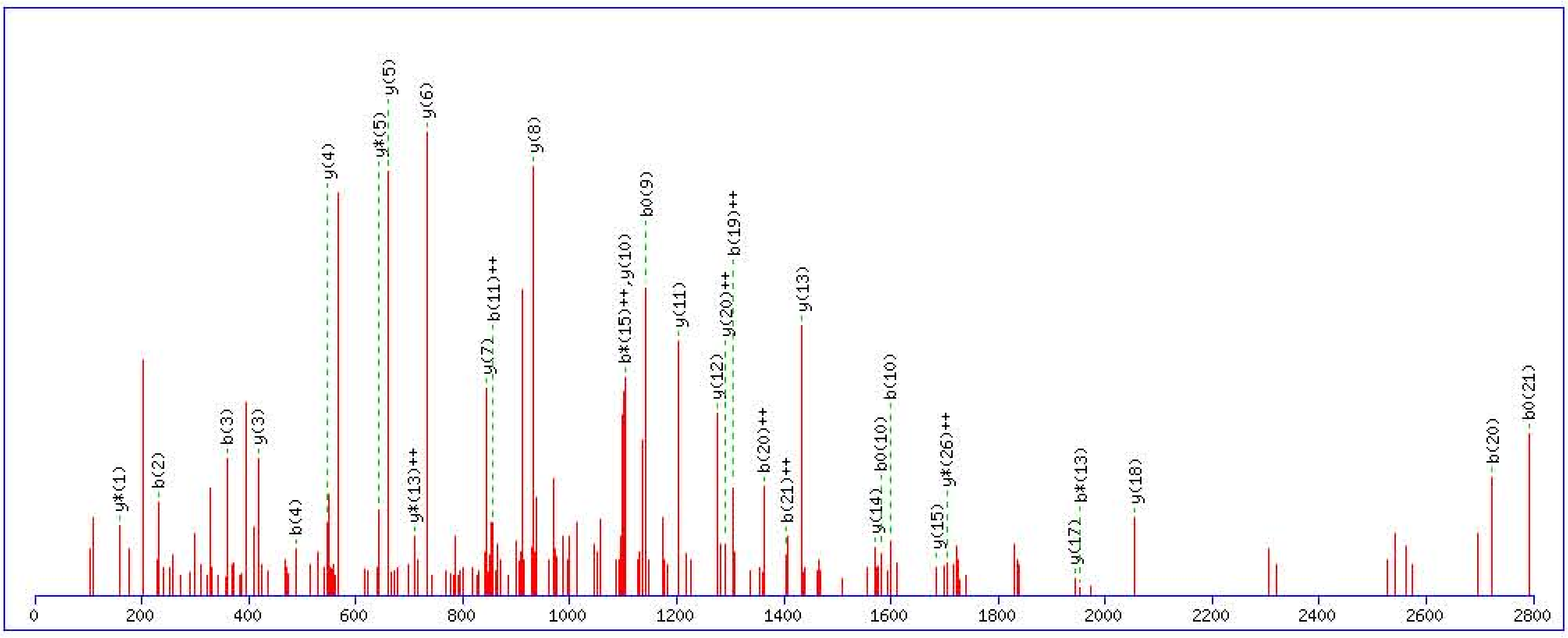
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

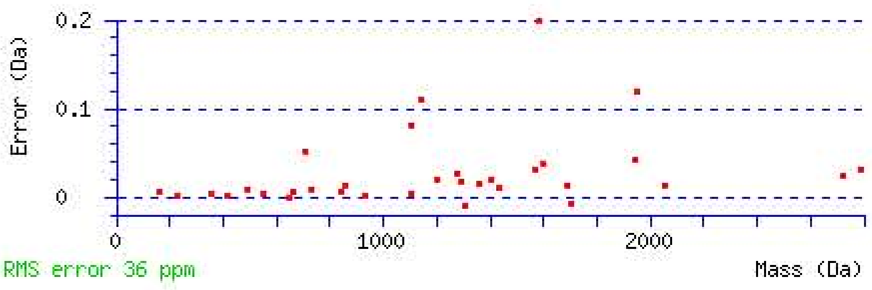
Match to Query 79330: 3653.662736 from(914.422960,4+) rtinseconds(2067) index(42549)
Title: Locus:1.1.1.3003.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

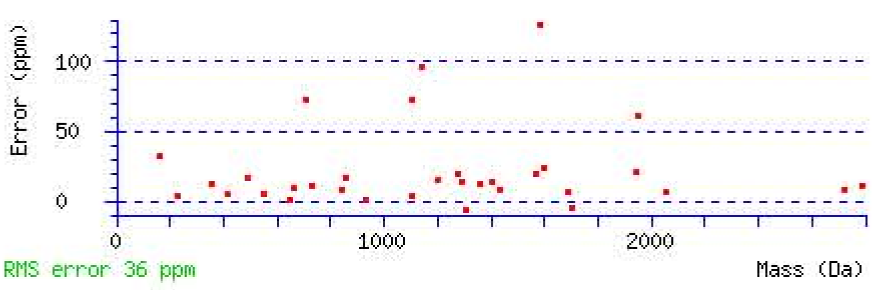
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 1.2e-005
Matches : 33/312 fragment ions using 66 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							28
2	**231.116175**	116.061725					V	3523.582122	1762.294699	3506.555573	1753.781424	3505.571557	1753.289416	27
3	**359.174753**	180.091015	342.148204	171.577740			Q	3424.513708	1712.760492	3407.487159	1704.247217	3406.503143	1703.755209	26
4	**488.217346**	244.612311	471.190797	236.099037	470.206781	235.607029	E	3296.455130	1648.731203	3279.428581	1640.217928	3278.444565	1639.725920	25
5	616.275924	308.641600	599.249375	300.128326	598.265359	299.636318	Q	3167.412537	1584.209906	3150.385988	1575.696632	3149.401972	1575.204624	24
6	776.306573	388.656925	759.280024	380.143650	758.296008	379.651642	C	3039.353959	1520.180617	3022.327410	1511.667343	3021.343394	1511.175335	23
7	936.337222	468.672249	919.310673	460.158975	918.326657	459.666967	C	2879.323310	1440.165293	2862.296761	1431.652018	2861.312745	1431.160010	22
8	1073.396134	537.201705	1056.369585	528.688431	1055.385569	528.196423	H	2719.292661	1360.149968	2702.266112	1351.636694	2701.282096	1351.144686	21
9	1160.428162	580.717719	1143.401613	572.204445	1142.417597	571.712437	S	2582.233749	1291.620512	2565.207200	1283.107238	2564.223184	1282.615230	20
10	**1599.653488**	800.330382	1582.626939	791.817108	1581.642923	791.325100	Q	2495.201721	1248.104498	2478.175172	1239.591224	2477.191156	1239.099216	19
11	1712.737552	**856.872414**	1695.711003	848.359140	1694.726987	847.867132	L	***2055.976395***	1028.491835	2038.949846	1019.978561	2037.965830	1019.486553	18
12	1841.780145	921.393711	1824.753596	912.880436	1823.769580	912.388428	E	***1942.892331***	971.949804	1925.865782	963.436529	1924.881766	962.944521	17
13	1970.822738	985.915007	1953.796189	977.401733	1952.812173	976.909725	E	1813.849738	907.428507	1796.823189	898.915233	1795.839173	898.423225	16
14	2083.906802	1042.457039	2066.880253	1033.943764	2065.896237	1033.451756	L	***1684.807145***	842.907211	1667.780596	834.393936	1666.796580	833.901928	15
15	2220.965714	1110.986495	2203.939165	1102.473220	2202.955149	1101.981212	H	***1571.723081***	786.365179	1554.696532	777.851904	1553.712516	777.359896	14
16	2380.996363	1191.001819	2363.969814	1182.488545	2362.985798	1181.996537	C	***1434.664169***	717.835723	1417.637620	709.322448	1416.653604	708.830440	13
17	2452.033477	1226.520376	2435.006928	1218.007102	2434.022912	1217.515094	A	***1274.633520***	637.820398	1257.606971	629.307124	1256.622955	628.815116	12
18	2553.081156	1277.044216	2536.054607	1268.530941	2535.070591	1268.038933	T	***1203.596406***	602.301841	1186.569857	593.788567	1185.585841	593.296559	11
19	2610.102620	**1305.554948**	2593.076071	1297.041673	2592.092055	1296.549665	G	***1102.548727***	551.778002	1085.522178	543.264727	1084.538162	542.772719	10
20	**2723.186684**	**1362.096980**	2706.160135	1353.583705	2705.176119	1353.091697	I	1045.527263	523.267270	1028.500714	514.753995	1027.516698	514.261987	9
21	2810.218712	**1405.612994**	2793.192163	1397.099719	2792.208147	1396.607711	S	***932.443199***	466.725238	915.416650	458.211963	914.432634	457.719955	8
22	2923.302776	1462.155026	2906.276227	1453.641751	2905.292211	1453.149743	L	***845.411171***	423.209224	828.384622	414.695949	827.400606	414.203941	7
23	2994.339890	1497.673583	2977.313341	1489.160308	2976.329325	1488.668301	A	***732.327107***	366.667192	715.300558	358.153917	714.316542	357.661909	6
24	3108.382817	1554.695047	3091.356268	1546.181772	3090.372252	1545.689764	N	***661.289993***	331.148635	644.263444	322.635360	643.279428	322.143352	5
25	3237.425410	1619.216343	3220.398861	1610.703069	3219.414845	1610.211061	E	***547.247066***	274.127171	530.220517	265.613897	529.236501	265.121889	4
26	3365.483988	1683.245632	3348.457439	1674.732358	3347.473423	1674.240350	Q	***418.204473***	209.605874	401.177924	201.092600	400.193908	200.600592	3
27	3480.510931	1740.759104	3463.484382	1732.245829	3462.500366	1731.753821	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
28							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.7	3653.615311	0.047425	MVQEQCCHSQLEELHCATGISLANEQDR
59.6	3653.615311	0.047425	MVQEQCCHSQLEELHCATGISLANEQDR
56.6	3653.615311	0.047425	MVQEQCCHSQLEELHCATGISLANEQDR

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

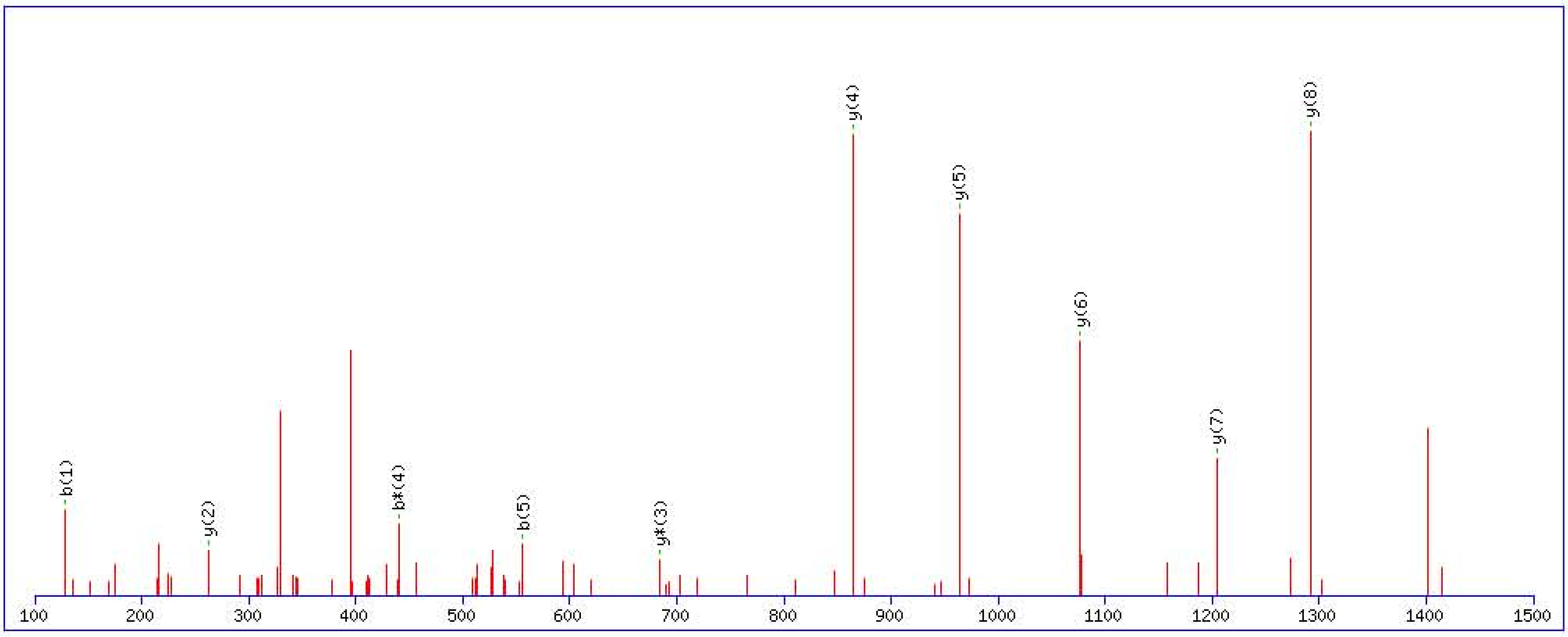
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSQLVYQSR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

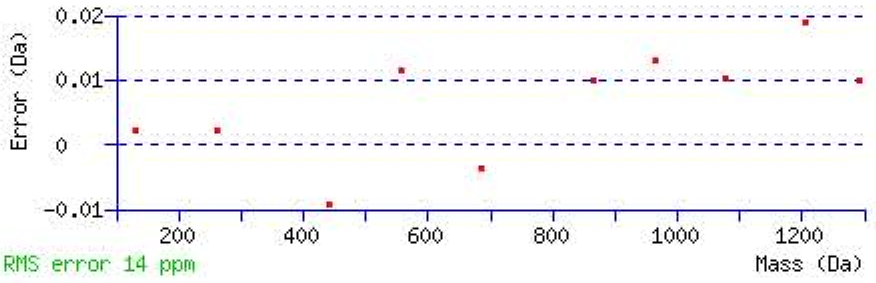
Match to Query 35746: 1418.780188 from(710.397370,2+) rtinseconds(1461) index(56642)
Title: Locus:1.1.1.2814.25 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

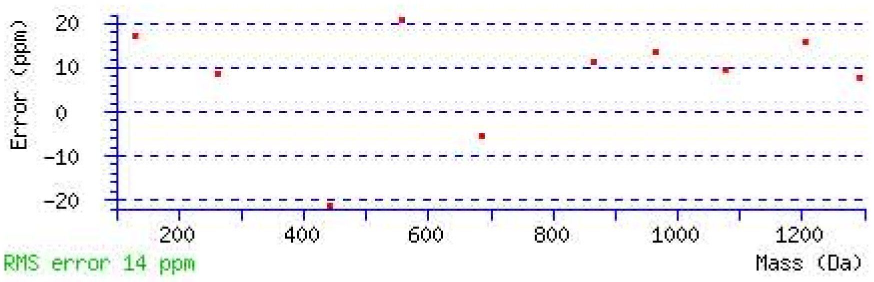
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1418.770386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00012
Matches : 10/92 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.102239**	65.054757	112.075690	56.541483			K							9
2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	S	***1291.682719***	646.344998	1274.656170	637.831723	1273.672154	637.339715	8
3	344.192845	172.600060	327.166296	164.086786	326.182280	163.594778	Q	***1204.650691***	602.828984	1187.624142	594.315709	1186.640126	593.823701	7
4	457.276909	229.142092	440.250360	220.628818	439.266344	220.136810	L	***1076.592113***	538.799695	1059.565564	530.286420	1058.581548	529.794412	6
5	**556.345323**	278.676300	539.318774	270.163025	538.334758	269.671017	V	***963.508049***	482.257663	946.481500	473.744388	945.497484	473.252380	5
6	719.408652	360.207964	702.382103	351.694690	701.398087	351.202682	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
7	1158.633978	579.820627	1141.607429	571.307353	1140.623413	570.815345	Q	701.376306	351.191791	684.349757	342.678517	683.365741	342.186509	3
8	1245.666006	623.336641	1228.639457	614.823367	1227.655441	614.331359	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
9							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.2	1418.770386	0.009802	KSQLVYQSR
15.3	1418.770386	0.009802	KSQLVYQSR
8.7	1418.788147	-0.007959	QSQVDRLYVALK
5.9	1418.780273	-0.000085	TNQLMETLKTIK
3.1	1418.799377	-0.019189	QRKLLEPVDHGK
3.1	1418.799347	-0.019159	KNIEIYIQRSR
3.0	1418.774231	0.005957	KGRPPGHILSSDR
0.8	1418.787659	-0.007471	KEILLAMLMVDK

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

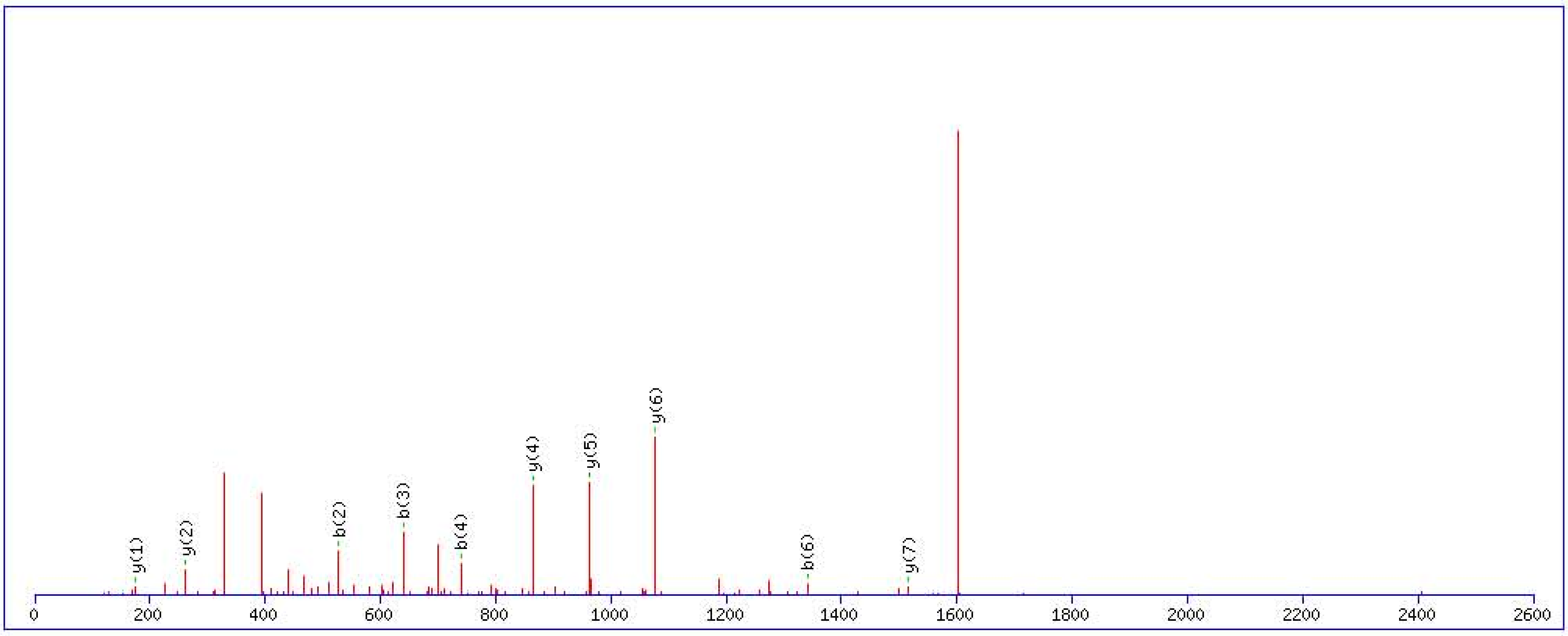
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQLVYQSR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

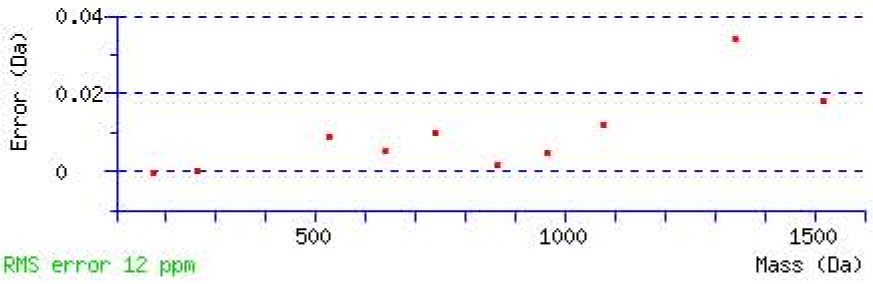
Match to Query 42236: 1601.861108 from(801.937830,2+) rtinseconds(2043) index(60841)
Title: Locus:1.1.1.3016.15 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

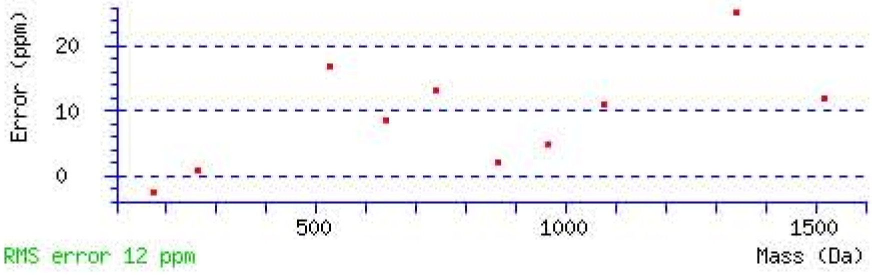
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1601.842178
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0024
Matches : 10/80 fragment ions using 15 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	**527.264630**	264.135953	510.238081	255.622679	509.254065	255.130671	Q	***1515.817439***	758.412358	1498.790890	749.899083	1497.806874	749.407075	7
3	**640.348694**	320.677985	623.322145	312.164711	622.338129	311.672703	L	***1076.592113***	538.799695	1059.565564	530.286420	1058.581548	529.794412	6
4	**739.417108**	370.212192	722.390559	361.698917	721.406543	361.206909	V	***963.508049***	482.257663	946.481500	473.744388	945.497484	473.252380	5
5	902.480437	451.743856	885.453888	443.230582	884.469872	442.738574	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
6	**1341.705763**	671.356520	1324.679214	662.843245	1323.695198	662.351237	Q	701.376306	351.191791	684.349757	342.678517	683.365741	342.186509	3
7	1428.737791	714.872534	1411.711242	706.359259	1410.727226	705.867251	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.6	1601.842178	0.018930	SQLVYQSR
13.5	1601.846024	0.015084	RFVLSCSLLSHQR
3.9	1601.852051	0.009057	SQISELNLLMK
2.9	1601.841995	0.019113	RPGTMTLQDGRKSR
2.0	1601.871155	-0.010047	FNQANTILKSR
1.8	1601.855881	0.005227	ELQRLQQAETMKK
0.4	1601.867126	-0.006018	RLGLAQKLMDQASR

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

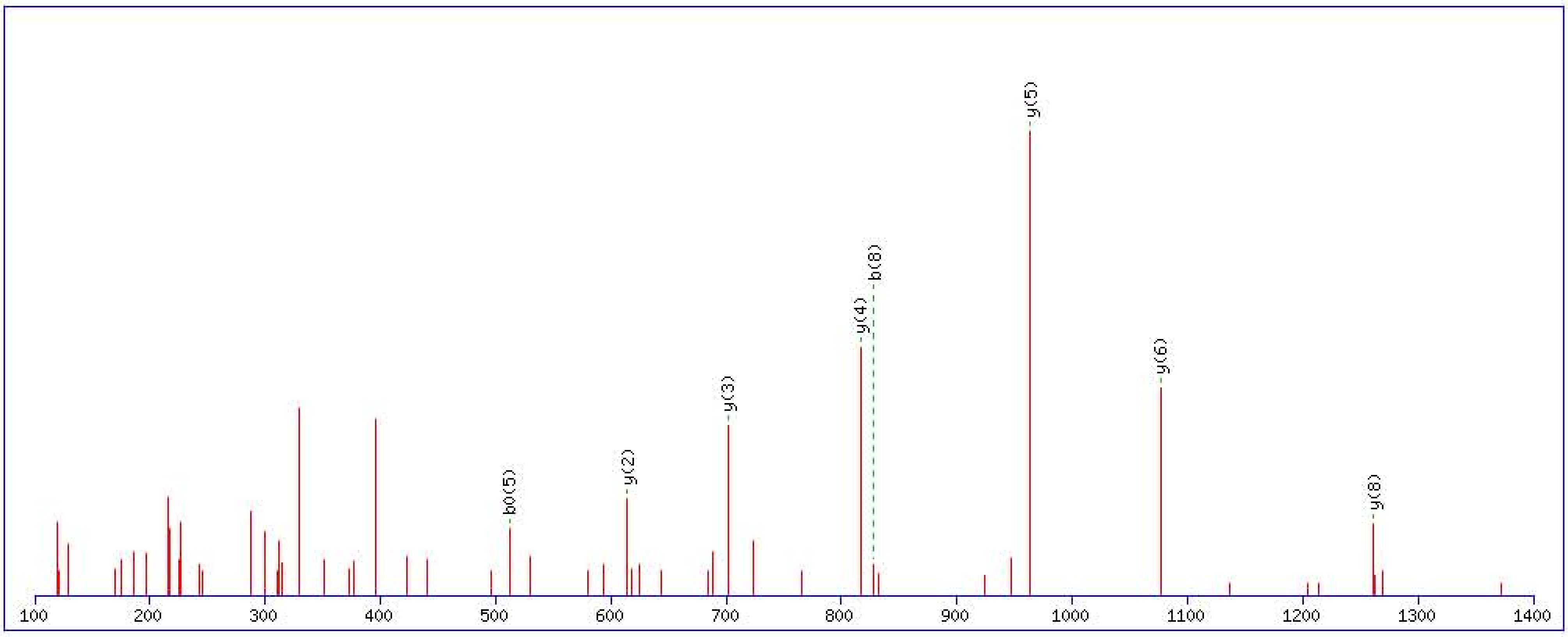
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELSEALGQIFDSQR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

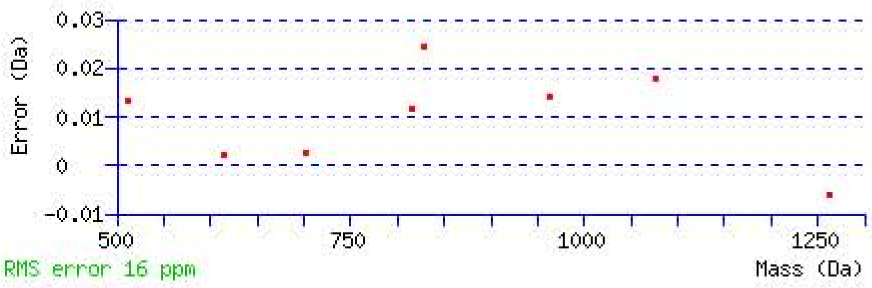
Match to Query 50602: 1902.976302 from(635.332710,3+) rtinseconds(2670) index(65059)
Title: Locus:1.1.1.3234.3 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

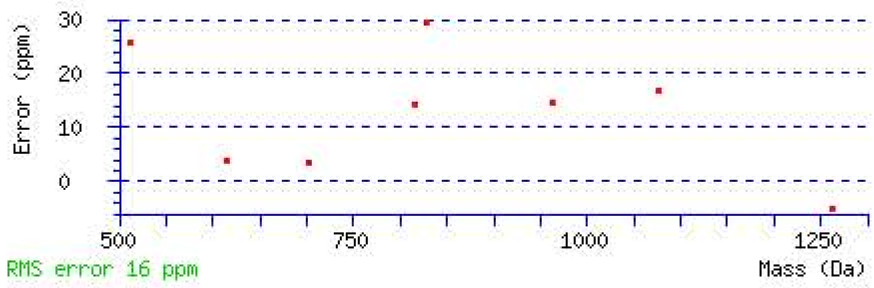
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1902.950928
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0068
Matches : 8/138 fragment ions using 13 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							14
2	243.133933	122.070605			225.123368	113.065322	L	1774.915632	887.961454	1757.889083	879.448180	1756.905067	878.956172	13
3	330.165961	165.586618			312.155396	156.581336	S	1661.831568	831.419422	1644.805019	822.906148	1643.821003	822.414140	12
4	459.208554	230.107915			441.197989	221.102633	E	1574.799540	787.903408	1557.772991	779.390134	1556.788975	778.898126	11
5	530.245668	265.626472			512.235103	256.621190	A	1445.756947	723.382112	1428.730398	714.868837	1427.746382	714.376829	10
6	643.329732	322.168504			625.319167	313.163222	L	1374.719833	687.863555	1357.693284	679.350280	1356.709268	678.858272	9
7	700.351196	350.679236			682.340631	341.673954	G	***1261.635769***	631.321523	1244.609220	622.808248	1243.625204	622.316240	8
8	**828.409774**	414.708525	811.383225	406.195251	810.399209	405.703243	Q	1204.614305	602.810791	1187.587756	594.297516	1186.603740	593.805508	7
9	941.493838	471.250557	924.467289	462.737283	923.483273	462.245275	I	***1076.555727***	538.781502	1059.529178	530.268227	1058.545162	529.776219	6
10	1088.562252	544.784764	1071.535703	536.271490	1070.551687	535.779482	F	***963.471663***	482.239470	946.445114	473.726195	945.461098	473.234187	5
11	1203.589195	602.298236	1186.562646	593.784961	1185.578630	593.292953	D	***816.403249***	408.705263	799.376700	400.191988	798.392684	399.699980	4
12	1290.621223	645.814250	1273.594674	637.300975	1272.610658	636.808967	S	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
13	1729.846549	865.426913	1712.820000	856.913638	1711.835984	856.421630	Q	***614.344278***	307.675777	597.317729	299.162503			2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.9	1902.950928	0.025374	ELSEALGQIFDSQR
2.5	1902.950928	0.025374	ELSEALGQIFDSQR

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

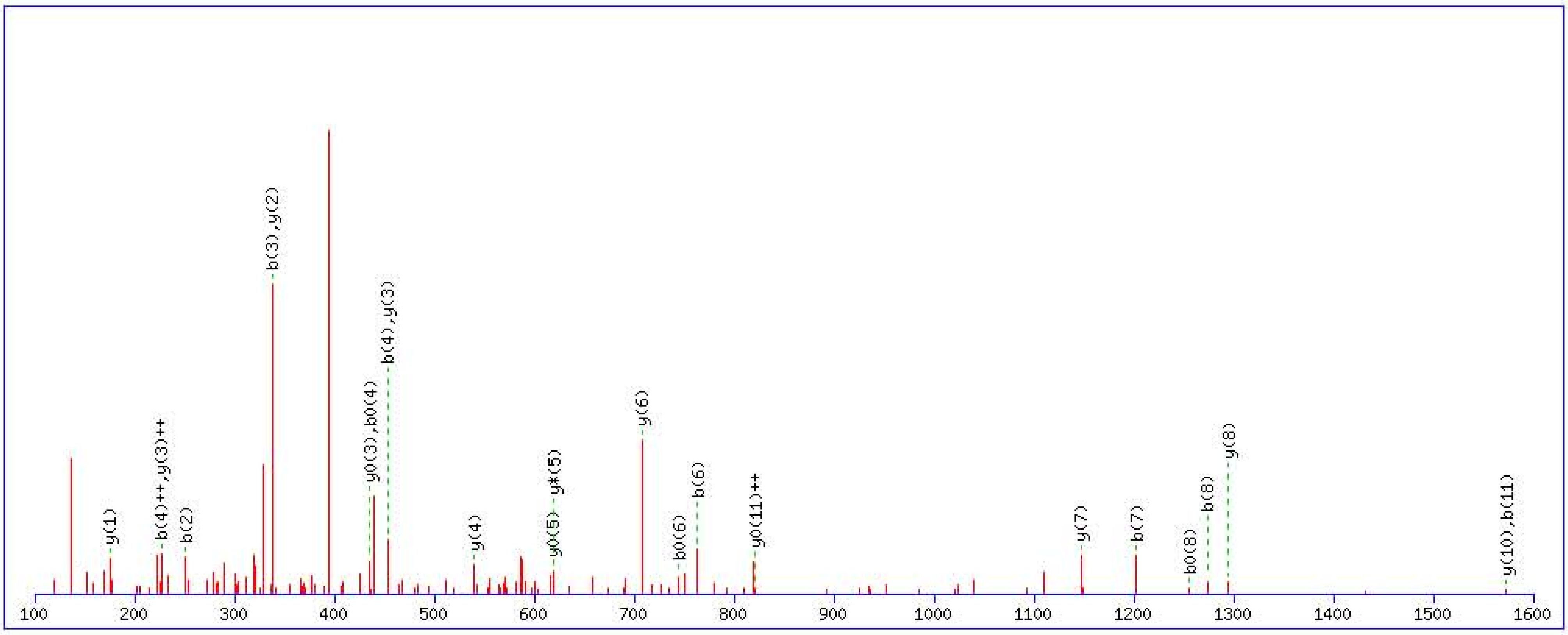
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSSDYFQAPSDYR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

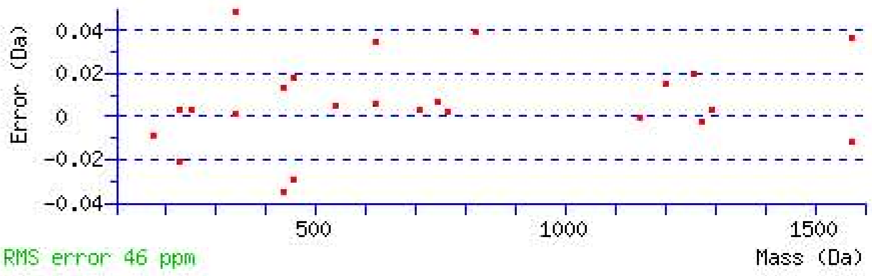
Match to Query 50785: 1908.848892 from(637.290240,3+) rtinseconds(2071) index(42576)
Title: Locus:1.1.1.3005.9 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

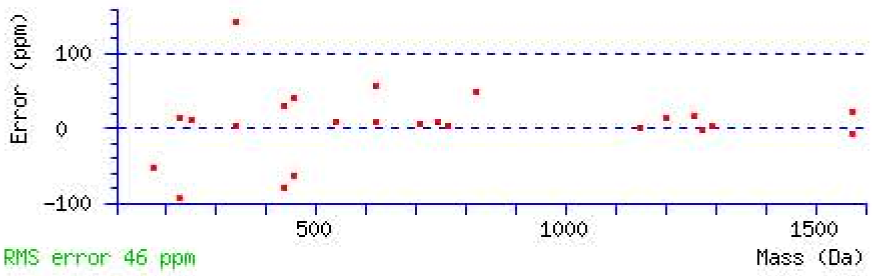
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1908.835236
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0007
Matches : 24/126 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	164.070605	82.538940					Y							13
2	***251.102633***	126.054954			233.092068	117.049672	S	1746.779198	873.893237	1729.752649	865.379963	1728.768633	864.887955	12
3	***338.134661***	169.570968			320.124096	160.565686	S	1659.747170	830.377223	1642.720621	821.863949	1641.736605	821.371941	11
4	***453.161604***	227.084440			435.151039	218.079158	D	***1572.715142***	786.861209	1555.688593	778.347935	1554.704577	777.855927	10
5	616.224933	308.616105			598.214368	299.610822	Y	1457.688199	729.347738	1440.661650	720.834463	1439.677634	720.342455	9
6	***763.293347***	382.150312			745.282782	373.145029	F	***1294.624870***	647.816073	1277.598321	639.302799	1276.614305	638.810791	8
7	***1202.518673***	601.762975	1185.492124	593.249700	1184.508108	592.757692	Q	***1147.556456***	574.281866	1130.529907	565.768592	1129.545891	565.276584	7
8	***1273.555787***	637.281532	1256.529238	628.768257	1255.545222	628.276249	A	***708.331130***	354.669203	691.304581	346.155929	690.320565	345.663921	6
9	1370.608551	685.807914	1353.582002	677.294639	1352.597986	676.802631	P	637.294016	319.150646	620.267467	310.637372	619.283451	310.145364	5
10	1457.640579	729.323928	1440.614030	720.810653	1439.630014	720.318645	S	***540.241252***	270.624264	523.214703	262.110990	522.230687	261.618982	4
11	***1572.667522***	786.837399	1555.640973	778.324125	1554.656957	777.832117	D	***453.209224***	227.108250	436.182675	218.594976	435.198659	218.102968	3
12	1735.730851	868.369064	1718.704302	859.855789	1717.720286	859.363781	Y	***338.182281***	169.594778	321.155732	161.081504			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.2	1908.835236	0.013656	YSSDYFQAPSDYR

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

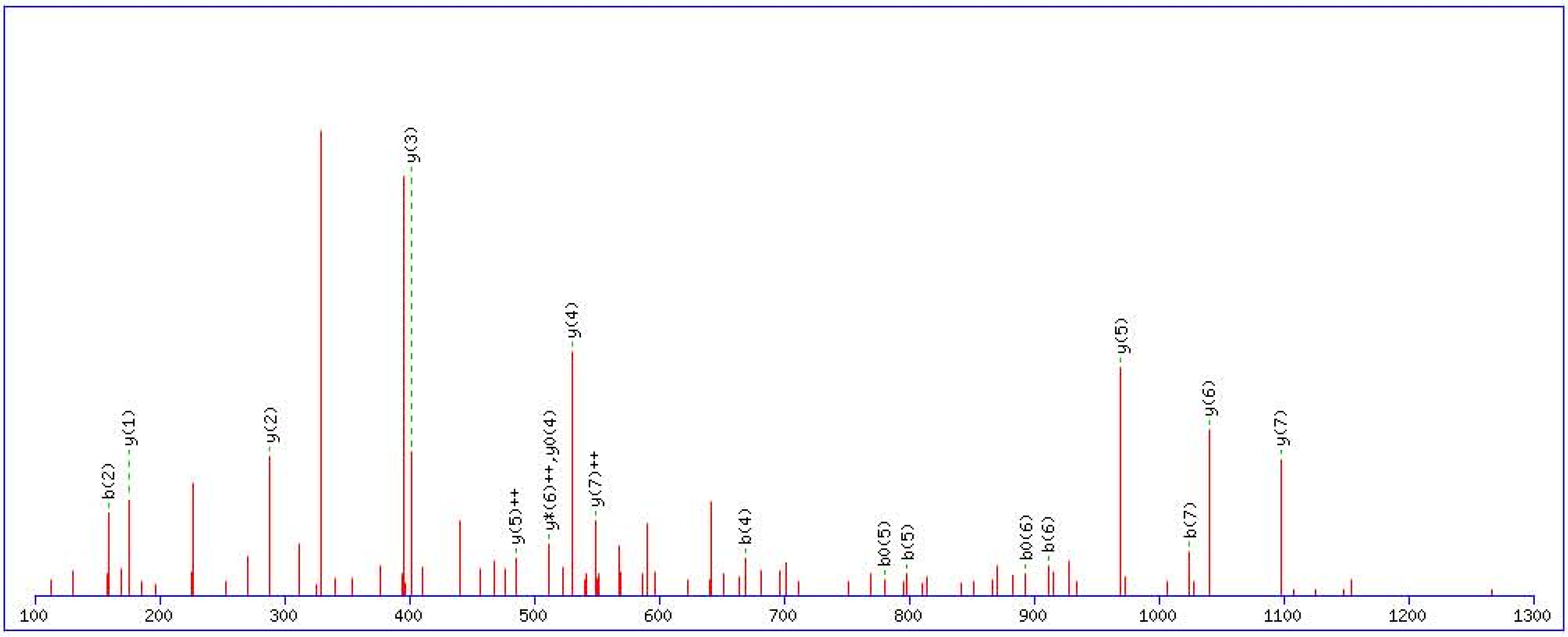
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGAQELLR**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

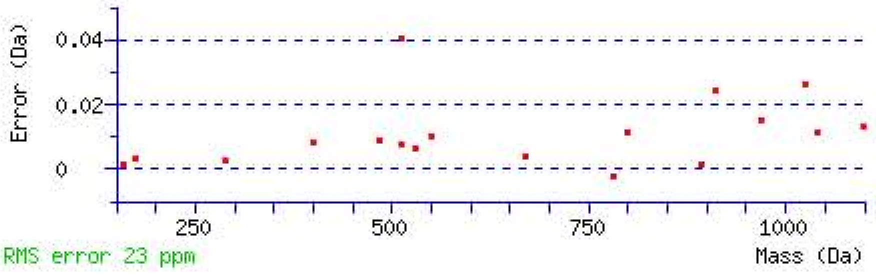
Match to Query 27650: 1197.667508 from(599.841030,2+) rtinseconds(1867) index(6117)
Title: Locus:1.1.1.2782.18 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

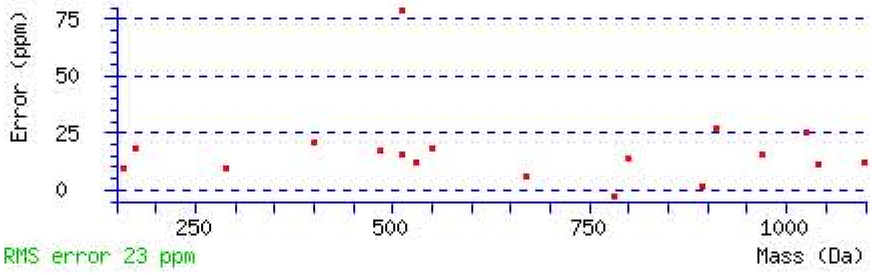
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1197.653961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0016
Matches : 18/72 fragment ions using 33 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							8
2	**159.076419**	80.041847			141.065854	71.036565	G	***1097.613577***	549.310427	1080.587028	540.797152	1079.603012	540.305144	7
3	230.113533	115.560404			212.102968	106.555122	A	***1040.592113***	520.799695	1023.565564	512.286420	1022.581548	511.794412	6
4	**669.338859**	335.173068	652.312310	326.659793	651.328294	326.167785	Q	***969.554999***	485.281138	952.528450	476.767863	951.544434	476.275855	5
5	**798.381452**	399.694364	781.354903	391.181090	780.370887	390.689082	E	***530.329673***	265.668475	513.303124	257.155200	512.319108	256.663192	4
6	**911.465516**	456.236396	894.438967	447.723122	893.454951	447.231114	L	***401.287080***	201.147178	384.260531	192.633903			3
7	**1024.549580**	512.778428	1007.523031	504.265153	1006.539015	503.773145	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 TGAQELLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.7	1197.653961	0.013547	TGAQELLR
17.3	1197.653961	0.013547	QTQEILR
16.6	1197.653961	0.013547	QTQEILR
12.1	1197.671692	-0.004184	LGLENAEALIR
8.5	1197.653961	0.013547	QQEITIR
7.7	1197.653961	0.013547	QTEQLLR
7.5	1197.671722	-0.004214	GTLDPVEKALR
7.2	1197.653961	0.013547	TQQLLER
6.9	1197.657776	0.009732	AAADALNRQIR
6.9	1197.671707	-0.004199	EAQDIILQLR

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

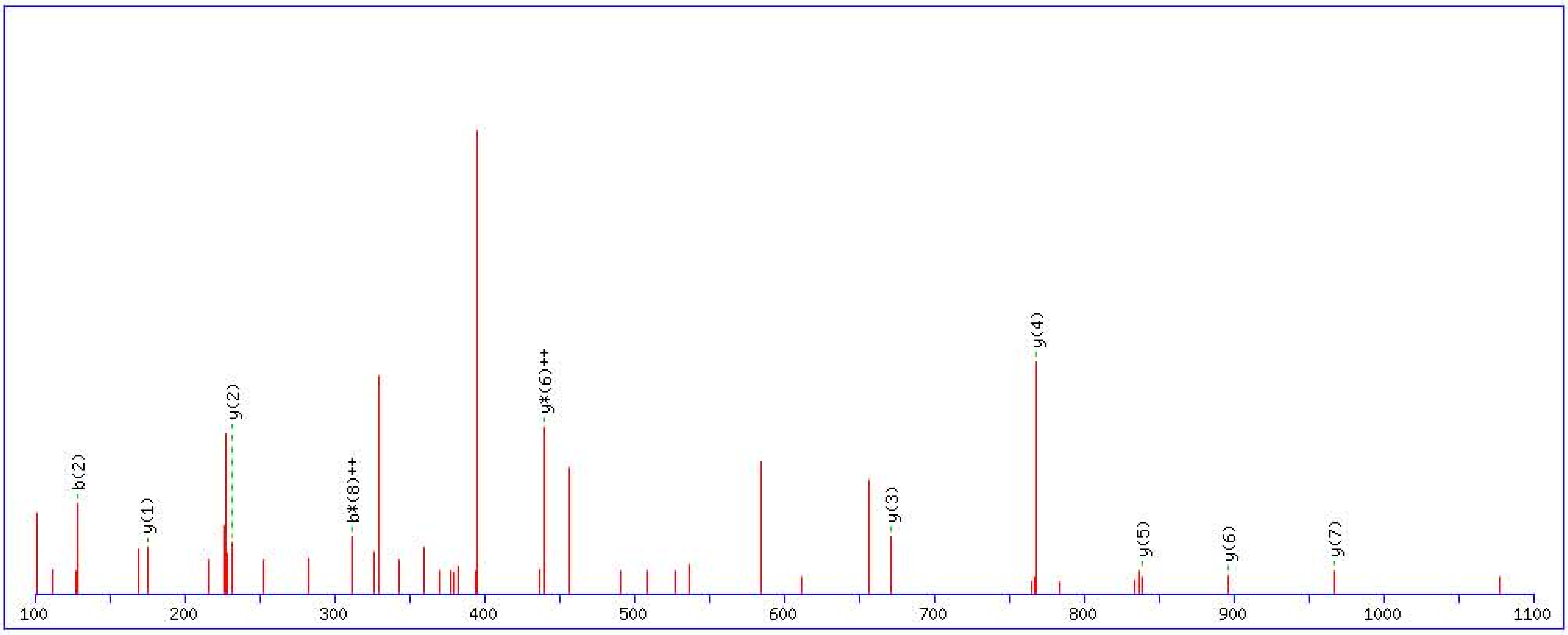
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GASQAGAPQGR**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

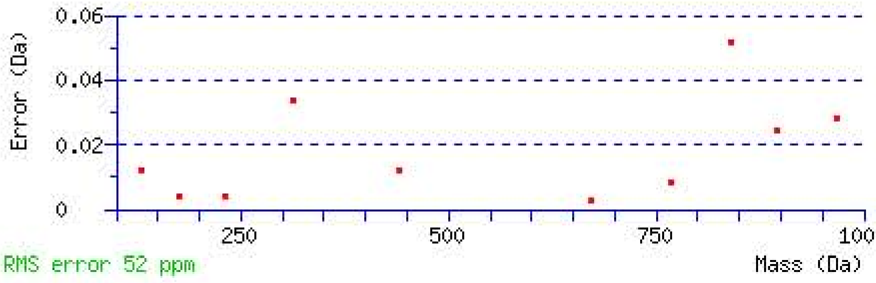
Match to Query 31151: 1309.662642 from(437.561490,3+) rtinseconds(1204) index(1657)
Title: Locus:1.1.1.2551.11 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

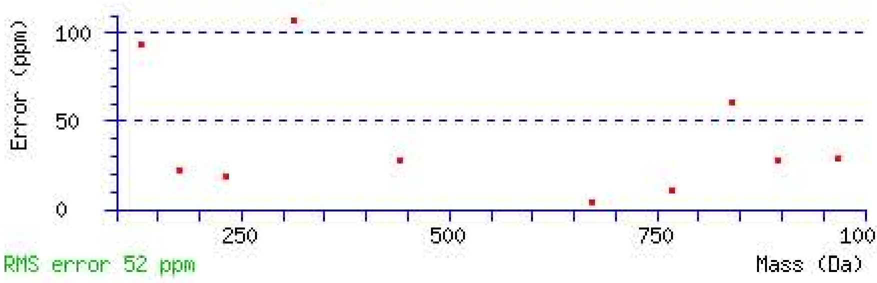
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1309.656097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.029
Matches : 10/94 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							11
2	129.065854	65.036565					A	1253.641918	627.324597	1236.615369	618.811323	1235.631353	618.319315	10
3	216.097882	108.552579			198.087317	99.547296	S	1182.604804	591.806040	1165.578255	583.292765	1164.594239	582.800757	9
4	344.156460	172.581868	327.129911	164.068593	326.145895	163.576585	Q	1095.572776	548.290026	1078.546227	539.776752			8
5	415.193574	208.100425	398.167025	199.587150	397.183009	199.095142	A	***967.514198***	484.260737	950.487649	475.747462			7
6	472.215038	236.611157	455.188489	228.097882	454.204473	227.605874	G	***896.477084***	448.742180	879.450535	440.228906			6
7	543.252152	272.129714	526.225603	263.616440	525.241587	263.124432	A	***839.455620***	420.231448	822.429071	411.718173			5
8	640.304916	320.656096	623.278367	312.142822	622.294351	311.650814	P	***768.418506***	384.712891	751.391957	376.199616			4
9	1079.530242	540.268759	1062.503693	531.755485	1061.519677	531.263477	Q	***671.365742***	336.186509	654.339193	327.673234			3
10	1136.551706	568.779491	1119.525157	560.266217	1118.541141	559.774208	G	***232.140416***	116.573846	215.113867	108.060571			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	1309.656097	0.006545	GASQAGAPQGR
24.0	1309.656097	0.006545	GASQAGAPQGR

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

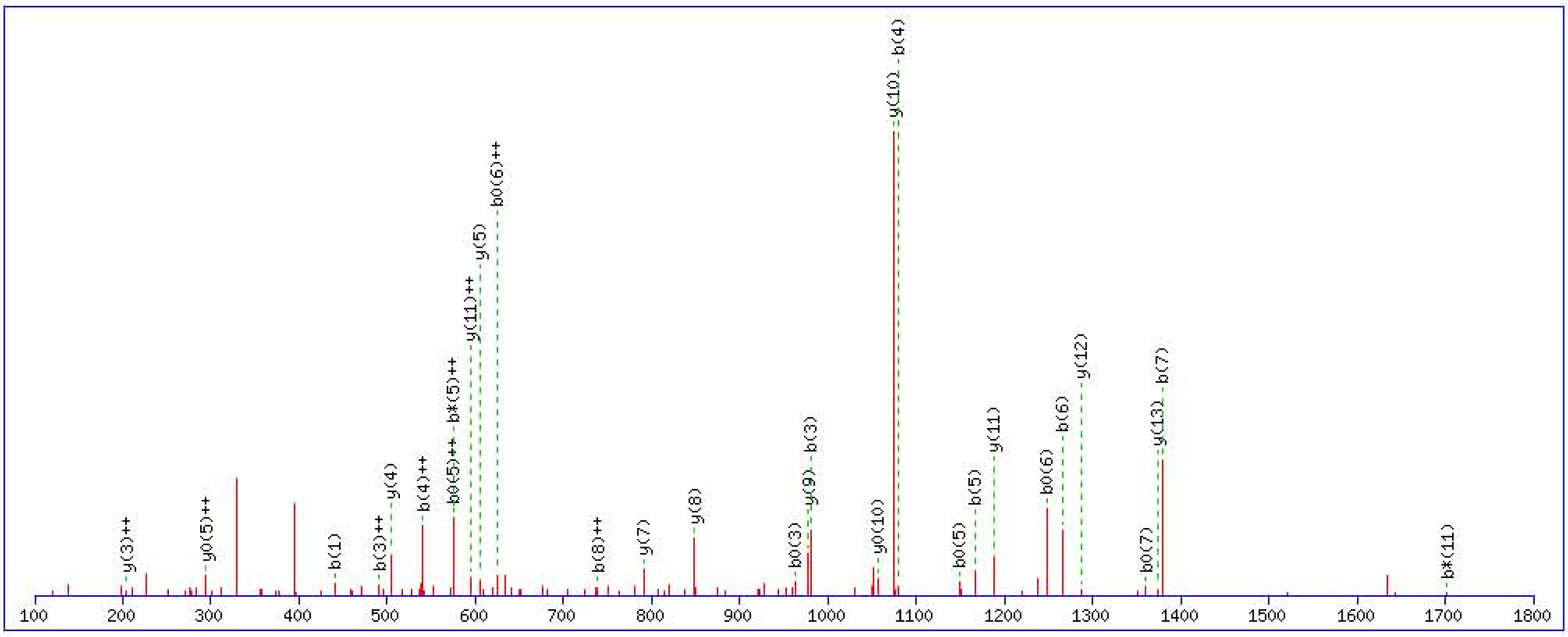
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QTQVSVLPEGGETPLFK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

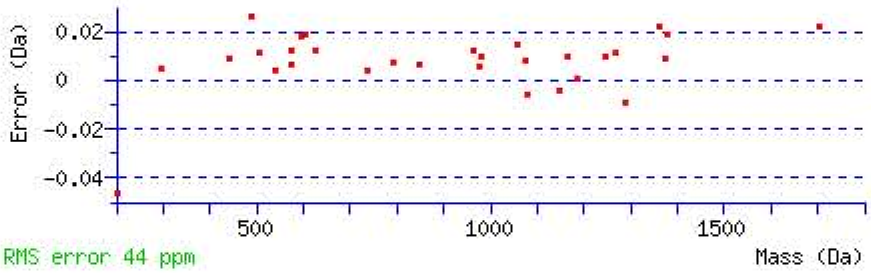
Match to Query 63850: 2451.318822 from(818.113550,3+) rtinseconds(2584) index(45789)
Title: Locus:1.1.1.3183.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

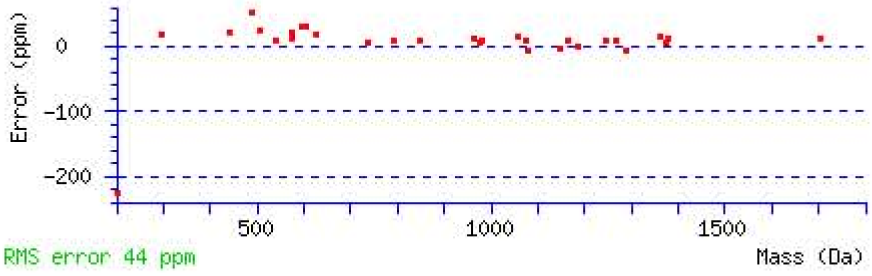
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2451.290588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.00024
Matches : 31/182 fragment ions using 68 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**440.232602**	220.619939	423.206053	212.106664			Q							17
2	541.280281	271.143779	524.253732	262.630504	523.269716	262.138496	T	2013.072528	1007.039902	1996.045979	998.526628	1995.061963	998.034620	16
3	**980.505607**	**490.756442**	963.479058	482.243167	962.495042	481.751159	Q	1912.024849	956.516063	1894.998300	948.002788	1894.014284	947.510780	15
4	**1079.574021**	**540.290649**	1062.547472	531.777374	1061.563456	531.285366	V	1472.799523	736.903400	1455.772974	728.390125	1454.788958	727.898117	14
5	**1166.606049**	583.806663	1149.579500	575.293388	1148.595484	574.801380	S	***1373.731109***	687.369193	1356.704560	678.855918	1355.720544	678.363910	13
6	**1265.674463**	633.340870	1248.647914	624.827595	1247.663898	624.335587	V	***1286.699081***	643.853179	1269.672532	635.339904	1268.688516	634.847896	12
7	**1378.758527**	689.882902	1361.731978	681.369627	1360.747962	680.877619	L	***1187.630667***	594.318971	1170.604118	585.805697	1169.620102	585.313689	11
8	1475.811291	**738.409284**	1458.784742	729.896009	1457.800726	729.404001	P	***1074.546603***	537.776940	1057.520054	529.263665	1056.536038	528.771657	10
9	1604.853884	802.930580	1587.827335	794.417306	1586.843319	793.925298	E	***977.493839***	489.250558	960.467290	480.737283	959.483274	480.245275	9
10	1661.875348	831.441312	1644.848799	822.928038	1643.864783	822.436030	G	***848.451246***	424.729261	831.424697	416.215986	830.440681	415.723978	8
11	1718.896812	859.952044	1701.870263	851.438770	1700.886247	850.946762	G	***791.429782***	396.218529	774.403233	387.705254	773.419217	387.213246	7
12	1847.939405	924.473341	1830.912856	915.960066	1829.928840	915.468058	E	734.408318	367.707797	717.381769	359.194523	716.397753	358.702515	6
13	1948.987084	974.997180	1931.960535	966.483906	1930.976519	965.991898	T	***605.365725***	303.186500	588.339176	294.673226	587.355160	294.181218	5
14	2046.039848	1023.523562	2029.013299	1015.010288	2028.029283	1014.518280	P	***504.318046***	252.662661	487.291497	244.149386			4
15	2159.123912	1080.065594	2142.097363	1071.552319	2141.113347	1071.060311	L	407.265282	204.136279	390.238733	195.623004			3
16	2306.192326	1153.599801	2289.165777	1145.086526	2288.181761	1144.594518	F	***294.181218***	147.594247	277.154669	139.080972			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.7	2451.290588	0.028234	QTQVSVLPEGGETPLFK
0.1	2451.301590	0.017232	ATKRISHMPSRPELSAVATDLR

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

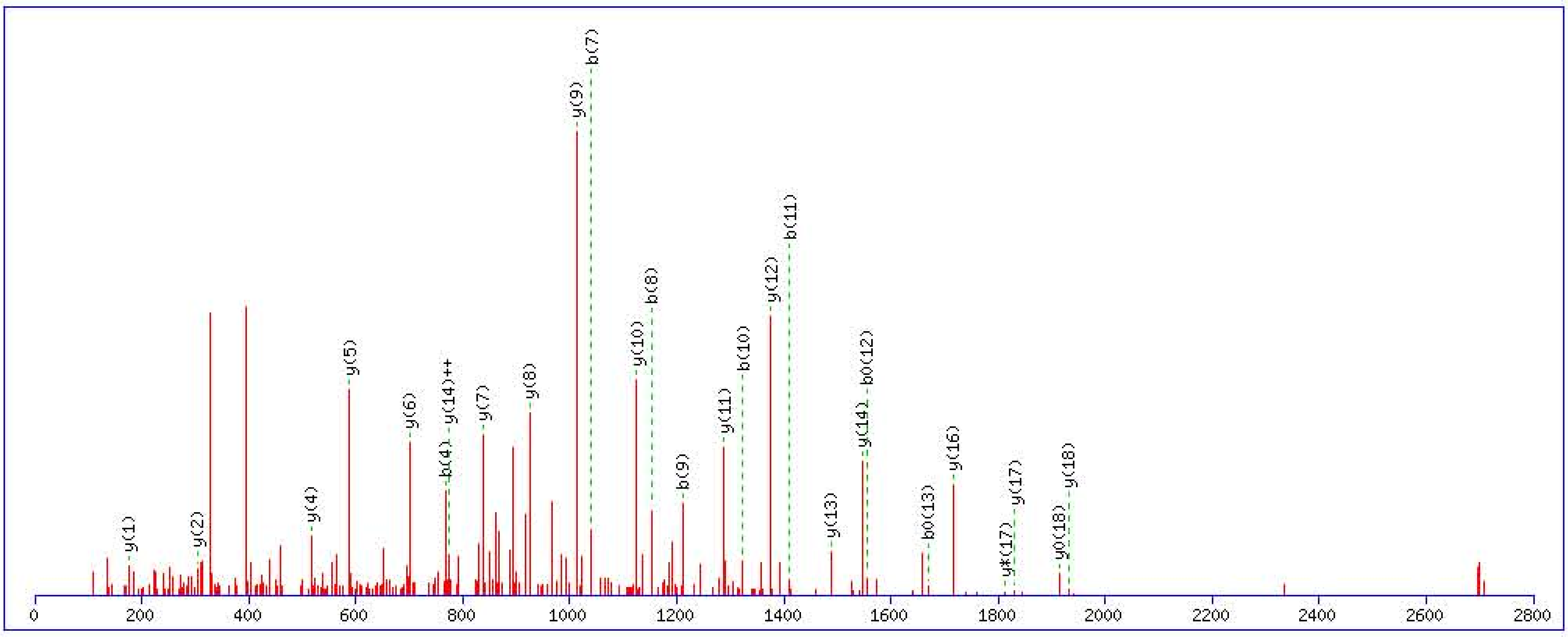
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DPDQTDGLGLSYLSSHIANVER**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

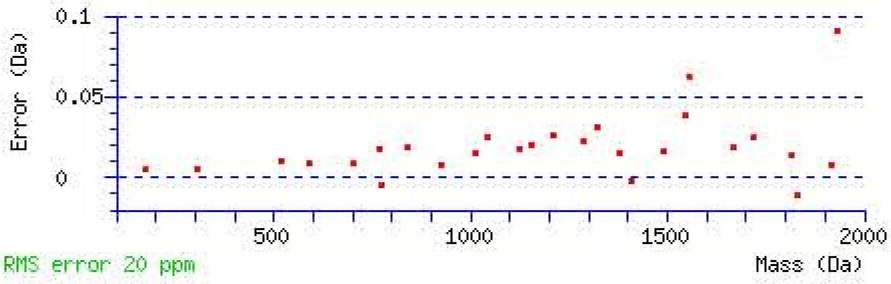
Match to Query 67469: 2697.345672 from(900.122500,3+) rtinseconds(2542) index(10440)
Title: Locus:1.1.1.3017.7 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

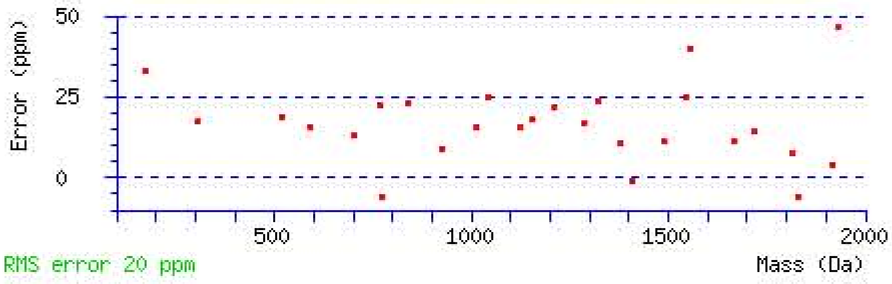
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2697.306824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 120  Expect: 2.9e-011
Matches : 27/244 fragment ions using 40 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							22
2	213.086983	107.047129			195.076418	98.041847	P	2583.287164	1292.147220	2566.260615	1283.633945	2565.276599	1283.141937	21
3	328.113926	164.560601			310.103361	155.555319	D	2486.234400	1243.620838	2469.207851	1235.107563	2468.223835	1234.615555	20
4	**767.339252**	384.173264	750.312703	375.659989	749.328687	375.167982	Q	2371.207457	1186.107366	2354.180908	1177.594092	2353.196892	1177.102084	19
5	868.386931	434.697104	851.360382	426.183829	850.376366	425.691821	T	***1931.982131***	966.494704	1914.955582	957.981429	1913.971566	957.489421	18
6	983.413874	492.210575	966.387325	483.697300	965.403309	483.205292	D	***1830.934452***	915.970864	1813.907903	907.457590	1812.923887	906.965581	17
7	**1040.435338**	520.721307	1023.408789	512.208032	1022.424773	511.716025	G	***1715.907509***	858.457392	1698.880960	849.944118	1697.896944	849.452110	16
8	**1153.519402**	577.263339	1136.492853	568.750065	1135.508837	568.258056	L	1658.886045	829.946661	1641.859496	821.433386	1640.875480	820.941378	15
9	**1210.540866**	605.774071	1193.514317	597.260796	1192.530301	596.768788	G	***1545.801981***	773.404629	1528.775432	764.891354	1527.791416	764.399346	14
10	**1323.624930**	662.316103	1306.598381	653.802828	1305.614365	653.310820	L	***1488.780517***	744.893897	1471.753968	736.380622	1470.769952	735.888614	13
11	**1410.656958**	705.832117	1393.630409	697.318842	1392.646393	696.826834	S	***1375.696453***	688.351865	1358.669904	679.838590	1357.685888	679.346582	12
12	1573.720287	787.363781	1556.693738	778.850507	1555.709722	778.358499	Y	***1288.664425***	644.835851	1271.637876	636.322576	1270.653860	635.830568	11
13	1686.804351	843.905813	1669.777802	835.392539	1668.793786	834.900531	L	***1125.601096***	563.304186	1108.574547	554.790912	1107.590531	554.298904	10
14	1773.836379	887.421827	1756.809830	878.908553	1755.825814	878.416545	S	***1012.517032***	506.762154	995.490483	498.248880	994.506467	497.756872	9
15	1860.868407	930.937841	1843.841858	922.424567	1842.857842	921.932559	S	***925.485004***	463.246140	908.458455	454.732866	907.474439	454.240858	8
16	1997.927319	999.467297	1980.900770	990.954023	1979.916754	990.462015	H	***838.452976***	419.730126	821.426427	411.216852	820.442411	410.724844	7
17	2111.011383	1056.009329	2093.984834	1047.496055	2093.000818	1047.004047	I	***701.394064***	351.200670	684.367515	342.687396	683.383499	342.195388	6
18	2182.048497	1091.527886	2165.021948	1083.014612	2164.037932	1082.522604	A	***588.310000***	294.658638	571.283451	286.145364	570.299435	285.653356	5
19	2296.091424	1148.549350	2279.064875	1140.036075	2278.080859	1139.544067	N	***517.272886***	259.140081	500.246337	250.626806	499.262321	250.134798	4
20	2395.159838	1198.083557	2378.133289	1189.570282	2377.149273	1189.078274	V	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
21	2524.202431	1262.604853	2507.175882	1254.091579	2506.191866	1253.599571	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
120.0	2697.306824	0.038848	DPDQTDGLGLSYLSSHIANVER

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

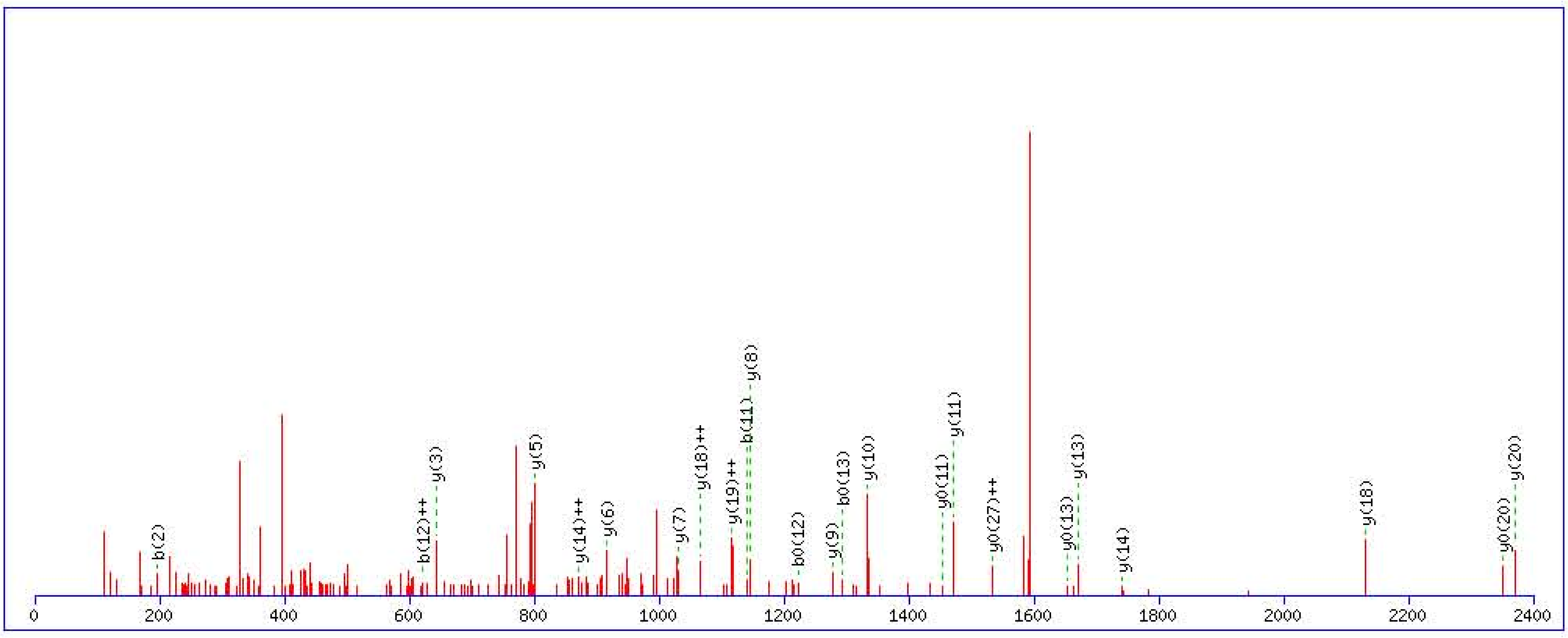
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPFDAATLHTSTAMAAQHGMDDDGTGQK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

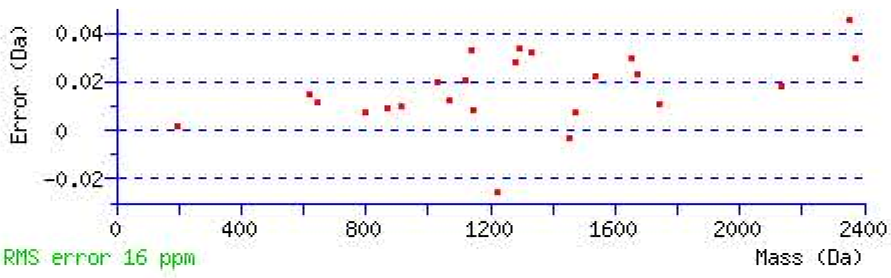
Match to Query 73262: 3183.477576 from(796.876670,4+) rtinseconds(1934) index(6623)
Title: Locus:1.1.1.2805.22 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

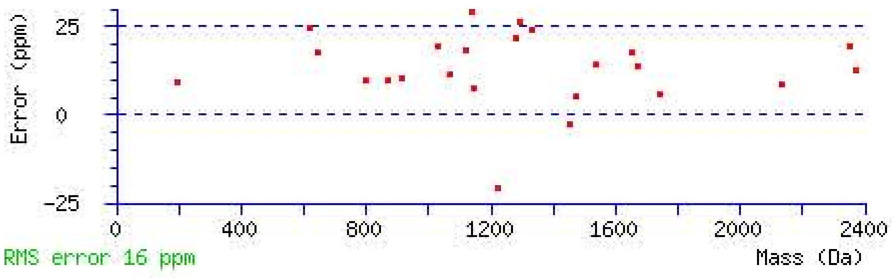
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3183.442383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q27    : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0024
Matches : 24/280 fragment ions using 69 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							28
2	**197.128454**	99.067865					P	3085.381222	1543.194249	3068.354673	1534.680974	3067.370657	1534.188966	27
3	344.196868	172.602072					F	2988.328458	1494.667867	2971.301909	1486.154592	2970.317893	1485.662584	26
4	459.223811	230.115543			441.213246	221.110261	D	2841.260044	1421.133660	2824.233495	1412.620385	2823.249479	1412.128377	25
5	530.260925	265.634101			512.250360	256.628818	A	2726.233101	1363.620188	2709.206552	1355.106914	2708.222536	1354.614906	24
6	601.298039	301.152658			583.287474	292.147375	A	2655.195987	1328.101631	2638.169438	1319.588357	2637.185422	1319.096349	23
7	702.345718	351.676497			684.335153	342.671215	T	2584.158873	1292.583074	2567.132324	1284.069800	2566.148308	1283.577792	22
8	815.429782	408.218529			797.419217	399.213247	L	2483.111194	1242.059235	2466.084645	1233.545960	2465.100629	1233.053952	21
9	952.488694	476.747985			934.478129	467.742703	H	***2370.027130***	1185.517203	2353.000581	1177.003928	2352.016565	1176.511920	20
10	1053.536373	527.271824			1035.525808	518.266542	T	2232.968218	1116.987747	2215.941669	1108.474472	2214.957653	1107.982464	19
11	**1140.568401**	570.787839			1122.557836	561.782556	S	***2131.920539***	1066.463907	2114.893990	1057.950633	2113.909974	1057.458625	18
12	1241.616080	621.311678			1223.605515	612.306396	T	2044.888511	1022.947893	2027.861962	1014.434619	2026.877946	1013.942611	17
13	1312.653194	656.830235			1294.642629	647.824952	A	1943.840832	972.424054	1926.814283	963.910779	1925.830267	963.418771	16
14	1443.693679	722.350478			1425.683114	713.345195	M	1872.803718	936.905497	1855.777169	928.392222	1854.793153	927.900214	15
15	1514.730793	757.869035			1496.720228	748.863752	A	***1741.763233***	871.385254	1724.736684	862.871980	1723.752668	862.379972	14
16	1585.767907	793.387591			1567.757342	784.382309	A	***1670.726119***	835.866697	1653.699570	827.353423	1652.715554	826.861415	13
17	1713.826485	857.416880	1696.799936	848.903606	1695.815920	848.411598	Q	1599.689005	800.348140	1582.662456	791.834866	1581.678440	791.342858	12
18	1850.885397	925.946336	1833.858848	917.433062	1832.874832	916.941054	H	***1471.630427***	736.318851	1454.603878	727.805577	1453.619862	727.313569	11
19	1907.906861	954.457068	1890.880312	945.943794	1889.896296	945.451786	G	***1334.571515***	667.789395	1317.544966	659.276121	1316.560950	658.784113	10
20	2038.947346	1019.977311	2021.920797	1011.464036	2020.936781	1010.972028	M	***1277.550051***	639.278663	1260.523502	630.765389	1259.539486	630.273381	9
21	2153.974289	1077.490782	2136.947740	1068.977508	2135.963724	1068.485500	D	***1146.509566***	573.758421	1129.483017	565.245146	1128.499001	564.753138	8
22	2269.001232	1135.004254	2251.974683	1126.490979	2250.990667	1125.998971	D	***1031.482623***	516.244949	1014.456074	507.731675	1013.472058	507.239667	7
23	2384.028175	1192.517725	2367.001626	1184.004451	2366.017610	1183.512443	D	***916.455680***	458.731478	899.429131	450.218203	898.445115	449.726195	6
24	2441.049639	1221.028457	2424.023090	1212.515183	2423.039074	1212.023175	G	***801.428737***	401.218007	784.402188	392.704732	783.418172	392.212724	5
25	2542.097318	1271.552297	2525.070769	1263.039022	2524.086753	1262.547014	T	744.407273	372.707275	727.380724	364.194000	726.396708	363.701992	4
26	2599.118782	1300.063029	2582.092233	1291.549754	2581.108217	1291.057746	G	***643.359594***	322.183435	626.333045	313.670161			3
27	3038.344108	1519.675692	3021.317559	1511.162417	3020.333543	1510.670409	Q	586.338130	293.672703	569.311581	285.159429			2
28							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.9	3183.442383	0.035193	VPFDAATLHTSTAMAAQHGMDDDGTGQK
5.3	3183.442383	0.035193	VPFDAATLHTSTAMAAQHGMDDDGTGQK

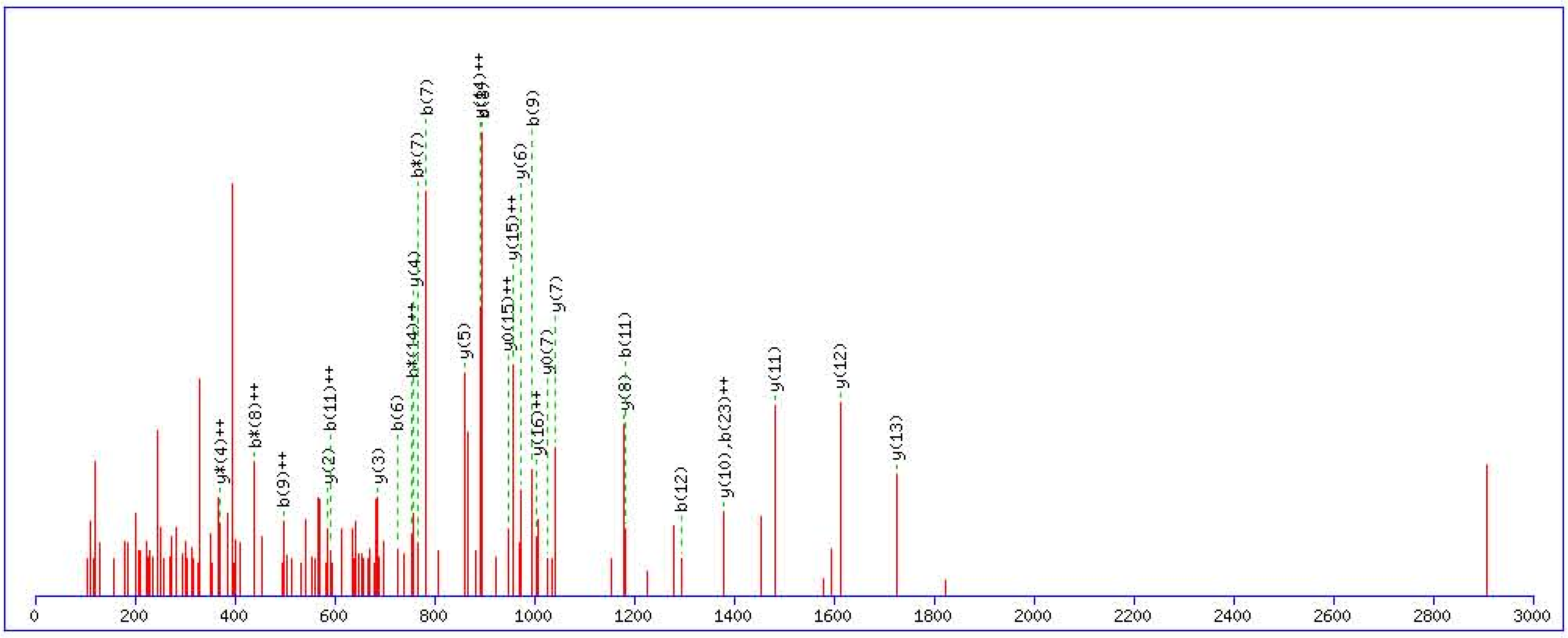
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIHDNFGIVEGLMTTVHAITATQK**
Found in **G3P_HUMAN**, Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3

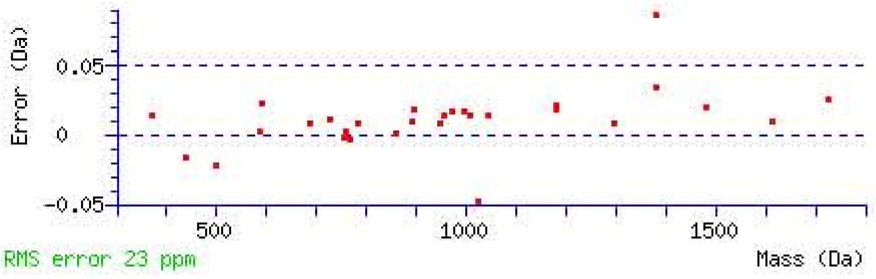
Match to Query 70634: 2905.559296 from(727.397100,4+) rtinseconds(3068) index(68142)
Title: Locus:1.1.1.3369.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

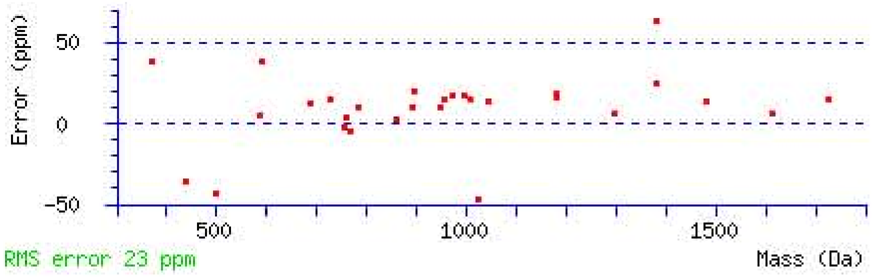


```
Monoisotopic mass of neutral peptide Mr(calc): 2905.519424
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q23     : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00054
Matches : 29/258 fragment ions using 66 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							24
2	213.159754	107.083515					I	2807.458272	1404.232774	2790.431723	1395.719499	2789.447707	1395.227491	23
3	350.218666	175.612971					H	2694.374208	1347.690742	2677.347659	1339.177467	2676.363643	1338.685459	22
4	465.245609	233.126443			447.235044	224.121160	D	2557.315296	1279.161286	2540.288747	1270.648011	2539.304731	1270.156003	21
5	579.288536	290.147906	562.261987	281.634632	561.277971	281.142624	N	2442.288353	1221.647814	2425.261804	1213.134540	2424.277788	1212.642532	20
6	***726.356950***	363.682113	709.330401	355.168838	708.346385	354.676830	F	2328.245426	1164.626351	2311.218877	1156.113076	2310.234861	1155.621068	19
7	***783.378414***	392.192845	766.351865	383.679571	765.367849	383.187563	G	2181.177012	1091.092144	2164.150463	1082.578869	2163.166447	1082.086861	18
8	***896.462478***	448.734877	879.435929	440.221603	878.451913	439.729595	I	2124.155548	1062.581412	2107.128999	1054.068137	2106.144983	1053.576129	17
9	***995.530892***	**498.269084**	978.504343	489.755810	977.520327	489.263802	V	2011.071484	1006.039380	1994.044935	997.526105	1993.060919	997.034097	16
10	1124.573485	562.790381	1107.546936	554.277106	1106.562920	553.785098	E	1912.003070	956.505173	1894.976521	947.991899	1893.992505	947.499890	15
11	***1181.594949***	**591.301113**	1164.568400	582.787838	1163.584384	582.295830	G	1782.960477	891.983876	1765.933928	883.470602	1764.949912	882.978594	14
12	***1294.679013***	647.843144	1277.652464	639.329870	1276.668448	638.837862	L	***1725.939013***	863.473144	1708.912464	854.959870	1707.928448	854.467862	13
13	1425.719498	713.363387	1408.692949	704.850113	1407.708933	704.358104	M	***1612.854949***	806.931113	1595.828400	798.417838	1594.844384	797.925830	12
14	1526.767177	763.887227	1509.740628	755.373952	1508.756612	754.881944	T	***1481.814464***	741.410870	1464.787915	732.897596	1463.803899	732.405588	11
15	1627.814856	814.411066	1610.788307	805.897792	1609.804291	805.405783	T	***1380.766785***	690.887031	1363.740236	682.373756	1362.756220	681.881748	10
16	1726.883270	863.945273	1709.856721	855.431999	1708.872705	854.939991	V	1279.719106	640.363191	1262.692557	631.849917	1261.708541	631.357909	9
17	1863.942182	932.474729	1846.915633	923.961455	1845.931617	923.469447	H	***1180.650692***	590.828984	1163.624143	582.315710	1162.640127	581.823701	8
18	1934.979296	967.993286	1917.952747	959.480012	1916.968731	958.988003	A	***1043.591780***	522.299528	1026.565231	513.786254	1025.581215	513.294245	7
19	2048.063360	1024.535318	2031.036811	1016.022044	2030.052795	1015.530036	I	***972.554666***	486.780971	955.528117	478.267697	954.544101	477.775689	6
20	2149.111039	1075.059157	2132.084490	1066.545883	2131.100474	1066.053875	T	***859.470602***	430.238939	842.444053	421.725665	841.460037	421.233657	5
21	2220.148153	1110.577714	2203.121604	1102.064440	2202.137588	1101.572432	A	***758.422923***	379.715100	741.396374	371.201825	740.412358	370.709817	4
22	2321.195832	1161.101554	2304.169283	1152.588279	2303.185267	1152.096271	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
23	2760.421158	**1380.714217**	2743.394609	1372.200942	2742.410593	1371.708934	Q	***586.338130***	293.672703	569.311581	285.159429			2
24							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 23 ppm



RMS error 23 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	2905.519424	0.039872	VIHDNFGIVEGLMTTVHAITATQK

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

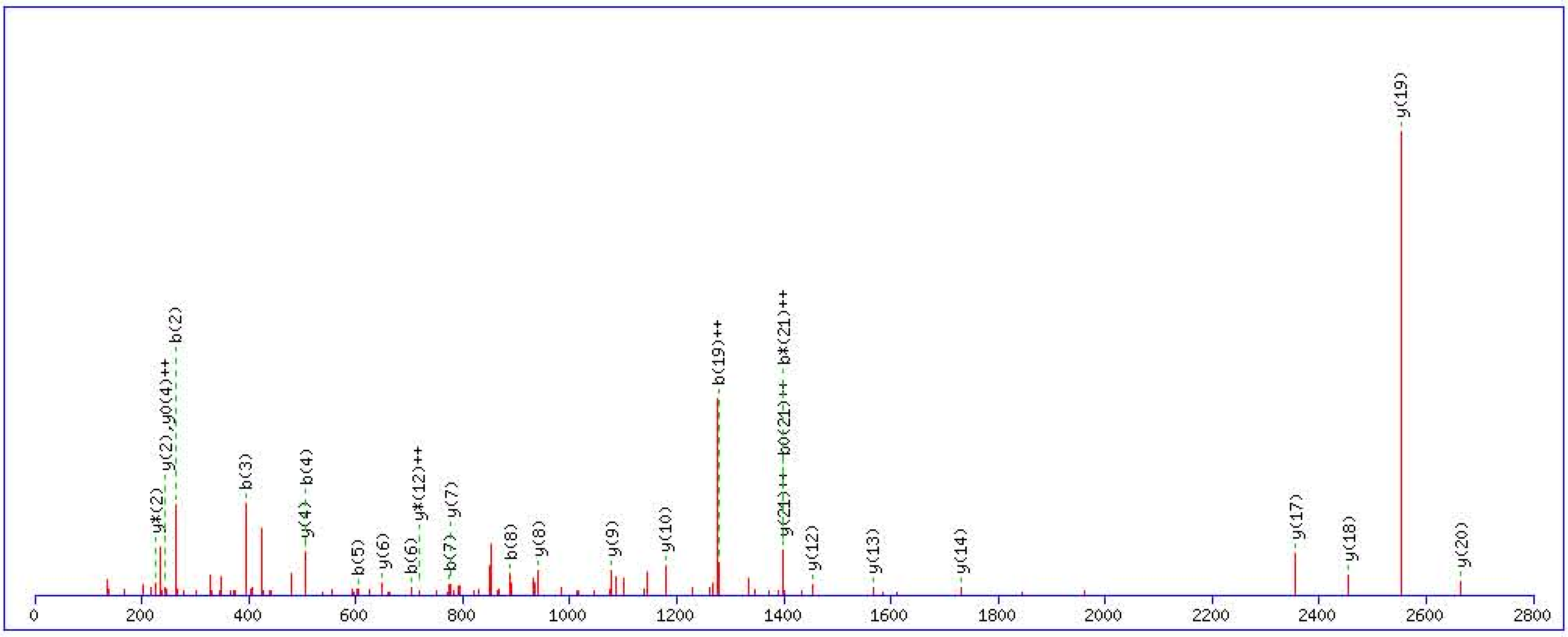
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVMLPVADQYDCITHYEGSTCPK**
Found in **HPTR_HUMAN**, Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2

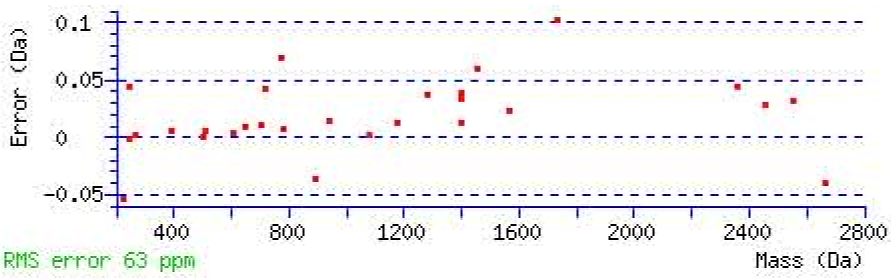
Match to Query 72122: 3057.413142 from(1020.144990,3+) rtinseconds(2443) index(44926)
Title: Locus:1.1.1.3134.13 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

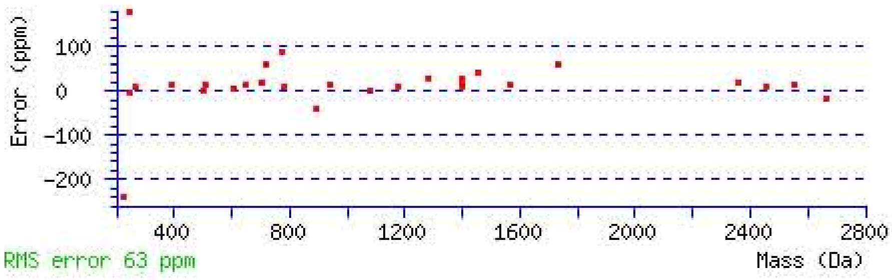
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3057.374466
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 74  Expect: 6.4e-007
Matches : 28/228 fragment ions using 51 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.070605	82.538940					Y							23
2	**263.139019**	132.073148					V	2895.318410	1448.162843	2878.291861	1439.649568	2877.307845	1439.157560	22
3	**394.179504**	197.593390					M	2796.249996	1398.628636	2779.223447	1390.115361	2778.239431	1389.623353	21
4	**507.263568**	254.135422					L	***2665.209511***	1333.108393	2648.182962	1324.595119	2647.198946	1324.103111	20
5	**604.316332**	302.661804					P	***2552.125447***	1276.566361	2535.098898	1268.053087	2534.114882	1267.561079	19
6	**703.384746**	352.196011					V	***2455.072683***	1228.039979	2438.046134	1219.526705	2437.062118	1219.034697	18
7	**774.421860**	387.714568					A	***2356.004269***	1178.505772	2338.977720	1169.992498	2337.993704	1169.500490	17
8	**889.448803**	445.228040			871.438238	436.222757	D	2284.967155	1142.987215	2267.940606	1134.473941	2266.956590	1133.981933	16
9	1328.674129	664.840703	1311.647580	656.327428	1310.663564	655.835420	Q	2169.940212	1085.473744	2152.913663	1076.960469	2151.929647	1076.468461	15
10	1491.737458	746.372367	1474.710909	737.859093	1473.726893	737.367085	Y	***1730.714886***	865.861081	1713.688337	857.347807	1712.704321	856.855799	14
11	1606.764401	803.885839	1589.737852	795.372564	1588.753836	794.880556	D	***1567.651557***	784.329417	1550.625008	775.816142	1549.640992	775.324134	13
12	1766.795050	883.901163	1749.768501	875.387889	1748.784485	874.895881	C	***1452.624614***	726.815945	1435.598065	718.302671	1434.614049	717.810663	12
13	1879.879114	940.443195	1862.852565	931.929921	1861.868549	931.437913	I	1292.593965	646.800621	1275.567416	638.287346	1274.583400	637.795338	11
14	1980.926793	990.967035	1963.900244	982.453760	1962.916228	981.961752	T	***1179.509901***	590.258589	1162.483352	581.745314	1161.499336	581.253306	10
15	2117.985705	1059.496490	2100.959156	1050.983216	2099.975140	1050.491208	H	***1078.462222***	539.734749	1061.435673	531.221475	1060.451657	530.729467	9
16	2281.049034	1141.028155	2264.022485	1132.514880	2263.038469	1132.022872	Y	***941.403310***	471.205293	924.376761	462.692018	923.392745	462.200010	8
17	2410.091627	1205.549452	2393.065078	1197.036177	2392.081062	1196.544169	E	***778.339981***	389.673628	761.313432	381.160354	760.329416	380.668346	7
18	2467.113091	1234.060184	2450.086542	1225.546909	2449.102526	1225.054901	G	***649.297388***	325.152332	632.270839	316.639057	631.286823	316.147049	6
19	2554.145119	1277.576198	2537.118570	1269.062923	2536.134554	1268.570915	S	592.275924	296.641600	575.249375	288.128325	574.265359	287.636317	5
20	2655.192798	1328.100037	2638.166249	1319.586762	2637.182233	1319.094754	T	***505.243896***	253.125586	488.217347	244.612311	487.233331	244.120303	4
21	2815.223447	1408.115361	2798.196898	1399.602087	2797.212882	1399.110079	C	404.196217	202.601746	387.169668	194.088472			3
22	2912.276211	1456.641743	2895.249662	1448.128469	2894.265646	1447.636461	P	***244.165568***	122.586422	227.139019	114.073148			2
23							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.8	3057.374466	0.038676	YVMLPVADQYDCITHYEGSTCPK

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

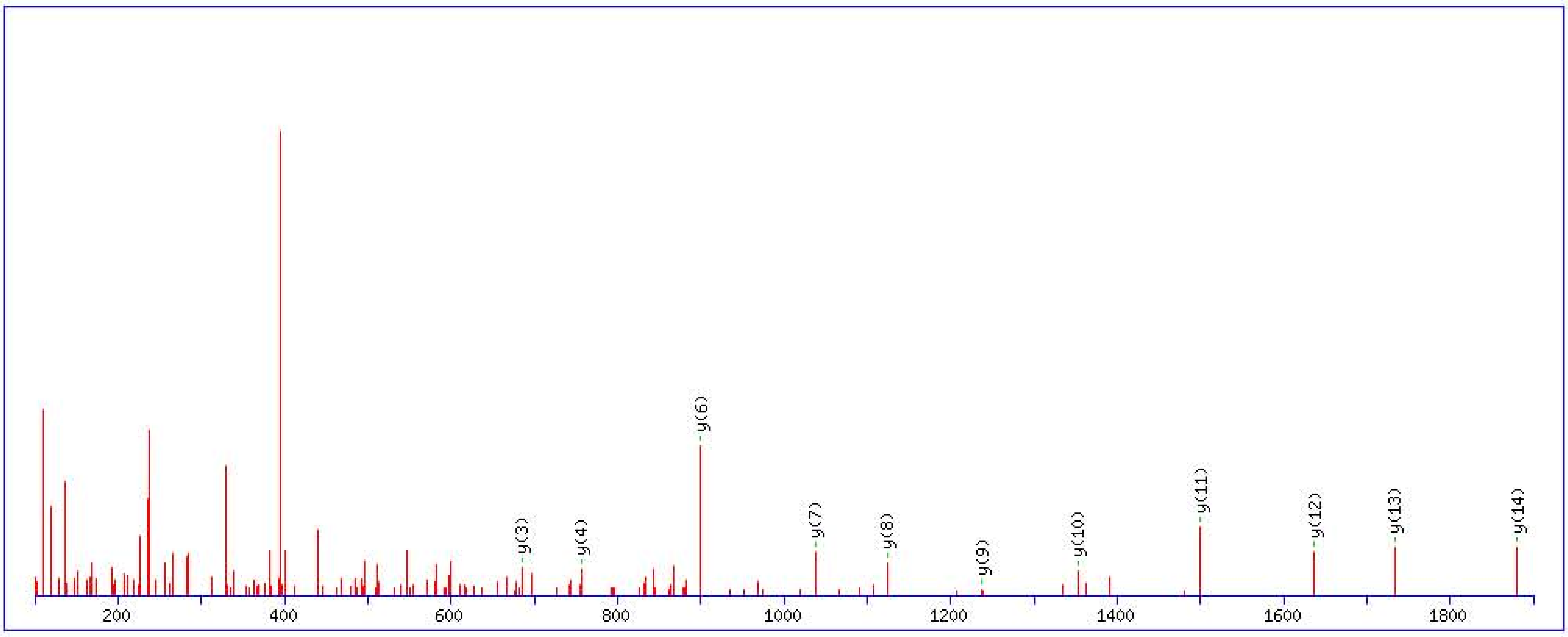
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYFPHFDLSHGSAQVK**
Found in **HBA_HUMAN**, Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2

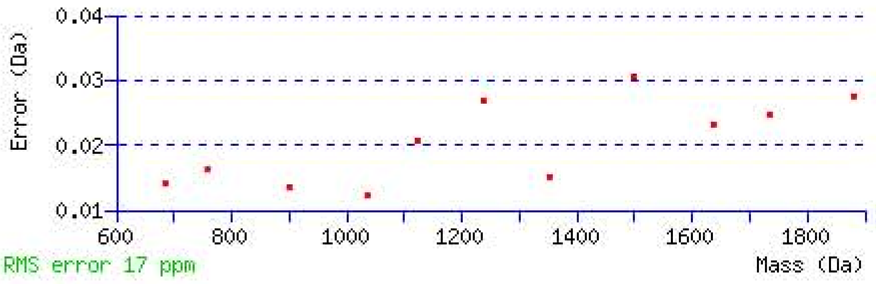
Match to Query 56870: 2144.069376 from(537.024620,4+) rtinseconds(2050) index(7355)
Title: Locus:1.1.1.2846.10 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

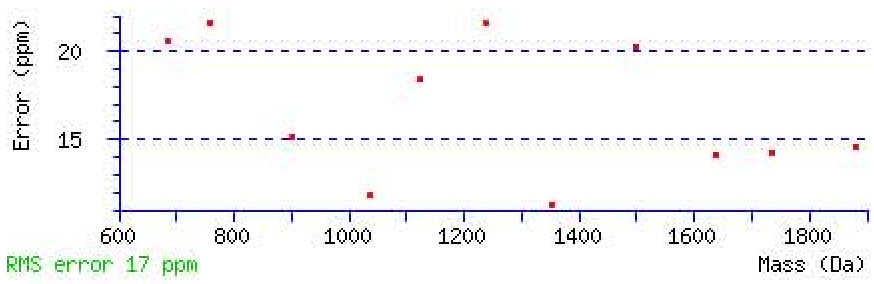
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2144.051346
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 80 **Expect:** 2.6e-007
Matches : 11/146 fragment ions using 17 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							16
2	265.118284	133.062780			247.107719	124.057498	Y	2044.010930	1022.509103	2026.984381	1013.995829	2026.000365	1013.503821	15
3	412.186698	206.596987			394.176133	197.591705	F	*1880.947601*	940.977438	1863.921052	932.464164	1862.937036	931.972156	14
4	509.239462	255.123369			491.228897	246.118087	P	*1733.879187*	867.443231	1716.852638	858.929957	1715.868622	858.437949	13
5	646.298374	323.652825			628.287809	314.647543	H	*1636.826423*	818.916849	1619.799874	810.403575	1618.815858	809.911567	12
6	793.366788	397.187032			775.356223	388.181750	F	*1499.767511*	750.387393	1482.740962	741.874119	1481.756946	741.382111	11
7	908.393731	454.700504			890.383166	445.695221	D	*1352.699097*	676.853186	1335.672548	668.339912	1334.688532	667.847904	10
8	1021.477795	511.242536			1003.467230	502.237253	L	*1237.672154*	619.339715	1220.645605	610.826441	1219.661589	610.334433	9
9	1108.509823	554.758550			1090.499258	545.753267	S	*1124.588090*	562.797683	1107.561541	554.284409	1106.577525	553.792400	8
10	1245.568735	623.288006			1227.558170	614.282723	H	*1037.556062*	519.281669	1020.529513	510.768394	1019.545497	510.276386	7
11	1302.590199	651.798738			1284.579634	642.793455	G	*900.497150*	450.752213	883.470601	442.238938	882.486585	441.746930	6
12	1389.622227	695.314752			1371.611662	686.309469	S	843.475686	422.241481	826.449137	413.728207	825.465121	413.236199	5
13	1460.659341	730.833309			1442.648776	721.828026	A	*756.443658*	378.725467	739.417109	370.212192			4
14	1899.884667	950.445972	1882.858118	941.932697	1881.874102	941.440689	Q	*685.406544*	343.206910	668.379995	334.693635			3
15	1998.953081	999.980179	1981.926532	991.466904	1980.942516	990.974896	V	246.181218	123.594247	229.154669	115.080972			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.3	2144.051346	0.018030	TYFPHFDLSHGSAQVK

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

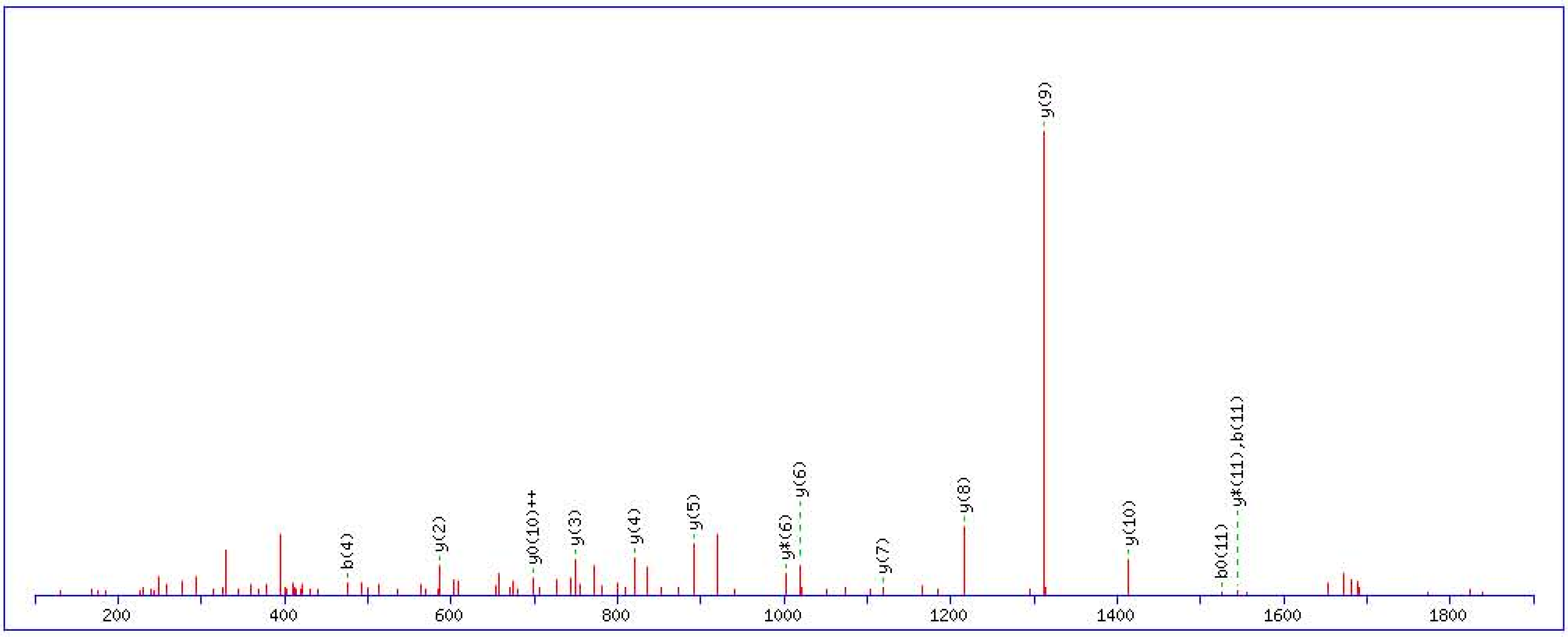
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFTPPVQAAYQK**
Found in **HBB_HUMAN**, Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2

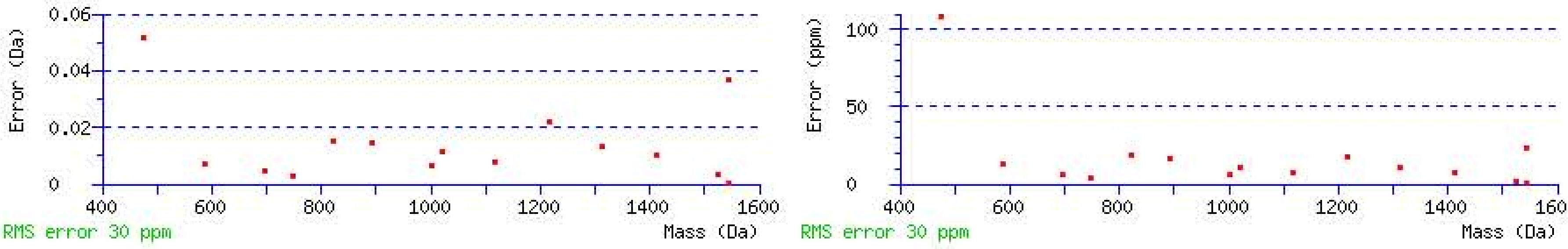
Match to Query 45534: 1688.881668 from(845.448110,2+) rtinseconds(1989) index(6936)
Title: Locus:1.1.1.2824.16 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1688.859604
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 3.7e-005
Matches : 15/102 fragment ions using 30 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							12
2	277.118283	139.062779			259.107718	130.057497	F	1560.824300	780.915788	1543.797751	772.402514	1542.813735	771.910506	11
3	378.165962	189.586619			360.155397	180.581336	T	***1413.755886***	707.381581	1396.729337	698.868307	1395.745321	698.376299	10
4	**475.218726**	238.113001			457.208161	229.107719	P	***1312.708207***	656.857742	1295.681658	648.344467			9
5	572.271490	286.639383			554.260925	277.634101	P	***1215.655443***	608.331360	1198.628894	599.818085			8
6	671.339904	336.173590			653.329339	327.168308	V	***1118.602679***	559.804978	1101.576130	551.291703			7
7	799.398482	400.202879	782.371933	391.689605	781.387917	391.197597	Q	***1019.534265***	510.270771	1002.507716	501.757496			6
8	870.435596	435.721436	853.409047	427.208162	852.425031	426.716154	A	***891.475687***	446.241482	874.449138	437.728207			5
9	941.472710	471.239993	924.446161	462.726719	923.462145	462.234711	A	***820.438573***	410.722925	803.412024	402.209650			4
10	1104.536039	552.771658	1087.509490	544.258383	1086.525474	543.766375	Y	***749.401459***	375.204368	732.374910	366.691093			3
11	**1543.761365**	772.384321	1526.734816	763.871046	1525.750800	763.379038	Q	***586.338130***	293.672703	569.311581	285.159429			2
12							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.1	1688.859604	0.022064	EFTPPVQAAYQK
25.2	1688.859604	0.022064	EFTPPVQAAYQK
5.5	1688.891937	-0.010269	TLYEALERQQK
4.3	1688.891937	-0.010269	DCGAAAEPFLLKAKAK
2.3	1688.887955	-0.006287	STVPDAVTKCRSAGIK
2.2	1688.870819	0.010849	YLFIFSVANMRNSK
1.9	1688.880692	0.000976	EEAQKLLEQYK
0.8	1688.896667	-0.014999	RFGNQITMQRK
0.8	1688.878052	0.003616	ITLFNHMRTDTRGK
0.6	1688.866837	0.014831	GGDVWVVAQNRMTLK

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

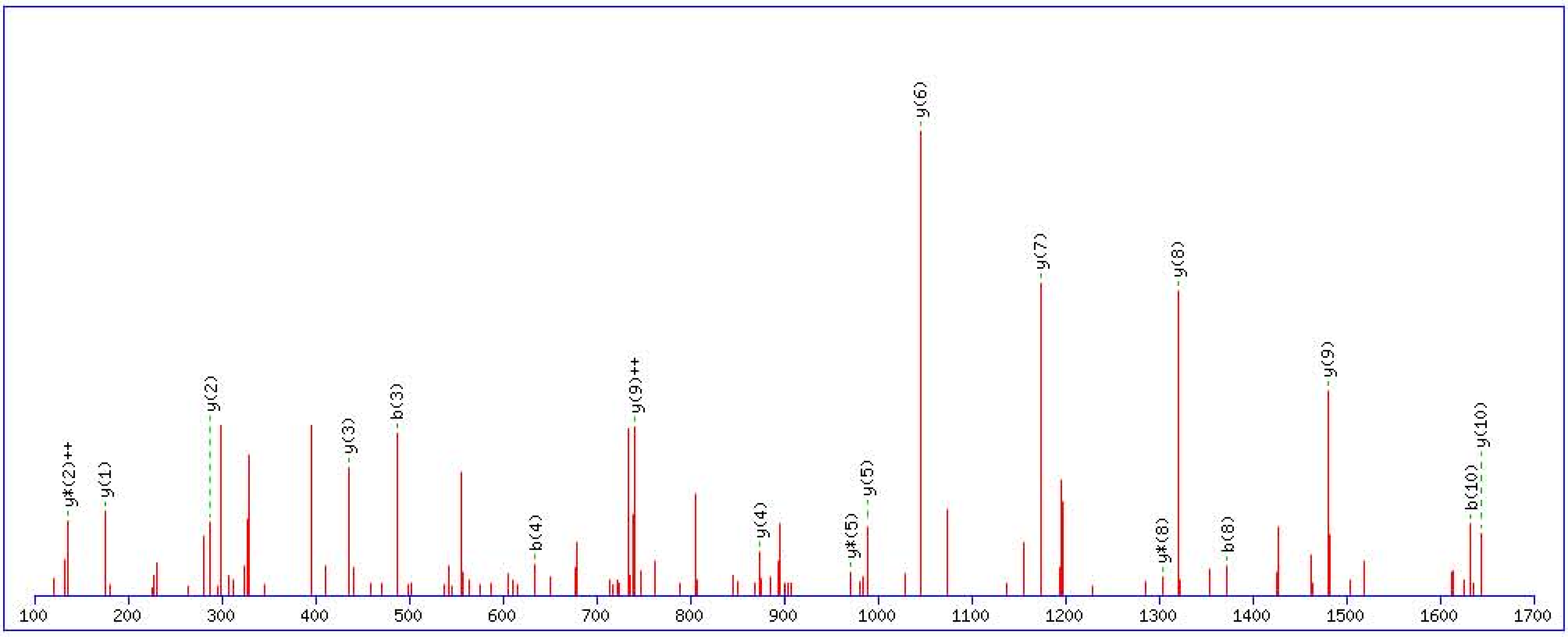
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YYCFQGNQFLR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

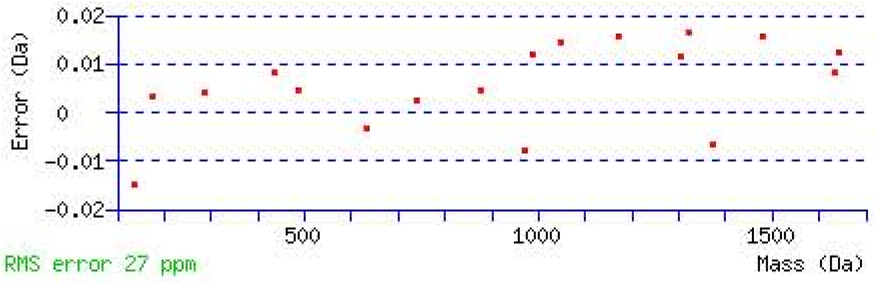
Match to Query 48515: 1805.854048 from(903.934300,2+) rtinseconds(2289) index(80527)
Title: Locus:1.1.1.3011.17 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

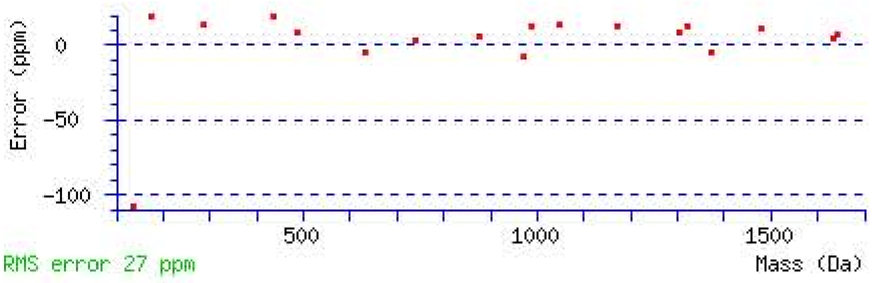
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1805.838165
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 2e-006
Matches : 18/72 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	164.070605	82.538940			Y					11
2	327.133934	164.070605			Y	*1643.782117*	822.394697	1626.755568	813.881422	10
3	**487.164583**	244.085930			C	*1480.718788*	740.863032	1463.692239	732.349758	9
4	**634.232997**	317.620137			F	*1320.688139*	660.847708	1303.661590	652.334433	8
5	762.291575	381.649426	745.265026	373.136151	Q	*1173.619725*	587.313501	1156.593176	578.800226	7
6	819.313039	410.160158	802.286490	401.646883	G	*1045.561147*	523.284212	1028.534598	514.770937	6
7	933.355966	467.181621	916.329417	458.668347	N	*988.539683*	494.773480	971.513134	486.260205	5
8	**1372.581292**	686.794284	1355.554743	678.281010	Q	*874.496756*	437.752016	857.470207	429.238742	4
9	1519.649706	760.328491	1502.623157	751.815217	F	*435.271430*	218.139353	418.244881	209.626078	3
10	**1632.733770**	816.870523	1615.707221	808.357249	L	*288.203016*	144.605146	271.176467	136.091871	2
11					R	*175.118952*	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.9	1805.838165	0.015883	YYCFQGNQFLR
38.3	1805.838165	0.015883	YYCFQGNQFLR
2.8	1805.845383	0.008665	WGTRGGFNGQMER
2.1	1805.873032	-0.018984	VSTGDNWNGIMKDTLR
1.7	1805.830154	0.023894	VSLHCGKSGGGDGCFLR
1.2	1805.844055	0.009993	LLQAPFTDCGDGPMLR
0.4	1805.877045	-0.022997	MFITHGVYEPEKPSR

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

{MATRIX SCIENCE}

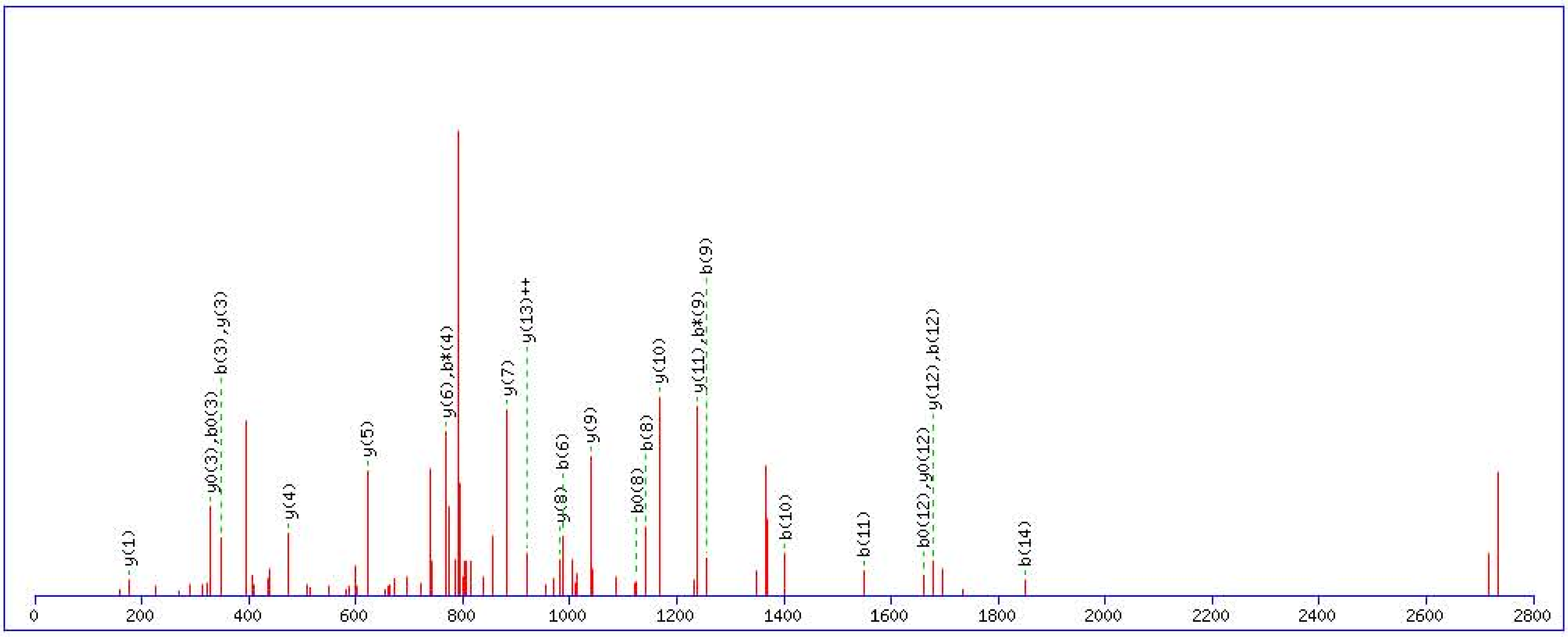
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GECQAEGVLFFQGDR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

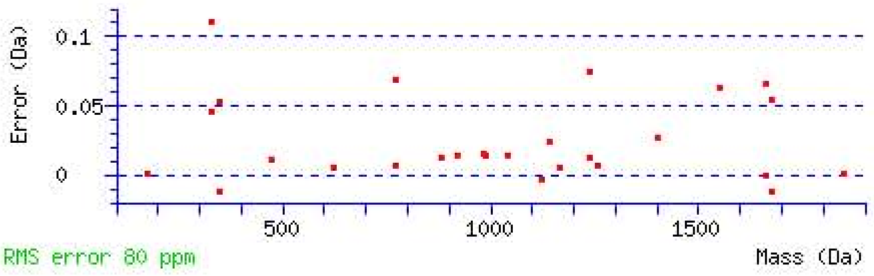
Match to Query 54323: 2022.952268 from(1012.483410,2+) rtinseconds(2402) index(81273)
Title: Locus:1.1.1.3050.19 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

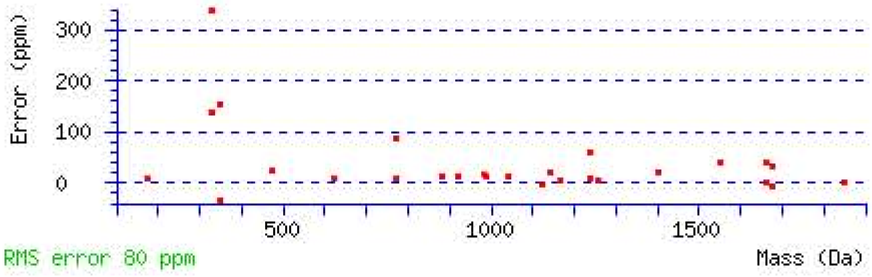
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2022.929184
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 1.1e-005
Matches : 27/158 fragment ions using 44 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							15
2	187.071333	94.039305			169.060768	85.034022	E	1966.914982	983.961129	1949.888433	975.447855	1948.904417	974.955847	14
3	**347.101982**	174.054629			329.091417	165.049347	C	1837.872389	919.439833	1820.845840	910.926558	1819.861824	910.434550	13
4	786.327308	393.667292	769.300759	385.154018	768.316743	384.662010	Q	***1677.841740***	839.424508	1660.815191	830.911234	1659.831175	830.419226	12
5	857.364422	429.185849	840.337873	420.672575	839.353857	420.180567	A	***1238.616414***	619.811845	1221.589865	611.298571	1220.605849	610.806563	11
6	**986.407015**	493.707146	969.380466	485.193871	968.396450	484.701863	E	***1167.579300***	584.293288	1150.552751	575.780014	1149.568735	575.288006	10
7	1043.428479	522.217878	1026.401930	513.704603	1025.417914	513.212595	G	***1038.536707***	519.771992	1021.510158	511.258717	1020.526142	510.766709	9
8	**1142.496893**	571.752085	1125.470344	563.238810	1124.486328	562.746802	V	***981.515243***	491.261260	964.488694	482.747985	963.504678	482.255977	8
9	**1255.580957**	628.294117	1238.554408	619.780842	1237.570392	619.288834	L	***882.446829***	441.727053	865.420280	433.213778	864.436264	432.721770	7
10	**1402.649371**	701.828324	1385.622822	693.315049	1384.638806	692.823041	F	***769.362765***	385.185021	752.336216	376.671746	751.352200	376.179738	6
11	**1549.717785**	775.362531	1532.691236	766.849256	1531.707220	766.357248	F	***622.294351***	311.650814	605.267802	303.137539	604.283786	302.645531	5
12	**1677.776363**	839.391820	1660.749814	830.878545	1659.765798	830.386537	Q	***475.225937***	238.116606	458.199388	229.603332	457.215372	229.111324	4
13	1734.797827	867.902552	1717.771278	859.389277	1716.787262	858.897269	G	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	3
14	**1849.824770**	925.416023	1832.798221	916.902749	1831.814205	916.410741	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.7	2022.929184	0.023084	GECQAEGVLFFQGDR
11.7	2022.929184	0.023084	GECQAEGVLFFQGDR
5.0	2022.980133	-0.027865	QHMEQKEQTAR
4.9	2022.950317	0.001951	NMSFVNDLTVTQDGR

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

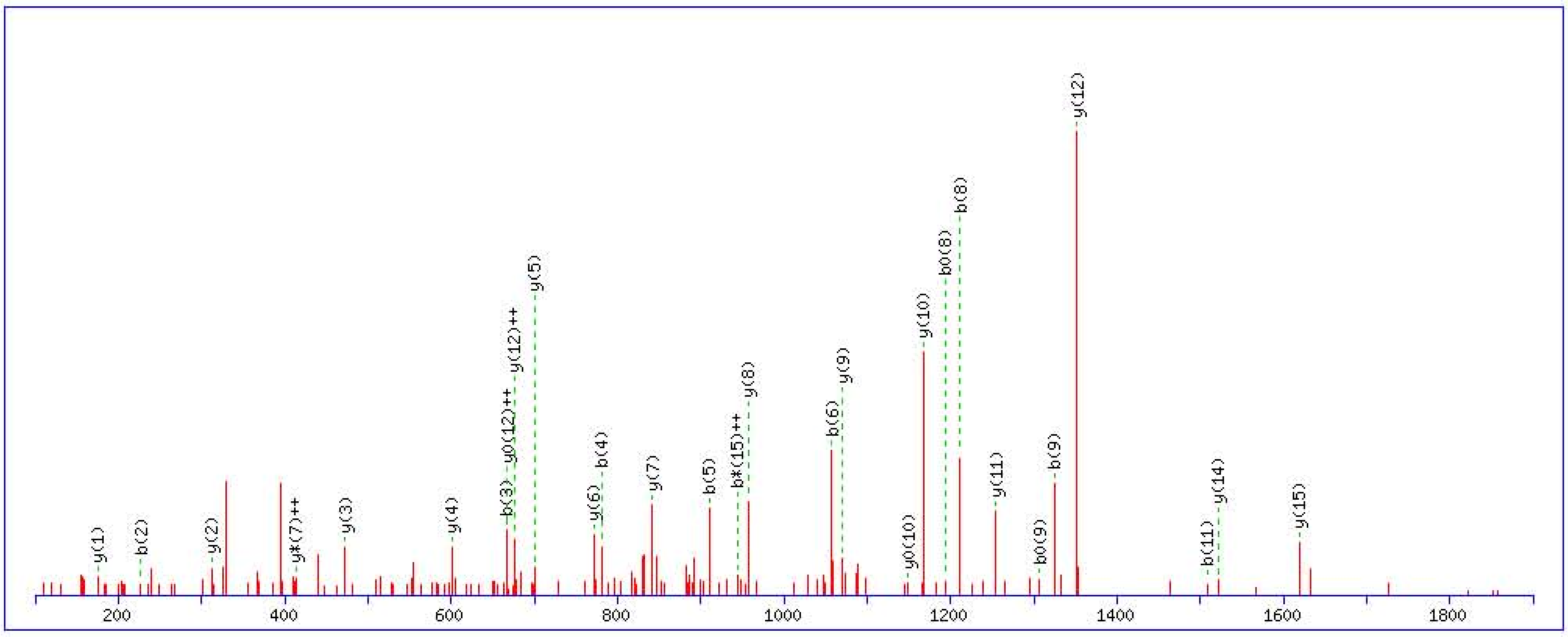
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLQDEFPGIPSPLDAAVECHR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

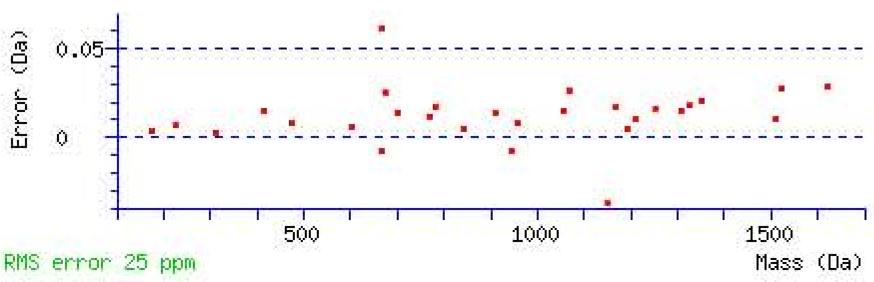
Match to Query 67251: 2674.355682 from(892.459170,3+) rtinseconds(2646) index(82572)
Title: Locus:1.1.1.3135.13 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

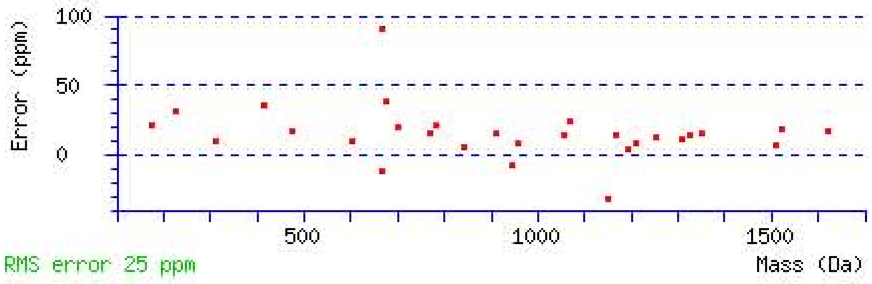
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1900 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2674.324722
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 76  Expect: 7.3e-007
Matches : 29/224 fragment ions using 62 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							21
2	***227.175404***	114.091340					L	2562.247943	1281.627609	2545.221394	1273.114335	2544.237378	1272.622327	20
3	***666.400730***	333.704003	649.374181	325.190729			Q	2449.163879	1225.085577	2432.137330	1216.572303	2431.153314	1216.080295	19
4	***781.427673***	391.217475	764.401124	382.704200	763.417108	382.212192	D	2009.938553	1005.472914	1992.912004	996.959640	1991.927988	996.467632	18
5	***910.470266***	455.738771	893.443717	447.225497	892.459701	446.733489	E	1894.911610	947.959443	1877.885061	939.446169	1876.901045	938.954160	17
6	***1057.538680***	529.272978	1040.512131	520.759704	1039.528115	520.267696	F	1765.869017	883.438146	1748.842468	874.924872	1747.858452	874.432864	16
7	1154.591444	577.799360	1137.564895	569.286086	1136.580879	568.794078	P	***1618.800603***	809.903939	1601.774054	801.390665	1600.790038	800.898657	15
8	***1211.612908***	606.310092	1194.586359	597.796818	1193.602343	597.304810	G	***1521.747839***	761.377557	1504.721290	752.864283	1503.737274	752.372275	14
9	***1324.696972***	662.852124	1307.670423	654.338850	1306.686407	653.846841	I	1464.726375	732.866825	1447.699826	724.353551	1446.715810	723.861543	13
10	1421.749736	711.378506	1404.723187	702.865232	1403.739171	702.373223	P	***1351.642311***	676.324793	1334.615762	667.811519	1333.631746	667.319511	12
11	***1508.781764***	754.894520	1491.755215	746.381246	1490.771199	745.889238	S	***1254.589547***	627.798411	1237.562998	619.285137	1236.578982	618.793129	11
12	1605.834528	803.420902	1588.807979	794.907628	1587.823963	794.415620	P	***1167.557519***	584.282397	1150.530970	575.769123	1149.546954	575.277115	10
13	1718.918592	859.962934	1701.892043	851.449660	1700.908027	850.957652	L	***1070.504755***	535.756015	1053.478206	527.242741	1052.494190	526.750733	9
14	1833.945535	917.476406	1816.918986	908.963131	1815.934970	908.471123	D	***957.420691***	479.213983	940.394142	470.700709	939.410126	470.208701	8
15	1904.982649	952.994963	1887.956100	944.481688	1886.972084	943.989680	A	***842.393748***	421.700512	825.367199	413.187237	824.383183	412.695229	7
16	1976.019763	988.513520	1958.993214	980.000245	1958.009198	979.508237	A	***771.356634***	386.181955	754.330085	377.668680	753.346069	377.176672	6
17	2075.088177	1038.047726	2058.061628	1029.534452	2057.077612	1029.042444	V	***700.319520***	350.663398	683.292971	342.150123	682.308955	341.658115	5
18	2204.130770	1102.569023	2187.104221	1094.055748	2186.120205	1093.563740	E	***601.251106***	301.129191	584.224557	292.615916	583.240541	292.123908	4
19	2364.161419	1182.584347	2347.134870	1174.071073	2346.150854	1173.579065	C	***472.208513***	236.607894	455.181964	228.094620			3
20	2501.220331	1251.113803	2484.193782	1242.600529	2483.209766	1242.108521	H	***312.177864***	156.592570	295.151315	148.079295			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.9	2674.324722	0.030960	LLQDEFPGIPSPLDAAVECHR

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

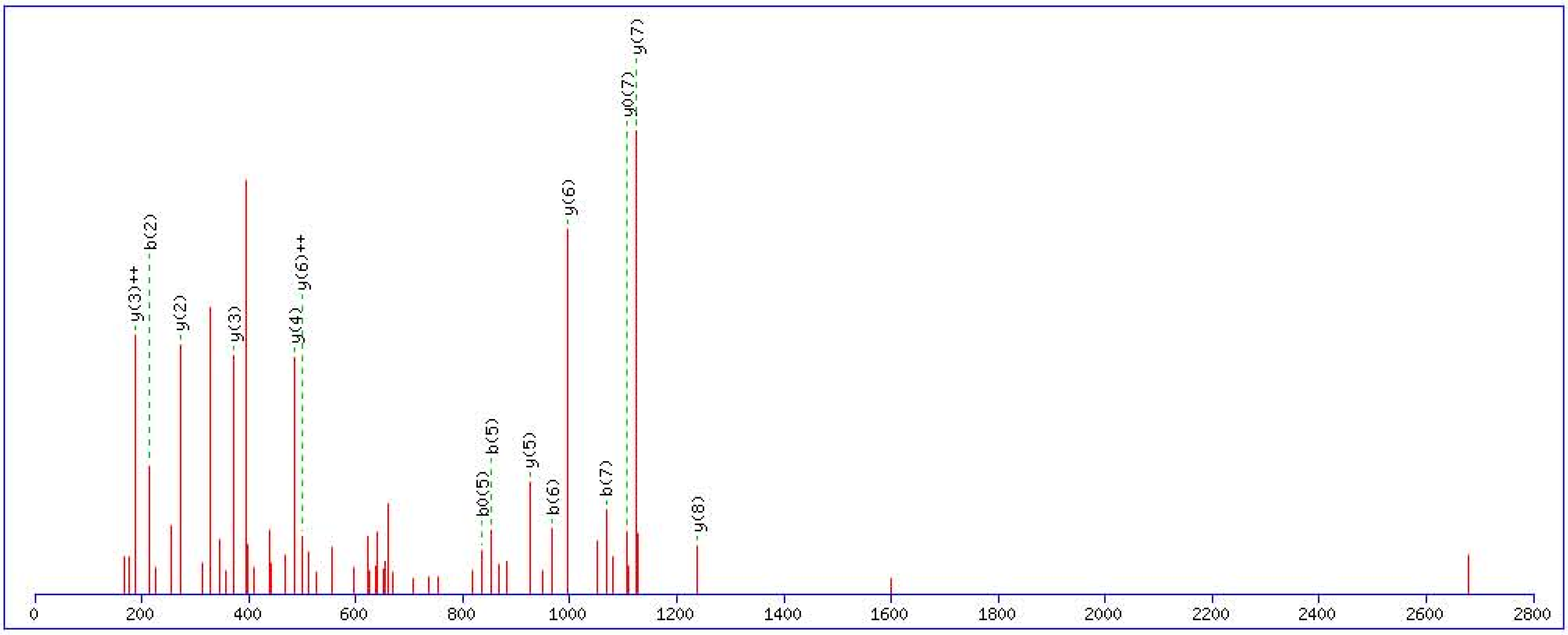
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLEAQLTPR**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

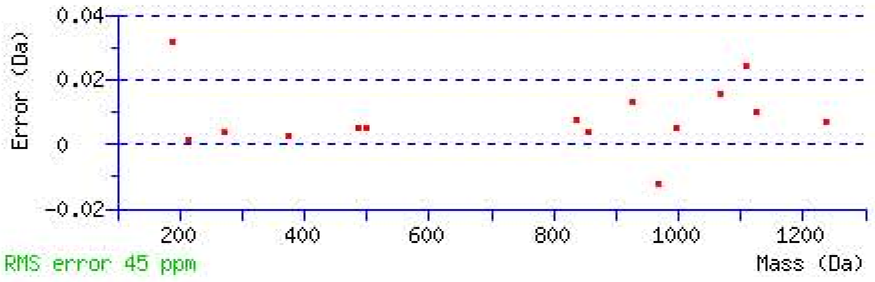
Match to Query 31767: 1338.738828 from(670.376690,2+) rtinseconds(1925) index(41624)
Title: Locus:1.1.1.2954.16 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

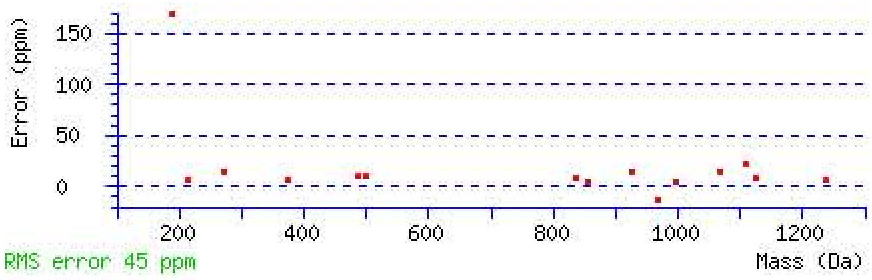
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1338.732941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 55 **Expect:** 4.8e-005
Matches : 15/84 fragment ions using 21 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							9
2	**215.139019**	108.073147			197.128454	99.067865	L	***1238.692556***	619.849916	1221.666007	611.336642	1220.681991	610.844633	8
3	344.181612	172.594444			326.171047	163.589162	E	***1125.608492***	563.307884	1108.581943	554.794610	1107.597927	554.302602	7
4	415.218726	208.113001			397.208161	199.107719	A	***996.565899***	498.786588	979.539350	490.273313	978.555334	489.781305	6
5	**854.444052**	427.725664	837.417503	419.212390	836.433487	418.720382	Q	***925.528785***	463.268031	908.502236	454.754756	907.518220	454.262748	5
6	**967.528116**	484.267696	950.501567	475.754422	949.517551	475.262414	L	***486.303459***	243.655367	469.276910	235.142093	468.292894	234.650085	4
7	**1068.575795**	534.791536	1051.549246	526.278261	1050.565230	525.786253	T	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
8	1165.628559	583.317918	1148.602010	574.804643	1147.617994	574.312635	P	***272.171716***	136.589496	255.145167	128.076221			2
9							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.2	1338.732941	0.005887	TLEAQLTPR
8.6	1338.732956	0.005872	VDLQSLPTR
8.5	1338.725555	0.013273	VDTVAAEHLTRK
0.5	1338.732941	0.005887	TDRIYAMKVVK

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

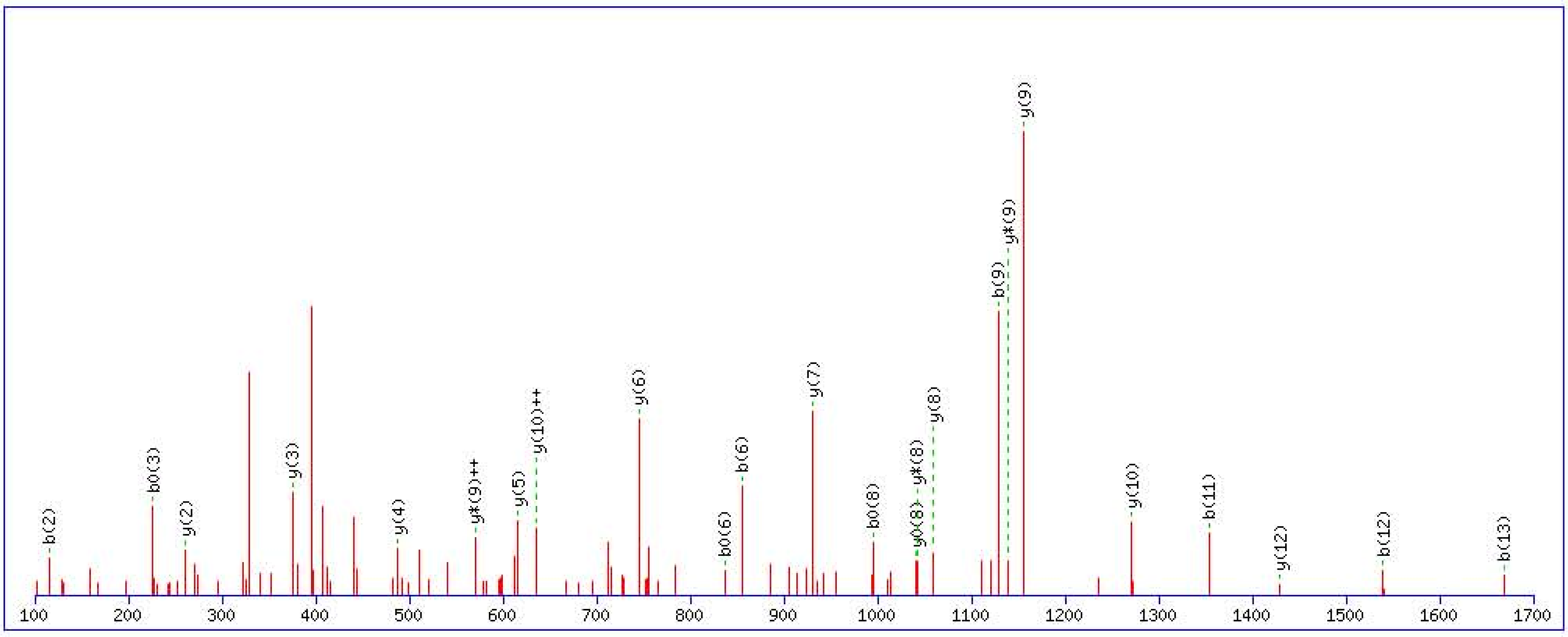
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

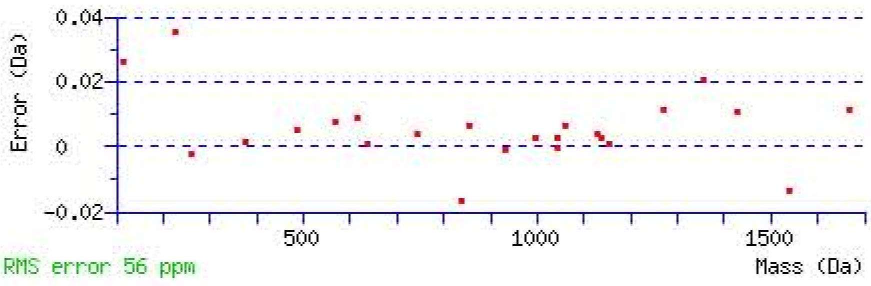
Match to Query 60277: 2283.078312 from(762.033380,3+) rtinseconds(1880) index(41240)
Title: Locus:1.1.1.2938.24 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

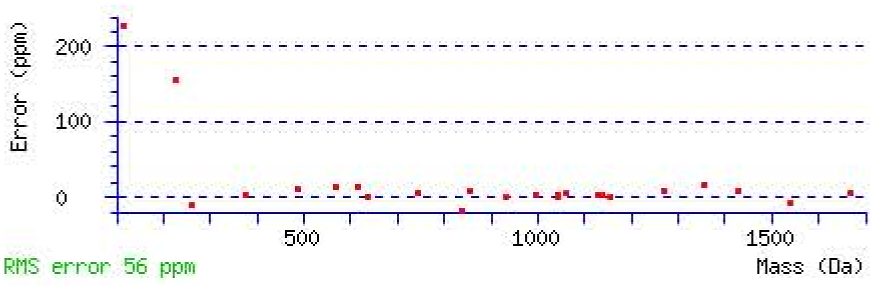
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2283.058975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 4.8e-005
Matches : 24/180 fragment ions using 41 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							18
2	**115.050204**	58.028740					G	2227.044809	1114.026042	2210.018260	1105.512768	2209.034244	1105.020760	17
3	244.092797	122.550037			226.082232	113.544754	E	2170.023345	1085.515310	2152.996796	1077.002036	2152.012780	1076.510028	16
4	345.140476	173.073876			327.129911	164.068594	T	2040.980752	1020.994014	2023.954203	1012.480740	2022.970187	1011.988732	15
5	416.177590	208.592433			398.167025	199.587151	A	1939.933073	970.470175	1922.906524	961.956900	1921.922508	961.464892	14
6	**855.402916**	428.205096	838.376367	419.691822	837.392351	419.199814	Q	1868.895959	934.951618	1851.869410	926.438343	1850.885394	925.946335	13
7	942.434944	471.721110	925.408395	463.207836	924.424379	462.715828	S	***1429.670633***	715.338955	1412.644084	706.825680	1411.660068	706.333672	12
8	1013.472058	507.239667	996.445509	498.726393	995.461493	498.234385	A	1342.638605	671.822941	1325.612056	663.309666	1324.628040	662.817658	11
9	**1128.499001**	564.753139	1111.472452	556.239864	1110.488436	555.747856	D	***1271.601491***	636.304384	1254.574942	627.791109	1253.590926	627.299101	10
10	1225.551765	613.279521	1208.525216	604.766246	1207.541200	604.274238	P	***1156.574548***	578.790912	1139.547999	570.277638	1138.563983	569.785630	9
11	**1353.610343**	677.308810	1336.583794	668.795535	1335.599778	668.303527	Q	***1059.521784***	530.264530	1042.495235	521.751256	1041.511219	521.259248	8
12	**1539.689656**	770.348466	1522.663107	761.835192	1521.679091	761.343184	W	***931.463206***	466.235241	914.436657	457.721967	913.452641	457.229959	7
13	**1668.732249**	834.869762	1651.705700	826.356488	1650.721684	825.864480	E	***745.383893***	373.195585	728.357344	364.682310	727.373328	364.190302	6
14	1796.790827	898.899052	1779.764278	890.385777	1778.780262	889.893769	Q	***616.341300***	308.674288	599.314751	300.161014			5
15	1909.874891	955.441083	1892.848342	946.927809	1891.864326	946.435801	L	***488.282722***	244.644999	471.256173	236.131725			4
16	2023.917818	1012.462547	2006.891269	1003.949273	2005.907253	1003.457265	N	***375.198658***	188.102967	358.172109	179.589693			3
17	2137.960745	1069.484010	2120.934196	1060.970736	2119.950180	1060.478728	N	***261.155731***	131.081504	244.129182	122.568229			2
18							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.5	2283.058975	0.019337	GGETAQSADPQWEQLNNK
10.7	2283.058975	0.019337	GGETAQSADPQWEQLNNK

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

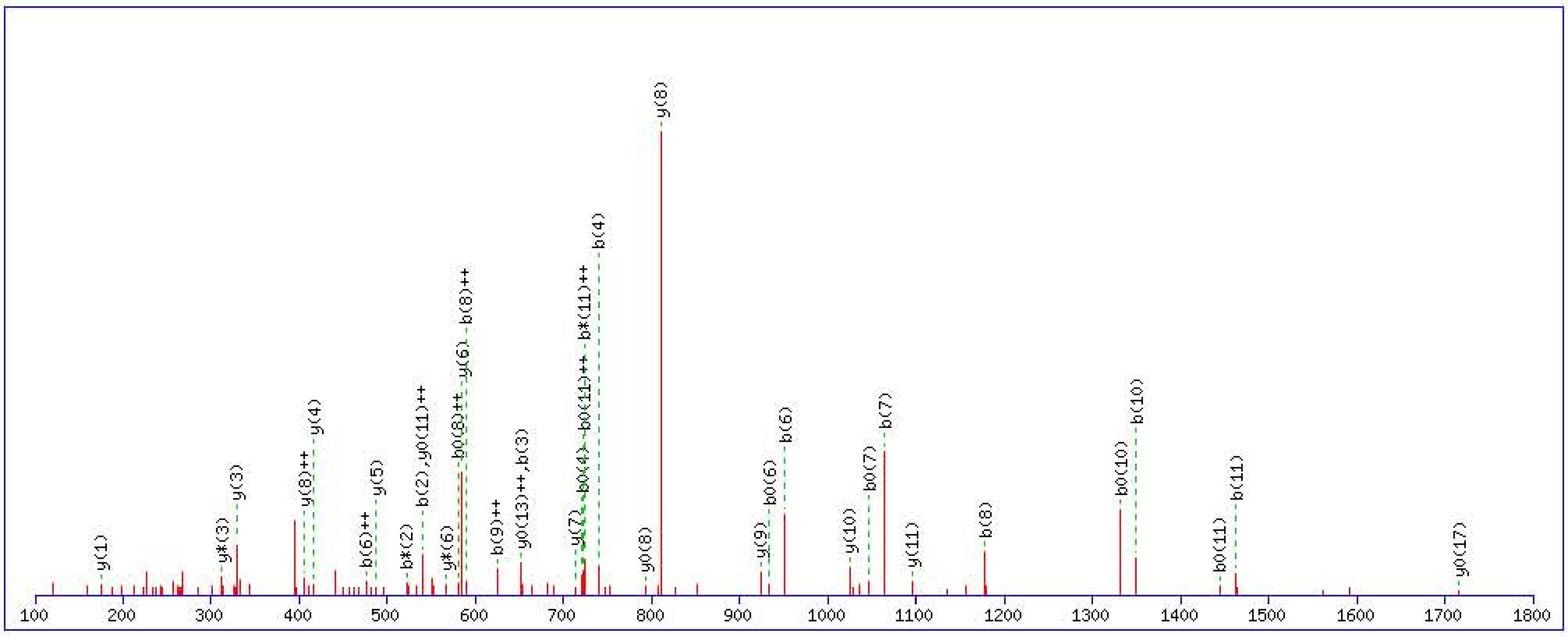
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQLSPDLLATLPEPASPGR**
Found in **HGFA_HUMAN**, Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1

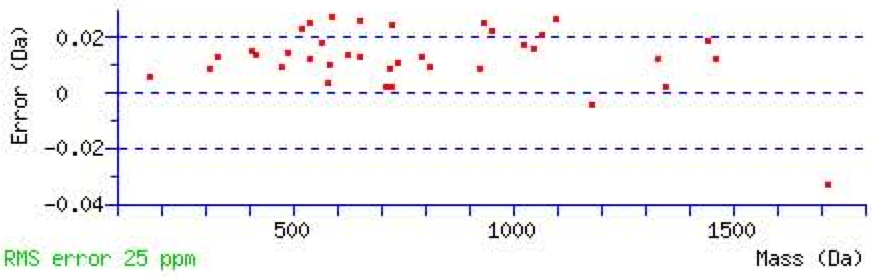
Match to Query 59977: 2271.258762 from(758.093530,3+) rtinseconds(2648) index(10991)
Title: Locus:1.1.1.3054.18 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

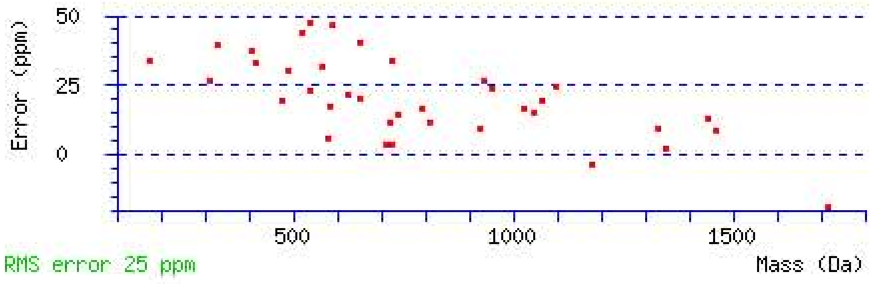
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2271.229675
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 2.4e-005
Matches : 37/202 fragment ions using 71 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							19
2	***539.301016***	270.154146	522.274467	261.640872			Q	2173.168553	1087.087914	2156.142004	1078.574640	2155.157988	1078.082632	18
3	***652.385080***	326.696178	635.358531	318.182904			L	1733.943227	867.475252	1716.916678	858.961977	1715.932662	858.469969	17
4	***739.417108***	370.212192	722.390559	361.698918	721.406543	361.206910	S	1620.859163	810.933219	1603.832614	802.419945	1602.848598	801.927937	16
5	836.469872	418.738574	819.443323	410.225300	818.459307	409.733292	P	1533.827135	767.417206	1516.800586	758.903931	1515.816570	758.411923	15
6	***951.496815***	**476.252046**	934.470266	467.738771	933.486250	467.246763	D	1436.774371	718.890824	1419.747822	710.377549	1418.763806	709.885541	14
7	***1064.580879***	532.794078	1047.554330	524.280803	1046.570314	523.788795	L	1321.747428	661.377352	1304.720879	652.864078	1303.736863	652.372069	13
8	***1177.664943***	**589.336110**	1160.638394	580.822835	1159.654378	580.330827	L	1208.663364	604.835320	1191.636815	596.322046	1190.652799	595.830038	12
9	1248.702057	**624.854667**	1231.675508	616.341392	1230.691492	615.849384	A	***1095.579300***	548.293288	1078.552751	539.780014	1077.568735	539.288006	11
10	***1349.749736***	675.378506	1332.723187	666.865232	1331.739171	666.373223	T	***1024.542186***	512.774731	1007.515637	504.261456	1006.531621	503.769448	10
11	***1462.833800***	731.920538	1445.807251	723.407264	1444.823235	722.915255	L	***923.494507***	462.250892	906.467958	453.737617	905.483942	453.245609	9
12	1559.886564	780.446920	1542.860015	771.933646	1541.875999	771.441637	P	***810.410443***	405.708860	793.383894	397.195585	792.399878	396.703577	8
13	1688.929157	844.968216	1671.902608	836.454942	1670.918592	835.962934	E	***713.357679***	357.182478	696.331130	348.669203	695.347114	348.177195	7
14	1785.981921	893.494598	1768.955372	884.981324	1767.971356	884.489316	P	***584.315086***	292.661181	567.288537	284.147907	566.304521	283.655899	6
15	1857.019035	929.013155	1839.992486	920.499881	1839.008470	920.007873	A	***487.262322***	244.134799	470.235773	235.621525	469.251757	235.129517	5
16	1944.051063	972.529169	1927.024514	964.015895	1926.040498	963.523887	S	***416.225208***	208.616242	399.198659	200.102968	398.214643	199.610960	4
17	2041.103827	1021.055552	2024.077278	1012.542277	2023.093262	1012.050269	P	***329.193180***	165.100228	312.166631	156.586954			3
18	2098.125291	1049.566283	2081.098742	1041.053009	2080.114726	1040.561001	G	232.140416	116.573846	215.113867	108.060572			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.1	2271.229675	0.029087	VQLSPDLLATLPEPASPGR
6.5	2271.226303	0.032459	IAKSDPPTLLTPSKWSVEFR
3.2	2271.277283	-0.018521	IIQGDIIASNGLLHILDR

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

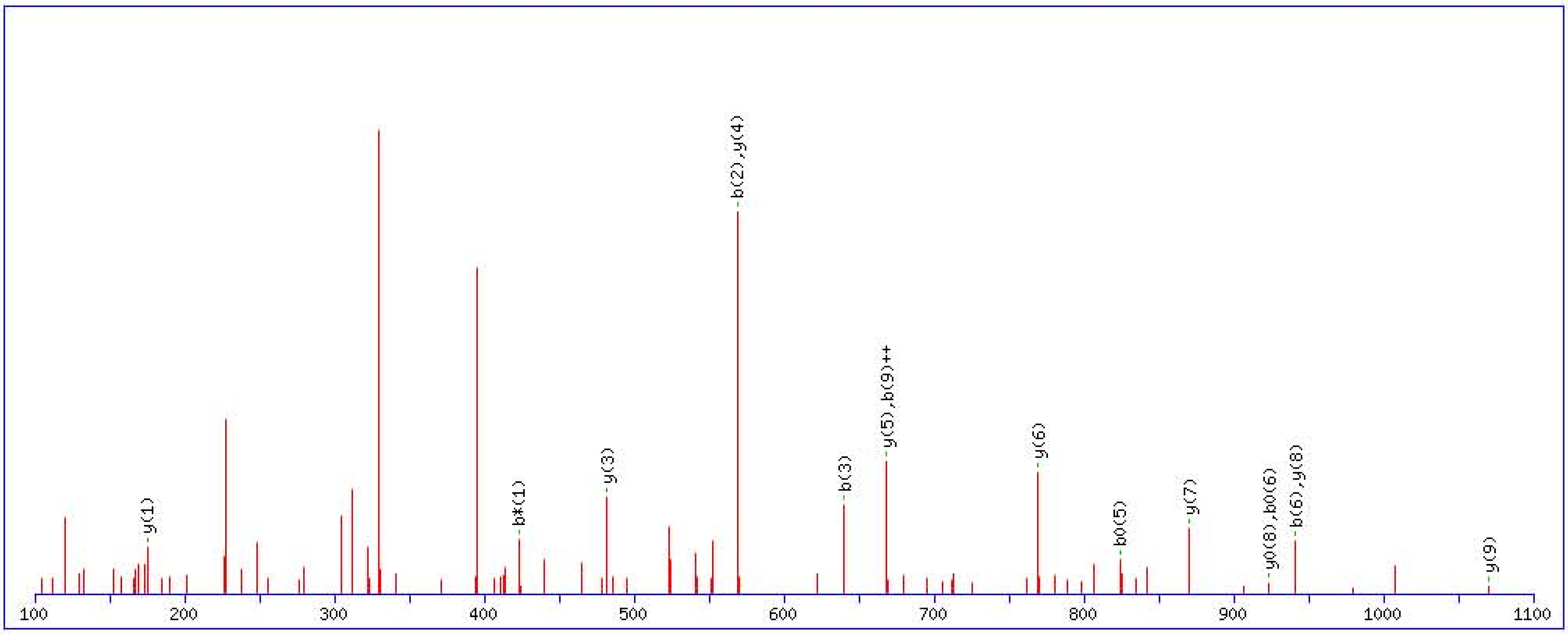
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEATTVSCFR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

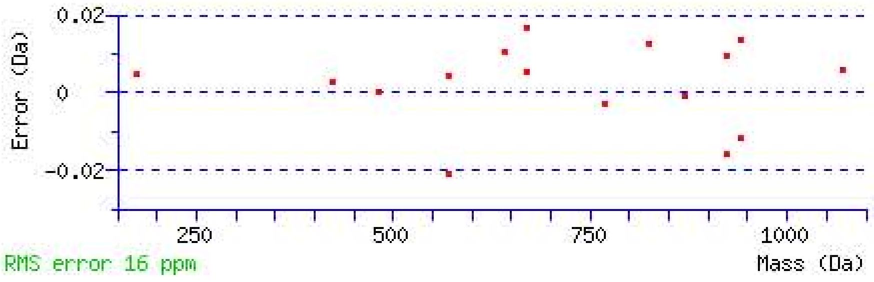
Match to Query 38917: 1508.717532 from(503.913120,3+) rtinseconds(1748) index(76806)
Title: Locus:1.1.1.2823.7 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

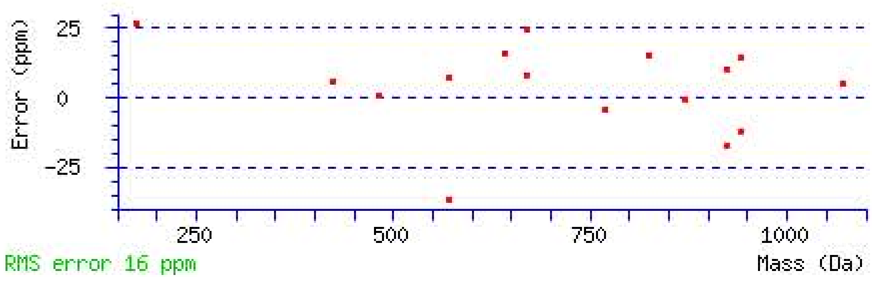
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1508.711578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 6.4e-005
Matches : 16/100 fragment ions using 20 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							10
2	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	E	***1070.493522***	535.750399	1053.466973	527.237125	1052.482957	526.745117	9
3	**640.312309**	320.659793	623.285760	312.146518	622.301744	311.654510	A	***941.450929***	471.229103	924.424380	462.715828	923.440364	462.223820	8
4	741.359988	371.183632	724.333439	362.670358	723.349423	362.178350	T	***870.413815***	435.710546	853.387266	427.197271	852.403250	426.705263	7
5	842.407667	421.707472	825.381118	413.194197	824.397102	412.702189	T	***769.366136***	385.186706	752.339587	376.673432	751.355571	376.181424	6
6	**941.476081**	471.241679	924.449532	462.728404	923.465516	462.236396	V	***668.318457***	334.662867	651.291908	326.149592	650.307892	325.657584	5
7	1028.508109	514.757693	1011.481560	506.244418	1010.497544	505.752410	S	***569.250043***	285.128660	552.223494	276.615385	551.239478	276.123377	4
8	1188.538758	594.773017	1171.512209	586.259743	1170.528193	585.767735	C	***482.218015***	241.612646	465.191466	233.099371			3
9	1335.607172	668.307224	1318.580623	659.793950	1317.596607	659.301942	F	322.187366	161.597321	305.160817	153.084047			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	1508.711578	0.005954	QEATTVSCFR

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

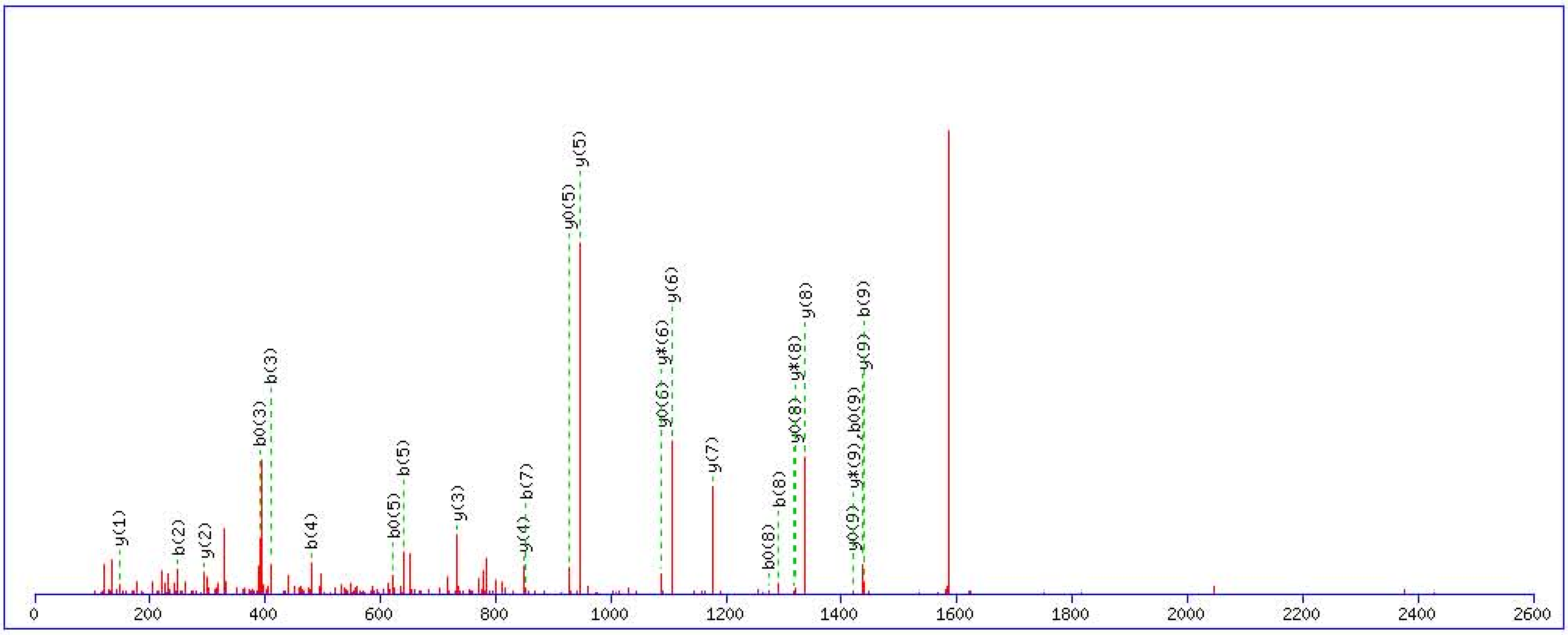
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FTCACPDQFK**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

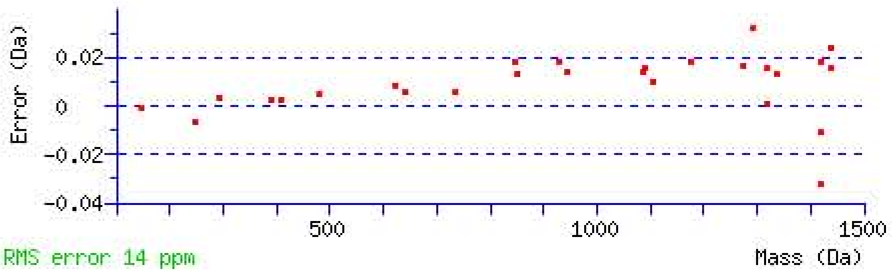
Match to Query 41378: 1583.711648 from(792.863100,2+) rtinseconds(1854) index(59397)
Title: Locus:1.1.1.2951.18 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

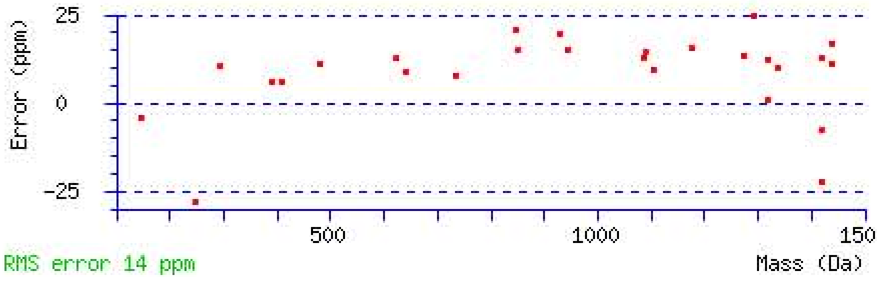
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1583.693497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00034
Matches : 27/86 fragment ions using 59 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							10
2	**249.123369**	125.065322			231.112804	116.060040	T	***1437.632342***	719.319809	1420.605793	710.806535	1419.621777	710.314527	9
3	**409.154018**	205.080647			391.143453	196.075365	C	***1336.584663***	668.795970	1319.558114	660.282695	1318.574098	659.790687	8
4	**480.191132**	240.599204			462.180567	231.593921	A	***1176.554014***	588.780645	1159.527465	580.267371	1158.543449	579.775363	7
5	**640.221781**	320.614529			622.211216	311.609246	C	***1105.516900***	553.262088	1088.490351	544.748814	1087.506335	544.256806	6
6	737.274545	369.140911			719.263980	360.135628	P	***945.486251***	473.246764	928.459702	464.733489	927.475686	464.241481	5
7	**852.301488**	426.654382			834.290923	417.649100	D	***848.433487***	424.720382	831.406938	416.207107	830.422922	415.715099	4
8	**1291.526814**	646.267045	1274.500265	637.753771	1273.516249	637.261763	Q	***733.406544***	367.206910	716.379995	358.693636			3
9	**1438.595228**	719.801252	1421.568679	711.287978	1420.584663	710.795970	F	***294.181218***	147.594247	277.154669	139.080973			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.1	1583.693497	0.018151	FTCACPDQFK

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

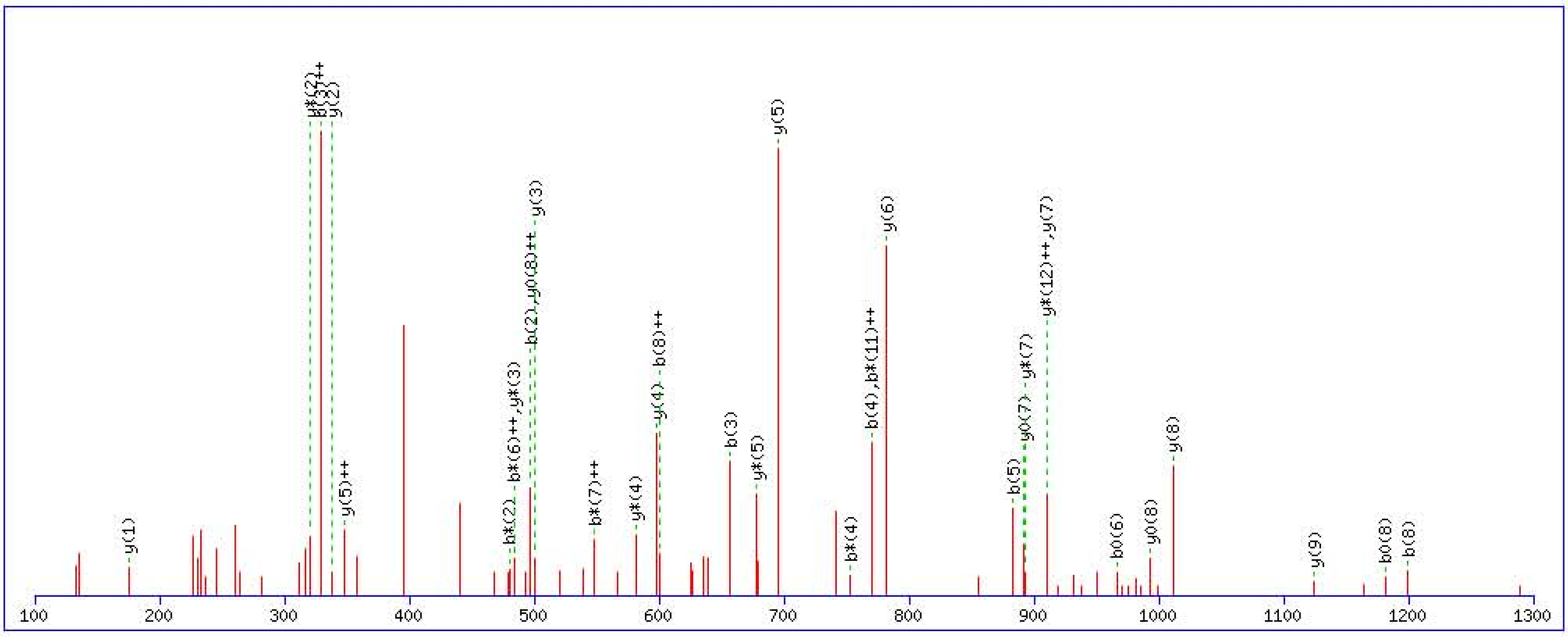
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQCLITQSPPYYR**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

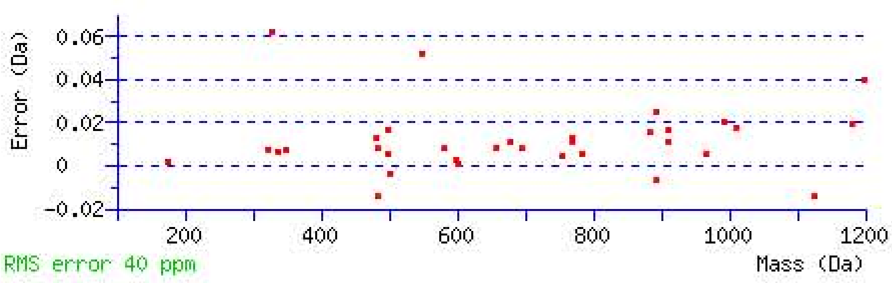
Match to Query 50461: 1892.945862 from(631.989230,3+) rtinseconds(2059) index(60982)
Title: Locus:1.1.1.3022.8 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

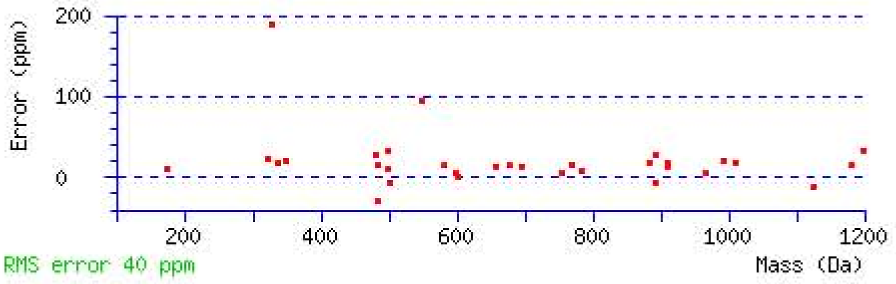
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1892.927704
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 0.00023
Matches : 33/122 fragment ions using 48 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							13
2	**497.254066**	249.130671	480.227517	240.617397			Q	1836.913526	918.960401	1819.886977	910.447127	1818.902961	909.955119	12
3	**657.284715**	**329.145996**	640.258166	320.632721			C	1397.688200	699.347738	1380.661651	690.834464	1379.677635	690.342456	11
4	**770.368779**	385.688028	753.342230	377.174753			L	1237.657551	619.332414	1220.631002	610.819139	1219.646986	610.327131	10
5	**883.452843**	442.230060	866.426294	433.716785			I	***1124.573487***	562.790382	1107.546938	554.277107	1106.562922	553.785099	9
6	984.500522	492.753899	967.473973	484.240625	966.489957	483.748617	T	***1011.489423***	506.248350	994.462874	497.735075	993.478858	497.243067	8
7	1112.559100	556.783188	1095.532551	548.269914	1094.548535	547.777906	Q	***910.441744***	455.724510	893.415195	447.211236	892.431179	446.719228	7
8	**1199.591128**	**600.299202**	1182.564579	591.785928	1181.580563	591.293920	S	***782.383166***	391.695221	765.356617	383.181947	764.372601	382.689939	6
9	1296.643892	648.825584	1279.617343	640.312310	1278.633327	639.820302	P	***695.351138***	348.179207	678.324589	339.665933			5
10	1393.696656	697.351966	1376.670107	688.838692	1375.686091	688.346684	P	***598.298374***	299.652825	581.271825	291.139551			4
11	1556.759985	778.883631	1539.733436	770.370356	1538.749420	769.878348	Y	***501.245610***	251.126443	484.219061	242.613169			3
12	1719.823314	860.415295	1702.796765	851.902021	1701.812749	851.410013	Y	***338.182281***	169.594778	321.155732	161.081504			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.2	1892.927704	0.018158	GQCLITQSPPYYR
12.8	1892.927704	0.018158	GQCLITQSPPYYR

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

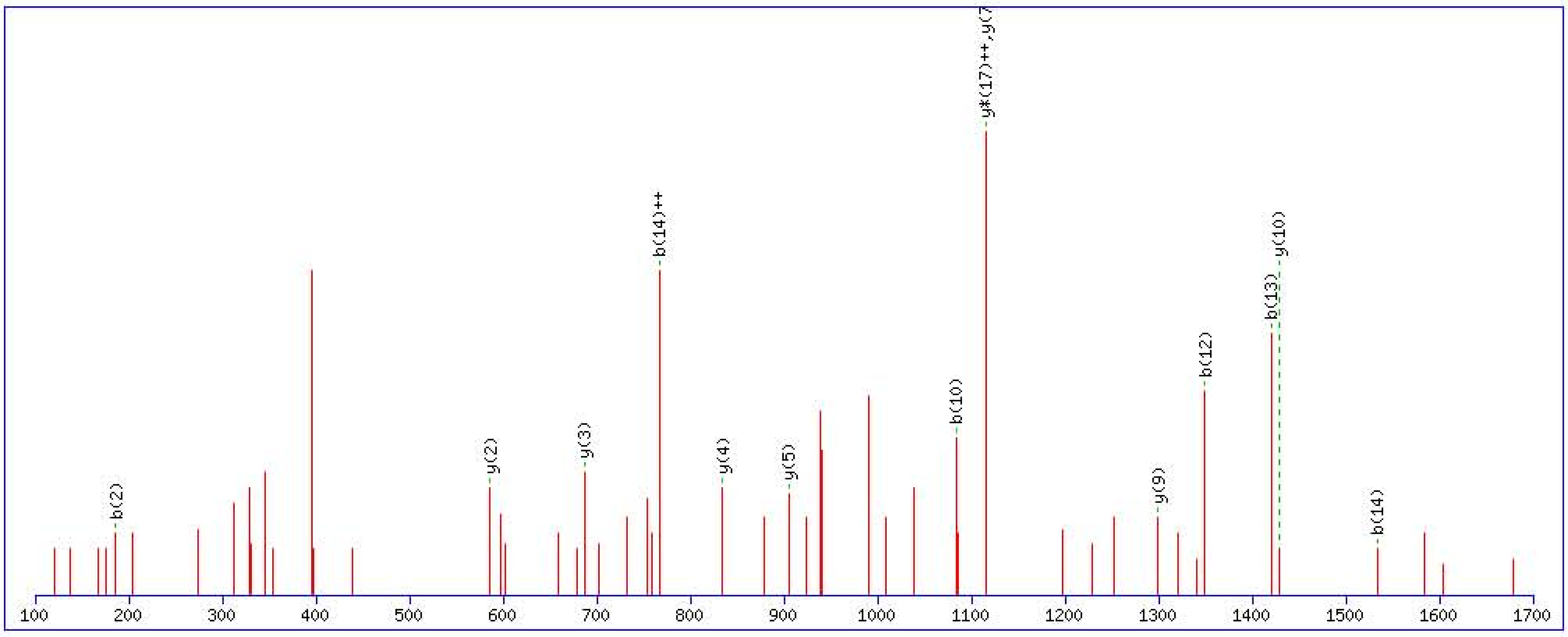
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGDTFSCMVGHEALPLAFTQK**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

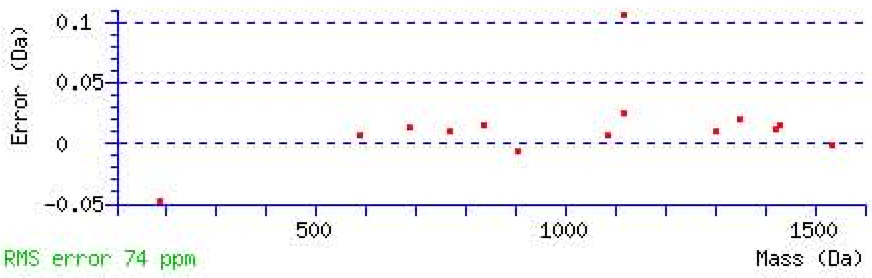
Match to Query 67025: 2647.331802 from(883.451210,3+) rtinseconds(2337) index(44302)
Title: Locus:1.1.1.3097.24 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

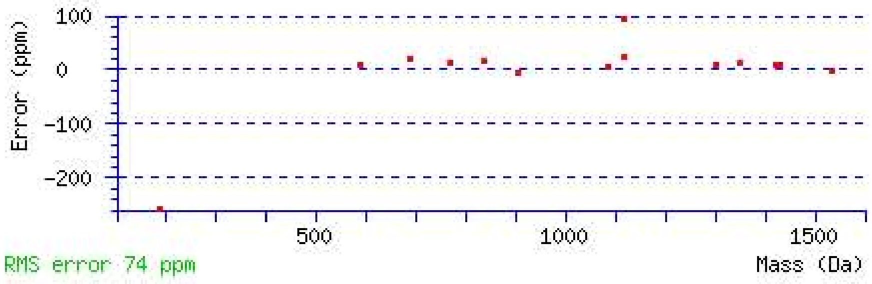
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2647.296082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.036
Matches : 14/232 fragment ions using 29 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			K							21
2	***186.123703***	93.565489	169.097154	85.052215			G	2520.208388	1260.607832	2503.181839	1252.094557	2502.197823	1251.602549	20
3	301.150646	151.078961	284.124097	142.565687	283.140081	142.073679	D	2463.186924	1232.097100	2446.160375	1223.583825	2445.176359	1223.091817	19
4	402.198325	201.602801	385.171776	193.089526	384.187760	192.597518	T	2348.159981	1174.583628	2331.133432	1166.070354	2330.149416	1165.578346	18
5	549.266739	275.137008	532.240190	266.623733	531.256174	266.131725	F	2247.112302	1124.059789	2230.085753	1115.546514	2229.101737	1115.054506	17
6	636.298767	318.653022	619.272218	310.139747	618.288202	309.647739	S	2100.043888	1050.525582	2083.017339	1042.012307	2082.033323	1041.520299	16
7	796.329416	398.668346	779.302867	390.155072	778.318851	389.663064	C	2013.011860	1007.009568	1995.985311	998.496294	1995.001295	998.004286	15
8	927.369901	464.188589	910.343352	455.675314	909.359336	455.183306	M	1852.981211	926.994244	1835.954662	918.480969	1834.970646	917.988961	14
9	1026.438315	513.722796	1009.411766	505.209521	1008.427750	504.717513	V	1721.940726	861.474001	1704.914177	852.960727	1703.930161	852.468719	13
10	***1083.459779***	542.233528	1066.433230	533.720253	1065.449214	533.228245	G	1622.872312	811.939794	1605.845763	803.426520	1604.861747	802.934512	12
11	1220.518691	610.762984	1203.492142	602.249709	1202.508126	601.757701	H	1565.850848	783.429062	1548.824299	774.915788	1547.840283	774.423780	11
12	***1349.561284***	675.284280	1332.534735	666.771006	1331.550719	666.278998	E	***1428.791936***	714.899606	1411.765387	706.386332	1410.781371	705.894324	10
13	***1420.598398***	710.802837	1403.571849	702.289563	1402.587833	701.797555	A	***1299.749343***	650.378310	1282.722794	641.865035	1281.738778	641.373027	9
14	***1533.682462***	767.344869	1516.655913	758.831595	1515.671897	758.339587	L	1228.712229	614.859753	1211.685680	606.346478	1210.701664	605.854470	8
15	1630.735226	815.871251	1613.708677	807.357977	1612.724661	806.865969	P	***1115.628165***	558.317721	1098.601616	549.804446	1097.617600	549.312438	7
16	1743.819290	872.413283	1726.792741	863.900009	1725.808725	863.408000	L	1018.575401	509.791339	1001.548852	501.278064	1000.564836	500.786056	6
17	1814.856404	907.931840	1797.829855	899.418566	1796.845839	898.926557	A	***905.491337***	453.249307	888.464788	444.736032	887.480772	444.244024	5
18	1961.924818	981.466047	1944.898269	972.952773	1943.914253	972.460764	F	***834.454223***	417.730750	817.427674	409.217475	816.443658	408.725467	4
19	2062.972497	1031.989886	2045.945948	1023.476612	2044.961932	1022.984604	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
20	2502.197823	1251.602549	2485.171274	1243.089275	2484.187258	1242.597267	Q	***586.338130***	293.672703	569.311581	285.159429			2
21							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.4	2647.296082	0.035720	KGDTFSCMVGHEALPLAFTQK

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

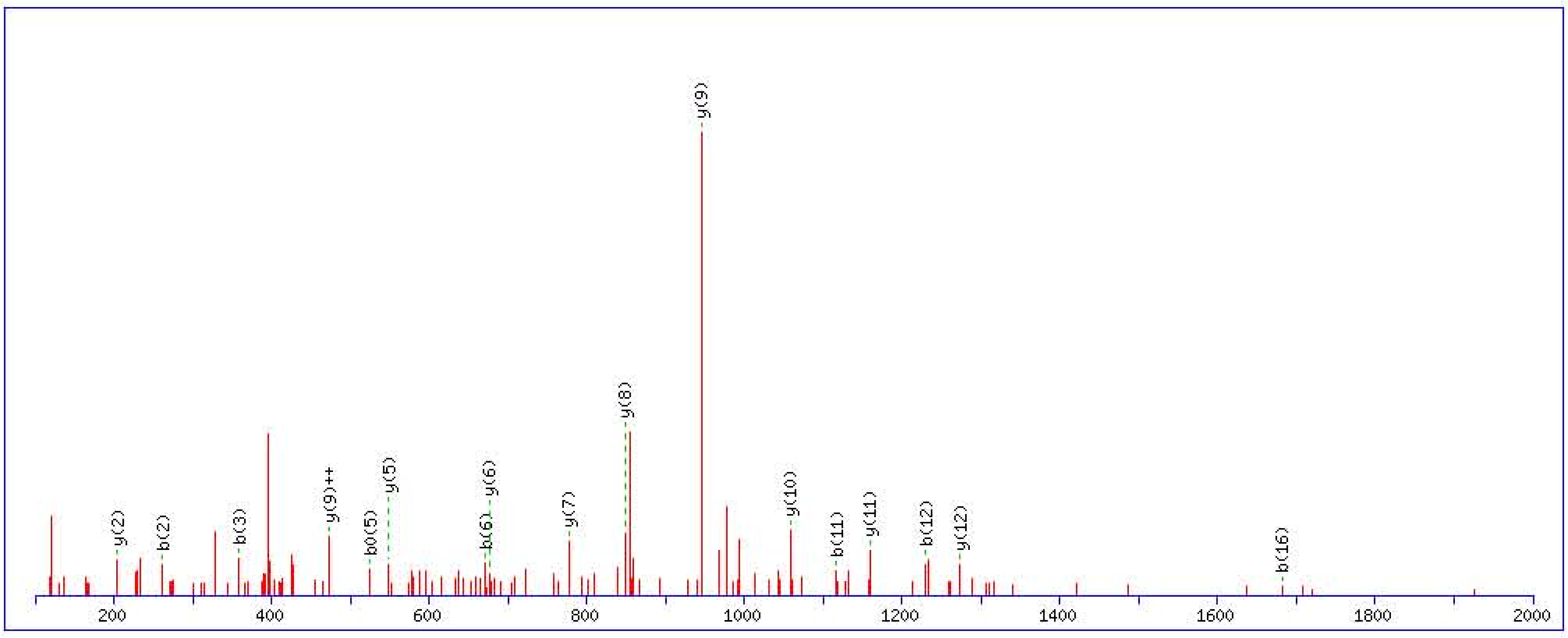
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NFPPSQDASGDLYTTSSQLTLPATQCLAGK**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

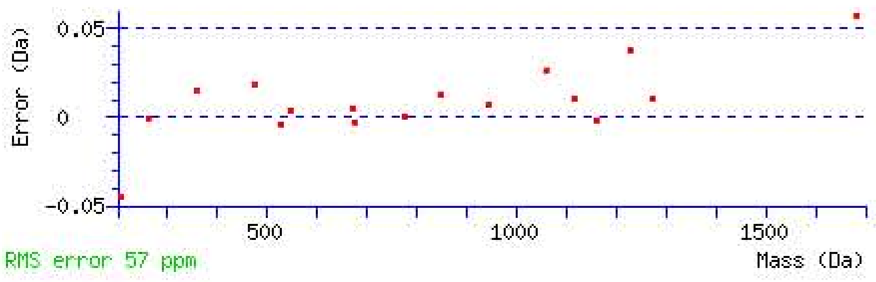
Match to Query 77658: 3478.717136 from(870.686560,4+) rtinseconds(2575) index(45717)
Title: Locus:1.1.1.3180.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

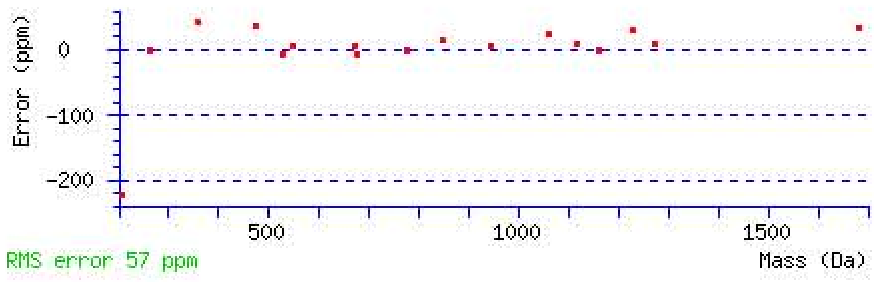
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3478.674866
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0094
Matches : 17/328 fragment ions using 44 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							30
2	***262.118617***	131.562946	245.092068	123.049672			F	3365.639210	1683.323243	3348.612661	1674.809968	3347.628645	1674.317960	29
3	***359.171381***	180.089328	342.144832	171.576054			P	3218.570796	1609.789036	3201.544247	1601.275761	3200.560231	1600.783753	28
4	456.224145	228.615710	439.197596	220.102436			P	3121.518032	1561.262654	3104.491483	1552.749379	3103.507467	1552.257371	27
5	543.256173	272.131725	526.229624	263.618450	525.245608	263.126442	S	3024.465268	1512.736272	3007.438719	1504.222997	3006.454703	1503.730989	26
6	***671.314751***	336.161014	654.288202	327.647739	653.304186	327.155731	Q	2937.433240	1469.220258	2920.406691	1460.706983	2919.422675	1460.214975	25
7	786.341694	393.674485	769.315145	385.161210	768.331129	384.669202	D	2809.374662	1405.190969	2792.348113	1396.677694	2791.364097	1396.185686	24
8	857.378808	429.193042	840.352259	420.679767	839.368243	420.187759	A	2694.347719	1347.677497	2677.321170	1339.164223	2676.337154	1338.672215	23
9	944.410836	472.709056	927.384287	464.195781	926.400271	463.703773	S	2623.310605	1312.158941	2606.284056	1303.645666	2605.300040	1303.153658	22
10	1001.432300	501.219788	984.405751	492.706513	983.421735	492.214505	G	2536.278577	1268.642926	2519.252028	1260.129652	2518.268012	1259.637644	21
11	***1116.459243***	558.733260	1099.432694	550.219985	1098.448678	549.727977	D	2479.257113	1240.132195	2462.230564	1231.618920	2461.246548	1231.126912	20
12	***1229.543307***	615.275291	1212.516758	606.762017	1211.532742	606.270009	L	2364.230170	1182.618723	2347.203621	1174.105448	2346.219605	1173.613440	19
13	1392.606636	696.806956	1375.580087	688.293682	1374.596071	687.801673	Y	2251.146106	1126.076691	2234.119557	1117.563416	2233.135541	1117.071408	18
14	1493.654315	747.330796	1476.627766	738.817521	1475.643750	738.325513	T	2088.082777	1044.545026	2071.056228	1036.031752	2070.072212	1035.539744	17
15	1594.701994	797.854635	1577.675445	789.341361	1576.691429	788.849353	T	1987.035098	994.021187	1970.008549	985.507913	1969.024533	985.015905	16
16	***1681.734022***	841.370649	1664.707473	832.857375	1663.723457	832.365367	S	1885.987419	943.497348	1868.960870	934.984073	1867.976854	934.492065	15
17	1768.766050	884.886663	1751.739501	876.373389	1750.755485	875.881381	S	1798.955391	899.981334	1781.928842	891.468059	1780.944826	890.976051	14
18	2207.991376	1104.499326	2190.964827	1095.986051	2189.980811	1095.494043	Q	1711.923363	856.465320	1694.896814	847.952045	1693.912798	847.460037	13
19	2321.075440	1161.041358	2304.048891	1152.528083	2303.064875	1152.036075	L	***1272.698037***	636.852657	1255.671488	628.339382	1254.687472	627.847374	12
20	2422.123119	1211.565197	2405.096570	1203.051923	2404.112554	1202.559915	T	***1159.613973***	580.310625	1142.587424	571.797350	1141.603408	571.305342	11
21	2535.207183	1268.107229	2518.180634	1259.593955	2517.196618	1259.101947	L	***1058.566294***	529.786785	1041.539745	521.273511	1040.555729	520.781503	10
22	2632.259947	1316.633611	2615.233398	1308.120337	2614.249382	1307.628329	P	***945.482230***	473.244753	928.455681	464.731479	927.471665	464.239471	9
23	2703.297061	1352.152169	2686.270512	1343.638894	2685.286496	1343.146886	A	***848.429466***	424.718371	831.402917	416.205097	830.418901	415.713089	8
24	2804.344740	1402.676008	2787.318191	1394.162733	2786.334175	1393.670725	T	***777.392352***	389.199814	760.365803	380.686540	759.381787	380.194532	7
25	2932.403318	1466.705297	2915.376769	1458.192022	2914.392753	1457.700015	Q	***676.344673***	338.675975	659.318124	330.162700			6
26	3092.433967	1546.720621	3075.407418	1538.207347	3074.423402	1537.715339	C	***548.286095***	274.646686	531.259546	266.133411			5
27	3205.518031	1603.262653	3188.491482	1594.749379	3187.507466	1594.257371	L	388.255446	194.631361	371.228897	186.118087			4
28	3276.555145	1638.781211	3259.528596	1630.267936	3258.544580	1629.775928	A	275.171382	138.089329	258.144833	129.576055			3
29	3333.576609	1667.291943	3316.550060	1658.778668	3315.566044	1658.286660	G	***204.134268***	102.570772	187.107719	94.057497			2
30							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.4	3478.674866	0.042270	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
20.1	3478.674866	0.042270	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
2.8	3478.674866	0.042270	NFPPSQDASGDLYTTSSQLTLPATQCLAGK

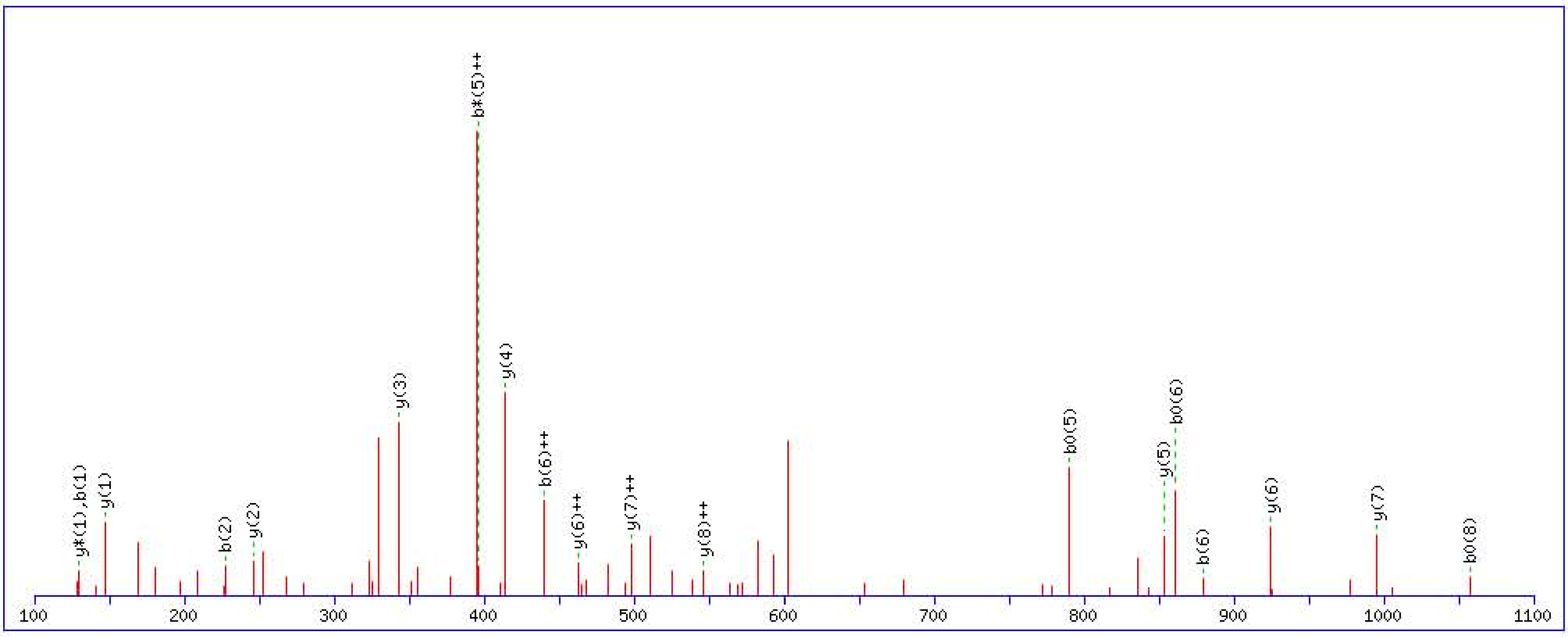
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPAAQAPVK**
Found in **IGHD_HUMAN**, Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2

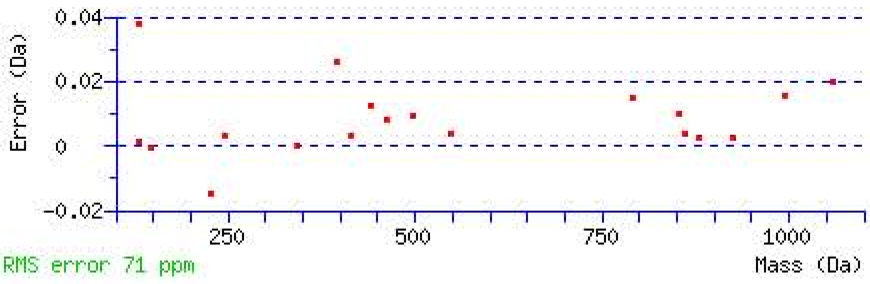
Match to Query 28242: 1220.663928 from(611.339240,2+) rtinseconds(1431) index(74721)
Title: Locus:1.1.1.2712.23 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

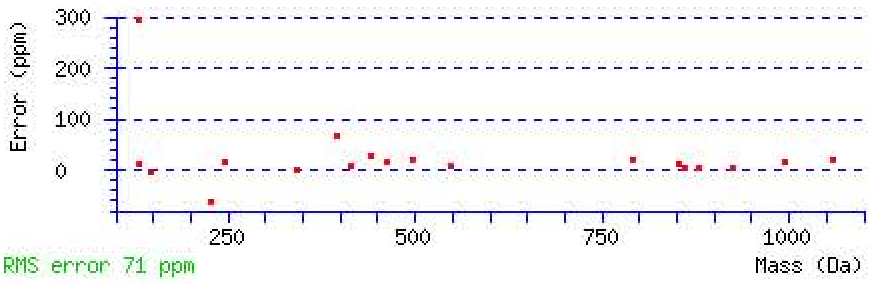
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1220.658707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0023
Matches : 19/72 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	**130.049869**	65.528572			112.039304	56.523290	E					9
2	**227.102633**	114.054954			209.092068	105.049672	P	1092.623414	546.815345	1075.596865	538.302071	8
3	298.139747	149.573512			280.129182	140.568229	A	***995.570650***	498.288963	978.544101	489.775689	7
4	369.176861	185.092068			351.166296	176.086786	A	***924.533536***	462.770406	907.506987	454.257132	6
5	808.402187	404.704732	791.375638	396.191457	790.391622	395.699449	Q	***853.496422***	427.251849	836.469873	418.738575	5
6	**879.439301**	440.223289	862.412752	431.710014	861.428736	431.218006	A	***414.271096***	207.639186	397.244547	199.125911	4
7	976.492065	488.749671	959.465516	480.236396	958.481500	479.744388	P	***343.233982***	172.120629	326.207433	163.607354	3
8	1075.560479	538.283878	1058.533930	529.770603	1057.549914	529.278595	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 EPAAQAPVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.4	1220.658707	0.005221	EPAAQAPVK
10.3	1220.658722	0.005206	EQNVPVPK
4.3	1220.676468	-0.012540	AEPPPSKPTVAK
2.1	1220.658722	0.005206	QPNLPDVK
2.1	1220.651321	0.012607	GQVLIAASSYGR
1.7	1220.654663	0.009265	QASKKTAMAAAK
1.4	1220.666580	-0.002652	EPAIVRFFSR
0.7	1220.651306	0.012622	ILSHTEEHKK

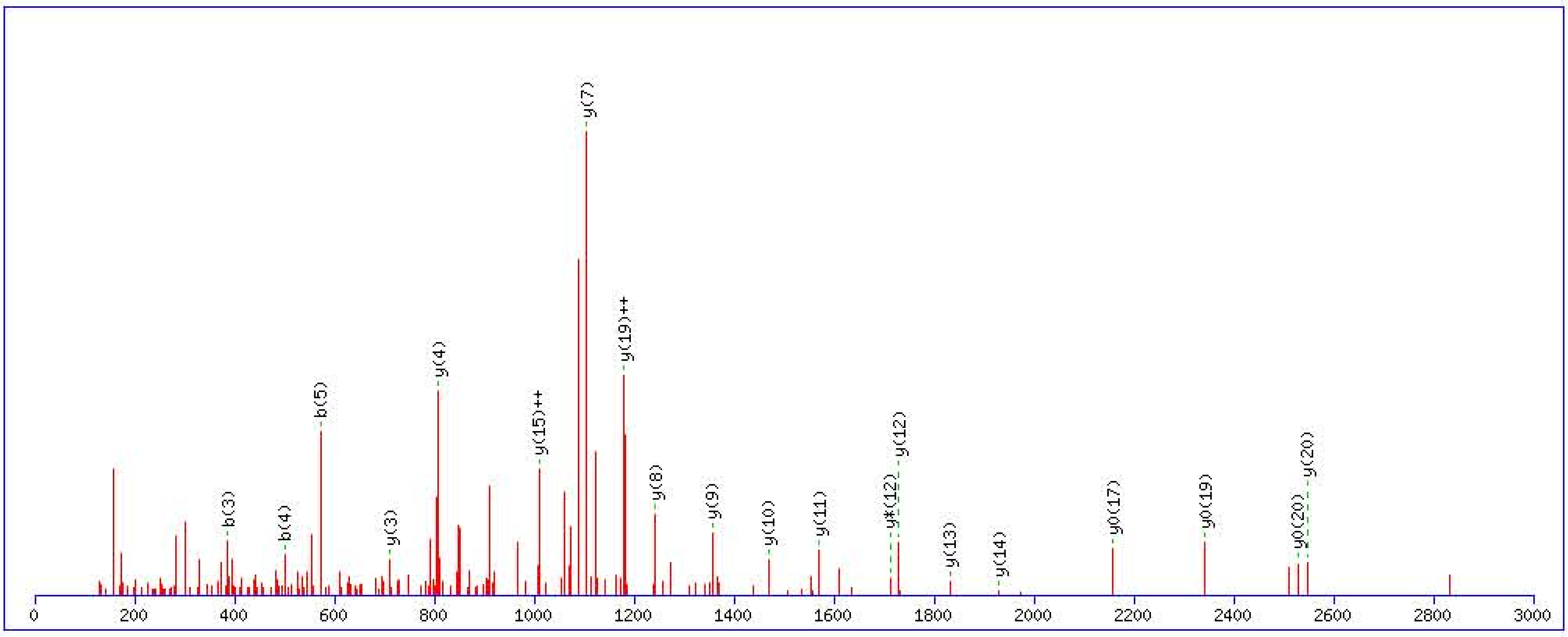
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLWNAGTSVTCTLNHPSLPPQR**
Found in **IGHD_HUMAN**, Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2

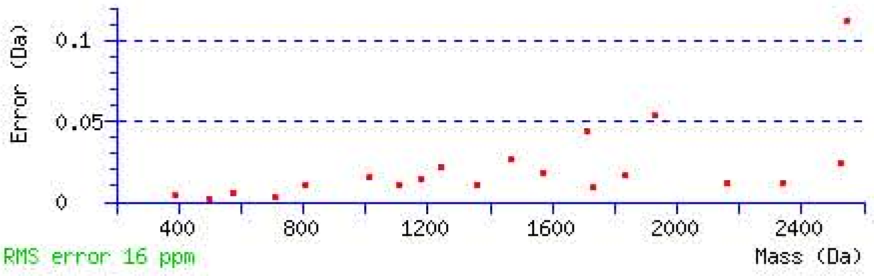
Match to Query 68075: 2746.399962 from(916.473930,3+) rtinseconds(2221) index(8542)
Title: Locus:1.1.1.2905.25 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

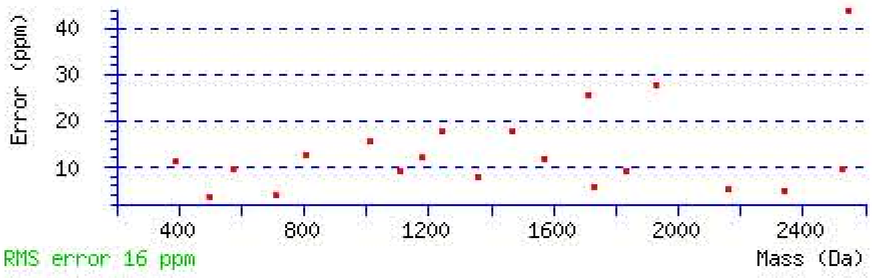
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2746.368332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21 : Biotin:Thermo-21345 (Q)
Ions Score: 91 **Expect:** 2.4e-008
Matches : 20/236 fragment ions using 23 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							22
2	201.123368	101.065322			183.112803	92.060039	L	2660.343575	1330.675425	2643.317026	1322.162151	2642.333010	1321.670143	21
3	**387.202681**	194.104978			369.192116	185.099696	W	***2547.259511***	1274.133393	2530.232962	1265.620119	2529.248946	1265.128111	20
4	**501.245608**	251.126442	484.219059	242.613168	483.235043	242.121160	N	2361.180198	1181.093737	2344.153649	1172.580462	2343.169633	1172.088454	19
5	**572.282722**	286.644999	555.256173	278.131725	554.272157	277.639717	A	2247.137271	1124.072273	2230.110722	1115.558999	2229.126706	1115.066991	18
6	629.304186	315.155731	612.277637	306.642457	611.293621	306.150449	G	2176.100157	1088.553716	2159.073608	1080.040442	2158.089592	1079.548434	17
7	730.351865	365.679571	713.325316	357.166296	712.341300	356.674288	T	2119.078693	1060.042984	2102.052144	1051.529710	2101.068128	1051.037702	16
8	817.383893	409.195585	800.357344	400.682310	799.373328	400.190302	S	2018.031014	1009.519145	2001.004465	1001.005871	2000.020449	1000.513863	15
9	916.452307	458.729792	899.425758	450.216517	898.441742	449.724509	V	***1930.998986***	966.003131	1913.972437	957.489857	1912.988421	956.997849	14
10	1017.499986	509.253631	1000.473437	500.740357	999.489421	500.248349	T	***1831.930572***	916.468924	1814.904023	907.955650	1813.920007	907.463642	13
11	1177.530635	589.268956	1160.504086	580.755681	1159.520070	580.263673	C	***1730.882893***	865.945085	1713.856344	857.431810	1712.872328	856.939802	12
12	1278.578314	639.792795	1261.551765	631.279521	1260.567749	630.787513	T	***1570.852244***	785.929760	1553.825695	777.416486	1552.841679	776.924478	11
13	1391.662378	696.334827	1374.635829	687.821553	1373.651813	687.329545	L	***1469.804565***	735.405921	1452.778016	726.892646	1451.794000	726.400638	10
14	1505.705305	753.356291	1488.678756	744.843016	1487.694740	744.351008	N	***1356.720501***	678.863889	1339.693952	670.350614	1338.709936	669.858606	9
15	1642.764217	821.885746	1625.737668	813.372472	1624.753652	812.880464	H	***1242.677574***	621.842425	1225.651025	613.329151	1224.667009	612.837143	8
16	1739.816981	870.412128	1722.790432	861.898854	1721.806416	861.406846	P	***1105.618662***	553.312969	1088.592113	544.799695	1087.608097	544.307687	7
17	1826.849009	913.928143	1809.822460	905.414868	1808.838444	904.922860	S	1008.565898	504.786587	991.539349	496.273313	990.555333	495.781305	6
18	1939.933073	970.470174	1922.906524	961.956900	1921.922508	961.464892	L	921.533870	461.270573	904.507321	452.757299			5
19	2036.985837	1018.996557	2019.959288	1010.483282	2018.975272	1009.991274	P	***808.449806***	404.728541	791.423257	396.215267			4
20	2134.038601	1067.522938	2117.012052	1059.009664	2116.028036	1058.517656	P	***711.397042***	356.202159	694.370493	347.688885			3
21	2573.263927	1287.135601	2556.237378	1278.622327	2555.253362	1278.130319	Q	614.344278	307.675777	597.317729	299.162503			2
22							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
90.8	2746.368332	0.031630	SLWNAGTSVTCTLNHPSLPPQR

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

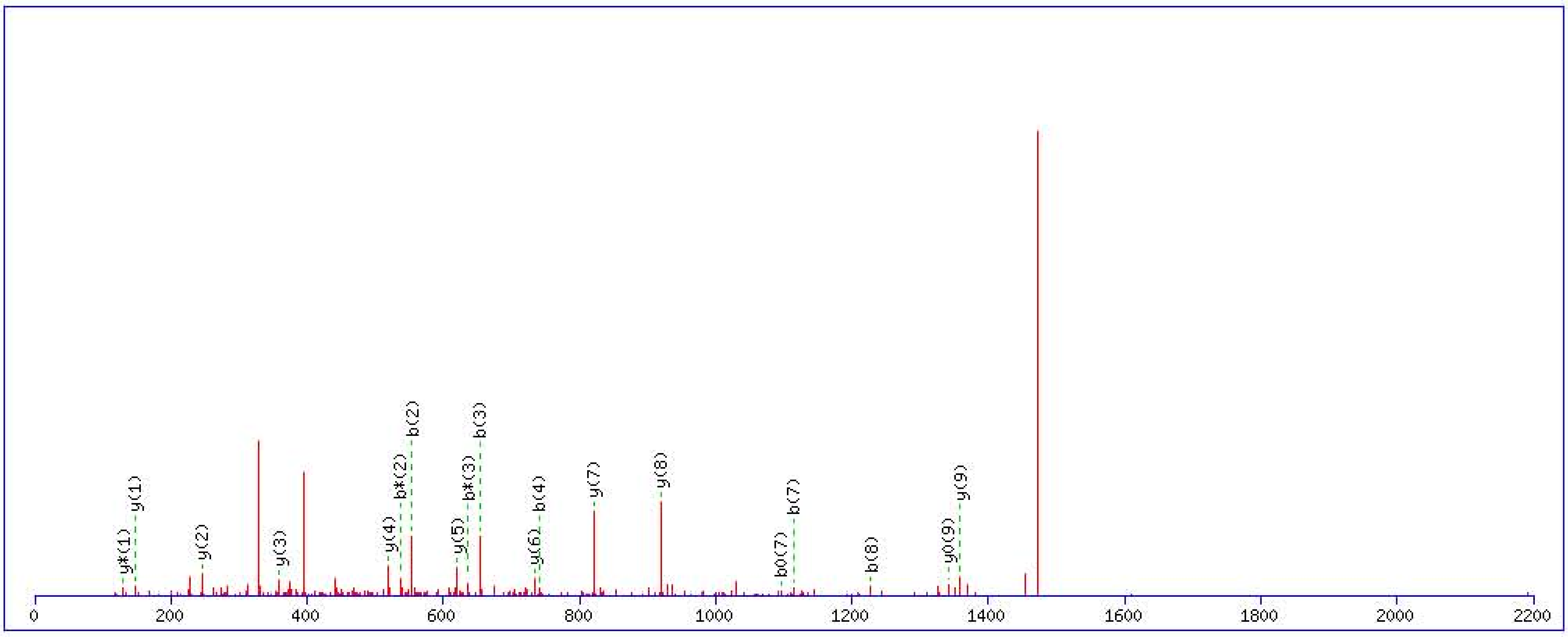
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

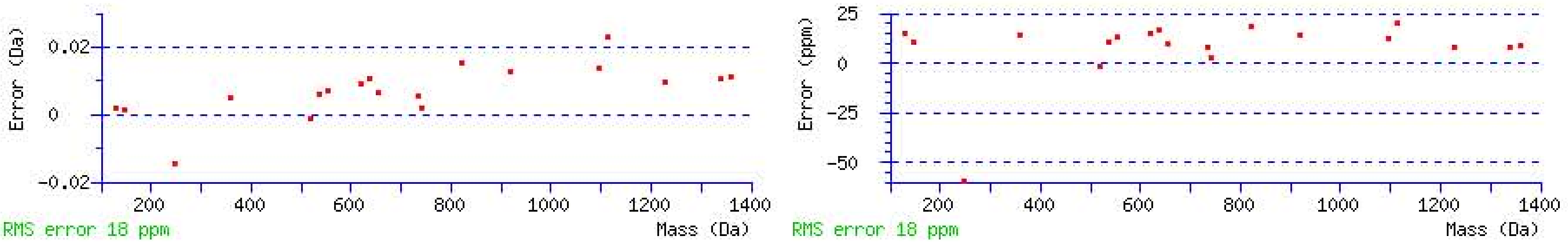
Match to Query 37736: 1471.800048 from(736.907300,2+) rtinseconds(2225) index(80100)
Title: Locus:1.1.1.2989.8 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 6e-005
Matches : 19/94 fragment ions using 40 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							10
2	**554.275529**	277.641403	537.248980	269.128128			Q	***1358.753442***	679.880359	1341.726893	671.367085	1340.742877	670.875076	9
3	**653.343943**	327.175610	636.317394	318.662335			V	***919.528116***	460.267696	902.501567	451.754421	901.517551	451.262413	8
4	**740.375971**	370.691623	723.349422	362.178349	722.365406	361.686341	S	***820.459702***	410.733489	803.433153	402.220215	802.449137	401.728207	7
5	853.460035	427.233656	836.433486	418.720381	835.449470	418.228373	L	***733.427674***	367.217475	716.401125	358.704201	715.417109	358.212193	6
6	954.507714	477.757495	937.481165	469.244220	936.497149	468.752212	T	***620.343610***	310.675443	603.317061	302.162169	602.333045	301.670161	5
7	**1114.538363**	557.772819	1097.511814	549.259545	1096.527798	548.767537	C	***519.295931***	260.151604	502.269382	251.638329			4
8	**1227.622427**	614.314851	1210.595878	605.801577	1209.611862	605.309569	L	***359.265282***	180.136279	342.238733	171.623004			3
9	1326.690841	663.849058	1309.664292	655.335784	1308.680276	654.843776	V	***246.181218***	123.594247	229.154669	115.080973			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.3	1471.789093	0.010955	NQVSLTCLVK
5.9	1471.792908	0.007140	NITINCVKGINAR
4.4	1471.797592	0.002456	KYFWDRAFLVK
3.9	1471.803467	-0.003419	EKQGPLLDLFGQK
0.2	1471.806793	-0.006745	AAALLAKQAEMEVK
0.1	1471.792221	0.007827	NESIIPLSPFEVK

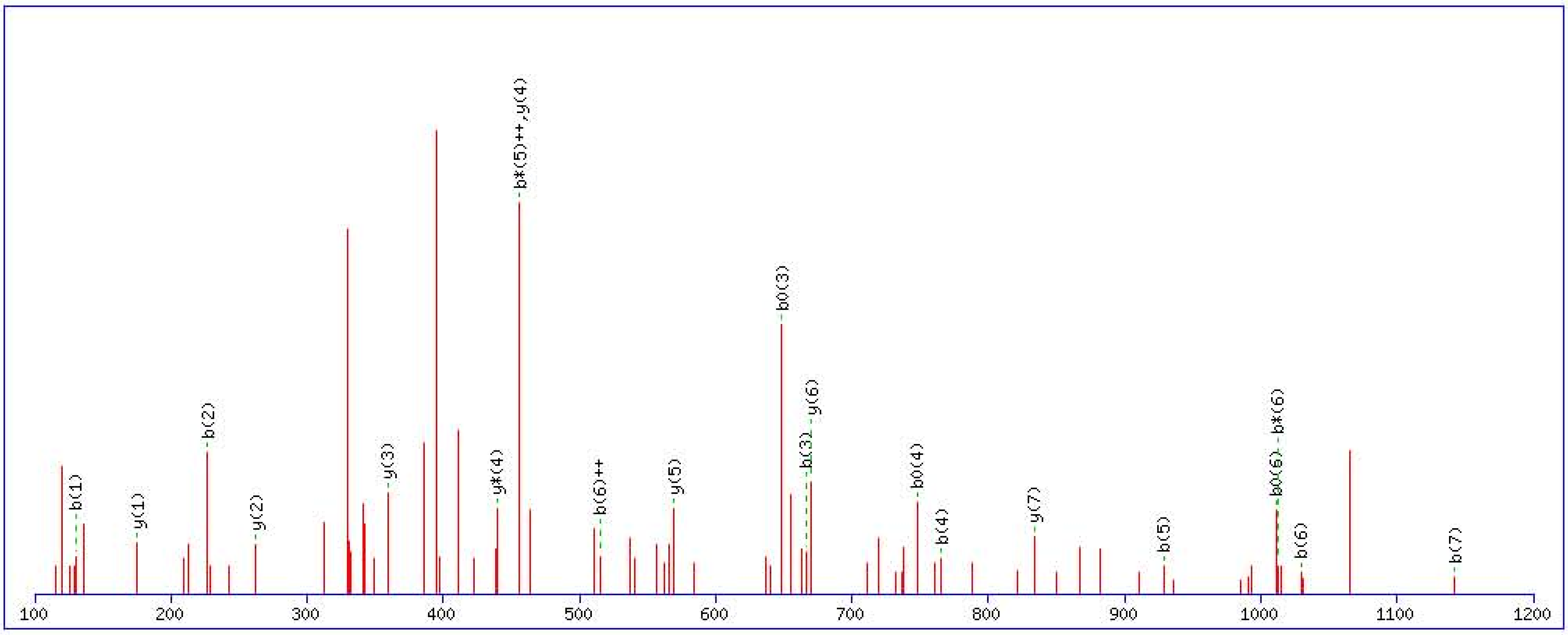
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPQVYTLPPSR**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

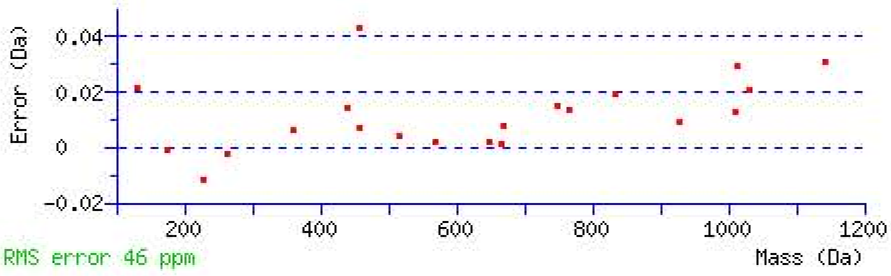
Match to Query 42103: 1596.834552 from(533.285460,3+) rtinseconds(1979) index(78345)
Title: Locus:1.1.1.2903.14 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

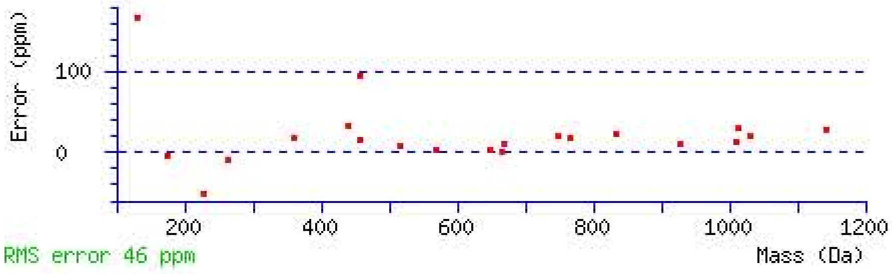
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0021
Matches : 21/114 fragment ions using 49 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							11
2	***227.102633***	114.054954			209.092068	105.049672	P	1468.798084	734.902680	1451.771535	726.389406	1450.787519	725.897398	10
3	***666.327959***	333.667618	649.301410	325.154343	648.317394	324.662335	Q	1371.745320	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
4	***765.396373***	383.201825	748.369824	374.688550	747.385808	374.196542	V	932.519994	466.763635	915.493445	458.250361	914.509429	457.758353	8
5	***928.459702***	464.733489	911.433153	456.220215	910.449137	455.728207	Y	***833.451580***	417.229428	816.425031	408.716154	815.441015	408.224146	7
6	***1029.507381***	515.257329	1012.480832	506.744054	1011.496816	506.252046	T	***670.388251***	335.697764	653.361702	327.184489	652.377686	326.692481	6
7	***1142.591445***	571.799361	1125.564896	563.286086	1124.580880	562.794078	L	***569.340572***	285.173924	552.314023	276.660650	551.330007	276.168642	5
8	1239.644209	620.325743	1222.617660	611.812468	1221.633644	611.320460	P	***456.256508***	228.631892	439.229959	220.118618	438.245943	219.626610	4
9	1336.696973	668.852125	1319.670424	660.338850	1318.686408	659.846842	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	1423.729001	712.368139	1406.702452	703.854864	1405.718436	703.362856	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1596.833389	0.001163	EPQVYTLPPSR
4.2	1596.855850	-0.021298	MLLLTRSPTAWHR
3.1	1596.825974	0.008578	KLSDLEAQWAPSPR

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

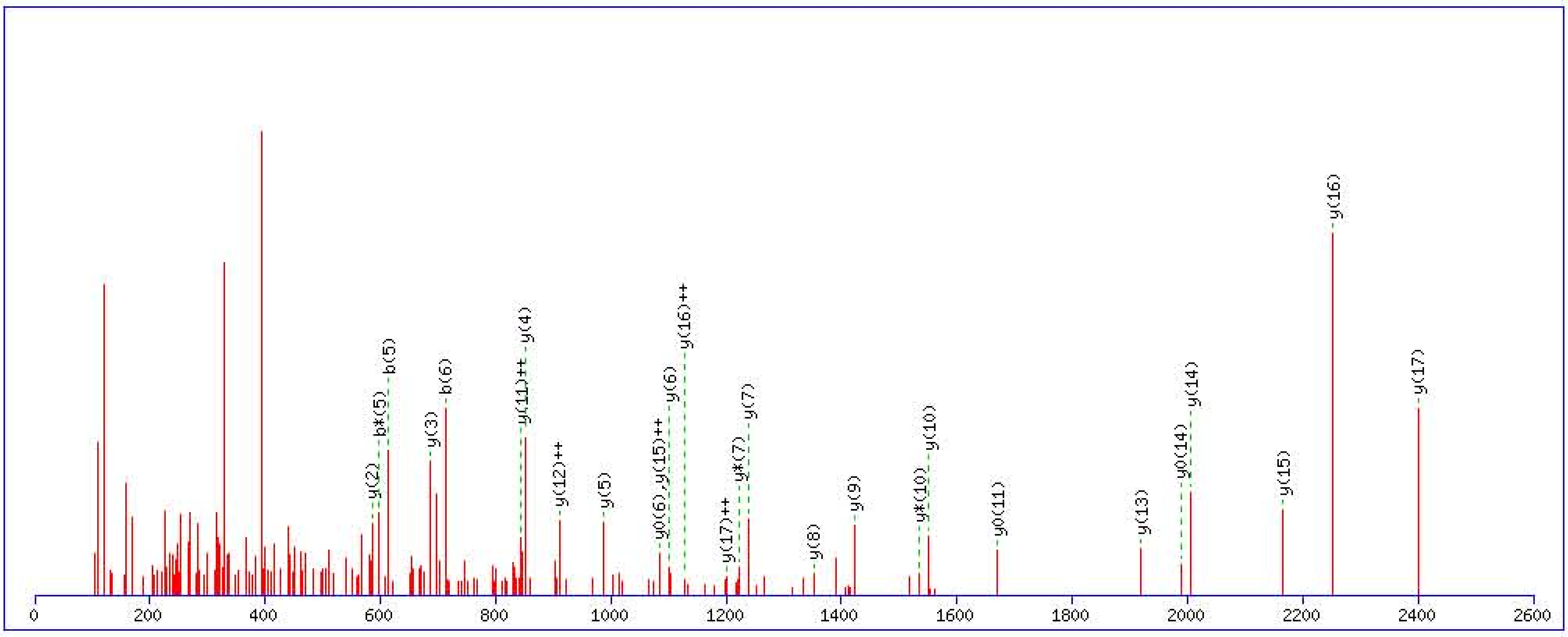
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WQQGNVFSCSVMHEALHNHYTQK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

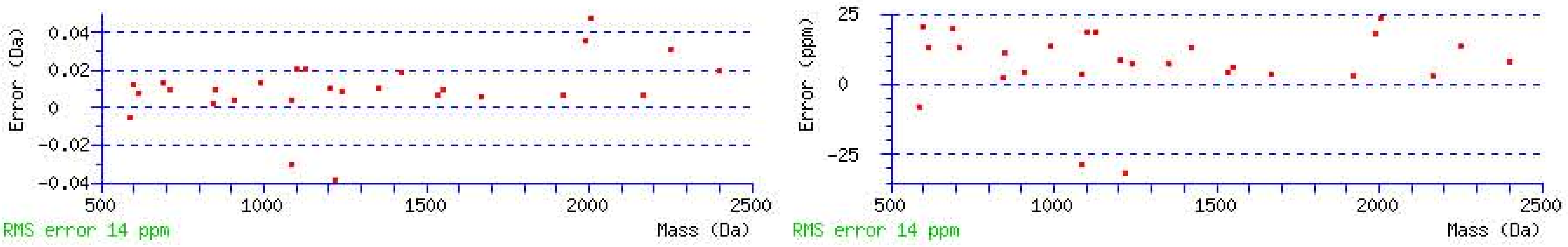
Match to Query 72537: 3111.448470 from(623.296970,5+) rtinseconds(2044) index(78812)
Title: Locus:1.1.1.2926.11 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3111.426590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q22 : Biotin:Thermo-21345 (Q)
Ions Score: 97 **Expect:** 3e-009
Matches : 27/244 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932					W							23
2	315.145167	158.076222	298.118618	149.562947			Q	2926.354551	1463.680913	2909.328002	1455.167639	2908.343986	1454.675631	22
3	443.203745	222.105511	426.177196	213.592236			Q	2798.295973	1399.651624	2781.269424	1391.138350	2780.285408	1390.646342	21
4	500.225209	250.616243	483.198660	242.102968			G	2670.237395	1335.622335	2653.210846	1327.109061	2652.226830	1326.617053	20
5	**614.268136**	307.637706	597.241587	299.124432			N	2613.215931	1307.111603	2596.189382	1298.598329	2595.205366	1298.106321	19
6	**713.336550**	357.171913	696.310001	348.658639			V	2499.173004	1250.090140	2482.146455	1241.576865	2481.162439	1241.084857	18
7	860.404964	430.706120	843.378415	422.192845			F	***2400.104590***	1200.555933	2383.078041	1192.042658	2382.094025	1191.550650	17
8	947.436992	474.222134	930.410443	465.708859	929.426427	465.216851	S	***2253.036176***	1127.021726	2236.009627	1118.508451	2235.025611	1118.016443	16
9	1107.467641	554.237459	1090.441092	545.724184	1089.457076	545.232176	C	***2166.004148***	1083.505712	2148.977599	1074.992437	2147.993583	1074.500429	15
10	1194.499669	597.753473	1177.473120	589.240198	1176.489104	588.748190	S	***2005.973499***	1003.490388	1988.946950	994.977113	1987.962934	994.485105	14
11	1293.568083	647.287680	1276.541534	638.774405	1275.557518	638.282397	V	***1918.941471***	959.974373	1901.914922	951.461099	1900.930906	950.969091	13
12	1424.608568	712.807922	1407.582019	704.294648	1406.598003	703.802640	M	1819.873057	910.440166	1802.846508	901.926892	1801.862492	901.434884	12
13	1561.667480	781.337378	1544.640931	772.824104	1543.656915	772.332096	H	1688.832572	844.919924	1671.806023	836.406649	1670.822007	835.914641	11
14	1690.710073	845.858675	1673.683524	837.345400	1672.699508	836.853392	E	***1551.773660***	776.390468	1534.747111	767.877193	1533.763095	767.385185	10
15	1761.747187	881.377231	1744.720638	872.863957	1743.736622	872.371949	A	***1422.731067***	711.869171	1405.704518	703.355897	1404.720502	702.863889	9
16	1874.831251	937.919263	1857.804702	929.405989	1856.820686	928.913981	L	***1351.693953***	676.350615	1334.667404	667.837340	1333.683388	667.345332	8
17	2011.890163	1006.448719	1994.863614	997.935445	1993.879598	997.443437	H	***1238.609889***	619.808583	1221.583340	611.295308	1220.599324	610.803300	7
18	2125.933090	1063.470183	2108.906541	1054.956908	2107.922525	1054.464900	N	***1101.550977***	551.279127	1084.524428	542.765852	1083.540412	542.273844	6
19	2262.992002	1131.999639	2245.965453	1123.486364	2244.981437	1122.994356	H	***987.508050***	494.257663	970.481501	485.744389	969.497485	485.252381	5
20	2426.055331	1213.531303	2409.028782	1205.018029	2408.044766	1204.526021	Y	***850.449138***	425.728207	833.422589	417.214933	832.438573	416.722925	4
21	2527.103010	1264.055143	2510.076461	1255.541868	2509.092445	1255.049860	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
22	2966.328336	1483.667806	2949.301787	1475.154531	2948.317771	1474.662523	Q	***586.338130***	293.672703	569.311581	285.159429			2
23							K	147.112804	74.060040	130.086255	65.546765			1

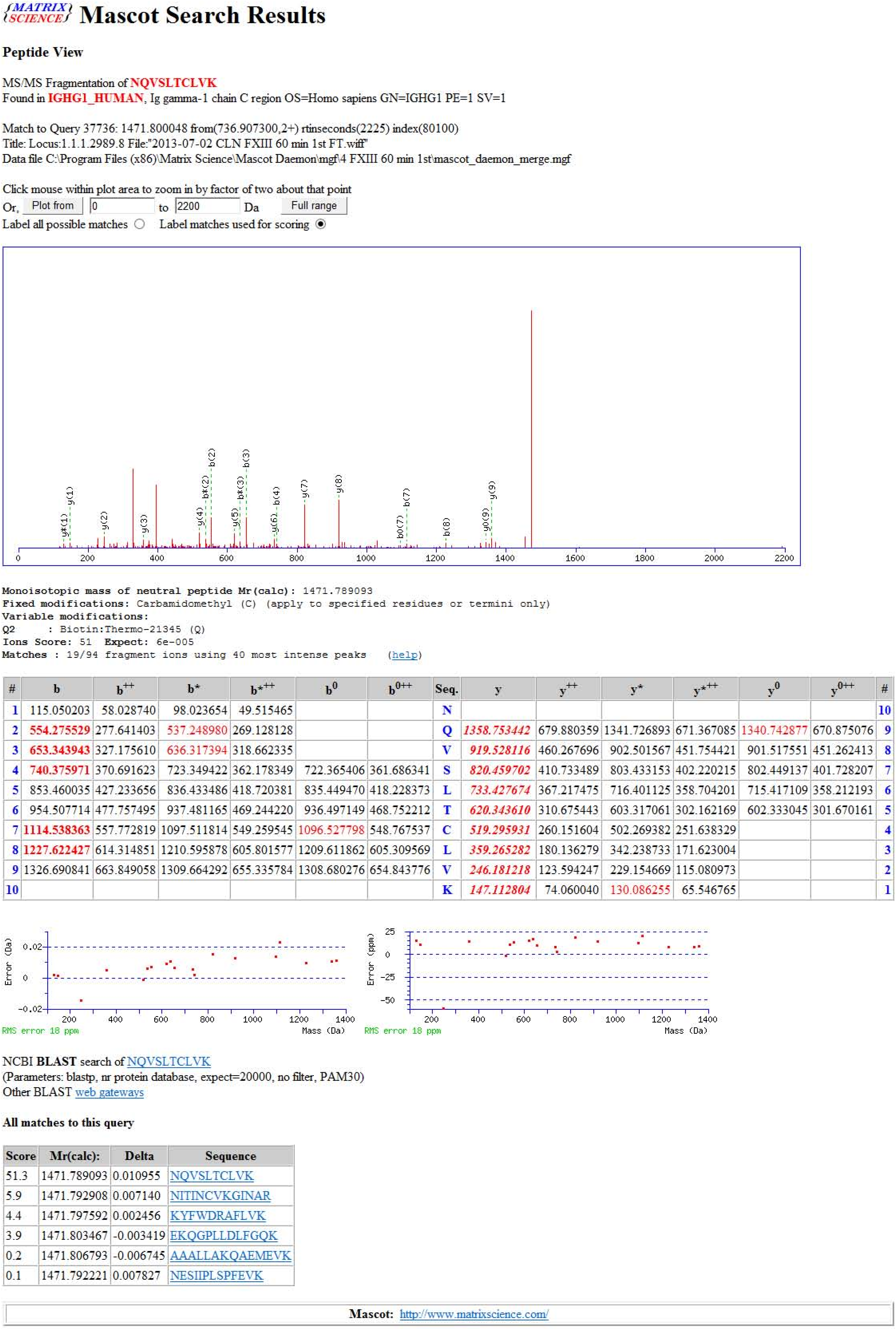


NCBI **BLAST** search of WQQGNVFSCSVMHEALHNHYTQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
97.4	3111.426590	0.021880	WQQGNVFSCSVMHEALHNHYTQK

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



{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

Match to Query 37736: 1471.800048 from(736.907300,2+) rtinseconds(2225) index(80100)
Title: Locus:1.1.1.2989.8 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 6e-005
Matches : 19/94 fragment ions using 40 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.050203	58.028740	98.023654	49.515465			N							10
2	**554.275529**	277.641403	537.248980	269.128128			Q	***1358.753442***	679.880359	1341.726893	671.367085	1340.742877	670.875076	9
3	**653.343943**	327.175610	636.317394	318.662335			V	***919.528116***	460.267696	902.501567	451.754421	901.517551	451.262413	8
4	**740.375971**	370.691623	723.349422	362.178349	722.365406	361.686341	S	***820.459702***	410.733489	803.433153	402.220215	802.449137	401.728207	7
5	853.460035	427.233656	836.433486	418.720381	835.449470	418.228373	L	***733.427674***	367.217475	716.401125	358.704201	715.417109	358.212193	6
6	954.507714	477.757495	937.481165	469.244220	936.497149	468.752212	T	***620.343610***	310.675443	603.317061	302.162169	602.333045	301.670161	5
7	**1114.538363**	557.772819	1097.511814	549.259545	1096.527798	548.767537	C	***519.295931***	260.151604	502.269382	251.638329			4
8	**1227.622427**	614.314851	1210.595878	605.801577	1209.611862	605.309569	L	***359.265282***	180.136279	342.238733	171.623004			3
9	1326.690841	663.849058	1309.664292	655.335784	1308.680276	654.843776	V	***246.181218***	123.594247	229.154669	115.080973			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.3	1471.789093	0.010955	NQVSLTCLVK
5.9	1471.792908	0.007140	NITINCVKGINAR
4.4	1471.797592	0.002456	KYFWDRAFLVK
3.9	1471.803467	-0.003419	EKQGPLLDLFGQK
0.2	1471.806793	-0.006745	AAALLAKQAEMEVK
0.1	1471.792221	0.007827	NESIIPLSPFEVK

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

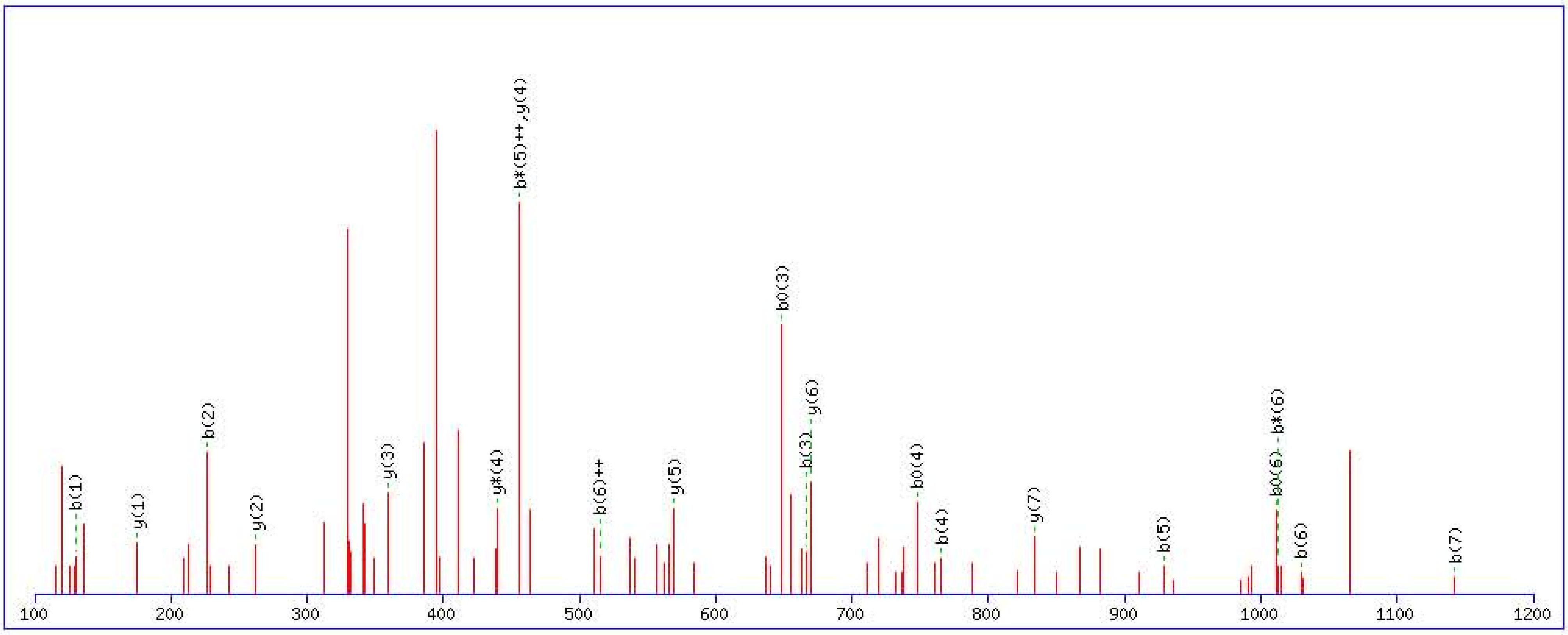
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPQVYTLPPSR**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

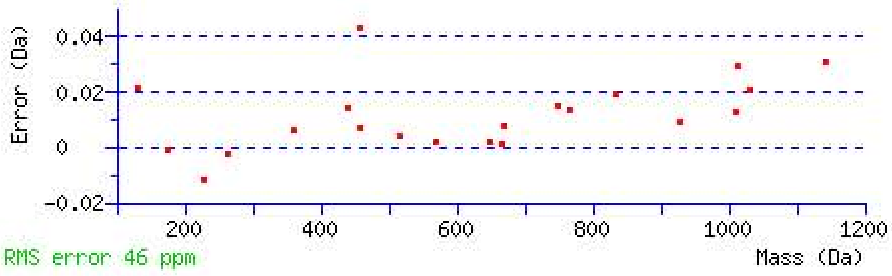
Match to Query 42103: 1596.834552 from(533.285460,3+) rtinseconds(1979) index(78345)
Title: Locus:1.1.1.2903.14 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

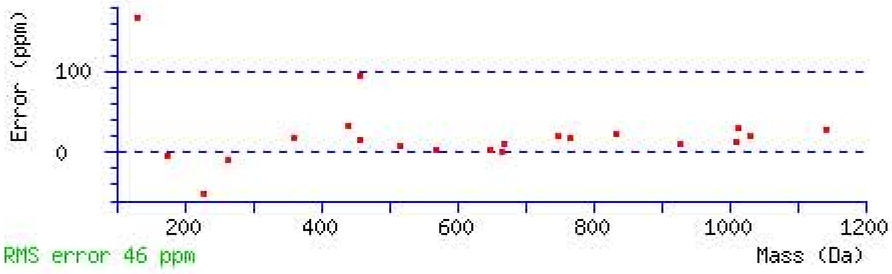
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0021
Matches : 21/114 fragment ions using 49 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							11
2	*227.102633*	114.054954			209.092068	105.049672	P	1468.798084	734.902680	1451.771535	726.389406	1450.787519	725.897398	10
3	*666.327959*	333.667618	649.301410	325.154343	648.317394	324.662335	Q	1371.745320	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
4	*765.396373*	383.201825	748.369824	374.688550	747.385808	374.196542	V	932.519994	466.763635	915.493445	458.250361	914.509429	457.758353	8
5	*928.459702*	464.733489	911.433153	456.220215	910.449137	455.728207	Y	*833.451580*	417.229428	816.425031	408.716154	815.441015	408.224146	7
6	*1029.507381*	515.257329	1012.480832	506.744054	1011.496816	506.252046	T	*670.388251*	335.697764	653.361702	327.184489	652.377686	326.692481	6
7	*1142.591445*	571.799361	1125.564896	563.286086	1124.580880	562.794078	L	*569.340572*	285.173924	552.314023	276.660650	551.330007	276.168642	5
8	1239.644209	620.325743	1222.617660	611.812468	1221.633644	611.320460	P	*456.256508*	228.631892	439.229959	220.118618	438.245943	219.626610	4
9	1336.696973	668.852125	1319.670424	660.338850	1318.686408	659.846842	P	*359.203744*	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	1423.729001	712.368139	1406.702452	703.854864	1405.718436	703.362856	S	*262.150980*	131.579128	245.124431	123.065854	244.140415	122.573846	2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1596.833389	0.001163	EPQVYTLPPSR
4.2	1596.855850	-0.021298	MLLLTRSPTAWHR
3.1	1596.825974	0.008578	KLSDLEAQWAPSPR

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

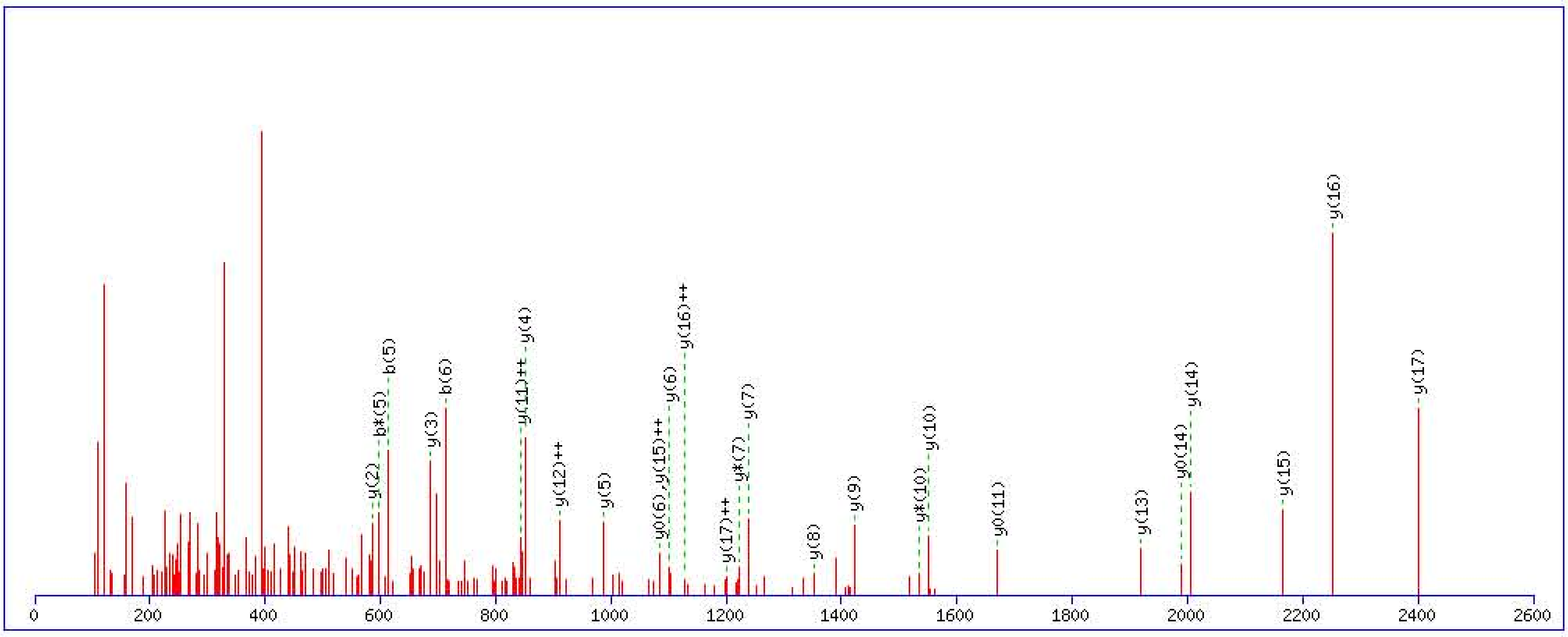
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WQQGNVFSCSVMHEALHNHYTQK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

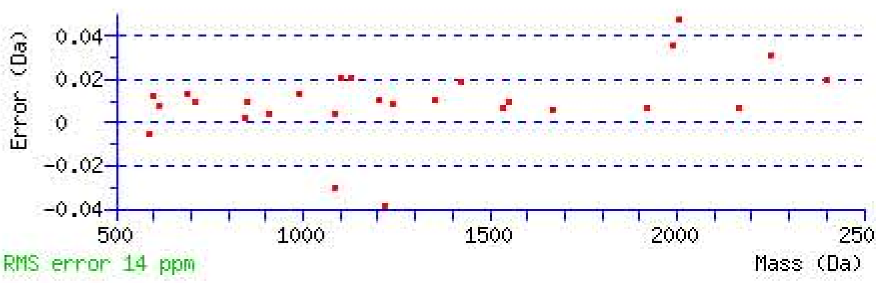
Match to Query 72537: 3111.448470 from(623.296970,5+) rtinseconds(2044) index(78812)
Title: Locus:1.1.1.2926.11 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

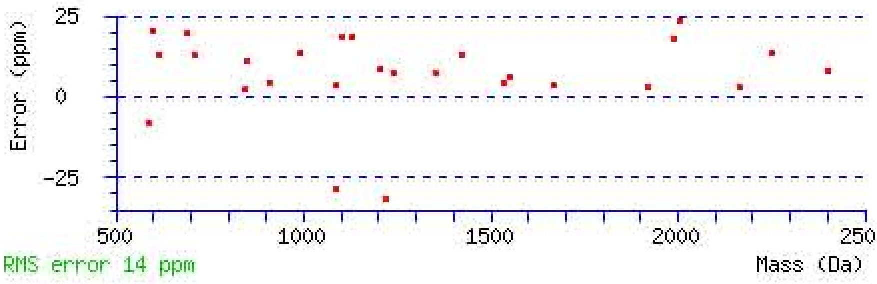
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3111.426590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q22     : Biotin:Thermo-21345 (Q)
Ions Score: 97  Expect: 3e-009
Matches : 27/244 fragment ions using 37 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	187.086589	94.046932					W							23
2	315.145167	158.076222	298.118618	149.562947			Q	2926.354551	1463.680913	2909.328002	1455.167639	2908.343986	1454.675631	22
3	443.203745	222.105511	426.177196	213.592236			Q	2798.295973	1399.651624	2781.269424	1391.138350	2780.285408	1390.646342	21
4	500.225209	250.616243	483.198660	242.102968			G	2670.237395	1335.622335	2653.210846	1327.109061	2652.226830	1326.617053	20
5	**614.268136**	307.637706	597.241587	299.124432			N	2613.215931	1307.111603	2596.189382	1298.598329	2595.205366	1298.106321	19
6	**713.336550**	357.171913	696.310001	348.658639			V	2499.173004	1250.090140	2482.146455	1241.576865	2481.162439	1241.084857	18
7	860.404964	430.706120	843.378415	422.192845			F	***2400.104590***	1200.555933	2383.078041	1192.042658	2382.094025	1191.550650	17
8	947.436992	474.222134	930.410443	465.708859	929.426427	465.216851	S	***2253.036176***	1127.021726	2236.009627	1118.508451	2235.025611	1118.016443	16
9	1107.467641	554.237459	1090.441092	545.724184	1089.457076	545.232176	C	***2166.004148***	1083.505712	2148.977599	1074.992437	2147.993583	1074.500429	15
10	1194.499669	597.753473	1177.473120	589.240198	1176.489104	588.748190	S	***2005.973499***	1003.490388	1988.946950	994.977113	1987.962934	994.485105	14
11	1293.568083	647.287680	1276.541534	638.774405	1275.557518	638.282397	V	***1918.941471***	959.974373	1901.914922	951.461099	1900.930906	950.969091	13
12	1424.608568	712.807922	1407.582019	704.294648	1406.598003	703.802640	M	1819.873057	910.440166	1802.846508	901.926892	1801.862492	901.434884	12
13	1561.667480	781.337378	1544.640931	772.824104	1543.656915	772.332096	H	1688.832572	844.919924	1671.806023	836.406649	1670.822007	835.914641	11
14	1690.710073	845.858675	1673.683524	837.345400	1672.699508	836.853392	E	***1551.773660***	776.390468	1534.747111	767.877193	1533.763095	767.385185	10
15	1761.747187	881.377231	1744.720638	872.863957	1743.736622	872.371949	A	***1422.731067***	711.869171	1405.704518	703.355897	1404.720502	702.863889	9
16	1874.831251	937.919263	1857.804702	929.405989	1856.820686	928.913981	L	***1351.693953***	676.350615	1334.667404	667.837340	1333.683388	667.345332	8
17	2011.890163	1006.448719	1994.863614	997.935445	1993.879598	997.443437	H	***1238.609889***	619.808583	1221.583340	611.295308	1220.599324	610.803300	7
18	2125.933090	1063.470183	2108.906541	1054.956908	2107.922525	1054.464900	N	***1101.550977***	551.279127	1084.524428	542.765852	1083.540412	542.273844	6
19	2262.992002	1131.999639	2245.965453	1123.486364	2244.981437	1122.994356	H	***987.508050***	494.257663	970.481501	485.744389	969.497485	485.252381	5
20	2426.055331	1213.531303	2409.028782	1205.018029	2408.044766	1204.526021	Y	***850.449138***	425.728207	833.422589	417.214933	832.438573	416.722925	4
21	2527.103010	1264.055143	2510.076461	1255.541868	2509.092445	1255.049860	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
22	2966.328336	1483.667806	2949.301787	1475.154531	2948.317771	1474.662523	Q	***586.338130***	293.672703	569.311581	285.159429			2
23							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
97.4	3111.426590	0.021880	WQQGNVFSCSVMHEALHNHYTQK

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

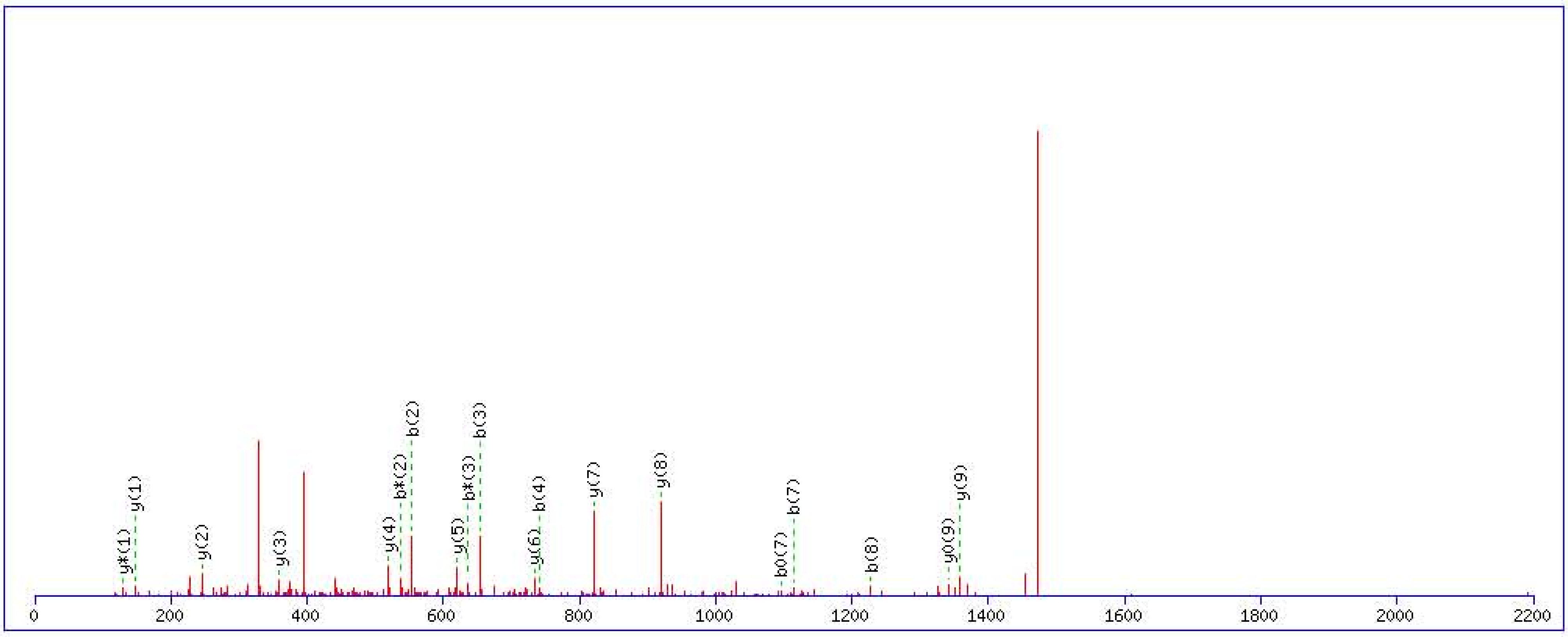
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

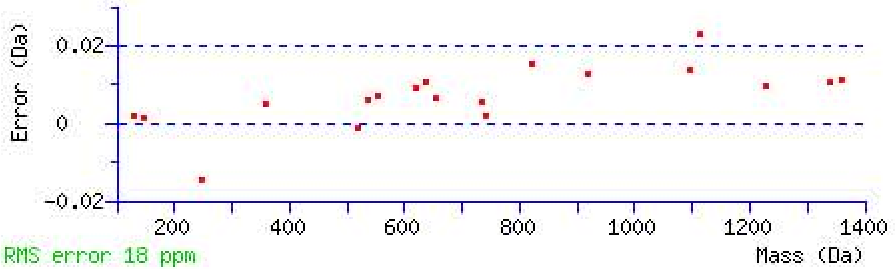
Match to Query 37736: 1471.800048 from(736.907300,2+) rtinseconds(2225) index(80100)
Title: Locus:1.1.1.2989.8 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

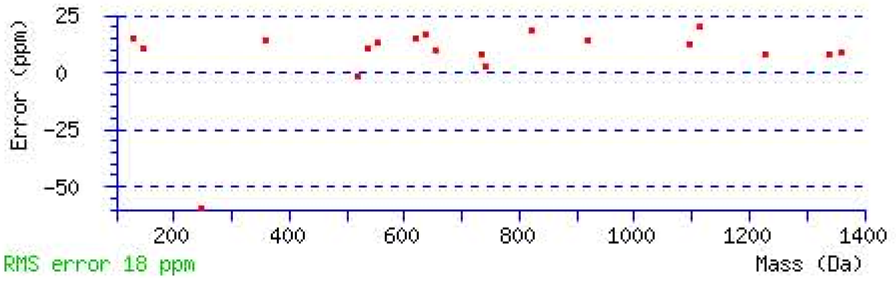
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 6e-005
Matches : 19/94 fragment ions using 40 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							10
2	**554.275529**	277.641403	537.248980	269.128128			Q	***1358.753442***	679.880359	1341.726893	671.367085	1340.742877	670.875076	9
3	**653.343943**	327.175610	636.317394	318.662335			V	***919.528116***	460.267696	902.501567	451.754421	901.517551	451.262413	8
4	**740.375971**	370.691623	723.349422	362.178349	722.365406	361.686341	S	***820.459702***	410.733489	803.433153	402.220215	802.449137	401.728207	7
5	853.460035	427.233656	836.433486	418.720381	835.449470	418.228373	L	***733.427674***	367.217475	716.401125	358.704201	715.417109	358.212193	6
6	954.507714	477.757495	937.481165	469.244220	936.497149	468.752212	T	***620.343610***	310.675443	603.317061	302.162169	602.333045	301.670161	5
7	**1114.538363**	557.772819	1097.511814	549.259545	1096.527798	548.767537	C	***519.295931***	260.151604	502.269382	251.638329			4
8	**1227.622427**	614.314851	1210.595878	605.801577	1209.611862	605.309569	L	***359.265282***	180.136279	342.238733	171.623004			3
9	1326.690841	663.849058	1309.664292	655.335784	1308.680276	654.843776	V	***246.181218***	123.594247	229.154669	115.080973			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.3	1471.789093	0.010955	NQVSLTCLVK
5.9	1471.792908	0.007140	NITINCVKGINAR
4.4	1471.797592	0.002456	KYFWDRAFLVK
3.9	1471.803467	-0.003419	EKQGPLLDLFGQK
0.2	1471.806793	-0.006745	AAALLAKQAEMEVK
0.1	1471.792221	0.007827	NESIIPLSPFEVK

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

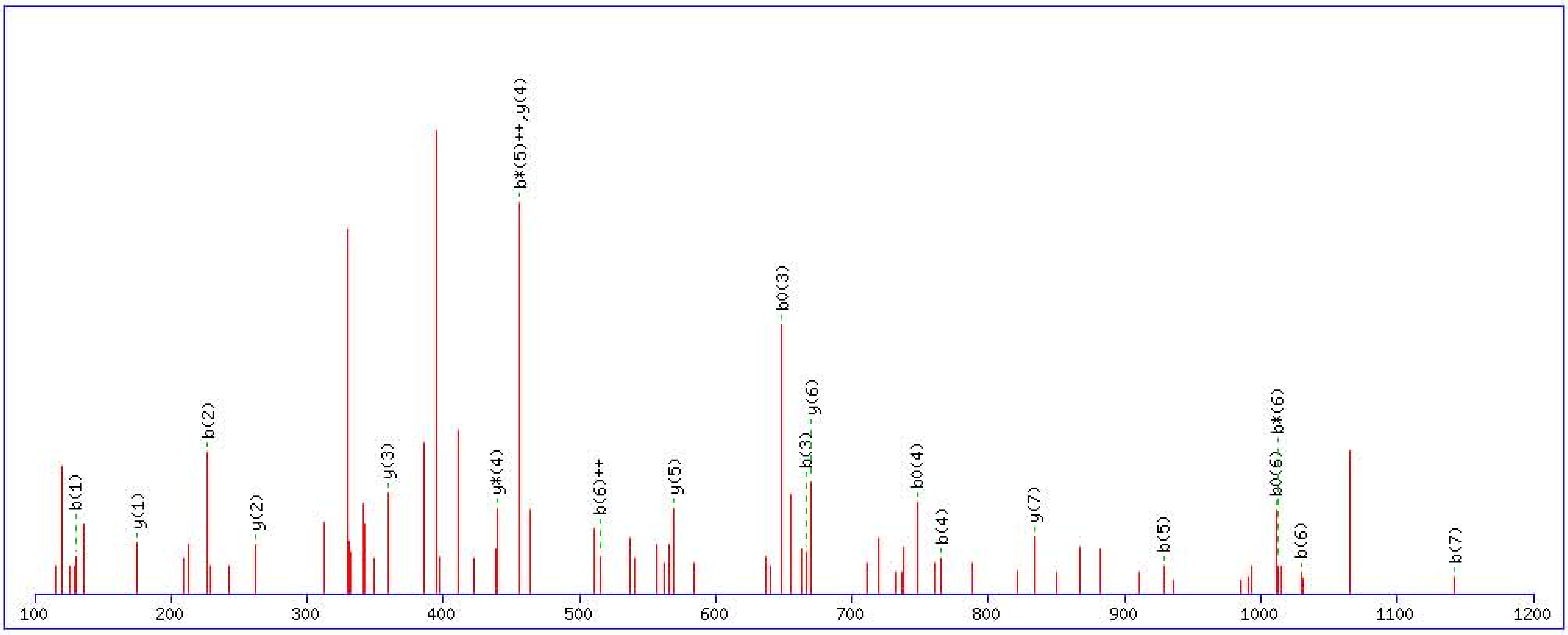
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPQVYTLPPSR**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

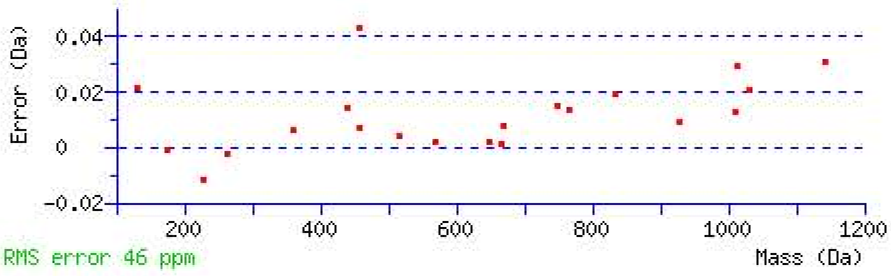
Match to Query 42103: 1596.834552 from(533.285460,3+) rtinseconds(1979) index(78345)
Title: Locus:1.1.1.2903.14 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

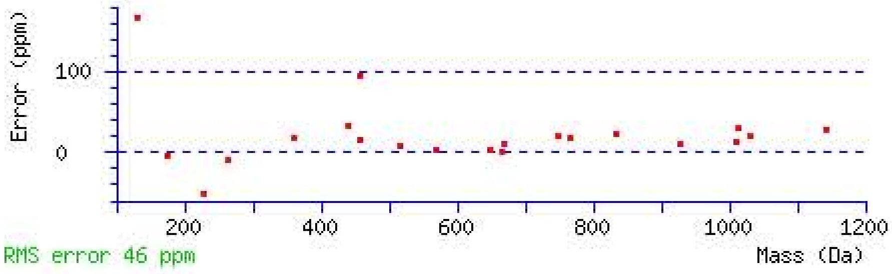
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0021
Matches : 21/114 fragment ions using 49 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							11
2	***227.102633***	114.054954			209.092068	105.049672	P	1468.798084	734.902680	1451.771535	726.389406	1450.787519	725.897398	10
3	***666.327959***	333.667618	649.301410	325.154343	648.317394	324.662335	Q	1371.745320	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
4	***765.396373***	383.201825	748.369824	374.688550	747.385808	374.196542	V	932.519994	466.763635	915.493445	458.250361	914.509429	457.758353	8
5	***928.459702***	464.733489	911.433153	456.220215	910.449137	455.728207	Y	***833.451580***	417.229428	816.425031	408.716154	815.441015	408.224146	7
6	***1029.507381***	515.257329	1012.480832	506.744054	1011.496816	506.252046	T	***670.388251***	335.697764	653.361702	327.184489	652.377686	326.692481	6
7	***1142.591445***	571.799361	1125.564896	563.286086	1124.580880	562.794078	L	***569.340572***	285.173924	552.314023	276.660650	551.330007	276.168642	5
8	1239.644209	620.325743	1222.617660	611.812468	1221.633644	611.320460	P	***456.256508***	228.631892	439.229959	220.118618	438.245943	219.626610	4
9	1336.696973	668.852125	1319.670424	660.338850	1318.686408	659.846842	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	1423.729001	712.368139	1406.702452	703.854864	1405.718436	703.362856	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1596.833389	0.001163	EPQVYTLPPSR
4.2	1596.855850	-0.021298	MLLLTRSPTAWHR
3.1	1596.825974	0.008578	KLSDLEAQWAPSPR

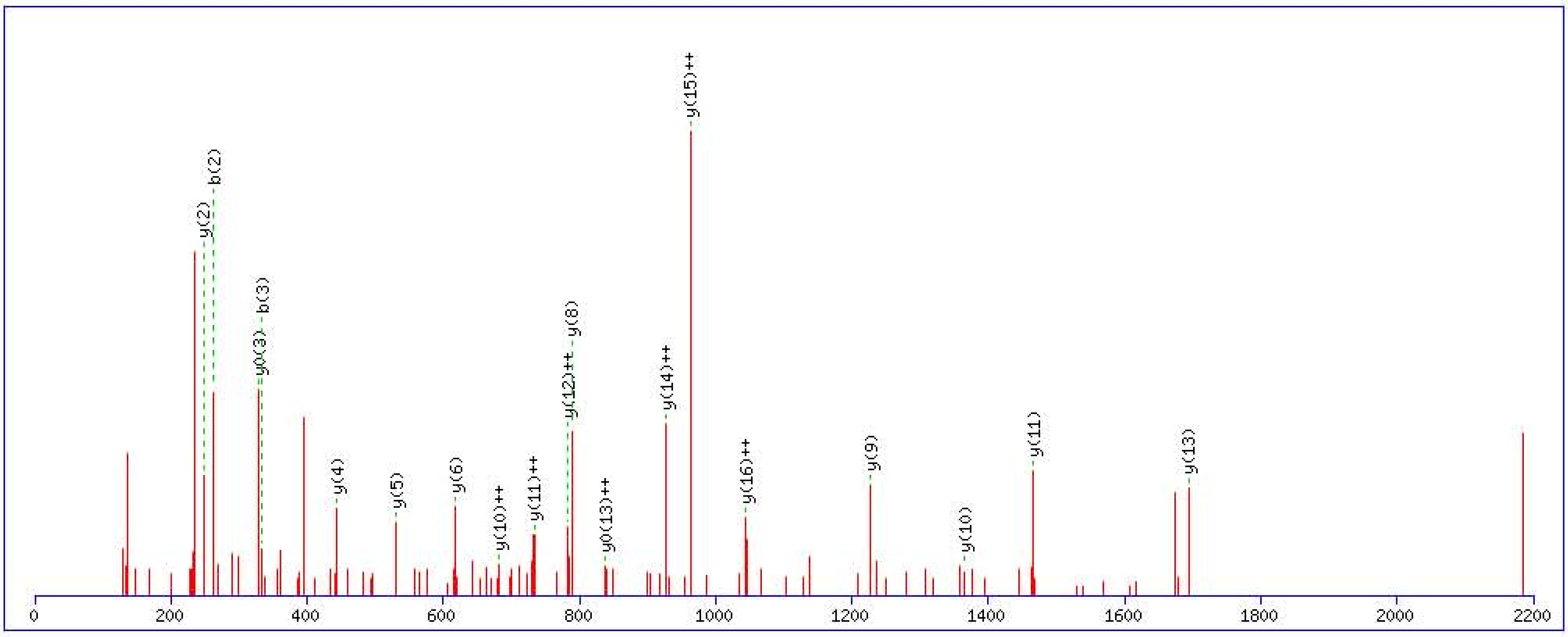
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYACEVTHQGLSSPVTK**
Found in **IGKC_HUMAN**, Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1

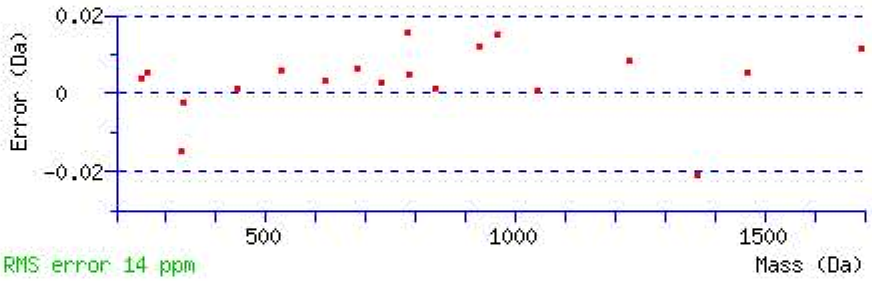
Match to Query 57890: 2186.103162 from(729.708330,3+) rtinseconds(1772) index(76970)
Title: Locus:1.1.1.2831.21 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

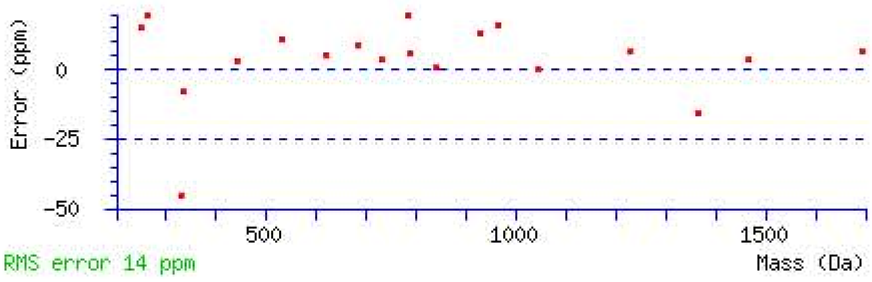
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2186.086411
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0021
Matches : 19/166 fragment ions using 48 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							17
2	**263.139019**	132.073148					Y	2088.025261	1044.516268	2070.998712	1036.002994	2070.014696	1035.510986	16
3	**334.176133**	167.591704					A	1924.961932	962.984604	1907.935383	954.471330	1906.951367	953.979322	15
4	494.206782	247.607029					C	1853.924818	927.466047	1836.898269	918.952773	1835.914253	918.460765	14
5	623.249375	312.128326			605.238810	303.123043	E	***1693.894169***	847.450723	1676.867620	838.937448	1675.883604	838.445440	13
6	722.317789	361.662533			704.307224	352.657250	V	1564.851576	782.929426	1547.825027	774.416152	1546.841011	773.924144	12
7	823.365468	412.186372			805.354903	403.181090	T	***1465.783162***	733.395219	1448.756613	724.881945	1447.772597	724.389937	11
8	960.424380	480.715828			942.413815	471.710546	H	***1364.735483***	682.871380	1347.708934	674.358105	1346.724918	673.866097	10
9	1399.649706	700.328491	1382.623157	691.815217	1381.639141	691.323208	Q	***1227.676571***	614.341924	1210.650022	605.828649	1209.666006	605.336641	9
10	1456.671170	728.839223	1439.644621	720.325948	1438.660605	719.833940	G	***788.451245***	394.729261	771.424696	386.215986	770.440680	385.723978	8
11	1569.755234	785.381255	1552.728685	776.867980	1551.744669	776.375972	L	731.429781	366.218529	714.403232	357.705254	713.419216	357.213246	7
12	1656.787262	828.897269	1639.760713	820.383994	1638.776697	819.891986	S	***618.345717***	309.676497	601.319168	301.163222	600.335152	300.671214	6
13	1743.819290	872.413283	1726.792741	863.900009	1725.808725	863.408000	S	***531.313689***	266.160483	514.287140	257.647208	513.303124	257.155200	5
14	1840.872054	920.939665	1823.845505	912.426391	1822.861489	911.934382	P	***444.281661***	222.644469	427.255112	214.131194	426.271096	213.639186	4
15	1939.940468	970.473872	1922.913919	961.960598	1921.929903	961.468590	V	347.228897	174.118087	330.202348	165.604812	329.218332	165.112804	3
16	2040.988147	1020.997712	2023.961598	1012.484437	2022.977582	1011.992429	T	***248.160483***	124.583880	231.133934	116.070605	230.149918	115.578597	2
17							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.5	2186.086411	0.016751	VYACEVTHQGLSSPVTK

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

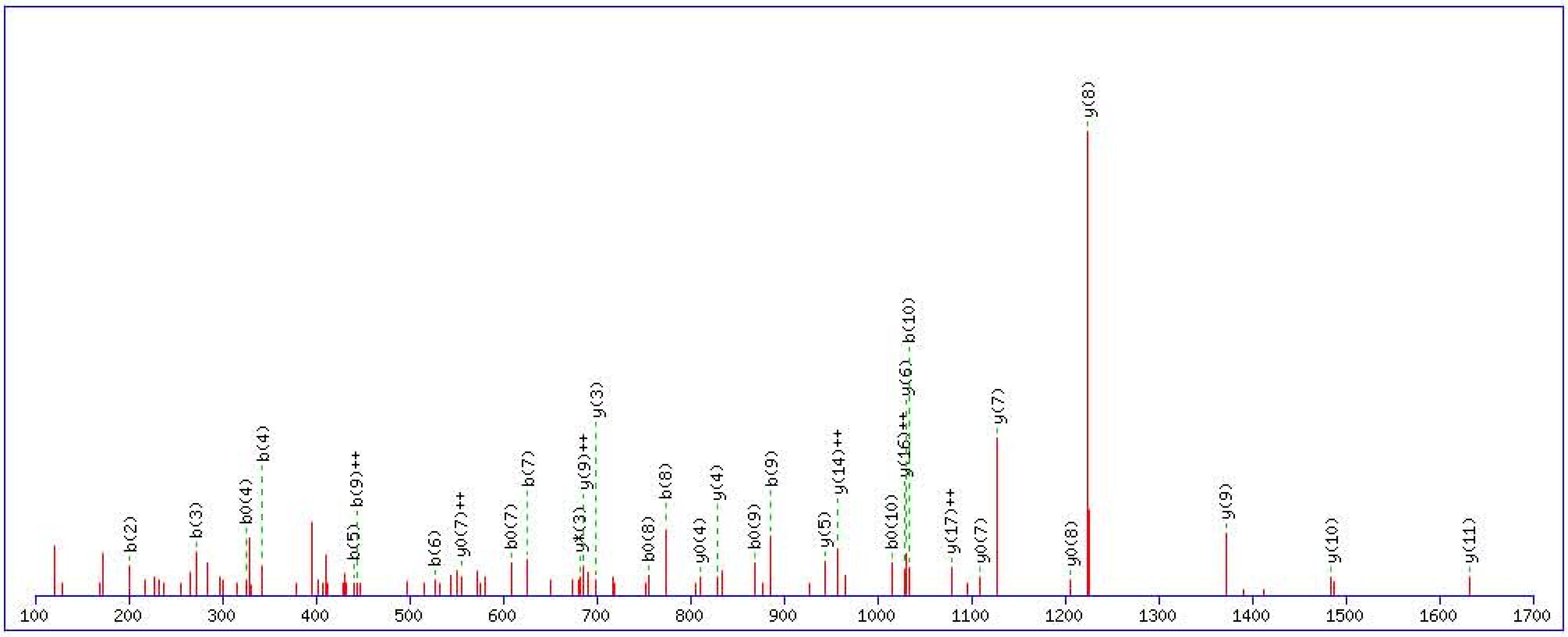
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVAAPSVFIFPPSDEQLK**
Found in **IGKC_HUMAN**, Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1

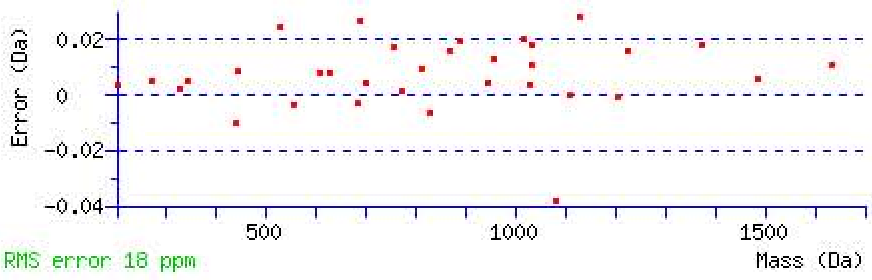
Match to Query 59485: 2256.210732 from(753.077520,3+) rtinseconds(2651) index(82598)
Title: Locus:1.1.1.3137.14 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

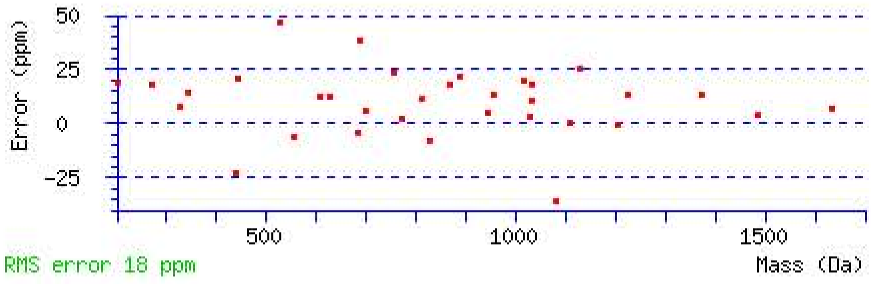
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2256.186432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00058
Matches : 33/168 fragment ions using 76 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							18
2	***201.123369***	101.065322			183.112804	92.060040	V	2156.146026	1078.576651	2139.119477	1070.063377	2138.135461	1069.571369	17
3	***272.160483***	136.583879			254.149918	127.578597	A	2057.077612	1029.042444	2040.051063	1020.529170	2039.067047	1020.037162	16
4	***343.197597***	172.102437			325.187032	163.097154	A	1986.040498	993.523887	1969.013949	985.010613	1968.029933	984.518605	15
5	***440.250361***	220.628819			422.239796	211.623536	P	1915.003384	958.005330	1897.976835	949.492056	1896.992819	949.000048	14
6	***527.282389***	264.144833			509.271824	255.139550	S	1817.950620	909.478948	1800.924071	900.965674	1799.940055	900.473666	13
7	***626.350803***	313.679040			608.340238	304.673757	V	1730.918592	865.962934	1713.892043	857.449660	1712.908027	856.957652	12
8	***773.419217***	387.213247			755.408652	378.207964	F	***1631.850178***	816.428727	1614.823629	807.915453	1613.839613	807.423445	11
9	***886.503281***	443.755279			868.492716	434.749996	I	***1484.781764***	742.894520	1467.755215	734.381246	1466.771199	733.889238	10
10	***1033.571695***	517.289486			1015.561130	508.284203	F	***1371.697700***	686.352488	1354.671151	677.839214	1353.687135	677.347206	9
11	1130.624459	565.815868			1112.613894	556.810585	P	***1224.629286***	612.818281	1207.602737	604.305007	1206.618721	603.812999	8
12	1227.677223	614.342250			1209.666658	605.336967	P	***1127.576522***	564.291899	1110.549973	555.778625	1109.565957	555.286617	7
13	1314.709251	657.858264			1296.698686	648.852981	S	***1030.523758***	515.765517	1013.497209	507.252243	1012.513193	506.760235	6
14	1429.736194	715.371735			1411.725629	706.366453	D	***943.491730***	472.249503	926.465181	463.736229	925.481165	463.244221	5
15	1558.778787	779.893032			1540.768222	770.887749	E	***828.464787***	414.736032	811.438238	406.222757	810.454222	405.730749	4
16	1998.004113	999.505695	1980.977564	990.992420	1979.993548	990.500412	Q	***699.422194***	350.214735	682.395645	341.701461			3
17	2111.088177	1056.047727	2094.061628	1047.534452	2093.077612	1047.042444	L	260.196868	130.602072	243.170319	122.088798			2
18							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.4	2256.186432	0.024300	TVAAPSVFIFPPSDEQLK

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

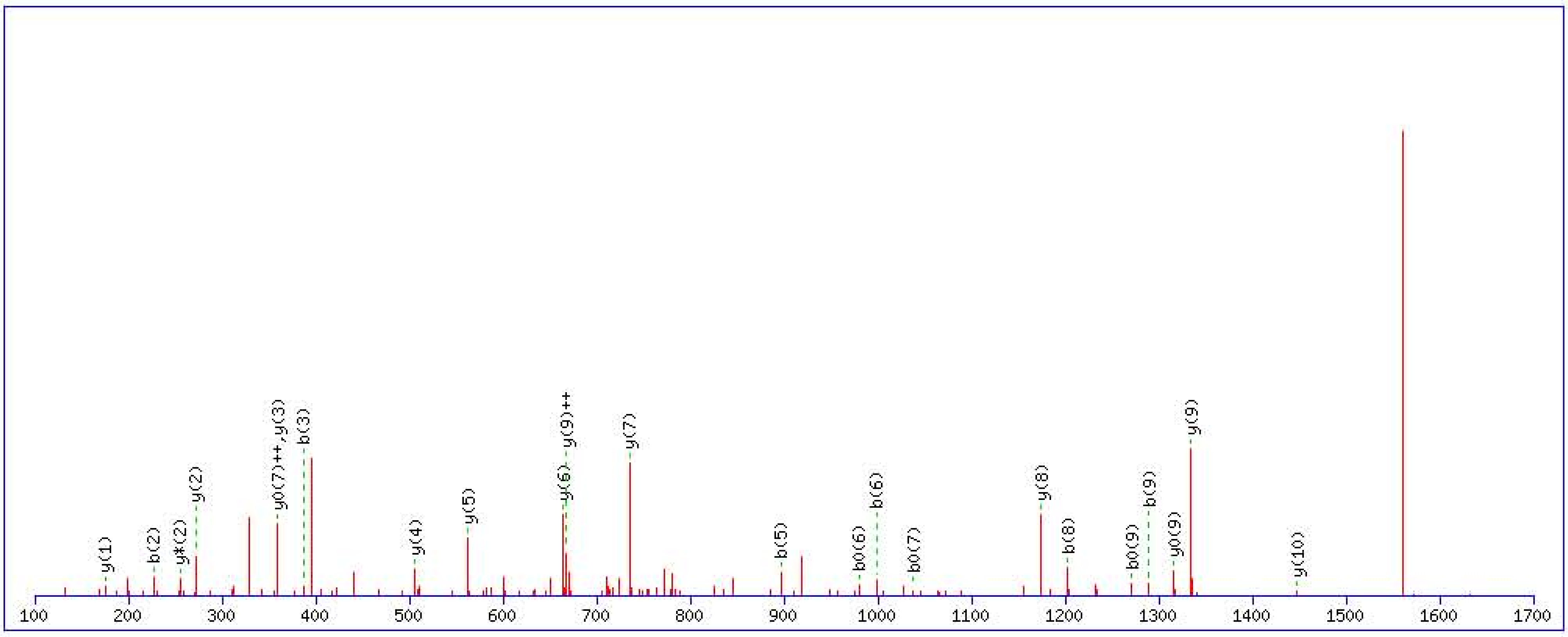
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LICQATGFSPR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

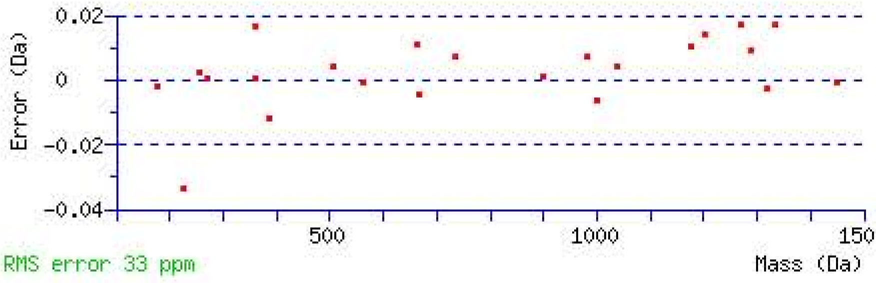
Match to Query 40173: 1559.805448 from(780.910000,2+) rtinseconds(1969) index(41950)
Title: Locus:1.1.1.2969.9 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

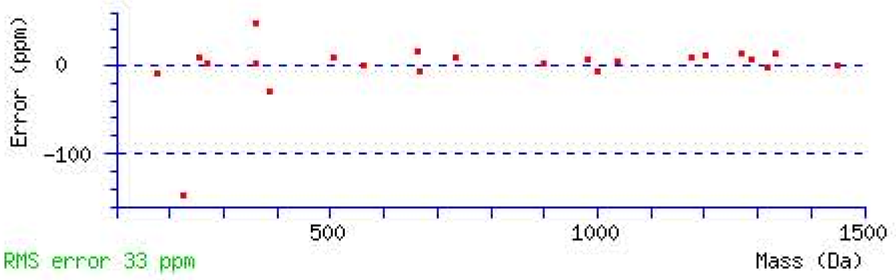
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1559.795242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 6e-006
Matches : 23/100 fragment ions using 40 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							11
2	**227.175404**	114.091340					I	***1447.718454***	724.362865	1430.691905	715.849591	1429.707889	715.357583	10
3	**387.206053**	194.106664					C	***1334.634390***	667.820833	1317.607841	659.307559	1316.623825	658.815551	9
4	826.431379	413.719328	809.404830	405.206053			Q	***1174.603741***	587.805509	1157.577192	579.292234	1156.593176	578.800226	8
5	**897.468493**	449.237885	880.441944	440.724610			A	***735.378415***	368.192846	718.351866	359.679571	717.367850	359.187563	7
6	**998.516172**	499.761724	981.489623	491.248449	980.505607	490.756441	T	***664.341301***	332.674289	647.314752	324.161014	646.330736	323.669006	6
7	1055.537636	528.272456	1038.511087	519.759182	1037.527071	519.267174	G	***563.293622***	282.150449	546.267073	273.637175	545.283057	273.145167	5
8	**1202.606050**	601.806663	1185.579501	593.293389	1184.595485	592.801381	F	***506.272158***	253.639717	489.245609	245.126443	488.261593	244.634435	4
9	**1289.638078**	645.322677	1272.611529	636.809403	1271.627513	636.317395	S	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	1386.690842	693.849059	1369.664293	685.335785	1368.680277	684.843777	P	***272.171716***	136.589496	255.145167	128.076221			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.3	1559.795242	0.010206	LICQATGFSPR
8.3	1559.808960	-0.003512	LDRLSGLADQMVAR
7.7	1559.820190	-0.014742	MTRSATQAAKQVPR
3.0	1559.812943	-0.007495	EPMNIYNLNAIIR

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

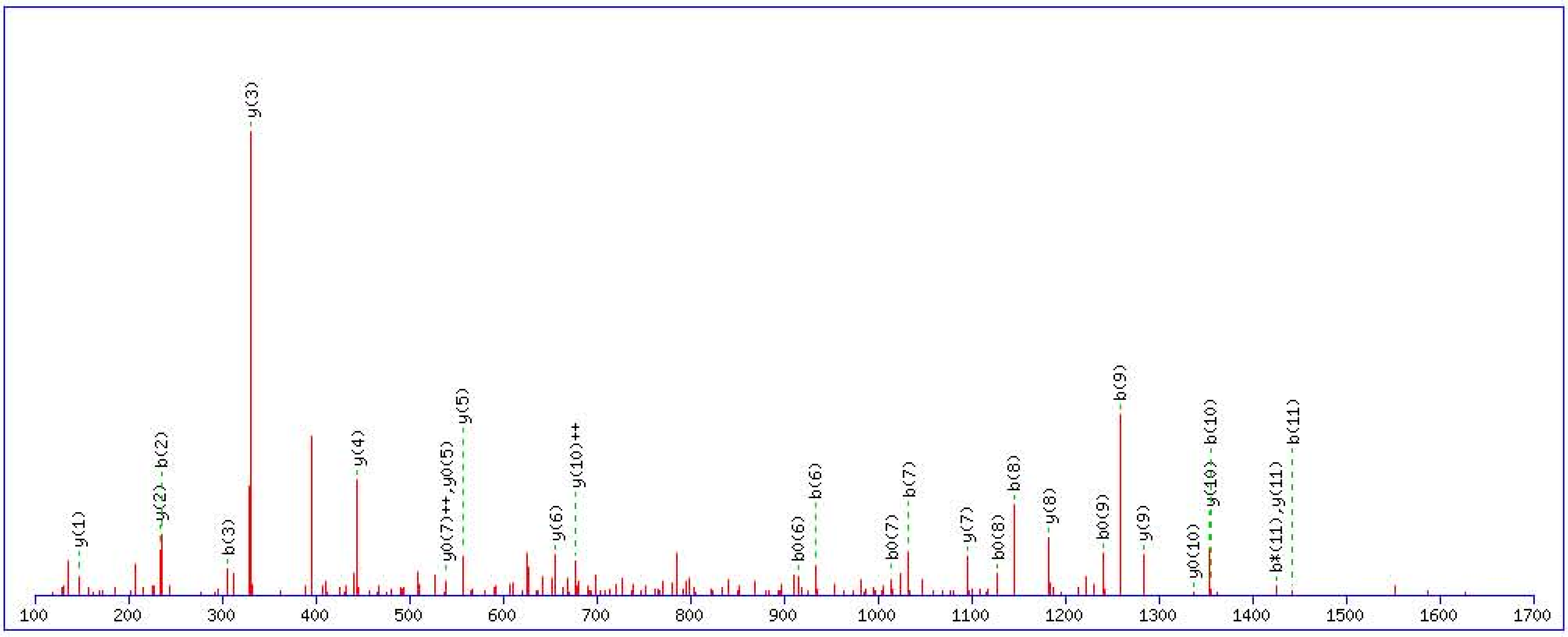
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAATSQVLLPSK**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

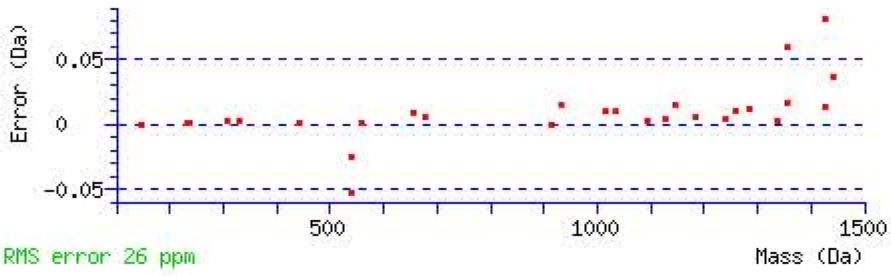
Match to Query 41545: 1587.883468 from(794.949010,2+) rtinseconds(2020) index(42255)
Title: Locus:1.1.1.2987.16 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

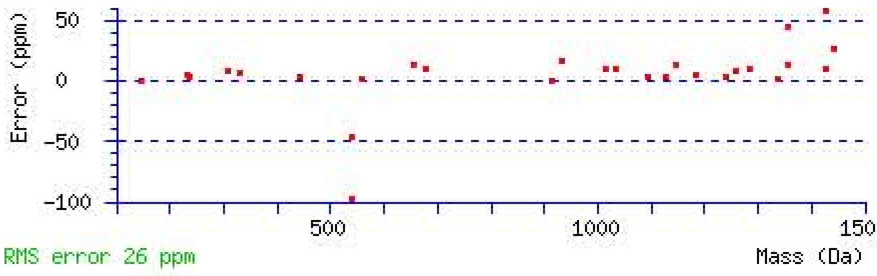


```
Monoisotopic mass of neutral peptide Mr(calc): 1587.869431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 81  Expect: 1.6e-007
Matches : 28/114 fragment ions using 43 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	164.070605	82.538940					Y							12
2	**235.107719**	118.057498					A	***1425.813399***	713.410337	1408.786850	704.897063	1407.802834	704.405055	11
3	**306.144833**	153.576055					A	***1354.776285***	677.891780	1337.749736	669.378506	1336.765720	668.886498	10
4	407.192512	204.099894			389.181947	195.094612	T	***1283.739171***	642.373223	1266.712622	633.859949	1265.728606	633.367941	9
5	494.224540	247.615908			476.213975	238.610626	S	***1182.691492***	591.849384	1165.664943	583.336110	1164.680927	582.844101	8
6	**933.449866**	467.228571	916.423317	458.715297	915.439301	458.223289	Q	***1095.659464***	548.333370	1078.632915	539.820096	1077.648899	539.328088	7
7	**1032.518280**	516.762778	1015.491731	508.249504	1014.507715	507.757496	V	***656.434138***	328.720707	639.407589	320.207432	638.423573	319.715424	6
8	**1145.602344**	573.304810	1128.575795	564.791536	1127.591779	564.299527	L	***557.365724***	279.186500	540.339175	270.673226	539.355159	270.181218	5
9	**1258.686408**	629.846842	1241.659859	621.333567	1240.675843	620.841559	L	***444.281660***	222.644468	427.255111	214.131193	426.271095	213.639186	4
10	**1355.739172**	678.373224	1338.712623	669.859949	1337.728607	669.367941	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
11	**1442.771200**	721.889238	1425.744651	713.375964	1424.760635	712.883955	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
12							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 26 ppm



RMS error 26 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.5	1587.869431	0.014037	YAATSQVLLPSK
14.5	1587.862045	0.021423	VTGQNQEQFLLLAK
9.0	1587.865402	0.018066	ENGLRDILAVLTMK
7.0	1587.890533	-0.007065	EPTTKAEMLKIISK
6.3	1587.891220	-0.007752	TIQTIVFLYSLYK
5.2	1587.862030	0.021438	EDAKLSFKHVSSLK
5.1	1587.862045	0.021423	DGASLSPATLFIQIR
2.6	1587.862045	0.021423	SKDLTAADVVKQWK
2.3	1587.870773	0.012695	FSWMKLLAHKVGR
2.1	1587.873276	0.010192	DLLTGEQFIQLRR

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

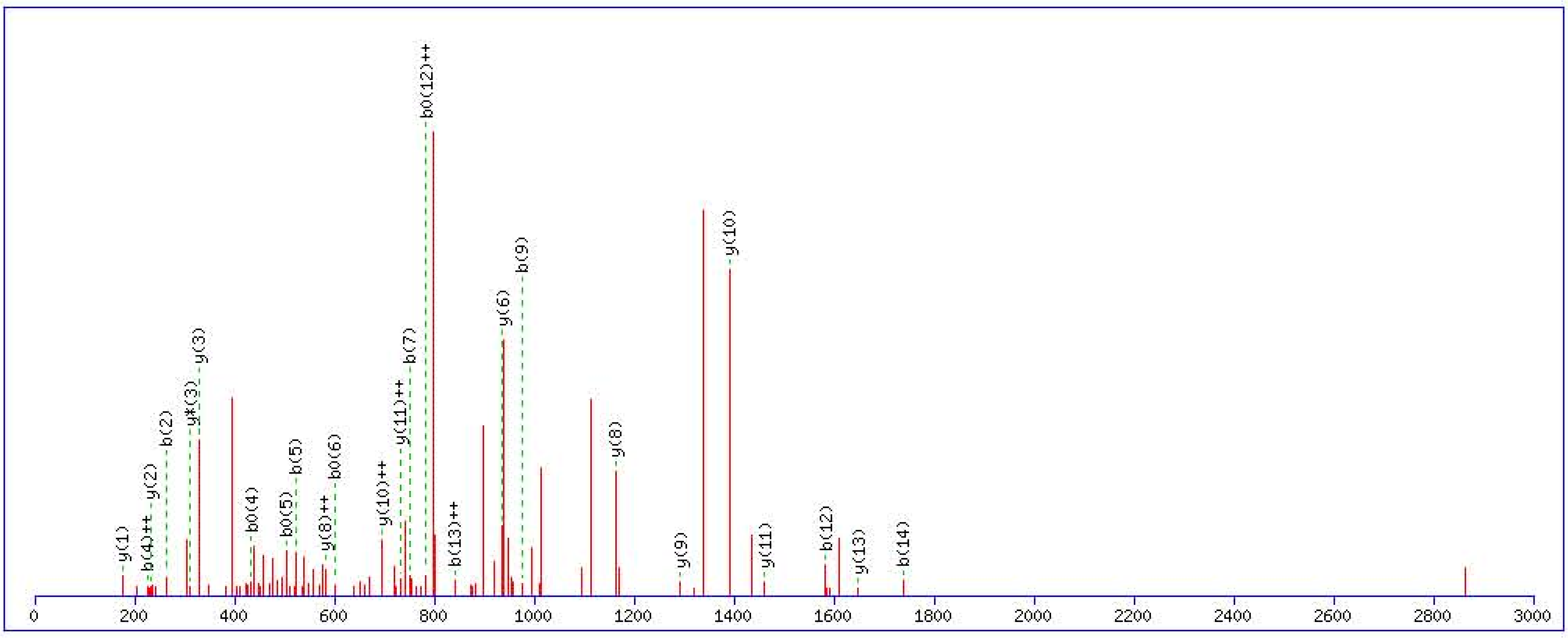
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVTSAPMPEPQAPGR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

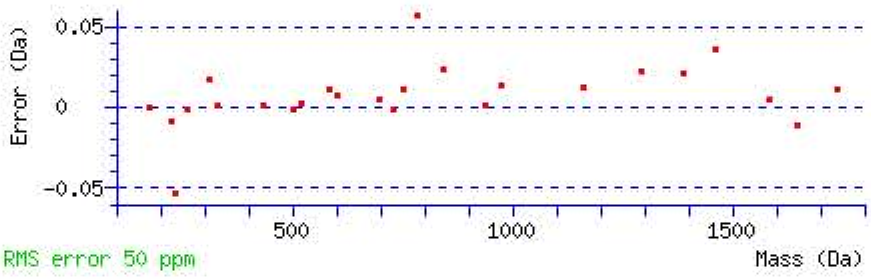
Match to Query 50875: 1910.940228 from(956.477390,2+) rtinseconds(1851) index(41009)
Title: Locus:1.1.1.2928.22 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

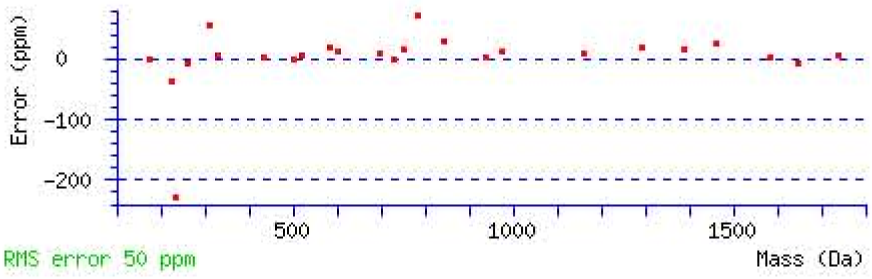
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1910.938263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.053
Matches : 25/132 fragment ions using 69 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	164.070605	82.538940					**Y**							**15**
2	**263.139019**	132.073148					**V**	1748.882225	874.944750	1731.855676	866.431476	1730.871660	865.939468	**14**
3	364.186698	182.596987			346.176133	173.591705	**T**	***1649.813811***	825.410543	1632.787262	816.897269	1631.803246	816.405261	**13**
4	451.218726	**226.113001**			433.208161	217.107719	**S**	1548.766132	774.886704	1531.739583	766.373430	1530.755567	765.881421	**12**
5	**522.255840**	261.631558			504.245275	252.626276	**A**	***1461.734104***	731.370690	1444.707555	722.857416	1443.723539	722.365407	**11**
6	619.308604	310.157940			601.298039	301.152658	**P**	***1390.696990***	695.852133	1373.670441	687.338859	1372.686425	686.846850	**10**
7	**750.349089**	375.678183			732.338524	366.672900	**M**	***1293.644226***	647.325751	1276.617677	638.812477	1275.633661	638.320468	**9**
8	847.401853	424.204565			829.391288	415.199282	**P**	***1162.603741***	581.805508	1145.577192	573.292234	1144.593176	572.800226	**8**
9	**976.444446**	488.725861			958.433881	479.720579	**E**	1065.550977	533.279126	1048.524428	524.765852	1047.540412	524.273844	**7**
10	1073.497210	537.252243			1055.486645	528.246961	**P**	***936.508384***	468.757830	919.481835	460.244555			**6**
11	1512.722536	756.864906	1495.695987	748.351632	1494.711971	747.859624	**Q**	839.455620	420.231448	822.429071	411.718173			**5**
12	**1583.759650**	792.383463	1566.733101	783.870189	1565.749085	783.378180	**A**	400.230294	200.618785	383.203745	192.105510			**4**
13	1680.812414	**840.909845**	1663.785865	832.396571	1662.801849	831.904563	**P**	***329.193180***	165.100228	312.166631	156.586953			**3**
14	**1737.833878**	869.420577	1720.807329	860.907303	1719.823313	860.415294	**G**	***232.140416***	116.573846	215.113867	108.060571			**2**
15							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	1910.934265	0.005963	SGSDEVQVGQQR
31.6	1910.938263	0.001965	YVTSAPMPEPQAPGR
27.7	1910.934265	0.005963	SGSDEVQVGQQR
5.0	1910.934265	0.005963	SGSDEVQVGQQR
3.9	1910.930725	0.009503	AGSGGLGGGAGGGQGAGAGQGAALR
3.9	1910.963196	-0.022968	EQQRQEELEKQR
3.1	1910.913101	0.027127	TLNMDMFTWEPRKAR
2.7	1910.955811	-0.015583	RLAALGADPAARDSDAEGR
2.3	1910.957382	-0.017154	DPWRFGNTPVQQR
1.4	1910.938721	0.001507	QEAEGLALDSPWHRFR

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

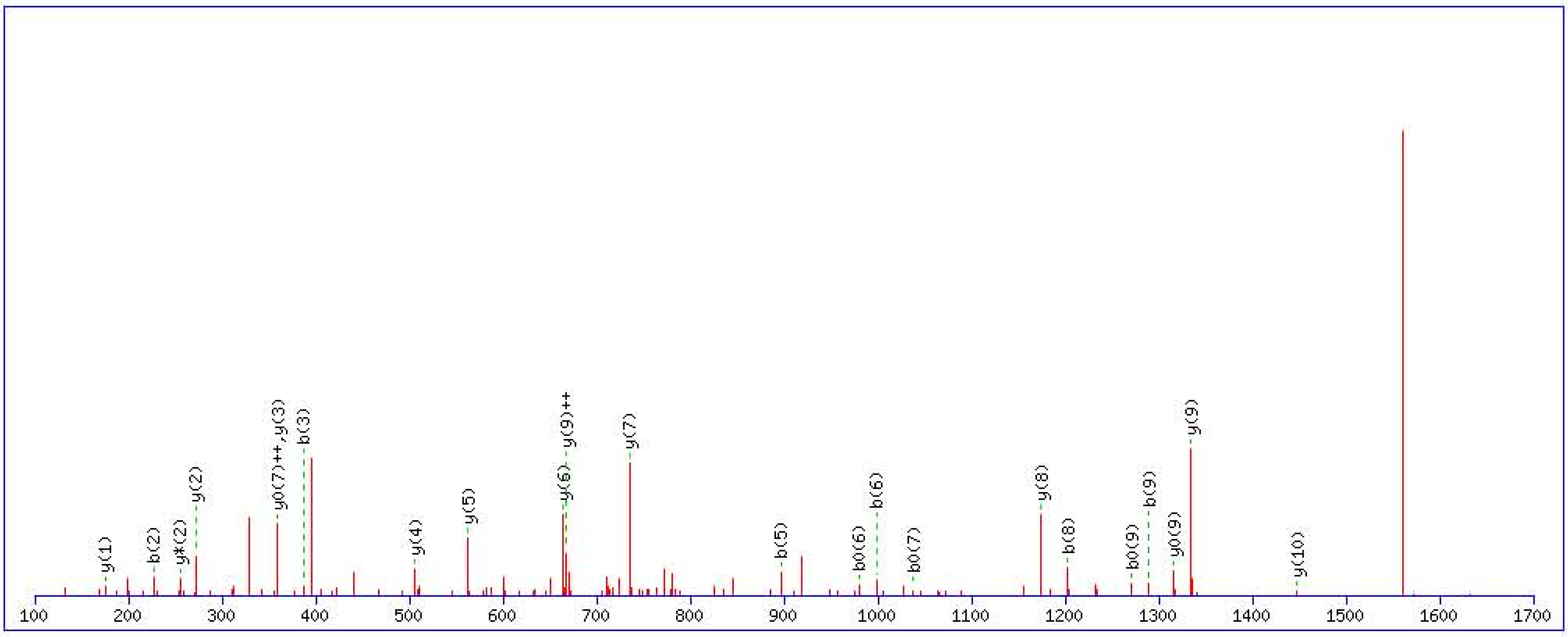
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LICQATGFSPR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

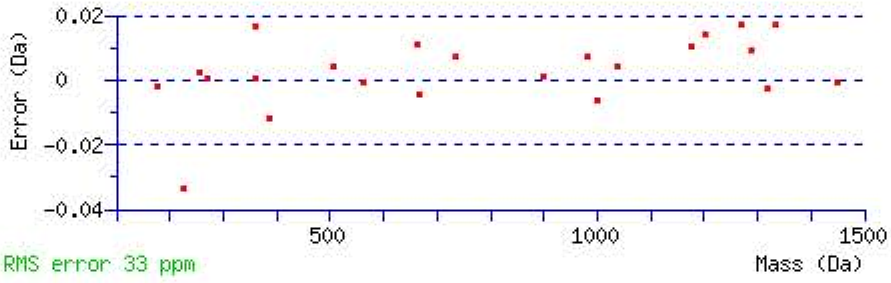
Match to Query 40173: 1559.805448 from(780.910000,2+) rtinseconds(1969) index(41950)
Title: Locus:1.1.1.2969.9 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

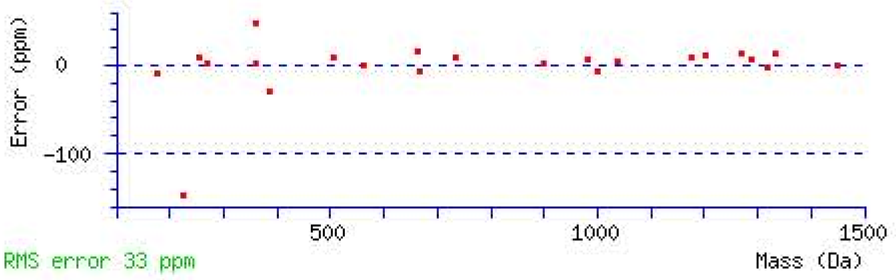
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1559.795242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 6e-006
Matches : 23/100 fragment ions using 40 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							11
2	**227.175404**	114.091340					I	***1447.718454***	724.362865	1430.691905	715.849591	1429.707889	715.357583	10
3	**387.206053**	194.106664					C	***1334.634390***	667.820833	1317.607841	659.307559	1316.623825	658.815551	9
4	826.431379	413.719328	809.404830	405.206053			Q	***1174.603741***	587.805509	1157.577192	579.292234	1156.593176	578.800226	8
5	**897.468493**	449.237885	880.441944	440.724610			A	***735.378415***	368.192846	718.351866	359.679571	717.367850	359.187563	7
6	**998.516172**	499.761724	981.489623	491.248449	980.505607	490.756441	T	***664.341301***	332.674289	647.314752	324.161014	646.330736	323.669006	6
7	1055.537636	528.272456	1038.511087	519.759182	1037.527071	519.267174	G	***563.293622***	282.150449	546.267073	273.637175	545.283057	273.145167	5
8	**1202.606050**	601.806663	1185.579501	593.293389	1184.595485	592.801381	F	***506.272158***	253.639717	489.245609	245.126443	488.261593	244.634435	4
9	**1289.638078**	645.322677	1272.611529	636.809403	1271.627513	636.317395	S	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	1386.690842	693.849059	1369.664293	685.335785	1368.680277	684.843777	P	***272.171716***	136.589496	255.145167	128.076221			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.3	1559.795242	0.010206	LICQATGFSPR
8.3	1559.808960	-0.003512	LDRLSGLADQMVAR
7.7	1559.820190	-0.014742	MTRSATQAAKQVPR
3.0	1559.812943	-0.007495	EPMNIYNLNAIIR

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

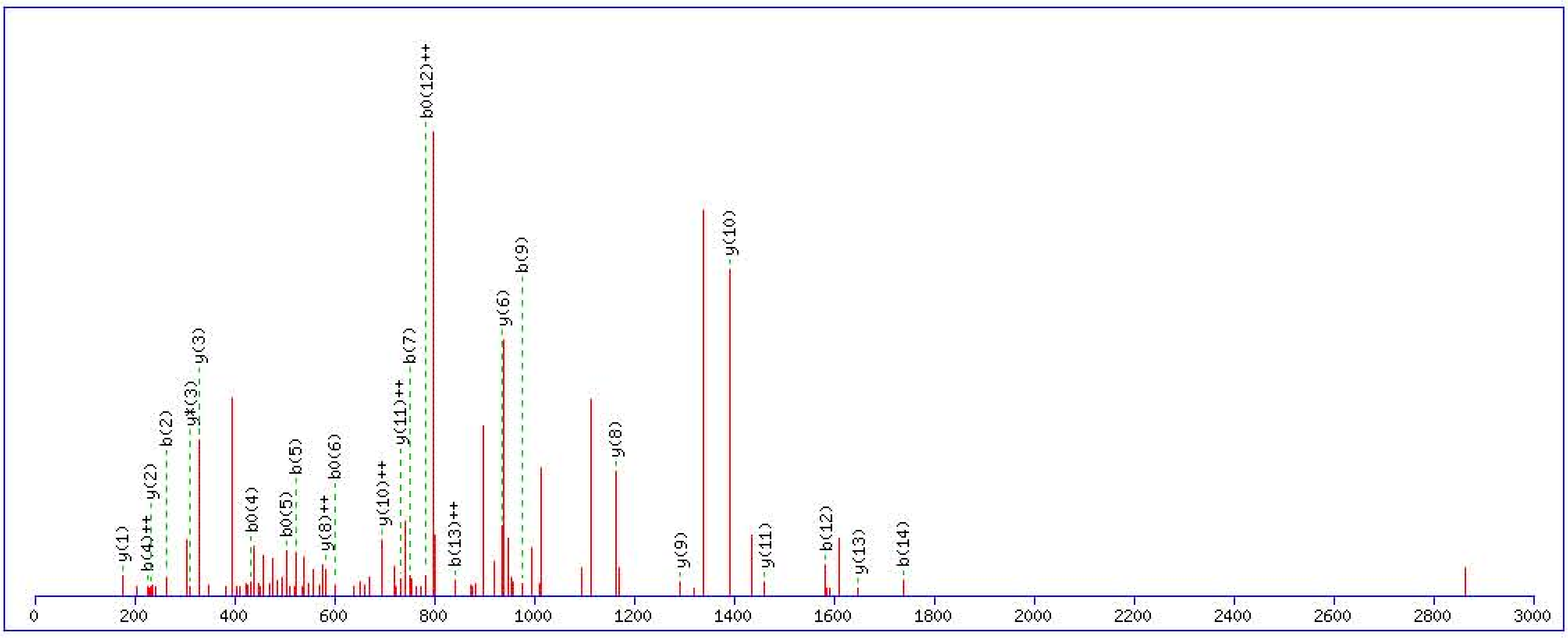
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVTSAPMPEPQAPGR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

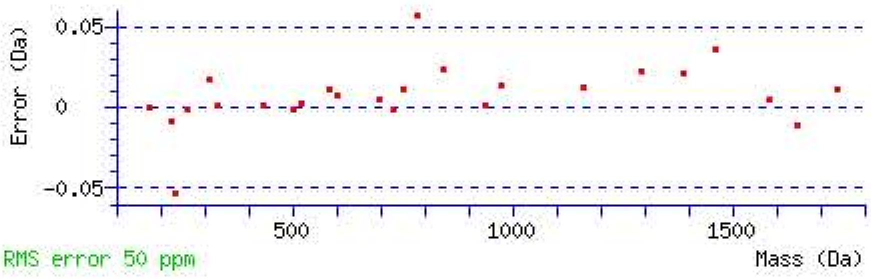
Match to Query 50875: 1910.940228 from(956.477390,2+) rtinseconds(1851) index(41009)
Title: Locus:1.1.1.2928.22 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

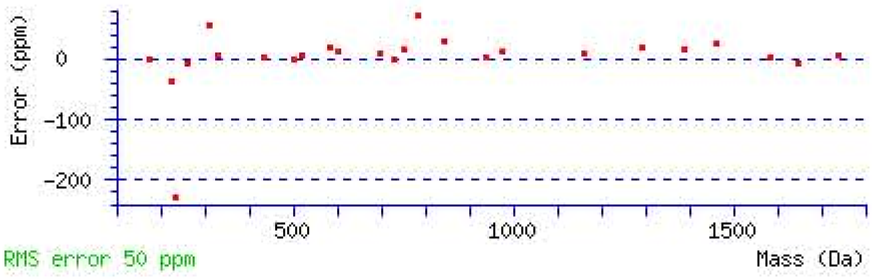
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1910.938263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.053
Matches : 25/132 fragment ions using 69 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	164.070605	82.538940					Y							15
2	**263.139019**	132.073148					V	1748.882225	874.944750	1731.855676	866.431476	1730.871660	865.939468	14
3	364.186698	182.596987			346.176133	173.591705	T	***1649.813811***	825.410543	1632.787262	816.897269	1631.803246	816.405261	13
4	451.218726	**226.113001**			433.208161	217.107719	S	1548.766132	774.886704	1531.739583	766.373430	1530.755567	765.881421	12
5	**522.255840**	261.631558			504.245275	252.626276	A	***1461.734104***	731.370690	1444.707555	722.857416	1443.723539	722.365407	11
6	619.308604	310.157940			601.298039	301.152658	P	***1390.696990***	695.852133	1373.670441	687.338859	1372.686425	686.846850	10
7	**750.349089**	375.678183			732.338524	366.672900	M	***1293.644226***	647.325751	1276.617677	638.812477	1275.633661	638.320468	9
8	847.401853	424.204565			829.391288	415.199282	P	***1162.603741***	581.805508	1145.577192	573.292234	1144.593176	572.800226	8
9	**976.444446**	488.725861			958.433881	479.720579	E	1065.550977	533.279126	1048.524428	524.765852	1047.540412	524.273844	7
10	1073.497210	537.252243			1055.486645	528.246961	P	***936.508384***	468.757830	919.481835	460.244555			6
11	1512.722536	756.864906	1495.695987	748.351632	1494.711971	747.859624	Q	839.455620	420.231448	822.429071	411.718173			5
12	**1583.759650**	792.383463	1566.733101	783.870189	1565.749085	783.378180	A	400.230294	200.618785	383.203745	192.105510			4
13	1680.812414	**840.909845**	1663.785865	832.396571	1662.801849	831.904563	P	***329.193180***	165.100228	312.166631	156.586953			3
14	**1737.833878**	869.420577	1720.807329	860.907303	1719.823313	860.415294	G	***232.140416***	116.573846	215.113867	108.060571			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	1910.934265	0.005963	SGSDEVQVGQQR
31.6	1910.938263	0.001965	YVTSAPMPEPQAPGR
27.7	1910.934265	0.005963	SGSDEVQVGQQR
5.0	1910.934265	0.005963	SGSDEVQVGQQR
3.9	1910.930725	0.009503	AGSGGLGGGAGGGQGAGAGQGAALR
3.9	1910.963196	-0.022968	EQQRQEELEKQR
3.1	1910.913101	0.027127	TLNMDMFTWEPRKAR
2.7	1910.955811	-0.015583	RLAALGADPAARDSDAEGR
2.3	1910.957382	-0.017154	DPWRFGNTPVQQR
1.4	1910.938721	0.001507	QEAEGLALDSPWHRFR

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

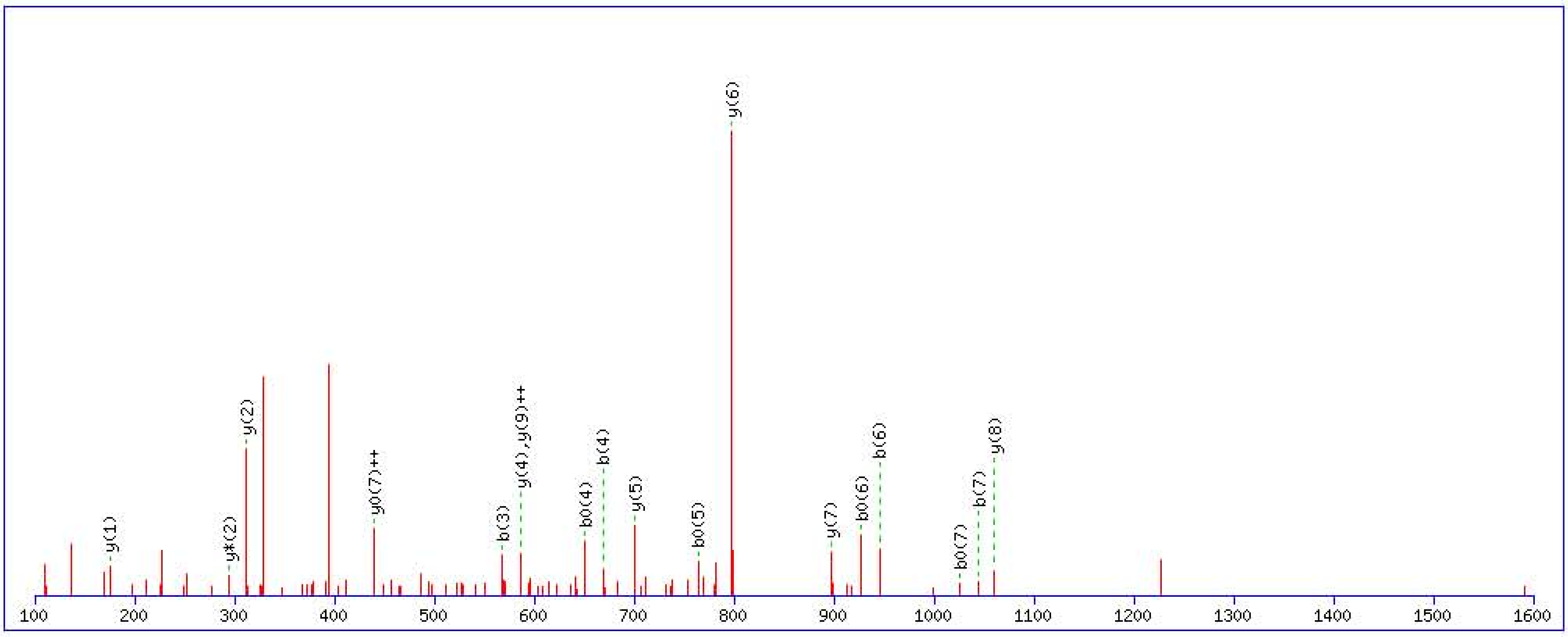
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAQTLYVPNCDHR**
Found in **IBP6_HUMAN**, Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1

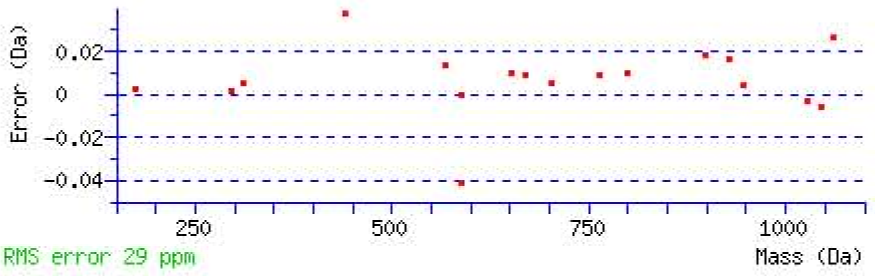
Match to Query 49323: 1840.882752 from(614.634860,3+) rtinseconds(1743) index(76775)
Title: Locus:1.1.1.2821.14 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

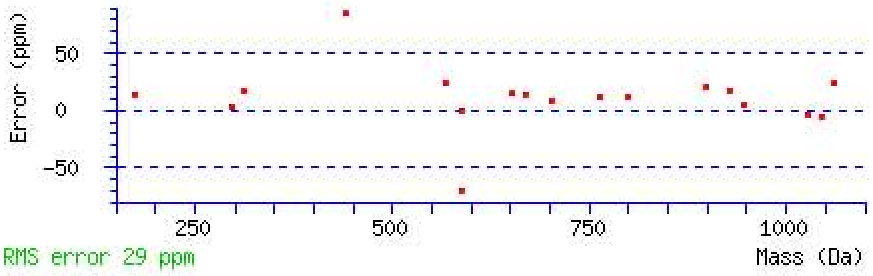
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1840.871262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0014
Matches : 18/130 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	58.028740	29.518008					G							13
2	129.065854	65.036565					A	1784.857073	892.932175	1767.830524	884.418900	1766.846508	883.926892	12
3	***568.291180***	284.649228	551.264631	276.135954			Q	1713.819959	857.413618	1696.793410	848.900343	1695.809394	848.408335	11
4	***669.338859***	335.173068	652.312310	326.659793	651.328294	326.167785	T	1274.594633	637.800955	1257.568084	629.287680	1256.584068	628.795672	10
5	782.422923	391.715100	765.396374	383.201825	764.412358	382.709817	L	1173.546954	587.277115	1156.520405	578.763841	1155.536389	578.271833	9
6	***945.486252***	473.246764	928.459703	464.733490	927.475687	464.241482	Y	***1060.462890***	530.735083	1043.436341	522.221809	1042.452325	521.729801	8
7	***1044.554666***	522.780971	1027.528117	514.267697	1026.544101	513.775689	V	***897.399561***	449.203419	880.373012	440.690144	879.388996	440.198136	7
8	1141.607430	571.307353	1124.580881	562.794079	1123.596865	562.302071	P	***798.331147***	399.669212	781.304598	391.155937	780.320582	390.663929	6
9	1255.650357	628.328817	1238.623808	619.815542	1237.639792	619.323534	N	***701.278383***	351.142830	684.251834	342.629555	683.267818	342.137547	5
10	1415.681006	708.344141	1398.654457	699.830867	1397.670441	699.338859	C	***587.235456***	294.121366	570.208907	285.608092	569.224891	285.116084	4
11	1530.707949	765.857613	1513.681400	757.344338	1512.697384	756.852330	D	427.204807	214.106041	410.178258	205.592767	409.194242	205.100759	3
12	1667.766861	834.387069	1650.740312	825.873794	1649.756296	825.381786	H	***312.177864***	156.592570	295.151315	148.079295			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.5	1840.871262	0.011490	GAQTLYVPNCDHR
3.8	1840.887650	-0.004898	AALSASEGEEVPQDK
0.3	1840.910141	-0.027389	RTSMPLLNDPQSVPDR

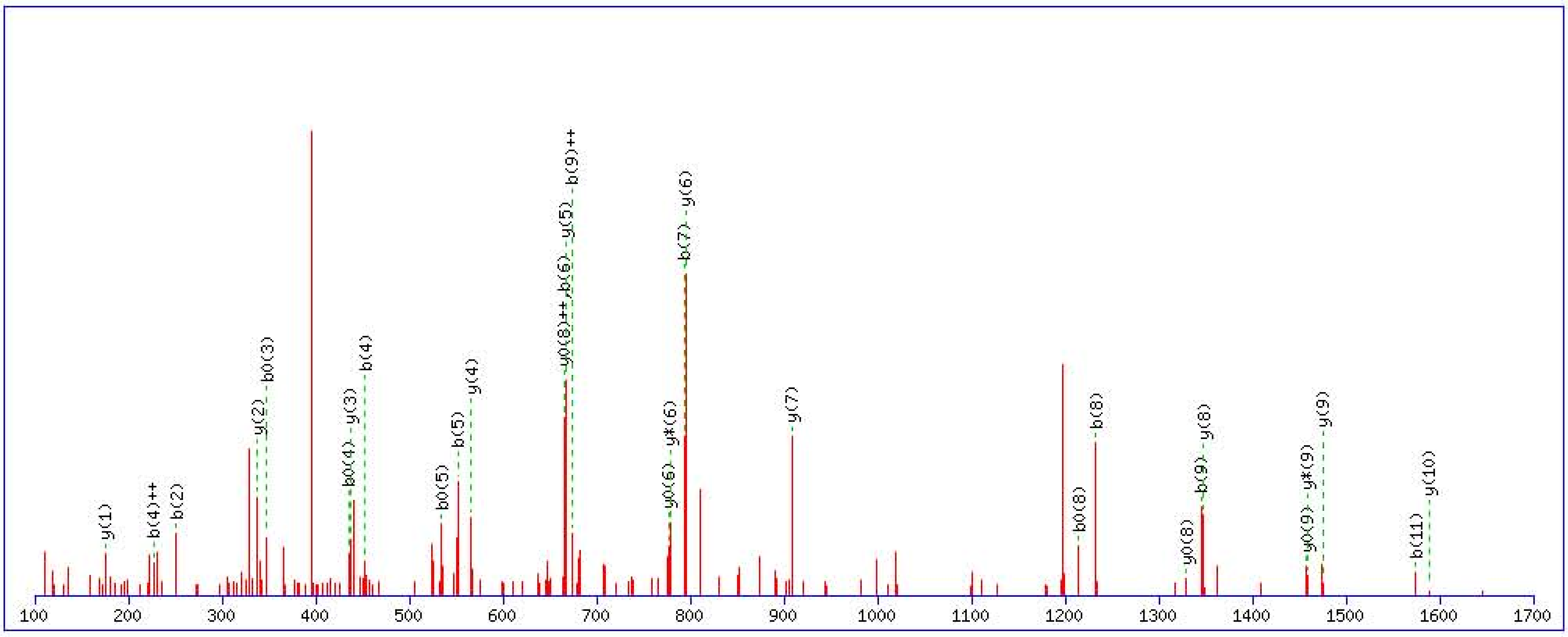
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLDSVLQQLQTEVYR**
Found in **IBP6_HUMAN**, Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1

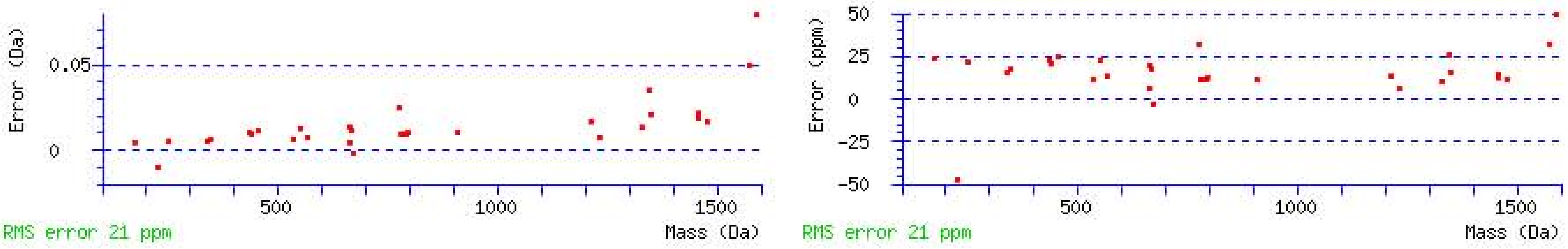
Match to Query 56814: 2139.142152 from(714.054660,3+) rtinseconds(2550) index(82080)
Title: Locus:1.1.1.3102.6 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2139.114655
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 3e-005
Matches : 30/146 fragment ions using 58 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	138.066188	69.536732					H							15
2	***251.150252***	126.078764					L	2003.063026	1002.035151	1986.036477	993.521877	1985.052461	993.029869	14
3	366.177195	183.592235			348.166630	174.586953	D	1889.978962	945.493119	1872.952413	936.979845	1871.968397	936.487836	13
4	***453.209223***	**227.108250**			435.198658	218.102967	S	1774.952019	887.979648	1757.925470	879.466373	1756.941454	878.974365	12
5	***552.277637***	276.642457			534.267072	267.637174	V	1687.919991	844.463634	1670.893442	835.950359	1669.909426	835.458351	11
6	***665.361701***	333.184489			647.351136	324.179206	L	***1588.851577***	794.929427	1571.825028	786.416152	1570.841012	785.924144	10
7	***793.420279***	397.213778	776.393730	388.700503	775.409714	388.208495	Q	***1475.767513***	738.387395	1458.740964	729.874120	1457.756948	729.382112	9
8	***1232.645605***	616.826440	1215.619056	608.313166	1214.635040	607.821158	Q	***1347.708935***	674.358105	1330.682386	665.844831	1329.698370	665.352823	8
9	***1345.729669***	**673.368472**	1328.703120	664.855198	1327.719104	664.363190	L	***908.483609***	454.745443	891.457060	446.232168	890.473044	445.740160	7
10	1473.788247	737.397761	1456.761698	728.884487	1455.777682	728.392479	Q	***795.399545***	398.203411	778.372996	389.690136	777.388980	389.198128	6
11	***1574.835926***	787.921601	1557.809377	779.408326	1556.825361	778.916318	T	***667.340967***	334.174122	650.314418	325.660847	649.330402	325.168839	5
12	1703.878519	852.442897	1686.851970	843.929623	1685.867954	843.437615	E	***566.293288***	283.650282	549.266739	275.137008	548.282723	274.645000	4
13	1802.946933	901.977104	1785.920384	893.463830	1784.936368	892.971822	V	***437.250695***	219.128986	420.224146	210.615711			3
14	1966.010262	983.508769	1948.983713	974.995494	1947.999697	974.503486	Y	***338.182281***	169.594779	321.155732	161.081504			2
15							R	***175.118952***	88.063114	158.092403	79.549840			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.5	2139.114655	0.027497	HLDSVLQQLQTEVYR
37.9	2139.114655	0.027497	HLDSVLQQLQTEVYR
24.4	2139.114655	0.027497	HLDSVLQQLQTEVYR
0.3	2139.122025	0.020127	FNVETMAQLLNIPPNK

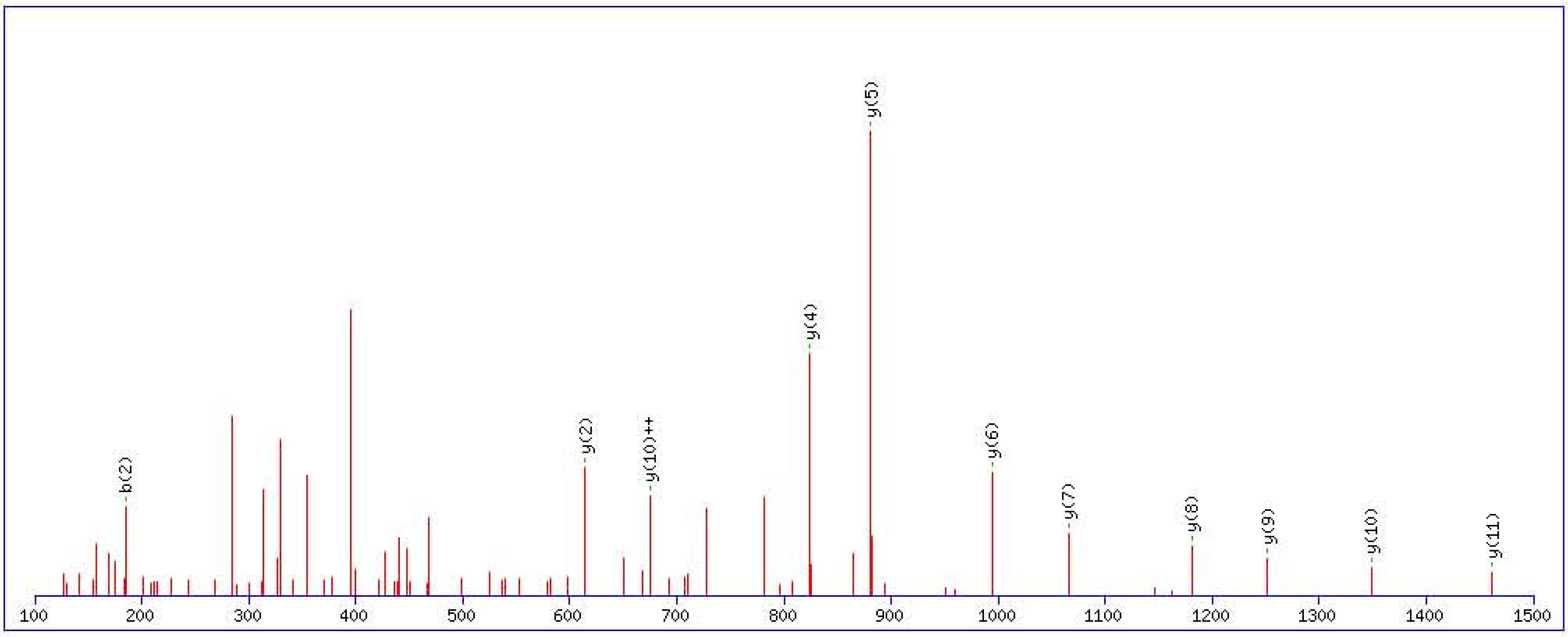
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAELPADALGPLQR**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

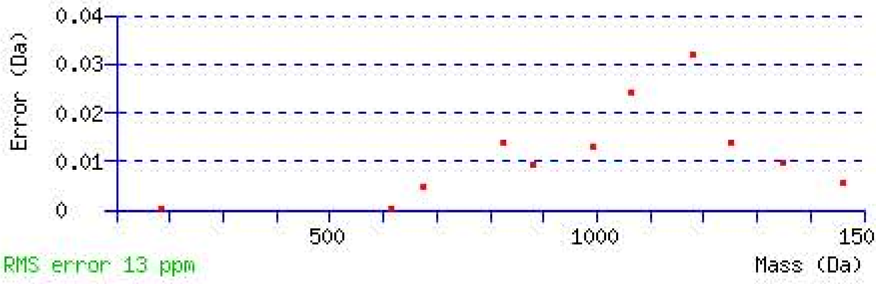
Match to Query 47889: 1773.996042 from(592.339290,3+) rtinseconds(2450) index(44945)
Title: Locus:1.1.1.3137.4 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

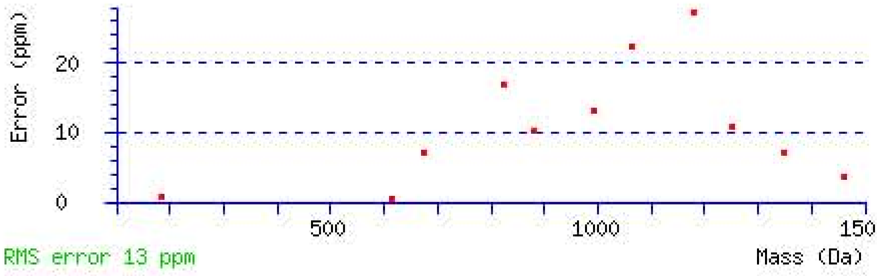
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1773.981094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 77  Expect: 2.3e-007
Matches : 11/114 fragment ions using 14 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							14
2	**185.128454**	93.067865					A	1661.904340	831.455808	1644.877791	822.942534	1643.893775	822.450526	13
3	314.171047	157.589161			296.160482	148.583879	E	1590.867226	795.937251	1573.840677	787.423977	1572.856661	786.931969	12
4	427.255111	214.131193			409.244546	205.125911	L	***1461.824633***	731.415955	1444.798084	722.902680	1443.814068	722.410672	11
5	524.307875	262.657576			506.297310	253.652293	P	***1348.740569***	674.873922	1331.714020	666.360648	1330.730004	665.868640	10
6	595.344989	298.176133			577.334424	289.170850	A	***1251.687805***	626.347540	1234.661256	617.834266	1233.677240	617.342258	9
7	710.371932	355.689604			692.361367	346.684322	D	***1180.650691***	590.828984	1163.624142	582.315709	1162.640126	581.823701	8
8	781.409046	391.208161			763.398481	382.202879	A	***1065.623748***	533.315512	1048.597199	524.802238			7
9	894.493110	447.750193			876.482545	438.744911	L	***994.586634***	497.796955	977.560085	489.283681			6
10	951.514574	476.260925			933.504009	467.255643	G	***881.502570***	441.254923	864.476021	432.741649			5
11	1048.567338	524.787307			1030.556773	515.782025	P	***824.481106***	412.744191	807.454557	404.230916			4
12	1161.651402	581.329339			1143.640837	572.324056	L	727.428342	364.217809	710.401793	355.704534			3
13	1600.876728	800.942002	1583.850179	792.428728	1582.866163	791.936719	Q	***614.344278***	307.675777	597.317729	299.162503			2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.4	1773.981094	0.014948	LAELPADALGPLQR

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

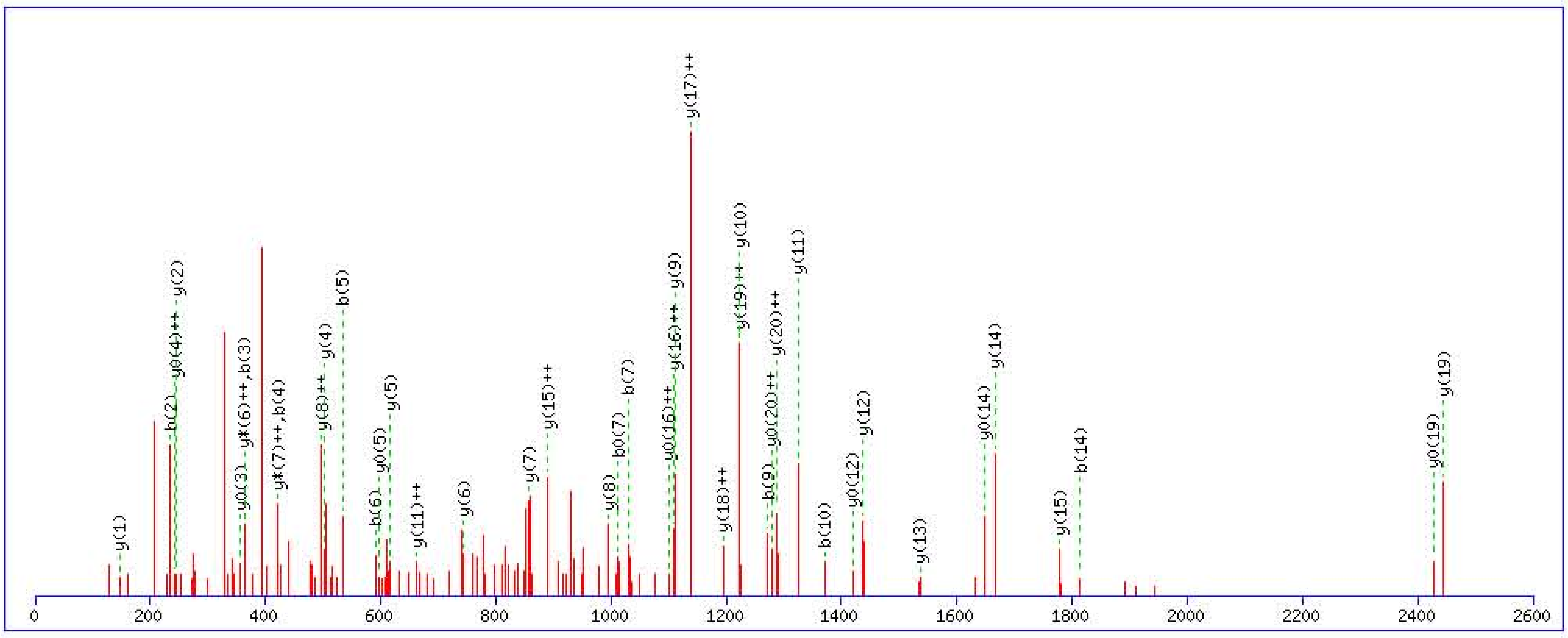
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFEGLGQLEVLTLDHNQLQEVK**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

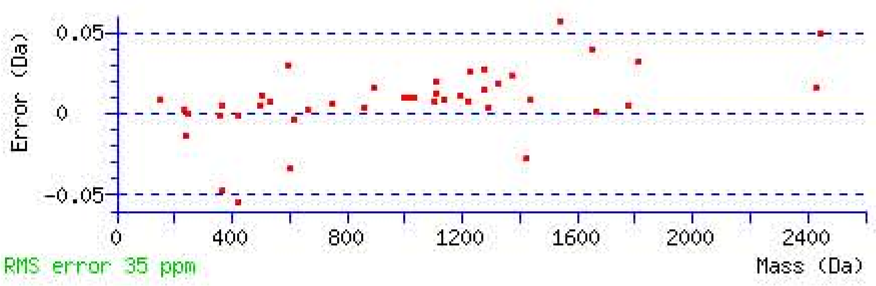
Match to Query 68874: 2807.486022 from(936.835950,3+) rtinseconds(2683) index(46419)
Title: Locus:1.1.1.3217.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

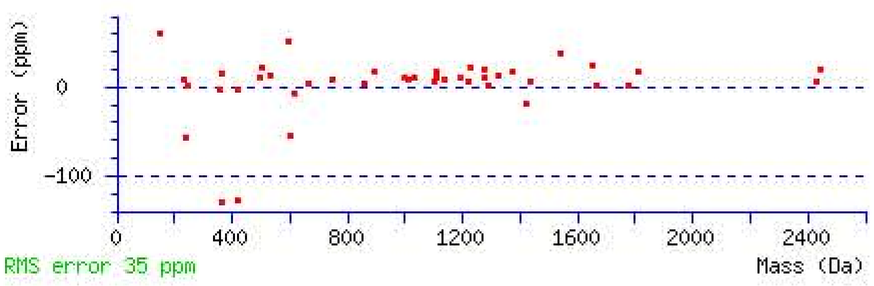
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2807.452759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 72 **Expect:** 1.3e-006
Matches : 43/236 fragment ions using 87 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							22
2	***235.107718***	118.057497			217.097153	109.052214	F	2721.428016	1361.217646	2704.401467	1352.704371	2703.417451	1352.212363	21
3	***364.150311***	182.578793			346.139746	173.573511	E	2574.359602	1287.683439	2557.333053	1279.170164	2556.349037	1278.678156	20
4	***421.171775***	211.089525			403.161210	202.084243	G	***2445.317009***	1223.162142	2428.290460	1214.648868	2427.306444	1214.156860	19
5	***534.255839***	267.631558			516.245274	258.626275	L	2388.295545	1194.651410	2371.268996	1186.138136	2370.284980	1185.646128	18
6	***591.277303***	296.142290			573.266738	287.137007	G	2275.211481	1138.109378	2258.184932	1129.596104	2257.200916	1129.104096	17
7	***1030.502629***	515.754953	1013.476080	507.241678	1012.492064	506.749670	Q	2218.190017	1109.598646	2201.163468	1101.085372	2200.179452	1100.593364	16
8	1143.586693	572.296985	1126.560144	563.783710	1125.576128	563.291702	L	***1778.964691***	889.985984	1761.938142	881.472709	1760.954126	880.980701	15
9	***1272.629286***	636.818281	1255.602737	628.305007	1254.618721	627.812999	E	***1665.880627***	833.443952	1648.854078	824.930677	1647.870062	824.438669	14
10	***1371.697700***	686.352488	1354.671151	677.839214	1353.687135	677.347206	V	***1536.838034***	768.922655	1519.811485	760.409381	1518.827469	759.917373	13
11	1484.781764	742.894520	1467.755215	734.381246	1466.771199	733.889238	L	***1437.769620***	719.388448	1420.743071	710.875174	1419.759055	710.383166	12
12	1585.829443	793.418360	1568.802894	784.905085	1567.818878	784.413077	T	***1324.685556***	662.846416	1307.659007	654.333142	1306.674991	653.841134	11
13	1698.913507	849.960392	1681.886958	841.447117	1680.902942	840.955109	L	***1223.637877***	612.322577	1206.611328	603.809302	1205.627312	603.317294	10
14	***1813.940450***	907.473863	1796.913901	898.960589	1795.929885	898.468581	D	***1110.553813***	555.780545	1093.527264	547.267270	1092.543248	546.775262	9
15	1950.999362	976.003319	1933.972813	967.490045	1932.988797	966.998037	H	***995.526870***	498.267073	978.500321	489.753799	977.516305	489.261791	8
16	2065.042289	1033.024782	2048.015740	1024.511508	2047.031724	1024.019500	N	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	7
17	2193.100867	1097.054072	2176.074318	1088.540797	2175.090302	1088.048789	Q	***744.425031***	372.716154	727.398482	364.202879	726.414466	363.710871	6
18	2306.184931	1153.596104	2289.158382	1145.082829	2288.174366	1144.590821	L	***616.366453***	308.686865	599.339904	300.173590	598.355888	299.681582	5
19	2434.243509	1217.625393	2417.216960	1209.112118	2416.232944	1208.620110	Q	***503.282389***	252.144833	486.255840	243.631558	485.271824	243.139550	4
20	2563.286102	1282.146689	2546.259553	1273.633415	2545.275537	1273.141407	E	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
21	2662.354516	1331.680896	2645.327967	1323.167622	2644.343951	1322.675614	V	***246.181218***	123.594247	229.154669	115.080972			2
22							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SFEGLGQLEVLTLDHNQLQEVK
(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	2807.452759	0.033263	SFEGLGQLEVLTLDHNQLQEVK
5.2	2807.452759	0.033263	SFEGLGQLEVLTLDHNQLQEVK

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

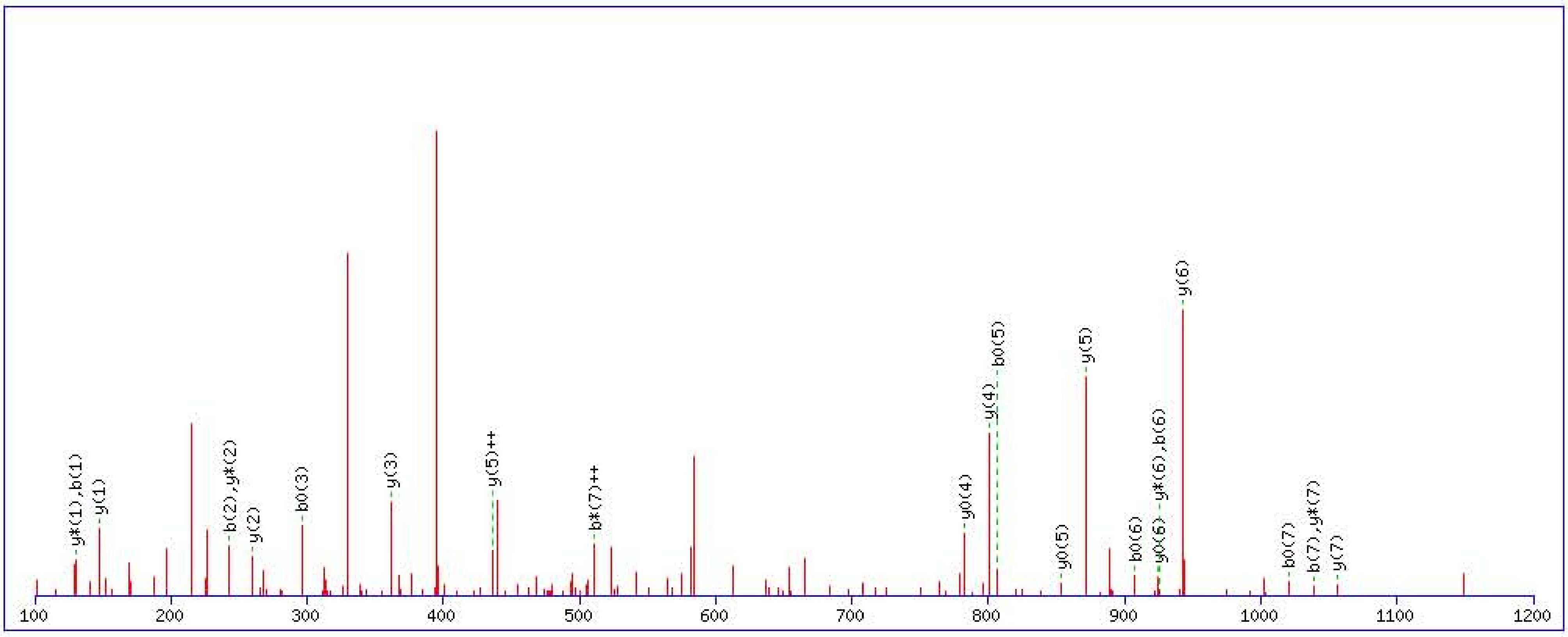
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELAAQTIK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

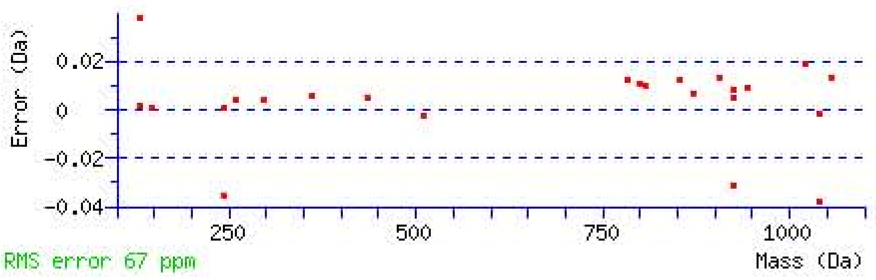
Match to Query 27183: 1183.671048 from(592.842800,2+) rtinseconds(1695) index(58271)
Title: Locus:1.1.1.2896.7 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

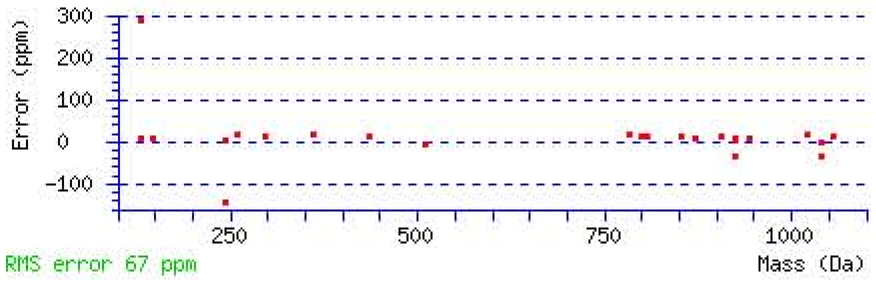
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1183.663452
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.02
Matches : 24/72 fragment ions using 51 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							8
2	**243.133933**	122.070605			225.123368	113.065322	L	***1055.628165***	528.317720	1038.601616	519.804446	1037.617600	519.312438	7
3	314.171047	157.589161			296.160482	148.583879	A	***942.544101***	471.775689	925.517552	463.262414	924.533536	462.770406	6
4	385.208161	193.107718			367.197596	184.102436	A	***871.506987***	436.257132	854.480438	427.743857	853.496422	427.251849	5
5	824.433487	412.720382	807.406938	404.207107	806.422922	403.715099	Q	***800.469873***	400.738575	783.443324	392.225300	782.459308	391.733292	4
6	**925.481166**	463.244221	908.454617	454.730947	907.470601	454.238939	T	***361.244547***	181.125911	344.217998	172.612637	343.233982	172.120629	3
7	**1038.565230**	519.786253	1021.538681	511.272978	1020.554665	510.780970	I	***260.196868***	130.602072	243.170319	122.088797			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.3	1183.663452	0.007596	ELAAQTIK
25.2	1183.663452	0.007596	ELAAQITK
12.6	1183.663467	0.007581	TQLSPSIK
7.0	1183.681198	-0.010150	LEALLEAAGIGK
6.5	1183.660080	0.010968	AIEAVAISPWK
6.5	1183.667282	0.003766	GKQASEPALRK
5.3	1183.663452	0.007596	LEQAATLK
4.5	1183.656937	0.014111	MRPQTLK
4.4	1183.674698	-0.003650	TQVRELK
3.4	1183.667297	0.003751	EPTGRVEIRK

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

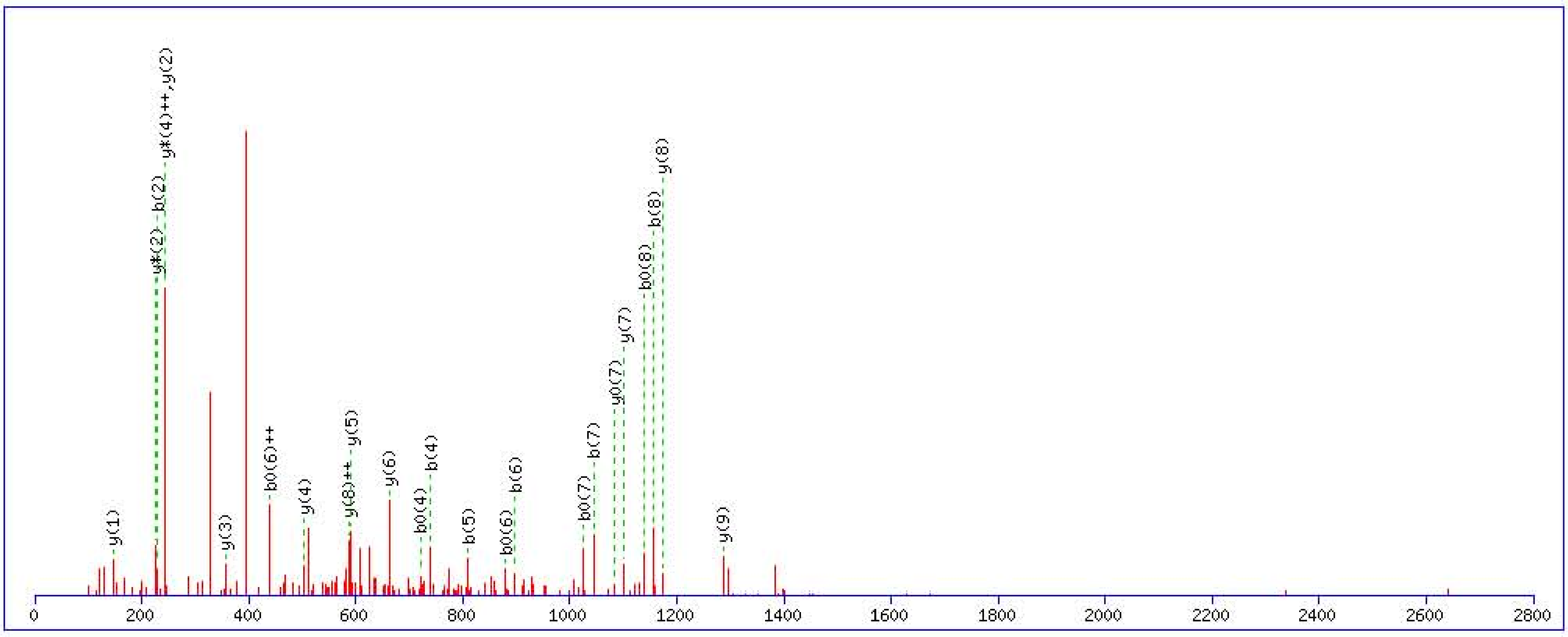
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDAQASFLPK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

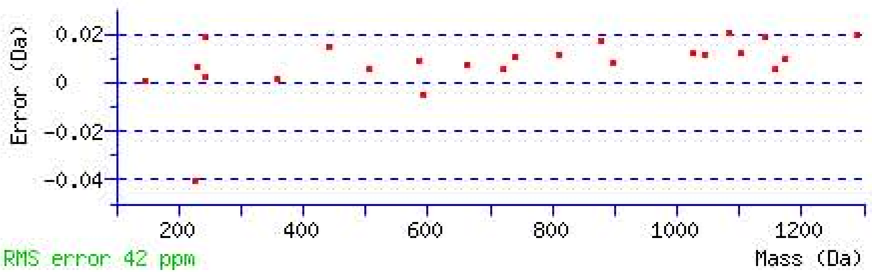
Match to Query 34574: 1399.765468 from(700.890010,2+) rtinseconds(2167) index(61710)
Title: Locus:1.1.1.3059.15 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

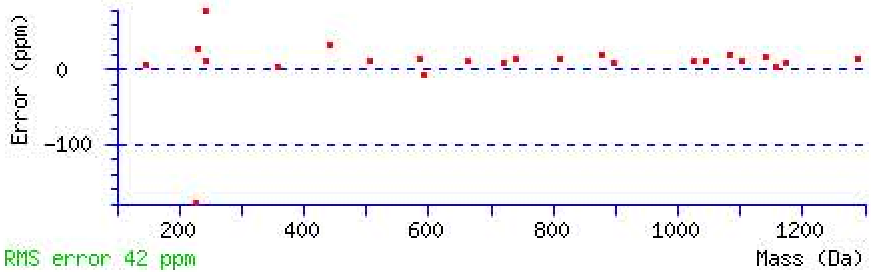
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1399.753342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00015
Matches : 24/92 fragment ions using 51 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							10
2	**229.118283**	115.062779			211.107718	106.057497	D	***1287.676571***	644.341924	1270.650022	635.828649	1269.666006	635.336641	9
3	300.155397	150.581336			282.144832	141.576054	A	***1172.649628***	586.828452	1155.623079	578.315178	1154.639063	577.823169	8
4	**739.380723**	370.194000	722.354174	361.680725	721.370158	361.188717	Q	***1101.612514***	551.309895	1084.585965	542.796621	1083.601949	542.304612	7
5	**810.417837**	405.712557	793.391288	397.199282	792.407272	396.707274	A	***662.387188***	331.697232	645.360639	323.183957	644.376623	322.691949	6
6	**897.449865**	449.228570	880.423316	440.715296	879.439300	440.223288	S	***591.350074***	296.178675	574.323525	287.665400	573.339509	287.173392	5
7	**1044.518279**	522.762777	1027.491730	514.249503	1026.507714	513.757495	F	***504.318046***	252.662661	487.291497	244.149386			4
8	**1157.602343**	579.304809	1140.575794	570.791535	1139.591778	570.299527	L	***357.249632***	179.128454	340.223083	170.615179			3
9	1254.655107	627.831191	1237.628558	619.317917	1236.644542	618.825909	P	***244.165568***	122.586422	227.139019	114.073148			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.0	1399.753342	0.012126	LDAQASFLPK
6.0	1399.785660	-0.020192	LNENIKNAMLIK
5.3	1399.753342	0.012126	LLDFAASQPK
5.3	1399.755859	0.009609	LSTPDTLTQISPK
4.4	1399.745972	0.019496	IDAATGIPVTTWR
4.4	1399.755814	0.009654	KTELGPLKEEEK
2.5	1399.771103	-0.005635	QKEPSVLFEVPK
2.4	1399.771973	-0.006505	IWQGMLTIK
2.4	1399.756714	0.008754	LSQVPMSALK
2.3	1399.782318	-0.016850	RGFLAQEELLPK

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

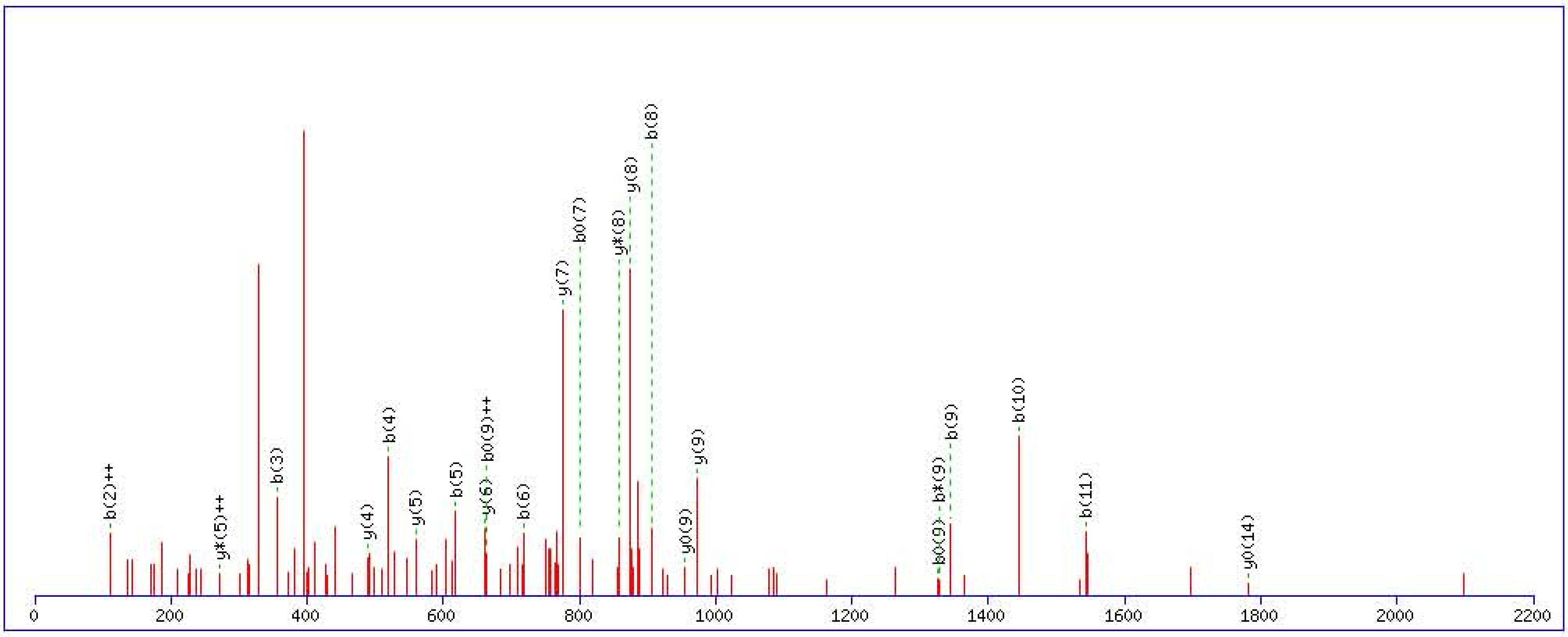
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FAHYVVTSQVVNTANEAR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

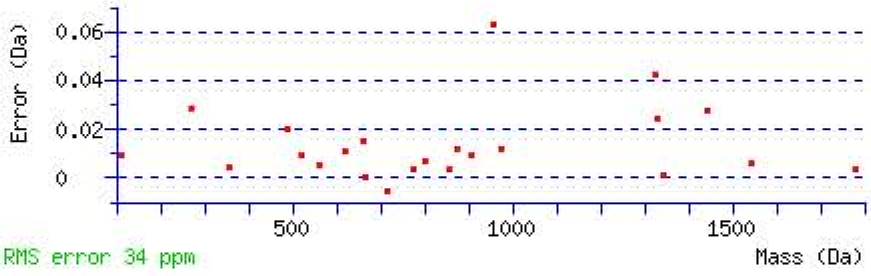
Match to Query 61007: 2316.190332 from(773.070720,3+) rtinseconds(1924) index(59977)
Title: Locus:1.1.1.2975.23 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

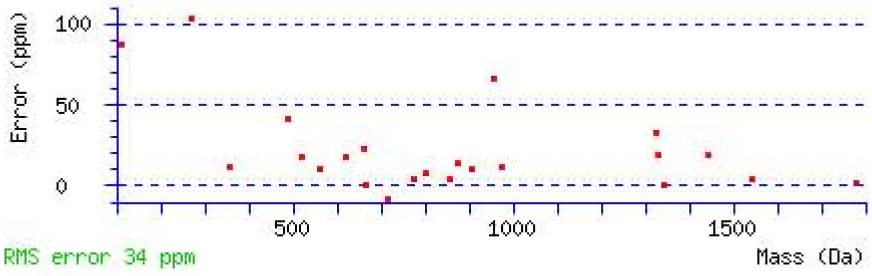
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2316.168488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.024
Matches : 23/172 fragment ions using 54 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							18
2	219.112804	110.060040					A	2170.107350	1085.557313	2153.080801	1077.044038	2152.096785	1076.552030	17
3	***356.171716***	178.589496					H	2099.070236	1050.038756	2082.043687	1041.525481	2081.059671	1041.033473	16
4	***519.235045***	260.121161					Y	1962.011324	981.509300	1944.984775	972.996026	1944.000759	972.504018	15
5	***618.303459***	309.655368					V	1798.947995	899.977636	1781.921446	891.464361	1780.937430	890.972353	14
6	***717.371873***	359.189575					V	1699.879581	850.443429	1682.853032	841.930154	1681.869016	841.438146	13
7	818.419552	409.713414			800.408987	400.708132	T	1600.811167	800.909222	1583.784618	792.395947	1582.800602	791.903939	12
8	***905.451580***	453.229428			887.441015	444.224146	S	1499.763488	750.385382	1482.736939	741.872108	1481.752923	741.380100	11
9	***1344.676906***	672.842091	1327.650357	664.328817	1326.666341	663.836808	Q	1412.731460	706.869368	1395.704911	698.356094	1394.720895	697.864086	10
10	***1443.745320***	722.376298	1426.718771	713.863024	1425.734755	713.371016	V	***973.506134***	487.256705	956.479585	478.743431	955.495569	478.251423	9
11	***1542.813734***	771.910505	1525.787185	763.397231	1524.803169	762.905223	V	***874.437720***	437.722498	857.411171	429.209224	856.427155	428.717216	8
12	1656.856661	828.931969	1639.830112	820.418694	1638.846096	819.926686	N	***775.369306***	388.188291	758.342757	379.675017	757.358741	379.183009	7
13	1757.904340	879.455808	1740.877791	870.942534	1739.893775	870.450526	T	***661.326379***	331.166828	644.299830	322.653553	643.315814	322.161545	6
14	1828.941454	914.974365	1811.914905	906.461091	1810.930889	905.969083	A	***560.278700***	280.642988	543.252151	272.129714	542.268135	271.637706	5
15	1942.984381	971.995829	1925.957832	963.482554	1924.973816	962.990546	N	***489.241586***	245.124431	472.215037	236.611157	471.231021	236.119149	4
16	2072.026974	1036.517125	2055.000425	1028.003850	2054.016409	1027.511842	E	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
17	2143.064088	1072.035682	2126.037539	1063.522407	2125.053523	1063.030399	A	246.156066	123.581671	229.129517	115.068397			2
18							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.4	2316.168488	0.021844	FAHYVVTSQVVNTANEAR

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

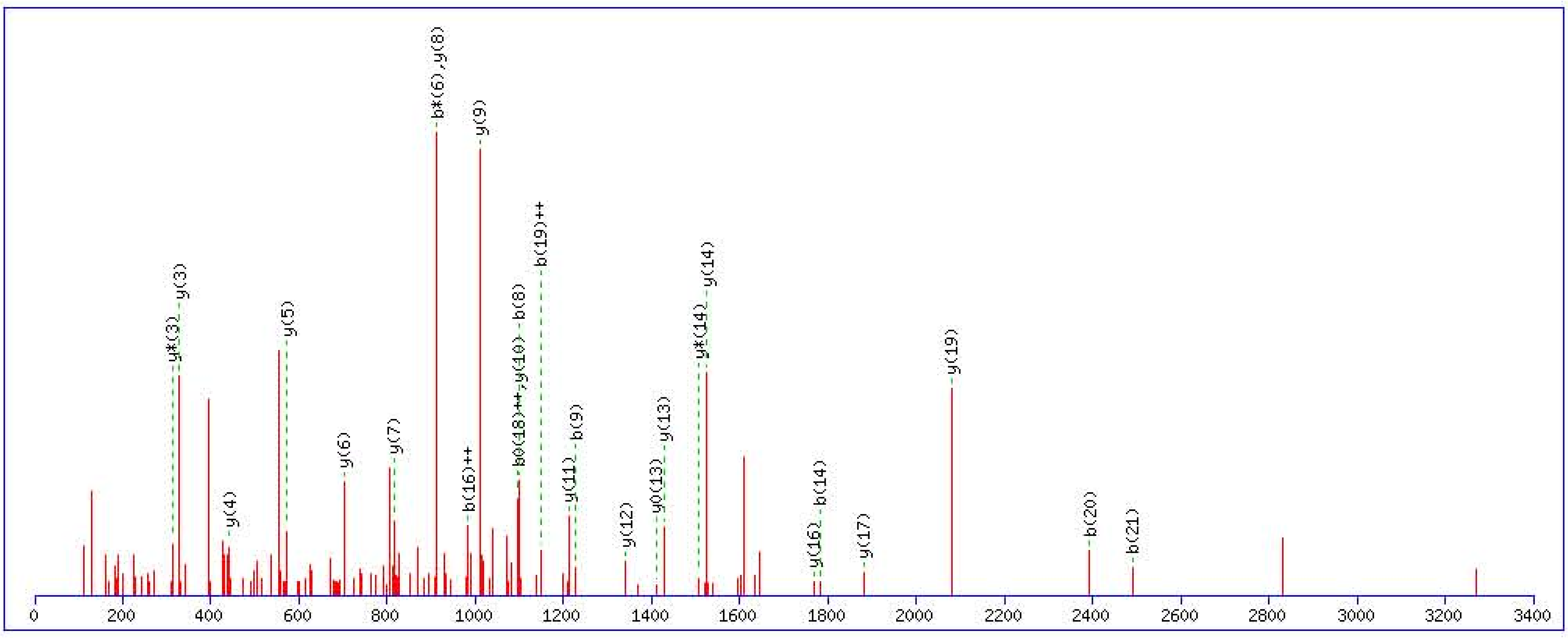
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GMADQDGLKPTIDKPSEDSPPLEMLGPR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

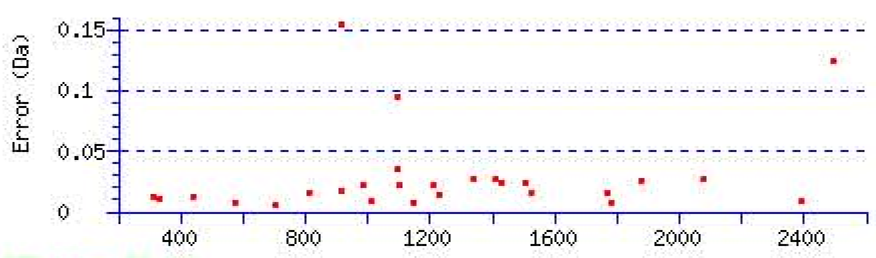
Match to Query 76174: 3304.656256 from(827.171340,4+) rtinseconds(2207) index(62024)
Title: Locus:1.1.1.3073.19 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

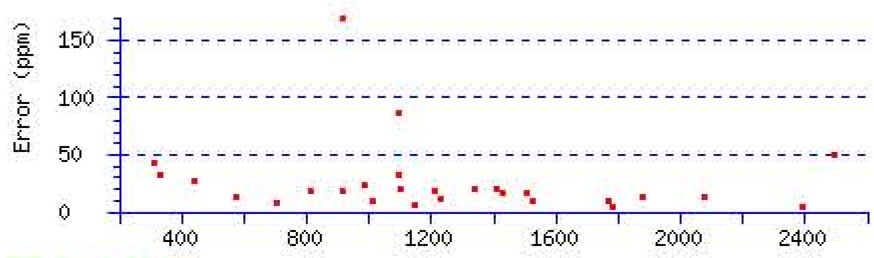
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3304.614151
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 106  Expect: 1.3e-010
Matches : 27/300 fragment ions using 39 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							28
2	189.069225	95.038250					M	3248.599985	1624.803630	3231.573436	1616.290356	3230.589420	1615.798348	27
3	260.106339	130.556807					A	3117.559500	1559.283388	3100.532951	1550.770113	3099.548935	1550.278105	26
4	375.133282	188.070279			357.122717	179.064997	D	3046.522386	1523.764831	3029.495837	1515.251556	3028.511821	1514.759548	25
5	814.358608	407.682942	797.332059	399.169668	796.348043	398.677660	Q	2931.495443	1466.251359	2914.468894	1457.738085	2913.484878	1457.246077	24
6	929.385551	465.196414	912.359002	456.683139	911.374986	456.191131	D	2492.270117	1246.638696	2475.243568	1238.125422	2474.259552	1237.633414	23
7	986.407015	493.707146	969.380466	485.193871	968.396450	484.701863	G	2377.243174	1189.125225	2360.216625	1180.611950	2359.232609	1180.119942	22
8	**1099.491079**	550.249177	1082.464530	541.735903	1081.480514	541.243895	L	2320.221710	1160.614493	2303.195161	1152.101218	2302.211145	1151.609210	21
9	**1227.586042**	614.296659	1210.559493	605.783385	1209.575477	605.291376	K	2207.137646	1104.072461	2190.111097	1095.559186	2189.127081	1095.067178	20
10	1324.638806	662.823041	1307.612257	654.309767	1306.628241	653.817758	P	***2079.042683***	1040.024980	2062.016134	1031.511705	2061.032118	1031.019697	19
11	1425.686485	713.346881	1408.659936	704.833606	1407.675920	704.341598	T	1981.989919	991.498598	1964.963370	982.985323	1963.979354	982.493315	18
12	1538.770549	769.888912	1521.744000	761.375638	1520.759984	760.883630	I	***1880.942240***	940.974758	1863.915691	932.461484	1862.931675	931.969476	17
13	1653.797492	827.402384	1636.770943	818.889110	1635.786927	818.397101	D	***1767.858176***	884.432726	1750.831627	875.919452	1749.847611	875.427444	16
14	**1781.892455**	891.449865	1764.865906	882.936591	1763.881890	882.444583	K	1652.831233	826.919255	1635.804684	818.405980	1634.820668	817.913972	15
15	1878.945219	939.976248	1861.918670	931.462973	1860.934654	930.970965	P	***1524.736270***	762.871773	1507.709721	754.358499	1506.725705	753.866491	14
16	1965.977247	**983.492262**	1948.950698	974.978987	1947.966682	974.486979	S	***1427.683506***	714.345391	1410.656957	705.832117	1409.672941	705.340109	13
17	2095.019840	1048.013558	2077.993291	1039.500283	2077.009275	1039.008275	E	***1340.651478***	670.829377	1323.624929	662.316103	1322.640913	661.824095	12
18	2210.046783	1105.527029	2193.020234	1097.013755	2192.036218	1096.521747	D	***1211.608885***	606.308081	1194.582336	597.794806	1193.598320	597.302798	11
19	2297.078811	**1149.043043**	2280.052262	1140.529769	2279.068246	1140.037761	S	***1096.581942***	548.794609	1079.555393	540.281335	1078.571377	539.789327	10
20	**2394.131575**	1197.569425	2377.105026	1189.056151	2376.121010	1188.564143	P	***1009.549914***	505.278595	992.523365	496.765321	991.539349	496.273313	9
21	**2491.184339**	1246.095807	2474.157790	1237.582533	2473.173774	1237.090525	P	***912.497150***	456.752213	895.470601	448.238939	894.486585	447.746931	8
22	2604.268403	1302.637839	2587.241854	1294.124565	2586.257838	1293.632557	L	***815.444386***	408.225831	798.417837	399.712557	797.433821	399.220549	7
23	2733.310996	1367.159136	2716.284447	1358.645861	2715.300431	1358.153854	E	***702.360322***	351.683799	685.333773	343.170525	684.349757	342.678517	6
24	2864.351481	1432.679379	2847.324932	1424.166104	2846.340916	1423.674096	M	***573.317729***	287.162503	556.291180	278.649228			5
25	2977.435545	1489.221411	2960.408996	1480.708136	2959.424980	1480.216128	L	***442.277244***	221.642260	425.250695	213.128986			4
26	3034.457009	1517.732143	3017.430460	1509.218868	3016.446444	1508.726860	G	***329.193180***	165.100228	312.166631	156.586953			3
27	3131.509773	1566.258525	3114.483224	1557.745250	3113.499208	1557.253242	P	272.171716	136.589496	255.145167	128.076221			2
28							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
106.1	3304.614151	0.042105	GMADQDGLKPTIDKPSEDSPPLEMLGPR
0.8	3304.683334	-0.027078	QNAIVAKMEDPLSNRAPDSLENVISNAVPGR

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

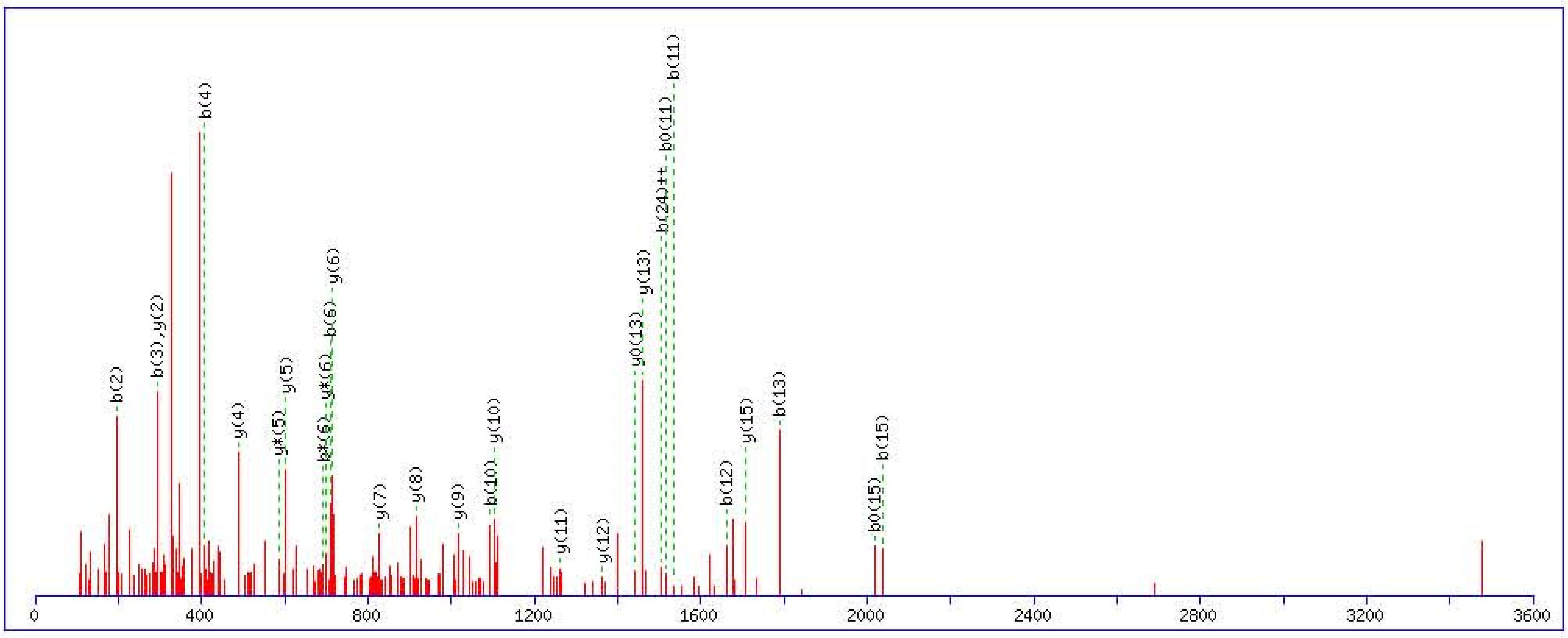
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHVLFRPTVSQQQSCPTCSTSLLNGHFK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

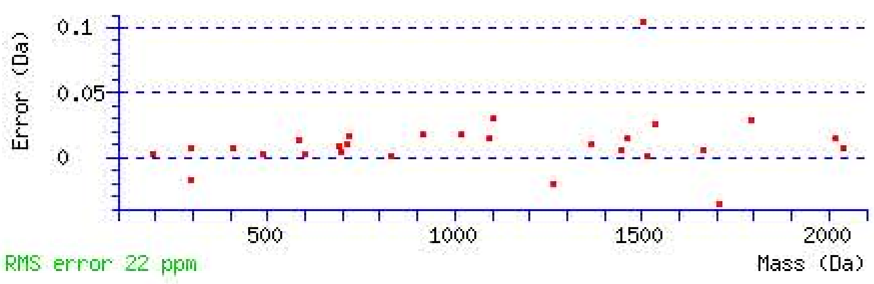
Match to Query 77860: 3496.755870 from(700.358450,5+) rtinseconds(1930) index(60020)
Title: Locus:1.1.1.2977.16 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

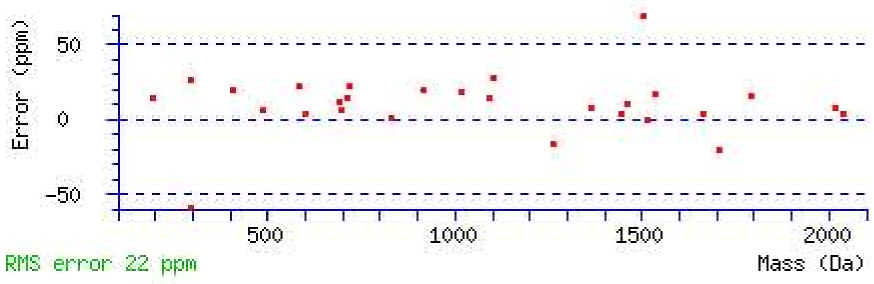
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3496.716660
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 0.00034
Matches : 28/286 fragment ions using 70 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							28
2	***195.087652***	98.047464					H	3440.702435	1720.854855	3423.675886	1712.341581	3422.691870	1711.849573	27
3	***294.156066***	147.581671					V	3303.643523	1652.325399	3286.616974	1643.812125	3285.632958	1643.320117	26
4	***407.240130***	204.123703					L	3204.575109	1602.791192	3187.548560	1594.277918	3186.564544	1593.785910	25
5	554.308544	277.657910					F	3091.491045	1546.249160	3074.464496	1537.735886	3073.480480	1537.243878	24
6	***710.409655***	355.708466	693.383106	347.195191			R	2944.422631	1472.714953	2927.396082	1464.201679	2926.412066	1463.709671	23
7	807.462419	404.234848	790.435870	395.721573			P	2788.321520	1394.664398	2771.294971	1386.151123	2770.310955	1385.659115	22
8	908.510098	454.758687	891.483549	446.245413	890.499533	445.753405	T	2691.268756	1346.138016	2674.242207	1337.624741	2673.258191	1337.132733	21
9	1007.578512	504.292894	990.551963	495.779620	989.567947	495.287612	V	2590.221077	1295.614176	2573.194528	1287.100902	2572.210512	1286.608894	20
10	***1094.610540***	547.808908	1077.583991	539.295634	1076.599975	538.803626	S	2491.152663	1246.079969	2474.126114	1237.566695	2473.142098	1237.074687	19
11	***1533.835866***	767.421571	1516.809317	758.908297	1515.825301	758.416289	Q	2404.120635	1202.563955	2387.094086	1194.050681	2386.110070	1193.558673	18
12	***1661.894444***	831.450860	1644.867895	822.937586	1643.883879	822.445578	Q	1964.895309	982.951292	1947.868760	974.438018	1946.884744	973.946010	17
13	***1789.953022***	895.480149	1772.926473	886.966875	1771.942457	886.474867	Q	1836.836731	918.922003	1819.810182	910.408729	1818.826166	909.916721	16
14	1876.985050	938.996163	1859.958501	930.482889	1858.974485	929.990881	S	***1708.778153***	854.892714	1691.751604	846.379440	1690.767588	845.887432	15
15	***2037.015699***	1019.011488	2019.989150	1010.498213	2019.005134	1010.006205	C	1621.746125	811.376700	1604.719576	802.863426	1603.735560	802.371418	14
16	2134.068463	1067.537869	2117.041914	1059.024595	2116.057898	1058.532587	P	***1461.715476***	731.361376	1444.688927	722.848101	1443.704911	722.356093	13
17	2235.116142	1118.061709	2218.089593	1109.548434	2217.105577	1109.056426	T	***1364.662712***	682.834994	1347.636163	674.321719	1346.652147	673.829711	12
18	2395.146791	1198.077033	2378.120242	1189.563759	2377.136226	1189.071751	C	***1263.615033***	632.311154	1246.588484	623.797880	1245.604468	623.305872	11
19	2482.178819	1241.593047	2465.152270	1233.079773	2464.168254	1232.587765	S	***1103.584384***	552.295830	1086.557835	543.782556	1085.573819	543.290548	10
20	2583.226498	1292.116887	2566.199949	1283.603612	2565.215933	1283.111604	T	***1016.552356***	508.779816	999.525807	500.266541	998.541791	499.774533	9
21	2670.258526	1335.632901	2653.231977	1327.119626	2652.247961	1326.627618	S	***915.504677***	458.255977	898.478128	449.742702	897.494112	449.250694	8
22	2783.342590	1392.174933	2766.316041	1383.661658	2765.332025	1383.169650	L	***828.472649***	414.739963	811.446100	406.226688			7
23	2896.426654	1448.716965	2879.400105	1440.203690	2878.416089	1439.711682	L	***715.388585***	358.197930	698.362036	349.684656			6
24	3010.469581	1505.738428	2993.443032	1497.225154	2992.459016	1496.733146	N	***602.304521***	301.655898	585.277972	293.142624			5
25	3067.491045	1534.249160	3050.464496	1525.735886	3049.480480	1525.243878	G	***488.261594***	244.634435	471.235045	236.121160			4
26	3204.549957	1602.778616	3187.523408	1594.265342	3186.539392	1593.773334	H	431.240130	216.123703	414.213581	207.610428			3
27	3351.618371	1676.312823	3334.591822	1667.799549	3333.607806	1667.307541	F	***294.181218***	147.594247	277.154669	139.080972			2
28							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.8	3496.716660	0.039210	GHVLFRPTVSQQQSCPTCSTSLLNGHFK
48.1	3496.716660	0.039210	GHVLFRPTVSQQQSCPTCSTSLLNGHFK
44.0	3496.716660	0.039210	GHVLFRPTVSQQQSCPTCSTSLLNGHFK

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

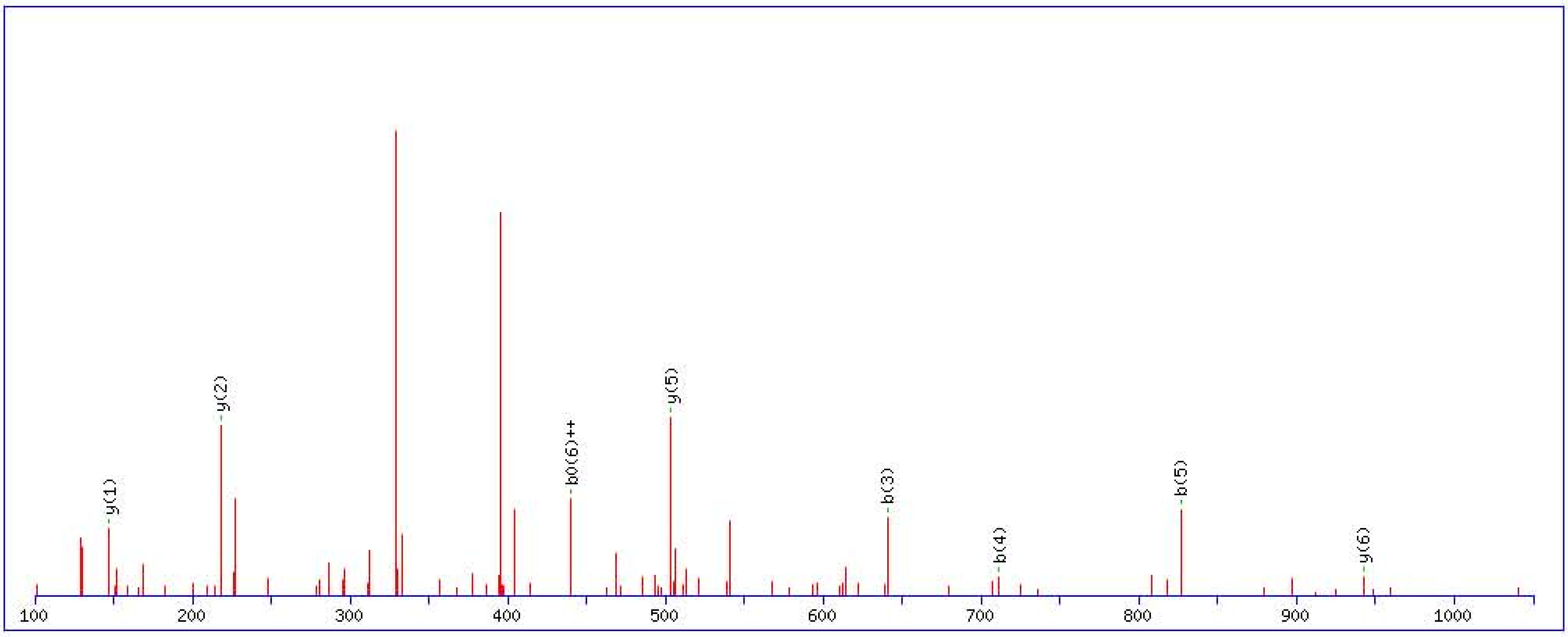
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQVADAK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

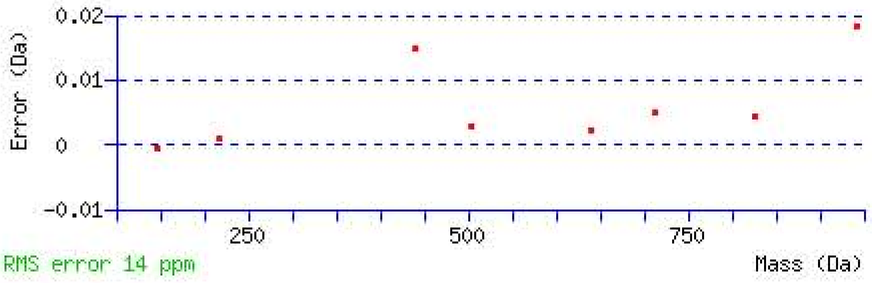
Match to Query 20726: 1042.549908 from(522.282230,2+) rtinseconds(1256) index(55231)
Title: Locus:1.1.1.2743.13 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

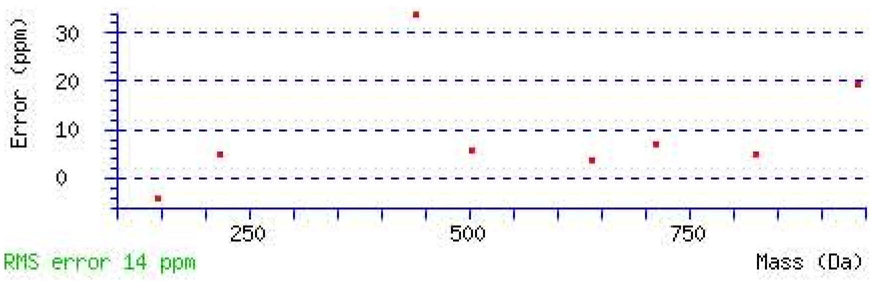
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1042.548111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0096
Matches : 8/66 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	102.054955	51.531116			84.044390	42.525833	**T**							7
2	541.280281	271.143779	524.253732	262.630504	523.269716	262.138496	**Q**	***942.507715***	471.757496	925.481166	463.244221	924.497150	462.752213	6
3	***640.348695***	320.677986	623.322146	312.164711	622.338130	311.672703	**V**	***503.282389***	252.144832	486.255840	243.631558	485.271824	243.139550	5
4	***711.385809***	356.196543	694.359260	347.683268	693.375244	347.191260	**A**	404.213975	202.610625	387.187426	194.097351	386.203410	193.605343	4
5	***826.412752***	413.710014	809.386203	405.196739	808.402187	404.704731	**D**	333.176861	167.092068	316.150312	158.578794	315.166296	158.086786	3
6	897.449866	449.228571	880.423317	440.715296	879.439301	440.223288	**A**	***218.149918***	109.578597	201.123369	101.065322			2
7							**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.0	1042.548111	0.001797	TQVADAK
13.2	1042.548096	0.001812	SLQADAK
10.2	1042.540726	0.009182	KPVSEVGDGR
9.4	1042.540680	0.009228	TPEERAAAAK
8.7	1042.540680	0.009228	EAEKRPADK
6.9	1042.548080	0.001828	EKEQAK
6.6	1042.540680	0.009228	SLENPAERK
5.5	1042.548080	0.001828	KEQEAK
5.5	1042.548080	0.001828	KQEEAK
5.3	1042.548096	0.001812	ISAQDAK

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

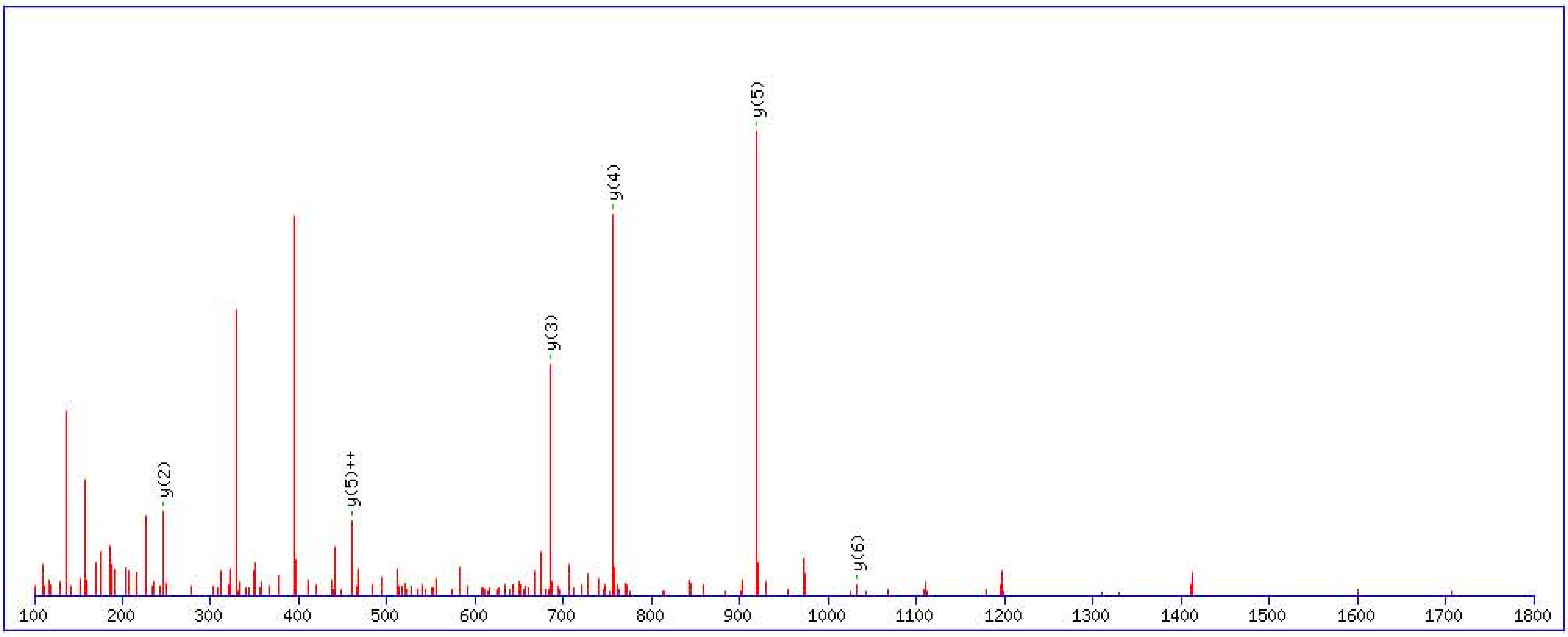
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALYAQAR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

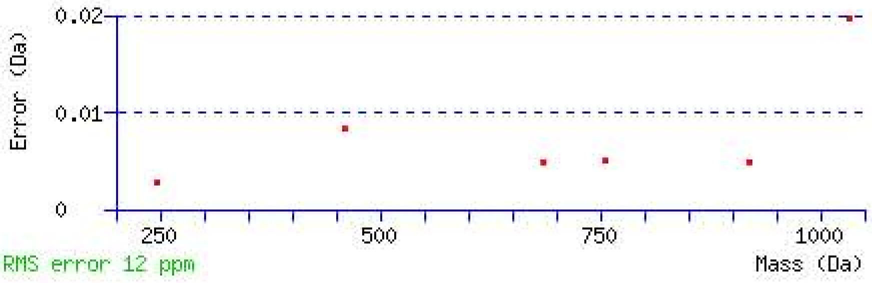
Match to Query 22541: 1102.599948 from(552.307250,2+) rtinseconds(1617) index(57695)
Title: Locus:1.1.1.2869.5 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

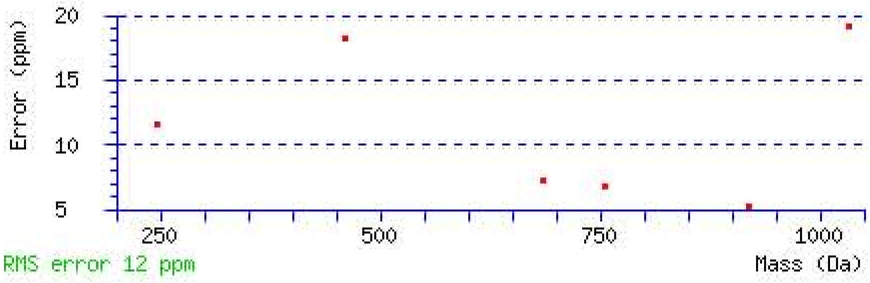
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1102.595703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0045
Matches : 6/40 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					7
2	185.128454	93.067865			L	*1032.565899*	516.786588	1015.539350	508.273313	6
3	348.191783	174.599529			Y	*919.481835*	460.244556	902.455286	451.731281	5
4	419.228897	210.118087			A	*756.418506*	378.712891	739.391957	370.199617	4
5	858.454223	429.730750	841.427674	421.217475	Q	*685.381392*	343.194334	668.354843	334.681060	3
6	929.491337	465.249307	912.464788	456.736032	A	*246.156066*	123.581671	229.129517	115.068397	2
7					R	175.118952	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.6	1102.595703	0.004245	ALYAQAR
8.1	1102.602234	-0.002286	AIELGYNPVK
4.0	1102.598190	0.001758	LAERSEASLK
3.0	1102.613495	-0.013547	SFIAVPVTNR
2.9	1102.598221	0.001727	LAGSLATDLSR
2.8	1102.613464	-0.013516	AIPEKYGAVR
2.8	1102.613495	-0.013547	ALTQGPLTFR
0.4	1102.602921	-0.002973	LLRQRMDR

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

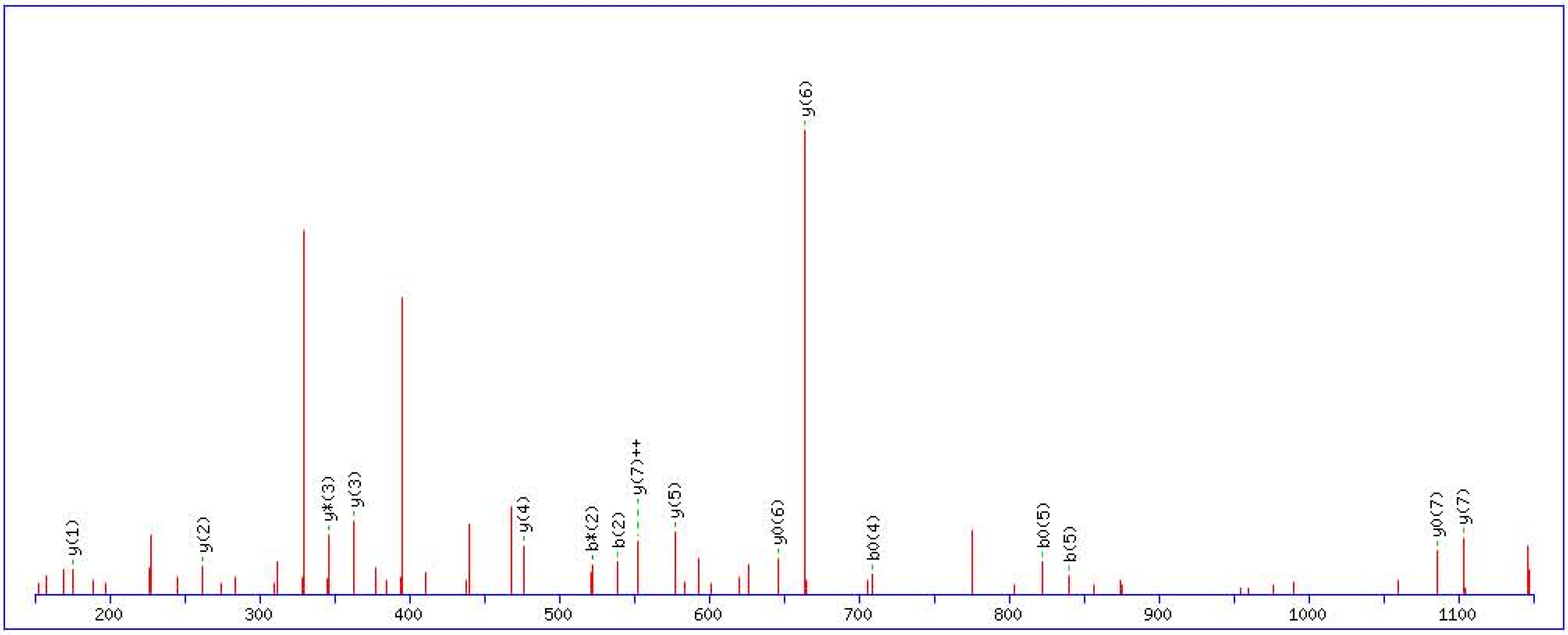
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQSTITSR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

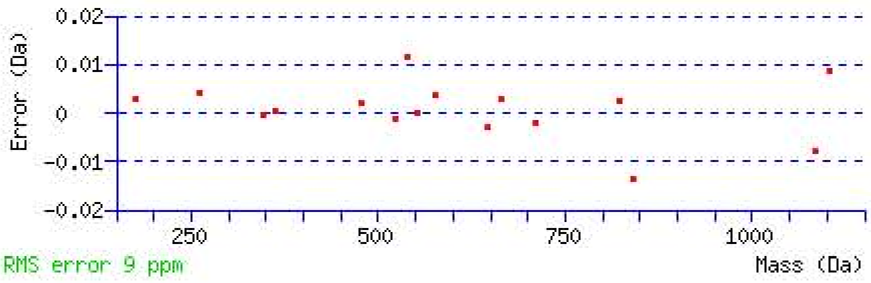
Match to Query 27708: 1201.653948 from(601.834250,2+) rtinseconds(1460) index(56636)
Title: Locus:1.1.1.2814.19 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

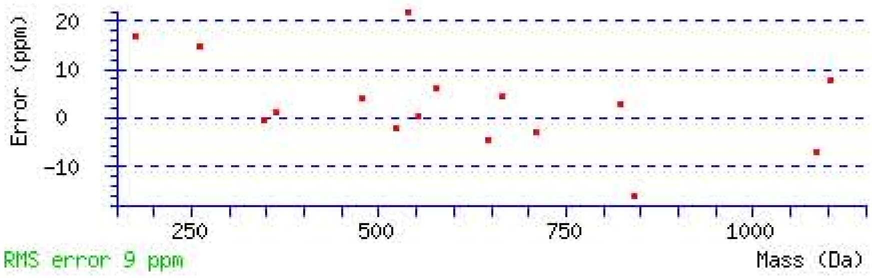
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1201.648895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.01
Matches : 16/76 fragment ions using 39 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	**539.301016**	270.154146	522.274467	261.640872			Q	***1103.587756***	552.297516	1086.561207	543.784242	1085.577191	543.292234	7
3	626.333044	313.670160	609.306495	305.156886	608.322479	304.664878	S	***664.362430***	332.684853	647.335881	324.171579	646.351865	323.679571	6
4	727.380723	364.194000	710.354174	355.680725	709.370158	355.188717	T	***577.330402***	289.168839	560.303853	280.655565	559.319837	280.163557	5
5	**840.464787**	420.736032	823.438238	412.222757	822.454222	411.730749	I	***476.282723***	238.645000	459.256174	230.131725	458.272158	229.639717	4
6	941.512466	471.259871	924.485917	462.746597	923.501901	462.254589	T	***363.198659***	182.102968	346.172110	173.589693	345.188094	173.097685	3
7	1028.544494	514.775885	1011.517945	506.262611	1010.533929	505.770603	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.3	1201.648895	0.005053	VQSTITSR

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

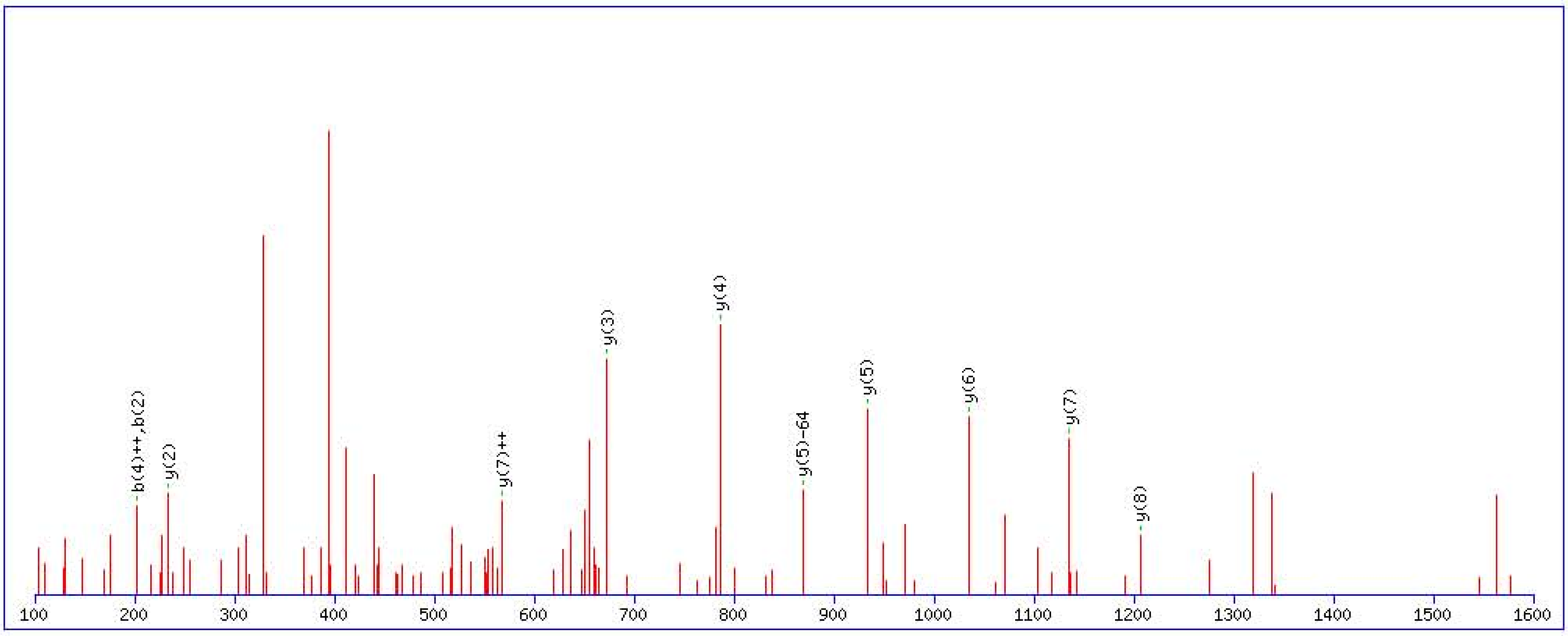
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MATTMIQSK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

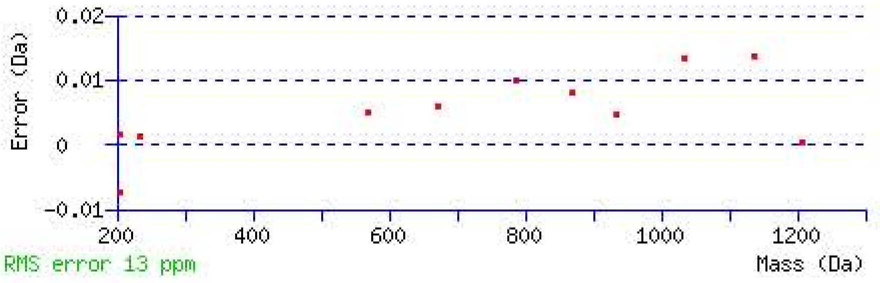
Match to Query 31705: 1336.667308 from(669.340930,2+) rtinseconds(1483) index(56786)
Title: Locus:1.1.1.2822.15 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

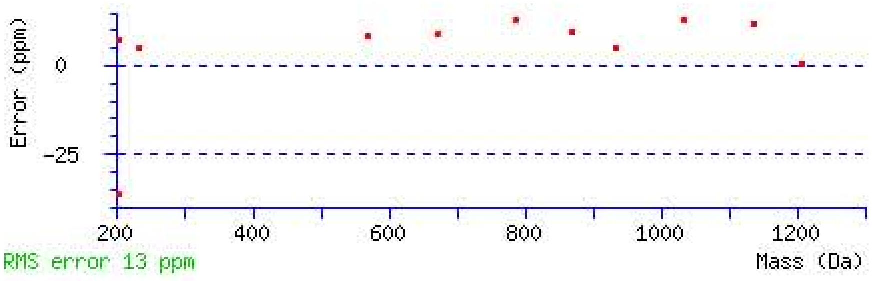
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1336.655289
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 5.1e-006
Matches : 11/122 fragment ions using 13 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.047761	66.527518					M							9
2	**203.084875**	102.046075					A	***1206.622094***	603.814685	1189.595545	595.301411	1188.611529	594.809403	8
3	304.132554	152.569915			286.121989	143.564632	T	***1135.584980***	568.296128	1118.558431	559.782854	1117.574415	559.290846	7
4	405.180233	**203.093754**			387.169668	194.088472	T	***1034.537301***	517.772289	1017.510752	509.259014	1016.526736	508.767006	6
5	552.215633	276.611455			534.205068	267.606172	M	***933.489622***	467.248449	916.463073	458.735175	915.479057	458.243167	5
6	665.299697	333.153487			647.289132	324.148204	I	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
7	1104.525023	552.766149	1087.498474	544.252875	1086.514458	543.760867	Q	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
8	1191.557051	596.282164	1174.530502	587.768889	1173.546486	587.276881	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.4	1336.655289	0.012019	MATTMIQSK
3.7	1336.680923	-0.013615	QSVPYGMATVIR
2.4	1336.662308	0.005000	KDTWGVVSSGSSK
2.3	1336.655289	0.012019	MATTMIQSK
2.3	1336.662262	0.005046	GYQEQIASLNSK
0.3	1336.684937	-0.017629	QFFEIQSK

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

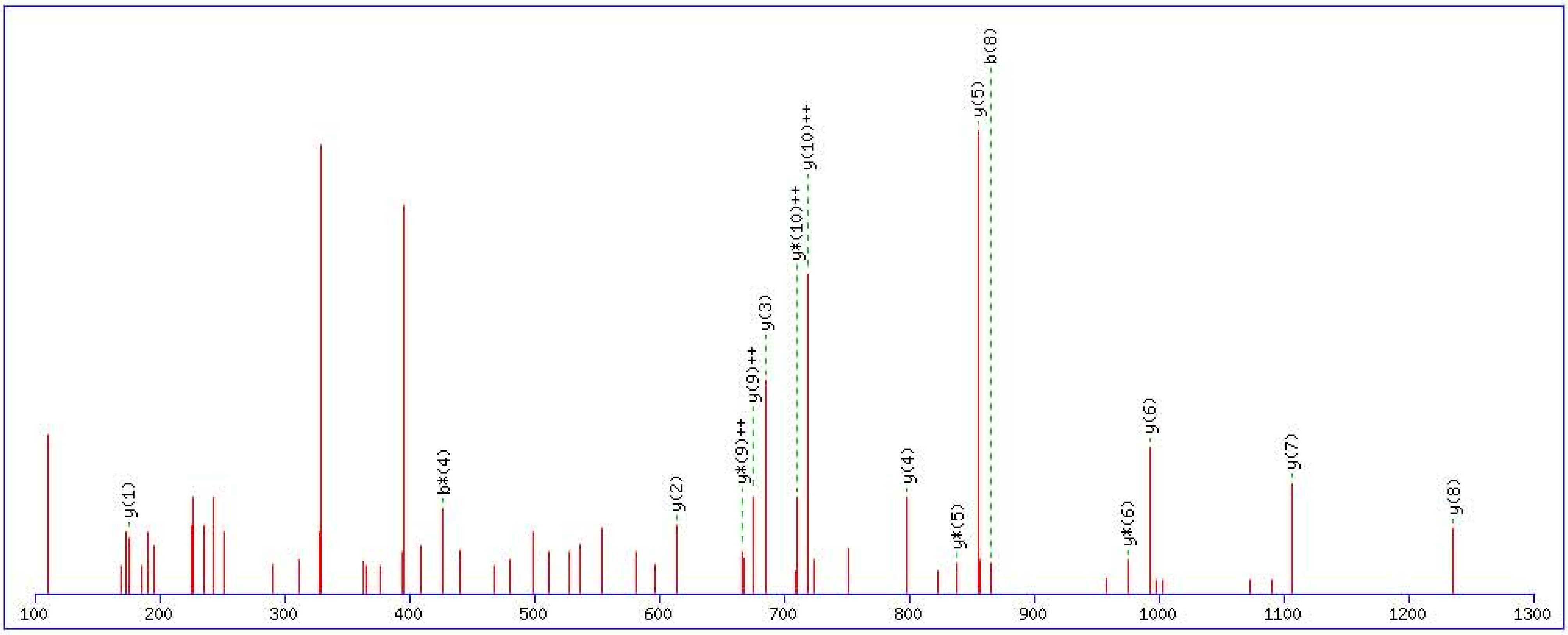
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSNENHGIAQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

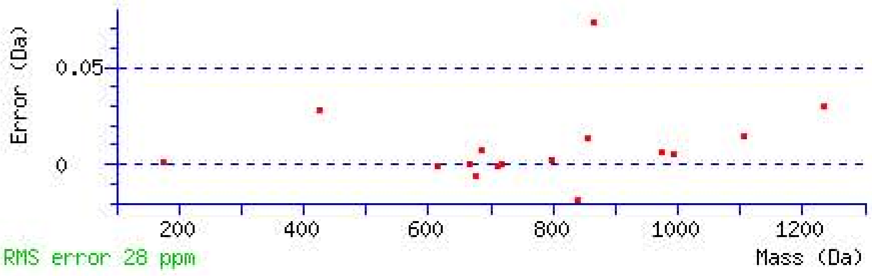
Match to Query 39900: 1548.783222 from(517.268350,3+) rtinseconds(1337) index(37692)
Title: Locus:1.1.1.2749.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

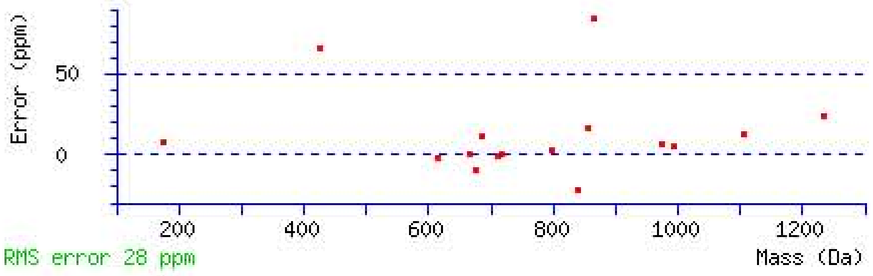
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1548.783066
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.012
Matches : 16/100 fragment ions using 40 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							11
2	201.123368	101.065322			183.112803	92.060039	S	1436.706307	718.856792	1419.679758	710.343517	1418.695742	709.851509	10
3	315.166295	158.086785	298.139746	149.573511	297.155730	149.081503	N	1349.674279	675.340778	1332.647730	666.827503	1331.663714	666.335495	9
4	444.208888	222.608082	427.182339	214.094808	426.198323	213.602800	E	***1235.631352***	618.319314	1218.604803	609.806040	1217.620787	609.314032	8
5	558.251815	279.629546	541.225266	271.116271	540.241250	270.624263	N	***1106.588759***	553.798018	1089.562210	545.284743			7
6	695.310727	348.159002	678.284178	339.645727	677.300162	339.153719	H	***992.545832***	496.776554	975.519283	488.263280			6
7	752.332191	376.669734	735.305642	368.156459	734.321626	367.664451	G	***855.486920***	428.247098	838.460371	419.733824			5
8	865.416255	433.211766	848.389706	424.698491	847.405690	424.206483	I	***798.465456***	399.736366	781.438907	391.223092			4
9	936.453369	468.730323	919.426820	460.217048	918.442804	459.725040	A	***685.381392***	343.194334	668.354843	334.681060			3
10	1375.678695	688.342986	1358.652146	679.829711	1357.668130	679.337703	Q	***614.344278***	307.675777	597.317729	299.162503			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	1548.783066	0.000156	LSNENHGIAQR

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

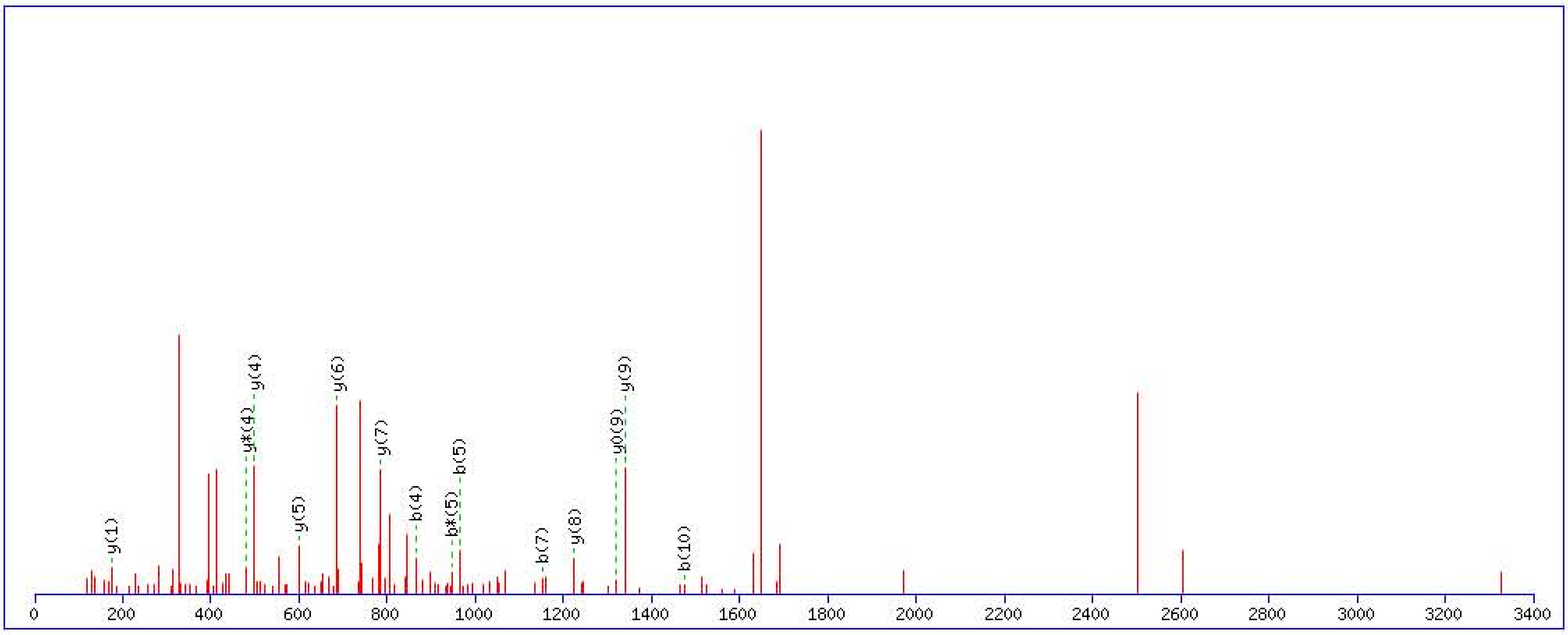
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FYNQVSTPLLR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

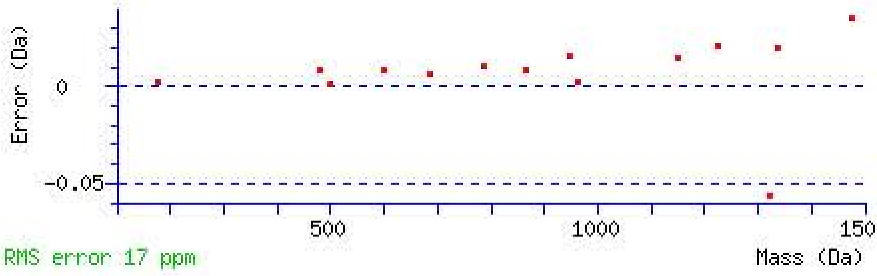
Match to Query 44577: 1647.901268 from(824.957910,2+) rtinseconds(2250) index(62376)
Title: Locus:1.1.1.3088.16 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

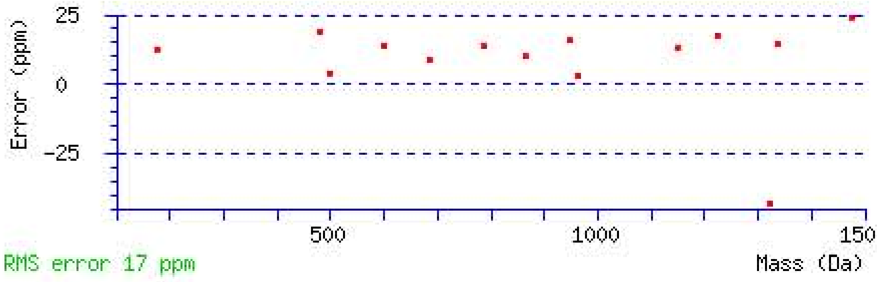
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1647.880676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0014
Matches : 14/98 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	148.075690	74.541483					F							11
2	311.139019	156.073148					Y	1501.819547	751.413411	1484.792998	742.900137	1483.808982	742.408129	10
3	425.181946	213.094611	408.155397	204.581337			N	***1338.756218***	669.881747	1321.729669	661.368472	1320.745653	660.876464	9
4	**864.407272**	432.707274	847.380723	424.194000			Q	***1224.713291***	612.860283	1207.686742	604.347009	1206.702726	603.855001	8
5	**963.475686**	482.241481	946.449137	473.728207			V	***785.487965***	393.247620	768.461416	384.734346	767.477400	384.242338	7
6	1050.507714	525.757495	1033.481165	517.244221	1032.497149	516.752213	S	***686.419551***	343.713414	669.393002	335.200139	668.408986	334.708131	6
7	**1151.555393**	576.281335	1134.528844	567.768060	1133.544828	567.276052	T	***599.387523***	300.197399	582.360974	291.684125	581.376958	291.192117	5
8	1248.608157	624.807717	1231.581608	616.294442	1230.597592	615.802434	P	***498.339844***	249.673560	481.313295	241.160285			4
9	1361.692221	681.349749	1344.665672	672.836474	1343.681656	672.344466	L	401.287080	201.147178	384.260531	192.633903			3
10	**1474.776285**	737.891780	1457.749736	729.378506	1456.765720	728.886498	L	288.203016	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.0	1647.880676	0.020592	FYNQVSTPLLR
2.7	1647.880508	0.020760	VTHSVQTDLSHLRR

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

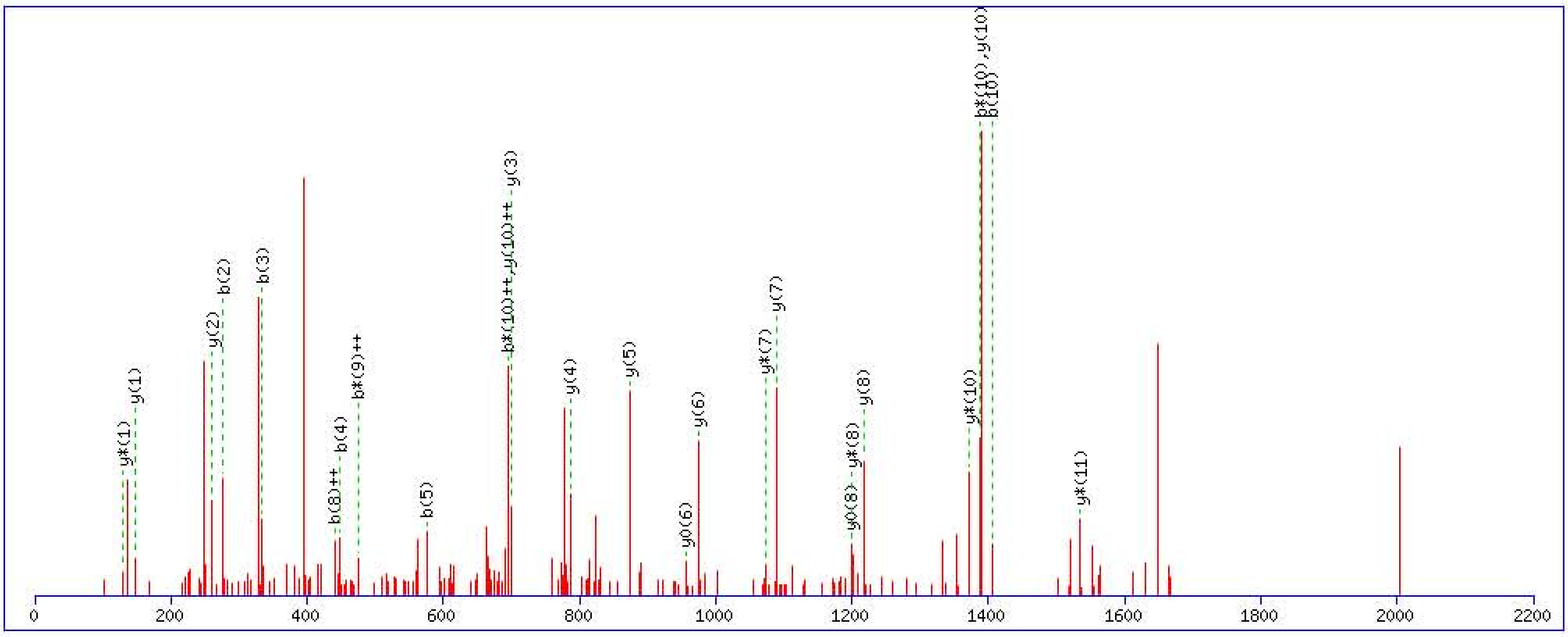
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYGNQDTSSQLK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

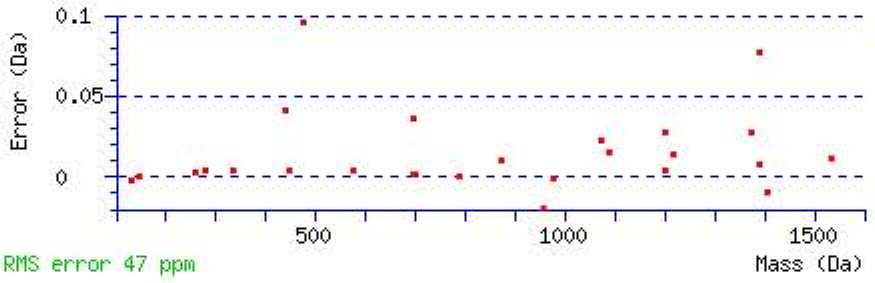
Match to Query 44937: 1663.839148 from(832.926850,2+) rtinseconds(1618) index(57705)
Title: Locus:1.1.1.2869.15 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

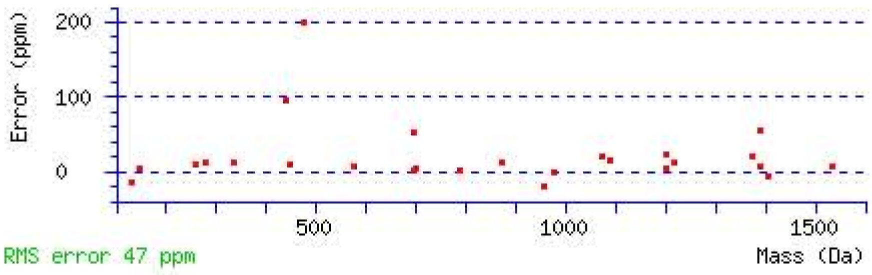
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1663.823944
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 47 **Expect:** 0.00011
Matches : 26/110 fragment ions using 47 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							12
2	**277.154669**	139.080973					Y	1551.747170	776.377223	1534.720621	767.863948	1533.736605	767.371940	11
3	**334.176133**	167.591704					G	***1388.683841***	694.845558	1371.657292	686.332284	1370.673276	685.840276	10
4	**448.219060**	224.613168	431.192511	216.099894			N	1331.662377	666.334826	1314.635828	657.821552	1313.651812	657.329544	9
5	**576.277638**	288.642457	559.251089	280.129183			Q	***1217.619450***	609.313363	1200.592901	600.800088	1199.608885	600.308080	8
6	691.304581	346.155929	674.278032	337.642654	673.294016	337.150646	D	***1089.560872***	545.284074	1072.534323	536.770799	1071.550307	536.278791	7
7	792.352260	396.679768	775.325711	388.166494	774.341695	387.674486	T	***974.533929***	487.770602	957.507380	479.257328	956.523364	478.765320	6
8	879.384288	440.195782	862.357739	431.682507	861.373723	431.190499	S	***873.486250***	437.246763	856.459701	428.733488	855.475685	428.241480	5
9	966.416316	483.711796	949.389767	475.198521	948.405751	474.706513	S	***786.454222***	393.730749	769.427673	385.217474	768.443657	384.725466	4
10	**1405.641642**	703.324459	1388.615093	694.811184	1387.631077	694.319176	Q	***699.422194***	350.214735	682.395645	341.701460			3
11	1518.725706	759.866491	1501.699157	751.353216	1500.715141	750.861208	L	***260.196868***	130.602072	243.170319	122.088797			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.9	1663.823944	0.015204	IYGNQDTSSQLK
24.8	1663.823944	0.015204	IYGNQDTSSQLK
4.5	1663.863663	-0.024515	EAQKEMQKIMTSLK

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SILQMSLDHHIVTPLTSLVIENEAGDER**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 46194: 3427.778696 from(857.951950,4+) rtinseconds(2697) index(65276)
Title: Locus:1.1.1.3243.14 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 3427.747940
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 6.1e-007
Matches : 25/316 fragment ions using 38 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							28
2	***201.123368***	101.065322			183.112803	92.060039	I	3341.723211	1671.365243	3324.696662	1662.851969	3323.712646	1662.359961	27
3	314.207432	157.607354			296.196867	148.602071	L	3228.639147	1614.823211	3211.612598	1606.309937	3210.628582	1605.817929	26
4	753.432758	377.220017	736.406209	368.706743	735.422193	368.214735	Q	3115.555083	1558.281179	3098.528534	1549.767905	3097.544518	1549.275897	25
5	884.473243	442.740260	867.446694	434.226985	866.462678	433.734977	M	2676.329757	1338.668516	2659.303208	1330.155242	2658.319192	1329.663234	24
6	971.505271	486.256274	954.478722	477.742999	953.494706	477.250991	S	2545.289272	1273.148274	2528.262723	1264.634999	2527.278707	1264.142991	23
7	1084.589335	542.798305	1067.562786	534.285031	1066.578770	533.793023	L	2458.257244	1229.632260	2441.230695	1221.118985	2440.246679	1220.626977	22
8	***1199.616278***	600.311777	1182.589729	591.798503	1181.605713	591.306494	D	2345.173180	1173.090228	2328.146631	1164.576953	2327.162615	1164.084945	21
9	***1336.675190***	668.841233	1319.648641	660.327959	1318.664625	659.835950	H	2230.146237	1115.576756	2213.119688	1107.063482	2212.135672	1106.571474	20
10	***1473.734102***	737.370689	1456.707553	728.857415	1455.723537	728.365406	H	2093.087325	1047.047300	2076.060776	1038.534026	2075.076760	1038.042018	19
11	***1586.818166***	793.912721	1569.791617	785.399446	1568.807601	784.907438	I	1956.028413	978.517845	1939.001864	970.004570	1938.017848	969.512562	18
12	***1685.886580***	843.446928	1668.860031	834.933653	1667.876015	834.441645	V	1842.944349	921.975813	1825.917800	913.462538	1824.933784	912.970530	17
13	***1786.934259***	893.970767	1769.907710	885.457493	1768.923694	884.965485	T	1743.875935	872.441606	1726.849386	863.928331	1725.865370	863.436323	16
14	1883.987023	942.497149	1866.960474	933.983875	1865.976458	933.491867	P	1642.828256	821.917766	1625.801707	813.404492	1624.817691	812.912484	15
15	1997.071087	999.039181	1980.044538	990.525907	1979.060522	990.033899	L	1545.775492	773.391384	1528.748943	764.878110	1527.764927	764.386102	14
16	2098.118766	1049.563021	2081.092217	1041.049746	2080.108201	1040.557738	T	1432.691428	716.849352	1415.664879	708.336078	1414.680863	707.844070	13
17	***2185.150794***	1093.079035	2168.124245	1084.565760	2167.140229	1084.073752	S	1331.643749	666.325513	1314.617200	657.812238	1313.633184	657.320230	12
18	2298.234858	**1149.621067**	2281.208309	1141.107792	2280.224293	1140.615784	L	1244.611721	622.809499	1227.585172	614.296224	1226.601156	613.804216	11
19	2397.303272	**1199.155274**	2380.276723	1190.641999	2379.292707	1190.149991	V	***1131.527657***	566.267467	1114.501108	557.754192	1113.517092	557.262184	10
20	2510.387336	1255.697306	2493.360787	1247.184031	2492.376771	1246.692023	I	***1032.459243***	516.733260	1015.432694	508.219985	1014.448678	507.727977	9
21	***2639.429929***	1320.218602	2622.403380	1311.705328	2621.419364	1311.213320	E	***919.375179***	460.191228	902.348630	451.677953	901.364614	451.185945	8
22	2753.472856	1377.240066	2736.446307	1368.726791	2735.462291	1368.234783	N	***790.332586***	395.669931	773.306037	387.156657	772.322021	386.664649	7
23	2882.515449	1441.761362	2865.488900	1433.248088	2864.504884	1432.756080	E	***676.289659***	338.648468	659.263110	330.135193	658.279094	329.643185	6
24	2953.552563	1477.279920	2936.526014	1468.766645	2935.541998	1468.274637	A	***547.247066***	274.127171	530.220517	265.613897	529.236501	265.121889	5
25	3010.574027	1505.790652	2993.547478	1497.277377	2992.563462	1496.785369	G	***476.209952***	238.608614	459.183403	230.095339	458.199387	229.603331	4
26	3125.600970	1563.304123	3108.574421	1554.790848	3107.590405	1554.298840	D	419.188488	210.097882	402.161939	201.584607	401.177923	201.092599	3
27	3254.643563	1627.825420	3237.617014	1619.312145	3236.632998	1618.820137	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
28							R	175.118952	88.063114	158.092403	79.549839			1

RMS error 39 ppm   RMS error 39 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.8	3427.747940	0.030756	SILQMSLDHHIVTPLTSLVIENEAGDER
0.6	3427.793747	-0.015051	PLWVFFFVILTLSNSSHCSPPPPLTLRMR

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

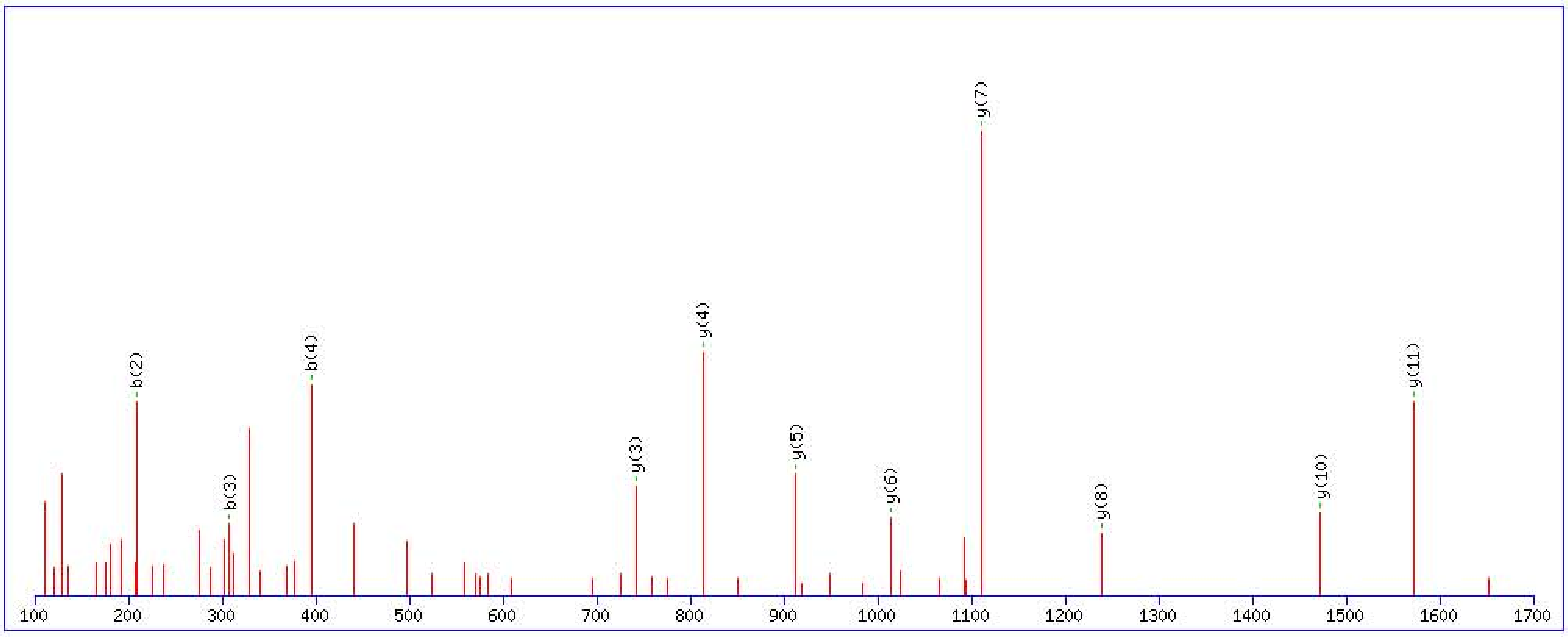
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AHVSFKPTVAQQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

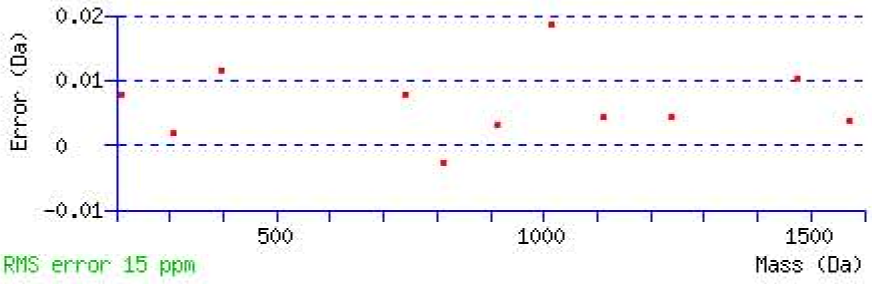
Match to Query 47958: 1778.960892 from(593.994240,3+) rtinseconds(1459) index(38595)
Title: Locus:1.1.1.2791.22 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

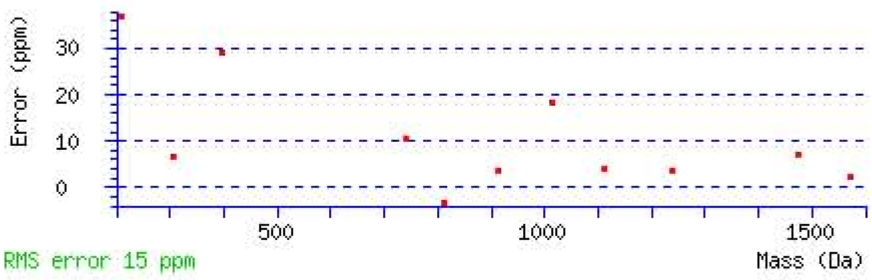
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1778.961395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1.4e-006
Matches : 11/118 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							13
2	**209.103302**	105.055289					H	1708.931558	854.969417	1691.905009	846.456143	1690.920993	845.964135	12
3	**308.171716**	154.589496					V	***1571.872646***	786.439961	1554.846097	777.926687	1553.862081	777.434679	11
4	**395.203744**	198.105510			377.193179	189.100227	S	***1472.804232***	736.905754	1455.777683	728.392480	1454.793667	727.900472	10
5	542.272158	271.639717			524.261593	262.634435	F	1385.772204	693.389740	1368.745655	684.876466	1367.761639	684.384458	9
6	670.367121	335.687199	653.340572	327.173924	652.356556	326.681916	K	***1238.703790***	619.855533	1221.677241	611.342259	1220.693225	610.850251	8
7	767.419885	384.213581	750.393336	375.700306	749.409320	375.208298	P	***1110.608827***	555.808052	1093.582278	547.294777	1092.598262	546.802769	7
8	868.467564	434.737420	851.441015	426.224146	850.456999	425.732138	T	***1013.556063***	507.281670	996.529514	498.768395	995.545498	498.276387	6
9	967.535978	484.271627	950.509429	475.758353	949.525413	475.266345	V	***912.508384***	456.757830	895.481835	448.244556			5
10	1038.573092	519.790184	1021.546543	511.276910	1020.562527	510.784902	A	***813.439970***	407.223623	796.413421	398.710349			4
11	1166.631670	583.819473	1149.605121	575.306199	1148.621105	574.814191	Q	***742.402856***	371.705066	725.376307	363.191792			3
12	1605.856996	803.432136	1588.830447	794.918862	1587.846431	794.426854	Q	614.344278	307.675777	597.317729	299.162503			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.4	1778.961395	-0.000503	AHVSFKPTVAQQR
62.4	1778.961395	-0.000503	AHVSFKPTVAQQR
0.1	1778.934906	0.025986	NSAPVSVSAVRTSFMVK

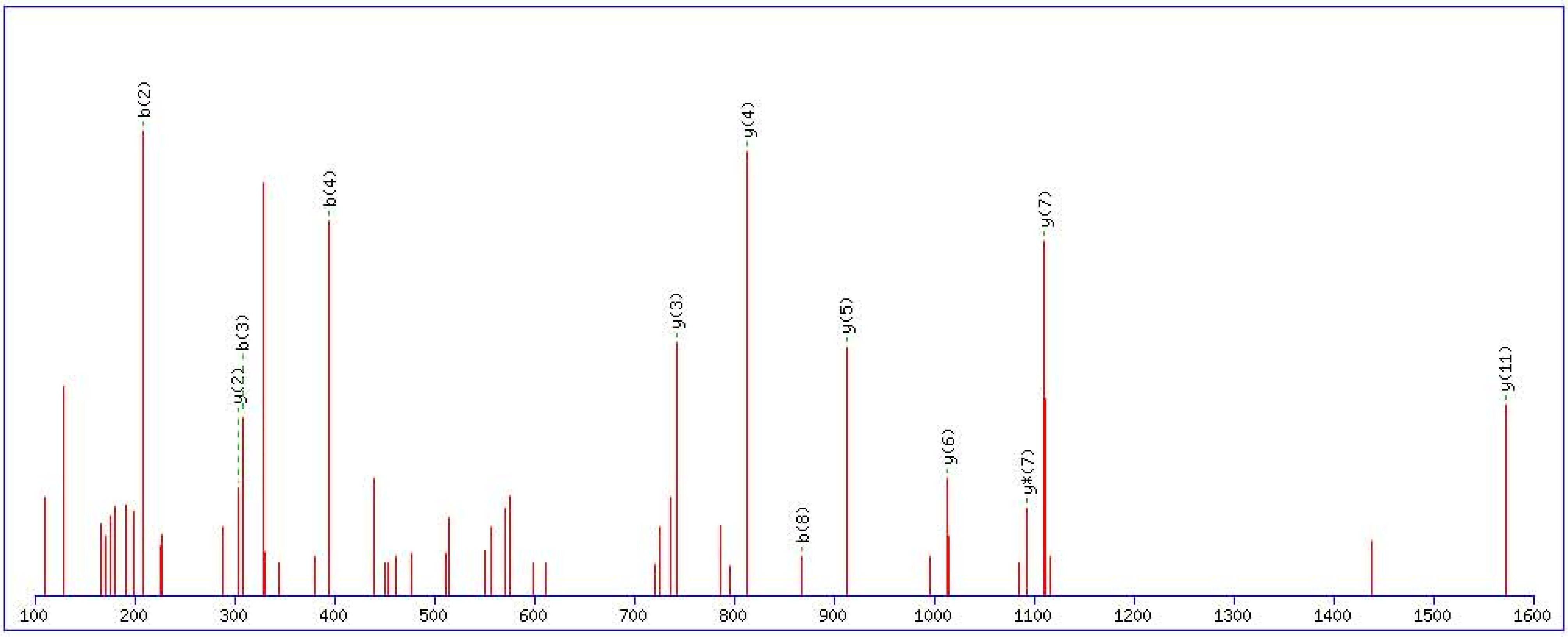
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AHVSFKPTVAQQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

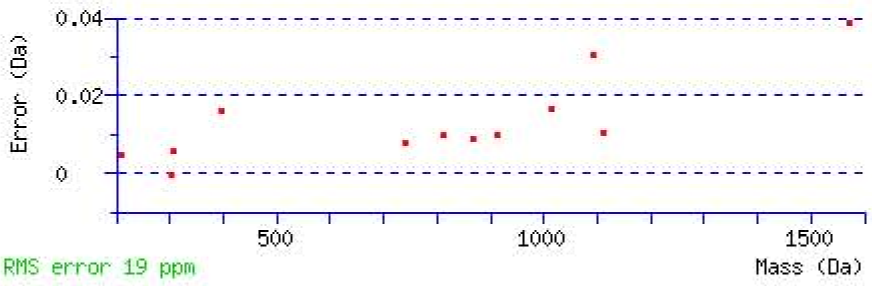
Match to Query 47966: 1778.972202 from(593.998010,3+) rtinseconds(1385) index(56100)
Title: Locus:1.1.1.2788.17 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

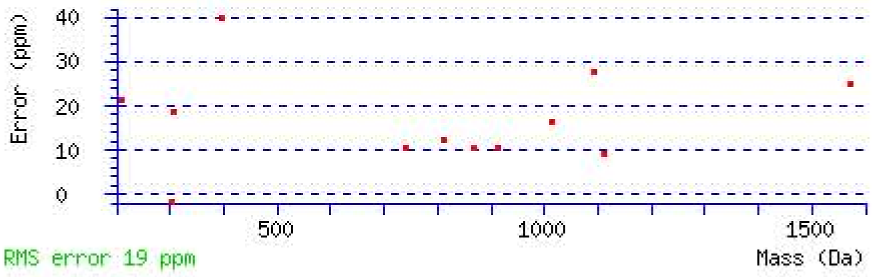
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1778.961395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0032
Matches : 12/118 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							13
2	***209.103302***	105.055289					H	1708.931558	854.969417	1691.905009	846.456143	1690.920993	845.964135	12
3	***308.171716***	154.589496					V	***1571.872646***	786.439961	1554.846097	777.926687	1553.862081	777.434679	11
4	***395.203744***	198.105510			377.193179	189.100227	S	1472.804232	736.905754	1455.777683	728.392480	1454.793667	727.900472	10
5	542.272158	271.639717			524.261593	262.634435	F	1385.772204	693.389740	1368.745655	684.876466	1367.761639	684.384458	9
6	670.367121	335.687199	653.340572	327.173924	652.356556	326.681916	K	1238.703790	619.855533	1221.677241	611.342259	1220.693225	610.850251	8
7	767.419885	384.213581	750.393336	375.700306	749.409320	375.208298	P	***1110.608827***	555.808052	1093.582278	547.294777	1092.598262	546.802769	7
8	***868.467564***	434.737420	851.441015	426.224146	850.456999	425.732138	T	***1013.556063***	507.281670	996.529514	498.768395	995.545498	498.276387	6
9	967.535978	484.271627	950.509429	475.758353	949.525413	475.266345	V	***912.508384***	456.757830	895.481835	448.244556			5
10	1038.573092	519.790184	1021.546543	511.276910	1020.562527	510.784902	A	***813.439970***	407.223623	796.413421	398.710349			4
11	1477.798418	739.402847	1460.771869	730.889573	1459.787853	730.397565	Q	***742.402856***	371.705066	725.376307	363.191792			3
12	1605.856996	803.432136	1588.830447	794.918862	1587.846431	794.426854	Q	***303.177530***	152.092403	286.150981	143.579129			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.7	1778.961395	0.010807	AHVSFKPTVAQQR
36.2	1778.961395	0.010807	AHVSFKPTVAQQR

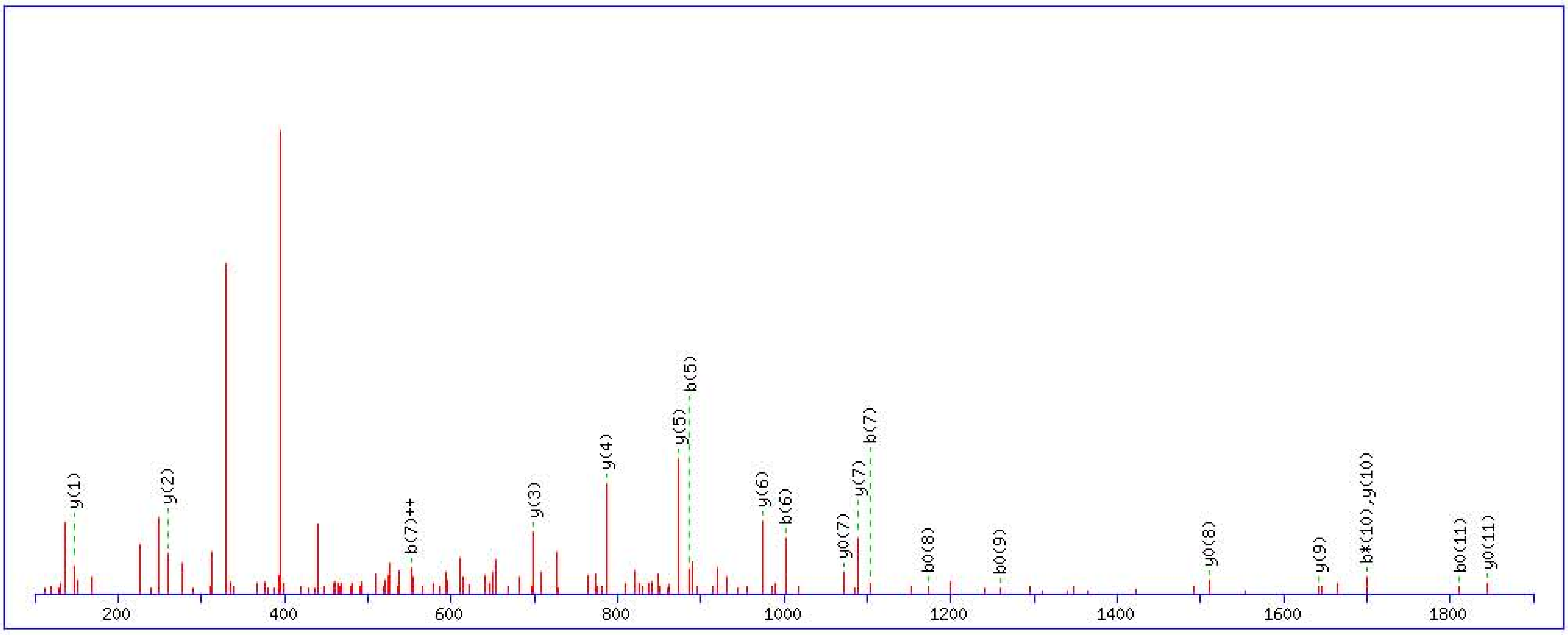
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYGNQDTSSQLK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

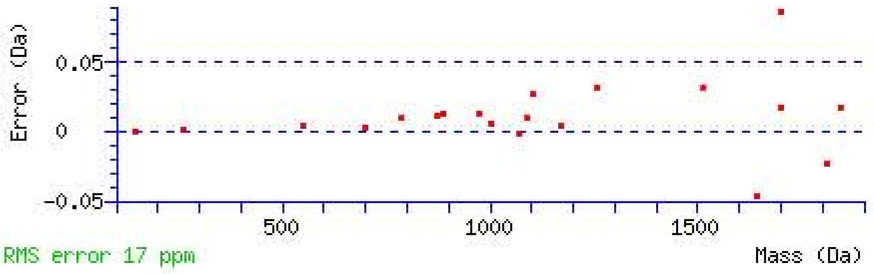
Match to Query 52365: 1975.009662 from(659.343830,3+) rtinseconds(1970) index(60353)
Title: Locus:1.1.1.2991.5 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

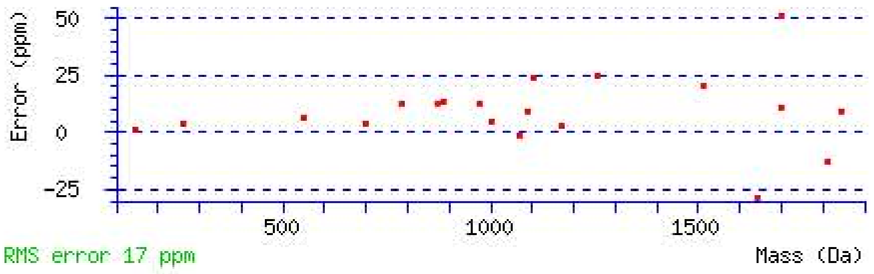
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1974.990692
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.014
Matches : 20/110 fragment ions using 48 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							12
2	277.154669	139.080973					Y	1862.913918	931.960597	1845.887369	923.447323	1844.903353	922.955315	11
3	334.176133	167.591704					G	***1699.850589***	850.428933	1682.824040	841.915658	1681.840024	841.423650	10
4	448.219060	224.613168	431.192511	216.099894			N	***1642.829125***	821.918201	1625.802576	813.404926	1624.818560	812.912918	9
5	**887.444386**	444.225831	870.417837	435.712557			Q	1528.786198	764.896737	1511.759649	756.383463	1510.775633	755.891455	8
6	**1002.471329**	501.739303	985.444780	493.226028	984.460764	492.734020	D	***1089.560872***	545.284074	1072.534323	536.770800	1071.550307	536.278792	7
7	**1103.519008**	552.263142	1086.492459	543.749868	1085.508443	543.257860	T	***974.533929***	487.770603	957.507380	479.257328	956.523364	478.765320	6
8	1190.551036	595.779156	1173.524487	587.265882	1172.540471	586.773874	S	***873.486250***	437.246763	856.459701	428.733489	855.475685	428.241481	5
9	1277.583064	639.295170	1260.556515	630.781896	1259.572499	630.289888	S	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
10	1716.808390	858.907833	1699.781841	850.394559	1698.797825	849.902551	Q	***699.422194***	350.214735	682.395645	341.701461			3
11	1829.892454	915.449865	1812.865905	906.936591	1811.881889	906.444583	L	***260.196868***	130.602072	243.170319	122.088797			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1974.990692	0.018970	IYGNQDTSSQLK

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

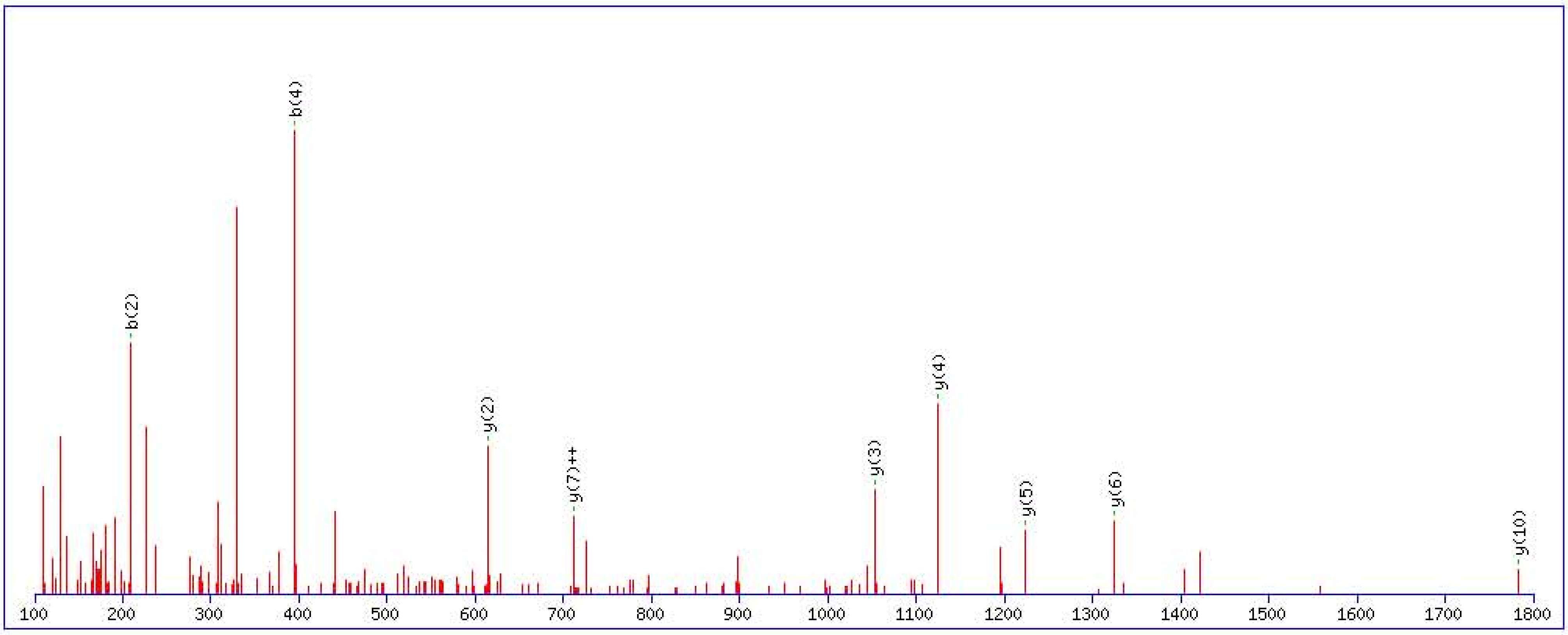
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AHVSFKPTVAQQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

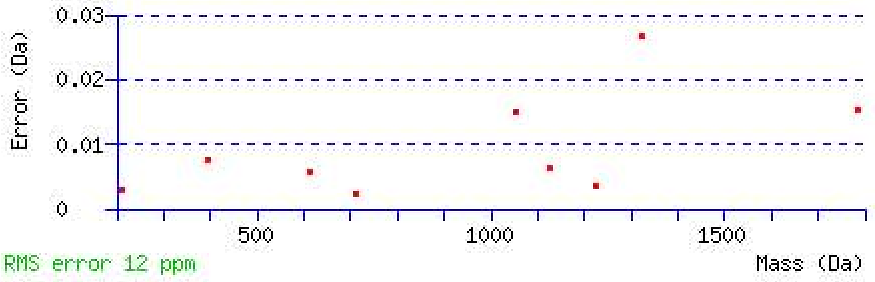
Match to Query 55875: 2090.136736 from(523.541460,4+) rtinseconds(1732) index(58580)
Title: Locus:1.1.1.2909.7 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

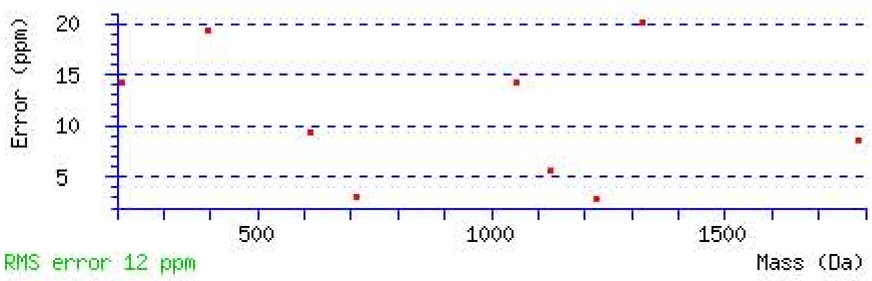
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2090.128143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.026
Matches : 9/118 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							13
2	**209.103302**	105.055289					H	2020.098306	1010.552791	2003.071757	1002.039517	2002.087741	1001.547509	12
3	308.171716	154.589496					V	1883.039394	942.023335	1866.012845	933.510061	1865.028829	933.018053	11
4	**395.203744**	198.105510			377.193179	189.100227	S	***1783.970980***	892.489128	1766.944431	883.975854	1765.960415	883.483846	10
5	542.272158	271.639717			524.261593	262.634435	F	1696.938952	848.973114	1679.912403	840.459840	1678.928387	839.967832	9
6	670.367121	335.687199	653.340572	327.173924	652.356556	326.681916	K	1549.870538	775.438907	1532.843989	766.925633	1531.859973	766.433625	8
7	767.419885	384.213581	750.393336	375.700306	749.409320	375.208298	P	1421.775575	711.391426	1404.749026	702.878151	1403.765010	702.386143	7
8	868.467564	434.737420	851.441015	426.224146	850.456999	425.732138	T	***1324.722811***	662.865044	1307.696262	654.351769	1306.712246	653.859761	6
9	967.535978	484.271627	950.509429	475.758353	949.525413	475.266345	V	***1223.675132***	612.341204	1206.648583	603.827930			5
10	1038.573092	519.790184	1021.546543	511.276910	1020.562527	510.784902	A	***1124.606718***	562.806997	1107.580169	554.293723			4
11	1477.798418	739.402847	1460.771869	730.889573	1459.787853	730.397565	Q	***1053.569604***	527.288440	1036.543055	518.775166			3
12	1917.023744	959.015510	1899.997195	950.502236	1899.013179	950.010228	Q	***614.344278***	307.675777	597.317729	299.162503			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.5	2090.128143	0.008593	AHVSFKPTVAQQR

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

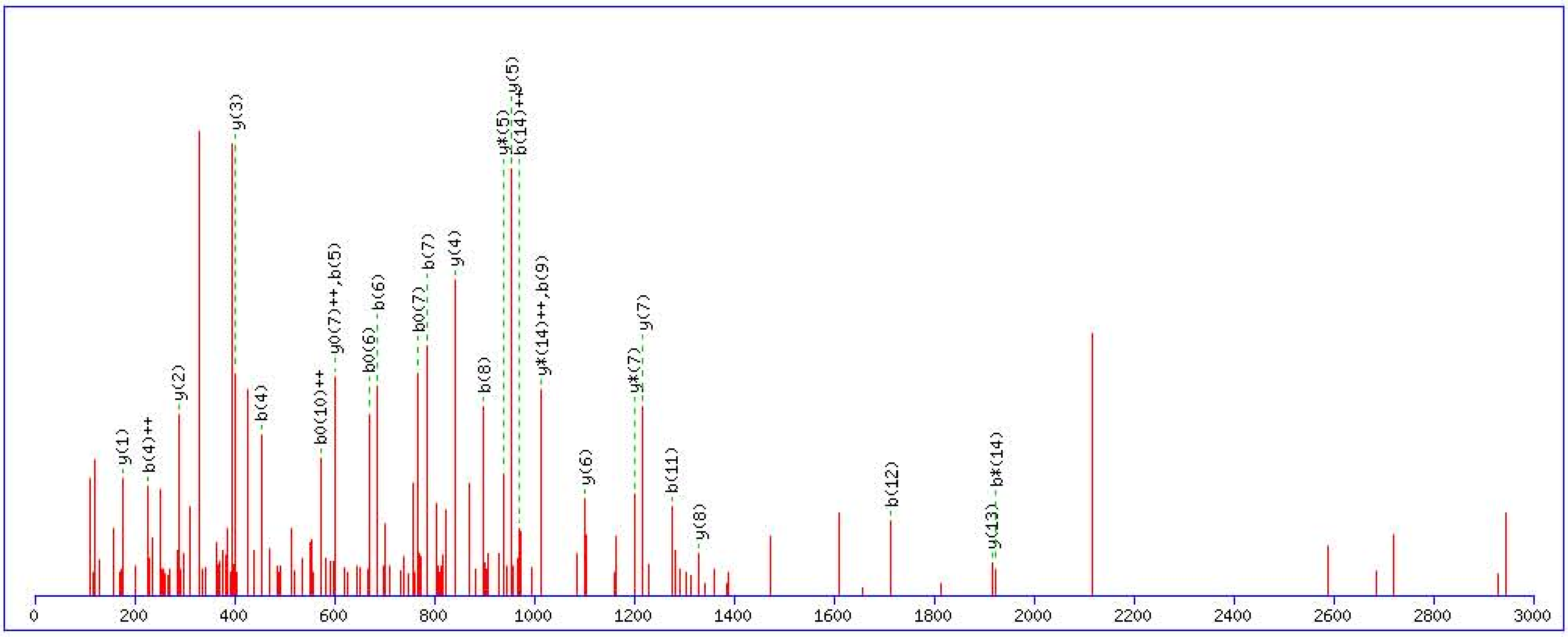
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEDHFSVIDFNQNIR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

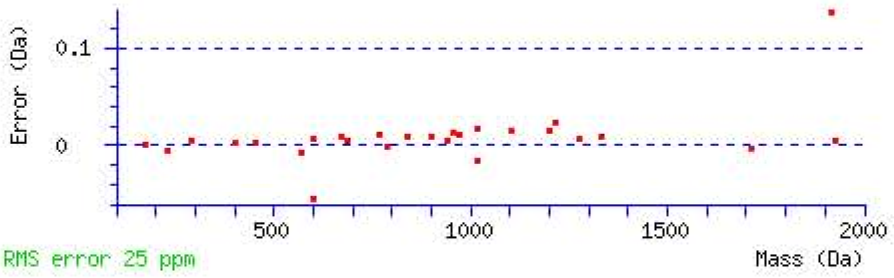
Match to Query 56375: 2115.042222 from(706.021350,3+) rtinseconds(2232) index(62231)
Title: Locus:1.1.1.3082.11 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

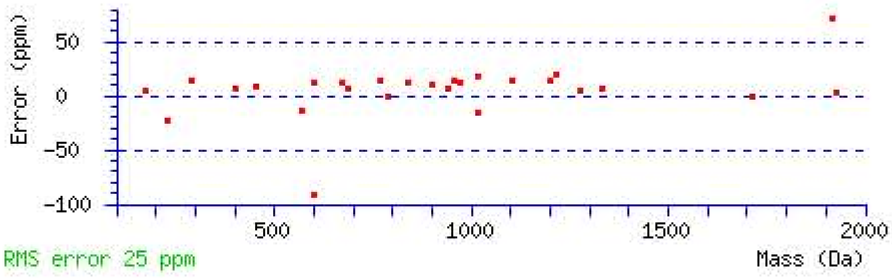
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2115.020752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 50 **Expect:** 3.1e-005
Matches : 27/134 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							15
2	201.086983	101.047130			183.076418	92.041847	E	2044.990921	1022.999099	2027.964372	1014.485824	2026.980356	1013.993816	14
3	316.113926	158.560601			298.103361	149.555319	D	***1915.948328***	958.477802	1898.921779	949.964528	1897.937763	949.472519	13
4	***453.172838***	**227.090057**			435.162273	218.084775	H	1800.921385	900.964331	1783.894836	892.451056	1782.910820	891.959048	12
5	***600.241252***	300.624264			582.230687	291.618982	F	1663.862473	832.434874	1646.835924	823.921600	1645.851908	823.429592	11
6	***687.273280***	344.140278			669.262715	335.134996	S	1516.794059	758.900668	1499.767510	750.387393	1498.783494	749.895385	10
7	***786.341694***	393.674485			768.331129	384.669202	V	1429.762031	715.384654	1412.735482	706.871379	1411.751466	706.379371	9
8	***899.425758***	450.216517			881.415193	441.211234	I	***1330.693617***	665.850447	1313.667068	657.337172	1312.683052	656.845164	8
9	***1014.452701***	507.729988			996.442136	498.724706	D	***1217.609553***	609.308415	1200.583004	600.795140	1199.598988	600.303132	7
10	1161.521115	581.264196			1143.510550	572.258913	F	***1102.582610***	551.794943	1085.556061	543.281669			6
11	***1275.564042***	638.285659	1258.537493	629.772385	1257.553477	629.280376	N	***955.514196***	478.260736	938.487647	469.747462			5
12	***1714.789368***	857.898322	1697.762819	849.385048	1696.778803	848.893039	Q	***841.471269***	421.239273	824.444720	412.725998			4
13	1828.832295	914.919785	1811.805746	906.406511	1810.821730	905.914503	N	***402.245943***	201.626610	385.219394	193.113335			3
14	1941.916359	**971.461817**	1924.889810	962.948543	1923.905794	962.456535	I	***288.203016***	144.605146	271.176467	136.091872			2
15							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.3	2115.020752	0.021470	AEDHFSVIDFNQNIR
2.2	2115.033981	0.008241	ESADRQVLMQEEEIK

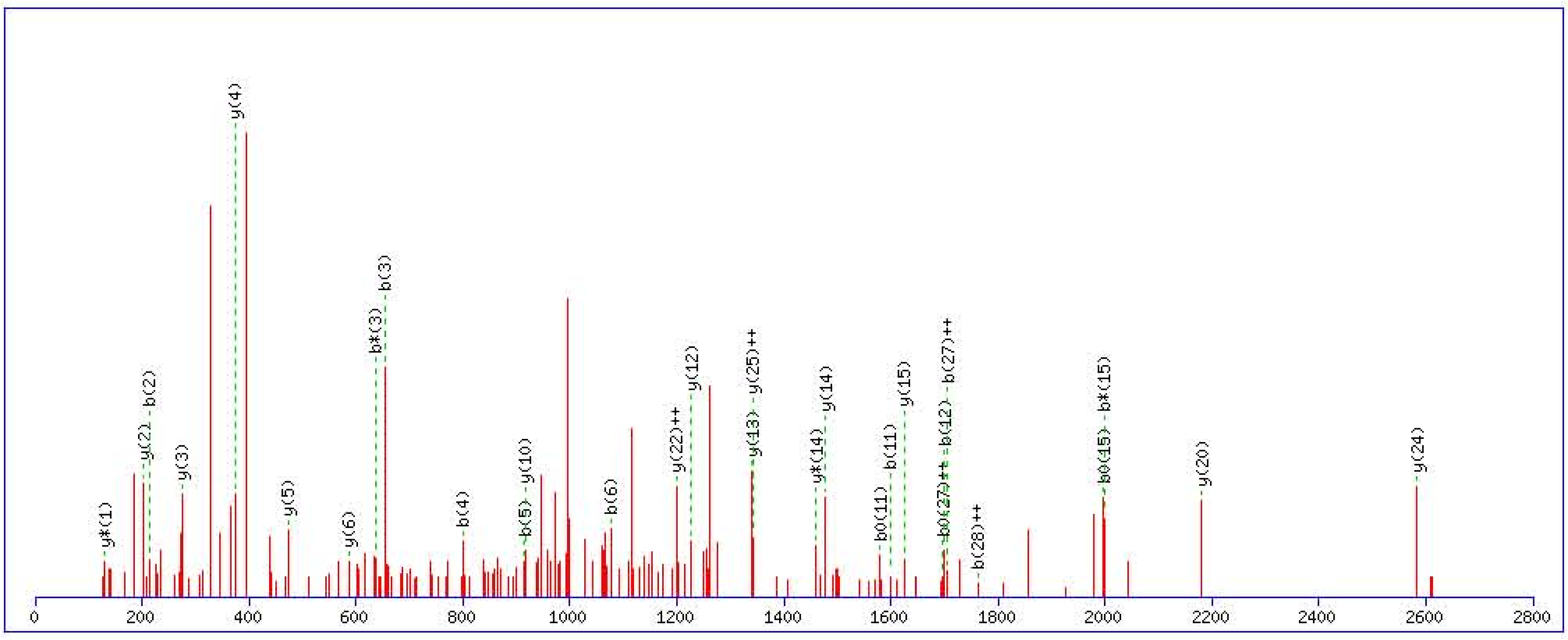
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

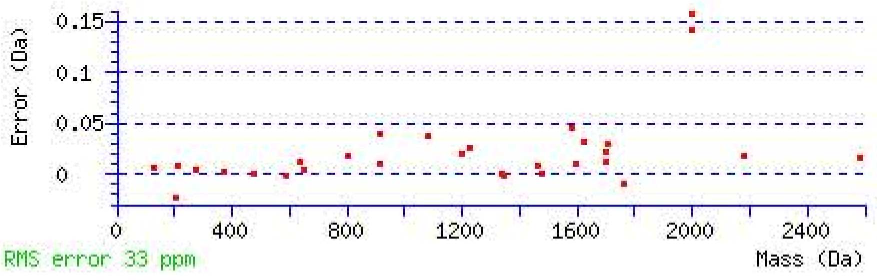
Match to Query 81203: 3993.969616 from(999.499680,4+) rtinseconds(2360) index(63158)
Title: Locus:1.1.1.3126.24 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

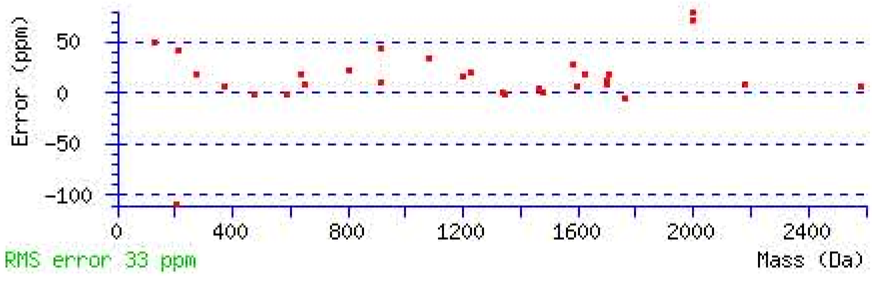
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3993.910858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0014
Matches : 30/356 fragment ions using 79 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							33
2	***214.118617***	107.562947	197.092068	99.049672			V	3880.875173	1940.941224	3863.848624	1932.427950	3862.864608	1931.935942	32
3	***653.343943***	327.175610	636.317394	318.662335			Q	3781.806759	1891.407017	3764.780210	1882.893743	3763.796194	1882.401735	31
4	***800.412357***	400.709817	783.385808	392.196542			F	3342.581433	1671.794354	3325.554884	1663.281080	3324.570868	1662.789072	30
5	***914.455284***	457.731280	897.428735	449.218006			N	3195.513019	1598.260147	3178.486470	1589.746873	3177.502454	1589.254865	29
6	***1077.518613***	539.262945	1060.492064	530.749670			Y	3081.470092	1541.238684	3064.443543	1532.725409	3063.459527	1532.233401	28
7	1174.571377	587.789327	1157.544828	579.276052			P	2918.406763	1459.707019	2901.380214	1451.193745	2900.396198	1450.701737	27
8	1311.630289	656.318783	1294.603740	647.805508			H	2821.353999	1411.180637	2804.327450	1402.667363	2803.343434	1402.175355	26
9	1412.677968	706.842622	1395.651419	698.329348	1394.667403	697.837339	T	2684.295087	1342.651181	2667.268538	1334.137907	2666.284522	1333.645899	25
10	1499.709996	750.358636	1482.683447	741.845362	1481.699431	741.353354	S	***2583.247408***	1292.127342	2566.220859	1283.614067	2565.236843	1283.122059	24
11	***1598.778410***	799.892843	1581.751861	791.379569	1580.767845	790.887561	V	2496.215380	1248.611328	2479.188831	1240.098053	2478.204815	1239.606045	23
12	***1699.826089***	850.416683	1682.799540	841.903408	1681.815524	841.411400	T	2397.146966	1199.077121	2380.120417	1190.563846	2379.136401	1190.071838	22
13	1814.853032	907.930154	1797.826483	899.416880	1796.842467	898.924872	D	2296.099287	1148.553281	2279.072738	1140.040007	2278.088722	1139.547999	21
14	1913.921446	957.464361	1896.894897	948.951087	1895.910881	948.459079	V	***2181.072344***	1091.039810	2164.045795	1082.526535	2163.061779	1082.034527	20
15	2014.969125	1007.988201	1997.942576	999.474926	1996.958560	998.982918	T	2082.003930	1041.505603	2064.977381	1032.992328	2063.993365	1032.500320	19
16	2143.027703	1072.017490	2126.001154	1063.504215	2125.017138	1063.012207	Q	1980.956251	990.981763	1963.929702	982.468489	1962.945686	981.976481	18
17	2257.070630	1129.038953	2240.044081	1120.525678	2239.060065	1120.033671	N	1852.897673	926.952474	1835.871124	918.439200	1834.887108	917.947192	17
18	2371.113557	1186.060417	2354.087008	1177.547142	2353.102992	1177.055134	N	1738.854746	869.931011	1721.828197	861.417736	1720.844181	860.925728	16
19	2518.181971	1259.594623	2501.155422	1251.081349	2500.171406	1250.589341	F	***1624.811819***	812.909547	1607.785270	804.396273	1606.801254	803.904265	15
20	2655.240883	1328.124079	2638.214334	1319.610805	2637.230318	1319.118797	H	***1477.743405***	739.375340	1460.716856	730.862066	1459.732840	730.370058	14
21	2769.283810	1385.145543	2752.257261	1376.632268	2751.273245	1376.140260	N	***1340.684493***	670.845885	1323.657944	662.332610	1322.673928	661.840602	13
22	2932.347139	1466.677207	2915.320590	1458.163933	2914.336574	1457.671925	Y	***1226.641566***	613.824421	1209.615017	605.311147	1208.631001	604.819139	12
23	3079.415553	1540.211414	3062.389004	1531.698140	3061.404988	1531.206132	F	1063.578237	532.292757	1046.551688	523.779482	1045.567672	523.287474	11
24	3136.437017	1568.722146	3119.410468	1560.208872	3118.426452	1559.716864	G	***916.509823***	458.758550	899.483274	450.245275	898.499258	449.753267	10
25	3193.458481	1597.232878	3176.431932	1588.719604	3175.447916	1588.227596	G	859.488359	430.247818	842.461810	421.734543	841.477794	421.242535	9
26	3280.490509	1640.748892	3263.463960	1632.235618	3262.479944	1631.743610	S	802.466895	401.737086	785.440346	393.223811	784.456330	392.731803	8
27	3409.533102	**1705.270189**	3392.506553	1696.756914	3391.522537	1696.264906	E	715.434867	358.221072	698.408318	349.707797	697.424302	349.215789	7
28	3522.617166	**1761.812221**	3505.590617	1753.298946	3504.606601	1752.806938	I	***586.392274***	293.699775	569.365725	285.186501			6
29	3621.685580	1811.346428	3604.659031	1802.833153	3603.675015	1802.341145	V	***473.308210***	237.157743	456.281661	228.644468			5
30	3720.753994	1860.880635	3703.727445	1852.367360	3702.743429	1851.875352	V	***374.239796***	187.623536	357.213247	179.110261			4
31	3791.791108	1896.399192	3774.764559	1887.885917	3773.780543	1887.393909	A	***275.171382***	138.089329	258.144833	129.576055			3
32	3848.812572	1924.909924	3831.786023	1916.396649	3830.802007	1915.904641	G	***204.134268***	102.570772	187.107719	94.057497			2
33							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.2	3993.910858	0.058758	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK
7.8	3993.910858	0.058758	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK

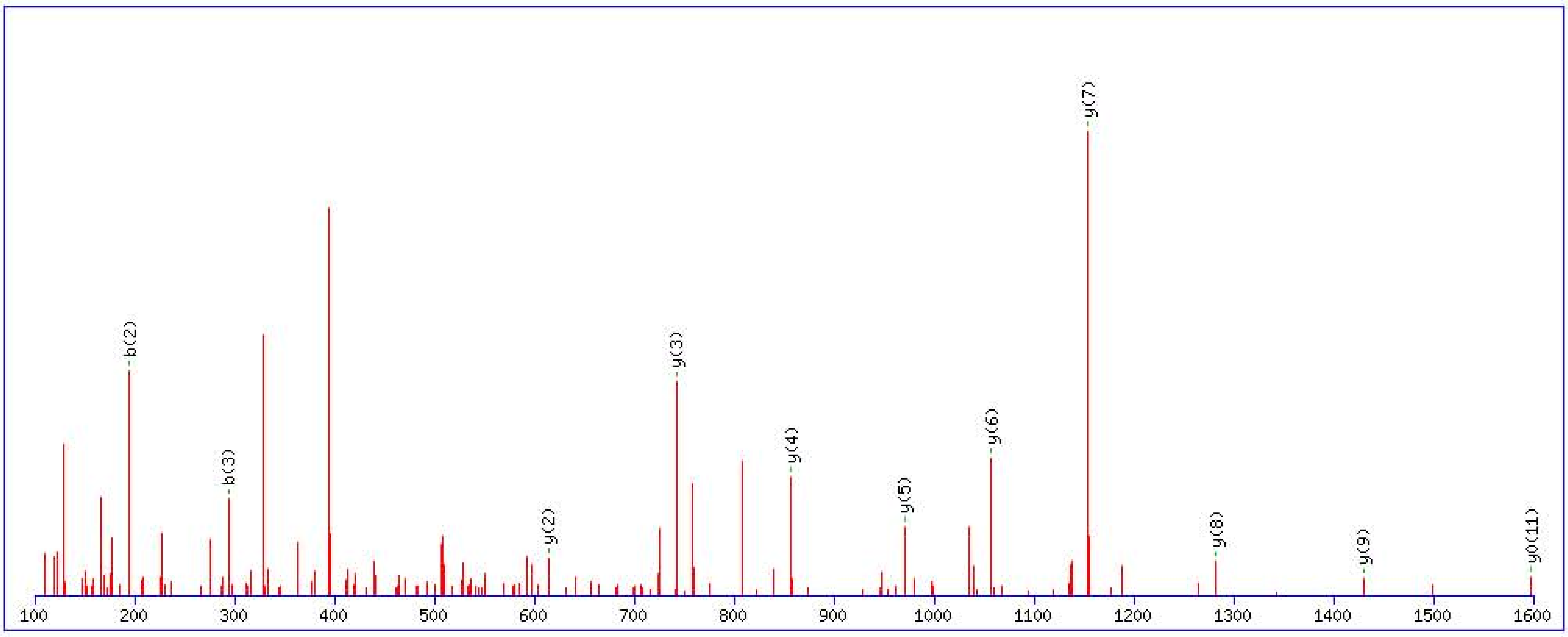
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHVSFKPSLDQQR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

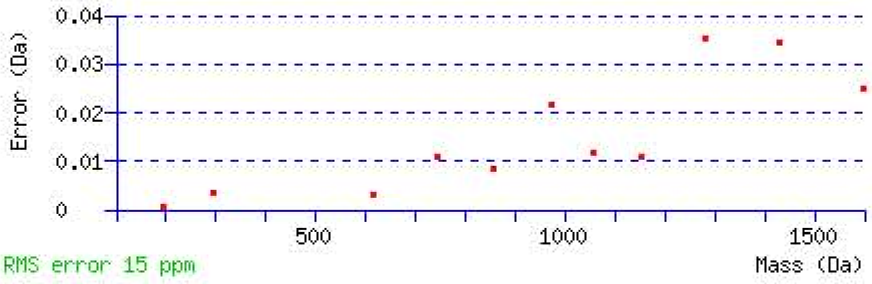
Match to Query 48630: 1808.945352 from(603.989060,3+) rtinseconds(1529) index(57152)
Title: Locus:1.1.1.2838.19 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

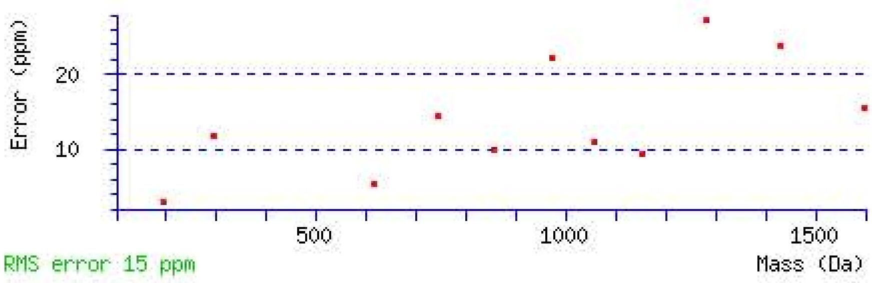


```
Monoisotopic mass of neutral peptide Mr(calc): 1808.935577
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 2.6e-005
Matches : 11/122 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							13
2	**195.087652**	98.047464					H	1752.921386	876.964331	1735.894837	868.451057	1734.910821	867.959049	12
3	**294.156066**	147.581671					V	1615.862474	808.434875	1598.835925	799.921601	1597.851909	799.429593	11
4	381.188094	191.097685			363.177529	182.092403	S	1516.794060	758.900668	1499.767511	750.387394	1498.783495	749.895386	10
5	528.256508	264.631892			510.245943	255.626610	F	***1429.762032***	715.384654	1412.735483	706.871380	1411.751467	706.379372	9
6	656.351471	328.679374	639.324922	320.166099	638.340906	319.674091	K	***1282.693618***	641.850447	1265.667069	633.337173	1264.683053	632.845165	8
7	753.404235	377.205756	736.377686	368.692481	735.393670	368.200473	P	***1154.598655***	577.802966	1137.572106	569.289691	1136.588090	568.797683	7
8	840.436263	420.721770	823.409714	412.208495	822.425698	411.716487	S	***1057.545891***	529.276584	1040.519342	520.763309	1039.535326	520.271301	6
9	953.520327	477.263802	936.493778	468.750527	935.509762	468.258519	L	***970.513863***	485.760570	953.487314	477.247295	952.503298	476.755287	5
10	1068.547270	534.777273	1051.520721	526.263999	1050.536705	525.771991	D	***857.429799***	429.218538	840.403250	420.705263	839.419234	420.213255	4
11	1196.605848	598.806562	1179.579299	590.293288	1178.595283	589.801279	Q	***742.402856***	371.705066	725.376307	363.191792			3
12	1635.831174	818.419225	1618.804625	809.905951	1617.820609	809.413943	Q	***614.344278***	307.675777	597.317729	299.162503			2
13							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 15 ppm



RMS error 15 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.0	1808.935577	0.009775	GHVSFKPSLDQQR
46.0	1808.935577	0.009775	GHVSFKPSLDQQR

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

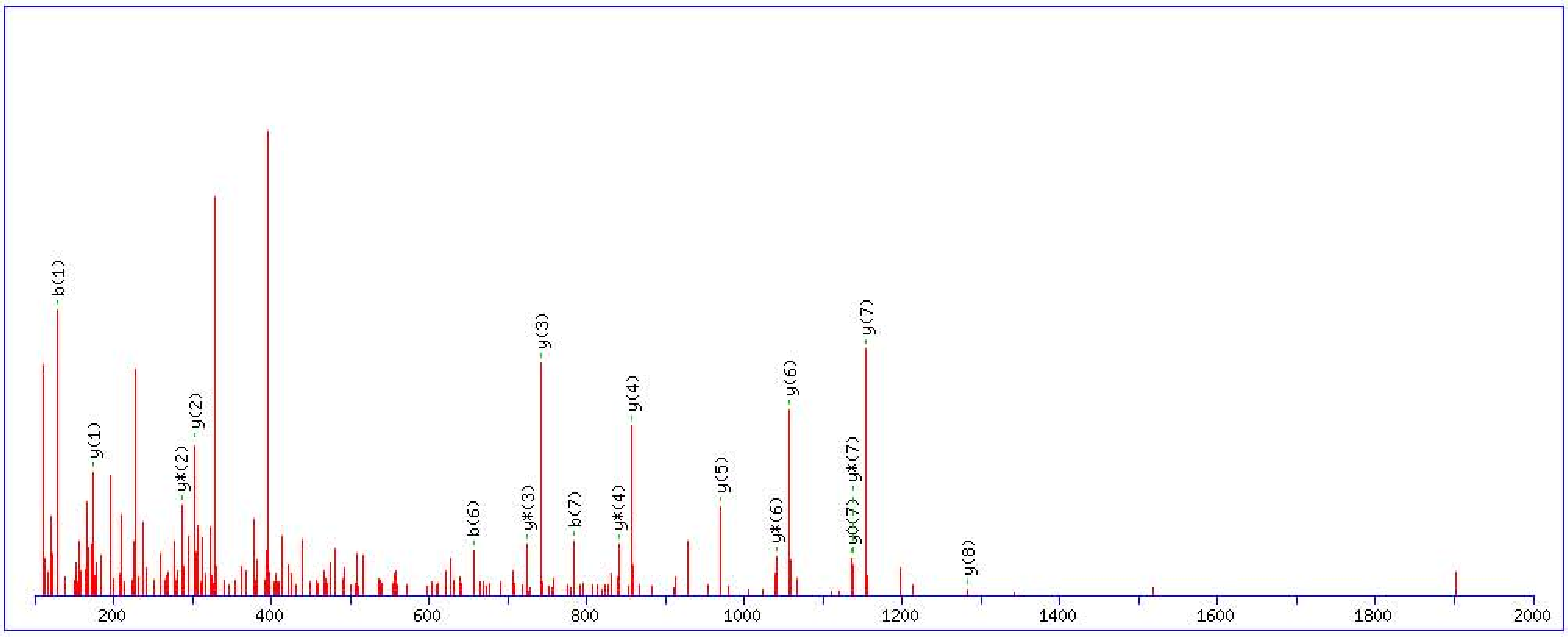
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGHVSFKPSLDQQR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

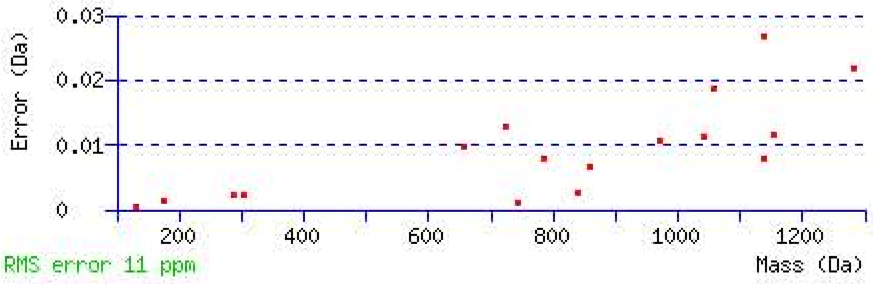
Match to Query 51445: 1937.037736 from(485.266710,4+) rtinseconds(1439) index(56489)
Title: Locus:1.1.1.2807.4 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

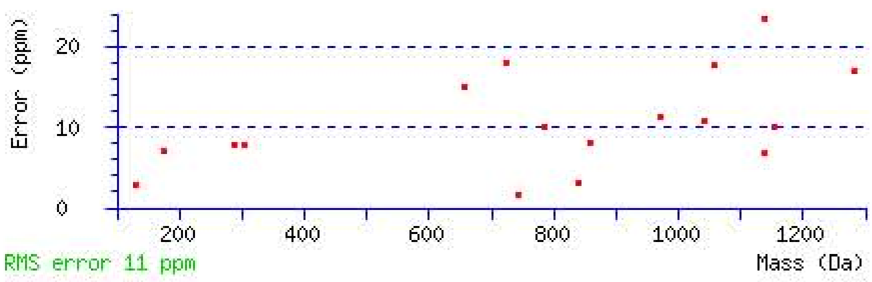
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1937.030533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.00053
Matches : 17/142 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	**129.102239**	65.054757	112.075690	56.541483			K							14
2	186.123703	93.565489	169.097154	85.052215			G	1809.942850	905.475063	1792.916301	896.961789	1791.932285	896.469781	13
3	323.182615	162.094945	306.156066	153.581671			H	1752.921386	876.964331	1735.894837	868.451057	1734.910821	867.959049	12
4	422.251029	211.629153	405.224480	203.115878			V	1615.862474	808.434875	1598.835925	799.921601	1597.851909	799.429593	11
5	509.283057	255.145167	492.256508	246.631892	491.272492	246.139884	S	1516.794060	758.900668	1499.767511	750.387394	1498.783495	749.895386	10
6	**656.351471**	328.679374	639.324922	320.166099	638.340906	319.674091	F	1429.762032	715.384654	1412.735483	706.871380	1411.751467	706.379372	9
7	**784.446434**	392.726855	767.419885	384.213581	766.435869	383.721573	K	***1282.693618***	641.850447	1265.667069	633.337173	1264.683053	632.845165	8
8	881.499198	441.253237	864.472649	432.739963	863.488633	432.247955	P	***1154.598655***	577.802966	1137.572106	569.289691	1136.588090	568.797683	7
9	968.531226	484.769251	951.504677	476.255977	950.520661	475.763969	S	***1057.545891***	529.276584	1040.519342	520.763309	1039.535326	520.271301	6
10	1081.615290	541.311283	1064.588741	532.798009	1063.604725	532.306000	L	***970.513863***	485.760570	953.487314	477.247295	952.503298	476.755287	5
11	1196.642233	598.824755	1179.615684	590.311480	1178.631668	589.819472	D	***857.429799***	429.218538	840.403250	420.705263	839.419234	420.213255	4
12	1635.867559	818.437418	1618.841010	809.924143	1617.856994	809.432135	Q	***742.402856***	371.705066	725.376307	363.191792			3
13	1763.926137	882.466707	1746.899588	873.953432	1745.915572	873.461424	Q	***303.177530***	152.092403	286.150981	143.579129			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.3	1937.030533	0.007203	KGHVSFKPSLDQQR
25.8	1937.030533	0.007203	KGHVSFKPSLDQQR
0.4	1937.051620	-0.013884	QPLEREQCLALLALGAR

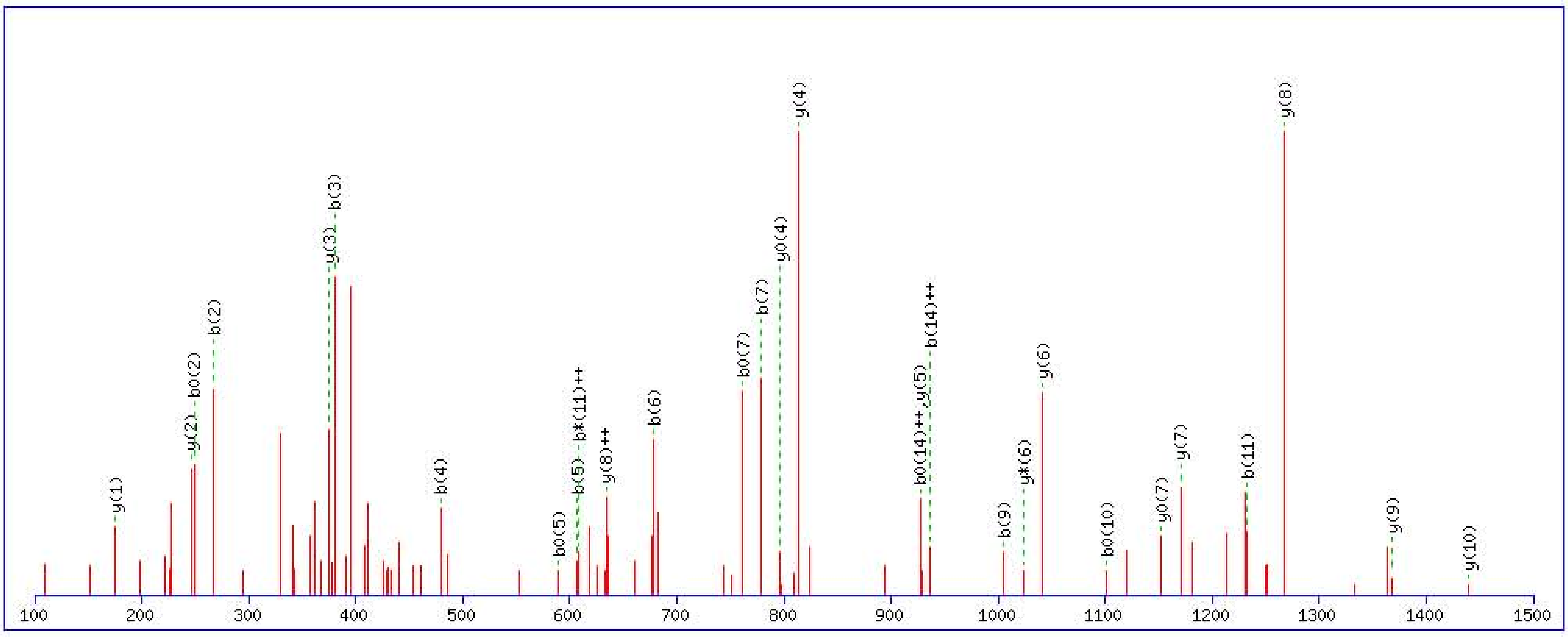
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHLVQATPENLQEAR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

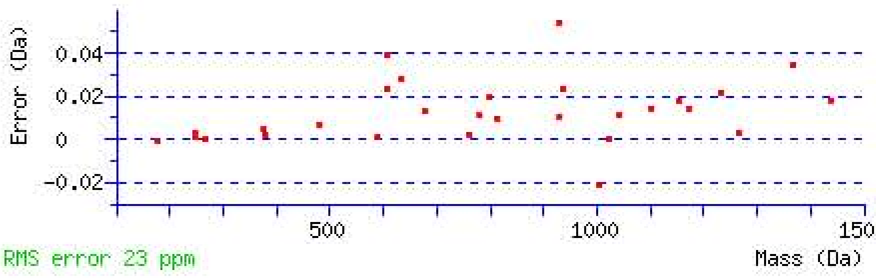
Match to Query 54861: 2045.053272 from(682.691700,3+) rtinseconds(1712) index(58410)
Title: Locus:1.1.1.2902.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

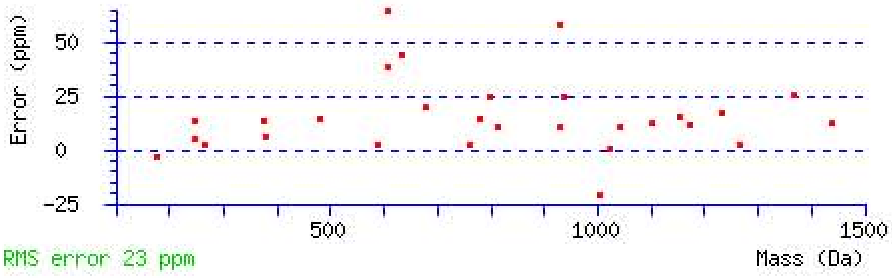


```
Monoisotopic mass of neutral peptide Mr(calc): 2045.036377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 73  Expect: 4.6e-007
Matches : 29/156 fragment ions using 40 most intense peaks   (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							15
2	***267.108781***	134.058028			249.098216	125.052746	H	1917.001094	959.004185	1899.974545	950.490911	1898.990529	949.998903	14
3	***380.192845***	190.600060			362.182280	181.594778	L	1779.942182	890.474729	1762.915633	881.961455	1761.931617	881.469447	13
4	***479.261259***	240.134267			461.250694	231.128985	V	1666.858118	833.932697	1649.831569	825.419423	1648.847553	824.927415	12
5	***607.319837***	304.163557	590.293288	295.650282	589.309272	295.158274	Q	1567.789704	784.398490	1550.763155	775.885216	1549.779139	775.393208	11
6	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	A	***1439.731126***	720.369201	1422.704577	711.855927	1421.720561	711.363919	10
7	***779.404630***	390.205953	762.378081	381.692679	761.394065	381.200671	T	***1368.694012***	684.850644	1351.667463	676.337370	1350.683447	675.845362	9
8	876.457394	438.732335	859.430845	430.219061	858.446829	429.727053	P	***1267.646333***	634.326805	1250.619784	625.813530	1249.635768	625.321522	8
9	***1005.499987***	503.253632	988.473438	494.740357	987.489422	494.248349	E	***1170.593569***	585.800423	1153.567020	577.287148	1152.583004	576.795140	7
10	1119.542914	560.275095	1102.516365	551.761821	1101.532349	551.269813	N	***1041.550976***	521.279126	1024.524427	512.765852	1023.540411	512.273844	6
11	***1232.626978***	616.817127	1215.600429	608.303853	1214.616413	607.811845	L	***927.508049***	464.257663	910.481500	455.744388	909.497484	455.252380	5
12	1671.852304	836.429790	1654.825755	827.916516	1653.841739	827.424508	Q	***814.423985***	407.715631	797.397436	399.202356	796.413420	398.710348	4
13	1800.894897	900.951087	1783.868348	892.437812	1782.884332	891.945804	E	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
14	1871.932011	936.469644	1854.905462	927.956369	1853.921446	927.464361	A	***246.156066***	123.581671	229.129517	115.068396			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 23 ppm



RMS error 23 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.6	2045.036377	0.016895	EHLVQATPENLQEAR
4.8	2045.051193	0.002079	VVGGYLLMLAYACVTMLR
3.0	2045.082687	-0.029415	QDTTGKIISIDTSSLR
2.6	2045.036377	0.016895	EHLVQATPENLQEAR
0.8	2045.040421	0.012851	QIEFNFPSQAITSPR

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

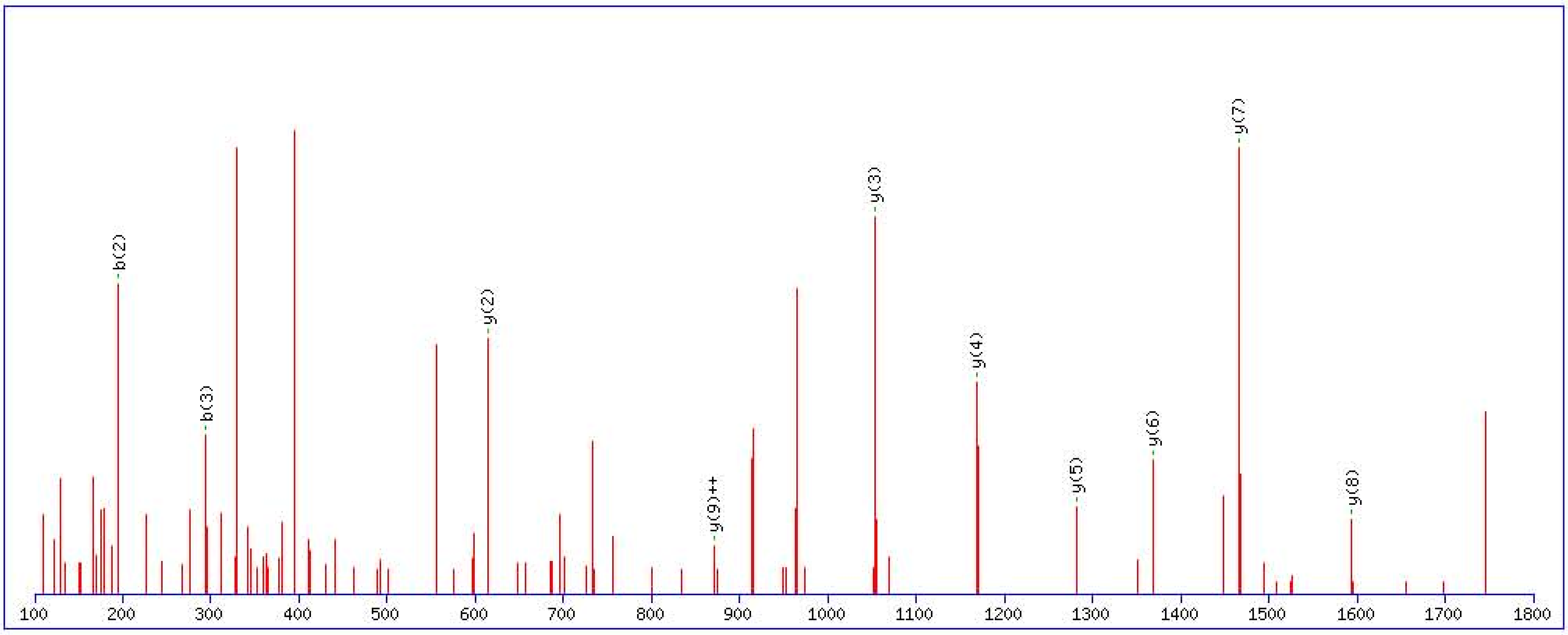
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHVSFKPSLDQQR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

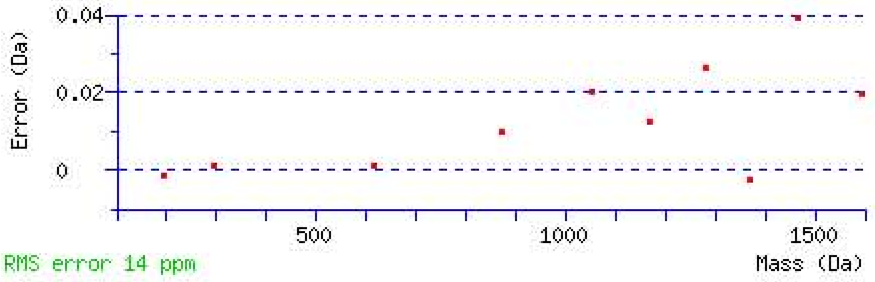
Match to Query 56445: 2120.126202 from(707.716010,3+) rtinseconds(1856) index(59420)
Title: Locus:1.1.1.2952.16 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

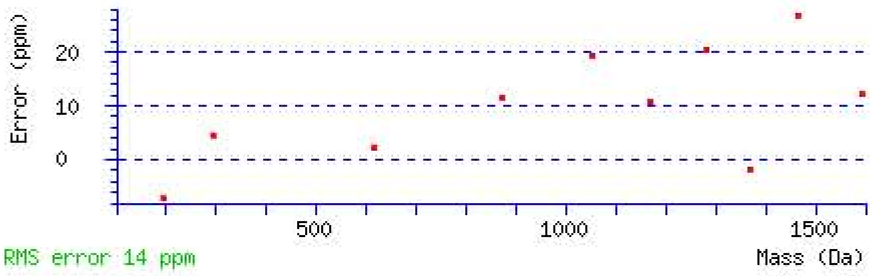
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2120.102325
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.006
Matches : 10/122 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							13
2	**195.087652**	98.047464					H	2064.088134	1032.547705	2047.061585	1024.034430	2046.077569	1023.542422	12
3	**294.156066**	147.581671					V	1927.029222	964.018249	1910.002673	955.504975	1909.018657	955.012967	11
4	381.188094	191.097685			363.177529	182.092403	S	1827.960808	914.484042	1810.934259	905.970768	1809.950243	905.478760	10
5	528.256508	264.631892			510.245943	255.626610	F	1740.928780	870.968028	1723.902231	862.454754	1722.918215	861.962746	9
6	656.351471	328.679374	639.324922	320.166099	638.340906	319.674091	K	***1593.860366***	797.433821	1576.833817	788.920547	1575.849801	788.428539	8
7	753.404235	377.205756	736.377686	368.692481	735.393670	368.200473	P	***1465.765403***	733.386340	1448.738854	724.873065	1447.754838	724.381057	7
8	840.436263	420.721770	823.409714	412.208495	822.425698	411.716487	S	***1368.712639***	684.859958	1351.686090	676.346683	1350.702074	675.854675	6
9	953.520327	477.263802	936.493778	468.750527	935.509762	468.258519	L	***1281.680611***	641.343944	1264.654062	632.830669	1263.670046	632.338661	5
10	1068.547270	534.777273	1051.520721	526.263999	1050.536705	525.771991	D	***1168.596547***	584.801912	1151.569998	576.288637	1150.585982	575.796629	4
11	1507.772596	754.389936	1490.746047	745.876662	1489.762031	745.384654	Q	***1053.569604***	527.288440	1036.543055	518.775166			3
12	1946.997922	974.002599	1929.971373	965.489325	1928.987357	964.997317	Q	***614.344278***	307.675777	597.317729	299.162503			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.9	2120.102325	0.023877	GHVSFKPSLDQQR

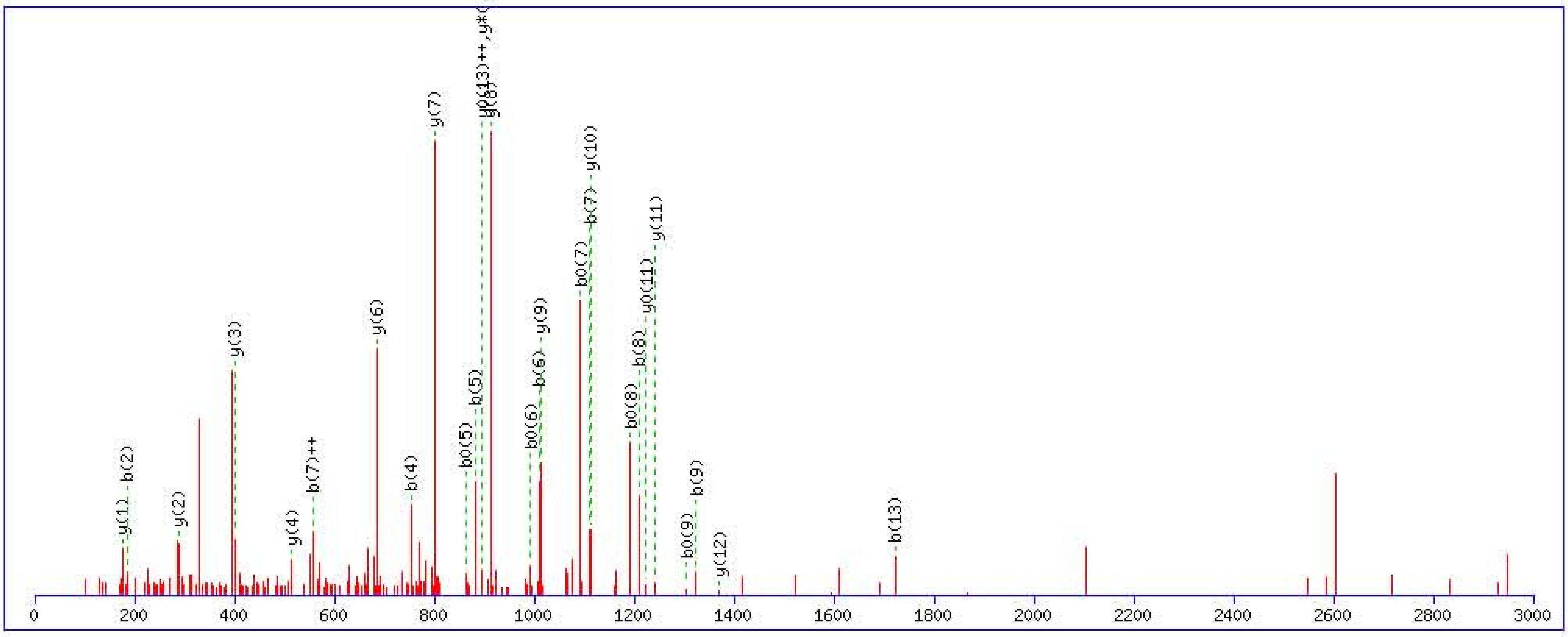
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPEQQETVLDGNLIIR**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

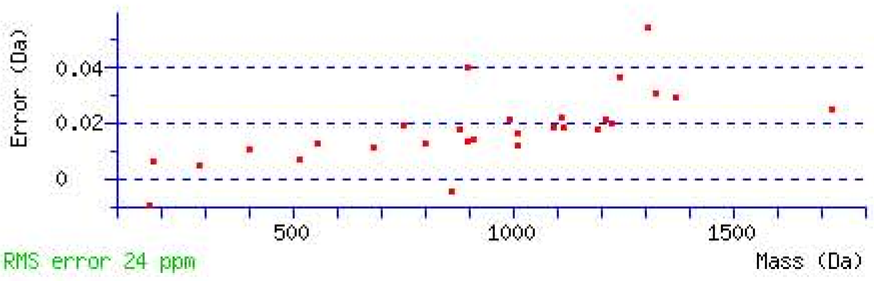
Match to Query 56497: 2122.134582 from(708.385470,3+) rtinseconds(2338) index(9314)
Title: Locus:1.1.1.2946.8 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

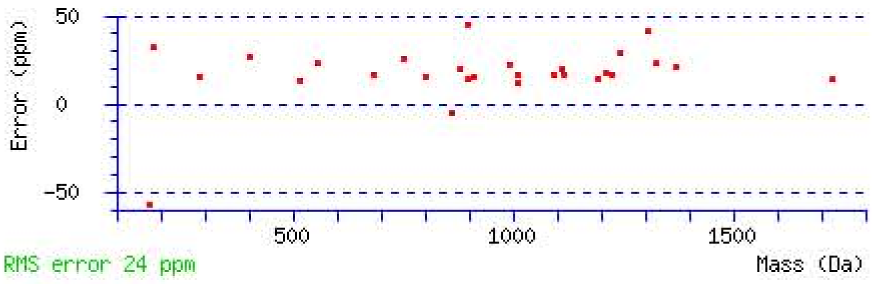
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2122.109222
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 1.3e-006
Matches : 28/162 fragment ions using 47 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							16
2	**185.092068**	93.049672			167.081503	84.044389	P	2036.084489	1018.545882	2019.057940	1010.032608	2018.073924	1009.540600	15
3	314.134661	157.570968			296.124096	148.565686	E	1939.031725	970.019500	1922.005176	961.506226	1921.021160	961.014218	14
4	**753.359987**	377.183632	736.333438	368.670357	735.349422	368.178349	Q	1809.989132	905.498204	1792.962583	896.984929	1791.978567	896.492921	13
5	**881.418565**	441.212921	864.392016	432.699646	863.408000	432.207638	Q	***1370.763806***	685.885541	1353.737257	677.372266	1352.753241	676.880258	12
6	**1010.461158**	505.734217	993.434609	497.220943	992.450593	496.728935	E	***1242.705228***	621.856252	1225.678679	613.342977	1224.694663	612.850969	11
7	**1111.508837**	556.258057	1094.482288	547.744782	1093.498272	547.252774	T	***1113.662635***	557.334955	1096.636086	548.821681	1095.652070	548.329673	10
8	**1210.577251**	605.792264	1193.550702	597.278989	1192.566686	596.786981	V	***1012.614956***	506.811116	995.588407	498.297841	994.604391	497.805833	9
9	**1323.661315**	662.334296	1306.634766	653.821021	1305.650750	653.329013	L	***913.546542***	457.276909	896.519993	448.763634	895.535977	448.271626	8
10	1438.688258	719.847767	1421.661709	711.334493	1420.677693	710.842485	D	***800.462478***	400.734877	783.435929	392.221602	782.451913	391.729594	7
11	1495.709722	748.358499	1478.683173	739.845225	1477.699157	739.353217	G	***685.435535***	343.221405	668.408986	334.708131			6
12	1609.752649	805.379963	1592.726100	796.866688	1591.742084	796.374680	N	628.414071	314.710673	611.387522	306.197399			5
13	**1722.836713**	861.921994	1705.810164	853.408720	1704.826148	852.916712	L	***514.371144***	257.689210	497.344595	249.175935			4
14	1835.920777	918.464026	1818.894228	909.950752	1817.910212	909.458744	I	***401.287080***	201.147178	384.260531	192.633903			3
15	1949.004841	975.006058	1931.978292	966.492784	1930.994276	966.000776	I	***288.203016***	144.605146	271.176467	136.091871			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.5	2122.109222	0.025360	SPEQQETVLDGNLIIR
52.9	2122.109222	0.025360	SPEQQETVLDGNLIIR
2.9	2122.156799	-0.022217	AERAALEELVKLQGER
2.5	2122.164246	-0.029664	TVIPIVNHSSKMTIQK

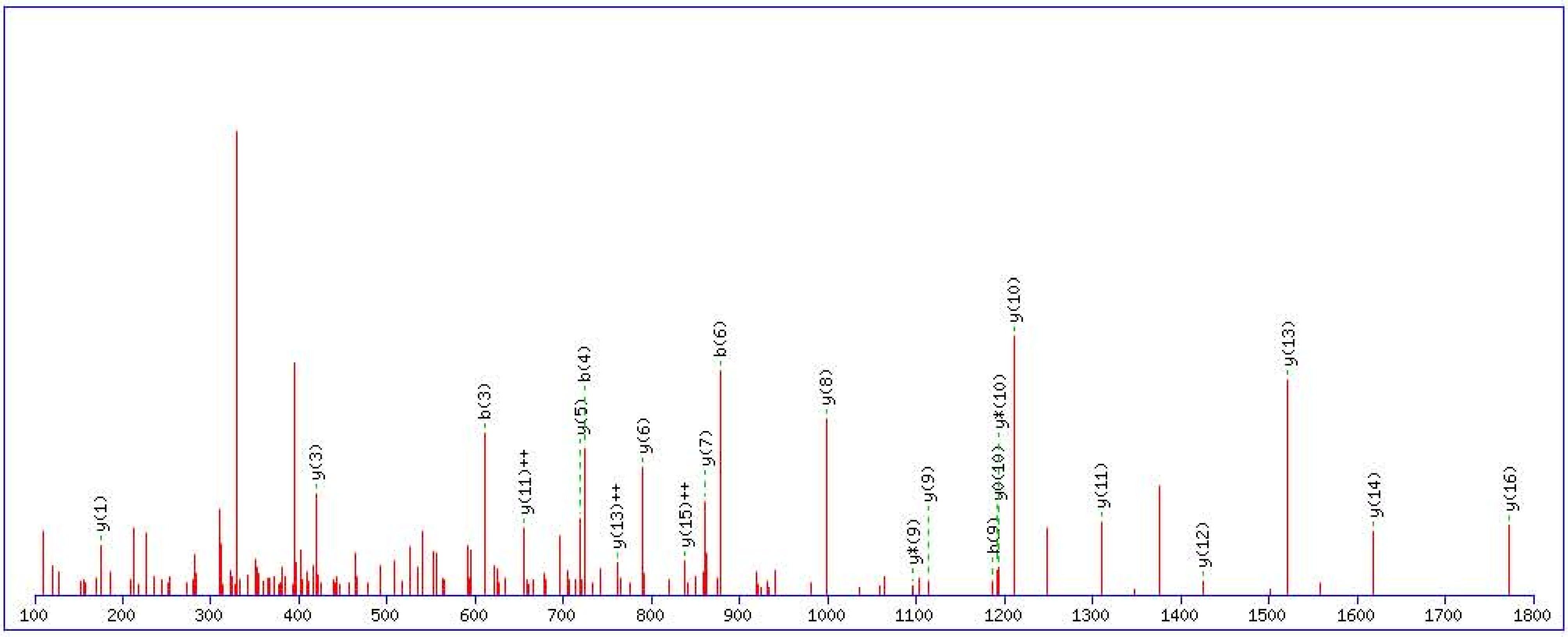
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLGLPGPPDVPDHAAYHPFR**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

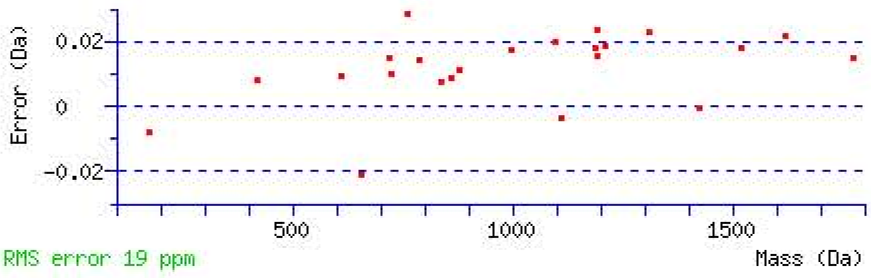
Match to Query 65269: 2494.274816 from(624.575980,4+) rtinseconds(2140) index(7943)
Title: Locus:1.1.1.2877.17 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

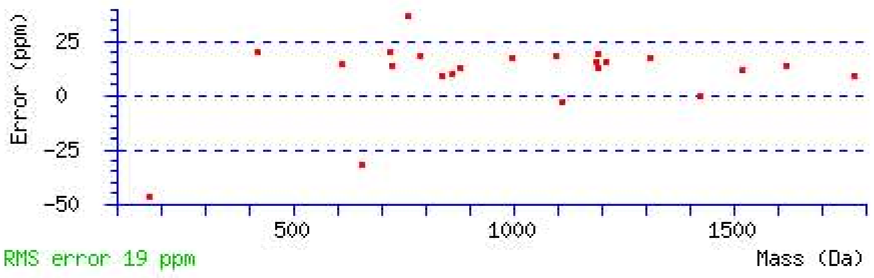
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2494.257980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 2.3e-006
Matches : 23/196 fragment ions using 56 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							20
2	553.316666	277.161971	536.290117	268.648697			L	2056.039923	1028.523599	2039.013374	1020.010325	2038.029358	1019.518317	19
3	**610.338130**	305.672703	593.311581	297.159429			G	1942.955859	971.981568	1925.929310	963.468293	1924.945294	962.976285	18
4	**723.422194**	362.214735	706.395645	353.701461			L	1885.934395	943.470836	1868.907846	934.957561	1867.923830	934.465553	17
5	820.474958	410.741117	803.448409	402.227843			P	***1772.850331***	886.928804	1755.823782	878.415529	1754.839766	877.923521	16
6	**877.496422**	439.251849	860.469873	430.738575			G	1675.797567	838.402422	1658.771018	829.889147	1657.787002	829.397139	15
7	974.549186	487.778231	957.522637	479.264957			P	***1618.776103***	809.891690	1601.749554	801.378415	1600.765538	800.886407	14
8	1071.601950	536.304613	1054.575401	527.791339			P	***1521.723339***	761.365308	1504.696790	752.852033	1503.712774	752.360025	13
9	**1186.628893**	593.818085	1169.602344	585.304810	1168.618328	584.812802	D	***1424.670575***	712.838926	1407.644026	704.325651	1406.660010	703.833643	12
10	1285.697307	643.352292	1268.670758	634.839017	1267.686742	634.347009	V	***1309.643632***	655.325454	1292.617083	646.812180	1291.633067	646.320172	11
11	1382.750071	691.878674	1365.723522	683.365399	1364.739506	682.873391	P	***1210.575218***	605.791247	1193.548669	597.277973	1192.564653	596.785964	10
12	1497.777014	749.392145	1480.750465	740.878871	1479.766449	740.386863	D	***1113.522454***	557.264865	1096.495905	548.751591	1095.511889	548.259582	9
13	1634.835926	817.921601	1617.809377	809.408327	1616.825361	808.916319	H	***998.495511***	499.751393	981.468962	491.238119			8
14	1705.873040	853.440158	1688.846491	844.926884	1687.862475	844.434876	A	***861.436599***	431.221937	844.410050	422.708663			7
15	1776.910154	888.958715	1759.883605	880.445441	1758.899589	879.953433	A	***790.399485***	395.703380	773.372936	387.190106			6
16	1939.973483	970.490380	1922.946934	961.977105	1921.962918	961.485097	Y	***719.362371***	360.184823	702.335822	351.671549			5
17	2077.032395	1039.019836	2060.005846	1030.506561	2059.021830	1030.014553	H	556.299042	278.653159	539.272493	270.139884			4
18	2174.085159	1087.546218	2157.058610	1079.032943	2156.074594	1078.540935	P	***419.240130***	210.123703	402.213581	201.610428			3
19	2321.153573	1161.080424	2304.127024	1152.567150	2303.143008	1152.075142	F	322.187366	161.597321	305.160817	153.084046			2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.2	2494.257980	0.016836	QLGLPGPPDVPDHAAYHPFR
1.0	2494.278381	-0.003565	MSAPLDAALHALQEEQARLKMR

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

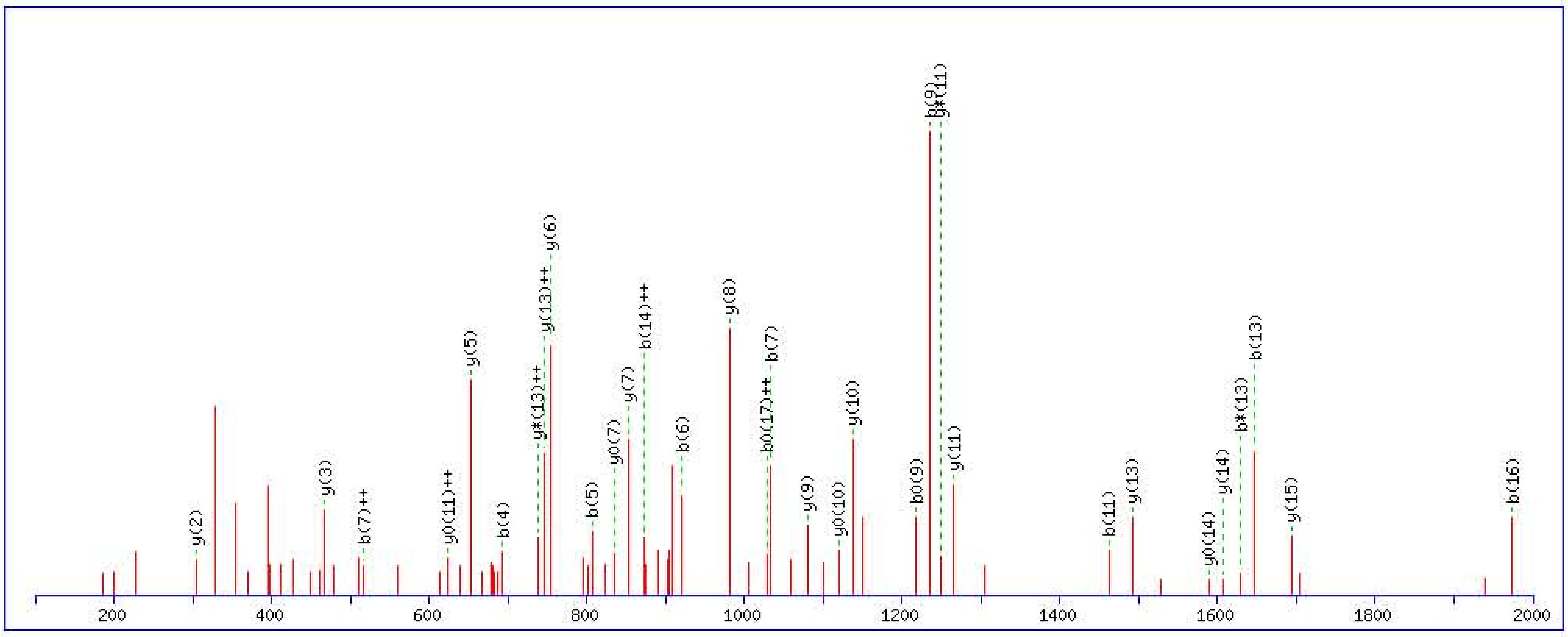
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGPVNLLSDPEQGVEVTGQYER**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

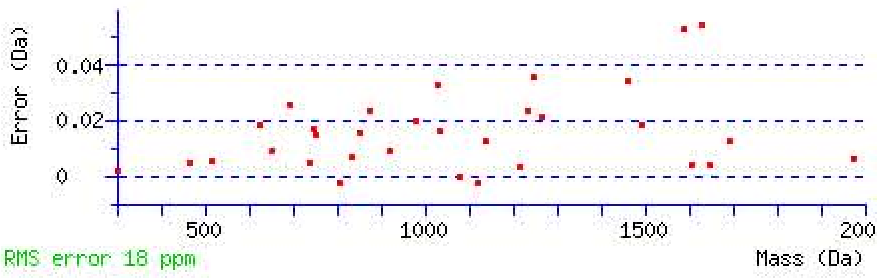
Match to Query 67847: 2725.372062 from(909.464630,3+) rtinseconds(2379) index(81122)
Title: Locus:1.1.1.3042.25 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

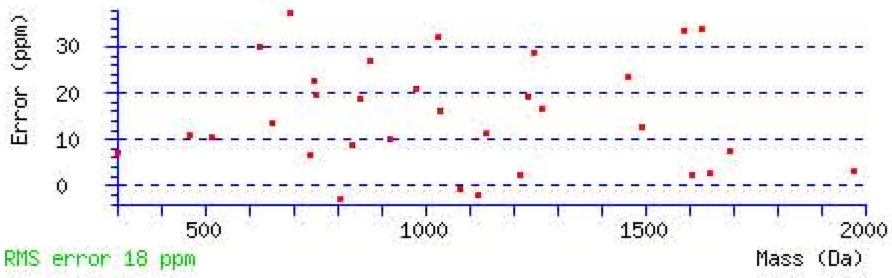
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2725.338135
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 6.3e-006
Matches : 32/236 fragment ions using 55 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							22
2	497.254066	249.130671	480.227517	240.617396			G	2287.120083	1144.063679	2270.093534	1135.550405	2269.109518	1135.058397	21
3	594.306830	297.657053	577.280281	289.143779			P	2230.098619	1115.552947	2213.072070	1107.039673	2212.088054	1106.547665	20
4	***693.375244***	347.191260	676.348695	338.677985			V	2133.045855	1067.026565	2116.019306	1058.513291	2115.035290	1058.021283	19
5	***807.418171***	404.212723	790.391622	395.699449			N	2033.977441	1017.492359	2016.950892	1008.979084	2015.966876	1008.487076	18
6	***920.502235***	460.754755	903.475686	452.241481			L	1919.934514	960.470895	1902.907965	951.957621	1901.923949	951.465613	17
7	***1033.586299***	**517.296787**	1016.559750	508.783513			L	1806.850450	903.928863	1789.823901	895.415589	1788.839885	894.923581	16
8	1120.618327	560.812801	1103.591778	552.299527	1102.607762	551.807519	S	***1693.766386***	847.386831	1676.739837	838.873557	1675.755821	838.381549	15
9	***1235.645270***	618.326273	1218.618721	609.812999	1217.634705	609.320990	D	***1606.734358***	803.870817	1589.707809	795.357543	1588.723793	794.865535	14
10	1332.698034	666.852655	1315.671485	658.339381	1314.687469	657.847373	P	***1491.707415***	746.357346	1474.680866	737.844071	1473.696850	737.352063	13
11	***1461.740627***	731.373951	1444.714078	722.860677	1443.730062	722.368669	E	1394.654651	697.830964	1377.628102	689.317689	1376.644086	688.825681	12
12	1589.799205	795.403241	1572.772656	786.889966	1571.788640	786.397958	Q	***1265.612058***	633.309667	1248.585509	624.796393	1247.601493	624.304385	11
13	***1646.820669***	823.913973	1629.794120	815.400698	1628.810104	814.908690	G	***1137.553480***	569.280378	1120.526931	560.767104	1119.542915	560.275096	10
14	1745.889083	**873.448180**	1728.862534	864.934905	1727.878518	864.442897	V	***1080.532016***	540.769646	1063.505467	532.256372	1062.521451	531.764364	9
15	1874.931676	937.969476	1857.905127	929.456202	1856.921111	928.964193	E	***981.463602***	491.235439	964.437053	482.722165	963.453037	482.230157	8
16	***1974.000090***	987.503683	1956.973541	978.990409	1955.989525	978.498401	V	***852.421009***	426.714143	835.394460	418.200868	834.410444	417.708860	7
17	2075.047769	1038.027522	2058.021220	1029.514248	2057.037204	1029.022240	T	***753.352595***	377.179936	736.326046	368.666661	735.342030	368.174653	6
18	2132.069233	1066.538254	2115.042684	1058.024980	2114.058668	1057.532972	G	***652.304916***	326.656096	635.278367	318.142822	634.294351	317.650814	5
19	2260.127811	1130.567543	2243.101262	1122.054269	2242.117246	1121.562261	Q	595.283452	298.145364	578.256903	289.632090	577.272887	289.140082	4
20	2423.191140	1212.099208	2406.164591	1203.585933	2405.180575	1203.093925	Y	***467.224874***	234.116075	450.198325	225.602801	449.214309	225.110793	3
21	2552.233733	1276.620504	2535.207184	1268.107230	2534.223168	1267.615222	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
22							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.6	2725.338135	0.033927	QGPVNLLSDPEQGVEVTGQYER
19.4	2725.338135	0.033927	QGPVNLLSDPEQGVEVTGQYER

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

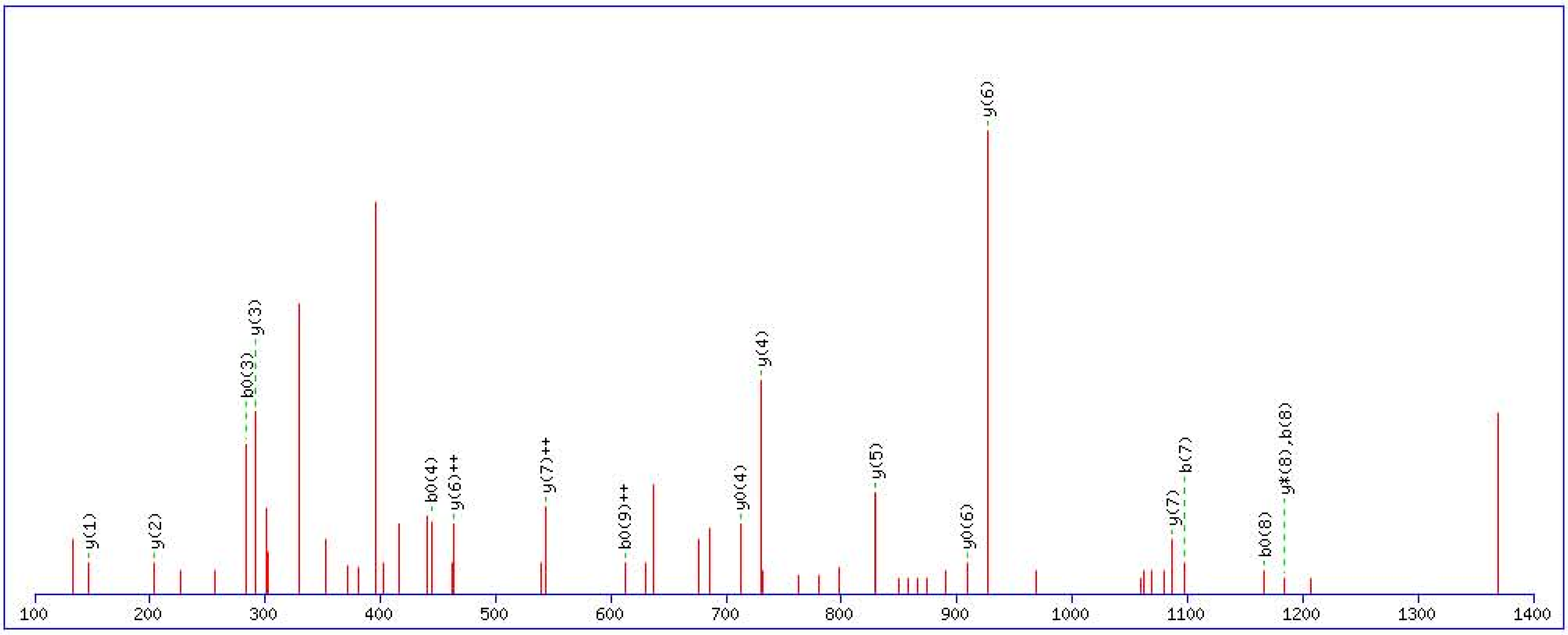
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGDCPVQSGK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

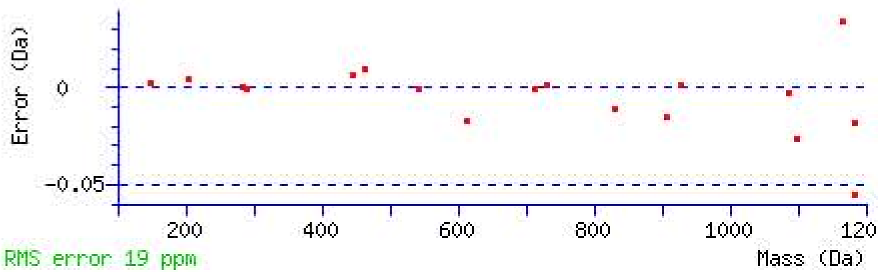
Match to Query 33950: 1386.631228 from(694.322890,2+) rtinseconds(1341) index(37722)
Title: Locus:1.1.1.2750.26 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

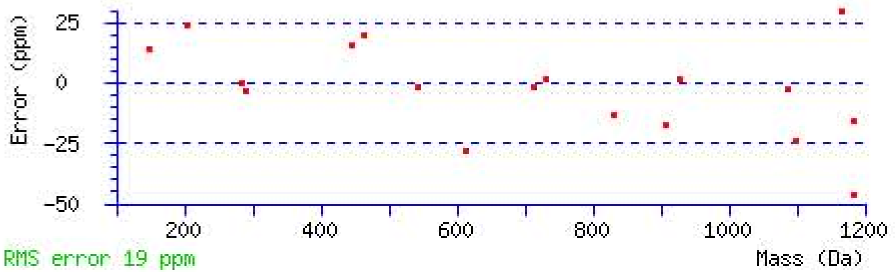
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1386.627182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.00029
Matches : 18/92 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							10
2	187.071333	94.039305			169.060768	85.034022	G	1258.591856	629.799566	1241.565307	621.286292	1240.581291	620.794284	9
3	302.098276	151.552776			284.087711	142.547494	D	1201.570392	601.288834	1184.543843	592.775560	1183.559827	592.283552	8
4	462.128925	231.568101			444.118360	222.562818	C	***1086.543449***	543.775363	1069.516900	535.262088	1068.532884	534.770080	7
5	559.181689	280.094483			541.171124	271.089200	P	***926.512800***	463.760038	909.486251	455.246764	908.502235	454.754756	6
6	658.250103	329.628690			640.239538	320.623407	V	***829.460036***	415.233656	812.433487	406.720382	811.449471	406.228374	5
7	**1097.475429**	549.241353	1080.448880	540.728078	1079.464864	540.236070	Q	***730.391622***	365.699449	713.365073	357.186175	712.381057	356.694167	4
8	**1184.507457**	592.757367	1167.480908	584.244092	1166.496892	583.752084	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
9	1241.528921	621.268099	1224.502372	612.754824	1223.518356	612.262816	G	***204.134268***	102.570772	187.107719	94.057497			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.5	1386.627182	0.004046	EGDCPVQSGK
2.9	1386.650269	-0.019041	YRNFSYLHCK

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

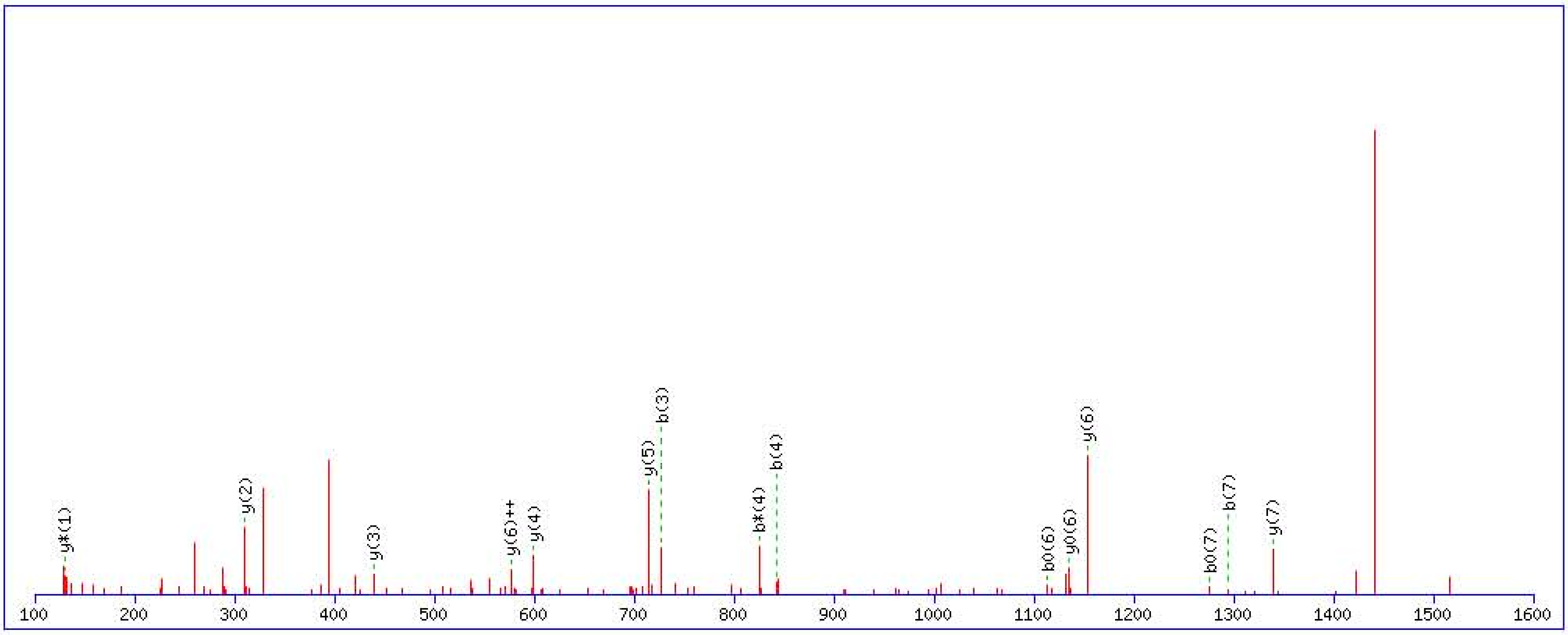
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TWQDCEYK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

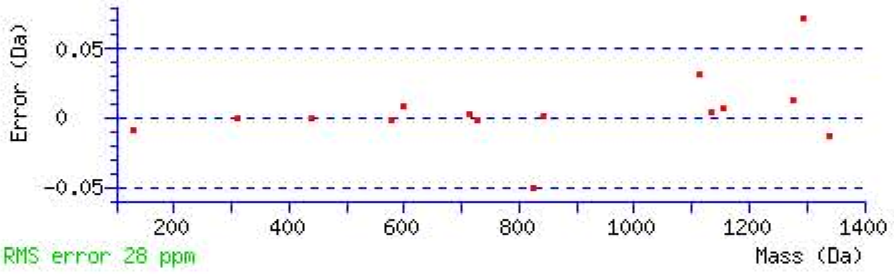
Match to Query 36673: 1439.633568 from(720.824060,2+) rtinseconds(1768) index(40538)
Title: Locus:1.1.1.2899.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

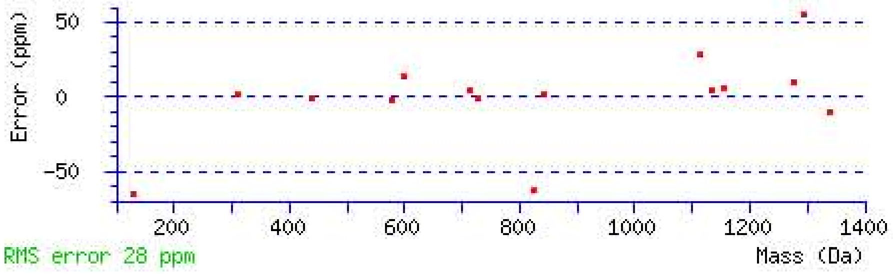
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1439.621353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0029
Matches : 15/76 fragment ions using 26 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							8
2	288.134268	144.570772			270.123703	135.565490	W	***1339.580957***	670.294117	1322.554408	661.780842	1321.570392	661.288834	7
3	**727.359594**	364.183435	710.333045	355.670161	709.349029	355.178153	Q	***1153.501644***	577.254460	1136.475095	568.741186	1135.491079	568.249178	6
4	**842.386537**	421.696907	825.359988	413.183632	824.375972	412.691624	D	***714.276318***	357.641797	697.249769	349.128523	696.265753	348.636515	5
5	1002.417186	501.712231	985.390637	493.198957	984.406621	492.706949	C	***599.249375***	300.128326	582.222826	291.615051	581.238810	291.123043	4
6	1131.459779	566.233528	1114.433230	557.720253	1113.449214	557.228245	E	***439.218726***	220.113001	422.192177	211.599727	421.208161	211.107719	3
7	**1294.523108**	647.765192	1277.496559	639.251918	1276.512543	638.759910	Y	***310.176133***	155.591705	293.149584	147.078430			2
8							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	1439.621353	0.012215	TWQDCEYK

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

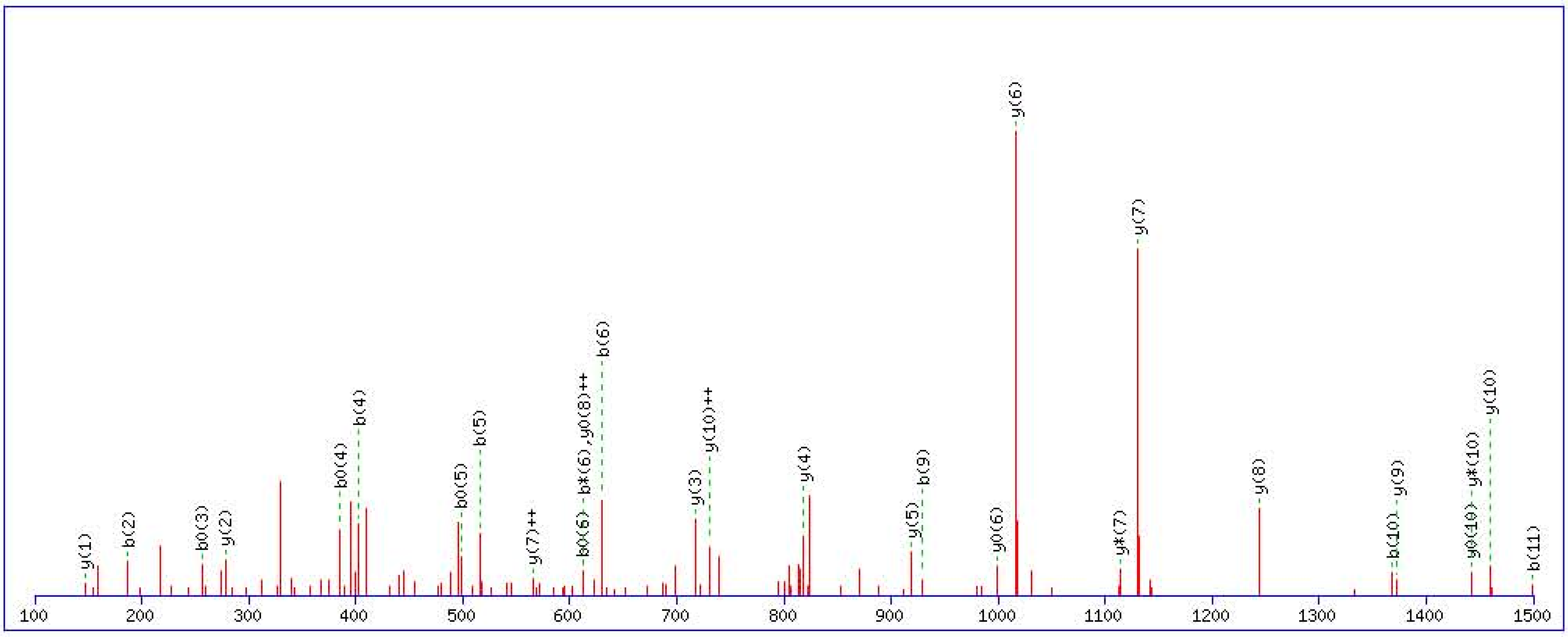
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVSEINPTTQMK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

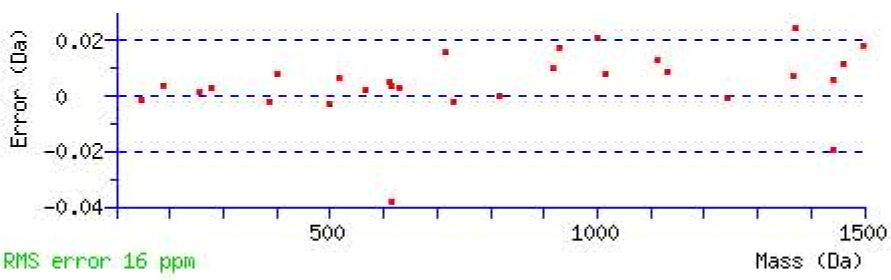
Match to Query 44488: 1644.832968 from(823.423760,2+) rtinseconds(1816) index(40828)
Title: Locus:1.1.1.2916.11 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

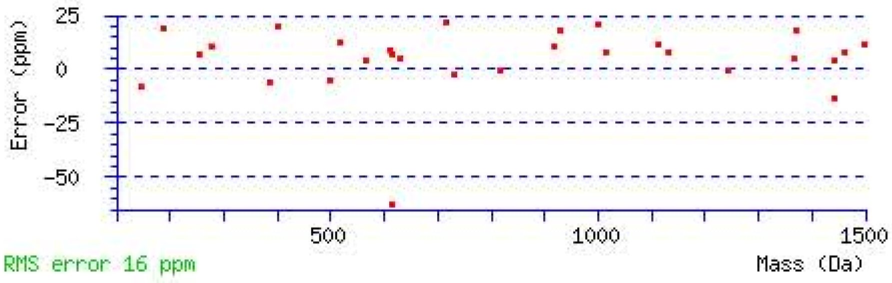
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1644.821503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 1.6e-006
Matches : 29/116 fragment ions using 50 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							12
2	**187.107718**	94.057497			169.097153	85.052214	V	1558.796763	779.902020	1541.770214	771.388745	1540.786198	770.896737	11
3	274.139746	137.573511			256.129181	128.568229	S	***1459.728349***	730.367813	1442.701800	721.854538	1441.717784	721.362530	10
4	**403.182339**	202.094808			385.171774	193.089525	E	***1372.696321***	686.851799	1355.669772	678.338524	1354.685756	677.846516	9
5	**516.266403**	258.636840			498.255838	249.631557	I	***1243.653728***	622.330502	1226.627179	613.817228	1225.643163	613.325220	8
6	**630.309330**	315.658303	613.282781	307.145029	612.298765	306.653021	N	***1130.569664***	565.788470	1113.543115	557.275196	1112.559099	556.783188	7
7	727.362094	364.184685	710.335545	355.671411	709.351529	355.179403	P	***1016.526737***	508.767007	999.500188	500.253732	998.516172	499.761724	6
8	828.409773	414.708525	811.383224	406.195250	810.399208	405.703242	T	***919.473973***	460.240625	902.447424	451.727350	901.463408	451.235342	5
9	**929.457452**	465.232364	912.430903	456.719090	911.446887	456.227082	T	***818.426294***	409.716785	801.399745	401.203511	800.415729	400.711503	4
10	**1368.682778**	684.845027	1351.656229	676.331753	1350.672213	675.839745	Q	***717.378615***	359.192946	700.352066	350.679671			3
11	**1499.723263**	750.365270	1482.696714	741.851995	1481.712698	741.359987	M	***278.153289***	139.580282	261.126740	131.067008			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.8	1644.821503	0.011465	SVSEINPTTQMK
2.8	1644.847092	-0.014124	LLSAIYSKQENHDK
0.8	1644.810745	0.022223	VSDGENVIISHFNSK

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

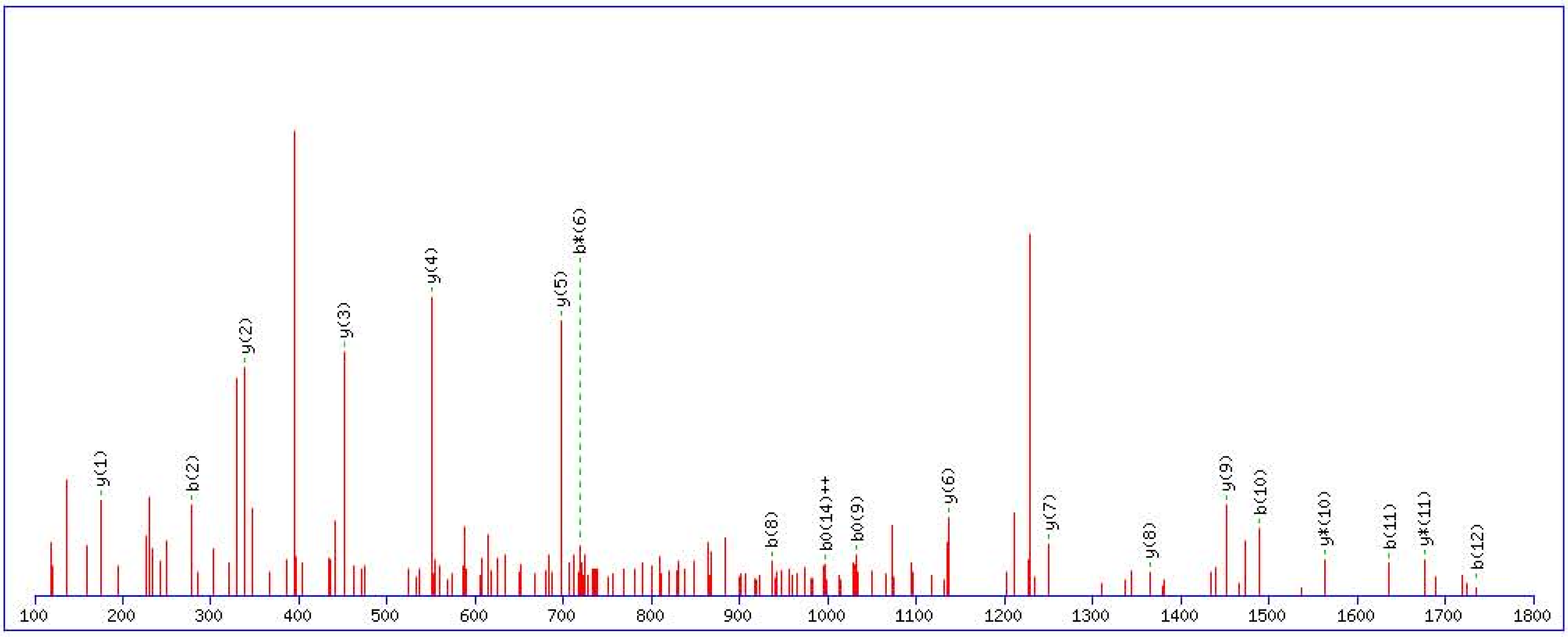
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

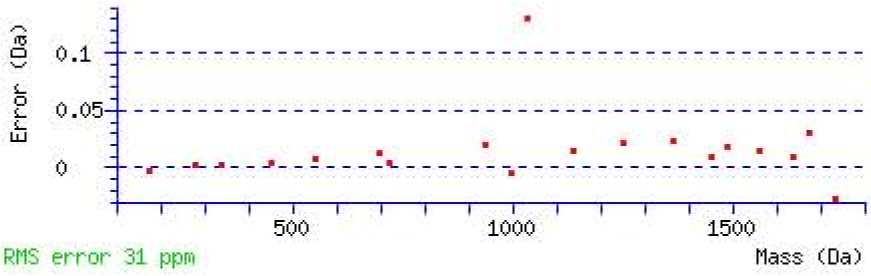
Match to Query 57849: 2185.065342 from(729.362390,3+) rtinseconds(2106) index(42779)
Title: Locus:1.1.1.3017.16 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

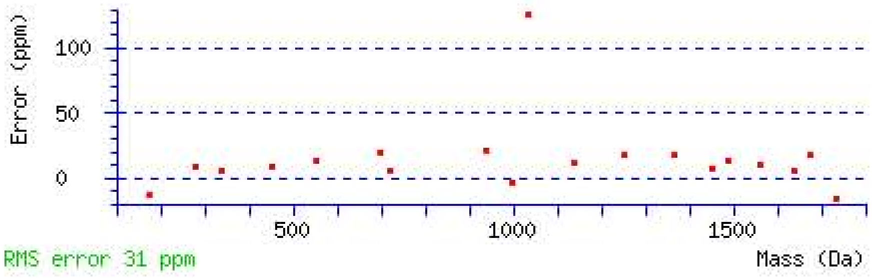
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2185.037445
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.0004
Matches : 19/146 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							15
2	**278.113532**	139.560404	261.086983	131.047130			N	2022.981419	1011.994348	2005.954870	1003.481073	2004.970854	1002.989065	14
3	365.145560	183.076418	348.119011	174.563144	347.134995	174.071136	S	1908.938492	954.972884	1891.911943	946.459610	1890.927927	945.967602	13
4	493.204138	247.105707	476.177589	238.592433	475.193573	238.100425	Q	1821.906464	911.456870	1804.879915	902.943596	1803.895899	902.451588	12
5	607.247065	304.127171	590.220516	295.613896	589.236500	295.121888	N	1693.847886	847.427581	1676.821337	838.914307	1675.837321	838.422299	11
6	735.305643	368.156460	718.279094	359.643185	717.295078	359.151177	Q	1579.804959	790.406118	1562.778410	781.892843	1561.794394	781.400835	10
7	822.337671	411.672474	805.311122	403.159199	804.327106	402.667191	S	***1451.746381***	726.376829	1434.719832	717.863554	1433.735816	717.371546	9
8	**936.380598**	468.693937	919.354049	460.180662	918.370033	459.688654	N	***1364.714353***	682.860815	1347.687804	674.347540			8
9	1050.423525	525.715400	1033.396976	517.202126	1032.412960	516.710118	N	***1250.671426***	625.839351	1233.644877	617.326077			7
10	**1489.648851**	745.328064	1472.622302	736.814789	1471.638286	736.322781	Q	***1136.628499***	568.817888	1119.601950	560.304613			6
11	**1636.717265**	818.862271	1619.690716	810.348996	1618.706700	809.856988	F	***697.403173***	349.205225	680.376624	340.691950			5
12	**1735.785679**	868.396478	1718.759130	859.883203	1717.775114	859.391195	V	***550.334759***	275.671018	533.308210	267.157743			4
13	1848.869743	924.938510	1831.843194	916.425235	1830.859178	915.933227	L	***451.266345***	226.136811	434.239796	217.623536			3
14	2011.933072	1006.470174	1994.906523	997.956900	1993.922507	997.464892	Y	***338.182281***	169.594779	321.155732	161.081504			2
15							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.4	2185.037445	0.027897	YNSQNQSNNQFVLYR
12.3	2185.037445	0.027897	YNSQNQSNNQFVLYR
12.2	2185.037445	0.027897	YNSQNQSNNQFVLYR

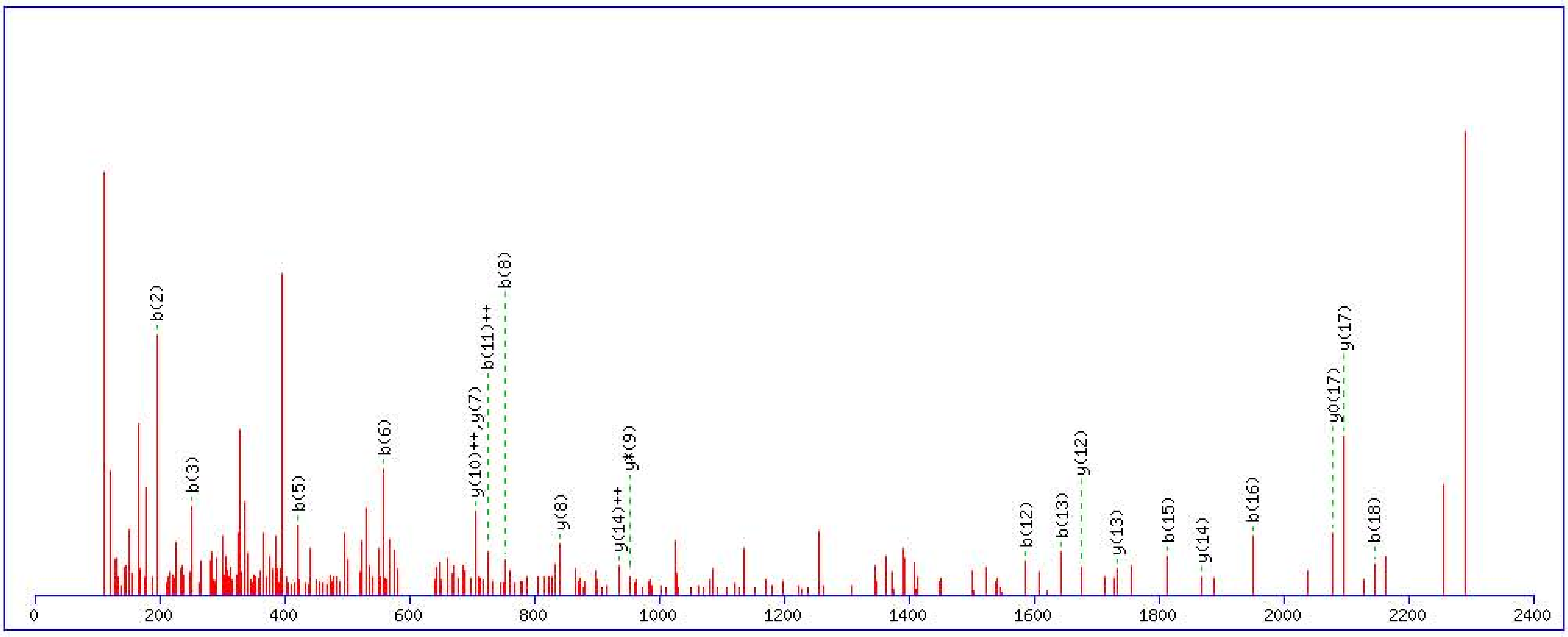
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHGLGHGHEQQHGLGHGHK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

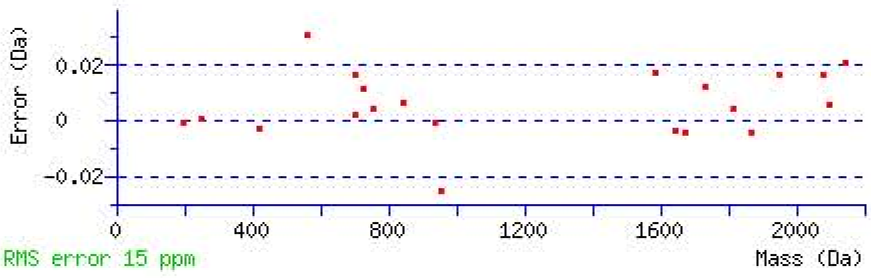
Match to Query 60482: 2290.104656 from(573.533440,4+) rtinseconds(754) index(35417)
Title: Locus:1.1.1.2466.3 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

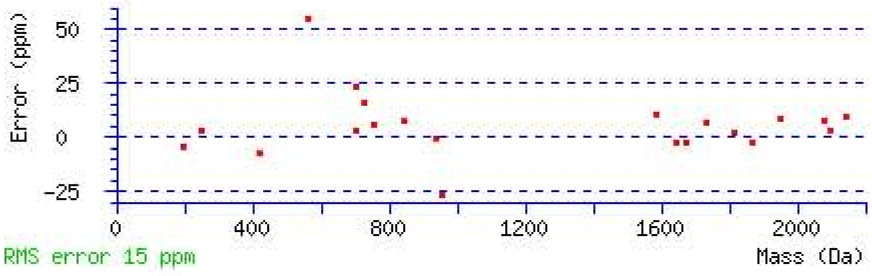
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2290.103897
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.0004
Matches : 21/162 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							19
2	***195.087652***	98.047464					H	2234.089685	1117.548480	2217.063136	1109.035206	2216.079120	1108.543198	18
3	***252.109116***	126.558196					G	**2097.030773**	1049.019024	2080.004224	1040.505750	2079.020208	1040.013742	17
4	365.193180	183.100228					L	2040.009309	1020.508293	2022.982760	1011.995018	2021.998744	1011.503010	16
5	***422.214644***	211.610960					G	1926.925245	963.966261	1909.898696	955.452986	1908.914680	954.960978	15
6	***559.273556***	280.140416					H	**1869.903781**	935.455529	1852.877232	926.942254	1851.893216	926.450246	14
7	616.295020	308.651148					G	**1732.844869**	866.926073	1715.818320	858.412798	1714.834304	857.920790	13
8	***753.353932***	377.180604					H	**1675.823405**	838.415341	1658.796856	829.902066	1657.812840	829.410058	12
9	882.396525	441.701901			864.385960	432.696618	E	1538.764493	769.885885	1521.737944	761.372610	1520.753928	760.880602	11
10	1321.621851	661.314564	1304.595302	652.801289	1303.611286	652.309281	Q	1409.721900	705.364588	1392.695351	696.851314			10
11	1449.680429	725.343853	1432.653880	716.830578	1431.669864	716.338570	Q	970.496574	485.751925	953.470025	477.238651			9
12	***1586.739341***	793.873309	1569.712792	785.360034	1568.728776	784.868026	H	**842.437996**	421.722636	825.411447	413.209361			8
13	***1643.760805***	822.384041	1626.734256	813.870766	1625.750240	813.378758	G	**705.379084**	353.193180	688.352535	344.679905			7
14	1756.844869	878.926073	1739.818320	870.412798	1738.834304	869.920790	L	648.357620	324.682448	631.331071	316.169174			6
15	***1813.866333***	907.436804	1796.839784	898.923530	1795.855768	898.431522	G	535.273556	268.140416	518.247007	259.627142			5
16	***1950.925245***	975.966260	1933.898696	967.452986	1932.914680	966.960978	H	478.252092	239.629684	461.225543	231.116410			4
17	2007.946709	1004.476992	1990.920160	995.963718	1989.936144	995.471710	G	341.193180	171.100228	324.166631	162.586954			3
18	***2145.005621***	1073.006448	2127.979072	1064.493174	2126.995056	1064.001166	H	284.171716	142.589496	267.145167	134.076222			2
19							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.7	2290.103897	0.000759	GHGLGHGHEQQHGLGHGHK
46.0	2290.103897	0.000759	GHGLGHGHEQQHGLGHGHK

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

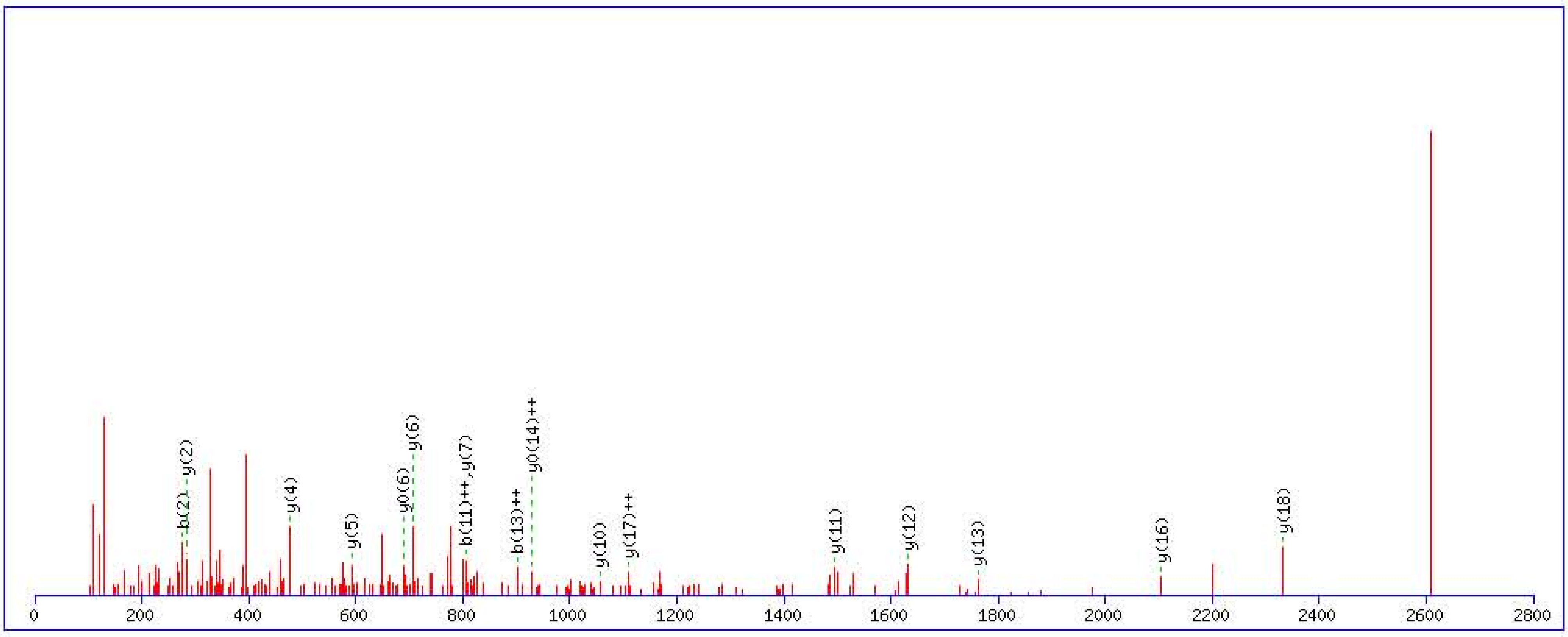
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FKLDDDLEHQGGHVLDHGHK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

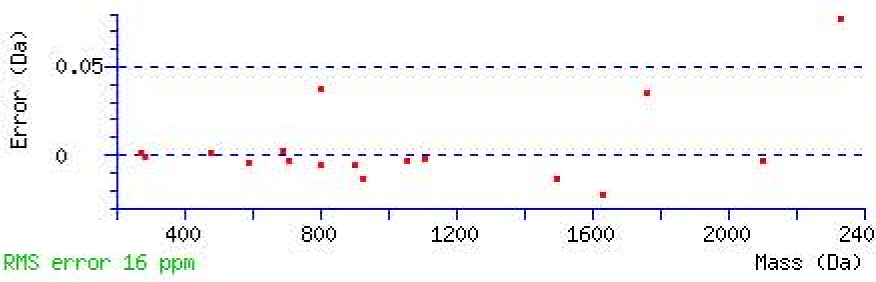
Match to Query 66683: 2607.273616 from(652.825680,4+) rtinseconds(1707) index(40132)
Title: Locus:1.1.1.2878.11 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

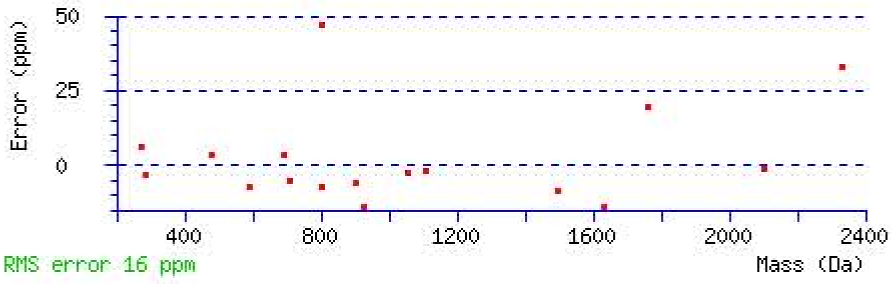
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2607.265259
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.00017
Matches : 17/212 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							20
2	276.170653	138.588964	259.144104	130.075690			K	2461.204104	1231.105690	2444.177555	1222.592415	2443.193539	1222.100407	19
3	389.254717	195.130996	372.228168	186.617722			L	***2333.109141***	1167.058208	2316.082592	1158.544934	2315.098576	1158.052926	18
4	504.281660	252.644468	487.255111	244.131193	486.271095	243.639186	D	2220.025077	1110.516176	2202.998528	1102.002902	2202.014512	1101.510894	17
5	619.308603	310.157940	602.282054	301.644665	601.298038	301.152657	D	***2104.998134***	1053.002705	2087.971585	1044.489430	2086.987569	1043.997422	16
6	734.335546	367.671411	717.308997	359.158137	716.324981	358.666129	D	1989.971191	995.489233	1972.944642	986.975959	1971.960626	986.483951	15
7	847.419610	424.213443	830.393061	415.700169	829.409045	415.208161	L	1874.944248	937.975762	1857.917699	929.462487	1856.933683	928.970479	14
8	976.462203	488.734740	959.435654	480.221465	958.451638	479.729457	E	***1761.860184***	881.433730	1744.833635	872.920455	1743.849619	872.428447	13
9	1113.521115	557.264196	1096.494566	548.750921	1095.510550	548.258913	H	***1632.817591***	816.912433	1615.791042	808.399159	1614.807026	807.907151	12
10	1552.746441	776.876859	1535.719892	768.363584	1534.735876	767.871576	Q	***1495.758679***	748.382977	1478.732130	739.869703	1477.748114	739.377695	11
11	1609.767905	**805.387590**	1592.741356	796.874316	1591.757340	796.382308	G	***1056.533353***	528.770314	1039.506804	520.257040	1038.522788	519.765032	10
12	1666.789369	833.898322	1649.762820	825.385048	1648.778804	824.893040	G	999.511889	500.259582	982.485340	491.746308	981.501324	491.254300	9
13	1803.848281	**902.427778**	1786.821732	893.914504	1785.837716	893.422496	H	942.490425	471.748850	925.463876	463.235576	924.479860	462.743568	8
14	1902.916695	951.961985	1885.890146	943.448711	1884.906130	942.956703	V	***805.431513***	403.219394	788.404964	394.706120	787.420948	394.214112	7
15	2016.000759	1008.504017	1998.974210	999.990743	1997.990194	999.498735	L	***706.363099***	353.685187	689.336550	345.171913	688.352534	344.679905	6
16	2131.027702	1066.017489	2114.001153	1057.504214	2113.017137	1057.012206	D	***593.279035***	297.143155	576.252486	288.629881	575.268470	288.137873	5
17	2268.086614	1134.546945	2251.060065	1126.033670	2250.076049	1125.541662	H	***478.252092***	239.629684	461.225543	231.116409			4
18	2325.108078	1163.057677	2308.081529	1154.544402	2307.097513	1154.052394	G	341.193180	171.100228	324.166631	162.586953			3
19	2462.166990	1231.587133	2445.140441	1223.073858	2444.156425	1222.581850	H	***284.171716***	142.589496	267.145167	134.076221			2
20							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.9	2607.265259	0.008357	FKLDDDLEHQGGHVLDHGHK
0.8	2607.256714	0.016902	KMTAADVSRHMNTLQLQMEVTR

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

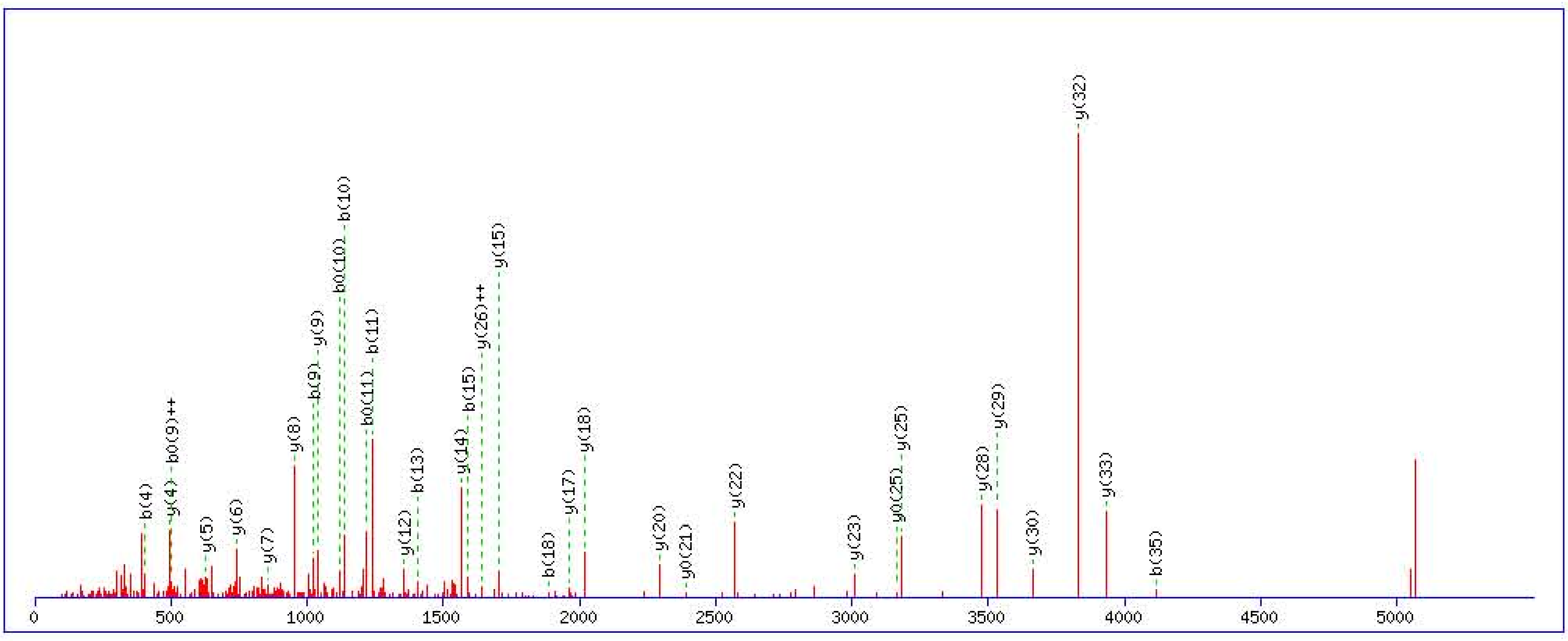
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

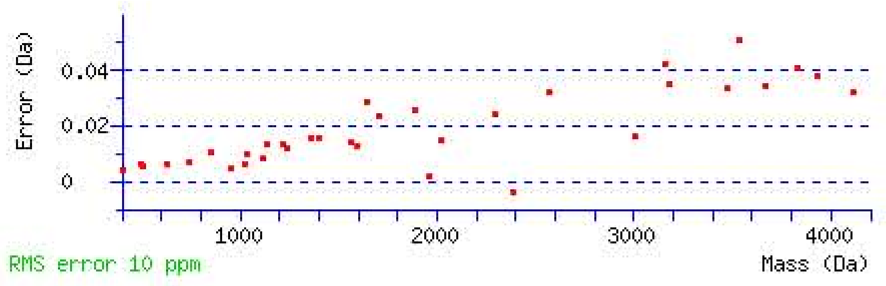
Match to Query 87461: 5066.537620 from(1014.314800,5+) rtinseconds(2627) index(46038)
Title: Locus:1.1.1.3198.6 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

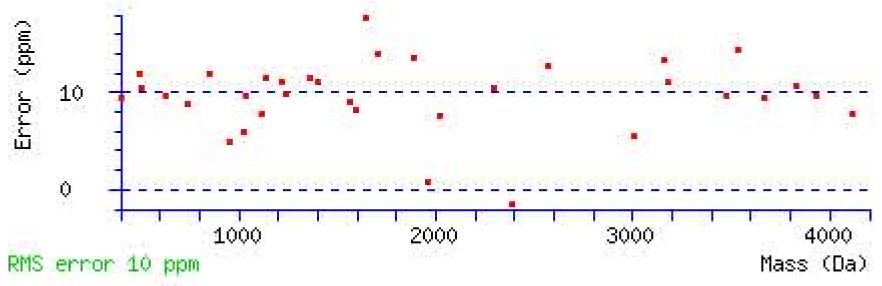
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 5500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 5066.465057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21    : Biotin:Thermo-21345 (Q)
Ions Score: 110  Expect: 1.8e-010
Matches : 34/484 fragment ions using 62 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							43
2	235.107718	118.057497			217.097153	109.052214	S	4920.403881	2460.705578	4903.377332	2452.192304	4902.393316	2451.700296	42
3	334.176132	167.591704			316.165567	158.586422	V	4833.371853	2417.189565	4816.345304	2408.676290	4815.361288	2408.184282	41
4	**405.213246**	203.110261			387.202681	194.104978	A	4734.303439	2367.655357	4717.276890	2359.142083	4716.292874	2358.650075	40
5	506.260925	253.634100			488.250360	244.628818	T	4663.266325	2332.136800	4646.239776	2323.623526	4645.255760	2323.131518	39
6	634.319503	317.663390	617.292954	309.150115	616.308938	308.658107	Q	4562.218646	2281.612961	4545.192097	2273.099686	4544.208081	2272.607679	38
7	735.367182	368.187229	718.340633	359.673955	717.356617	359.181947	T	4434.160068	2217.583672	4417.133519	2209.070397	4416.149503	2208.578390	37
8	895.397831	448.202554	878.371282	439.689279	877.387266	439.197271	C	4333.112389	2167.059833	4316.085840	2158.546558	4315.101824	2158.054550	36
9	**1023.456409**	512.231843	1006.429860	503.718568	1005.445844	503.226560	Q	4173.081740	2087.044508	4156.055191	2078.531233	4155.071175	2078.039226	35
10	**1136.540473**	568.773875	1119.513924	560.260600	1118.529908	559.768592	I	4045.023162	2023.015219	4027.996613	2014.501944	4027.012597	2014.009936	34
11	**1237.588152**	619.297714	1220.561603	610.784440	1219.577587	610.292432	T	***3931.939098***	1966.473187	3914.912549	1957.959912	3913.928533	1957.467904	33
12	1334.640916	667.824096	1317.614367	659.310822	1316.630351	658.818814	P	***3830.891419***	1915.949347	3813.864870	1907.436073	3812.880854	1906.944065	32
13	**1405.678030**	703.342653	1388.651481	694.829379	1387.667465	694.337371	A	3733.838655	1867.422965	3716.812106	1858.909691	3715.828090	1858.417683	31
14	1534.720623	767.863949	1517.694074	759.350675	1516.710058	758.858667	E	***3662.801541***	1831.904408	3645.774992	1823.391134	3644.790976	1822.899126	30
15	**1591.742087**	796.374681	1574.715538	787.861407	1573.731522	787.369399	G	***3533.758948***	1767.383112	3516.732399	1758.869837	3515.748383	1758.377829	29
16	1688.794851	844.901063	1671.768302	836.387789	1670.784286	835.895781	P	***3476.737484***	1738.872380	3459.710935	1730.359105	3458.726919	1729.867097	28
17	1787.863265	894.435271	1770.836716	885.921996	1769.852700	885.429988	V	3379.684720	1690.345998	3362.658171	1681.832723	3361.674155	1681.340715	27
18	**1886.931679**	943.969478	1869.905130	935.456203	1868.921114	934.964195	V	3280.616306	1640.811791	3263.589757	1632.298516	3262.605741	1631.806508	26
19	1987.979358	994.493317	1970.952809	985.980043	1969.968793	985.488035	T	***3181.547892***	1591.277584	3164.521343	1582.764309	3163.537327	1582.272301	25
20	2059.016472	1030.011874	2041.989923	1021.498600	2041.005907	1021.006591	A	3080.500213	1540.753744	3063.473664	1532.240470	3062.489648	1531.748462	24
21	2498.241798	1249.624537	2481.215249	1241.111262	2480.231233	1240.619254	Q	***3009.463099***	1505.235187	2992.436550	1496.721913	2991.452534	1496.229905	23
22	2661.305127	1331.156202	2644.278578	1322.642927	2643.294562	1322.150919	Y	***2570.237773***	1285.622524	2553.211224	1277.109250	2552.227208	1276.617242	22
23	2776.332070	1388.669673	2759.305521	1380.156398	2758.321505	1379.664390	D	2407.174444	1204.090860	2390.147895	1195.577585	2389.163879	1195.085577	21
24	2936.362719	1468.684997	2919.336170	1460.171723	2918.352154	1459.679715	C	***2292.147501***	1146.577388	2275.120952	1138.064114	2274.136936	1137.572106	20
25	3049.446783	1525.227029	3032.420234	1516.713755	3031.436218	1516.221747	L	2132.116852	1066.562064	2115.090303	1058.048789	2114.106287	1057.556781	19
26	3106.468247	1553.737761	3089.441698	1545.224487	3088.457682	1544.732479	G	***2019.032788***	1010.020032	2002.006239	1001.506757	2001.022223	1001.014749	18
27	3266.498896	1633.753086	3249.472347	1625.239811	3248.488331	1624.747803	C	***1962.011324***	981.509300	1944.984775	972.996025	1944.000759	972.504017	17
28	3365.567310	1683.287293	3348.540761	1674.774018	3347.556745	1674.282010	V	1801.980675	901.493975	1784.954126	892.980701	1783.970110	892.488693	16
29	3502.626222	1751.816749	3485.599673	1743.303474	3484.615657	1742.811466	H	***1702.912261***	851.959768	1685.885712	843.446494	1684.901696	842.954486	15
30	3599.678986	1800.343131	3582.652437	1791.829856	3581.668421	1791.337848	P	***1565.853349***	783.430312	1548.826800	774.917038	1547.842784	774.425030	14
31	3712.763050	1856.885163	3695.736501	1848.371888	3694.752485	1847.879880	I	1468.800585	734.903930	1451.774036	726.390656	1450.790020	725.898648	13
32	3799.795078	1900.401177	3782.768529	1891.887902	3781.784513	1891.395894	S	***1355.716521***	678.361898	1338.689972	669.848624	1337.705956	669.356616	12
33	3900.842757	1950.925016	3883.816208	1942.411742	3882.832192	1941.919734	T	1268.684493	634.845884	1251.657944	626.332610	1250.673928	625.840602	11
34	4028.901335	2014.954305	4011.874786	2006.441031	4010.890770	2005.949023	Q	1167.636814	584.322045	1150.610265	575.808770	1149.626249	575.316762	10
35	**4115.933363**	2058.470320	4098.906814	2049.957045	4097.922798	2049.465037	S	***1039.578236***	520.292756	1022.551687	511.779481	1021.567671	511.287473	9
36	4212.986127	2106.996702	4195.959578	2098.483427	4194.975562	2097.991419	P	***952.546208***	476.776742	935.519659	468.263467	934.535643	467.771459	8
37	4328.013070	2164.510173	4310.986521	2155.996899	4310.002505	2155.504891	D	***855.493444***	428.250360	838.466895	419.737085	837.482879	419.245077	7
38	4441.097134	2221.052205	4424.070585	2212.538930	4423.086569	2212.046923	L	***740.466501***	370.736888	723.439952	362.223614	722.455936	361.731606	6
39	4570.139727	2285.573502	4553.113178	2277.060227	4552.129162	2276.568219	E	***627.382437***	314.194856	610.355888	305.681582	609.371872	305.189574	5
40	4667.192491	2334.099884	4650.165942	2325.586609	4649.181926	2325.094601	P	***498.339844***	249.673560	481.313295	241.160285			4
41	4780.276555	2390.641915	4763.250006	2382.128641	4762.265990	2381.636633	I	401.287080	201.147178	384.260531	192.633903			3
42	4893.360619	2447.183947	4876.334070	2438.670673	4875.350054	2438.178665	L	288.203016	144.605146	271.176467	136.091871			2
43							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
110.2	5066.465057	0.072563	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
50.9	5066.465057	0.072563	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
33.1	5066.465057	0.072563	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
33.1	5066.465057	0.072563	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR

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

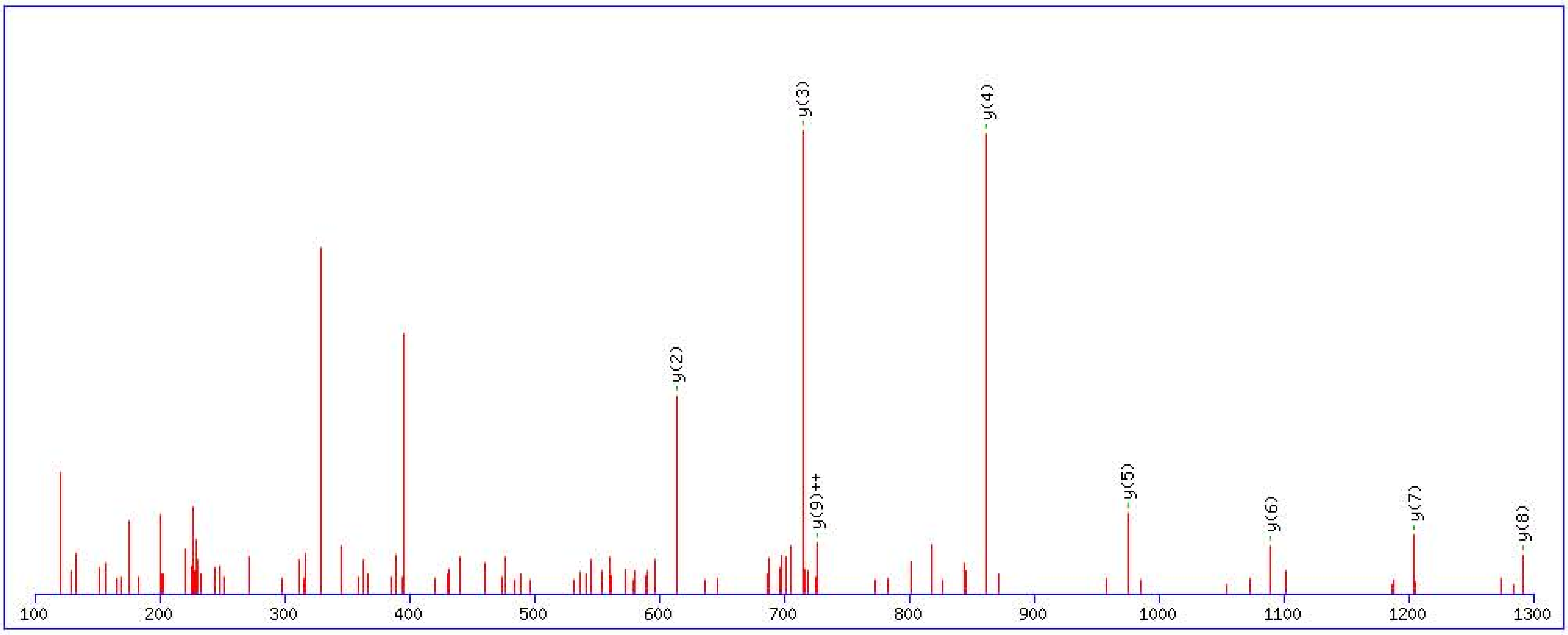
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VECSDNLFTQR**
Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

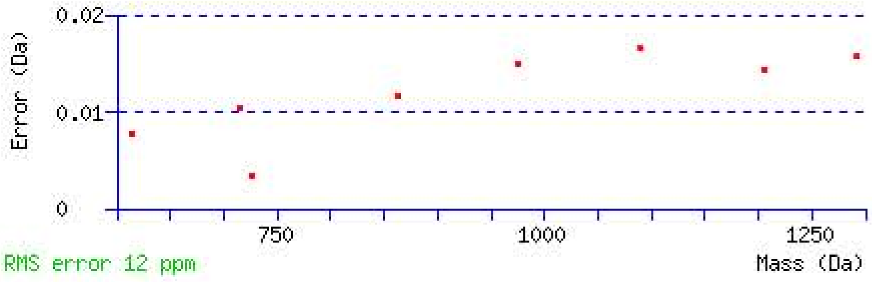
Match to Query 45320: 1678.791912 from(560.604580,3+) rtinseconds(2073) index(61068)
Title: Locus:1.1.1.3027.7 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

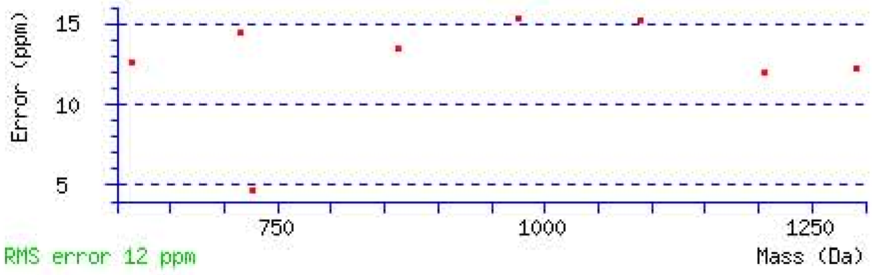
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1678.780716
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.0001
Matches : 8/104 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	100.075690	50.541483					V							11
2	229.118283	115.062780			211.107718	106.057497	E	1580.719575	790.863426	1563.693026	782.350151	1562.709010	781.858143	10
3	389.148932	195.078104			371.138367	186.072822	C	1451.676982	726.342129	1434.650433	717.828855	1433.666417	717.336847	9
4	476.180960	238.594118			458.170395	229.588835	S	***1291.646333***	646.326805	1274.619784	637.813530	1273.635768	637.321522	8
5	591.207903	296.107590			573.197338	287.102307	D	***1204.614305***	602.810791	1187.587756	594.297516	1186.603740	593.805508	7
6	705.250830	353.129053	688.224281	344.615778	687.240265	344.123770	N	***1089.587362***	545.297319	1072.560813	536.784045	1071.576797	536.292037	6
7	818.334894	409.671085	801.308345	401.157810	800.324329	400.665802	L	***975.544435***	488.275856	958.517886	479.762581	957.533870	479.270573	5
8	965.403308	483.205292	948.376759	474.692017	947.392743	474.200009	F	***862.460371***	431.733824	845.433822	423.220549	844.449806	422.728541	4
9	1066.450987	533.729131	1049.424438	525.215857	1048.440422	524.723849	T	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
10	1505.676313	753.341795	1488.649764	744.828520	1487.665748	744.336512	Q	***614.344278***	307.675777	597.317729	299.162503			2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.2	1678.780716	0.011196	VECSDNLFTQR
6.7	1678.769455	0.022457	VWDKEGEMEVAMQK

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

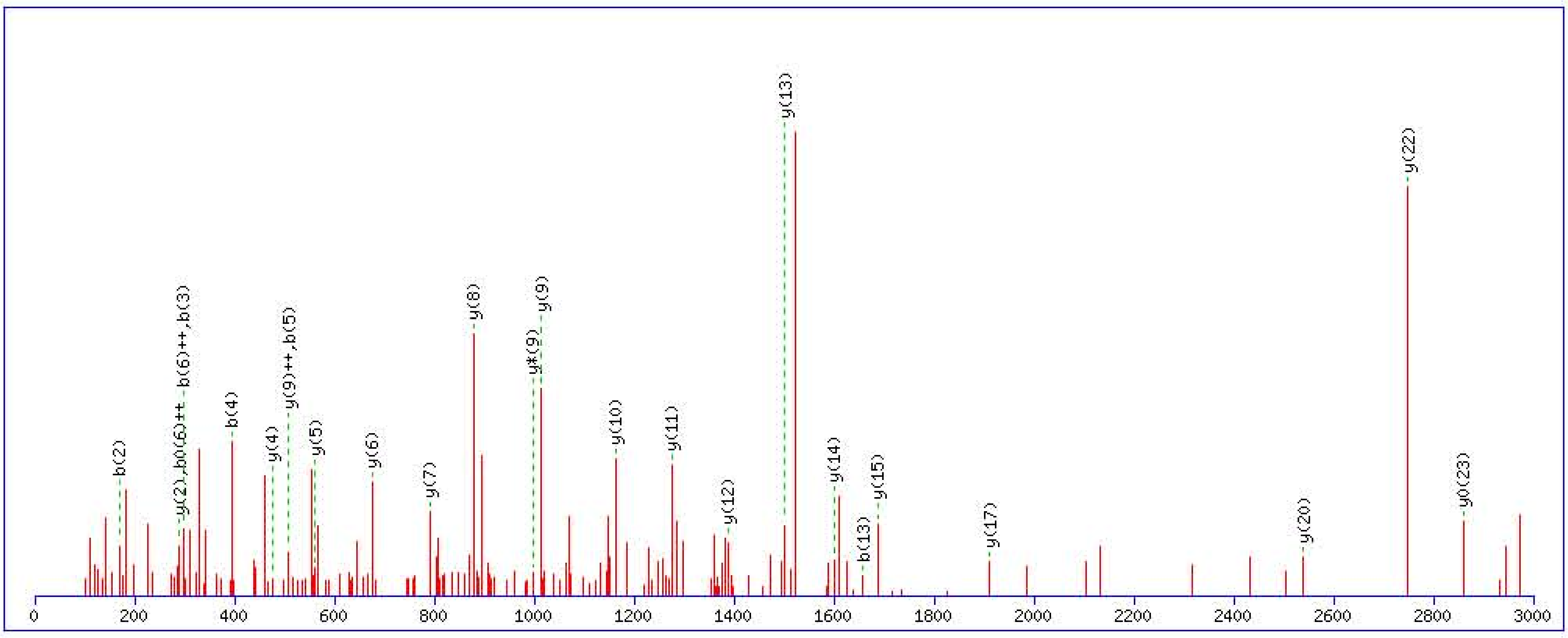
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APEPISTQSHSVLILFHSDNSGENR**
Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

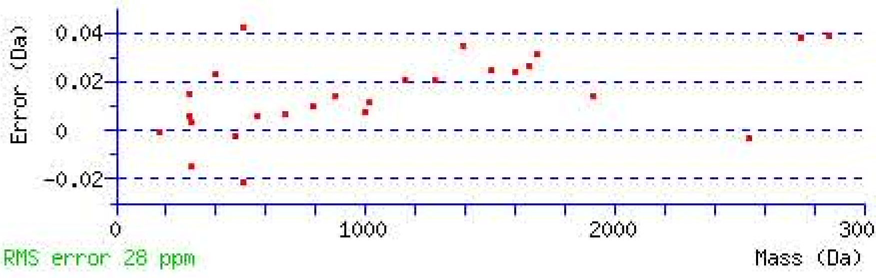
Match to Query 72046: 3045.534936 from(762.391010,4+) rtinseconds(2207) index(62019)
Title: Locus:1.1.1.3073.14 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

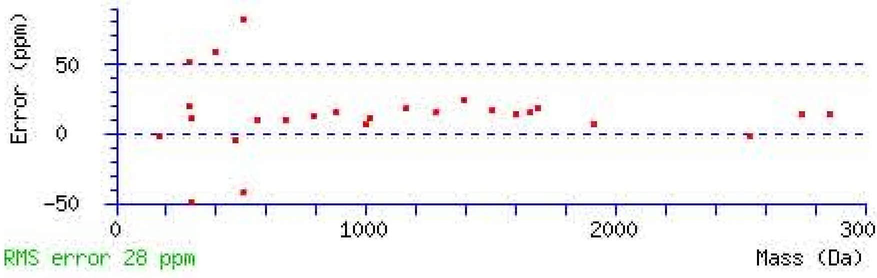
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3045.497803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 6.9e-005
Matches : 26/266 fragment ions using 82 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							25
2	**169.097154**	85.052215					P	2975.467980	1488.237628	2958.441431	1479.724353	2957.457415	1479.232345	24
3	**298.139747**	149.573512			280.129182	140.568229	E	2878.415216	1439.711246	2861.388667	1431.197971	2860.404651	1430.705963	23
4	**395.192511**	198.099894			377.181946	189.094611	P	***2749.372623***	1375.189949	2732.346074	1366.676675	2731.362058	1366.184667	22
5	**508.276575**	254.641926			490.266010	245.636643	I	2652.319859	1326.663567	2635.293310	1318.150293	2634.309294	1317.658285	21
6	595.308603	298.157940			577.298038	289.152657	S	***2539.235795***	1270.121535	2522.209246	1261.608261	2521.225230	1261.116253	20
7	696.356282	348.681779			678.345717	339.676497	T	2452.203767	1226.605521	2435.177218	1218.092247	2434.193202	1217.600239	19
8	1135.581608	568.294442	1118.555059	559.781168	1117.571043	559.289160	Q	2351.156088	1176.081682	2334.129539	1167.568407	2333.145523	1167.076399	18
9	1222.613636	611.810456	1205.587087	603.297182	1204.603071	602.805174	S	***1911.930762***	956.469019	1894.904213	947.955745	1893.920197	947.463737	17
10	1359.672548	680.339912	1342.645999	671.826638	1341.661983	671.334630	H	1824.898734	912.953005	1807.872185	904.439731	1806.888169	903.947723	16
11	1446.704576	723.855926	1429.678027	715.342652	1428.694011	714.850644	S	***1687.839822***	844.423549	1670.813273	835.910275	1669.829257	835.418267	15
12	1545.772990	773.390133	1528.746441	764.876859	1527.762425	764.384851	V	***1600.807794***	800.907535	1583.781245	792.394261	1582.797229	791.902253	14
13	**1658.857054**	829.932165	1641.830505	821.418891	1640.846489	820.926883	L	***1501.739380***	751.373328	1484.712831	742.860054	1483.728815	742.368045	13
14	1771.941118	886.474197	1754.914569	877.960923	1753.930553	877.468915	I	***1388.655316***	694.831296	1371.628767	686.318022	1370.644751	685.826014	12
15	1885.025182	943.016229	1867.998633	934.502955	1867.014617	934.010947	L	***1275.571252***	638.289264	1258.544703	629.775990	1257.560687	629.283982	11
16	2032.093596	1016.550436	2015.067047	1008.037162	2014.083031	1007.545154	F	***1162.487188***	581.747232	1145.460639	573.233958	1144.476623	572.741950	10
17	2169.152508	1085.079892	2152.125959	1076.566617	2151.141943	1076.074610	H	***1015.418774***	508.213025	998.392225	499.699751	997.408209	499.207743	9
18	2256.184536	1128.595906	2239.157987	1120.082631	2238.173971	1119.590624	S	***878.359862***	439.683569	861.333313	431.170295	860.349297	430.678287	8
19	2371.211479	1186.109377	2354.184930	1177.596103	2353.200914	1177.104095	D	***791.327834***	396.167555	774.301285	387.654280	773.317269	387.162272	7
20	2485.254406	1243.130841	2468.227857	1234.617566	2467.243841	1234.125558	N	***676.300891***	338.654084	659.274342	330.140809	658.290326	329.648801	6
21	2572.286434	1286.646855	2555.259885	1278.133580	2554.275869	1277.641572	S	***562.257964***	281.632620	545.231415	273.119346	544.247399	272.627338	5
22	2629.307898	1315.157587	2612.281349	1306.644312	2611.297333	1306.152304	G	***475.225936***	238.116606	458.199387	229.603331	457.215371	229.111323	4
23	2758.350491	1379.678884	2741.323942	1371.165609	2740.339926	1370.673601	E	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
24	2872.393418	1436.700347	2855.366869	1428.187072	2854.382853	1427.695064	N	***289.161879***	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.9	3045.497803	0.037133	APEPISTQSHSVLILFHSDNSGENR

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

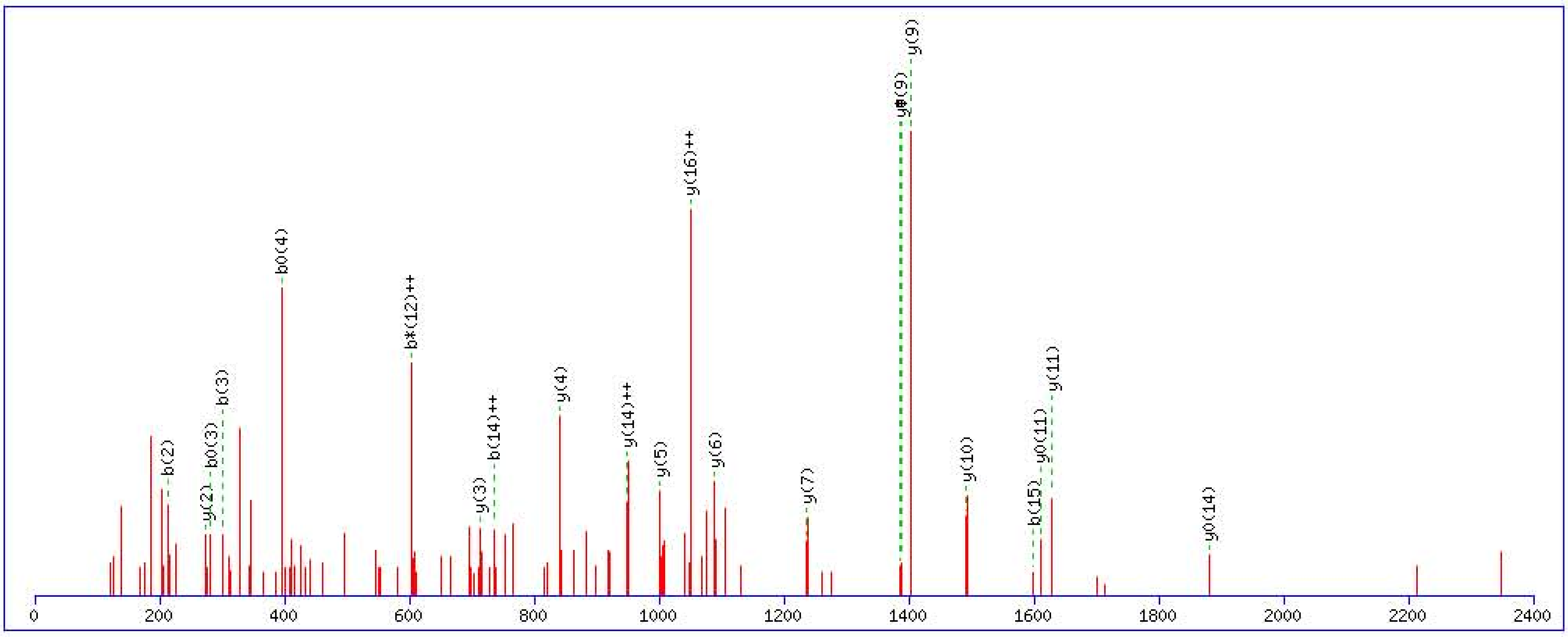
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSIAQAHSPAFSCEQVR**
Found in **CD14_HUMAN**, Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2

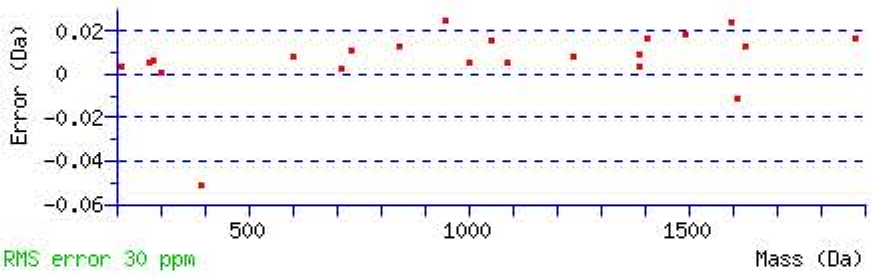
Match to Query 60893: 2310.172512 from(771.064780,3+) rtinseconds(1958) index(41882)
Title: Locus:1.1.1.2965.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

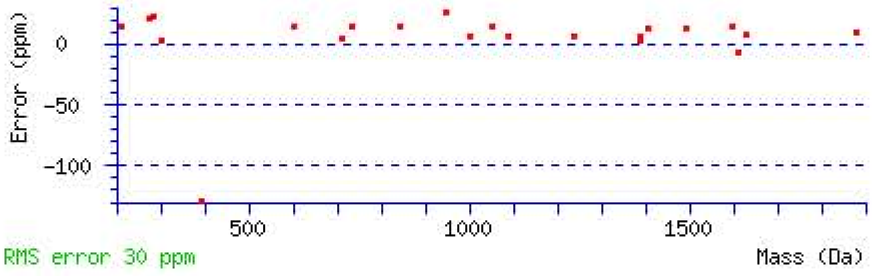
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2310.161285
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0051
Matches : 22/184 fragment ions using 46 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							18
2	**213.159754**	107.083515					L	2212.100156	1106.553716	2195.073607	1098.040441	2194.089591	1097.548433	17
3	**300.191782**	150.599529			282.181217	141.594247	S	2099.016092	1050.011684	2081.989543	1041.498409	2081.005527	1041.006401	16
4	413.275846	207.141561			395.265281	198.136279	I	2011.984064	1006.495670	1994.957515	997.982396	1993.973499	997.490388	15
5	484.312960	242.660118			466.302395	233.654836	A	1898.900000	949.953638	1881.873451	941.440364	1880.889435	940.948356	14
6	612.371538	306.689407	595.344989	298.176133	594.360973	297.684125	Q	1827.862886	914.435081	1810.836337	905.921807	1809.852321	905.429799	13
7	683.408652	342.207964	666.382103	333.694690	665.398087	333.202682	A	1699.804308	850.405792	1682.777759	841.892518	1681.793743	841.400510	12
8	820.467564	410.737420	803.441015	402.224146	802.456999	401.732138	H	***1628.767194***	814.887235	1611.740645	806.373961	1610.756629	805.881953	11
9	907.499592	454.253434	890.473043	445.740160	889.489027	445.248152	S	***1491.708282***	746.357779	1474.681733	737.844505	1473.697717	737.352497	10
10	1004.552356	502.779816	987.525807	494.266542	986.541791	493.774534	P	***1404.676254***	702.841765	1387.649705	694.328491	1386.665689	693.836483	9
11	1075.589470	538.298373	1058.562921	529.785099	1057.578905	529.293091	A	1307.623490	654.315383	1290.596941	645.802109	1289.612925	645.310101	8
12	1222.657884	611.832580	1205.631335	603.319306	1204.647319	602.827298	F	***1236.586376***	618.796826	1219.559827	610.283552	1218.575811	609.791544	7
13	1309.689912	655.348594	1292.663363	646.835320	1291.679347	646.343312	S	***1089.517962***	545.262619	1072.491413	536.749345	1071.507397	536.257337	6
14	1469.720561	735.363919	1452.694012	726.850644	1451.709996	726.358636	C	***1002.485934***	501.746605	985.459385	493.233331	984.475369	492.741323	5
15	**1598.763154**	799.885215	1581.736605	791.371941	1580.752589	790.879933	E	***842.455285***	421.731281	825.428736	413.218006	824.444720	412.725998	4
16	2037.988480	1019.497878	2020.961931	1010.984604	2019.977915	1010.492596	Q	***713.412692***	357.209984	696.386143	348.696710			3
17	2137.056894	1069.032085	2120.030345	1060.518811	2119.046329	1060.026803	V	***274.187366***	137.597321	257.160817	129.084046			2
18							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	2310.161285	0.011227	VLSIAQAHSPAFSCEQVR

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

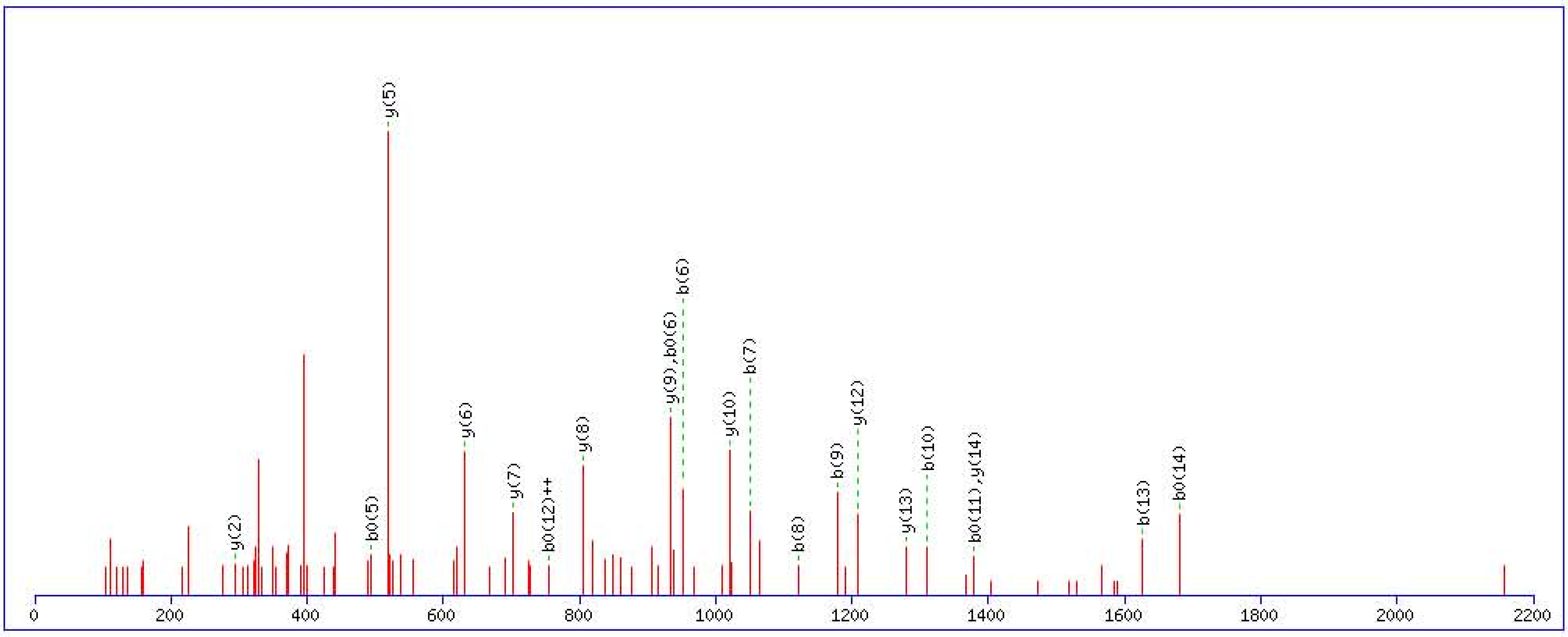
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIGLDQVAGMSETALPGAFK**
Found in **MYH9_HUMAN**, Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4

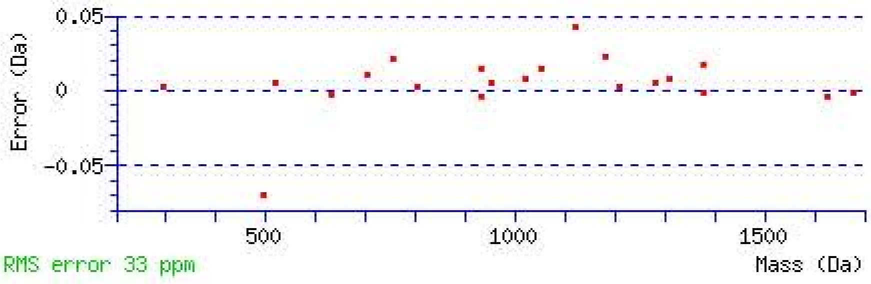
Match to Query 61307: 2328.250902 from(777.090910,3+) rtinseconds(2830) index(66390)
Title: Locus:1.1.1.3288.15 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

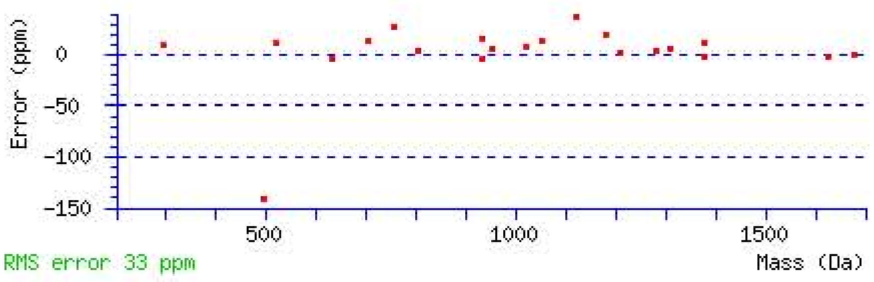
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2328.222153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 61 **Expect:** 1.7e-005
Matches : 21/196 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	114.091340	57.549308					I							20
2	227.175404	114.091340					I	2216.145376	1108.576326	2199.118827	1100.063051	2198.134811	1099.571043	19
3	284.196868	142.602072					G	2103.061312	1052.034294	2086.034763	1043.521019	2085.050747	1043.029011	18
4	397.280932	199.144104					L	2046.039848	1023.523562	2029.013299	1015.010288	2028.029283	1014.518279	17
5	512.307875	256.657576			494.297310	247.652293	D	1932.955784	966.981530	1915.929235	958.468255	1914.945219	957.976247	16
6	**951.533201**	476.270239	934.506652	467.756964	933.522636	467.264956	Q	1817.928841	909.468058	1800.902292	900.954784	1799.918276	900.462776	15
7	**1050.601615**	525.804446	1033.575066	517.291171	1032.591050	516.799163	V	***1378.703515***	689.855395	1361.676966	681.342121	1360.692950	680.850113	14
8	**1121.638729**	561.323003	1104.612180	552.809728	1103.628164	552.317720	A	***1279.635101***	640.321188	1262.608552	631.807914	1261.624536	631.315906	13
9	**1178.660193**	589.833734	1161.633644	581.320460	1160.649628	580.828452	G	***1208.597987***	604.802631	1191.571438	596.289357	1190.587422	595.797349	12
10	**1309.700678**	655.353977	1292.674129	646.840703	1291.690113	646.348694	M	1151.576523	576.291900	1134.549974	567.778625	1133.565958	567.286617	11
11	1396.732706	698.869991	1379.706157	690.356717	1378.722141	689.864709	S	***1020.536038***	510.771657	1003.509489	502.258382	1002.525473	501.766374	10
12	1525.775299	763.391288	1508.748750	754.878013	1507.764734	754.386005	E	***933.504010***	467.255643	916.477461	458.742368	915.493445	458.250360	9
13	**1626.822978**	813.915127	1609.796429	805.401853	1608.812413	804.909845	T	***804.461417***	402.734346	787.434868	394.221072	786.450852	393.729064	8
14	1697.860092	849.433684	1680.833543	840.920410	1679.849527	840.428402	A	***703.413738***	352.210507	686.387189	343.697232			7
15	1810.944156	905.975716	1793.917607	897.462442	1792.933591	896.970434	L	***632.376624***	316.691950	615.350075	308.178675			6
16	1907.996920	954.502098	1890.970371	945.988824	1889.986355	945.496816	P	***519.292560***	260.149918	502.266011	251.636643			5
17	1965.018384	983.012830	1947.991835	974.499556	1947.007819	974.007547	G	422.239796	211.623536	405.213247	203.110261			4
18	2036.055498	1018.531387	2019.028949	1010.018113	2018.044933	1009.526105	A	365.218332	183.112804	348.191783	174.599529			3
19	2183.123912	1092.065594	2166.097363	1083.552319	2165.113347	1083.060311	F	***294.181218***	147.594247	277.154669	139.080972			2
20							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.7	2328.222153	0.028749	IIGLDQVAGMSETALPGAFK

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

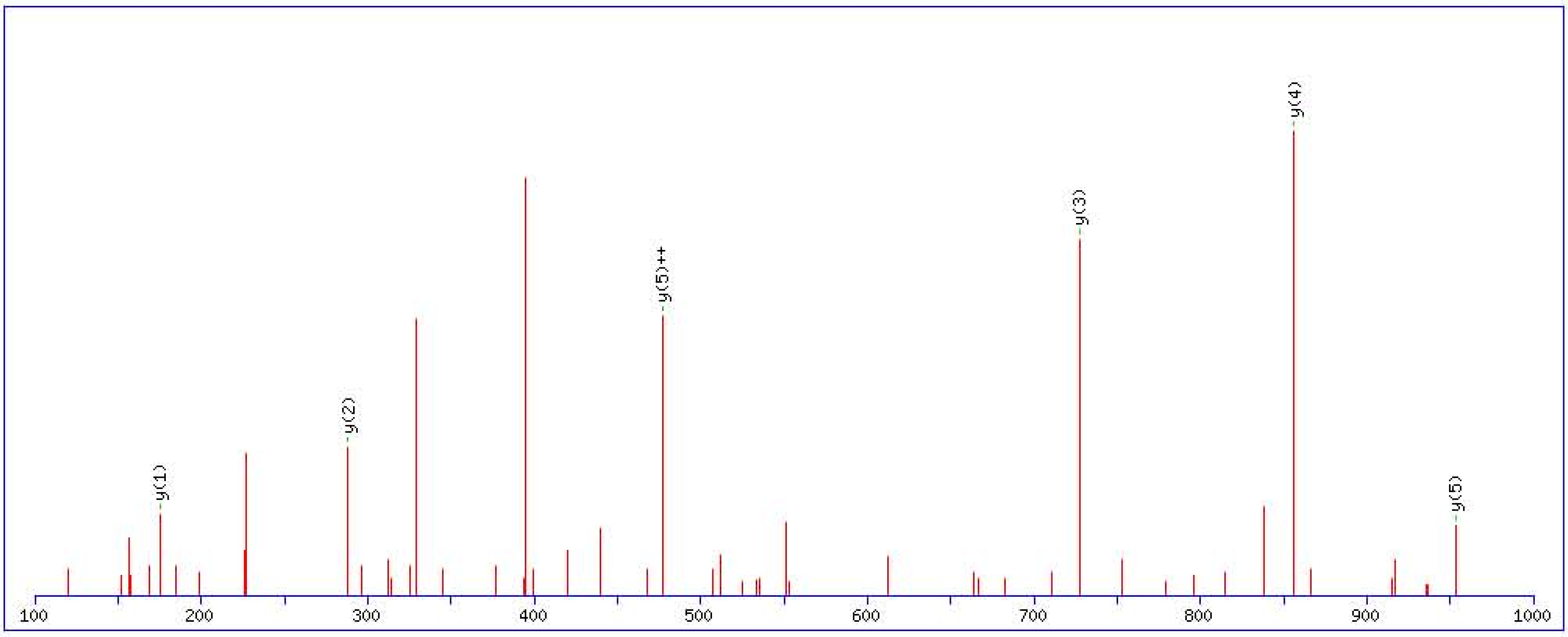
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPEQLR**
Found in **GNPTG_HUMAN**, N-acetylglucosamine-1-phosphotransferase subunit gamma OS=Homo sapiens GN=GNPTG PE=1 SV=1

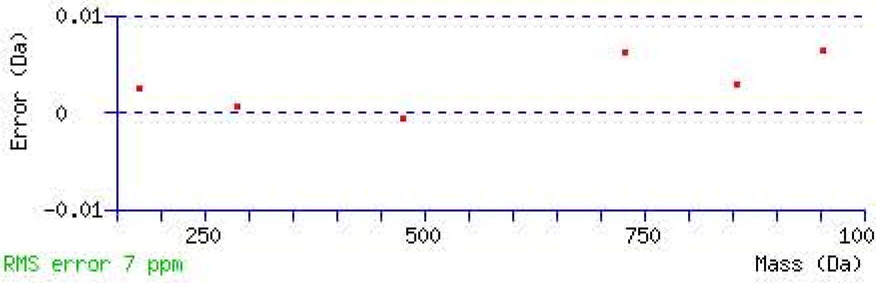
Match to Query 20638: 1039.548488 from(520.781520,2+) rtinseconds(1450) index(38519)
Title: Locus:1.1.1.2788.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

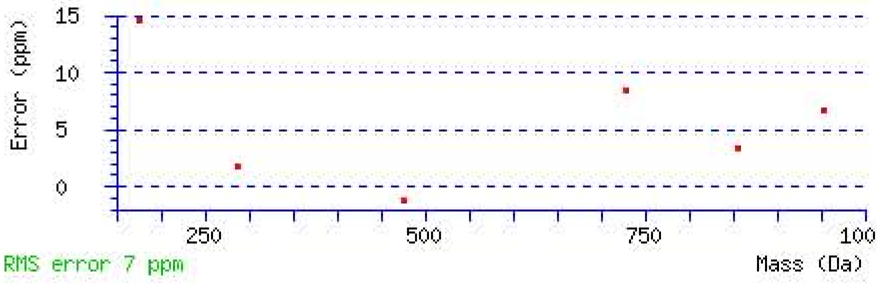
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1039.548431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0029
Matches : 6/48 fragment ions using 9 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							6
2	185.092068	93.049672			167.081503	84.044389	P	***953.523699***	477.265488	936.497150	468.752213	935.513134	468.260205	5
3	314.134661	157.570968			296.124096	148.565686	E	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
4	753.359987	377.183632	736.333438	368.670357	735.349422	368.178349	Q	***727.428342***	364.217809	710.401793	355.704535			3
5	866.444051	433.725664	849.417502	425.212389	848.433486	424.720381	L	***288.203016***	144.605146	271.176467	136.091872			2
6							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.1	1039.548431	0.000057	SPEQLR
23.4	1039.548431	0.000057	SPEIQR
19.8	1039.541031	0.007457	ALESNHTLR
17.6	1039.563492	-0.015004	SSLERHRR
7.3	1039.533813	0.014675	EALFYELR
6.6	1039.563492	-0.015004	SSHLRERR
5.4	1039.559662	-0.011174	SVILNHMAR
4.7	1039.541061	0.007427	SSRVTFSTR
2.7	1039.541046	0.007442	ALQSGPPQSR
2.5	1039.541061	0.007427	SPRTTVHDK

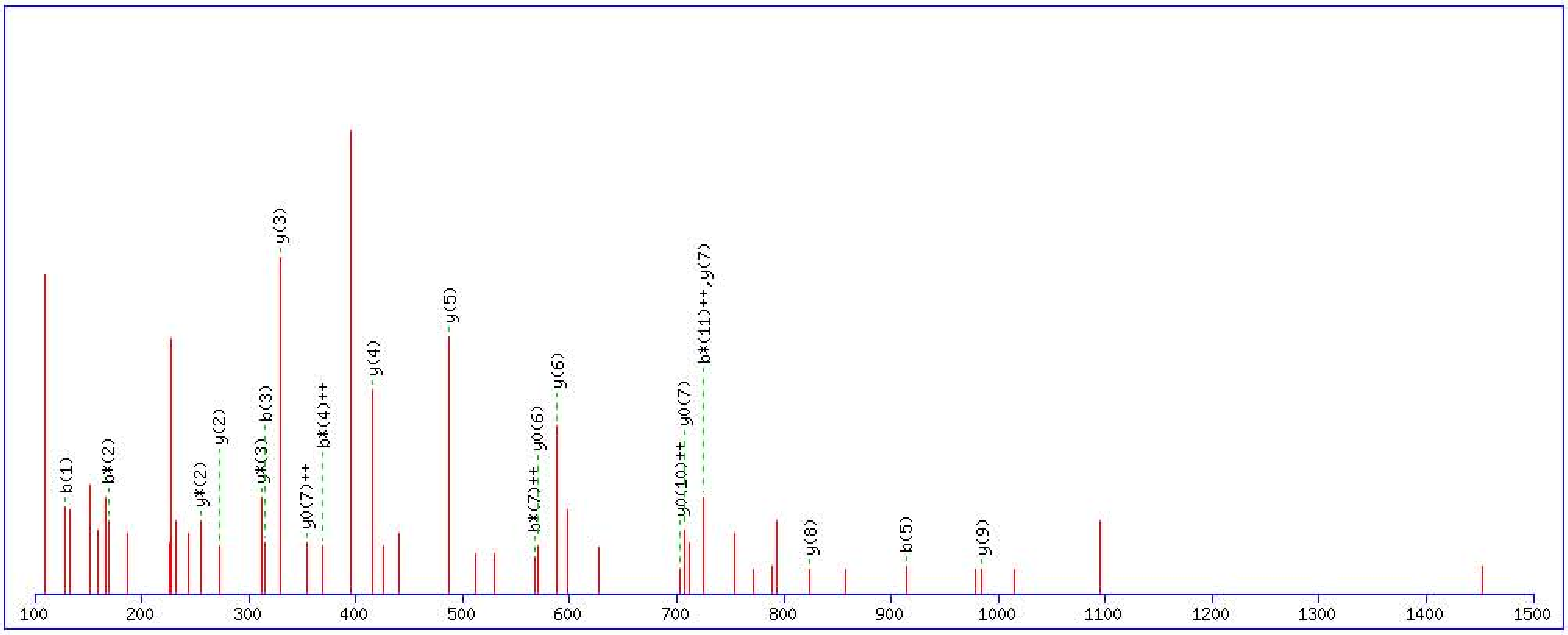
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGEQCVHTASGPR**
Found in **NOTC2_HUMAN**, Neurogenic locus notch homolog protein 2 OS=Homo sapiens GN=NOTCH2 PE=1 SV=3

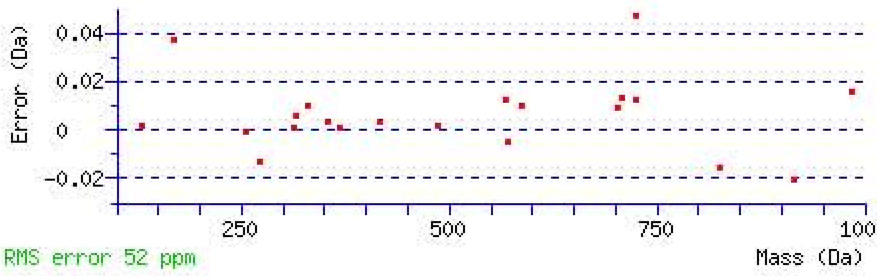
Match to Query 46699: 1736.839376 from(435.217120,4+) rtinseconds(1067) index(36004)
Title: Locus:1.1.1.2655.7 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

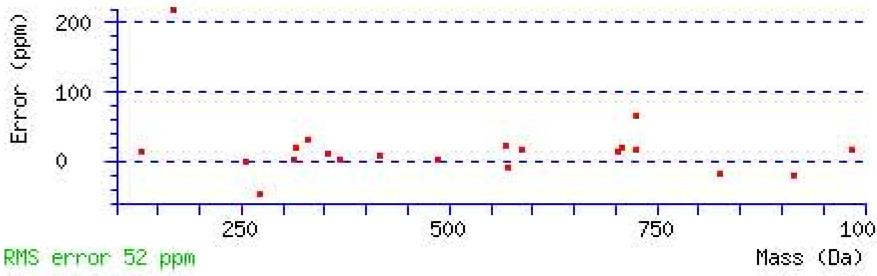
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1736.845047
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0059
Matches : 21/134 fragment ions using 45 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**129.102239**	65.054757	112.075690	56.541483			K							13
2	186.123703	93.565489	169.097154	85.052215			G	1609.757359	805.382318	1592.730810	796.869043	1591.746794	796.377035	12
3	**315.166296**	158.086786	298.139747	149.573512	297.155731	149.081504	E	1552.735895	776.871586	1535.709346	768.358311	1534.725330	767.866303	11
4	754.391622	377.699449	737.365073	369.186175	736.381057	368.694167	Q	1423.693302	712.350289	1406.666753	703.837015	1405.682737	703.345007	10
5	**914.422271**	457.714774	897.395722	449.201499	896.411706	448.709491	C	***984.467976***	492.737626	967.441427	484.224352	966.457411	483.732344	9
6	1013.490685	507.248981	996.464136	498.735706	995.480120	498.243698	V	***824.437327***	412.722302	807.410778	404.209027	806.426762	403.717019	8
7	1150.549597	575.778437	1133.523048	567.265162	1132.539032	566.773154	H	***725.368913***	363.188095	708.342364	354.674820	707.358348	354.182812	7
8	1251.597276	626.302276	1234.570727	617.789002	1233.586711	617.296994	T	***588.310001***	294.658639	571.283452	286.145364	570.299436	285.653356	6
9	1322.634390	661.820833	1305.607841	653.307559	1304.623825	652.815551	A	***487.262322***	244.134799	470.235773	235.621524	469.251757	235.129516	5
10	1409.666418	705.336847	1392.639869	696.823573	1391.655853	696.331565	S	***416.225208***	208.616242	399.198659	200.102967	398.214643	199.610959	4
11	1466.687882	733.847579	1449.661333	725.334305	1448.677317	724.842297	G	***329.193180***	165.100228	312.166631	156.586953			3
12	1563.740646	782.373961	1546.714097	773.860687	1545.730081	773.368679	P	***272.171716***	136.589496	255.145167	128.076221			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.9	1736.845047	-0.005671	KGEQCVHTASGPR

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

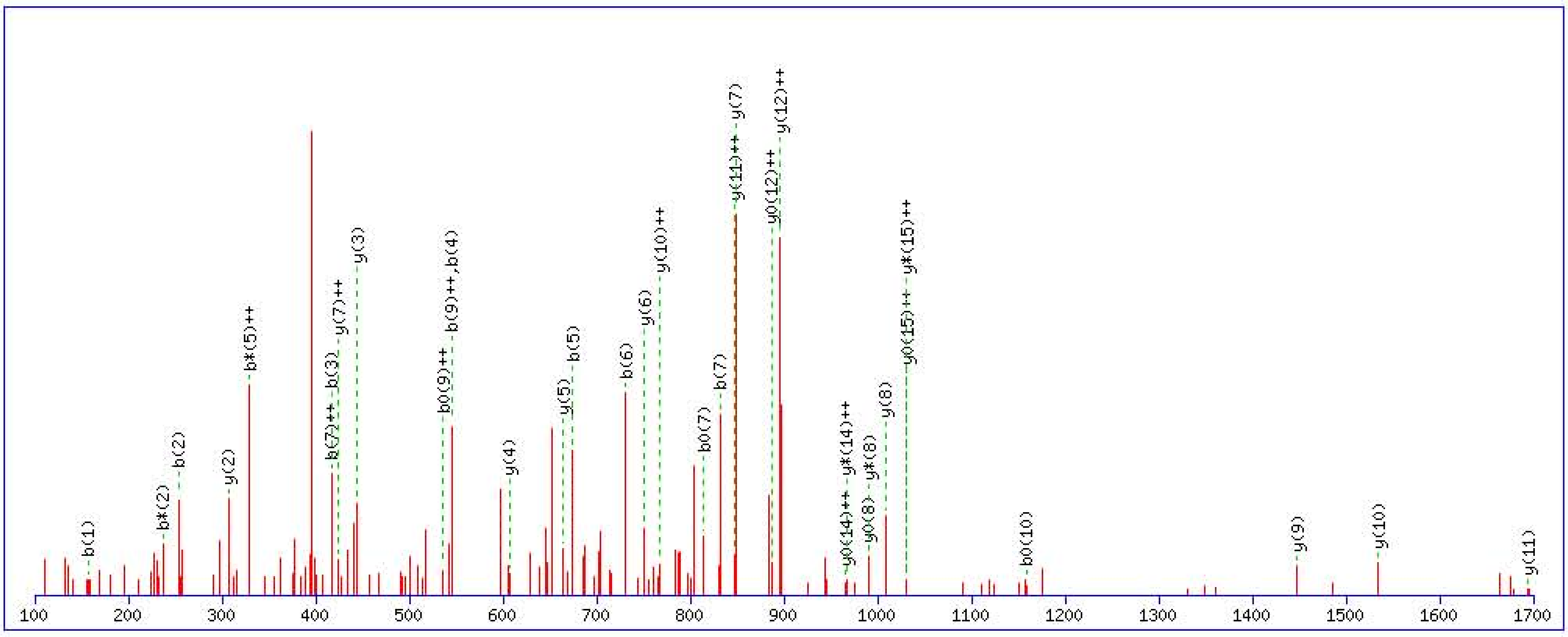
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPYQEGTPCSQCPSGYHCK**
Found in **PI16_HUMAN**, Peptidase inhibitor 16 OS=Homo sapiens GN=PI16 PE=1 SV=1

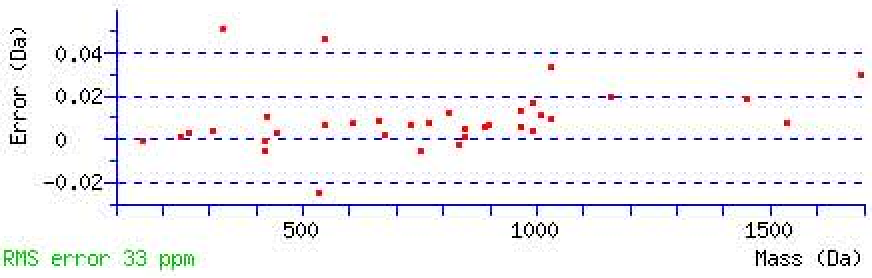
Match to Query 66782: 2622.140176 from(656.542320,4+) rtinseconds(1292) index(37366)
Title: Locus:1.1.1.2733.13 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

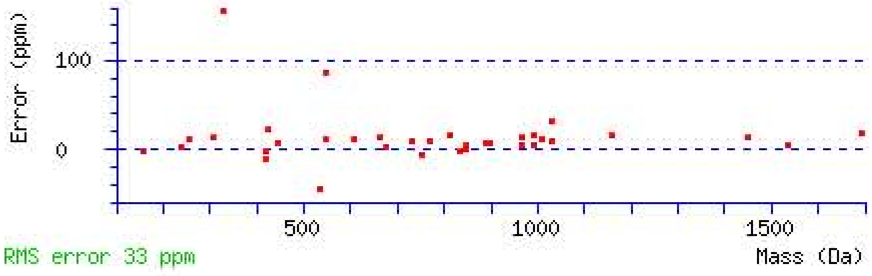


```
Monoisotopic mass of neutral peptide Mr(calc): 2622.123611
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0006
Matches : 35/198 fragment ions using 93 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	***157.108387***	79.057831	140.081838	70.544557			R							19
2	***254.161151***	127.584213	237.134602	119.070939			P	2467.029773	1234.018524	2450.003224	1225.505250	2449.019208	1225.013242	18
3	***417.224480***	209.115878	400.197931	200.602604			Y	2369.977009	1185.492142	2352.950460	1176.978868	2351.966444	1176.486860	17
4	***545.283058***	273.145167	528.256509	264.631893			Q	2206.913680	1103.960478	2189.887131	1095.447203	2188.903115	1094.955195	16
5	***674.325651***	337.666464	657.299102	329.153189	656.315086	328.661181	E	2078.855102	1039.931189	2061.828553	1031.417914	2060.844537	1030.925906	15
6	***731.347115***	366.177196	714.320566	357.663921	713.336550	357.171913	G	1949.812509	975.409892	1932.785960	966.896618	1931.801944	966.404610	14
7	***832.394794***	**416.701035**	815.368245	408.187761	814.384229	407.695753	T	1892.791045	946.899160	1875.764496	938.385886	1874.780480	937.893878	13
8	929.447558	465.227417	912.421009	456.714143	911.436993	456.222135	P	1791.743366	896.375321	1774.716817	887.862047	1773.732801	887.370038	12
9	1089.478207	**545.242742**	1072.451658	536.729467	1071.467642	536.237459	C	***1694.690602***	847.848939	1677.664053	839.335665	1676.680037	838.843656	11
10	1176.510235	588.758756	1159.483686	580.245481	1158.499670	579.753473	S	***1534.659953***	767.833614	1517.633404	759.320340	1516.649388	758.828332	10
11	1615.735561	808.371419	1598.709012	799.858144	1597.724996	799.366136	Q	***1447.627925***	724.317600	1430.601376	715.804326	1429.617360	715.312318	9
12	1775.766210	888.386743	1758.739661	879.873469	1757.755645	879.381461	C	***1008.402599***	504.704937	991.376050	496.191663	990.392034	495.699655	8
13	1872.818974	936.913125	1855.792425	928.399851	1854.808409	927.907843	P	***848.371950***	424.689613	831.345401	416.176338	830.361385	415.684330	7
14	1959.851002	980.429139	1942.824453	971.915865	1941.840437	971.423857	S	***751.319186***	376.163231	734.292637	367.649956	733.308621	367.157948	6
15	2016.872466	1008.939871	1999.845917	1000.426597	1998.861901	999.934589	G	***664.287158***	332.647217	647.260609	324.133942			5
16	2179.935795	1090.471535	2162.909246	1081.958261	2161.925230	1081.466253	Y	***607.265694***	304.136485	590.239145	295.623210			4
17	2316.994707	1159.000991	2299.968158	1150.487717	2298.984142	1149.995709	H	***444.202365***	222.604820	427.175816	214.091546			3
18	2477.025356	1239.016316	2459.998807	1230.503041	2459.014791	1230.011033	C	***307.143453***	154.075364	290.116904	145.562090			2
19							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 33 ppm



RMS error 33 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.1	2622.123611	0.016565	RPYQEGTPCSQCPSGYHCK

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

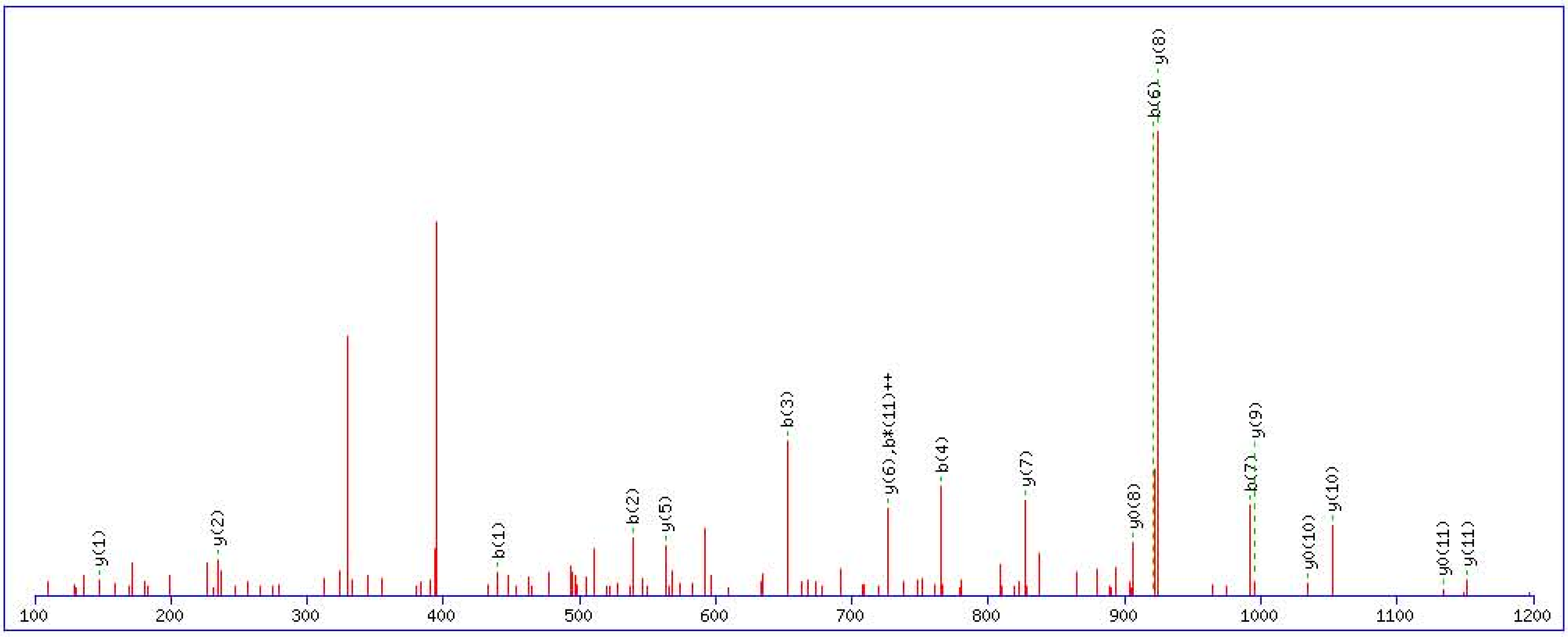
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVLLVGAPTYDDVSK**
Found in **PHLD_HUMAN**, Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

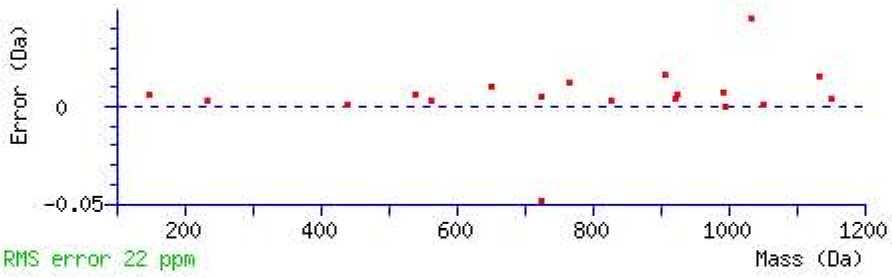
Match to Query 50952: 1915.026222 from(639.349350,3+) rtinseconds(2283) index(43958)
Title: Locus:1.1.1.3079.5 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

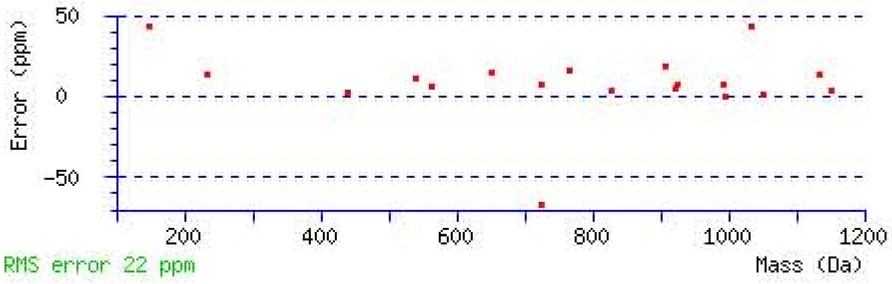
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1915.012497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 9e-005
Matches : 19/150 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***440.232602***	220.619939	423.206053	212.106664			Q							15
2	***539.301016***	270.154146	522.274467	261.640872			V	1476.794438	738.900857	1459.767889	730.387583	1458.783873	729.895575	14
3	***652.385080***	326.696178	635.358531	318.182904			L	1377.726024	689.366650	1360.699475	680.853376	1359.715459	680.361368	13
4	***765.469144***	383.238210	748.442595	374.724936			L	1264.641960	632.824618	1247.615411	624.311344	1246.631395	623.819336	12
5	864.537558	432.772417	847.511009	424.259143			V	***1151.557896***	576.282586	1134.531347	567.769312	1133.547331	567.277304	11
6	***921.559022***	461.283149	904.532473	452.769875			G	***1052.489482***	526.748379	1035.462933	518.235105	1034.478917	517.743097	10
7	***992.596136***	496.801706	975.569587	488.288432			A	***995.468018***	498.237647	978.441469	489.724373	977.457453	489.232365	9
8	1089.648900	545.328088	1072.622351	536.814814			P	***924.430904***	462.719090	907.404355	454.205816	906.420339	453.713808	8
9	1190.696579	595.851927	1173.670030	587.338653	1172.686014	586.846645	T	***827.378140***	414.192708	810.351591	405.679434	809.367575	405.187426	7
10	1353.759908	677.383592	1336.733359	668.870318	1335.749343	668.378310	Y	***726.330461***	363.668869	709.303912	355.155594	708.319896	354.663586	6
11	1468.786851	734.897064	1451.760302	726.383789	1450.776286	725.891781	D	***563.267132***	282.137204	546.240583	273.623930	545.256567	273.131922	5
12	1583.813794	792.410535	1566.787245	783.897261	1565.803229	783.405253	D	448.240189	224.623733	431.213640	216.110458	430.229624	215.618450	4
13	1682.882208	841.944742	1665.855659	833.431468	1664.871643	832.939460	V	333.213246	167.110261	316.186697	158.596987	315.202681	158.104979	3
14	1769.914236	885.460756	1752.887687	876.947482	1751.903671	876.455474	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
15							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.6	1915.012497	0.013725	QVLLVGAPTYDDVSK
1.4	1915.038925	-0.012703	CYALFLNLINKYQKK

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

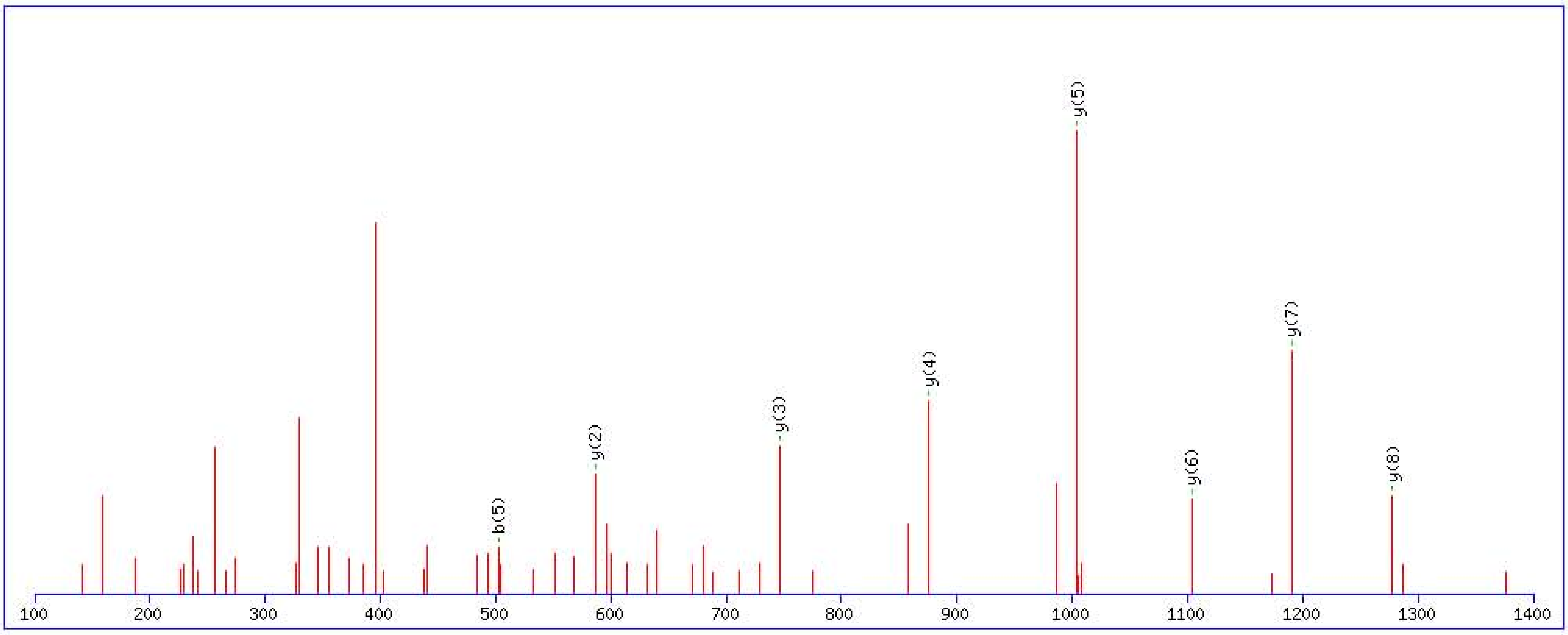
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSVEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

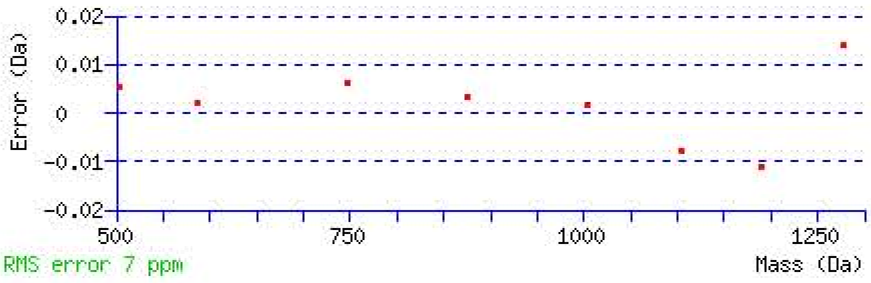
Match to Query 33692: 1375.650668 from(688.832610,2+) rtinseconds(1358) index(37850)
Title: Locus:1.1.1.2756.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

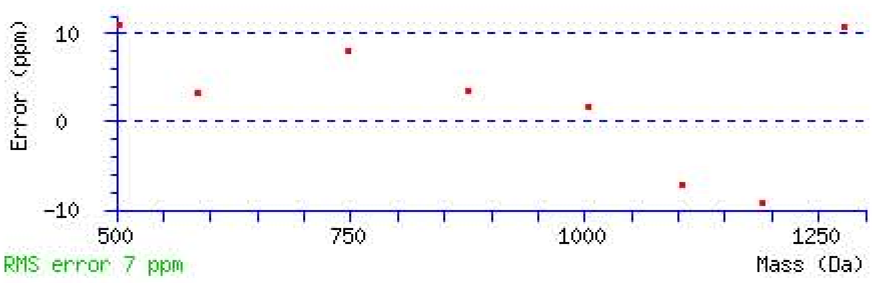
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1375.647568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 57 **Expect:** 1.9e-005
Matches : 8/74 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							9
2	187.107718	94.057497			169.097153	85.052214	S	***1277.586435***	639.296856	1260.559886	630.783581	1259.575870	630.291573	8
3	274.139746	137.573511			256.129181	128.568229	S	***1190.554407***	595.780842	1173.527858	587.267567	1172.543842	586.775559	7
4	373.208160	187.107718			355.197595	178.102436	V	***1103.522379***	552.264828	1086.495830	543.751553	1085.511814	543.259545	6
5	**502.250753**	251.629015			484.240188	242.623732	E	***1004.453965***	502.730621	987.427416	494.217346	986.443400	493.725338	5
6	631.293346	316.150311			613.282781	307.145029	E	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
7	791.323995	396.165636			773.313430	387.160353	C	***746.368779***	373.688028	729.342230	365.174753			3
8	1230.549321	615.778299	1213.522772	607.265024	1212.538756	606.773016	Q	***586.338130***	293.672703	569.311581	285.159429			2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.2	1375.647568	0.003100	VSSVEECQK
6.8	1375.662827	-0.012159	GFSIPECQK

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

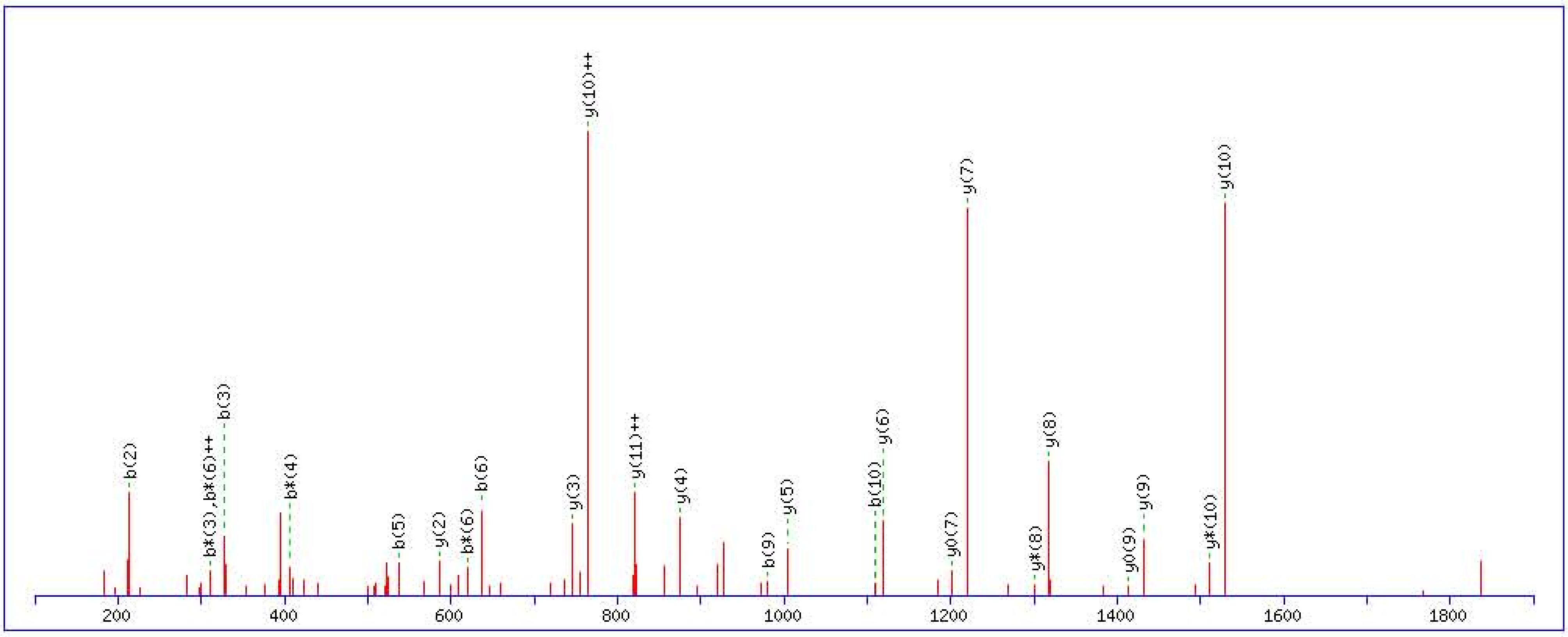
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNIPLVTNEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

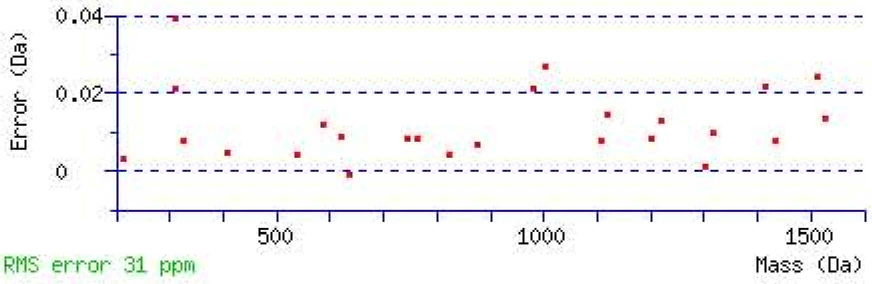
Match to Query 49763: 1853.959328 from(927.986940,2+) rtinseconds(2138) index(79453)
Title: Locus:1.1.1.2958.25 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

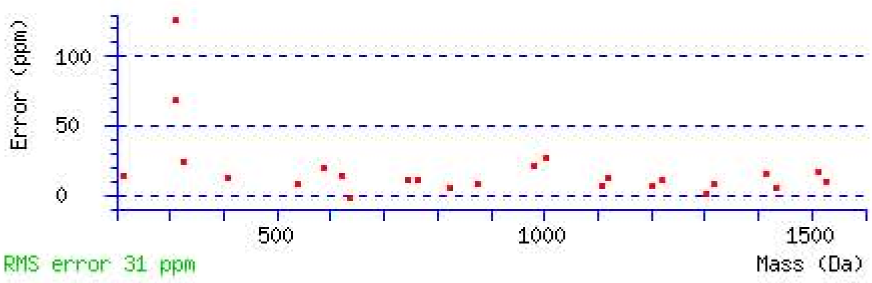
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1853.937927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 8.4e-006
Matches : 25/124 fragment ions using 42 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							13
2	**214.118617**	107.562947	197.092068	99.049672			N	1755.876804	878.442040	1738.850255	869.928766	1737.866239	869.436758	12
3	**327.202681**	164.104978	310.176132	155.591704			I	1641.833877	821.420577	1624.807328	812.907302	1623.823312	812.415294	11
4	424.255445	212.631360	407.228896	204.118086			P	***1528.749813***	764.878545	1511.723264	756.365270	1510.739248	755.873262	10
5	**537.339509**	269.173393	520.312960	260.660118			L	***1431.697049***	716.352163	1414.670500	707.838888	1413.686484	707.346880	9
6	**636.407923**	318.707600	619.381374	310.194325			V	***1318.612985***	659.810131	1301.586436	651.296856	1300.602420	650.804848	8
7	737.455602	369.231439	720.429053	360.718165	719.445037	360.226157	T	***1219.544571***	610.275924	1202.518022	601.762649	1201.534006	601.270641	7
8	851.498529	426.252903	834.471980	417.739628	833.487964	417.247620	N	***1118.496892***	559.752084	1101.470343	551.238810	1100.486327	550.746802	6
9	**980.541122**	490.774199	963.514573	482.260924	962.530557	481.768916	E	***1004.453965***	502.730621	987.427416	494.217346	986.443400	493.725338	5
10	**1109.583715**	555.295496	1092.557166	546.782221	1091.573150	546.290213	E	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
11	1269.614364	635.310820	1252.587815	626.797546	1251.603799	626.305538	C	***746.368779***	373.688028	729.342230	365.174753			3
12	1708.839690	854.923483	1691.813141	846.410209	1690.829125	845.918201	Q	***586.338130***	293.672703	569.311581	285.159429			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.9	1853.937927	0.021401	VNIPLVTNEECQK
1.8	1853.934341	0.024987	RGLSNPNELQAAIDSNR

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

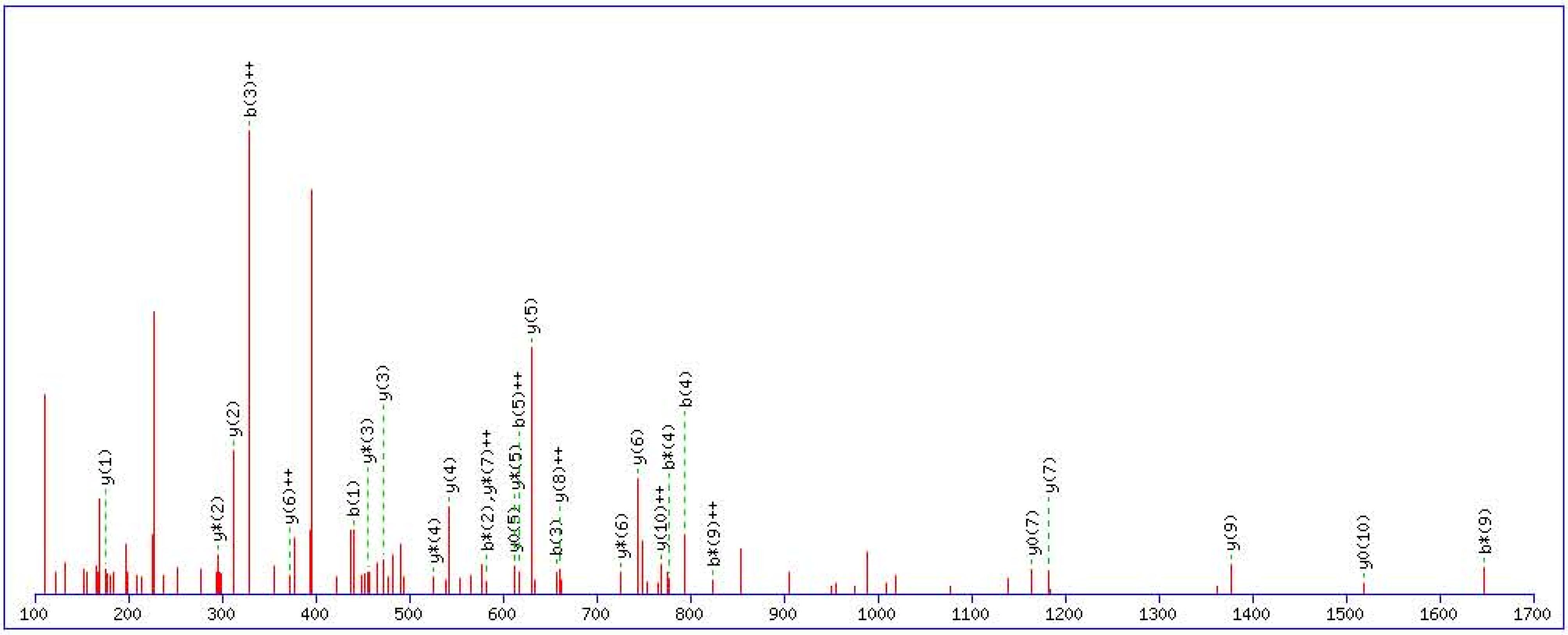
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QCGHQISACHR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

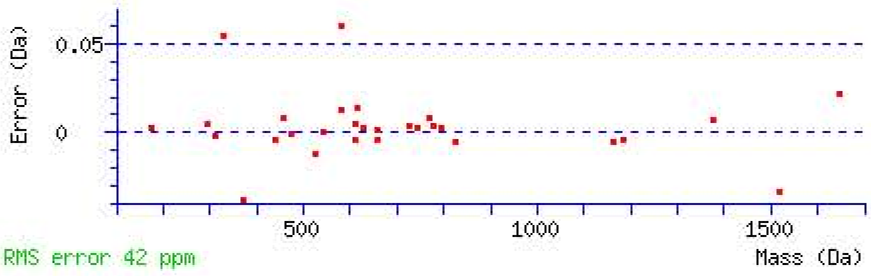
Match to Query 52355: 1974.912376 from(494.735370,4+) rtinseconds(1421) index(38269)
Title: Locus:1.1.1.2778.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

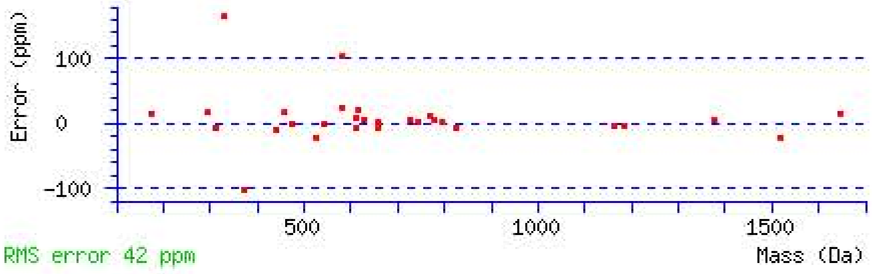
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1974.916122
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.026
Matches : 29/100 fragment ions using 68 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**440.232602**	220.619939	423.206053	212.106664			Q							11
2	600.263251	300.635264	583.236702	292.121989			C	1536.698070	768.852673	1519.671521	760.339399	1518.687505	759.847391	10
3	**657.284715**	**329.145996**	640.258166	320.632721			G	***1376.667421***	688.837349	1359.640872	680.324074	1358.656856	679.832066	9
4	**794.343627**	397.675452	777.317078	389.162177			H	1319.645957	660.326617	1302.619408	651.813342	1301.635392	651.321334	8
5	1233.568953	**617.288115**	1216.542404	608.774840			Q	***1182.587045***	591.797161	1165.560496	583.283886	1164.576480	582.791878	7
6	1346.653017	673.830147	1329.626468	665.316872			I	***743.361719***	372.184498	726.335170	363.671223	725.351154	363.179215	6
7	1433.685045	717.346161	1416.658496	708.832886	1415.674480	708.340878	S	***630.277655***	315.642466	613.251106	307.129191	612.267090	306.637183	5
8	1504.722159	752.864718	1487.695610	744.351443	1486.711594	743.859435	A	***543.245627***	272.126452	526.219078	263.613177			4
9	1664.752808	832.880042	1647.726259	824.366768	1646.742243	823.874760	C	***472.208513***	236.607894	455.181964	228.094620			3
10	1801.811720	901.409498	1784.785171	892.896224	1783.801155	892.404216	H	***312.177864***	156.592570	295.151315	148.079295			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.0	1974.916122	-0.003746	QCGHQISACHR

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

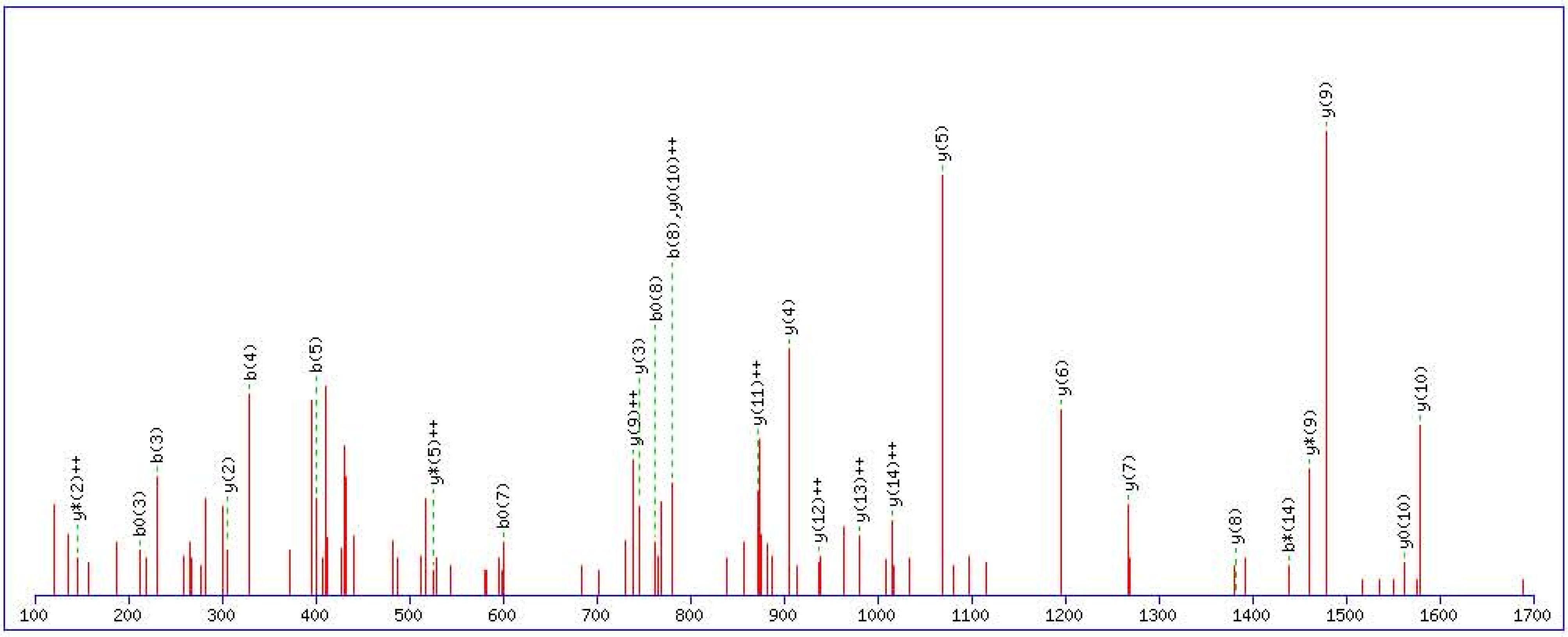
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGDVASMYTPNAQYCQMR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

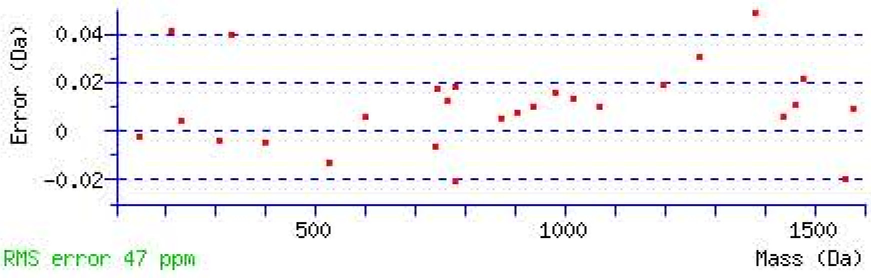
Match to Query 61802: 2359.038882 from(787.353570,3+) rtinseconds(2047) index(42417)
Title: Locus:1.1.1.2996.20 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

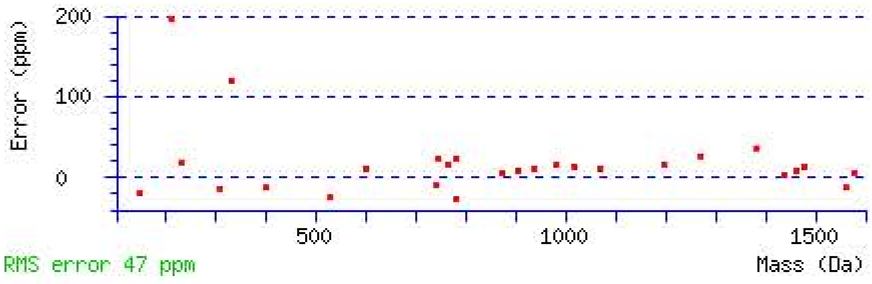
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2359.021759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0049
Matches : 27/162 fragment ions using 71 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							18
2	115.050204	58.028740					G	2303.007580	1152.007428	2285.981031	1143.494153	2284.997015	1143.002145	17
3	**230.077147**	115.542211			212.066582	106.536929	D	2245.986116	1123.496696	2228.959567	1114.983421	2227.975551	1114.491413	16
4	**329.145561**	165.076418			311.134996	156.071136	V	2130.959173	1065.983224	2113.932624	1057.469950	2112.948608	1056.977942	15
5	**400.182675**	200.594975			382.172110	191.589693	A	2031.890759	1016.449018	2014.864210	1007.935743	2013.880194	1007.443735	14
6	487.214703	244.110989			469.204138	235.105707	S	1960.853645	980.930461	1943.827096	972.417186	1942.843080	971.925178	13
7	618.255188	309.631232			600.244623	300.625949	M	1873.821617	937.414447	1856.795068	928.901172	1855.811052	928.409164	12
8	**781.318517**	391.162896			763.307952	382.157614	Y	1742.781132	871.894204	1725.754583	863.380930	1724.770567	862.888922	11
9	882.366196	441.686736			864.355631	432.681453	T	***1579.717803***	790.362540	1562.691254	781.849265	1561.707238	781.357257	10
10	979.418960	490.213118			961.408395	481.207835	P	***1478.670124***	739.838700	1461.643575	731.325426			9
11	1093.461887	547.234581	1076.435338	538.721307	1075.451322	538.229299	N	***1381.617360***	691.312318	1364.590811	682.799044			8
12	1164.499001	582.753138	1147.472452	574.239864	1146.488436	573.747856	A	***1267.574433***	634.290855	1250.547884	625.777580			7
13	1292.557579	646.782428	1275.531030	638.269153	1274.547014	637.777145	Q	***1196.537319***	598.772298	1179.510770	590.259023			6
14	1455.620908	728.314092	1438.594359	719.800818	1437.610343	719.308810	Y	***1068.478741***	534.743009	1051.452192	526.229734			5
15	1615.651557	808.329417	1598.625008	799.816142	1597.640992	799.324134	C	***905.415412***	453.211344	888.388863	444.698070			4
16	2054.876883	1027.942079	2037.850334	1019.428805	2036.866318	1018.936797	Q	***745.384763***	373.196020	728.358214	364.682745			3
17	2185.917368	1093.462322	2168.890819	1084.949047	2167.906803	1084.457039	M	***306.159437***	153.583356	289.132888	145.070082			2
18							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.0	2359.021759	0.017123	GGDVASMYTPNAQYCQMR
14.0	2359.021759	0.017123	GGDVASMYTPNAQYCQMR

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

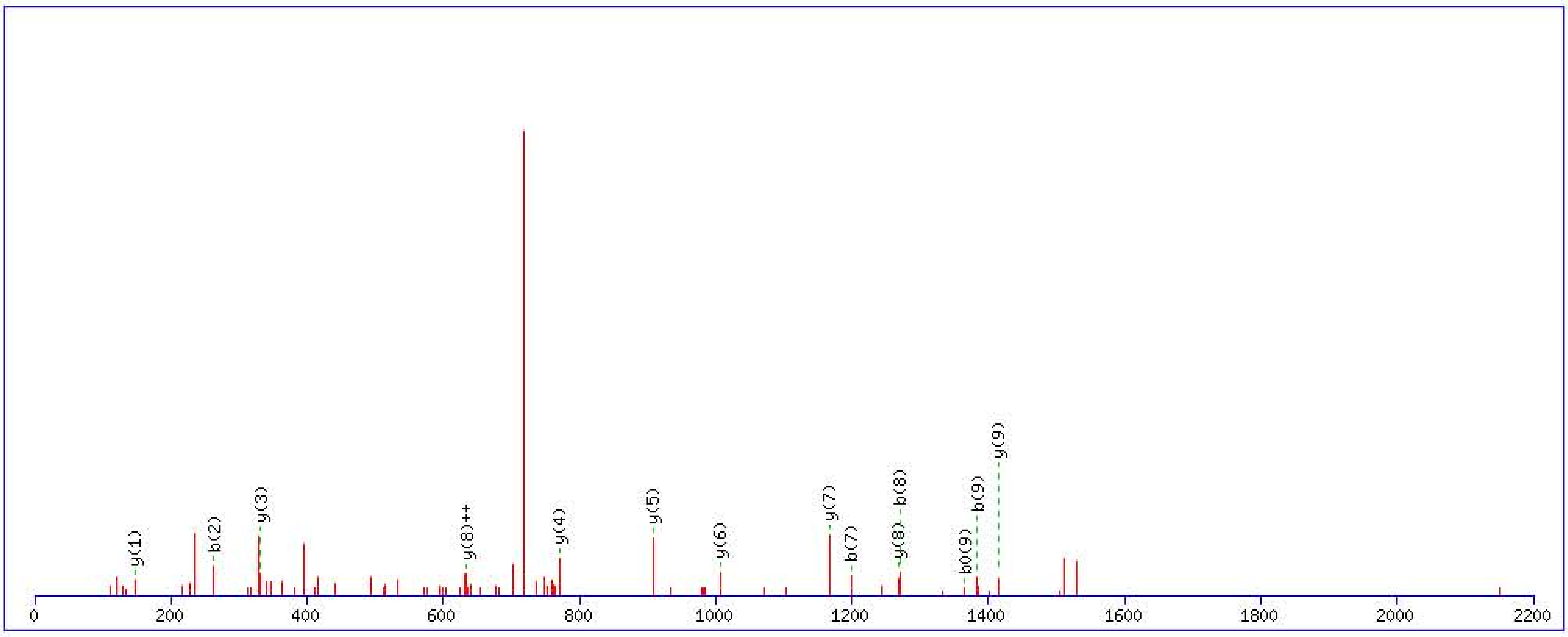
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFTCVHQALK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

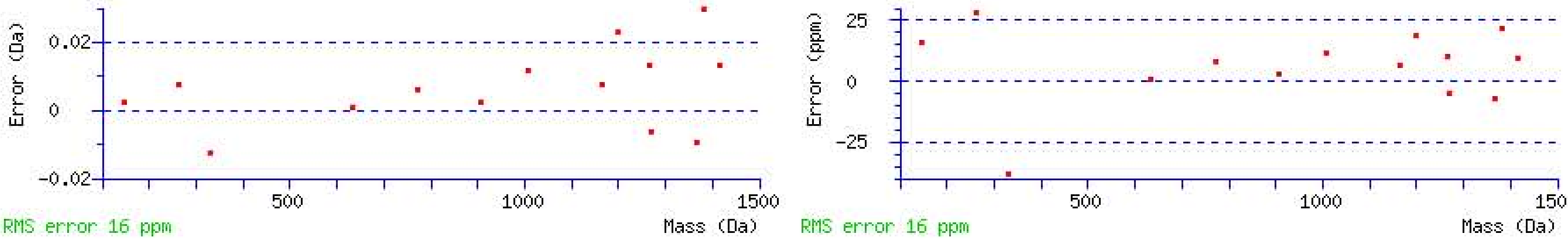
Match to Query 39444: 1528.762128 from(765.388340,2+) rtinseconds(1802) index(40763)
Title: Locus:1.1.1.2911.19 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1528.753052
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0026
Matches : 14/82 fragment ions using 40 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	**263.102633**	132.054954			245.092068	123.049672	F	***1414.733376***	707.870326	1397.706827	699.357051	1396.722811	698.865043	9
3	364.150312	182.578794			346.139747	173.573512	T	***1267.664962***	634.336119	1250.638413	625.822844	1249.654397	625.330836	8
4	524.180961	262.594119			506.170396	253.588836	C	***1166.617283***	583.812279	1149.590734	575.299005			7
5	623.249375	312.128326			605.238810	303.123043	V	***1006.586634***	503.796955	989.560085	495.283680			6
6	760.308287	380.657782			742.297722	371.652499	H	***907.518220***	454.262748	890.491671	445.749473			5
7	**1199.533613**	600.270444	1182.507064	591.757170	1181.523048	591.265162	Q	***770.459308***	385.733292	753.432759	377.220017			4
8	**1270.570727**	635.789001	1253.544178	627.275727	1252.560162	626.783719	A	***331.233982***	166.120629	314.207433	157.607354			3
9	**1383.654791**	692.331033	1366.628242	683.817759	1365.644226	683.325751	L	260.196868	130.602072	243.170319	122.088797			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	1528.753052	0.009076	DFTCVHQALK
4.9	1528.755524	0.006604	QQNEGDSIISK
4.5	1528.744293	0.017835	KDYTSGAMLTGELK
0.9	1528.755524	0.006604	QQNEGDSIISK
0.7	1528.773254	-0.011126	QEDILNGKENEIK
0.3	1528.773254	-0.011126	ENLQLNQETEAIK
0.3	1528.755524	0.006604	DQKATPLGPQEMAK
0.3	1528.780685	-0.018557	KYMATVTSISGDLK

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

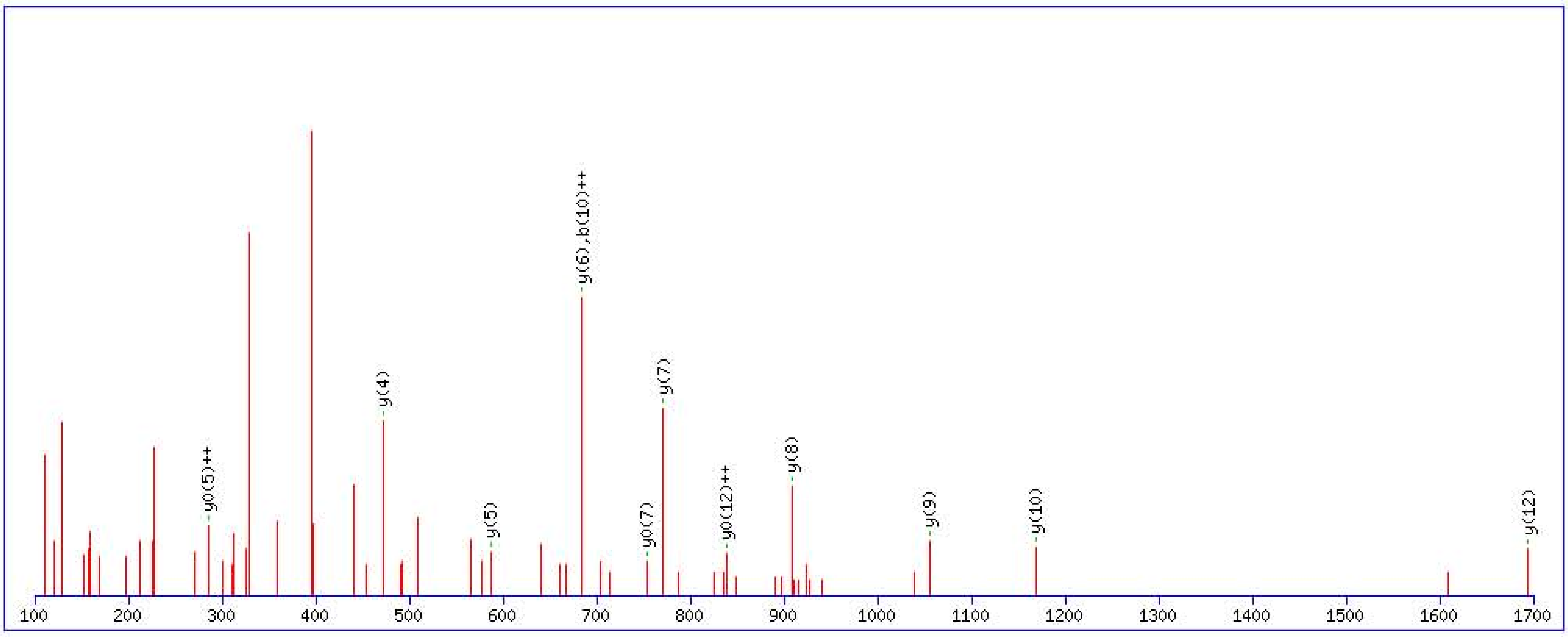
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVTSVSQIFHSPDLAIR**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

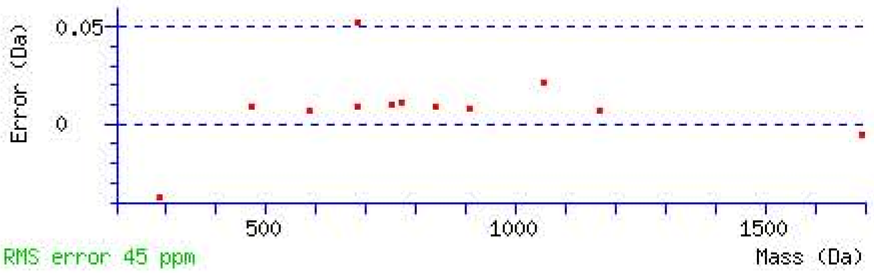
Match to Query 56782: 2137.149016 from(535.294530,4+) rtinseconds(2312) index(44108)
Title: Locus:1.1.1.3089.4 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

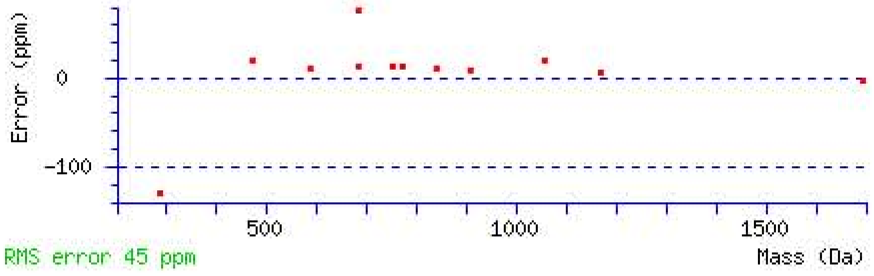
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2137.135406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.0027
Matches : 12/168 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							17
2	157.097154	79.052215					V	2081.121208	1041.064242	2064.094659	1032.550967	2063.110643	1032.058959	16
3	258.144833	129.576055			240.134268	120.570772	T	1982.052794	991.530035	1965.026245	983.016761	1964.042229	982.524753	15
4	345.176861	173.092068			327.166296	164.086786	S	1881.005115	941.006196	1863.978566	932.492921	1862.994550	932.000913	14
5	444.245275	222.626275			426.234710	213.620993	V	1793.973087	897.490182	1776.946538	888.976907	1775.962522	888.484899	13
6	531.277303	266.142290			513.266738	257.137007	S	***1694.904673***	847.955975	1677.878124	839.442700	1676.894108	838.950692	12
7	970.502629	485.754953	953.476080	477.241678	952.492064	476.749670	Q	1607.872645	804.439961	1590.846096	795.926686	1589.862080	795.434678	11
8	1083.586693	542.296985	1066.560144	533.783710	1065.576128	533.291702	I	***1168.647319***	584.827298	1151.620770	576.314023	1150.636754	575.822015	10
9	1230.655107	615.831192	1213.628558	607.317917	1212.644542	606.825909	F	***1055.563255***	528.285266	1038.536706	519.771991	1037.552690	519.279983	9
10	1367.714019	684.360648	1350.687470	675.847373	1349.703454	675.355365	H	***908.494841***	454.751059	891.468292	446.237784	890.484276	445.745776	8
11	1454.746047	727.876662	1437.719498	719.363387	1436.735482	718.871379	S	***771.435929***	386.221603	754.409380	377.708328	753.425364	377.216320	7
12	1551.798811	776.403044	1534.772262	767.889769	1533.788246	767.397761	P	***684.403901***	342.705589	667.377352	334.192314	666.393336	333.700306	6
13	1666.825754	833.916515	1649.799205	825.403241	1648.815189	824.911233	D	***587.351137***	294.179207	570.324588	285.665932	569.340572	285.173924	5
14	1779.909818	890.458547	1762.883269	881.945273	1761.899253	881.453265	L	***472.324194***	236.665735	455.297645	228.152460			4
15	1850.946932	925.977104	1833.920383	917.463830	1832.936367	916.971822	A	359.240130	180.123703	342.213581	171.610429			3
16	1964.030996	982.519136	1947.004447	974.005862	1946.020431	973.513853	I	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.8	2137.135406	0.013610	GVTSVSQIFHSPDLAIR

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

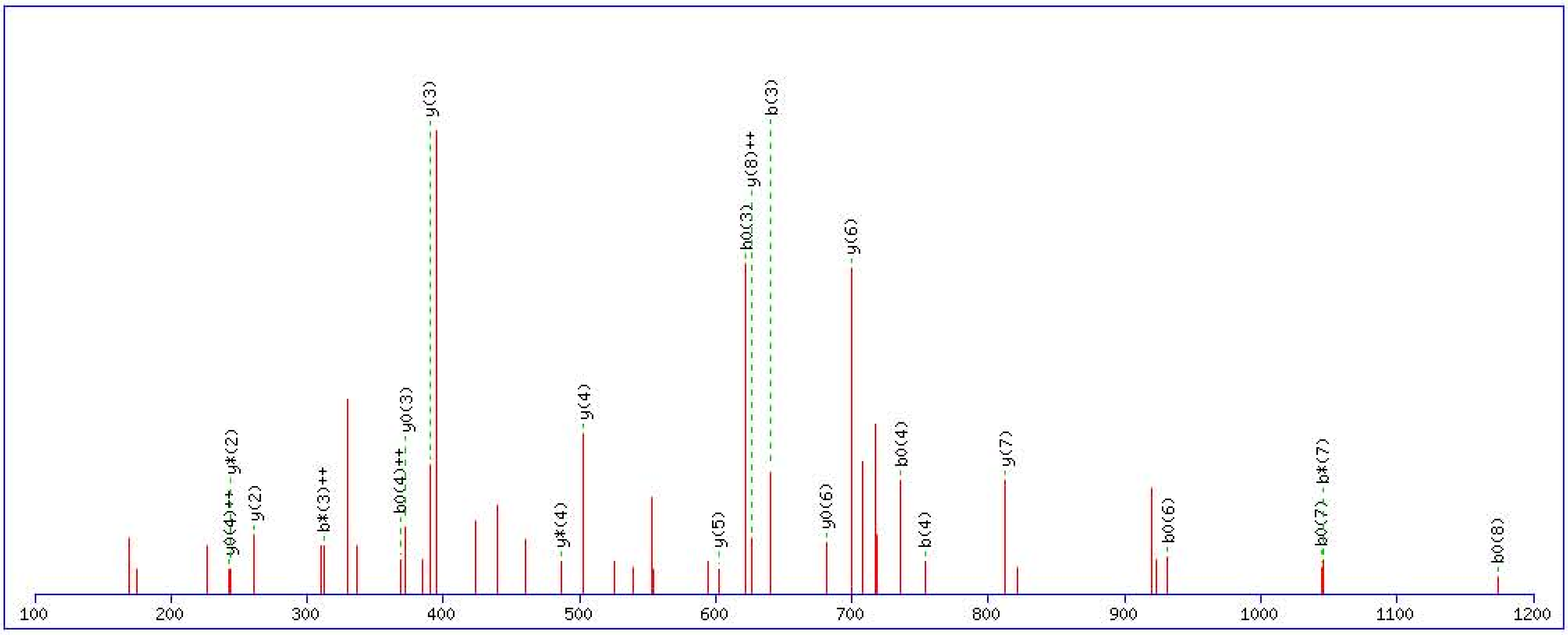
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAQLPVIENK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

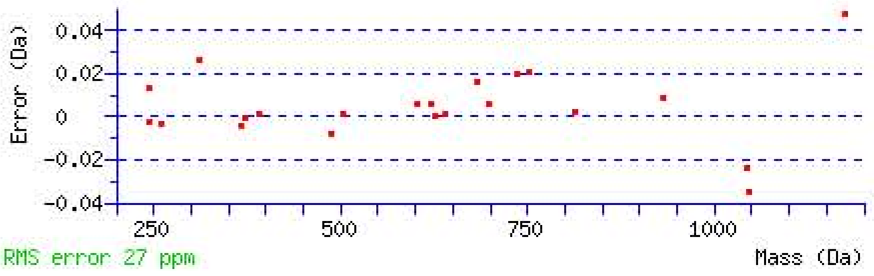
Match to Query 37055: 1450.791908 from(726.403230,2+) rtinseconds(1958) index(41880)
Title: Locus:1.1.1.2965.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

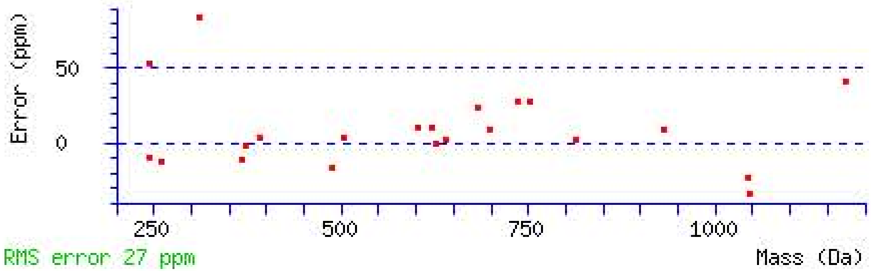
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1450.785355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0084
Matches : 22/100 fragment ions using 45 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							10
2	201.086983	101.047130			183.076418	92.041847	A	1322.750070	661.878673	1305.723521	653.365398	1304.739505	652.873390	9
3	**640.312309**	320.659793	623.285760	312.146518	622.301744	311.654510	Q	1251.712956	626.360116	1234.686407	617.846841	1233.702391	617.354833	8
4	**753.396373**	377.201825	736.369824	368.688550	735.385808	368.196542	L	***812.487630***	406.747453	795.461081	398.234178	794.477065	397.742170	7
5	850.449137	425.728207	833.422588	417.214932	832.438572	416.722924	P	***699.403566***	350.205421	682.377017	341.692146	681.393001	341.200138	6
6	949.517551	475.262414	932.491002	466.749139	931.506986	466.257131	V	***602.350802***	301.679039	585.324253	293.165764	584.340237	292.673756	5
7	1062.601615	531.804446	1045.575066	523.291171	1044.591050	522.799163	I	***503.282388***	252.144832	486.255839	243.631557	485.271823	243.139549	4
8	1191.644208	596.325742	1174.617659	587.812468	1173.633643	587.320459	E	***390.198324***	195.602800	373.171775	187.089525	372.187759	186.597517	3
9	1305.687135	653.347205	1288.660586	644.833931	1287.676570	644.341923	N	***261.155731***	131.081503	244.129182	122.568229			2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.8	1450.785355	0.006553	EAQLPVIENK
4.3	1450.811661	-0.019753	ILNGHSLTRRER
0.6	1450.789215	0.002693	NSSHTLLQVLSPR
0.1	1450.796600	-0.004692	QISAVHKETK

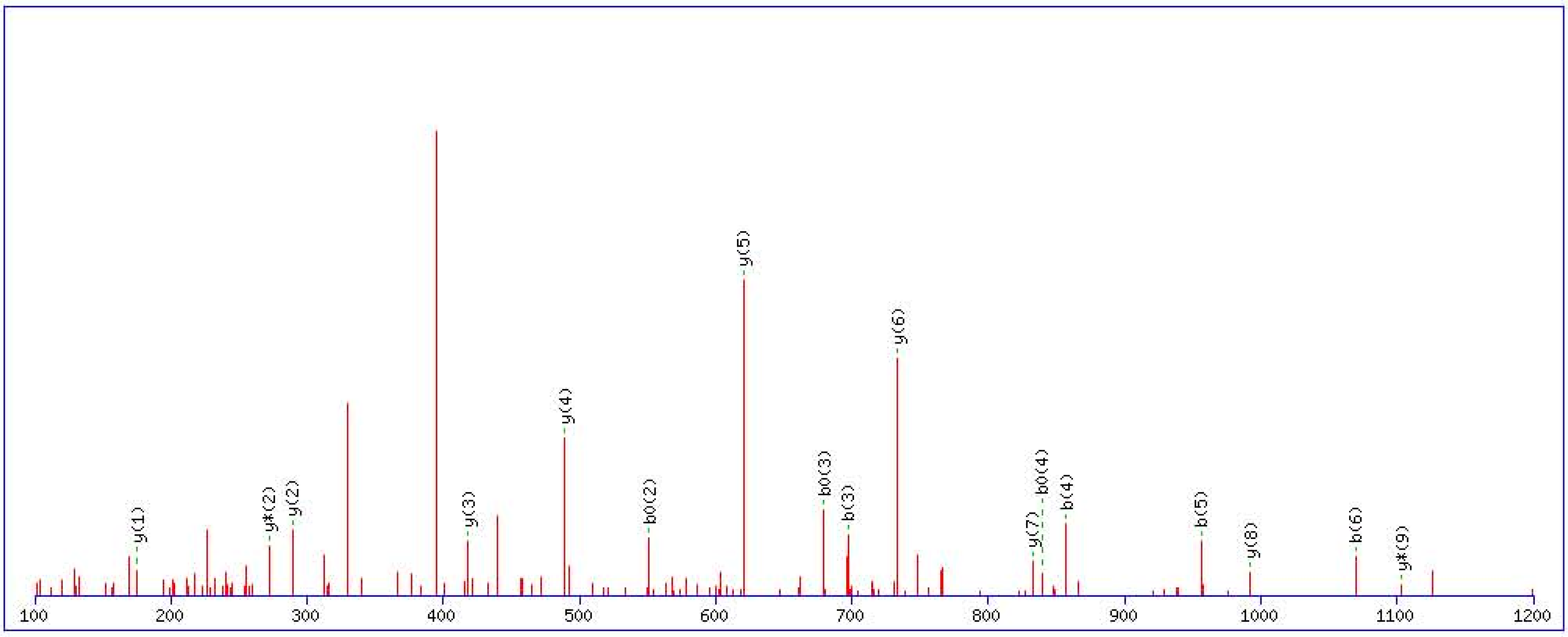
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

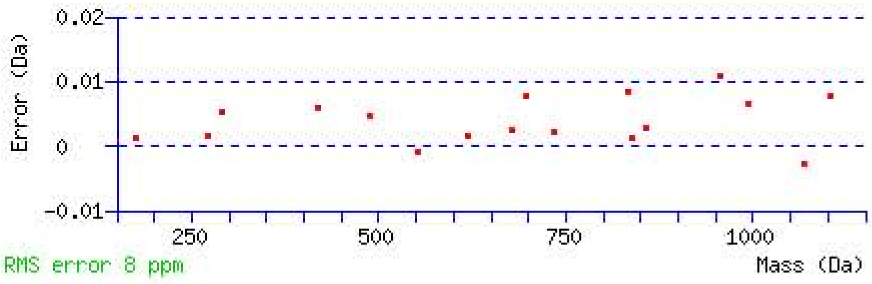
Match to Query 45515: 1687.789812 from(563.603880,3+) rtinseconds(1800) index(77144)
Title: Locus:1.1.1.2841.6 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

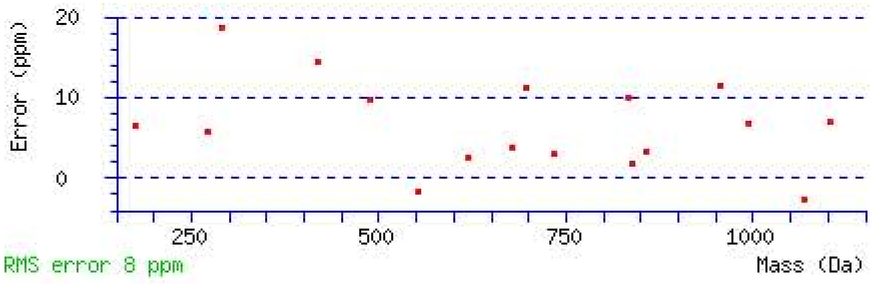
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1687.784393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 7.8e-005
Matches : 17/114 fragment ions using 31 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							11
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1559.749102	780.378189	1542.722553	771.864915	1541.738537	771.372907	10
3	**697.333773**	349.170525	680.307224	340.657250	679.323208	340.165242	Q	1120.523776	560.765526	1103.497227	552.252252	1102.513211	551.760244	9
4	**857.364422**	429.185849	840.337873	420.672575	839.353857	420.180567	C	***992.465198***	496.736237	975.438649	488.222963	974.454633	487.730955	8
5	**956.432836**	478.720056	939.406287	470.206782	938.422271	469.714774	V	***832.434549***	416.720913	815.408000	408.207638	814.423984	407.715630	7
6	**1069.516900**	535.262088	1052.490351	526.748814	1051.506335	526.256806	I	***733.366135***	367.186706	716.339586	358.673431	715.355570	358.181423	6
7	1200.557385	600.782331	1183.530836	592.269056	1182.546820	591.777048	M	***620.282071***	310.644674	603.255522	302.131399	602.271506	301.639391	5
8	1271.594499	636.300888	1254.567950	627.787613	1253.583934	627.295605	A	***489.241586***	245.124431	472.215037	236.611156	471.231021	236.119148	4
9	1400.637092	700.822184	1383.610543	692.308910	1382.626527	691.816902	E	***418.204472***	209.605874	401.177923	201.092600	400.193907	200.600592	3
10	1514.680019	757.843648	1497.653470	749.330373	1496.669454	748.838365	N	***289.161879***	145.084577	272.135330	136.571303			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.0	1687.784393	0.005419	EQQCVIMAENR
41.2	1687.784393	0.005419	EQQCVIMAENR
1.1	1687.776093	0.013719	QQEEAQAAAAAASAESR
1.0	1687.787552	0.002260	GASEDGEYFLMIRGK
0.8	1687.773666	0.016146	TTGPPSGQMPDNPPHR

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

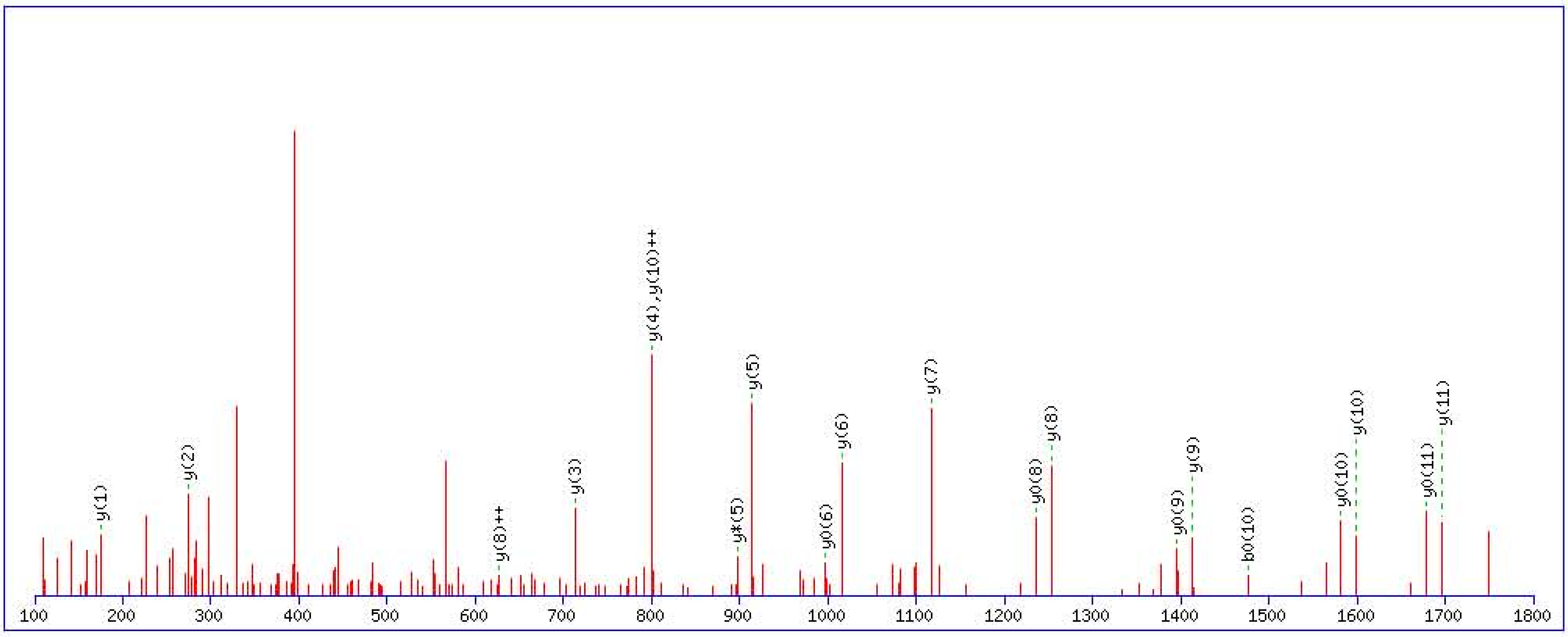
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **APWCHTTNSQVR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

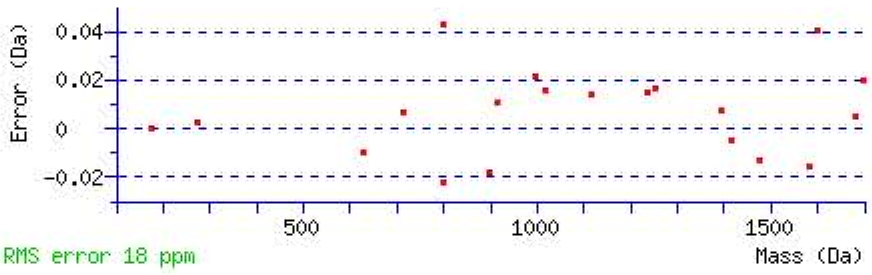
Match to Query 47630: 1766.840592 from(589.954140,3+) rtinseconds(1511) index(75329)
Title: Locus:1.1.1.2740.16 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

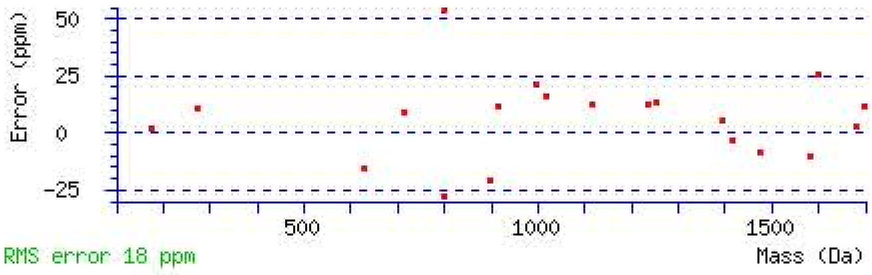


Monoisotopic mass of neutral peptide Mr(calc): 1766.834488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 77 **Expect:** 2.2e-007
Matches : 20/102 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							12
2	169.097154	85.052215					P	***1696.804643***	848.905960	1679.778094	840.392685	1678.794078	839.900677	11
3	355.176467	178.091872					W	***1599.751879***	800.379578	1582.725330	791.866303	1581.741314	791.374295	10
4	515.207116	258.107196					C	***1413.672566***	707.339921	1396.646017	698.826647	1395.662001	698.334639	9
5	652.266028	326.636652					H	***1253.641917***	627.324597	1236.615368	618.811322	1235.631352	618.319314	8
6	753.313707	377.160492			735.303142	368.155209	T	***1116.583005***	558.795141	1099.556456	550.281866	1098.572440	549.789858	7
7	854.361386	427.684331			836.350821	418.679049	T	***1015.535326***	508.271301	998.508777	499.758027	997.524761	499.266019	6
8	968.404313	484.705795	951.377764	476.192520	950.393748	475.700512	N	***914.487647***	457.747462	897.461098	449.234187	896.477082	448.742179	5
9	1055.436341	528.221809	1038.409792	519.708534	1037.425776	519.216526	S	***800.444720***	400.725998	783.418171	392.212724	782.434155	391.720716	4
10	1494.661667	747.834472	1477.635118	739.321197	1476.651102	738.829189	Q	***713.412692***	357.209984	696.386143	348.696710			3
11	1593.730081	797.368679	1576.703532	788.855404	1575.719516	788.363396	V	***274.187366***	137.597321	257.160817	129.084047			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 18 ppm



RMS error 18 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.7	1766.834488	0.006104	APWCHTTNSQVR
5.4	1766.829758	0.010834	WPSPSPTAMPSPEDLR
0.6	1766.833115	0.007477	SMLEVNYPMENGIVR

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

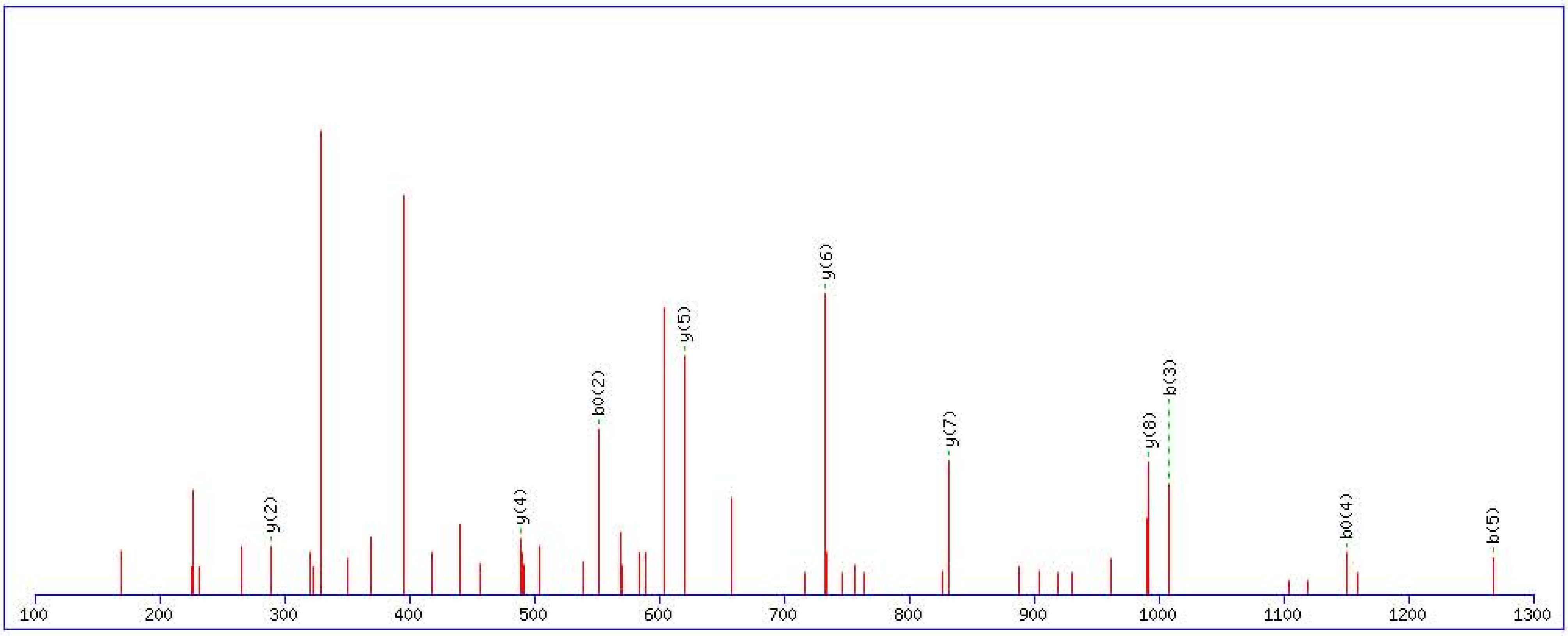
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

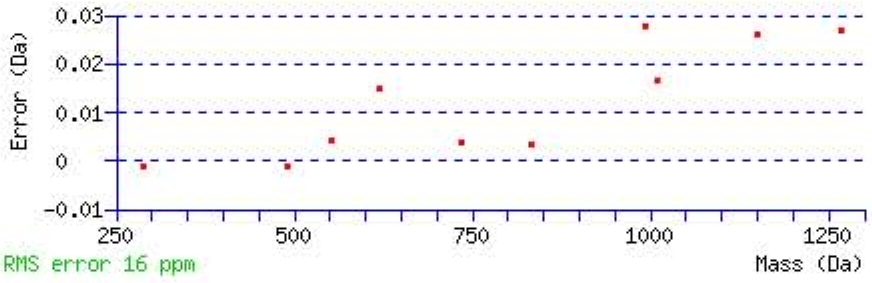
Match to Query 52899: 1998.971022 from(667.330950,3+) rtinseconds(2119) index(79326)
Title: Locus:1.1.1.2952.16 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

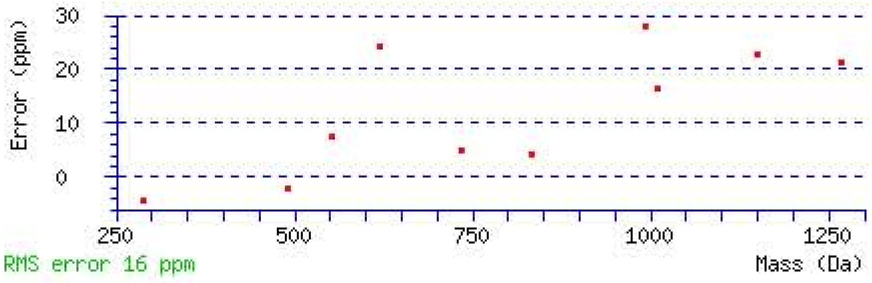
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1998.951141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.0052
Matches : 10/114 fragment ions using 21 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1870.915850	935.961563	1853.889301	927.448288	1852.905285	926.956280	10
3	**1008.500521**	504.753899	991.473972	496.240624	990.489956	495.748616	Q	1431.690524	716.348900	1414.663975	707.835625	1413.679959	707.343617	9
4	1168.531170	584.769223	1151.504621	576.255949	1150.520605	575.763940	C	***992.465198***	496.736237	975.438649	488.222962	974.454633	487.730954	8
5	**1267.599584**	634.303430	1250.573035	625.790156	1249.589019	625.298148	V	***832.434549***	416.720912	815.408000	408.207638	814.423984	407.715630	7
6	1380.683648	690.845462	1363.657099	682.332188	1362.673083	681.840179	I	***733.366135***	367.186705	716.339586	358.673431	715.355570	358.181423	6
7	1511.724133	756.365704	1494.697584	747.852430	1493.713568	747.360422	M	***620.282071***	310.644673	603.255522	302.131399	602.271506	301.639391	5
8	1582.761247	791.884261	1565.734698	783.370987	1564.750682	782.878979	A	***489.241586***	245.124431	472.215037	236.611156	471.231021	236.119148	4
9	1711.803840	856.405558	1694.777291	847.892283	1693.793275	847.400275	E	418.204472	209.605874	401.177923	201.092599	400.193907	200.600591	3
10	1825.846767	913.427021	1808.820218	904.913747	1807.836202	904.421739	N	***289.161879***	145.084577	272.135330	136.571303			2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.3	1998.951141	0.019881	EQQCVIMAENR
0.9	1998.980133	-0.009111	MNPQQQRMAAIGTDK
0.9	1998.980133	-0.009111	MNPQQQRMAAIGTDK
0.9	1998.980133	-0.009111	MNPQQQRMAAIGTDK

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

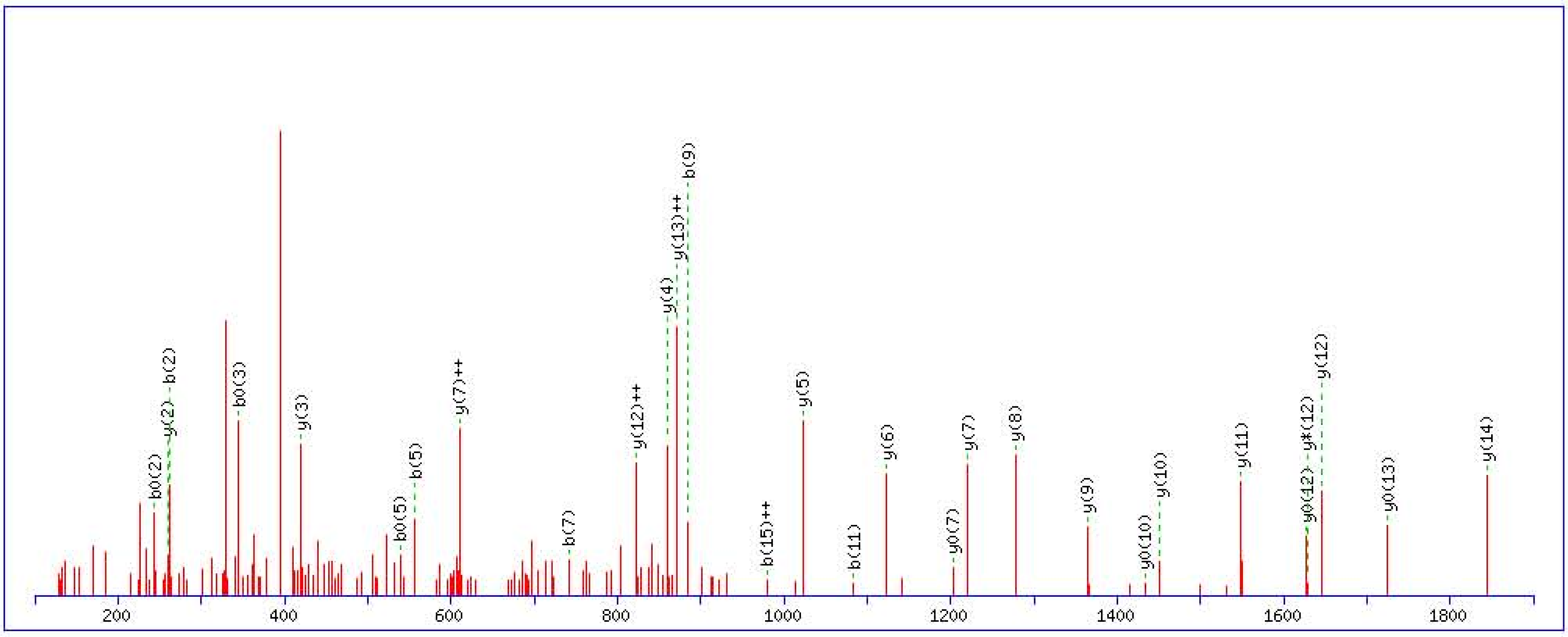
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CTTPPPSSGPTYQCLK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

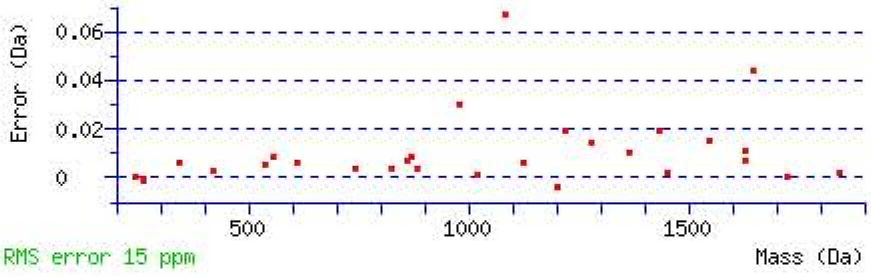
Match to Query 56202: 2103.990372 from(702.337400,3+) rtinseconds(1758) index(76880)
Title: Locus:1.1.1.2826.19 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

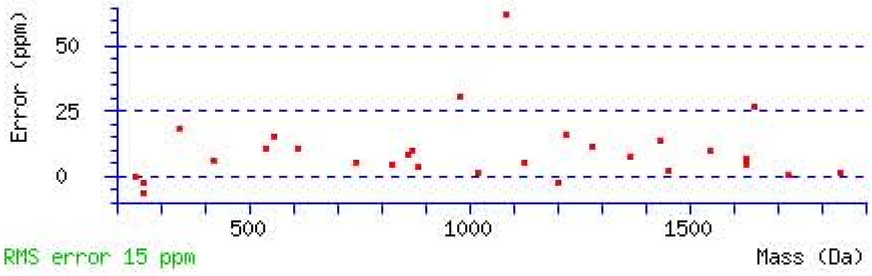
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2103.979172
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 2e-006
Matches : 29/144 fragment ions using 57 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.037925	81.022600					C							16
2	**262.085604**	131.546440			244.075039	122.541158	T	1944.955785	972.981531	1927.929236	964.468256	1926.945220	963.976248	15
3	363.133283	182.070280			345.122718	173.064997	T	***1843.908106***	922.457691	1826.881557	913.944417	1825.897541	913.452409	14
4	460.186047	230.596661			442.175482	221.591379	P	1742.860427	871.933852	1725.833878	863.420577	1724.849862	862.928569	13
5	**557.238811**	279.123044			539.228246	270.117761	P	***1645.807663***	823.407470	1628.781114	814.894195	1627.797098	814.402187	12
6	654.291575	327.649426			636.281010	318.644143	P	***1548.754899***	774.881088	1531.728350	766.367813	1530.744334	765.875805	11
7	**741.323603**	371.165440			723.313038	362.160157	S	***1451.702135***	726.354706	1434.675586	717.841431	1433.691570	717.349423	10
8	828.355631	414.681454			810.345066	405.676171	S	***1364.670107***	682.838692	1347.643558	674.325417	1346.659542	673.833409	9
9	**885.377095**	443.192186			867.366530	434.186903	G	***1277.638079***	639.322678	1260.611530	630.809403	1259.627514	630.317395	8
10	982.429859	491.718568			964.419294	482.713285	P	***1220.616615***	610.811946	1203.590066	602.298671	1202.606050	601.806663	7
11	**1083.477538**	542.242407			1065.466973	533.237125	T	***1123.563851***	562.285564	1106.537302	553.772289	1105.553286	553.280281	6
12	1246.540867	623.774072			1228.530302	614.768789	Y	***1022.516172***	511.761724	1005.489623	503.248450			5
13	1685.766193	843.386735	1668.739644	834.873460	1667.755628	834.381452	Q	***859.452843***	430.230060	842.426294	421.716785			4
14	1845.796842	923.402059	1828.770293	914.888785	1827.786277	914.396777	C	***420.227517***	210.617396	403.200968	202.104122			3
15	1958.880906	979.944091	1941.854357	971.430817	1940.870341	970.938809	L	***260.196868***	130.602072	243.170319	122.088797			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.0	2103.979172	0.011200	CTTPPPSSGPTYQCLK
5.2	2103.964554	0.025818	TAADTPAIMNWDLFFTMK

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

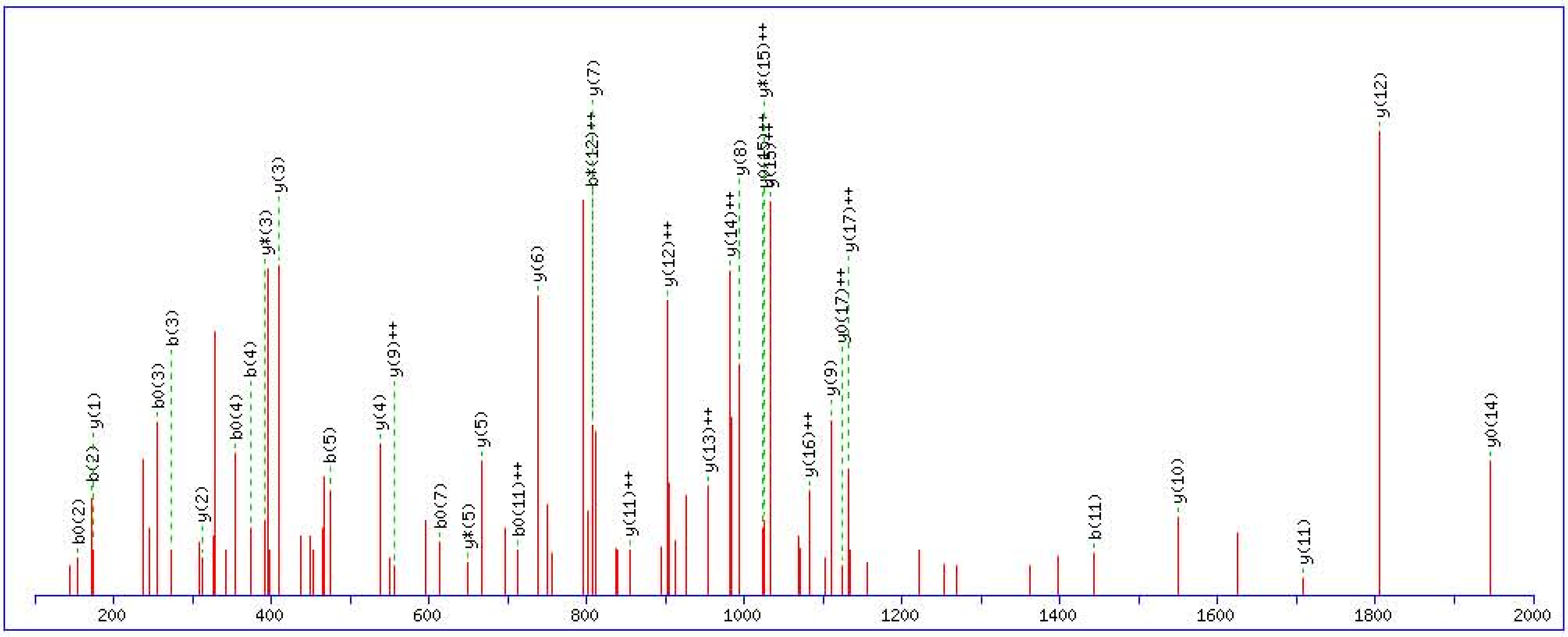
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATTVTGTPCQDWAAQEPHR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

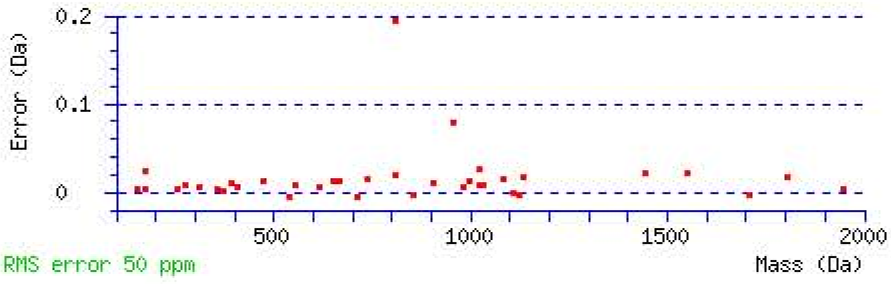
Match to Query 63553: 2436.141102 from(813.054310,3+) rtinseconds(1818) index(77219)
Title: Locus:1.1.1.2847.15 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

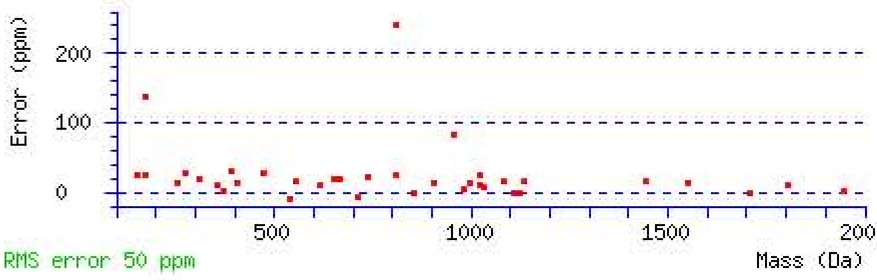
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2436.131470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 1.3e-005
Matches : 37/190 fragment ions using 83 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							19
2	**173.092069**	87.049672			155.081504	78.044390	T	2366.101616	1183.554446	2349.075067	1175.041171	2348.091051	1174.549163	18
3	**274.139748**	137.573512			256.129183	128.568230	T	2265.053937	1133.030606	2248.027388	1124.517332	2247.043372	1124.025324	17
4	**373.208162**	187.107719			355.197597	178.102437	V	2164.006258	1082.506767	2146.979709	1073.993492	2145.995693	1073.501484	16
5	**474.255841**	237.631559			456.245276	228.626276	T	2064.937844	1032.972560	2047.911295	1024.459285	2046.927279	1023.967277	15
6	531.277305	266.142291			513.266740	257.137008	G	1963.890165	982.448721	1946.863616	973.935446	1945.879600	973.443438	14
7	632.324984	316.666130			614.314419	307.660848	T	1906.868701	953.937989	1889.842152	945.424714	1888.858136	944.932706	13
8	729.377748	365.192512			711.367183	356.187230	P	***1805.821022***	903.414149	1788.794473	894.900875	1787.810457	894.408867	12
9	889.408397	445.207837			871.397832	436.202554	C	***1708.768258***	854.887767	1691.741709	846.374493	1690.757693	845.882485	11
10	1328.633723	664.820500	1311.607174	656.307225	1310.623158	655.815217	Q	***1548.737609***	774.872443	1531.711060	766.359168	1530.727044	765.867160	10
11	**1443.660666**	722.333971	1426.634117	713.820697	1425.650101	713.328689	D	***1109.512283***	555.259780	1092.485734	546.746505	1091.501718	546.254497	9
12	1629.739979	815.373628	1612.713430	806.860353	1611.729414	806.368345	W	***994.485340***	497.746308	977.458791	489.233034	976.474775	488.741026	8
13	1700.777093	850.892185	1683.750544	842.378910	1682.766528	841.886902	A	***808.406027***	404.706652	791.379478	396.193377	790.395462	395.701369	7
14	1771.814207	886.410742	1754.787658	877.897467	1753.803642	877.405459	A	***737.368913***	369.188095	720.342364	360.674820	719.358348	360.182812	6
15	1899.872785	950.440031	1882.846236	941.926756	1881.862220	941.434748	Q	***666.331799***	333.669538	649.305250	325.156263	648.321234	324.664255	5
16	2028.915378	1014.961327	2011.888829	1006.448053	2010.904813	1005.956045	E	***538.273221***	269.640249	521.246672	261.126974	520.262656	260.634966	4
17	2125.968142	1063.487709	2108.941593	1054.974434	2107.957577	1054.482427	P	***409.230628***	205.118952	392.204079	196.605677			3
18	2263.027054	1132.017165	2246.000505	1123.503890	2245.016489	1123.011883	H	***312.177864***	156.592570	295.151315	148.079295			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.8	2436.131470	0.009632	ATTVTGTPCQDWAAQEPHR
24.5	2436.131470	0.009632	ATTVTGTPCQDWAAQEPHR

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

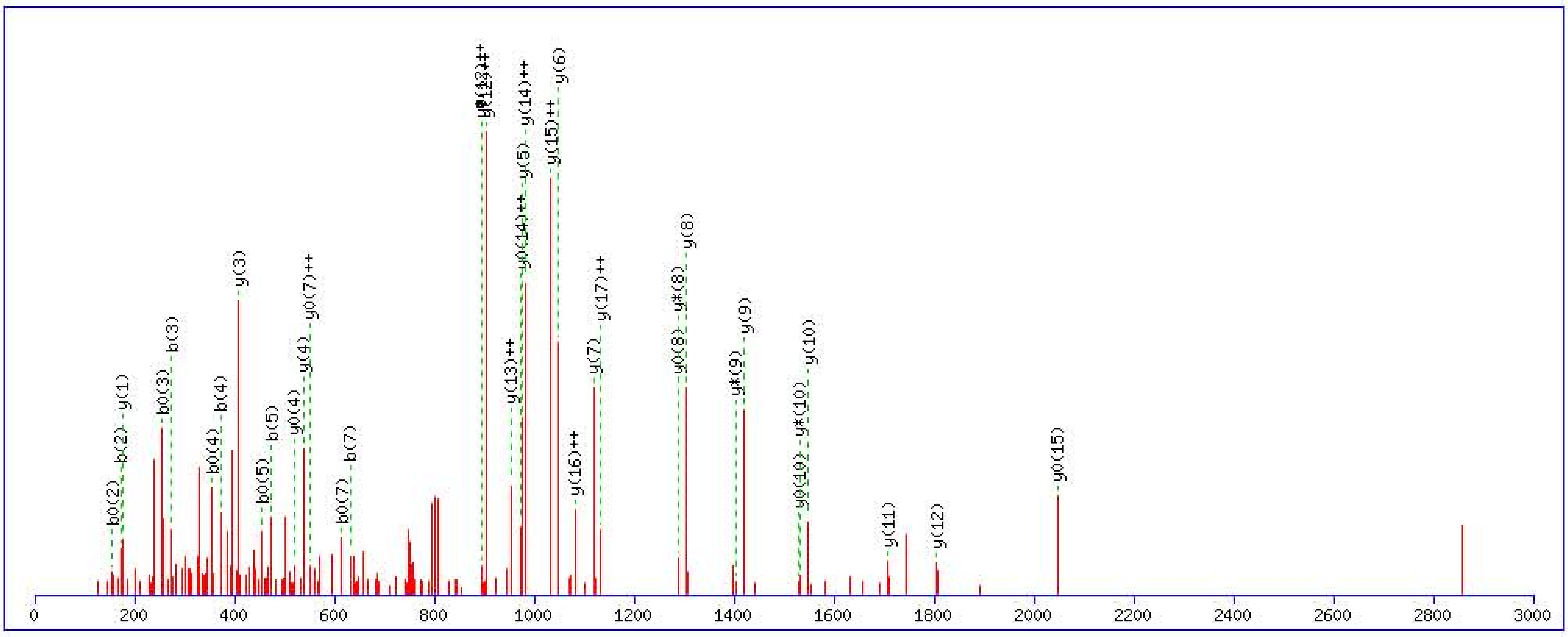
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATTVTGTPCQDWAAQEPHR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

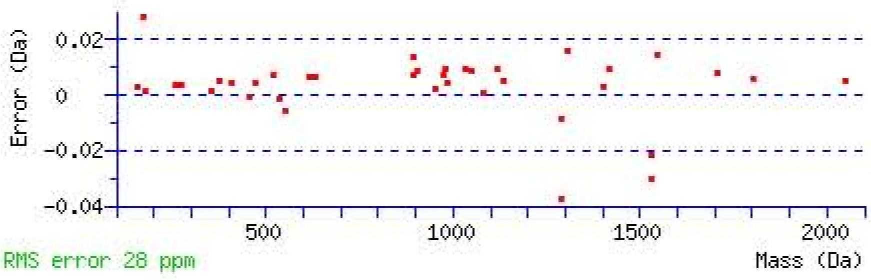
Match to Query 63555: 2436.149352 from(813.057060,3+) rtinseconds(1858) index(77395)
Title: Locus:1.1.1.2861.20 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

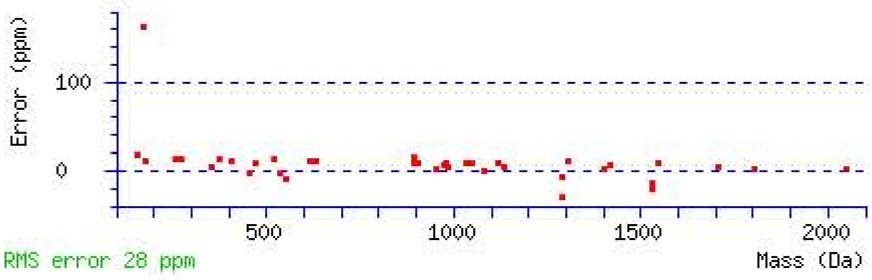
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2436.131470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 3.1e-005
Matches : 38/190 fragment ions using 75 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	72.044390	36.525833					A							19
2	**173.092069**	87.049672			155.081504	78.044390	T	2366.101616	1183.554446	2349.075067	1175.041171	2348.091051	1174.549163	18
3	**274.139748**	137.573512			256.129183	128.568230	T	2265.053937	1133.030606	2248.027388	1124.517332	2247.043372	1124.025324	17
4	**373.208162**	187.107719			355.197597	178.102437	V	2164.006258	1082.506767	2146.979709	1073.993492	2145.995693	1073.501484	16
5	**474.255841**	237.631559			456.245276	228.626276	T	2064.937844	1032.972560	2047.911295	1024.459285	2046.927279	1023.967277	15
6	531.277305	266.142291			513.266740	257.137008	G	1963.890165	982.448721	1946.863616	973.935446	1945.879600	973.443438	14
7	**632.324984**	316.666130			614.314419	307.660848	T	1906.868701	953.937989	1889.842152	945.424714	1888.858136	944.932706	13
8	729.377748	365.192512			711.367183	356.187230	P	***1805.821022***	903.414149	1788.794473	894.900875	1787.810457	894.408867	12
9	889.408397	445.207837			871.397832	436.202554	C	***1708.768258***	854.887767	1691.741709	846.374493	1690.757693	845.882485	11
10	1017.466975	509.237126	1000.440426	500.723851	999.456410	500.231843	Q	***1548.737609***	774.872443	1531.711060	766.359168	1530.727044	765.867160	10
11	1132.493918	566.750597	1115.467369	558.237323	1114.483353	557.745315	D	***1420.679031***	710.843154	1403.652482	702.329879	1402.668466	701.837871	9
12	1318.573231	659.790254	1301.546682	651.276979	1300.562666	650.784971	W	***1305.652088***	653.329682	1288.625539	644.816408	1287.641523	644.324400	8
13	1389.610345	695.308811	1372.583796	686.795536	1371.599780	686.303528	A	***1119.572775***	560.290026	1102.546226	551.776751	1101.562210	551.284743	7
14	1460.647459	730.827368	1443.620910	722.314093	1442.636894	721.822085	A	***1048.535661***	524.771469	1031.509112	516.258194	1030.525096	515.766186	6
15	1899.872785	950.440031	1882.846236	941.926756	1881.862220	941.434748	Q	***977.498547***	489.252912	960.471998	480.739637	959.487982	480.247629	5
16	2028.915378	1014.961327	2011.888829	1006.448053	2010.904813	1005.956045	E	***538.273221***	269.640249	521.246672	261.126974	520.262656	260.634966	4
17	2125.968142	1063.487709	2108.941593	1054.974434	2107.957577	1054.482427	P	***409.230628***	205.118952	392.204079	196.605677			3
18	2263.027054	1132.017165	2246.000505	1123.503890	2245.016489	1123.011883	H	312.177864	156.592570	295.151315	148.079295			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.6	2436.131470	0.017882	ATTVTGTPCQDWAAQEPHR
23.8	2436.131470	0.017882	ATTVTGTPCQDWAAQEPHR

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

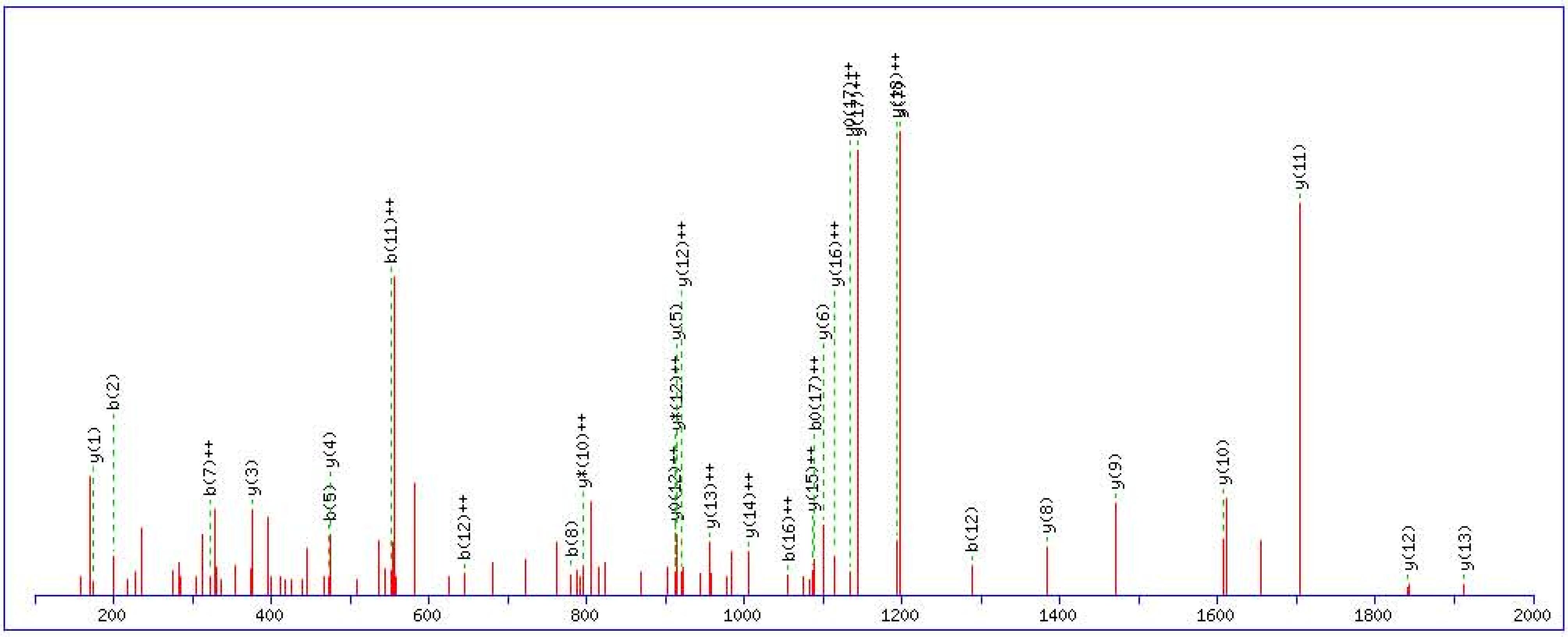
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVGGCVAHPHSWPWQVSLR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

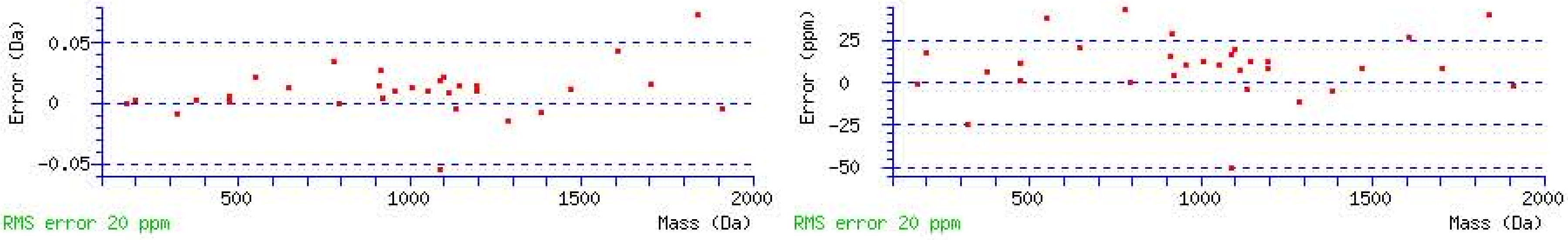
Match to Query 64752: 2482.273902 from(828.431910,3+) rtinseconds(2200) index(79937)
Title: Locus:1.1.1.2980.13 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2482.251480
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00036
Matches : 32/164 fragment ions using 87 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							19
2	**199.144104**	100.075690					V	2384.190309	1192.598792	2367.163760	1184.085518	2366.179744	1183.593510	18
3	256.165568	128.586422					G	2285.121895	1143.064585	2268.095346	1134.551311	2267.111330	1134.059303	17
4	313.187032	157.097154					G	2228.100431	1114.553853	2211.073882	1106.040579	2210.089866	1105.548571	16
5	**473.217681**	237.112479					C	2171.078967	1086.043121	2154.052418	1077.529847	2153.068402	1077.037839	15
6	572.286095	286.646686					V	2011.048318	1006.027797	1994.021769	997.514523	1993.037753	997.022515	14
7	643.323209	**322.165243**					A	***1911.979904***	956.493590	1894.953355	947.980316	1893.969339	947.488308	13
8	**780.382121**	390.694699					H	***1840.942790***	920.975033	1823.916241	912.461759	1822.932225	911.969751	12
9	877.434885	439.221081					P	***1703.883878***	852.445577	1686.857329	843.932303	1685.873313	843.440295	11
10	1014.493797	507.750537					H	***1606.831114***	803.919195	1589.804565	795.405921	1588.820549	794.913913	10
11	1101.525825	**551.266550**			1083.515260	542.261268	S	***1469.772202***	735.389739	1452.745653	726.876465	1451.761637	726.384457	9
12	**1287.605138**	**644.306207**			1269.594573	635.300924	W	***1382.740174***	691.873725	1365.713625	683.360451	1364.729609	682.868443	8
13	1384.657902	692.832589			1366.647337	683.827306	P	***1196.660861***	598.834069	1179.634312	590.320794	1178.650296	589.828786	7
14	1570.737215	785.872245			1552.726650	776.866963	W	***1099.608097***	550.307687	1082.581548	541.794412	1081.597532	541.302404	6
15	2009.962541	1005.484909	1992.935992	996.971634	1991.951976	996.479626	Q	***913.528784***	457.268030	896.502235	448.754756	895.518219	448.262748	5
16	2109.030955	**1055.019115**	2092.004406	1046.505841	2091.020390	1046.013833	V	***474.303458***	237.655367	457.276909	229.142092	456.292893	228.650084	4
17	2196.062983	1098.535129	2179.036434	1090.021855	2178.052418	1089.529847	S	***375.235044***	188.121160	358.208495	179.607886	357.224479	179.115878	3
18	2309.147047	1155.077161	2292.120498	1146.563887	2291.136482	1146.071879	L	288.203016	144.605146	271.176467	136.091872			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.3	2482.251480	0.022422	VVGGCVAHPHSWPWQVSLR

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

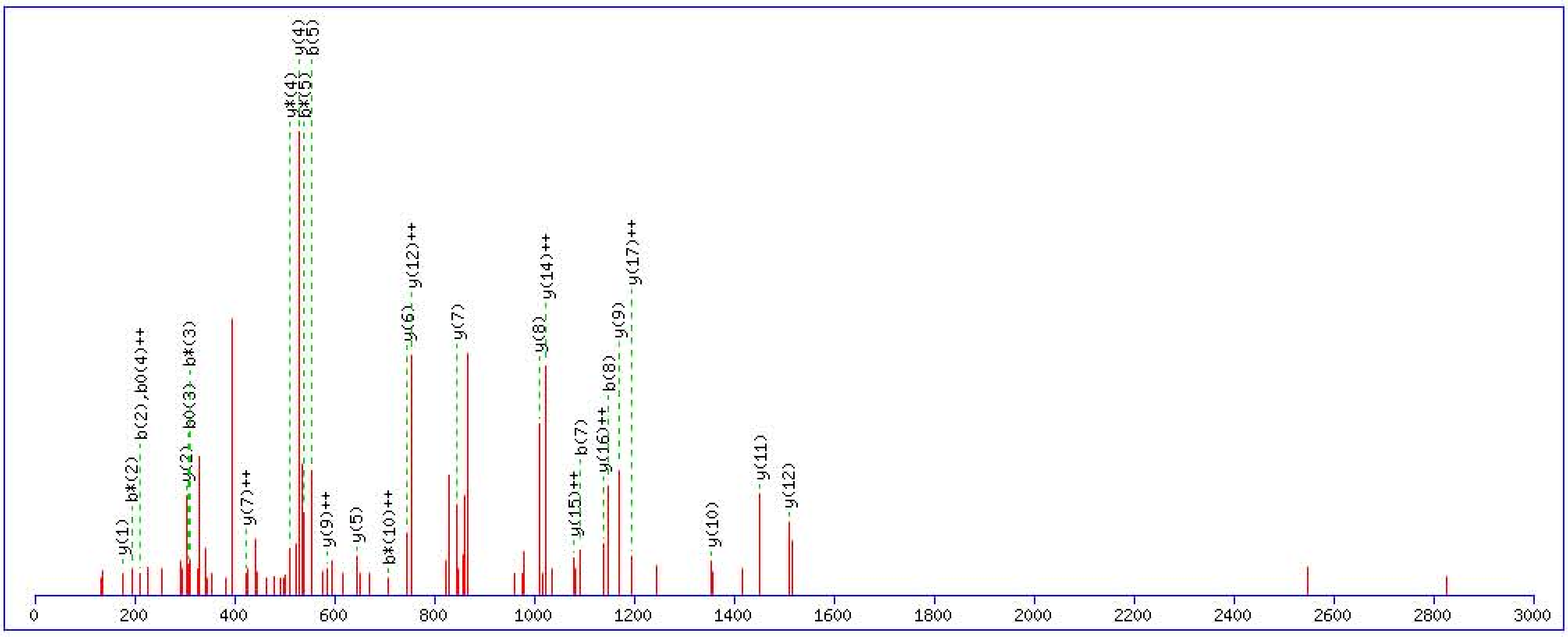
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPDNDPQGPWCYTTDPEKR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

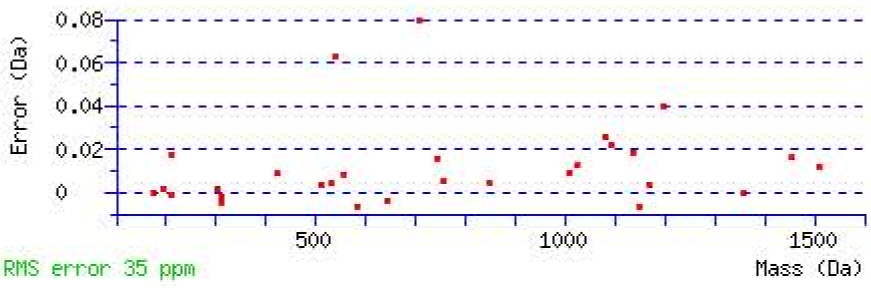
Match to Query 66606: 2600.165442 from(867.729090,3+) rtinseconds(1942) index(78055)
Title: Locus:1.1.1.2890.26 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

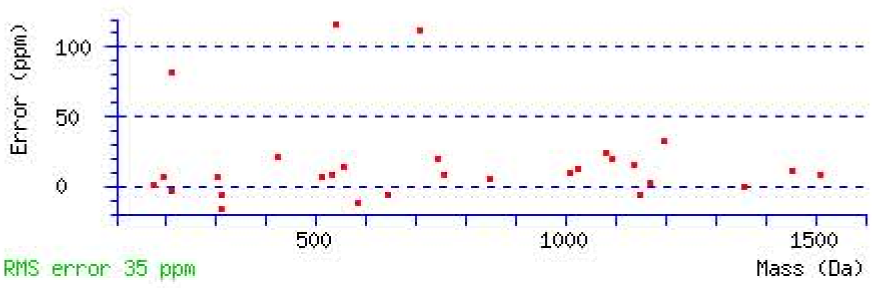
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2600.142410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00011
Matches : 29/208 fragment ions using 64 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							19
2	**212.102967**	106.555121	195.076418	98.041847			P	2487.106759	1244.057017	2470.080210	1235.543743	2469.096194	1235.051735	18
3	327.129910	164.068593	310.103361	155.555319	309.119345	155.063311	D	2390.053995	1195.530635	2373.027446	1187.017361	2372.043430	1186.525353	17
4	441.172837	221.090057	424.146288	212.576782	423.162272	212.084774	N	2275.027052	1138.017164	2258.000503	1129.503889	2257.016487	1129.011881	16
5	**556.199780**	278.603528	539.173231	270.090254	538.189215	269.598246	D	2160.984125	1080.995700	2143.957576	1072.482426	2142.973560	1071.990418	15
6	653.252544	327.129910	636.225995	318.616636	635.241979	318.124628	P	2045.957182	1023.482229	2028.930633	1014.968955	2027.946617	1014.476946	14
7	**1092.477870**	546.742573	1075.451321	538.229299	1074.467305	537.737290	Q	1948.904418	974.955847	1931.877869	966.442572	1930.893853	965.950564	13
8	**1149.499334**	575.253305	1132.472785	566.740030	1131.488769	566.248022	G	***1509.679092***	755.343184	1492.652543	746.829910	1491.668527	746.337902	12
9	1246.552098	623.779687	1229.525549	615.266413	1228.541533	614.774404	P	***1452.657628***	726.832452	1435.631079	718.319178	1434.647063	717.827170	11
10	1432.631411	716.819343	1415.604862	708.306069	1414.620846	707.814061	W	***1355.604864***	678.306070	1338.578315	669.792796	1337.594299	669.300788	10
11	1592.662060	796.834668	1575.635511	788.321394	1574.651495	787.829385	C	***1169.525551***	585.266414	1152.499002	576.753139	1151.514986	576.261131	9
12	1755.725389	878.366333	1738.698840	869.853058	1737.714824	869.361050	Y	***1009.494902***	505.251089	992.468353	496.737815	991.484337	496.245807	8
13	1856.773068	928.890172	1839.746519	920.376898	1838.762503	919.884889	T	***846.431573***	423.719425	829.405024	415.206150	828.421008	414.714142	7
14	1957.820747	979.414012	1940.794198	970.900737	1939.810182	970.408729	T	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	6
15	2072.847690	1036.927483	2055.821141	1028.414208	2054.837125	1027.922200	D	***644.336215***	322.671746	627.309666	314.158471	626.325650	313.666463	5
16	2169.900454	1085.453865	2152.873905	1076.940590	2151.889889	1076.448582	P	***529.309272***	265.158274	512.282723	256.645000	511.298707	256.152992	4
17	2298.943047	1149.975161	2281.916498	1141.461887	2280.932482	1140.969879	E	432.256508	216.631892	415.229959	208.118618	414.245943	207.626610	3
18	2427.038010	1214.022643	2410.011461	1205.509368	2409.027445	1205.017360	K	***303.213915***	152.110595	286.187366	143.597321			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.2	2600.142410	0.023032	NPDNDPQGPWCYTTDPEKR

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

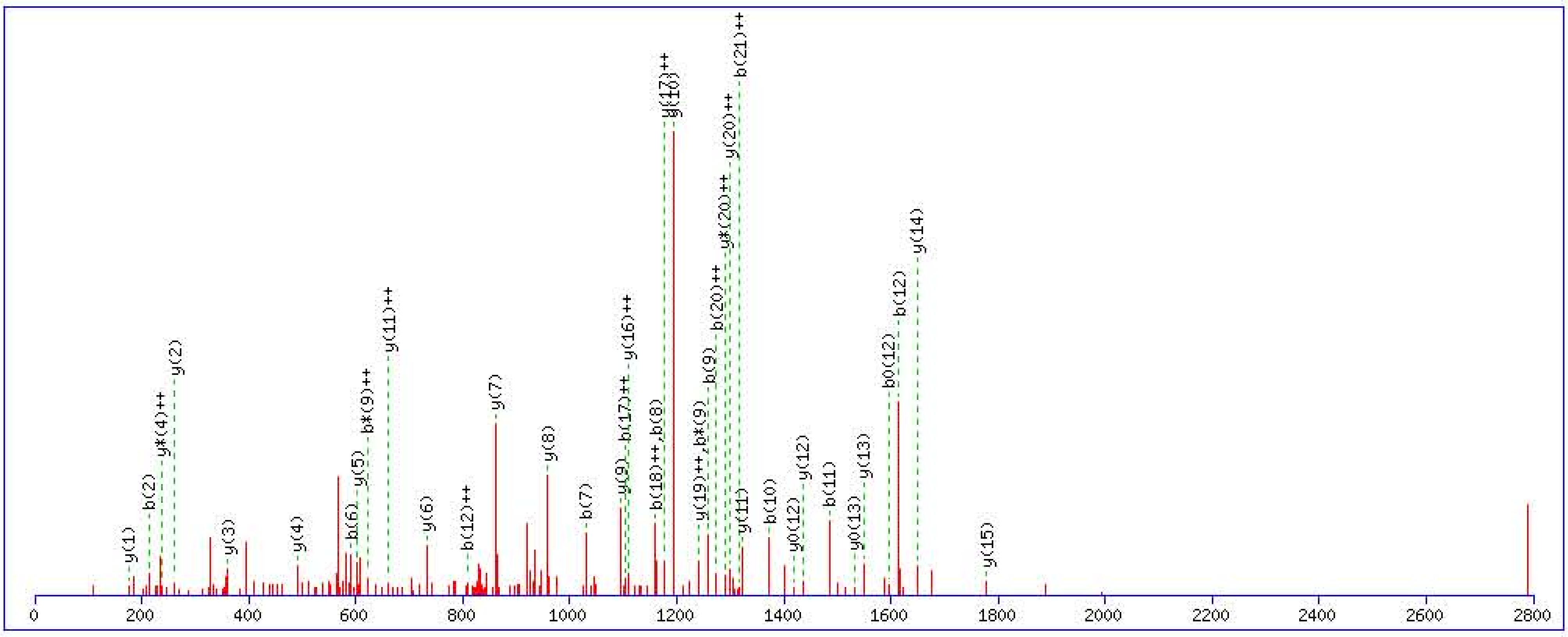
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

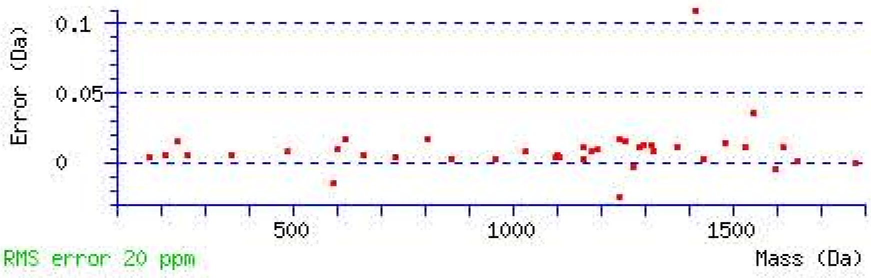
Match to Query 68869: 2806.505172 from(936.509000,3+) rtinseconds(2074) index(79021)
Title: Locus:1.1.1.2936.12 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

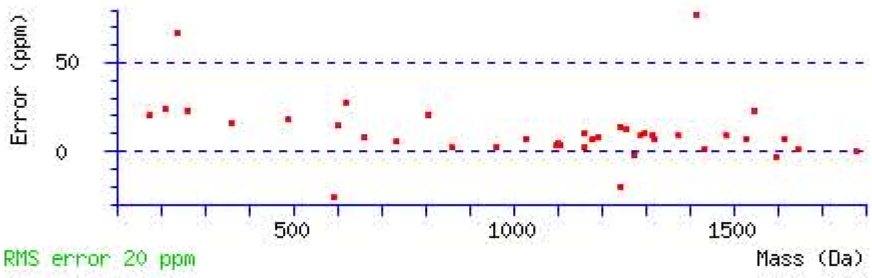
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2806.479965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 72 **Expect:** 1.1e-006
Matches : 40/224 fragment ions using 84 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							22
2	**213.159754**	107.083515					I	2708.418847	1354.713061	2691.392298	1346.199787	2690.408282	1345.707779	21
3	326.243818	163.625547					L	2595.334783	1298.171029	2578.308234	1289.657755	2577.324218	1289.165747	20
4	383.265282	192.136279					G	2482.250719	1241.628997	2465.224170	1233.115723	2464.240154	1232.623715	19
5	454.302396	227.654836					A	2425.229255	1213.118265	2408.202706	1204.604991	2407.218690	1204.112983	18
6	**591.361308**	296.184292					H	2354.192141	1177.599708	2337.165592	1169.086434	2336.181576	1168.594426	17
7	**1030.586634**	515.796955	1013.560085	507.283681			Q	2217.133229	1109.070252	2200.106680	1100.556978	2199.122664	1100.064970	16
8	**1159.629227**	580.318252	1142.602678	571.804977	1141.618662	571.312969	E	***1777.907903***	889.457590	1760.881354	880.944315	1759.897338	880.452307	15
9	**1258.697641**	629.852459	1241.671092	621.339184	1240.687076	620.847176	V	***1648.865310***	824.936293	1631.838761	816.423019	1630.854745	815.931011	14
10	**1372.740568**	686.873922	1355.714019	678.360648	1354.730003	677.868640	N	***1549.796896***	775.402086	1532.770347	766.888812	1531.786331	766.396804	13
11	**1485.824632**	743.415954	1468.798083	734.902680	1467.814067	734.410672	L	***1435.753969***	718.380623	1418.727420	709.867348	1417.743404	709.375340	12
12	**1614.867225**	**807.937251**	1597.840676	799.423976	1596.856660	798.931968	E	***1322.669905***	661.838591	1305.643356	653.325316	1304.659340	652.833308	11
13	1711.919989	856.463633	1694.893440	847.950358	1693.909424	847.458350	P	***1193.627312***	597.317294	1176.600763	588.804020	1175.616747	588.312012	10
14	1848.978901	924.993089	1831.952352	916.479814	1830.968336	915.987806	H	***1096.574548***	548.790912	1079.547999	540.277638	1078.563983	539.785630	9
15	1948.047315	974.527296	1931.020766	966.014021	1930.036750	965.522013	V	***959.515636***	480.261456	942.489087	471.748182	941.505071	471.256174	8
16	2076.105893	1038.556584	2059.079344	1030.043310	2058.095328	1029.551302	Q	***860.447222***	430.727249	843.420673	422.213975	842.436657	421.721967	7
17	2205.148486	**1103.077881**	2188.121937	1094.564606	2187.137921	1094.072598	E	***732.388644***	366.697960	715.362095	358.184686	714.378079	357.692678	6
18	2318.232550	**1159.619913**	2301.206001	1151.106638	2300.221985	1150.614631	I	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
19	2447.275143	1224.141210	2430.248594	1215.627935	2429.264578	1215.135927	E	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
20	2546.343557	**1273.675417**	2529.317008	1265.162142	2528.332992	1264.670134	V	***361.219394***	181.113335	344.192845	172.600060	343.208829	172.108052	3
21	2633.375585	**1317.191431**	2616.349036	1308.678156	2615.365020	1308.186148	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VILGAHQEVNLEPHVQEIEVSR
(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	2806.479965	0.025207	VILGAHQEVNLEPHVQEIEVSR
7.1	2806.479965	0.025207	VILGAHQEVNLEPHVQEIEVSR

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

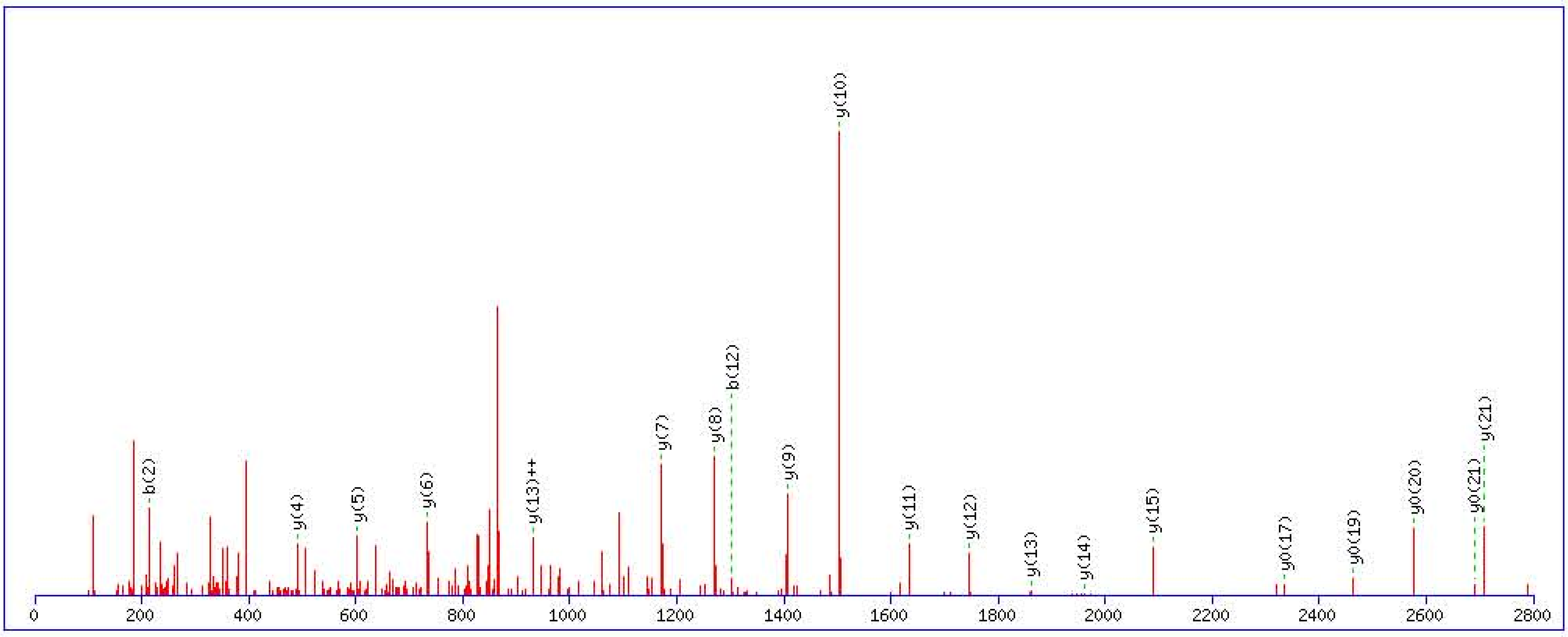
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

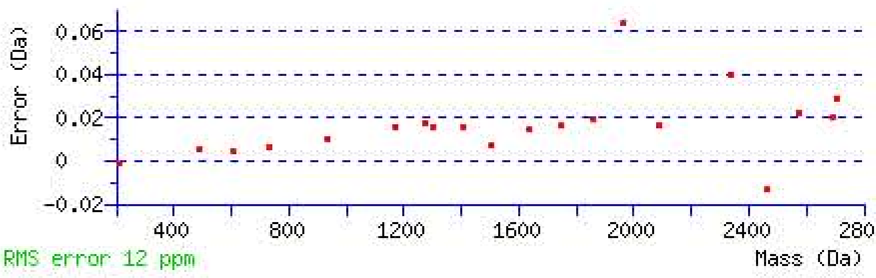
Match to Query 68870: 2806.505296 from(702.633600,4+) rtinseconds(2048) index(78835)
Title: Locus:1.1.1.2927.13 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

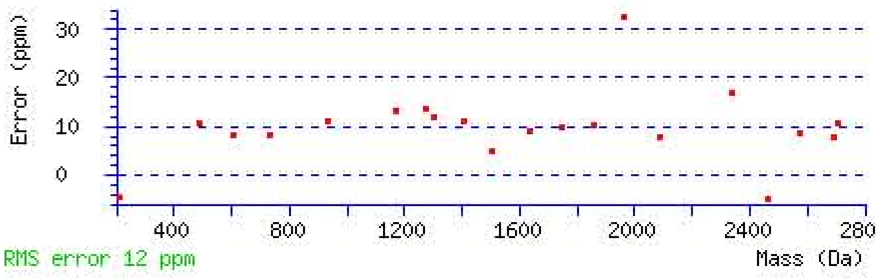
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2806.479965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 102  Expect: 1.2e-009
Matches : 20/224 fragment ions using 25 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							22
2	**213.159754**	107.083515					I	***2708.418847***	1354.713061	2691.392298	1346.199787	2690.408282	1345.707779	21
3	326.243818	163.625547					L	2595.334783	1298.171029	2578.308234	1289.657755	2577.324218	1289.165747	20
4	383.265282	192.136279					G	2482.250719	1241.628997	2465.224170	1233.115723	2464.240154	1232.623715	19
5	454.302396	227.654836					A	2425.229255	1213.118265	2408.202706	1204.604991	2407.218690	1204.112983	18
6	591.361308	296.184292					H	2354.192141	1177.599708	2337.165592	1169.086434	2336.181576	1168.594426	17
7	719.419886	360.213581	702.393337	351.700307			Q	2217.133229	1109.070252	2200.106680	1100.556978	2199.122664	1100.064970	16
8	848.462479	424.734878	831.435930	416.221603	830.451914	415.729595	E	***2089.074651***	1045.040963	2072.048102	1036.527689	2071.064086	1036.035681	15
9	947.530893	474.269085	930.504344	465.755810	929.520328	465.263802	V	***1960.032058***	980.519667	1943.005509	972.006393	1942.021493	971.514385	14
10	1061.573820	531.290548	1044.547271	522.777274	1043.563255	522.285266	N	***1860.963644***	930.985460	1843.937095	922.472186	1842.953079	921.980178	13
11	1174.657884	587.832580	1157.631335	579.319306	1156.647319	578.827297	L	***1746.920717***	873.963997	1729.894168	865.450722	1728.910152	864.958714	12
12	**1303.700477**	652.353877	1286.673928	643.840602	1285.689912	643.348594	E	***1633.836653***	817.421965	1616.810104	808.908690	1615.826088	808.416682	11
13	1400.753241	700.880259	1383.726692	692.366984	1382.742676	691.874976	P	***1504.794060***	752.900668	1487.767511	744.387394	1486.783495	743.895386	10
14	1537.812153	769.409715	1520.785604	760.896440	1519.801588	760.404432	H	***1407.741296***	704.374286	1390.714747	695.861012	1389.730731	695.369004	9
15	1636.880567	818.943922	1619.854018	810.430647	1618.870002	809.938639	V	***1270.682384***	635.844830	1253.655835	627.331556	1252.671819	626.839548	8
16	2076.105893	1038.556584	2059.079344	1030.043310	2058.095328	1029.551302	Q	***1171.613970***	586.310623	1154.587421	577.797349	1153.603405	577.305341	7
17	2205.148486	1103.077881	2188.121937	1094.564606	2187.137921	1094.072598	E	***732.388644***	366.697960	715.362095	358.184686	714.378079	357.692678	6
18	2318.232550	1159.619913	2301.206001	1151.106638	2300.221985	1150.614631	I	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
19	2447.275143	1224.141210	2430.248594	1215.627935	2429.264578	1215.135927	E	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
20	2546.343557	1273.675417	2529.317008	1265.162142	2528.332992	1264.670134	V	361.219394	181.113335	344.192845	172.600060	343.208829	172.108052	3
21	2633.375585	1317.191431	2616.349036	1308.678156	2615.365020	1308.186148	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
22							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
101.7	2806.479965	0.025331	VILGAHQEVNLEPHVQEIEVSR
3.8	2806.479965	0.025331	VILGAHQEVNLEPHVQEIEVSR

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

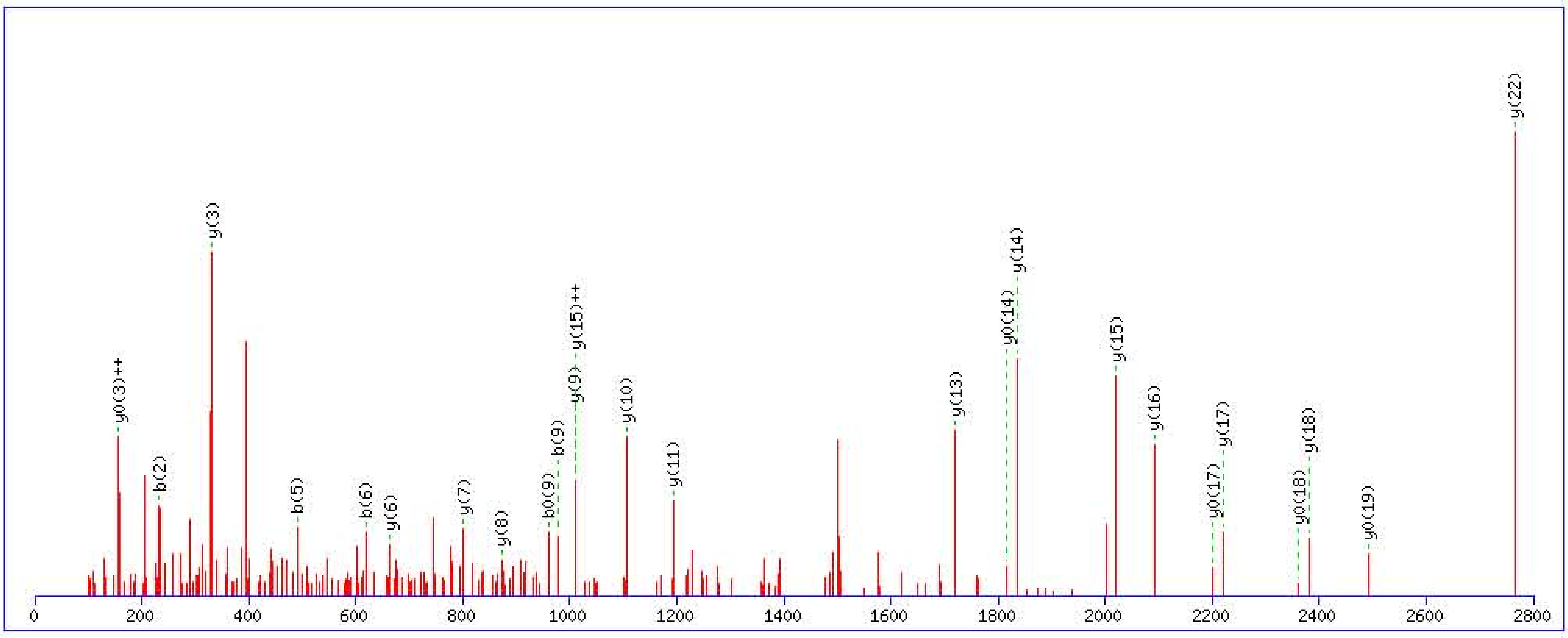
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMSGLECQAWDSQSPHAHGYIPSK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

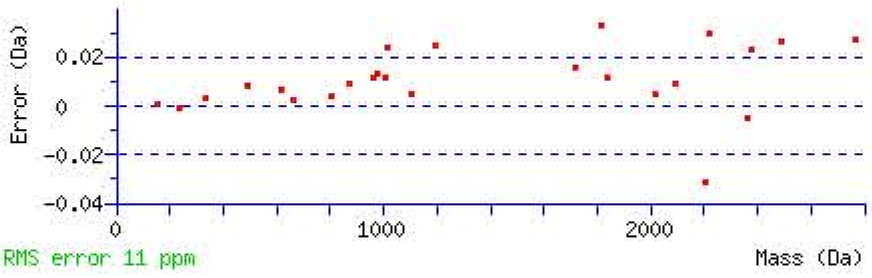
Match to Query 71590: 2997.382776 from(750.352970,4+) rtinseconds(1982) index(78376)
Title: Locus:1.1.1.2904.20 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

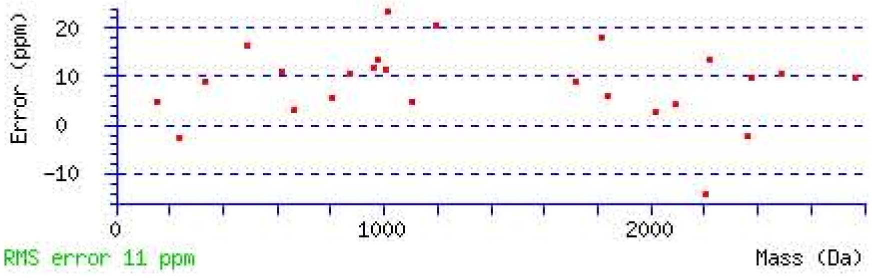
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2997.357162
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 80  Expect: 1.3e-007
Matches : 25/260 fragment ions using 46 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							24
2	**233.095440**	117.051358			215.084875	108.046076	M	2897.316768	1449.162022	2880.290219	1440.648748	2879.306203	1440.156740	23
3	320.127468	160.567372			302.116903	151.562089	S	***2766.276283***	1383.641780	2749.249734	1375.128505	2748.265718	1374.636497	22
4	377.148932	189.078104			359.138367	180.072821	G	2679.244255	1340.125766	2662.217706	1331.612491	2661.233690	1331.120483	21
5	**490.232996**	245.620136			472.222431	236.614853	L	2622.222791	1311.615034	2605.196242	1303.101759	2604.212226	1302.609751	20
6	**619.275589**	310.141433			601.265024	301.136150	E	2509.138727	1255.073002	2492.112178	1246.559727	2491.128162	1246.067719	19
7	779.306238	390.156757			761.295673	381.151475	C	***2380.096134***	1190.551705	2363.069585	1182.038431	2362.085569	1181.546423	18
8	907.364816	454.186046	890.338267	445.672772	889.354251	445.180764	Q	***2220.065485***	1110.536381	2203.038936	1102.023106	2202.054920	1101.531098	17
9	**978.401930**	489.704603	961.375381	481.191329	960.391365	480.699321	A	***2092.006907***	1046.507092	2074.980358	1037.993817	2073.996342	1037.501809	16
10	1164.481243	582.744260	1147.454694	574.230985	1146.470678	573.738977	W	***2020.969793***	1010.988535	2003.943244	1002.475260	2002.959228	1001.983252	15
11	1279.508186	640.257731	1262.481637	631.744457	1261.497621	631.252449	D	***1834.890480***	917.948878	1817.863931	909.435604	1816.879915	908.943596	14
12	1366.540214	683.773745	1349.513665	675.260471	1348.529649	674.768463	S	***1719.863537***	860.435407	1702.836988	851.922132	1701.852972	851.430124	13
13	1805.765540	903.386408	1788.738991	894.873134	1787.754975	894.381126	Q	1632.831509	816.919393	1615.804960	808.406118	1614.820944	807.914110	12
14	1892.797568	946.902422	1875.771019	938.389148	1874.787003	937.897140	S	***1193.606183***	597.306730	1176.579634	588.793455	1175.595618	588.301447	11
15	1989.850332	995.428804	1972.823783	986.915530	1971.839767	986.423522	P	***1106.574155***	553.790716	1089.547606	545.277441	1088.563590	544.785433	10
16	2126.909244	1063.958260	2109.882695	1055.444986	2108.898679	1054.952978	H	***1009.521391***	505.264334	992.494842	496.751059	991.510826	496.259051	9
17	2197.946358	1099.476817	2180.919809	1090.963543	2179.935793	1090.471535	A	***872.462479***	436.734878	855.435930	428.221603	854.451914	427.729595	8
18	2335.005270	1168.006273	2317.978721	1159.492999	2316.994705	1159.000991	H	***801.425365***	401.216321	784.398816	392.703046	783.414800	392.211038	7
19	2392.026734	1196.517005	2375.000185	1188.003731	2374.016169	1187.511723	G	***664.366453***	332.686865	647.339904	324.173590	646.355888	323.681582	6
20	2555.090063	1278.048670	2538.063514	1269.535395	2537.079498	1269.043387	Y	607.344989	304.176133	590.318440	295.662858	589.334424	295.170850	5
21	2668.174127	1334.590702	2651.147578	1326.077427	2650.163562	1325.585419	I	444.281660	222.644468	427.255111	214.131194	426.271095	213.639186	4
22	2765.226891	1383.117084	2748.200342	1374.603809	2747.216326	1374.111801	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
23	2852.258919	1426.633098	2835.232370	1418.119823	2834.248354	1417.627815	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
24							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.3	2997.357162	0.025614	TMSGLECQAWDSQSPHAHGYIPSK
35.2	2997.357162	0.025614	TMSGLECQAWDSQSPHAHGYIPSK

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

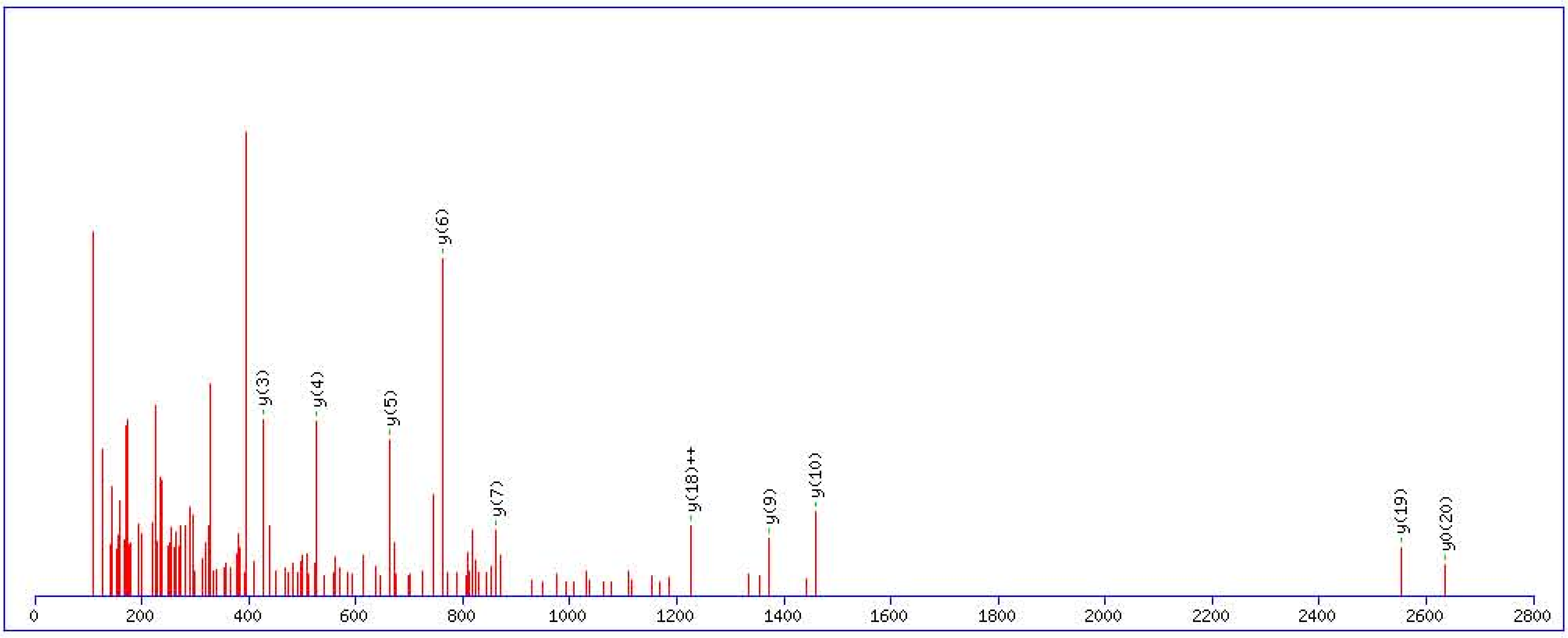
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

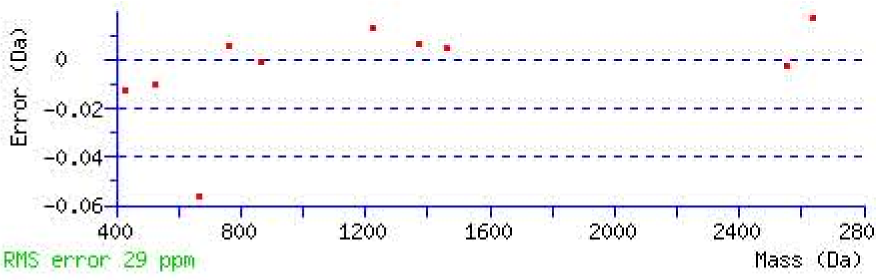
Match to Query 72401: 3092.465484 from(516.418190,6+) rtinseconds(1401) index(74471)
Title: Locus:1.1.1.2702.17 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

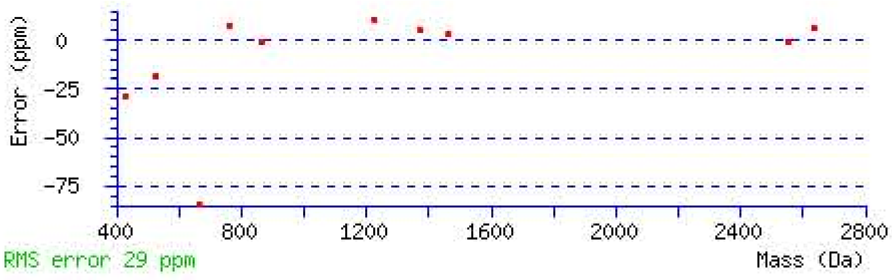
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3092.457016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.002
Matches : 10/270 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							25
2	172.071667	86.539471	155.045118	78.026197			N	3036.442790	1518.725033	3019.416241	1510.211758	3018.432225	1509.719750	24
3	271.140081	136.073679	254.113532	127.560404			V	2922.399863	1461.703569	2905.373314	1453.190295	2904.389298	1452.698287	23
4	342.177195	171.592236	325.150646	163.078961			A	2823.331449	1412.169362	2806.304900	1403.656088	2805.320884	1403.164080	22
5	441.245609	221.126443	424.219060	212.613168			V	2752.294335	1376.650805	2735.267786	1368.137531	2734.283770	1367.645523	21
6	542.293288	271.650282	525.266739	263.137008	524.282723	262.645000	T	2653.225921	1327.116598	2636.199372	1318.603324	2635.215356	1318.111316	20
7	641.361702	321.184489	624.335153	312.671215	623.351137	312.179207	V	***2552.178242***	1276.592759	2535.151693	1268.079484	2534.167677	1267.587476	19
8	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	S	2453.109828	1227.058552	2436.083279	1218.545277	2435.099263	1218.053269	18
9	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	G	2366.077800	1183.542538	2349.051251	1175.029263	2348.067235	1174.537255	17
10	922.474106	461.740691	905.447557	453.227417	904.463541	452.735409	H	2309.056336	1155.031806	2292.029787	1146.518531	2291.045771	1146.026523	16
11	1023.521785	512.264530	1006.495236	503.751256	1005.511220	503.259248	T	2171.997424	1086.502350	2154.970875	1077.989075	2153.986859	1077.497067	15
12	1183.552434	592.279855	1166.525885	583.766581	1165.541869	583.274572	C	2070.949745	1035.978510	2053.923196	1027.465236	2052.939180	1026.973228	14
13	1311.611012	656.309144	1294.584463	647.795870	1293.600447	647.303862	Q	1910.919096	955.963186	1893.892547	947.449911	1892.908531	946.957903	13
14	1448.669924	724.838600	1431.643375	716.325326	1430.659359	715.833318	H	1782.860518	891.933897	1765.833969	883.420622	1764.849953	882.928614	12
15	1634.749237	817.878257	1617.722688	809.364982	1616.738672	808.872974	W	1645.801606	823.404441	1628.775057	814.891166	1627.791041	814.399158	11
16	1721.781265	861.394271	1704.754716	852.880996	1703.770700	852.388988	S	***1459.722293***	730.364784	1442.695744	721.851510	1441.711728	721.359502	10
17	1792.818379	896.912828	1775.791830	888.399553	1774.807814	887.907545	A	***1372.690265***	686.848770	1355.663716	678.335496	1354.679700	677.843488	9
18	2232.043705	1116.525490	2215.017156	1108.012216	2214.033140	1107.520208	Q	1301.653151	651.330213	1284.626602	642.816939	1283.642586	642.324931	8
19	2333.091384	1167.049330	2316.064835	1158.536055	2315.080819	1158.044047	T	***862.427825***	431.717550	845.401276	423.204276	844.417260	422.712268	7
20	2430.144148	1215.575712	2413.117599	1207.062437	2412.133583	1206.570429	P	***761.380146***	381.193711	744.353597	372.680436	743.369581	372.188428	6
21	2567.203060	1284.105168	2550.176511	1275.591893	2549.192495	1275.099885	H	***664.327382***	332.667329	647.300833	324.154054	646.316817	323.662046	5
22	2668.250739	1334.629007	2651.224190	1326.115733	2650.240174	1325.623725	T	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	4
23	2805.309651	1403.158463	2788.283102	1394.645189	2787.299086	1394.153181	H	***426.220791***	213.614033	409.194242	205.100759			3
24	2919.352578	1460.179927	2902.326029	1451.666652	2901.342013	1451.174644	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.2	3092.457016	0.008468	GNVAVTVSGHTCQHWSAQTPHTHNR
20.0	3092.457016	0.008468	GNVAVTVSGHTCQHWSAQTPHTHNR

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

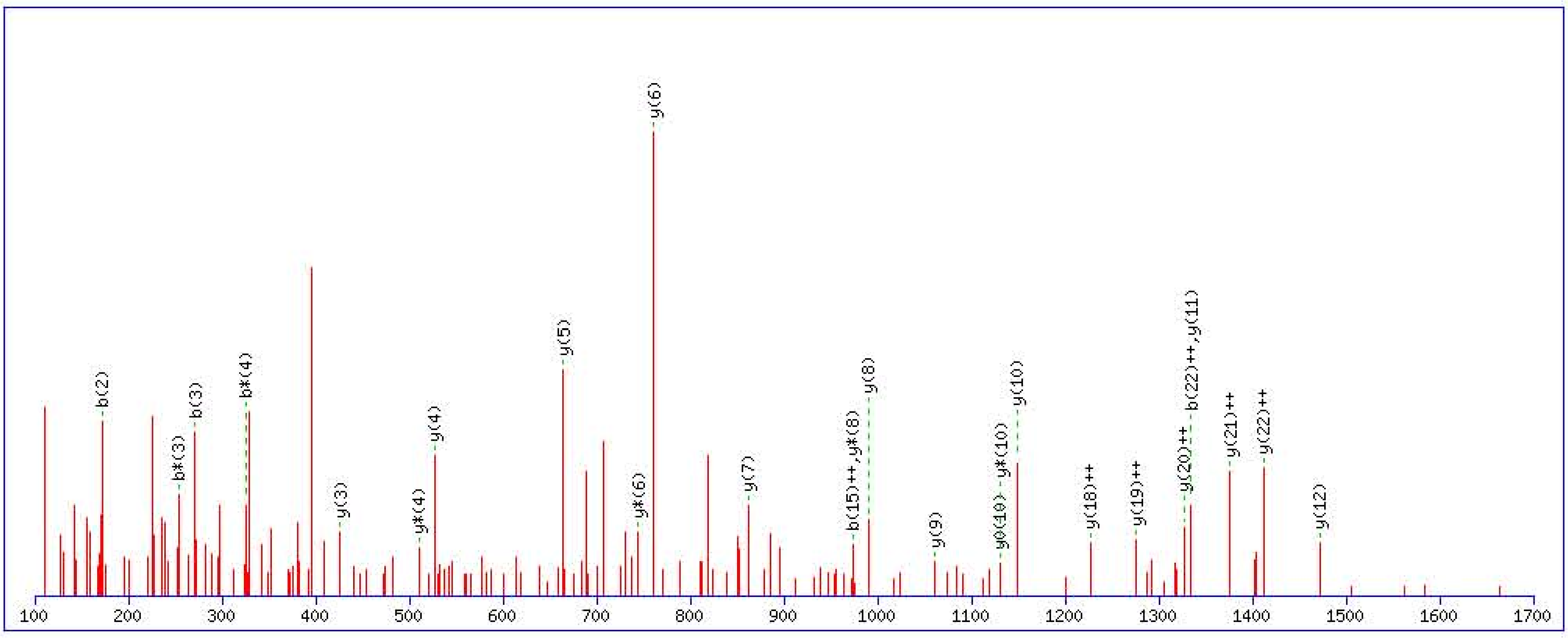
{MATRIX SCIENCE} **Mascot Search Results**

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 72404: 3092.468870 from(619.501050,5+) rtinseconds(1437) index(74770)
Title: Locus:1.1.1.2714.22 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3092.457016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00047
Matches : 26/270 fragment ions using 45 most intense peaks   (help)
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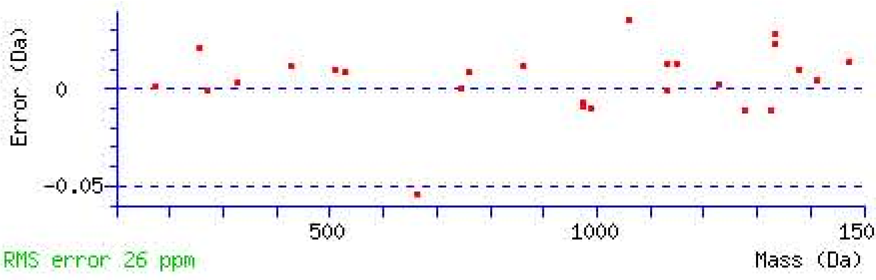
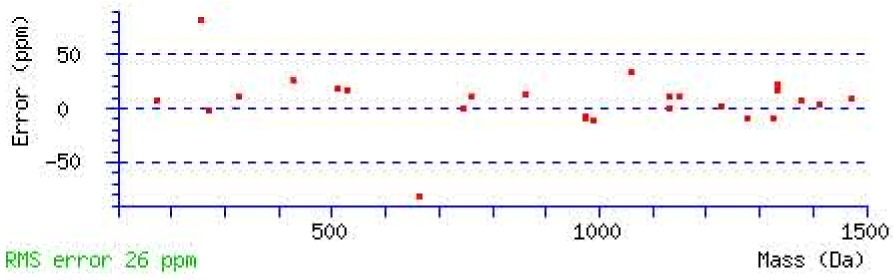
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							25
2	**172.071667**	86.539471	155.045118	78.026197			N	3036.442790	1518.725033	3019.416241	1510.211758	3018.432225	1509.719750	24
3	**271.140081**	136.073679	254.113532	127.560404			V	2922.399863	1461.703569	2905.373314	1453.190295	2904.389298	1452.698287	23
4	342.177195	171.592236	325.150646	163.078961			A	2823.331449	1412.169362	2806.304900	1403.656088	2805.320884	1403.164080	22
5	441.245609	221.126443	424.219060	212.613168			V	2752.294335	1376.650805	2735.267786	1368.137531	2734.283770	1367.645523	21
6	542.293288	271.650282	525.266739	263.137008	524.282723	262.645000	T	2653.225921	1327.116598	2636.199372	1318.603324	2635.215356	1318.111316	20
7	641.361702	321.184489	624.335153	312.671215	623.351137	312.179207	V	2552.178242	1276.592759	2535.151693	1268.079484	2534.167677	1267.587476	19
8	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	S	2453.109828	1227.058552	2436.083279	1218.545277	2435.099263	1218.053269	18
9	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	G	2366.077800	1183.542538	2349.051251	1175.029263	2348.067235	1174.537255	17
10	922.474106	461.740691	905.447557	453.227417	904.463541	452.735409	H	2309.056336	1155.031806	2292.029787	1146.518531	2291.045771	1146.026523	16
11	1023.521785	512.264530	1006.495236	503.751256	1005.511220	503.259248	T	2171.997424	1086.502350	2154.970875	1077.989075	2153.986859	1077.497067	15
12	1183.552434	592.279855	1166.525885	583.766581	1165.541869	583.274572	C	2070.949745	1035.978510	2053.923196	1027.465236	2052.939180	1026.973228	14
13	1622.777760	811.892518	1605.751211	803.379244	1604.767195	802.887236	Q	1910.919096	955.963186	1893.892547	947.449911	1892.908531	946.957903	13
14	1759.836672	880.421974	1742.810123	871.908700	1741.826107	871.416692	H	***1471.693770***	736.350523	1454.667221	727.837248	1453.683205	727.345240	12
15	1945.915985	**973.461631**	1928.889436	964.948356	1927.905420	964.456348	W	***1334.634858***	667.821067	1317.608309	659.307792	1316.624293	658.815784	11
16	2032.948013	1016.977645	2015.921464	1008.464370	2014.937448	1007.972362	S	***1148.555545***	574.781410	1131.528996	566.268136	1130.544980	565.776128	10
17	2103.985127	1052.496201	2086.958578	1043.982927	2085.974562	1043.490919	A	***1061.523517***	531.265396	1044.496968	522.752122	1043.512952	522.260114	9
18	2232.043705	1116.525490	2215.017156	1108.012216	2214.033140	1107.520208	Q	***990.486403***	495.746839	973.459854	487.233565	972.475838	486.741557	8
19	2333.091384	1167.049330	2316.064835	1158.536055	2315.080819	1158.044047	T	***862.427825***	431.717550	845.401276	423.204276	844.417260	422.712268	7
20	2430.144148	1215.575712	2413.117599	1207.062437	2412.133583	1206.570429	P	***761.380146***	381.193711	744.353597	372.680436	743.369581	372.188428	6
21	2567.203060	1284.105168	2550.176511	1275.591893	2549.192495	1275.099885	H	***664.327382***	332.667329	647.300833	324.154054	646.316817	323.662046	5
22	2668.250739	**1334.629007**	2651.224190	1326.115733	2650.240174	1325.623725	T	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	4
23	2805.309651	1403.158463	2788.283102	1394.645189	2787.299086	1394.153181	H	***426.220791***	213.614033	409.194242	205.100759			3
24	2919.352578	1460.179927	2902.326029	1451.666652	2901.342013	1451.174644	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.6	3092.457016	0.011854	GNVAVTVSGHTCQHWSAQTPHTHNR
14.6	3092.457016	0.011854	GNVAVTVSGHTCQHWSAQTPHTHNR

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

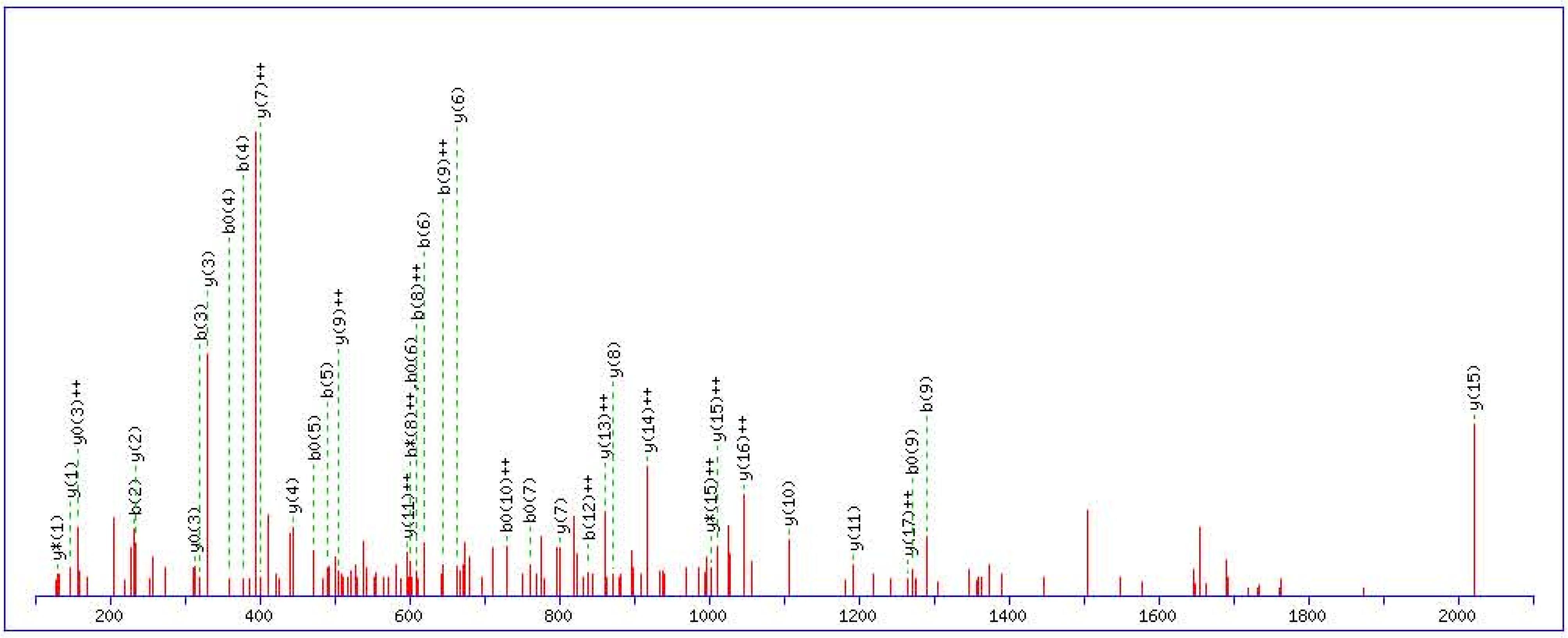
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMSGLECQAWDSQSPHAGYIPSK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

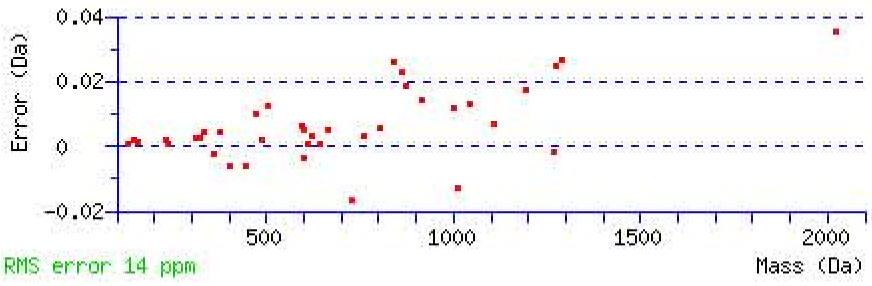
Match to Query 76203: 3308.567096 from(828.149050,4+) rtinseconds(2135) index(79429)
Title: Locus:1.1.1.2957.18 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

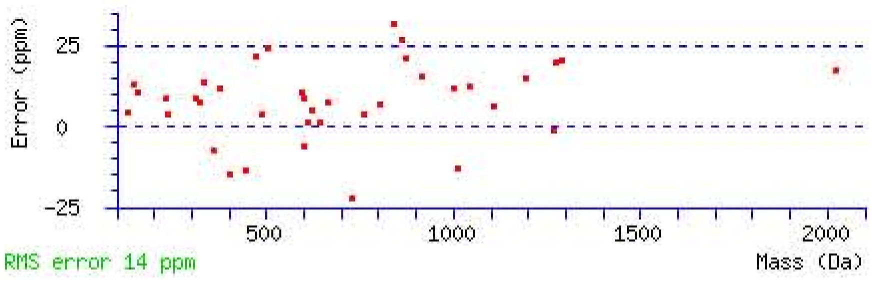
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3308.523911
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.026
Matches : 38/260 fragment ions using 123 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							24
2	***233.095440***	117.051358			215.084875	108.046076	M	3208.483516	1604.745396	3191.456967	1596.232121	3190.472951	1595.740114	23
3	***320.127468***	160.567372			302.116903	151.562089	S	3077.443031	1539.225154	3060.416482	1530.711879	3059.432466	1530.219871	22
4	***377.148932***	189.078104			359.138367	180.072821	G	2990.411003	1495.709140	2973.384454	1487.195865	2972.400438	1486.703857	21
5	***490.232996***	245.620136			472.222431	236.614853	L	2933.389539	1467.198408	2916.362990	1458.685133	2915.378974	1458.193125	20
6	***619.275589***	310.141433			601.265024	301.136150	E	2820.305475	1410.656376	2803.278926	1402.143101	2802.294910	1401.651093	19
7	779.306238	390.156757			761.295673	381.151475	C	2691.262882	1346.135079	2674.236333	1337.621804	2673.252317	1337.129796	18
8	1218.531564	**609.769420**	1201.505015	601.256146	1200.520999	600.764138	Q	2531.232233	1266.119755	2514.205684	1257.606480	2513.221668	1257.114472	17
9	***1289.568678***	**645.287977**	1272.542129	636.774703	1271.558113	636.282695	A	2092.006907	1046.507091	2074.980358	1037.993817	2073.996342	1037.501809	16
10	1475.647991	738.327634	1458.621442	729.814359	1457.637426	729.322351	W	***2020.969793***	1010.988535	2003.943244	1002.475260	2002.959228	1001.983252	15
11	1590.674934	795.841105	1573.648385	787.327831	1572.664369	786.835823	D	1834.890480	917.948878	1817.863931	909.435604	1816.879915	908.943596	14
12	1677.706962	**839.357119**	1660.680413	830.843845	1659.696397	830.351837	S	1719.863537	860.435407	1702.836988	851.922132	1701.852972	851.430124	13
13	2116.932288	1058.969782	2099.905739	1050.456507	2098.921723	1049.964499	Q	1632.831509	816.919393	1615.804960	808.406118	1614.820944	807.914110	12
14	2203.964316	1102.485796	2186.937767	1093.972521	2185.953751	1093.480513	S	***1193.606183***	597.306730	1176.579634	588.793455	1175.595618	588.301447	11
15	2301.017080	1151.012178	2283.990531	1142.498903	2283.006515	1142.006895	P	***1106.574155***	553.790716	1089.547606	545.277441	1088.563590	544.785433	10
16	2438.075992	1219.541634	2421.049443	1211.028359	2420.065427	1210.536351	H	1009.521391	505.264334	992.494842	496.751059	991.510826	496.259051	9
17	2509.113106	1255.060191	2492.086557	1246.546917	2491.102541	1246.054909	A	***872.462479***	436.734878	855.435930	428.221603	854.451914	427.729595	8
18	2646.172018	1323.589647	2629.145469	1315.076372	2628.161453	1314.584365	H	***801.425365***	401.216321	784.398816	392.703046	783.414800	392.211038	7
19	2703.193482	1352.100379	2686.166933	1343.587104	2685.182917	1343.095097	G	***664.366453***	332.686865	647.339904	324.173590	646.355888	323.681582	6
20	2866.256811	1433.632044	2849.230262	1425.118769	2848.246246	1424.626761	Y	607.344989	304.176133	590.318440	295.662858	589.334424	295.170850	5
21	2979.340875	1490.174076	2962.314326	1481.660801	2961.330310	1481.168793	I	***444.281660***	222.644468	427.255111	214.131194	426.271095	213.639186	4
22	3076.393639	1538.700458	3059.367090	1530.187183	3058.383074	1529.695175	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
23	3163.425667	1582.216472	3146.399118	1573.703197	3145.415102	1573.211189	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
24							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.1	3308.523911	0.043185	TMSGLECQAWDSQSPHAHGYIPSK

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

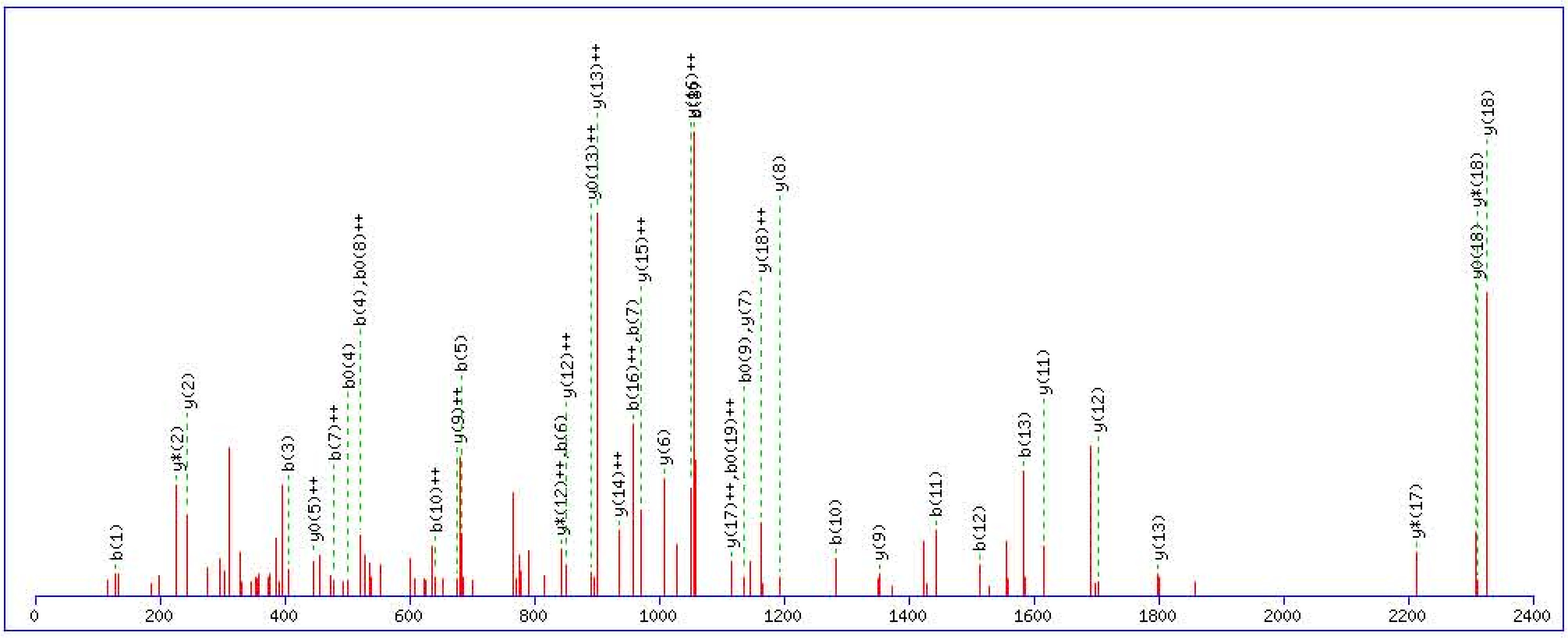
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

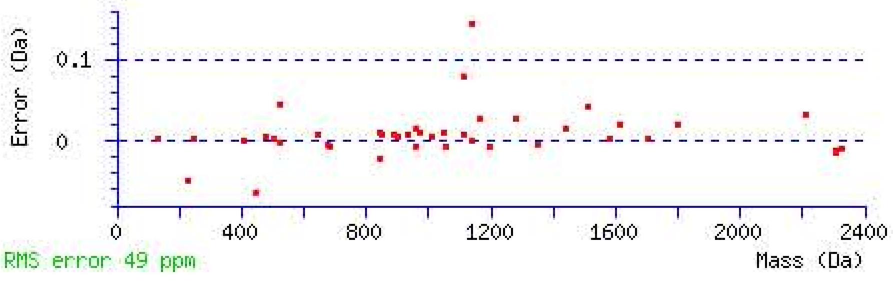
Match to Query 76689: 3382.574136 from(846.650810,4+) rtinseconds(1927) index(77930)
Title: Locus:1.1.1.2885.26 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

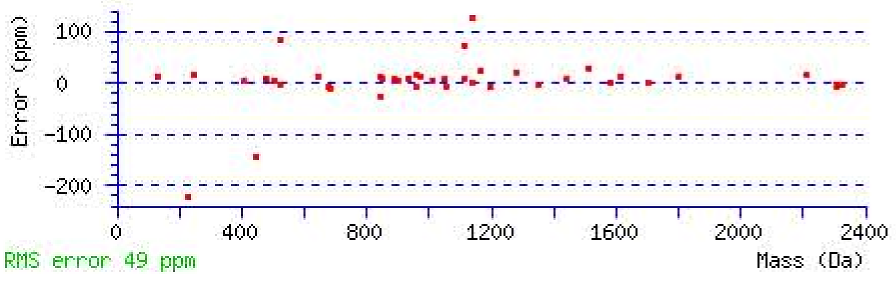
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3382.549469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q22     : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00024
Matches : 42/290 fragment ions using 91 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							26
2	242.186303	121.596790	225.159754	113.083515			L	3255.461780	1628.234528	3238.435231	1619.721253	3237.451215	1619.229245	25
3	***405.249632***	203.128454	388.223083	194.615180			Y	3142.377716	1571.692496	3125.351167	1563.179221	3124.367151	1562.687213	24
4	***520.276575***	260.641926	503.250026	252.128651	502.266010	251.636643	D	2979.314387	1490.160831	2962.287838	1481.647557	2961.303822	1481.155549	23
5	***683.339904***	342.173590	666.313355	333.660316	665.329339	333.168308	Y	2864.287444	1432.647360	2847.260895	1424.134085	2846.276879	1423.642077	22
6	***843.370553***	422.188915	826.344004	413.675640	825.359988	413.183632	C	2701.224115	1351.115695	2684.197566	1342.602421	2683.213550	1342.110413	21
7	***958.397496***	**479.702386**	941.370947	471.189112	940.386931	470.697104	D	2541.193466	1271.100371	2524.166917	1262.587096	2523.182901	1262.095089	20
8	***1057.465910***	529.236593	1040.439361	520.723319	1039.455345	520.231311	V	2426.166523	1213.586899	2409.139974	1205.073625	2408.155958	1204.581617	19
9	1154.518674	577.762975	1137.492125	569.249701	1136.508109	568.757693	P	***2327.098109***	1164.052692	2310.071560	1155.539418	2309.087544	1155.047410	18
10	***1282.577252***	**641.792264**	1265.550703	633.278990	1264.566687	632.786982	Q	2230.045345	1115.526310	2213.018796	1107.013036	2212.034780	1106.521028	17
11	***1442.607901***	721.807589	1425.581352	713.294314	1424.597336	712.802306	C	2101.986767	1051.497021	2084.960218	1042.983747	2083.976202	1042.491739	16
12	***1513.645015***	757.326146	1496.618466	748.812871	1495.634450	748.320863	A	1941.956118	971.481697	1924.929569	962.968423	1923.945553	962.476415	15
13	***1584.682129***	792.844703	1567.655580	784.331428	1566.671564	783.839420	A	1870.919004	935.963140	1853.892455	927.449866	1852.908439	926.957858	14
14	1681.734893	841.371085	1664.708344	832.857810	1663.724328	832.365802	P	***1799.881890***	900.444583	1782.855341	891.931309	1781.871325	891.439301	13
15	1768.766921	884.887099	1751.740372	876.373824	1750.756356	875.881816	S	***1702.829126***	851.918201	1685.802577	843.404927	1684.818561	842.912919	12
16	1915.835335	**958.421306**	1898.808786	949.908031	1897.824770	949.416023	F	***1615.797098***	808.402187	1598.770549	799.888913	1597.786533	799.396905	11
17	2030.862278	1015.934777	2013.835729	1007.421503	2012.851713	1006.929495	D	1468.728684	734.867980	1451.702135	726.354706	1450.718119	725.862698	10
18	2190.892927	1095.950102	2173.866378	1087.436827	2172.882362	1086.944819	C	***1353.701741***	677.354509	1336.675192	668.841234	1335.691176	668.349226	9
19	2247.914391	1124.460834	2230.887842	1115.947559	2229.903826	1115.455551	G	***1193.671092***	597.339184	1176.644543	588.825910	1175.660527	588.333902	8
20	2376.009354	1188.508315	2358.982805	1179.995041	2357.998789	1179.503033	K	***1136.649628***	568.828452	1119.623079	560.315178	1118.639063	559.823170	7
21	2473.062118	1237.034697	2456.035569	1228.521423	2455.051553	1228.029415	P	***1008.554665***	504.780971	991.528116	496.267696	990.544100	495.775688	6
22	2912.287444	1456.647360	2895.260895	1448.134086	2894.276879	1447.642078	Q	911.501901	456.254589	894.475352	447.741314	893.491336	447.249306	5
23	3011.355858	1506.181567	2994.329309	1497.668293	2993.345293	1497.176285	V	472.276575	236.641925	455.250026	228.128651	454.266010	227.636643	4
24	3140.398451	1570.702864	3123.371902	1562.189589	3122.387886	1561.697581	E	373.208161	187.107719	356.181612	178.594444	355.197596	178.102436	3
25	3237.451215	1619.229246	3220.424666	1610.715971	3219.440650	1610.223963	P	***244.165568***	122.586422	227.139019	114.073148			2
26							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KLYDYCDVPQCAAPSFDCGKPQVEPK
(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	3382.549469	0.024667	KLYDYCDVPQCAAPSFDCGKPQVEPK
3.3	3382.549469	0.024667	KLYDYCDVPQCAAPSFDCGKPQVEPK

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

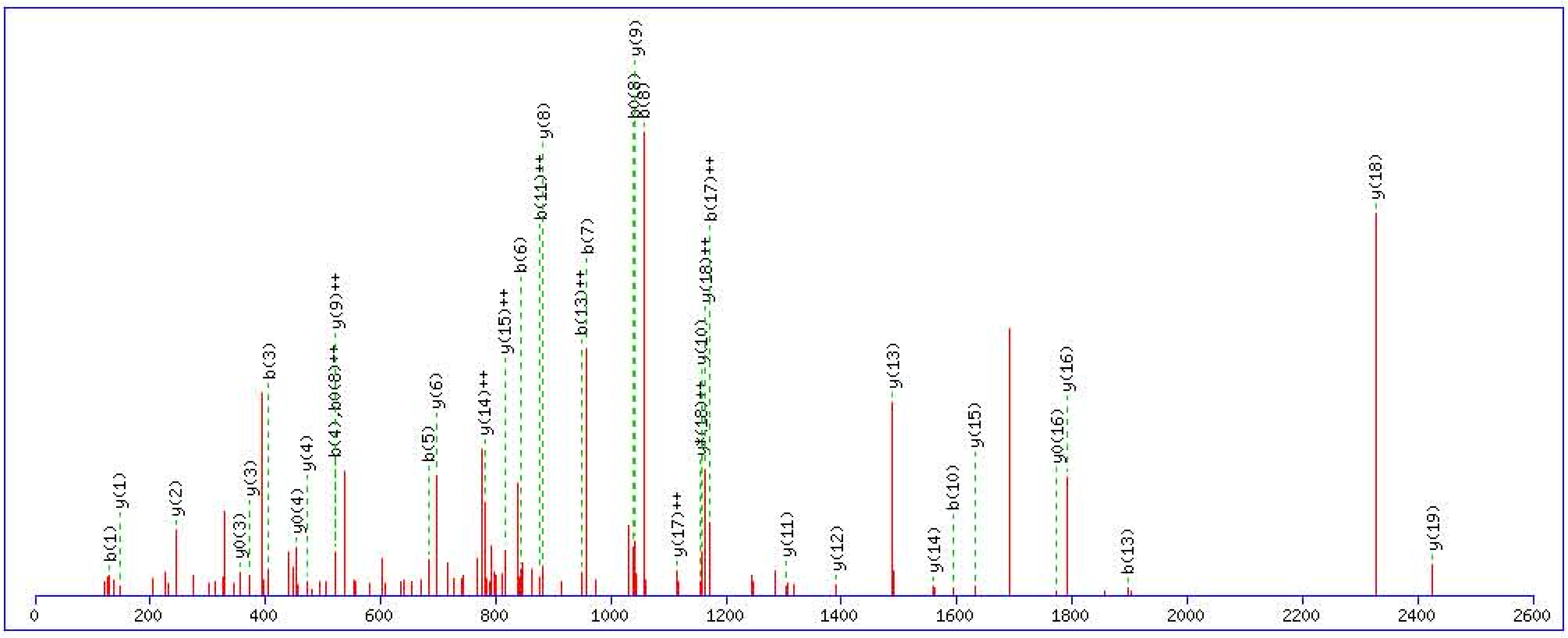
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 76690: 3382.582416 from(846.652880,4+) rtinseconds(1980) index(78355)
Title: Locus:1.1.1.2903.24 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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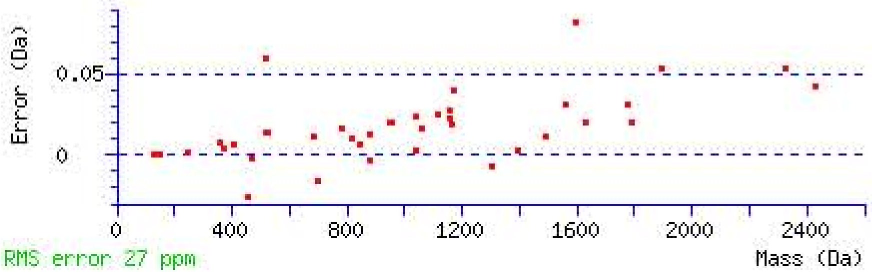
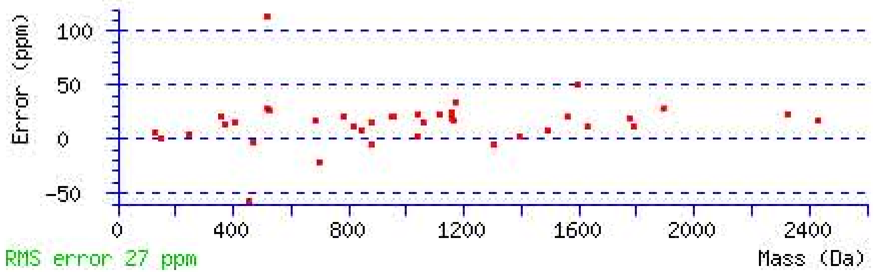
Monoisotopic mass of neutral peptide Mr(calc): 3382.549469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 75  Expect: 1.4e-007
Matches : 39/290 fragment ions using 86 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							26
2	242.186303	121.596790	225.159754	113.083515			L	3255.461780	1628.234528	3238.435231	1619.721253	3237.451215	1619.229245	25
3	***405.249632***	203.128454	388.223083	194.615180			Y	3142.377716	1571.692496	3125.351167	1563.179221	3124.367151	1562.687213	24
4	***520.276575***	260.641926	503.250026	252.128651	502.266010	251.636643	D	2979.314387	1490.160831	2962.287838	1481.647557	2961.303822	1481.155549	23
5	***683.339904***	342.173590	666.313355	333.660316	665.329339	333.168308	Y	2864.287444	1432.647360	2847.260895	1424.134085	2846.276879	1423.642077	22
6	***843.370553***	422.188915	826.344004	413.675640	825.359988	413.183632	C	2701.224115	1351.115695	2684.197566	1342.602421	2683.213550	1342.110413	21
7	***958.397496***	479.702386	941.370947	471.189112	940.386931	470.697104	D	2541.193466	1271.100371	2524.166917	1262.587096	2523.182901	1262.095088	20
8	***1057.465910***	529.236593	1040.439361	520.723319	1039.455345	520.231311	V	***2426.166523***	1213.586899	2409.139974	1205.073625	2408.155958	1204.581617	19
9	1154.518674	577.762975	1137.492125	569.249701	1136.508109	568.757693	P	***2327.098109***	1164.052692	2310.071560	1155.539418	2309.087544	1155.047410	18
10	***1593.744000***	797.375638	1576.717451	788.862364	1575.733435	788.370356	Q	2230.045345	1115.526310	2213.018796	1107.013036	2212.034780	1106.521028	17
11	1753.774649	**877.390963**	1736.748100	868.877688	1735.764084	868.385680	C	***1790.820019***	895.913647	1773.793470	887.400373	1772.809454	886.908365	16
12	1824.811763	912.909520	1807.785214	904.396245	1806.801198	903.904237	A	***1630.789370***	815.898323	1613.762821	807.385048	1612.778805	806.893040	15
13	***1895.848877***	**948.428077**	1878.822328	939.914802	1877.838312	939.422794	A	***1559.752256***	780.379766	1542.725707	771.866491	1541.741691	771.374483	14
14	1992.901641	996.954459	1975.875092	988.441184	1974.891076	987.949176	P	***1488.715142***	744.861209	1471.688593	736.347934	1470.704577	735.855926	13
15	2079.933669	1040.470472	2062.907120	1031.957198	2061.923104	1031.465190	S	***1391.662378***	696.334827	1374.635829	687.821552	1373.651813	687.329544	12
16	2227.002083	1114.004679	2209.975534	1105.491405	2208.991518	1104.999397	F	***1304.630350***	652.818813	1287.603801	644.305538	1286.619785	643.813530	11
17	2342.029026	**1171.518151**	2325.002477	1163.004876	2324.018461	1162.512868	D	***1157.561936***	579.284606	1140.535387	570.771331	1139.551371	570.279323	10
18	2502.059675	1251.533475	2485.033126	1243.020201	2484.049110	1242.528193	C	***1042.534993***	521.771135	1025.508444	513.257860	1024.524428	512.765852	9
19	2559.081139	1280.044207	2542.054590	1271.530933	2541.070574	1271.038925	G	***882.504344***	441.755810	865.477795	433.242536	864.493779	432.750528	8
20	2687.176102	1344.091689	2670.149553	1335.578414	2669.165537	1335.086406	K	825.482880	413.245078	808.456331	404.731804	807.472315	404.239796	7
21	2784.228866	1392.618071	2767.202317	1384.104796	2766.218301	1383.612788	P	***697.387917***	349.197597	680.361368	340.684322	679.377352	340.192314	6
22	2912.287444	1456.647360	2895.260895	1448.134085	2894.276879	1447.642077	Q	600.335153	300.671215	583.308604	292.157940	582.324588	291.665932	5
23	3011.355858	1506.181567	2994.329309	1497.668292	2993.345293	1497.176284	V	***472.276575***	236.641925	455.250026	228.128651	454.266010	227.636643	4
24	3140.398451	1570.702863	3123.371902	1562.189589	3122.387886	1561.697581	E	***373.208161***	187.107719	356.181612	178.594444	355.197596	178.102436	3
25	3237.451215	1619.229245	3220.424666	1610.715971	3219.440650	1610.223963	P	***244.165568***	122.586422	227.139019	114.073148			2
26							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
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11.1	3382.549469	0.032947	KLYDYCDVPQCAAPSFDCGKPQVEPK
1.6	3382.580414	0.002002	HLYPNTPYAYTFWTYMMNARSKNVGWR
1.6	3382.580414	0.002002	HLYPNTPYAYTFWTYMMNARSKNVGWR
0.4	3382.595993	-0.013577	GSTSNFYSQGLESIPQLCNENRVLREDNR

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

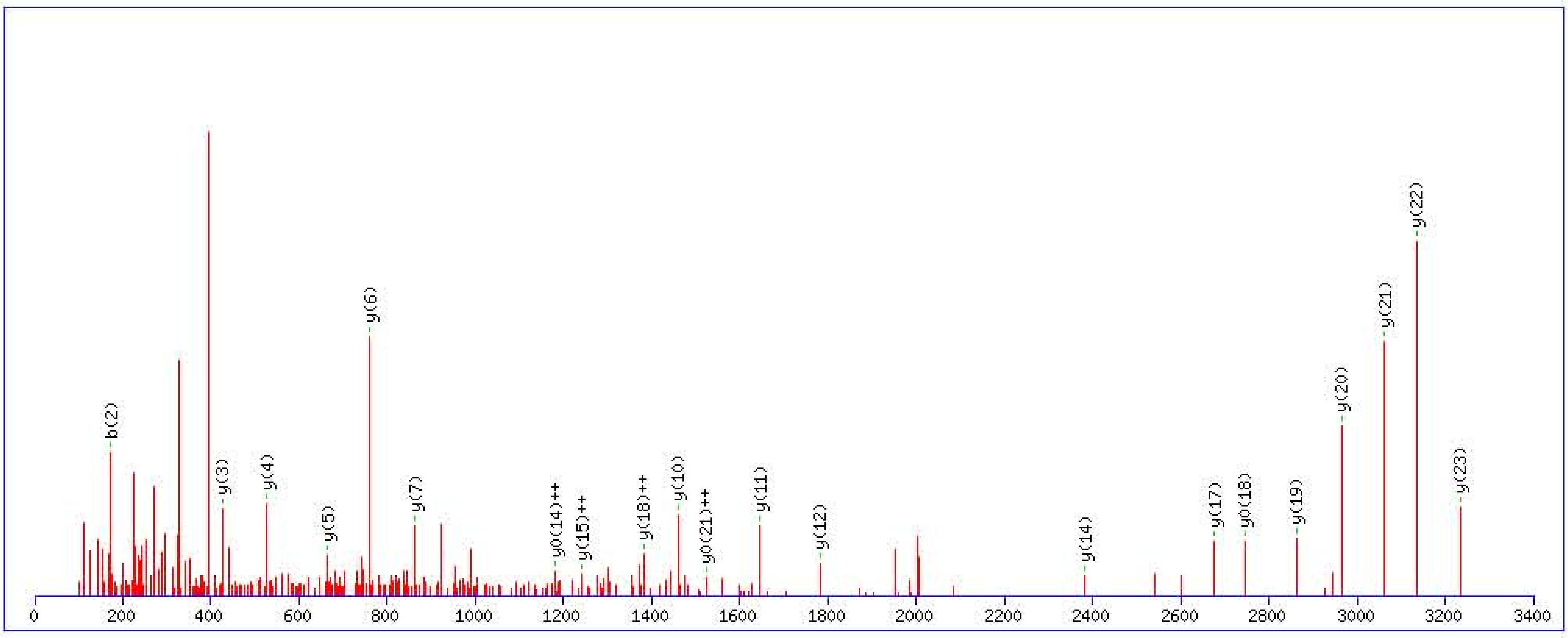
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 76999: 3403.637270 from(681.734730,5+) rtinseconds(1643) index(76167)
Title: Locus:1.1.1.2786.16 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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Monoisotopic mass of neutral peptide Mr(calc): 3403.623764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 109  Expect: 3.5e-010
Matches : 21/270 fragment ions using 29 most intense peaks   (help)
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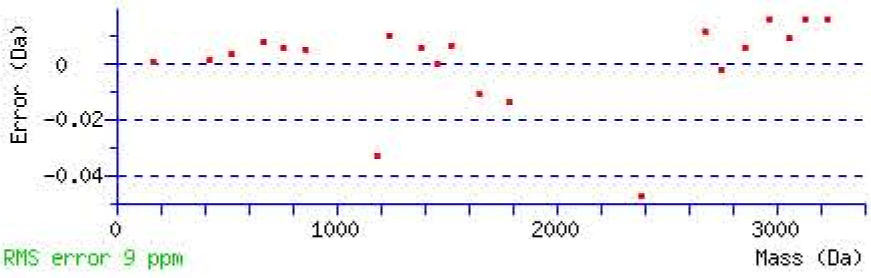
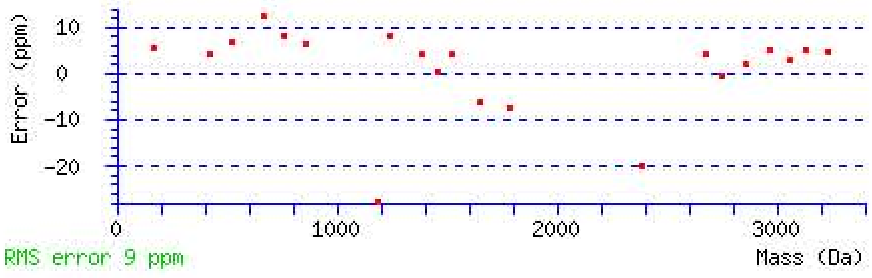
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							25
2	172.071667	86.539471	155.045118	78.026197			N	3347.609538	1674.308407	3330.582989	1665.795132	3329.598973	1665.303124	24
3	271.140081	136.073679	254.113532	127.560404			V	***3233.566611***	1617.286943	3216.540062	1608.773669	3215.556046	1608.281661	23
4	342.177195	171.592236	325.150646	163.078961			A	***3134.498197***	1567.752736	3117.471648	1559.239462	3116.487632	1558.747454	22
5	441.245609	221.126443	424.219060	212.613168			V	***3063.461083***	1532.234179	3046.434534	1523.720905	3045.450518	1523.228897	21
6	542.293288	271.650282	525.266739	263.137008	524.282723	262.645000	T	***2964.392669***	1482.699972	2947.366120	1474.186698	2946.382104	1473.694690	20
7	641.361702	321.184489	624.335153	312.671215	623.351137	312.179207	V	***2863.344990***	1432.176133	2846.318441	1423.662858	2845.334425	1423.170850	19
8	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	S	2764.276576	1382.641926	2747.250027	1374.128651	2746.266011	1373.636643	18
9	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	G	***2677.244548***	1339.125912	2660.217999	1330.612637	2659.233983	1330.120629	17
10	922.474106	461.740691	905.447557	453.227417	904.463541	452.735409	H	2620.223084	1310.615180	2603.196535	1302.101905	2602.212519	1301.609897	16
11	1023.521785	512.264530	1006.495236	503.751256	1005.511220	503.259248	T	2483.164172	1242.085724	2466.137623	1233.572449	2465.153607	1233.080441	15
12	1183.552434	592.279855	1166.525885	583.766581	1165.541869	583.274572	C	***2382.116493***	1191.561884	2365.089944	1183.048610	2364.105928	1182.556602	14
13	1622.777760	811.892518	1605.751211	803.379244	1604.767195	802.887236	Q	2222.085844	1111.546560	2205.059295	1103.033285	2204.075279	1102.541277	13
14	1759.836672	880.421974	1742.810123	871.908700	1741.826107	871.416692	H	***1782.860518***	891.933897	1765.833969	883.420622	1764.849953	882.928614	12
15	1945.915985	973.461631	1928.889436	964.948356	1927.905420	964.456348	W	***1645.801606***	823.404441	1628.775057	814.891166	1627.791041	814.399158	11
16	2032.948013	1016.977645	2015.921464	1008.464370	2014.937448	1007.972362	S	***1459.722293***	730.364784	1442.695744	721.851510	1441.711728	721.359502	10
17	2103.985127	1052.496201	2086.958578	1043.982927	2085.974562	1043.490919	A	1372.690265	686.848770	1355.663716	678.335496	1354.679700	677.843488	9
18	2543.210453	1272.108865	2526.183904	1263.595590	2525.199888	1263.103582	Q	1301.653151	651.330213	1284.626602	642.816939	1283.642586	642.324931	8
19	2644.258132	1322.632704	2627.231583	1314.119429	2626.247567	1313.627421	T	***862.427825***	431.717550	845.401276	423.204276	844.417260	422.712268	7
20	2741.310896	1371.159086	2724.284347	1362.645811	2723.300331	1362.153803	P	***761.380146***	381.193711	744.353597	372.680436	743.369581	372.188428	6
21	2878.369808	1439.688542	2861.343259	1431.175267	2860.359243	1430.683259	H	***664.327382***	332.667329	647.300833	324.154054	646.316817	323.662046	5
22	2979.417487	1490.212381	2962.390938	1481.699107	2961.406922	1481.207099	T	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	4
23	3116.476399	1558.741837	3099.449850	1550.228563	3098.465834	1549.736555	H	***426.220791***	213.614033	409.194242	205.100759			3
24	3230.519326	1615.763301	3213.492777	1607.250026	3212.508761	1606.758018	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
108.8	3403.623764	0.013506	GNVAVTVSGHTCQHWSAQTPHTHNR

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

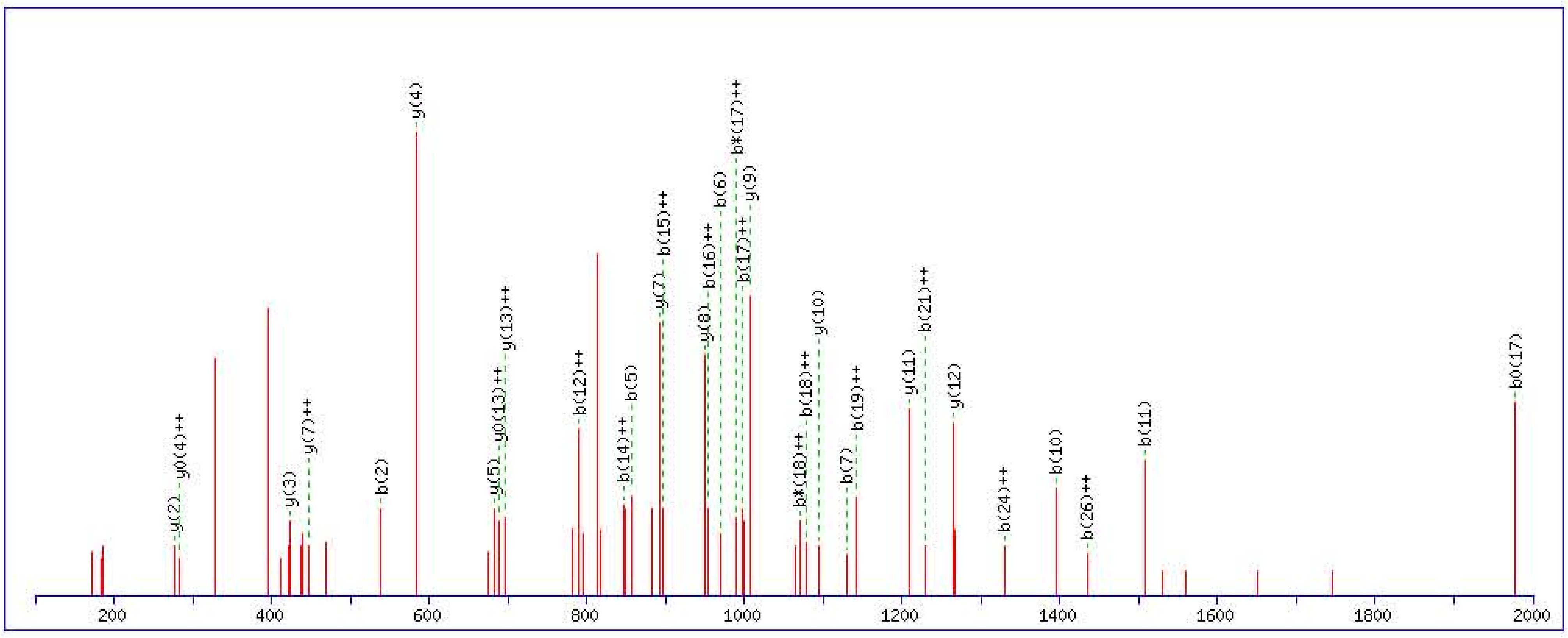
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 78346: 3547.618936 from(887.912010,4+) rtinseconds(2167) index(79697)
Title: Locus:1.1.1.2968.26 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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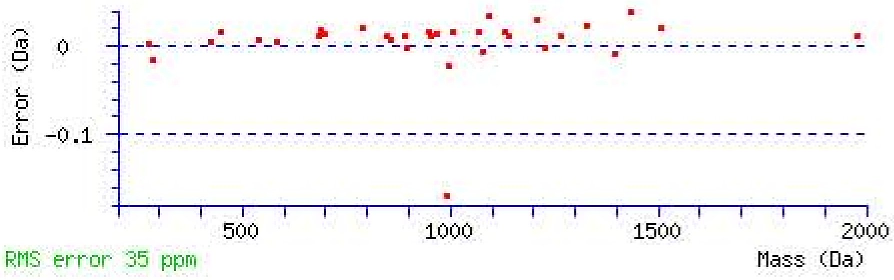
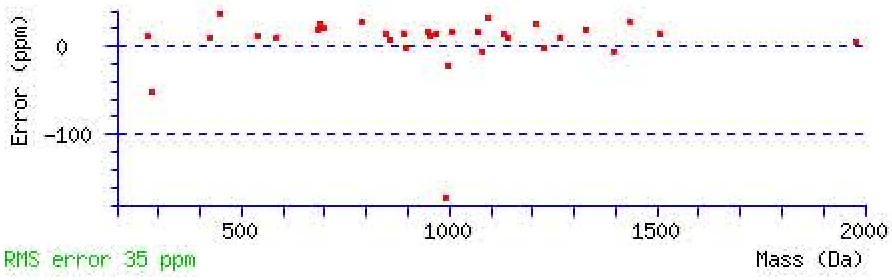
Monoisotopic mass of neutral peptide Mr(calc): 3547.584061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 71  Expect: 8.2e-007
Matches : 33/352 fragment ions using 57 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483					V							31
2	***539.301016***	270.154146	522.274467	261.640872			Q	3449.522877	1725.265076	3432.496328	1716.751802	3431.512312	1716.259794	30
3	626.333044	313.670160	609.306495	305.156886	608.322479	304.664878	S	3010.297551	1505.652413	2993.271002	1497.139139	2992.286986	1496.647131	29
4	727.380723	364.194000	710.354174	355.680725	709.370158	355.188717	T	2923.265523	1462.136399	2906.238974	1453.623125	2905.254958	1453.131117	28
5	***856.423316***	428.715296	839.396767	420.202022	838.412751	419.710014	E	2822.217844	1411.612560	2805.191295	1403.099285	2804.207279	1402.607277	27
6	***969.507380***	485.257328	952.480831	476.744054	951.496815	476.252046	L	2693.175251	1347.091263	2676.148702	1338.577989	2675.164686	1338.085981	26
7	***1129.538029***	565.272653	1112.511480	556.759378	1111.527464	556.267370	C	2580.091187	1290.549231	2563.064638	1282.035957	2562.080622	1281.543949	25
8	1200.575143	600.791210	1183.548594	592.277935	1182.564578	591.785927	A	2420.060538	1210.533907	2403.033989	1202.020632	2402.049973	1201.528624	24
9	1257.596607	629.301942	1240.570058	620.788667	1239.586042	620.296659	G	2349.023424	1175.015350	2331.996875	1166.502075	2331.012859	1166.010067	23
10	***1394.655519***	697.831397	1377.628970	689.318123	1376.644954	688.826115	H	2292.001960	1146.504618	2274.975411	1137.991343	2273.991395	1137.499335	22
11	***1507.739583***	754.373429	1490.713034	745.860155	1489.729018	745.368147	L	2154.943048	1077.975162	2137.916499	1069.461887	2136.932483	1068.969879	21
12	1578.776697	***789.891986***	1561.750148	781.378712	1560.766132	780.886704	A	2041.858984	1021.433130	2024.832435	1012.919855	2023.848419	1012.427847	20
13	1635.798161	818.402718	1618.771612	809.889444	1617.787596	809.397436	G	1970.821870	985.914573	1953.795321	977.401298	1952.811305	976.909290	19
14	1692.819625	***846.913450***	1675.793076	838.400176	1674.809060	837.908168	G	1913.800406	957.403841	1896.773857	948.890566	1895.789841	948.398558	18
15	1793.867304	***897.437290***	1776.840755	888.924015	1775.856739	888.432007	T	1856.778942	928.893109	1839.752393	920.379835	1838.768377	919.887826	17
16	1908.894247	***954.950761***	1891.867698	946.437487	1890.883682	945.945479	D	1755.731263	878.369269	1738.704714	869.855995	1737.720698	869.363987	16
17	1995.926275	***998.466775***	1978.899726	989.953501	1977.915710	989.461493	S	1640.704320	820.855798	1623.677771	812.342523	1622.693755	811.850515	15
18	2155.956924	***1078.482100***	2138.930375	1069.968825	2137.946359	1069.476817	C	1553.672292	777.339784	1536.645743	768.826509	1535.661727	768.334501	14
19	2284.015502	***1142.511389***	2266.988953	1133.998114	2266.004937	1133.506106	Q	1393.641643	697.324459	1376.615094	688.811185	1375.631078	688.319177	13
20	2341.036966	1171.022121	2324.010417	1162.508846	2323.026401	1162.016838	G	***1265.583065***	633.295170	1248.556516	624.781896	1247.572500	624.289888	12
21	2456.063909	***1228.535592***	2439.037360	1220.022318	2438.053344	1219.530310	D	***1208.561601***	604.784438	1191.535052	596.271164	1190.551036	595.779156	11
22	2543.095937	1272.051606	2526.069388	1263.538332	2525.085372	1263.046324	S	***1093.534658***	547.270967	1076.508109	538.757692	1075.524093	538.265684	10
23	2600.117401	1300.562338	2583.090852	1292.049064	2582.106836	1291.557056	G	***1006.502630***	503.754953	989.476081	495.241678	988.492065	494.749670	9
24	2657.138865	***1329.073070***	2640.112316	1320.559796	2639.128300	1320.067788	G	***949.481166***	475.244221	932.454617	466.730946	931.470601	466.238938	8
25	2754.191629	1377.599452	2737.165080	1369.086178	2736.181064	1368.594170	P	***892.459702***	446.733489	875.433153	438.220214	874.449137	437.728206	7
26	2867.275693	***1434.141484***	2850.249144	1425.628210	2849.265128	1425.136202	L	795.406938	398.207107	778.380389	389.693832	777.396373	389.201824	6
27	2966.344107	1483.675691	2949.317558	1475.162417	2948.333542	1474.670409	V	***682.322874***	341.665075	665.296325	333.151800	664.312309	332.659792	5
28	3126.374756	1563.691016	3109.348207	1555.177741	3108.364191	1554.685733	C	***583.254460***	292.130868	566.227911	283.617593	565.243895	283.125585	4
29	3273.443170	1637.225223	3256.416621	1628.711948	3255.432605	1628.219940	F	***423.223811***	212.115543	406.197262	203.602269	405.213246	203.110261	3
30	3402.485763	1701.746519	3385.459214	1693.233245	3384.475198	1692.741237	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
31							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.3	3547.584061	0.034875	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK
32.8	3547.584061	0.034875	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK

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

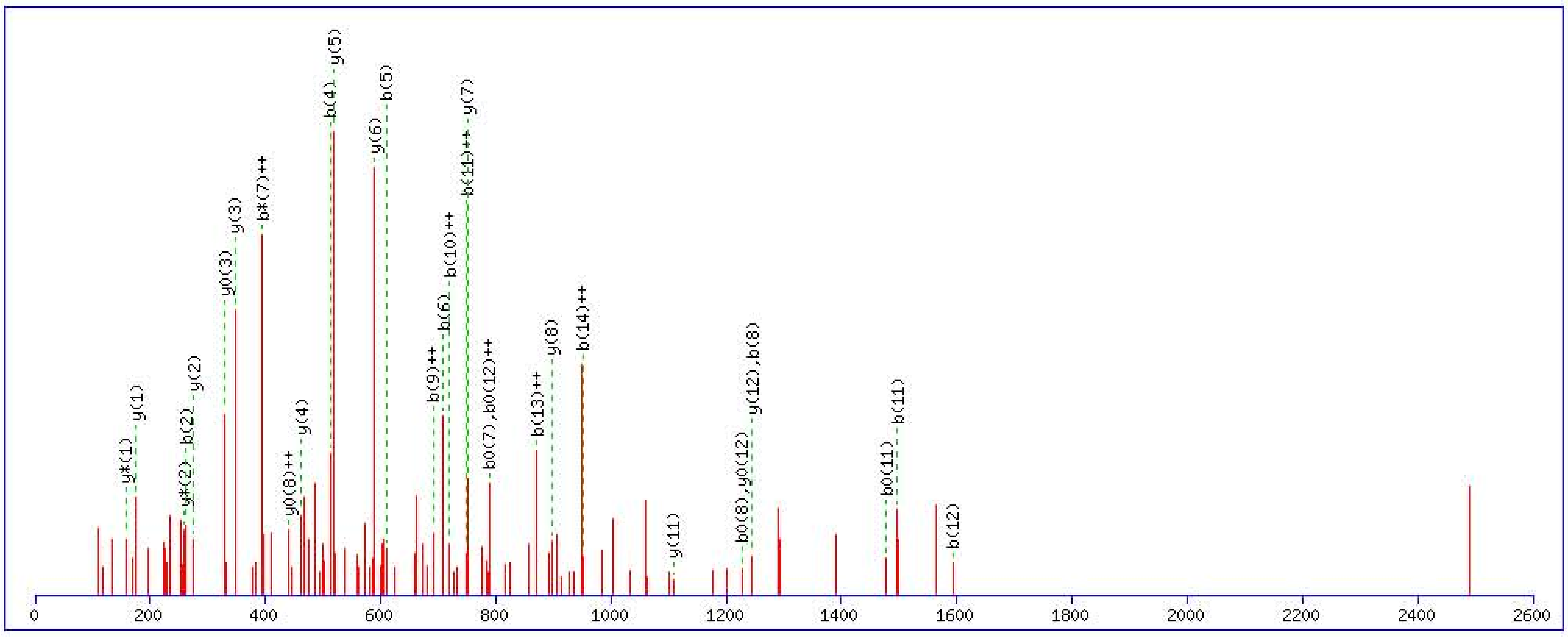
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TCNHPVPQHGGPFCAGDATR**
Found in **PROP_HUMAN**, Properdin OS=Homo sapiens GN=CFP PE=1 SV=2

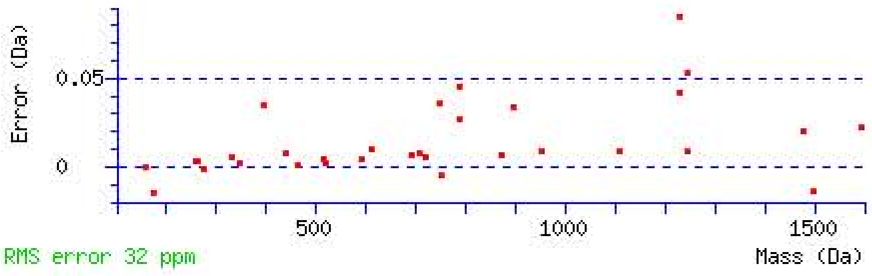
Match to Query 65057: 2489.126496 from(623.288900,4+) rtinseconds(1499) index(75253)
Title: Locus:1.1.1.2736.11 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

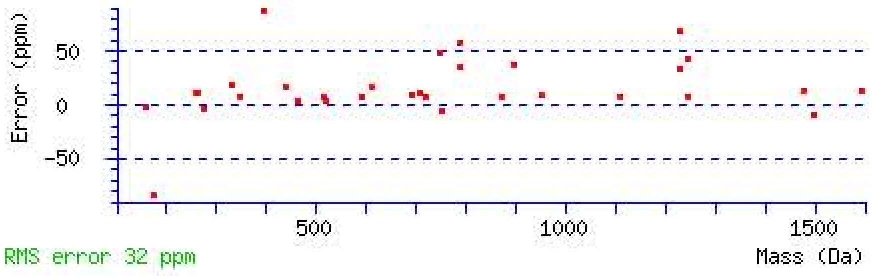
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2489.115128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 50 **Expect:** 9.5e-005
Matches : 32/222 fragment ions using 64 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							20
2	***262.085604***	131.546440			244.075039	122.541158	C	2389.074689	1195.040982	2372.048140	1186.527708	2371.064124	1186.035700	19
3	376.128531	188.567904	359.101982	180.054629	358.117966	179.562621	N	2229.044040	1115.025658	2212.017491	1106.512383	2211.033475	1106.020375	18
4	***513.187443***	257.097360	496.160894	248.584085	495.176878	248.092077	H	2115.001113	1058.004194	2097.974564	1049.490920	2096.990548	1048.998912	17
5	***610.240207***	305.623742	593.213658	297.110467	592.229642	296.618459	P	1977.942201	989.474739	1960.915652	980.961464	1959.931636	980.469456	16
6	***709.308621***	355.157949	692.282072	346.644674	691.298056	346.152666	V	1880.889437	940.948357	1863.862888	932.435082	1862.878872	931.943074	15
7	806.361385	403.684331	789.334836	395.171056	788.350820	394.679048	P	1781.821023	891.414150	1764.794474	882.900875	1763.810458	882.408867	14
8	***1245.586711***	623.296994	1228.560162	614.783719	1227.576146	614.291711	Q	1684.768259	842.887768	1667.741710	834.374493	1666.757694	833.882485	13
9	1382.645623	**691.826450**	1365.619074	683.313175	1364.635058	682.821167	H	***1245.542933***	623.275105	1228.516384	614.761830	1227.532368	614.269822	12
10	1439.667087	**720.337182**	1422.640538	711.823907	1421.656522	711.331899	G	***1108.484021***	554.745649	1091.457472	546.232374	1090.473456	545.740366	11
11	***1496.688551***	**748.847914**	1479.662002	740.334639	1478.677986	739.842631	G	1051.462557	526.234917	1034.436008	517.721642	1033.451992	517.229634	10
12	***1593.741315***	797.374296	1576.714766	788.861021	1575.730750	788.369013	P	994.441093	497.724185	977.414544	489.210910	976.430528	488.718902	9
13	1740.809729	**870.908503**	1723.783180	862.395228	1722.799164	861.903220	F	***897.388329***	449.197803	880.361780	440.684528	879.377764	440.192520	8
14	1900.840378	**950.923827**	1883.813829	942.410553	1882.829813	941.918545	C	***750.319915***	375.663596	733.293366	367.150321	732.309350	366.658313	7
15	1971.877492	986.442384	1954.850943	977.929110	1953.866927	977.437102	A	***590.289266***	295.648271	573.262717	287.134997	572.278701	286.642989	6
16	2028.898956	1014.953116	2011.872407	1006.439842	2010.888391	1005.947834	G	***519.252152***	260.129714	502.225603	251.616440	501.241587	251.124432	5
17	2143.925899	1072.466587	2126.899350	1063.953313	2125.915334	1063.461305	D	***462.230688***	231.618982	445.204139	223.105707	444.220123	222.613700	4
18	2214.963013	1107.985144	2197.936464	1099.471870	2196.952448	1098.979862	A	***347.203745***	174.105510	330.177196	165.592236	329.193180	165.100228	3
19	2316.010692	1158.508984	2298.984143	1149.995709	2298.000127	1149.503701	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.6	2489.115128	0.011368	TCNHPVPQHGGPFCAGDATR

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

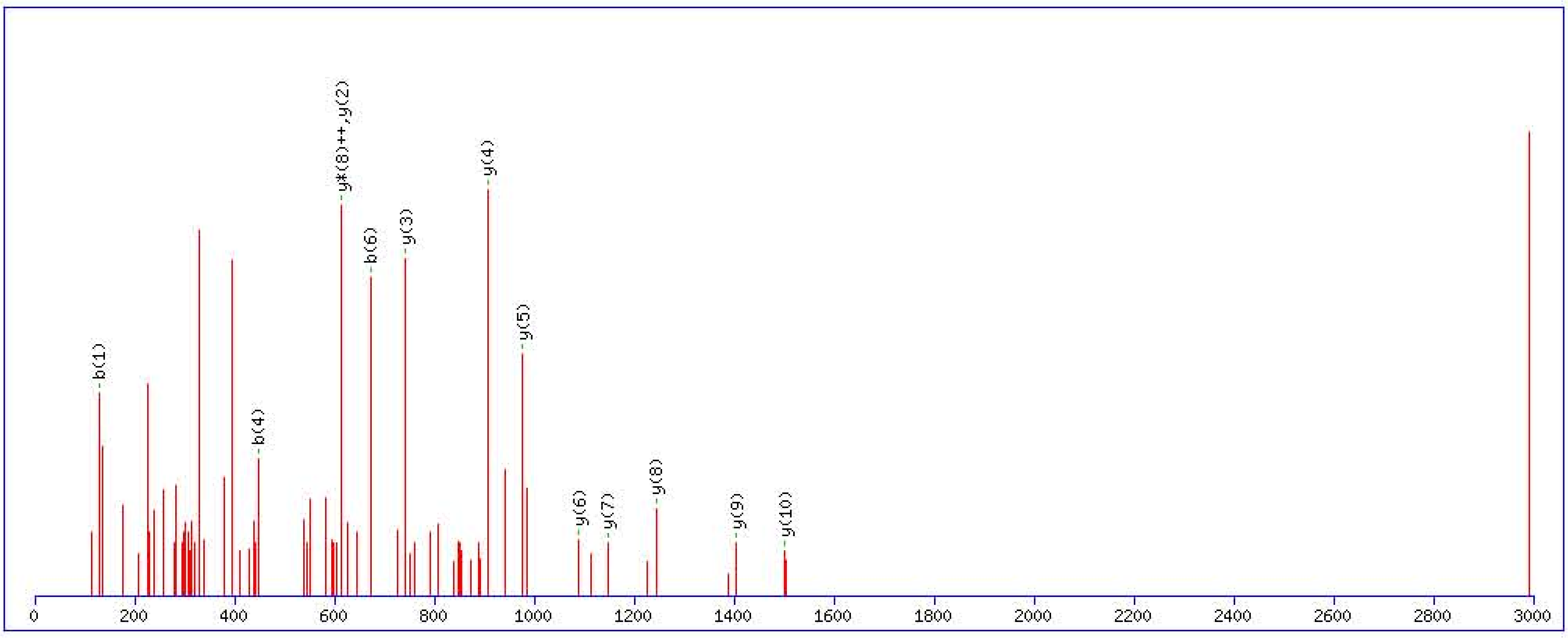
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KCSAPEPSQKPPGKPCPGLAYEQR**
Found in **PROP_HUMAN**, Properdin OS=Homo sapiens GN=CFP PE=1 SV=2

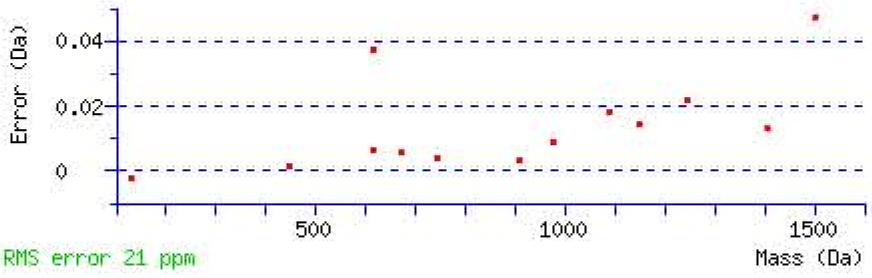
Match to Query 71547: 2992.483220 from(599.503920,5+) rtinseconds(1425) index(74673)
Title: Locus:1.1.1.2710.25 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

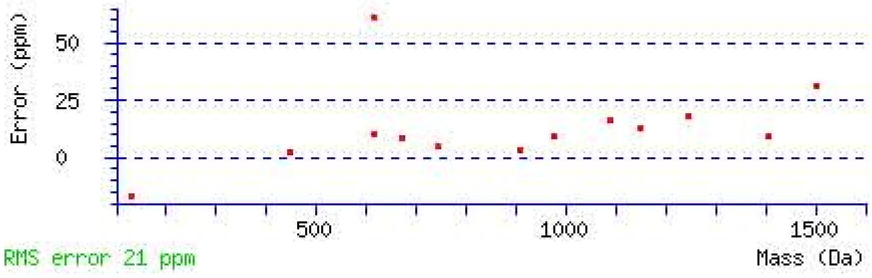
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2992.472107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q23    : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 8.1e-006
Matches : 13/268 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.102239**	65.054757	112.075690	56.541483			K							24
2	289.132888	145.070082	272.106339	136.556808			C	2865.384455	1433.195865	2848.357906	1424.682591	2847.373890	1424.190583	23
3	376.164916	188.586096	359.138367	180.072822	358.154351	179.580814	S	2705.353806	1353.180541	2688.327257	1344.667266	2687.343241	1344.175258	22
4	**447.202030**	224.104653	430.175481	215.591378	429.191465	215.099370	A	2618.321778	1309.664527	2601.295229	1301.151252	2600.311213	1300.659244	21
5	544.254794	272.631035	527.228245	264.117761	526.244229	263.625753	P	2547.284664	1274.145970	2530.258115	1265.632695	2529.274099	1265.140687	20
6	**673.297387**	337.152332	656.270838	328.639057	655.286822	328.147049	E	2450.231900	1225.619588	2433.205351	1217.106313	2432.221335	1216.614305	19
7	770.350151	385.678714	753.323602	377.165439	752.339586	376.673431	P	2321.189307	1161.098292	2304.162758	1152.585017	2303.178742	1152.093009	18
8	857.382179	429.194728	840.355630	420.681453	839.371614	420.189445	S	2224.136543	1112.571909	2207.109994	1104.058635	2206.125978	1103.566627	17
9	985.440757	493.224017	968.414208	484.710742	967.430192	484.218734	Q	2137.104515	1069.055895	2120.077966	1060.542621	2119.093950	1060.050613	16
10	1113.535720	557.271498	1096.509171	548.758224	1095.525155	548.266216	K	2009.045937	1005.026607	1992.019388	996.513332	1991.035372	996.021324	15
11	1210.588484	605.797880	1193.561935	597.284606	1192.577919	596.792598	P	1880.950974	940.979125	1863.924425	932.465851	1862.940409	931.973843	14
12	1307.641248	654.324262	1290.614699	645.810988	1289.630683	645.318980	P	1783.898210	892.452743	1766.871661	883.939469	1765.887645	883.447461	13
13	1364.662712	682.834994	1347.636163	674.321720	1346.652147	673.829712	G	1686.845446	843.926361	1669.818897	835.413087	1668.834881	834.921079	12
14	1492.757675	746.882476	1475.731126	738.369201	1474.747110	737.877193	K	1629.823982	815.415629	1612.797433	806.902355	1611.813417	806.410347	11
15	1589.810439	795.408858	1572.783890	786.895583	1571.799874	786.403575	P	***1501.729019***	751.368148	1484.702470	742.854873	1483.718454	742.362865	10
16	1749.841088	875.424182	1732.814539	866.910908	1731.830523	866.418900	C	***1404.676255***	702.841766	1387.649706	694.328491	1386.665690	693.836483	9
17	1846.893852	923.950564	1829.867303	915.437290	1828.883287	914.945282	P	***1244.645606***	622.826441	1227.619057	614.313167	1226.635041	613.821159	8
18	1903.915316	952.461296	1886.888767	943.948022	1885.904751	943.456014	G	***1147.592842***	574.300059	1130.566293	565.786785	1129.582277	565.294777	7
19	2016.999380	1009.003328	1999.972831	1000.490054	1998.988815	999.998045	L	***1090.571378***	545.789327	1073.544829	537.276053	1072.560813	536.784045	6
20	2088.036494	1044.521885	2071.009945	1036.008610	2070.025929	1035.516602	A	***977.487314***	489.247295	960.460765	480.734021	959.476749	480.242013	5
21	2251.099823	1126.053549	2234.073274	1117.540275	2233.089258	1117.048267	Y	***906.450200***	453.728738	889.423651	445.215464	888.439635	444.723456	4
22	2380.142416	1190.574846	2363.115867	1182.061571	2362.131851	1181.569564	E	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
23	2819.367742	1410.187509	2802.341193	1401.674235	2801.357177	1401.182227	Q	***614.344278***	307.675777	597.317729	299.162503			2
24							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.5	2992.472107	0.011113	KCSAPEPSQKPPGKPCPGLAYEQR

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

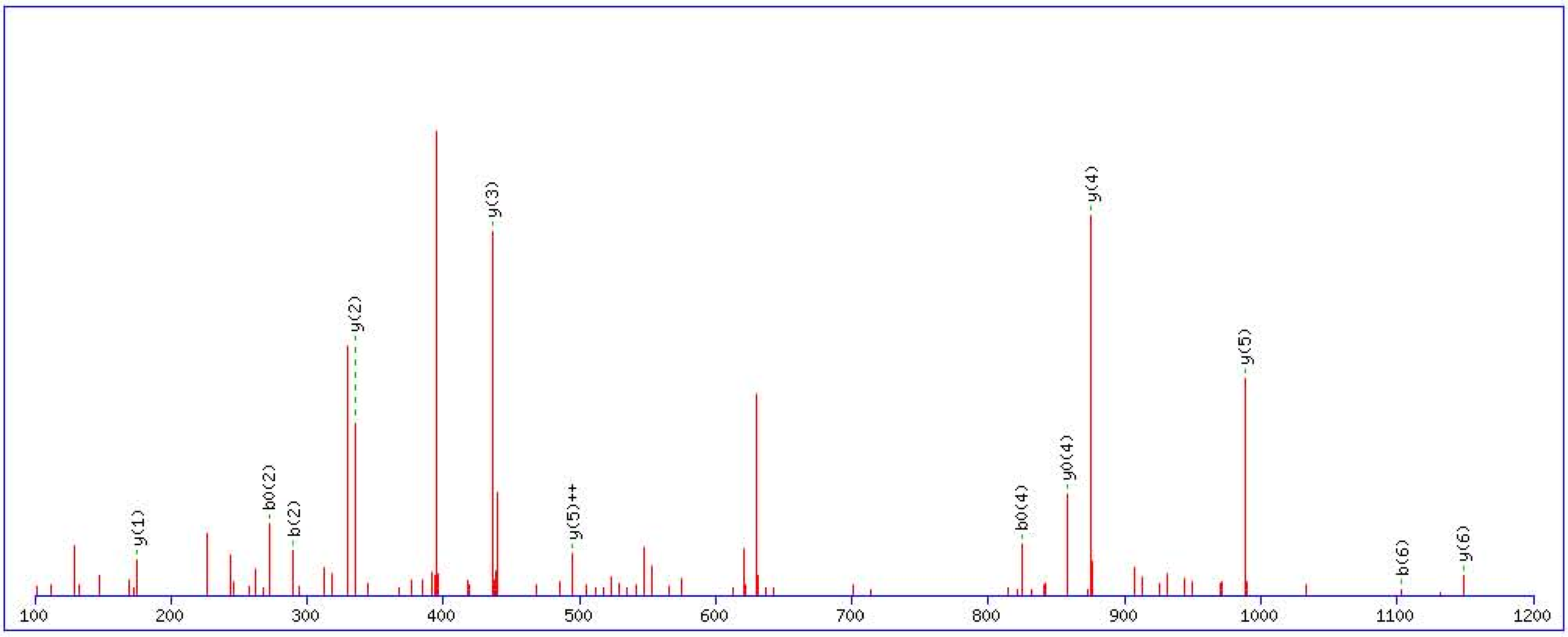
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ECLQTCR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

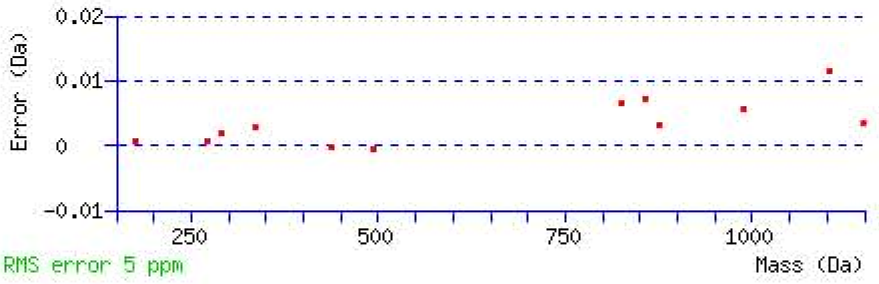
Match to Query 30126: 1276.573728 from(639.294140,2+) rtinseconds(1433) index(38374)
Title: Locus:1.1.1.2782.24 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

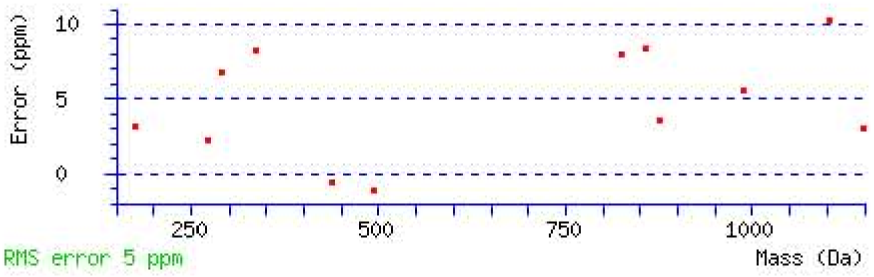
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1276.572632
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0064
Matches : 12/62 fragment ions using 29 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							7
2	**290.080518**	145.543897			272.069953	136.538615	C	***1148.537319***	574.772298	1131.510770	566.259023	1130.526754	565.767015	6
3	403.164582	202.085929			385.154017	193.080647	L	***988.506670***	494.756973	971.480121	486.243699	970.496105	485.751691	5
4	842.389908	421.698592	825.363359	413.185318	824.379343	412.693310	Q	***875.422606***	438.214941	858.396057	429.701667	857.412041	429.209659	4
5	943.437587	472.222432	926.411038	463.709157	925.427022	463.217149	T	***436.197280***	218.602278	419.170731	210.089003	418.186715	209.596995	3
6	**1103.468236**	552.237756	1086.441687	543.724482	1085.457671	543.232474	C	***335.149601***	168.078438	318.123052	159.565164			2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.0	1276.572632	0.001096	ECLQTCR
11.6	1276.590393	-0.016665	TMHTSVMALDR
9.9	1276.583862	-0.010134	KMSLSCHVCR
6.9	1276.560516	0.013212	QQVPSEDSMEK
6.3	1276.587006	-0.013278	EDGTWAPMRSK
5.7	1276.579605	-0.005877	EEQRSPFNDR
5.6	1276.571762	0.001966	AGAESPTMSVDGR
5.6	1276.590393	-0.016665	TMHTSVMALDR
4.0	1276.569229	0.004499	MTGRYEMYAR
1.6	1276.558029	0.015699	AGTVMFEYGMR

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

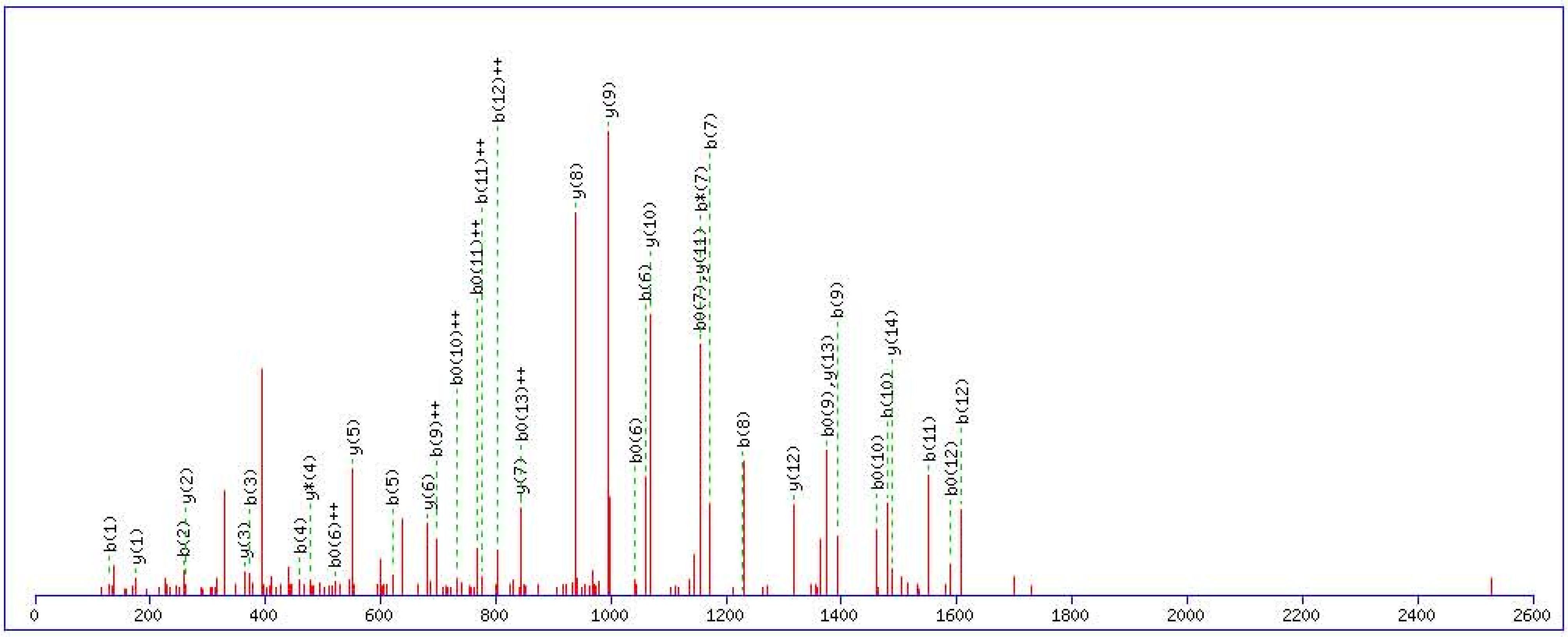
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KEDSCQLGYSAGPCMGMTSR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

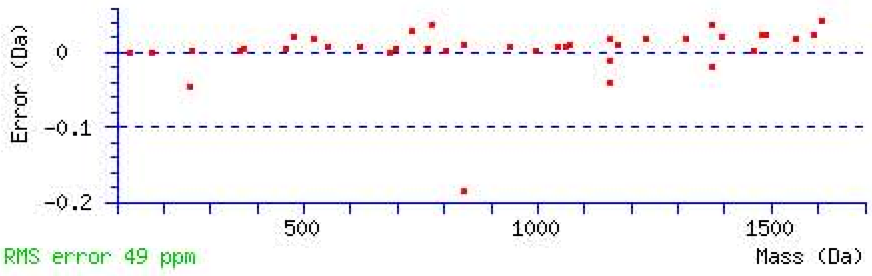
Match to Query 66052: 2545.121742 from(849.381190,3+) rtinseconds(1854) index(59399)
Title: Locus:1.1.1.2951.20 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

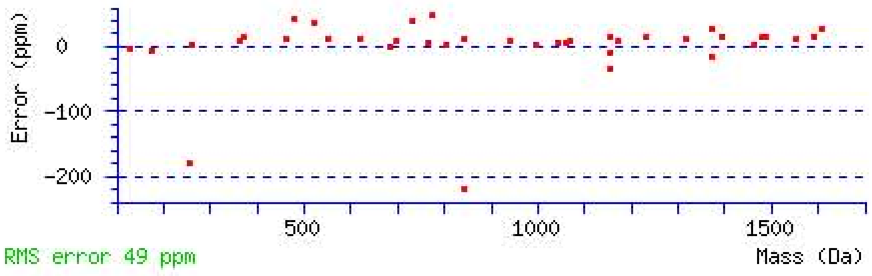
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2545.089188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 99  Expect: 6.2e-010
Matches : 39/224 fragment ions using 63 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							20
2	***258.144832***	129.576054	241.118283	121.062780	240.134267	120.570772	E	2418.001508	1209.504392	2400.974959	1200.991117	2399.990943	1200.499109	19
3	***373.171775***	187.089526	356.145226	178.576251	355.161210	178.084243	D	2288.958915	1144.983095	2271.932366	1136.469821	2270.948350	1135.977813	18
4	***460.203803***	230.605540	443.177254	222.092265	442.193238	221.600257	S	2173.931972	1087.469624	2156.905423	1078.956349	2155.921407	1078.464341	17
5	***620.234452***	310.620864	603.207903	302.107590	602.223887	301.615582	C	2086.899944	1043.953610	2069.873395	1035.440335	2068.889379	1034.948327	16
6	***1059.459778***	530.233527	1042.433229	521.720253	1041.449213	521.228245	Q	1926.869295	963.938286	1909.842746	955.425011	1908.858730	954.933003	15
7	***1172.543842***	586.775559	1155.517293	578.262285	1154.533277	577.770277	L	***1487.643969***	744.325623	1470.617420	735.812348	1469.633404	735.320340	14
8	***1229.565306***	615.286291	1212.538757	606.773017	1211.554741	606.281008	G	***1374.559905***	687.783591	1357.533356	679.270316	1356.549340	678.778308	13
9	***1392.628635***	**696.817956**	1375.602086	688.304681	1374.618070	687.812673	Y	***1317.538441***	659.272859	1300.511892	650.759584	1299.527876	650.267576	12
10	***1479.660663***	740.333970	1462.634114	731.820695	1461.650098	731.328687	S	***1154.475112***	577.741194	1137.448563	569.227920	1136.464547	568.735912	11
11	***1550.697777***	**775.852527**	1533.671228	767.339252	1532.687212	766.847244	A	***1067.443084***	534.225180	1050.416535	525.711906	1049.432519	525.219898	10
12	***1607.719241***	**804.363259**	1590.692692	795.849984	1589.708676	795.357976	G	***996.405970***	498.706623	979.379421	490.193349	978.395405	489.701341	9
13	1704.772005	852.889641	1687.745456	844.376366	1686.761440	843.884358	P	***939.384506***	470.195891	922.357957	461.682617	921.373941	461.190609	8
14	1864.802654	932.904965	1847.776105	924.391691	1846.792089	923.899683	C	***842.331742***	421.669509	825.305193	413.156235	824.321177	412.664227	7
15	1995.843139	998.425208	1978.816590	989.911933	1977.832574	989.419925	M	***682.301093***	341.654185	665.274544	333.140910	664.290528	332.648902	6
16	2052.864603	1026.935939	2035.838054	1018.422665	2034.854038	1017.930657	G	***551.260608***	276.133942	534.234059	267.620668	533.250043	267.128660	5
17	2183.905088	1092.456182	2166.878539	1083.942907	2165.894523	1083.450899	M	494.239144	247.623210	477.212595	239.109935	476.228579	238.617927	4
18	2284.952767	1142.980021	2267.926218	1134.466747	2266.942202	1133.974739	T	***363.198659***	182.102967	346.172110	173.589693	345.188094	173.097685	3
19	2371.984795	1186.496035	2354.958246	1177.982761	2353.974230	1177.490753	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
99.0	2545.089188	0.032554	KEDSCQLGYSAGPCMGMTSR
0.8	2545.119553	0.002189	MTCGSGFGGRAFSCISACGPRPGR

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

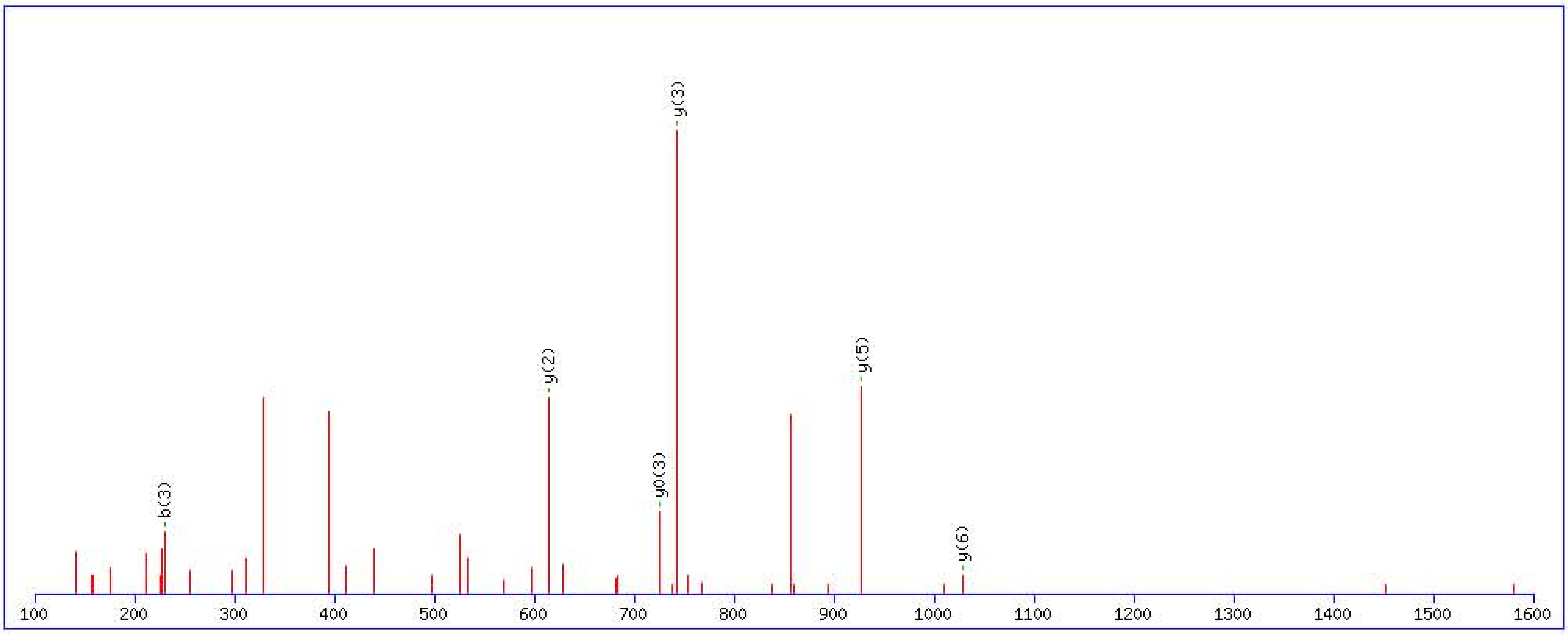
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTAIEQR**
Found in **HEG1_HUMAN**, Protein HEG homolog 1 OS=Homo sapiens GN=HEG1 PE=1 SV=3

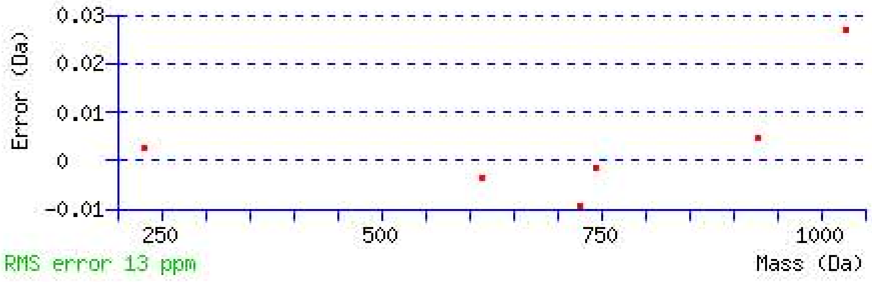
Match to Query 22120: 1084.566648 from(543.290600,2+) rtinseconds(1429) index(38345)
Title: Locus:1.1.1.2781.20 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

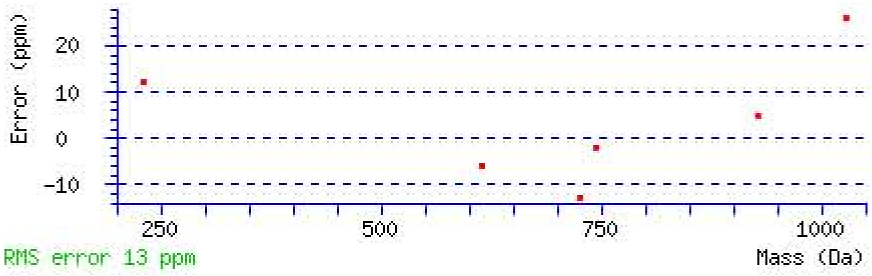
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1084.569901
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.016
Matches : 6/56 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							7
2	159.076419	80.041847			141.065854	71.036565	T	***1028.555728***	514.781502	1011.529179	506.268228	1010.545163	505.776220	6
3	**230.113533**	115.560404			212.102968	106.555122	A	***927.508049***	464.257663	910.481500	455.744388	909.497484	455.252380	5
4	343.197597	172.102436			325.187032	163.097154	I	856.470935	428.739106	839.444386	420.225831	838.460370	419.733823	4
5	472.240190	236.623733			454.229625	227.618450	E	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
6	911.465516	456.236396	894.438967	447.723122	893.454951	447.231114	Q	***614.344278***	307.675777	597.317729	299.162503			2
7							R	175.118952	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.1	1084.569901	-0.003253	GTAIEQR
10.4	1084.569885	-0.003237	ASAEIQR
6.0	1084.569916	-0.003268	TKMDLGGHVK
1.2	1084.569885	-0.003237	QELAASR
1.2	1084.569901	-0.003253	QELAGTR

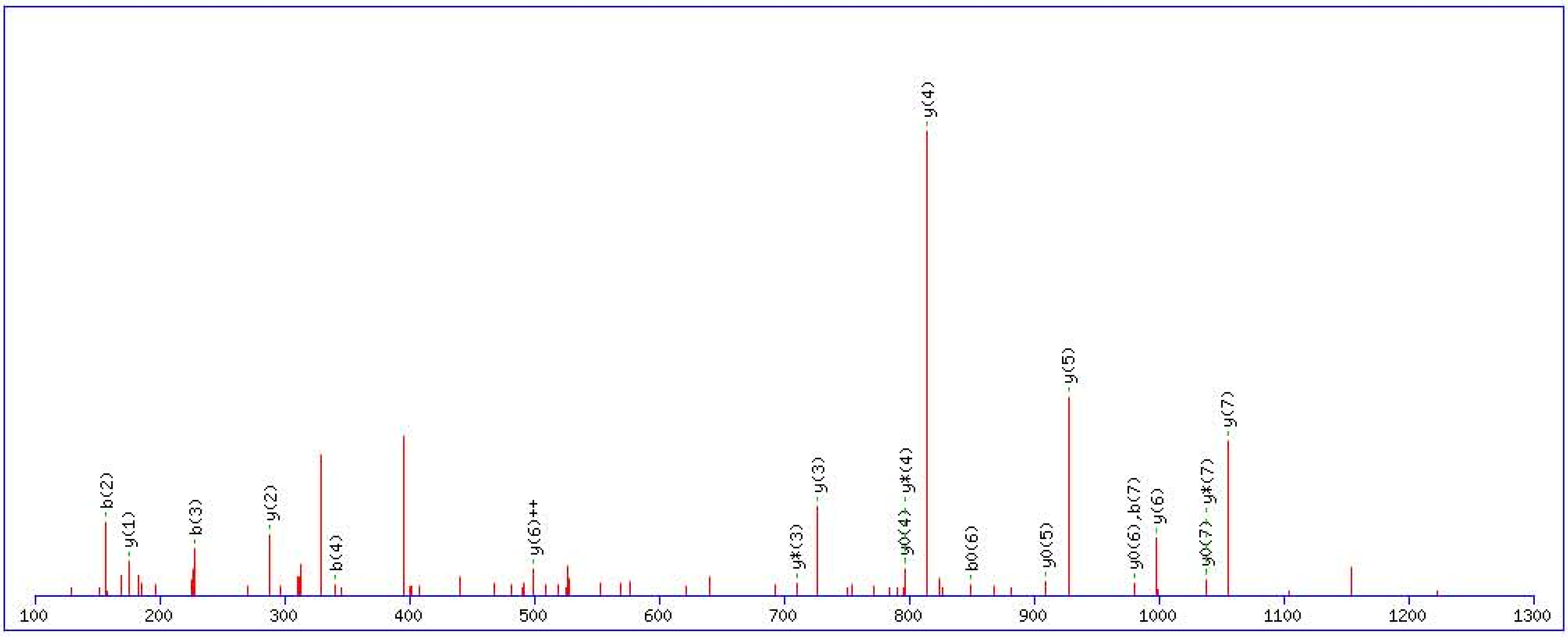
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGALSQLR**
Found in **MENT_HUMAN**, Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1

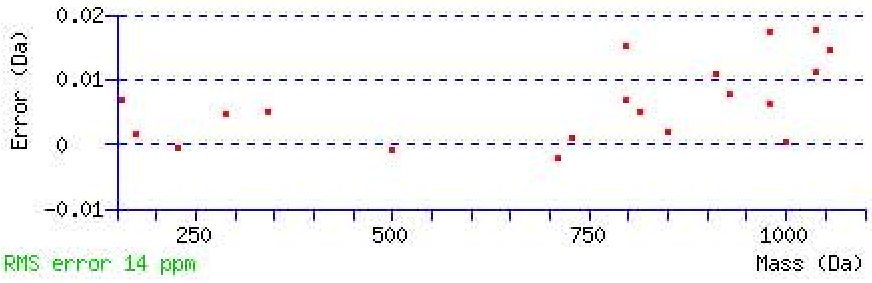
Match to Query 25893: 1153.665608 from(577.840080,2+) rtinseconds(1898) index(41398)
Title: Locus:1.1.1.2945.7 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

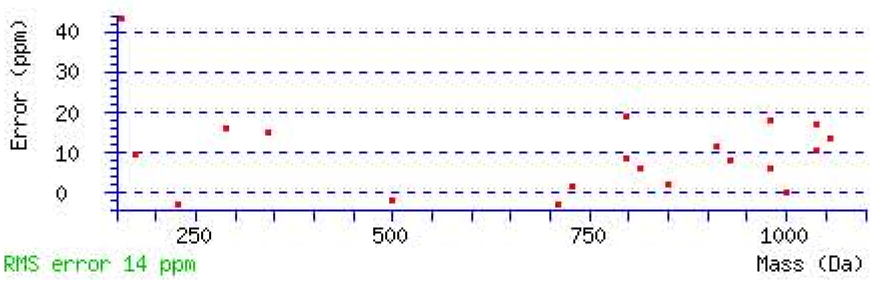
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1153.664139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00021
Matches : 20/60 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							8
2	**157.097154**	79.052215					G	***1055.603012***	528.305144	1038.576463	519.791870	1037.592447	519.299862	7
3	**228.134268**	114.570772					A	***998.581548***	499.794412	981.554999	491.281138	980.570983	490.789130	6
4	**341.218332**	171.112804					L	***927.544434***	464.275855	910.517885	455.762581	909.533869	455.270573	5
5	428.250360	214.628818			410.239795	205.623535	S	***814.460370***	407.733823	797.433821	399.220549	796.449805	398.728541	4
6	867.475686	434.241481	850.449137	425.728207	849.465121	425.236199	Q	***727.428342***	364.217809	710.401793	355.704535			3
7	**980.559750**	490.783513	963.533201	482.270239	962.549185	481.778231	L	***288.203016***	144.605146	271.176467	136.091872			2
8							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.8	1153.664139	0.001469	VGALSQLR
15.4	1153.667953	-0.002345	RANPNSIRVK
13.2	1153.675354	-0.009746	RALLSQR
13.2	1153.675369	-0.009761	RALTVQR
11.4	1153.681885	-0.016277	VQEKTALPLR
11.4	1153.664124	0.001484	VKQEALR
11.0	1153.681870	-0.016262	RALENLLPTK
8.7	1153.656723	0.008885	RPSADPGKKAK
6.8	1153.675369	-0.009761	QTVRALR
6.6	1153.660767	0.004841	VPTAAGAWLLR

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

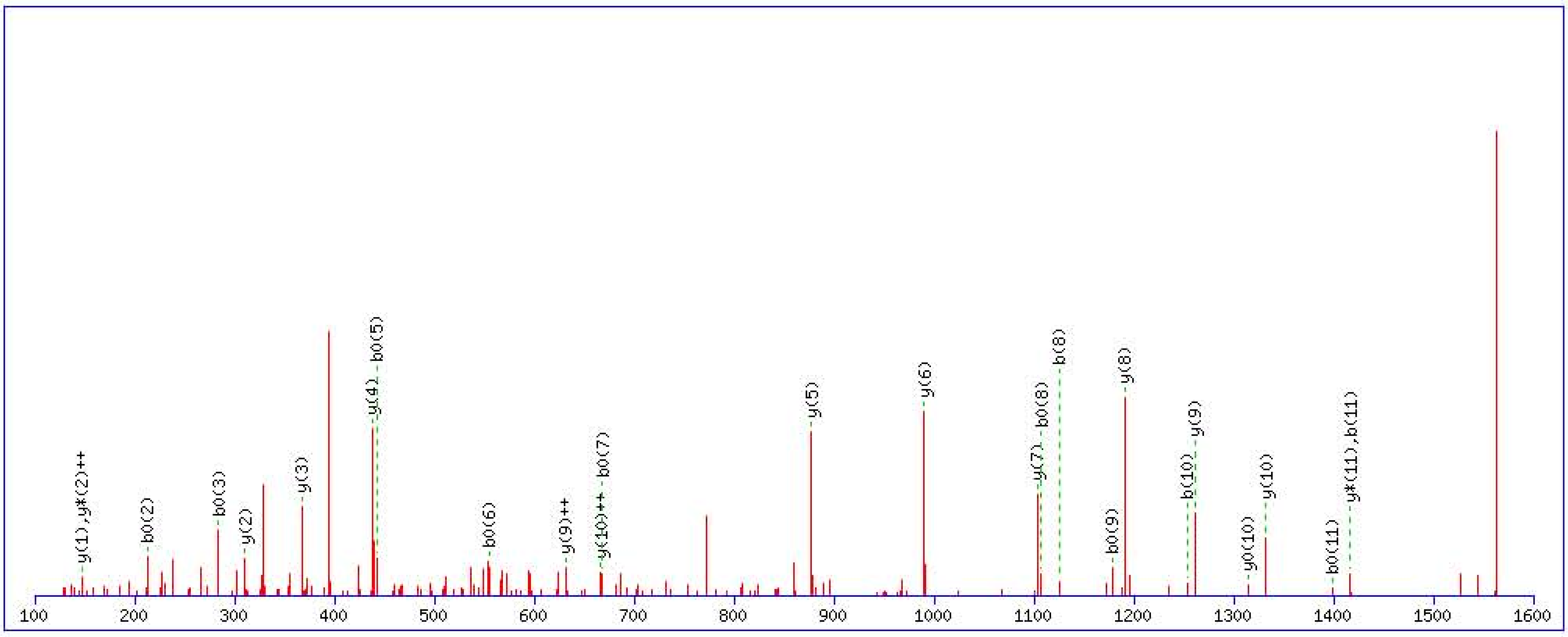
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETAASLLQAGYK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

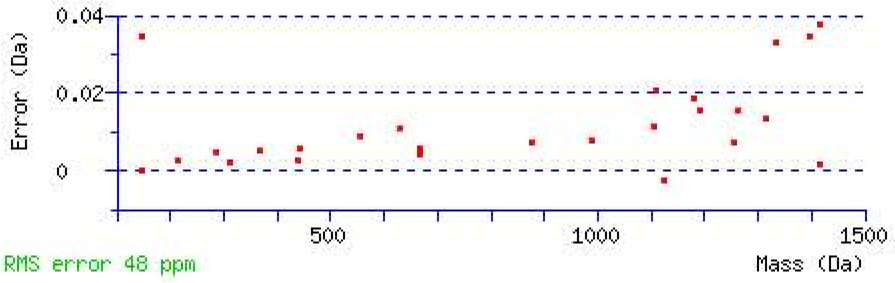
Match to Query 40247: 1561.823248 from(781.918900,2+) rtinseconds(2095) index(61200)
Title: Locus:1.1.1.3034.20 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

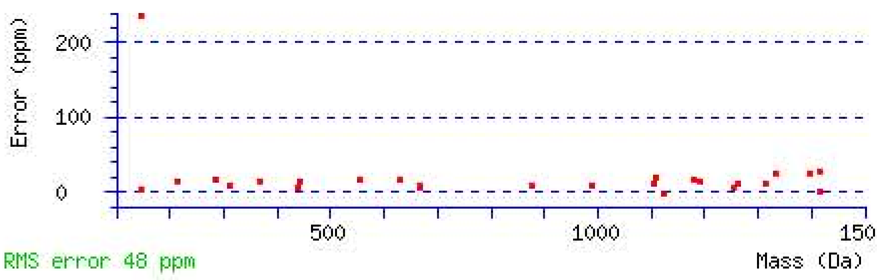
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1561.817383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 73  Expect: 5.2e-007
Matches : 26/104 fragment ions using 41 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							12
2	231.097548	116.052412			213.086983	107.047130	T	1433.782100	717.394688	1416.755551	708.881414	1415.771535	708.389406	11
3	302.134662	151.570969			284.124097	142.565687	A	***1332.734421***	666.870848	1315.707872	658.357574	1314.723856	657.865566	10
4	373.171776	187.089526			355.161211	178.084243	A	***1261.697307***	631.352292	1244.670758	622.839017	1243.686742	622.347009	9
5	460.203804	230.605540			442.193239	221.600257	S	***1190.660193***	595.833734	1173.633644	587.320460	1172.649628	586.828452	8
6	573.287868	287.147572			555.277303	278.142290	L	***1103.628165***	552.317721	1086.601616	543.804446			7
7	686.371932	343.689604			668.361367	334.684322	L	***990.544101***	495.775689	973.517552	487.262414			6
8	**1125.597258**	563.302267	1108.570709	554.788993	1107.586693	554.296985	Q	***877.460037***	439.233657	860.433488	430.720382			5
9	1196.634372	598.820824	1179.607823	590.307550	1178.623807	589.815541	A	***438.234711***	219.620993	421.208162	211.107719			4
10	**1253.655836**	627.331556	1236.629287	618.818282	1235.645271	618.326273	G	***367.197597***	184.102436	350.171048	175.589162			3
11	**1416.719165**	708.863221	1399.692616	700.349946	1398.708600	699.857938	Y	***310.176133***	155.591705	293.149584	147.078430			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.5	1561.817383	0.005865	ETAASLLQAGYK
6.3	1561.817398	0.005850	VLPEVLEKQCGYK
3.5	1561.824799	-0.001551	QDLLFLDMLK
3.3	1561.835144	-0.011896	ILKGDQLLQEDYK

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

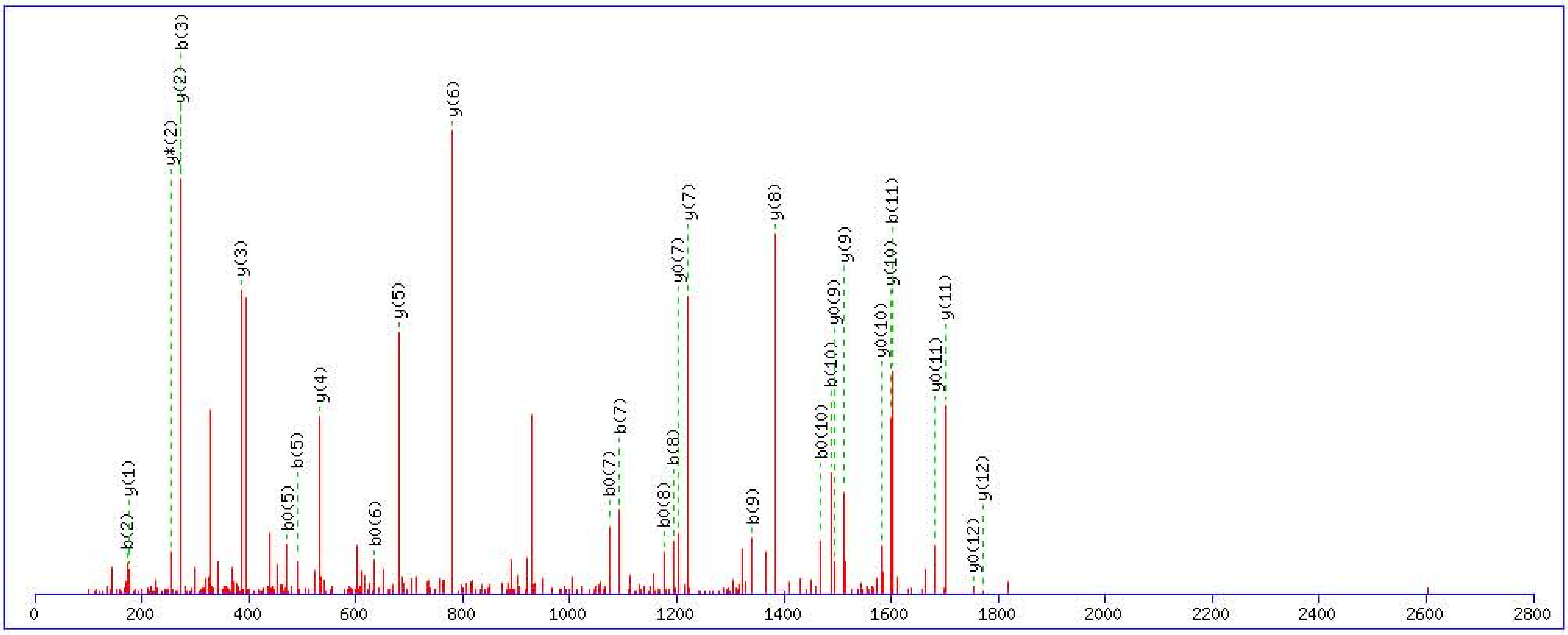
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TATSEYQTFFNPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

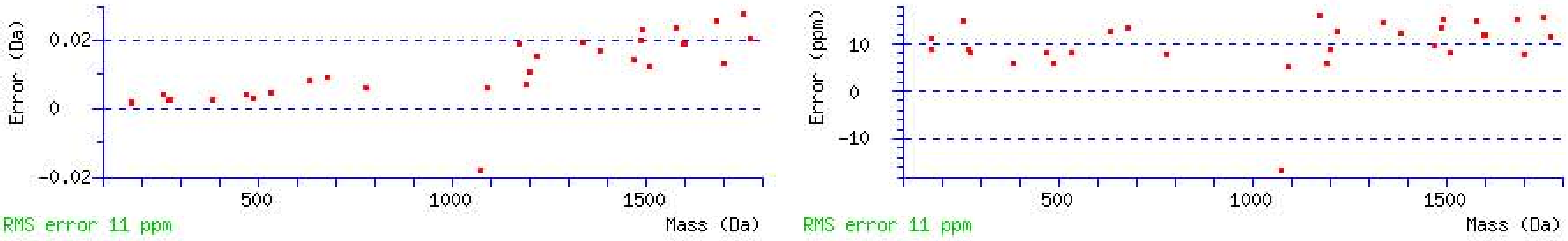
Match to Query 50115: 1871.911968 from(936.963260,2+) rtinseconds(2222) index(62151)
Title: Locus:1.1.1.3078.24 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1871.887619
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 87  Expect: 4.2e-008
Matches : 31/122 fragment ions using 52 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	**173.092069**	87.049672			155.081504	78.044390	A	***1771.847219***	886.427248	1754.820670	877.913973	1753.836654	877.421965	12
3	**274.139748**	137.573512			256.129183	128.568230	T	***1700.810105***	850.908691	1683.783556	842.395416	1682.799540	841.903408	11
4	361.171776	181.089526			343.161211	172.084243	S	***1599.762426***	800.384851	1582.735877	791.871577	1581.751861	791.379569	10
5	**490.214369**	245.610822			472.203804	236.605540	E	***1512.730398***	756.868837	1495.703849	748.355563	1494.719833	747.863555	9
6	653.277698	327.142487			635.267133	318.137205	Y	***1383.687805***	692.347541	1366.661256	683.834266	1365.677240	683.342258	8
7	**1092.503024**	546.755150	1075.476475	538.241876	1074.492459	537.749868	Q	***1220.624476***	610.815876	1203.597927	602.302602	1202.613911	601.810594	7
8	**1193.550703**	597.278990	1176.524154	588.765715	1175.540138	588.273707	T	***781.399150***	391.203213	764.372601	382.689939	763.388585	382.197931	6
9	**1340.619117**	670.813197	1323.592568	662.299922	1322.608552	661.807914	F	***680.351471***	340.679374	663.324922	332.166099			5
10	**1487.687531**	744.347404	1470.660982	735.834129	1469.676966	735.342121	F	***533.283057***	267.145167	516.256508	258.631892			4
11	**1601.730458**	801.368867	1584.703909	792.855593	1583.719893	792.363585	N	***386.214643***	193.610959	369.188094	185.097685			3
12	1698.783222	849.895249	1681.756673	841.381975	1680.772657	840.889967	P	***272.171716***	136.589496	255.145167	128.076221			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.2	1871.887619	0.024349	TATSEYQTFFNPR

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

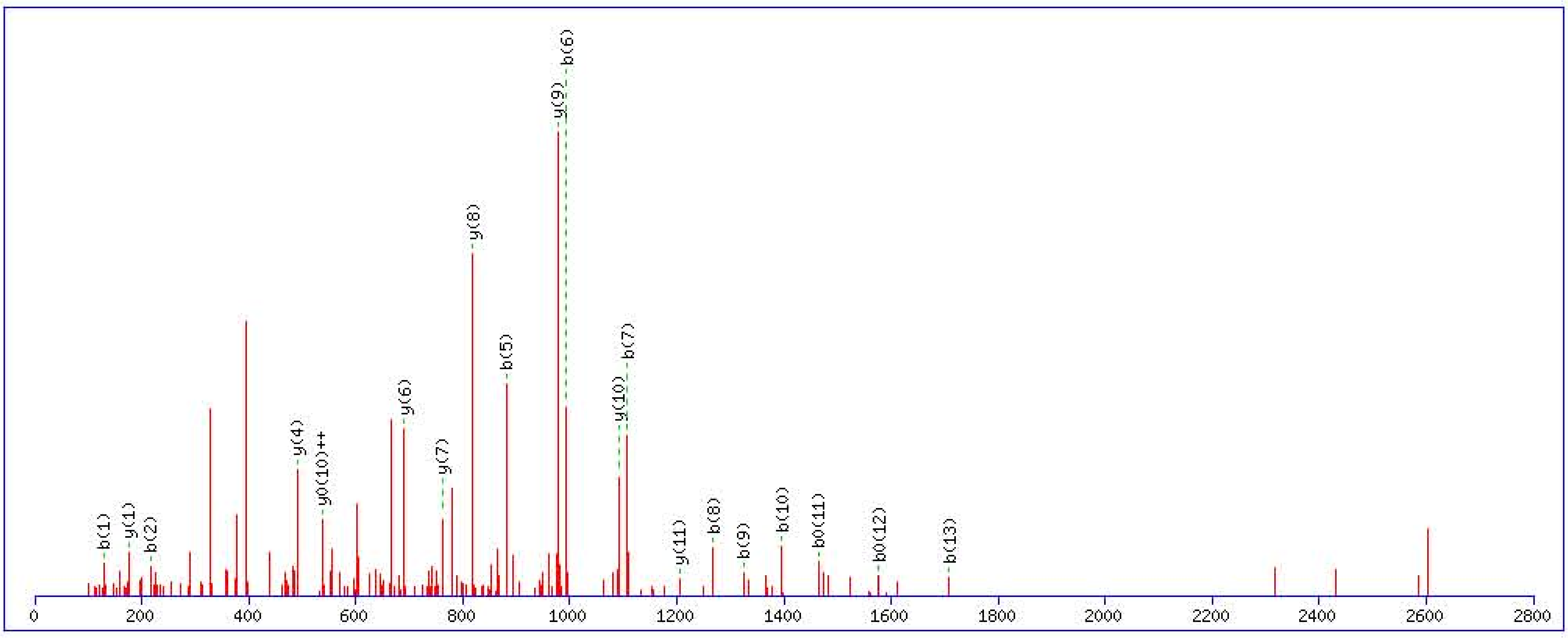
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KSPQELLCGASLISDR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

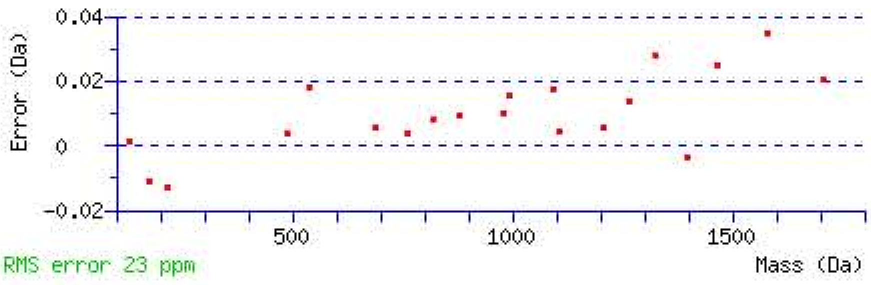
Match to Query 55699: 2084.094972 from(695.705600,3+) rtinseconds(2224) index(62162)
Title: Locus:1.1.1.3079.12 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

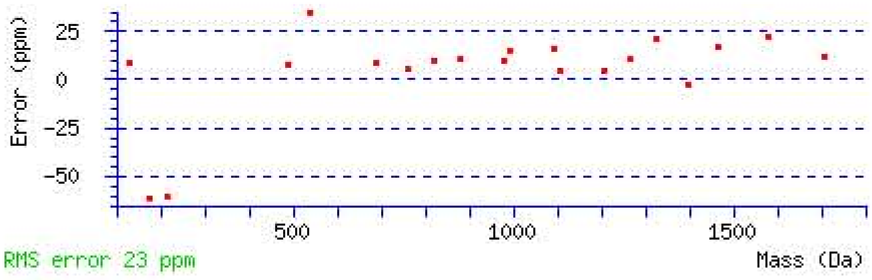
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2084.075806
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 5.4e-006
Matches : 20/176 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	***129.102239***	65.054757	112.075690	56.541483			K							16
2	***216.134267***	108.570771	199.107718	100.057497	198.123702	99.565489	S	1956.988145	978.997711	1939.961596	970.484436	1938.977580	969.992428	15
3	313.187031	157.097153	296.160482	148.583879	295.176466	148.091871	P	1869.956117	935.481697	1852.929568	926.968422	1851.945552	926.476414	14
4	752.412357	376.709817	735.385808	368.196542	734.401792	367.704534	Q	1772.903353	886.955314	1755.876804	878.442040	1754.892788	877.950032	13
5	***881.454950***	441.231113	864.428401	432.717839	863.444385	432.225831	E	1333.678027	667.342652	1316.651478	658.829377	1315.667462	658.337369	12
6	***994.539014***	497.773145	977.512465	489.259871	976.528449	488.767863	L	***1204.635434***	602.821355	1187.608885	594.308081	1186.624869	593.816073	11
7	***1107.623078***	554.315177	1090.596529	545.801903	1089.612513	545.309895	L	***1091.551370***	546.279323	1074.524821	537.766049	1073.540805	537.274040	10
8	***1267.653727***	634.330502	1250.627178	625.817227	1249.643162	625.325219	C	***978.467306***	489.737291	961.440757	481.224017	960.456741	480.732009	9
9	***1324.675191***	662.841234	1307.648642	654.327959	1306.664626	653.835951	G	***818.436657***	409.721967	801.410108	401.208692	800.426092	400.716684	8
10	***1395.712305***	698.359791	1378.685756	689.846516	1377.701740	689.354508	A	***761.415193***	381.211235	744.388644	372.697960	743.404628	372.205952	7
11	1482.744333	741.875805	1465.717784	733.362530	1464.733768	732.870522	S	***690.378079***	345.692678	673.351530	337.179403	672.367514	336.687395	6
12	1595.828397	798.417837	1578.801848	789.904562	1577.817832	789.412554	L	603.346051	302.176664	586.319502	293.663389	585.335486	293.171381	5
13	***1708.912461***	854.959868	1691.885912	846.446594	1690.901896	845.954586	I	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
14	1795.944489	898.475883	1778.917940	889.962608	1777.933924	889.470600	S	377.177923	189.092600	360.151374	180.579325	359.167358	180.087317	3
15	1910.971432	955.989354	1893.944883	947.476080	1892.960867	946.984072	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.6	2084.075806	0.019166	KSPQELLCGASLISDR
5.2	2084.097565	-0.002593	KEFIMAELIQTEKAYVR
5.2	2084.097565	-0.002593	KEFIMAELLQTEKAYVR
2.7	2084.113541	-0.018569	LQGQQQLIHQNR
2.7	2084.113541	-0.018569	LQGQQQLIHQNR
2.7	2084.113541	-0.018569	LQGQQQLIHQNR
2.7	2084.113541	-0.018569	LQGQQQLIHQNR
2.4	2084.090225	0.004747	SKYDVPGPPLNVTITDVNR
1.3	2084.083679	0.011293	EDLISFLCGKVPPPRNSR

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

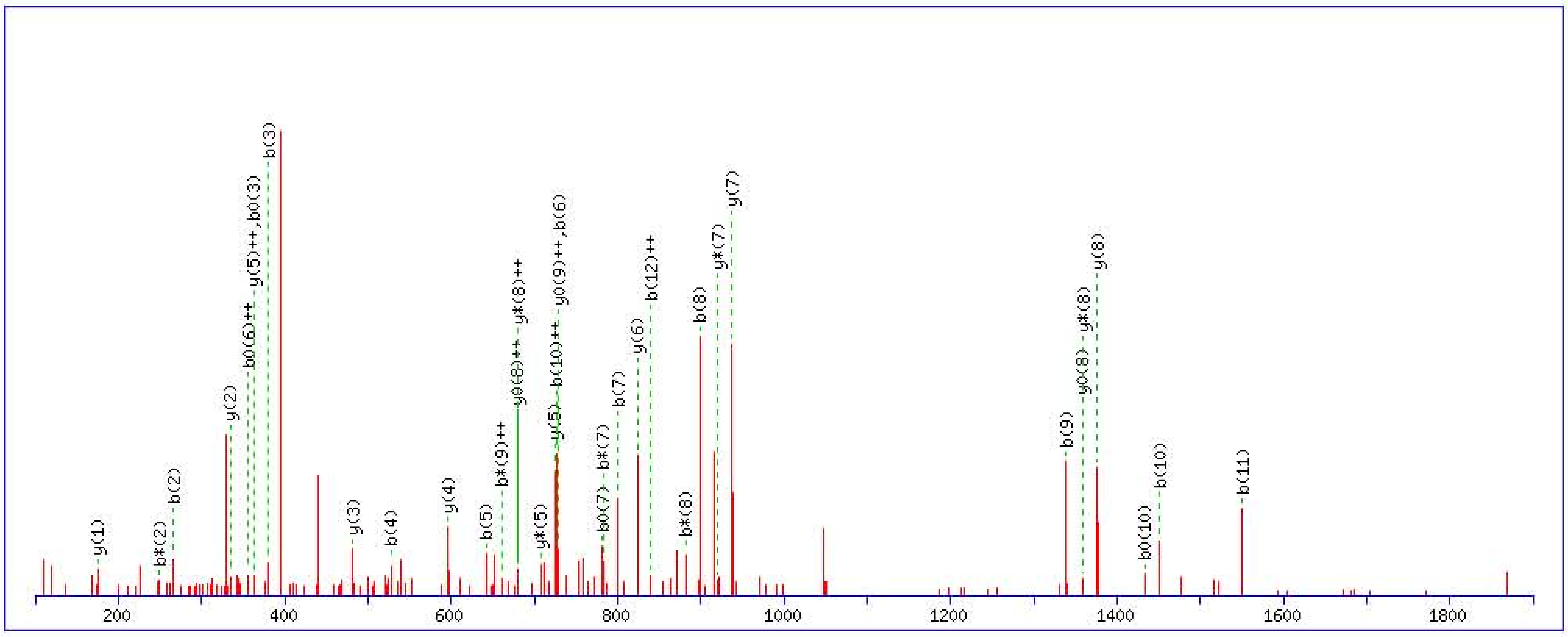
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQDFNSAVQLVENFCR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

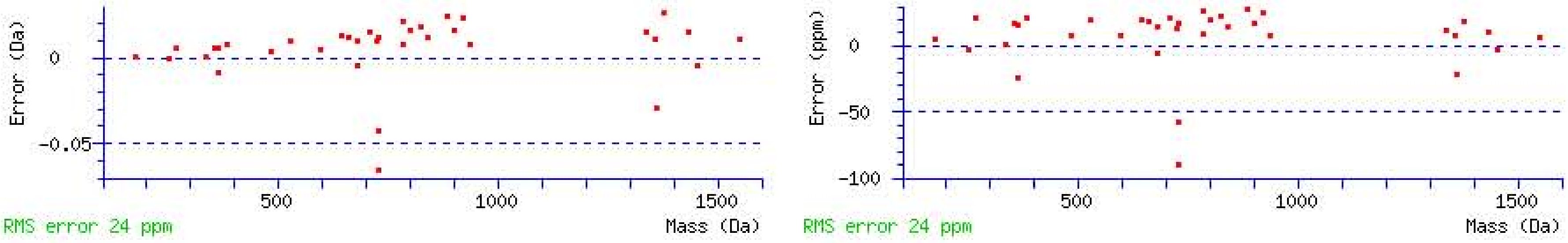
Match to Query 60016: 2274.085422 from(759.035750,3+) rtinseconds(2558) index(64329)
Title: Locus:1.1.1.3195.7 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2274.067398
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0042
Matches : 36/166 fragment ions using 93 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							16
2	***266.124766***	133.566021	249.098217	125.052746			Q	2138.015757	1069.511516	2120.989208	1060.998242	2120.005192	1060.506234	15
3	***381.151709***	191.079492	364.125160	182.566218	363.141144	182.074210	D	2009.957179	1005.482228	1992.930630	996.968953	1991.946614	996.476945	14
4	***528.220123***	264.613700	511.193574	256.100425	510.209558	255.608417	F	1894.930236	947.968756	1877.903687	939.455482	1876.919671	938.963474	13
5	***642.263050***	321.635163	625.236501	313.121889	624.252485	312.629881	N	1747.861822	874.434549	1730.835273	865.921275	1729.851257	865.429267	12
6	***729.295078***	365.151177	712.268529	356.637903	711.284513	356.145895	S	1633.818895	817.413086	1616.792346	808.899811	1615.808330	808.407803	11
7	***800.332192***	400.669734	783.305643	392.156459	782.321627	391.664451	A	1546.786867	773.897072	1529.760318	765.383797	1528.776302	764.891789	10
8	***899.400606***	450.203941	882.374057	441.690666	881.390041	441.198658	V	1475.749753	738.378515	1458.723204	729.865240	1457.739188	729.373232	9
9	***1338.625932***	669.816604	1321.599383	661.303330	1320.615367	660.811322	Q	***1376.681339***	688.844308	1359.654790	680.331033	1358.670774	679.839025	8
10	***1451.709996***	**726.358636**	1434.683447	717.845362	1433.699431	717.353354	L	***937.456013***	469.231645	920.429464	460.718370	919.445448	460.226362	7
11	***1550.778410***	775.892843	1533.751861	767.379569	1532.767845	766.887561	V	***824.371949***	412.689613	807.345400	404.176338	806.361384	403.684330	6
12	1679.821003	**840.414140**	1662.794454	831.900865	1661.810438	831.408857	E	***725.303535***	363.155406	708.276986	354.642131	707.292970	354.150123	5
13	1793.863930	897.435603	1776.837381	888.922329	1775.853365	888.430321	N	***596.260942***	298.634109	579.234393	290.120835			4
14	1940.932344	970.969810	1923.905795	962.456536	1922.921779	961.964528	F	***482.218015***	241.612646	465.191466	233.099371			3
15	2100.962993	1050.985135	2083.936444	1042.471860	2082.952428	1041.979852	C	***335.149601***	168.078438	318.123052	159.565164			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.2	2274.067398	0.018024	HQDFNSAVQLVENFCR
8.5	2274.067398	0.018024	HQDFNSAVQLVENFCR

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

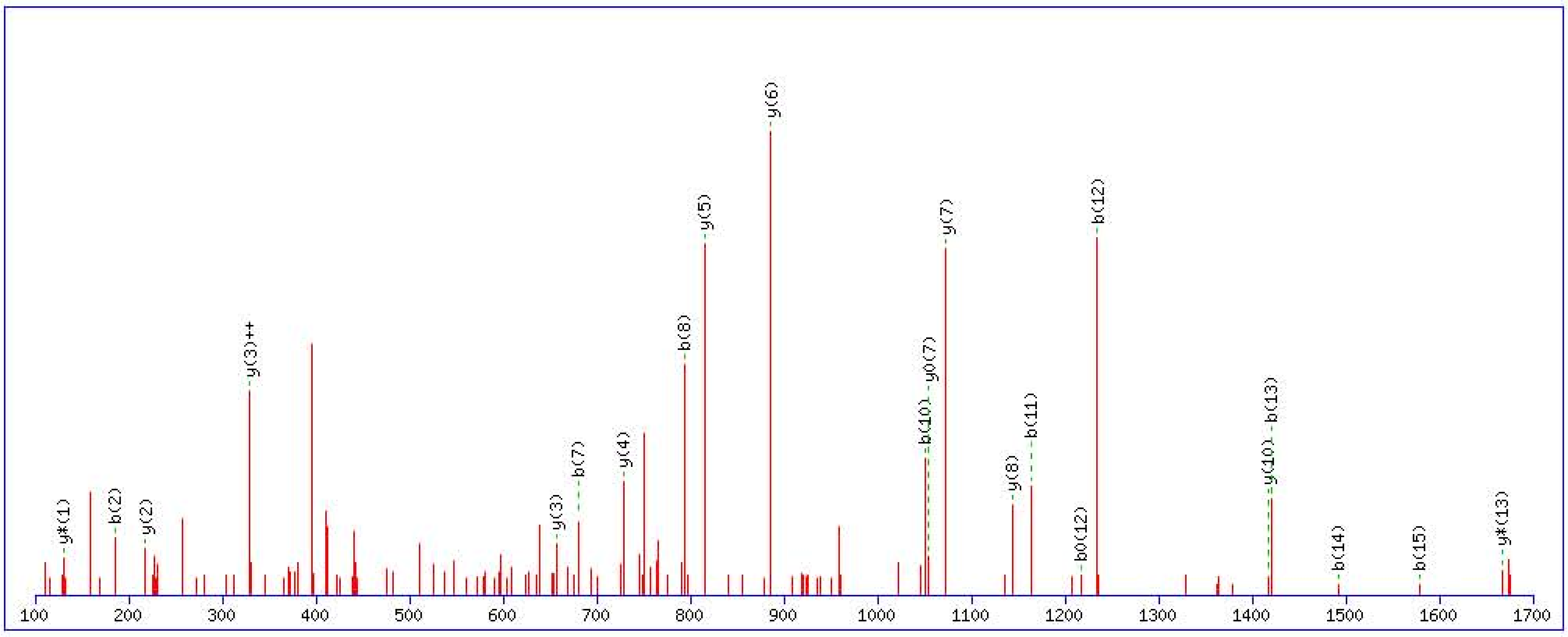
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAVTTHGLPCLAWASAQAK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

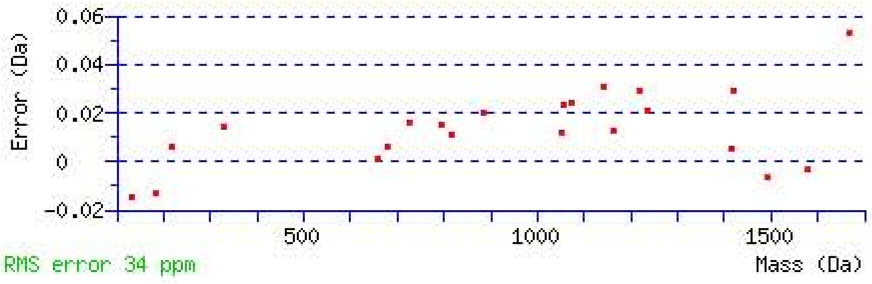
Match to Query 60793: 2305.240182 from(769.420670,3+) rtinseconds(2354) index(63105)
Title: Locus:1.1.1.3124.21 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

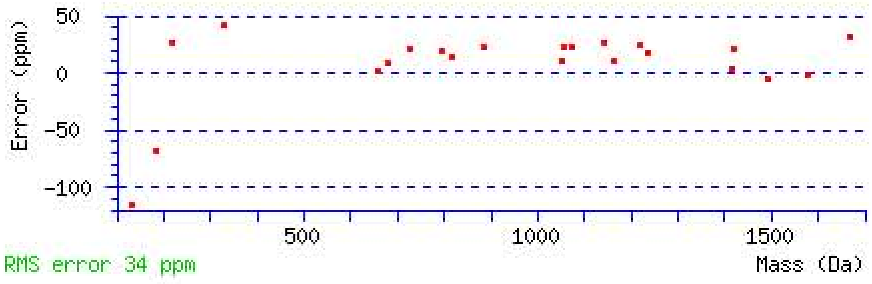
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2305.207504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17    : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 3.3e-005
Matches : 22/170 fragment ions using 46 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							19
2	***185.128454***	93.067865					A	2193.130730	1097.069003	2176.104181	1088.555728	2175.120165	1088.063720	18
3	284.196868	142.602072					V	2122.093616	1061.550446	2105.067067	1053.037171	2104.083051	1052.545163	17
4	385.244547	193.125912			367.233982	184.120629	T	2023.025202	1012.016239	2005.998653	1003.502965	2005.014637	1003.010957	16
5	486.292226	243.649751			468.281661	234.644469	T	1921.977523	961.492400	1904.950974	952.979125	1903.966958	952.487117	15
6	623.351138	312.179207			605.340573	303.173925	H	1820.929844	910.968560	1803.903295	902.455286	1802.919279	901.963278	14
7	***680.372602***	340.689939			662.362037	331.684657	G	1683.870932	842.439104	1666.844383	833.925830	1665.860367	833.433822	13
8	***793.456666***	397.231971			775.446101	388.226689	L	1626.849468	813.928372	1609.822919	805.415098	1608.838903	804.923090	12
9	890.509430	445.758353			872.498865	436.753071	P	1513.765404	757.386340	1496.738855	748.873066	1495.754839	748.381058	11
10	***1050.540079***	525.773678			1032.529514	516.768395	C	***1416.712640***	708.859958	1399.686091	700.346684	1398.702075	699.854675	10
11	***1163.624143***	582.315710			1145.613578	573.310427	L	1256.681991	628.844634	1239.655442	620.331359	1238.671426	619.839351	9
12	***1234.661257***	617.834267			1216.650692	608.828984	A	***1143.597927***	572.302602	1126.571378	563.789327	1125.587362	563.297319	8
13	***1420.740570***	710.873923			1402.730005	701.868640	W	***1072.560813***	536.784045	1055.534264	528.270770	1054.550248	527.778762	7
14	***1491.777684***	746.392480			1473.767119	737.387197	A	***886.481500***	443.744388	869.454951	435.231114	868.470935	434.739106	6
15	***1578.809712***	789.908494			1560.799147	780.903212	S	***815.444386***	408.225831	798.417837	399.712557	797.433821	399.220549	5
16	1649.846826	825.427051			1631.836261	816.421768	A	***728.412358***	364.709817	711.385809	356.196543			4
17	2089.072152	1045.039714	2072.045603	1036.526439	2071.061587	1036.034431	Q	***657.375244***	329.191260	640.348695	320.677986			3
18	2160.109266	1080.558271	2143.082717	1072.044996	2142.098701	1071.552988	A	***218.149918***	109.578597	201.123369	101.065323			2
19							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.0	2305.207504	0.032678	LAVTTHGLPCLAWASAQAK
0.2	2305.236481	0.003701	STLSQHLRIHTGEKPYK

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

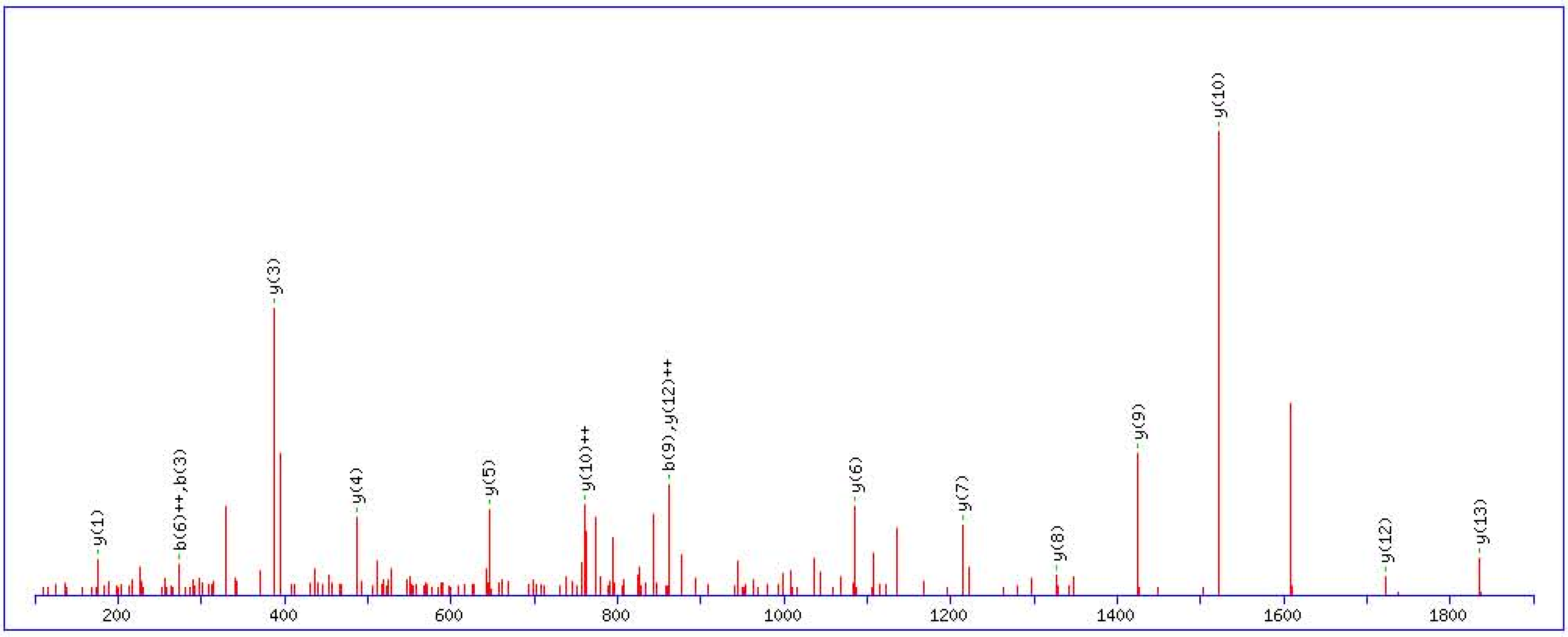
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEGSSVNLSPPLEQCVPDR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

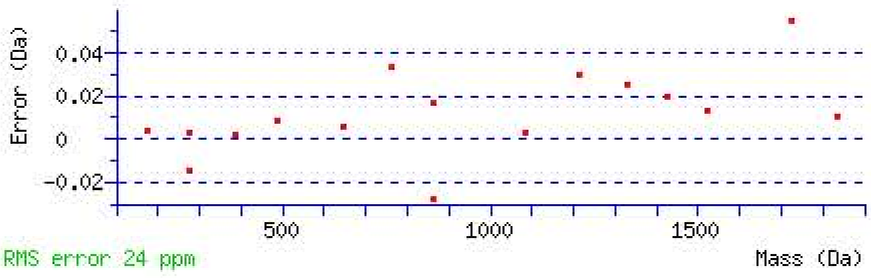
Match to Query 62037: 2381.164662 from(794.728830,3+) rtinseconds(2138) index(61466)
Title: Locus:1.1.1.3049.21 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

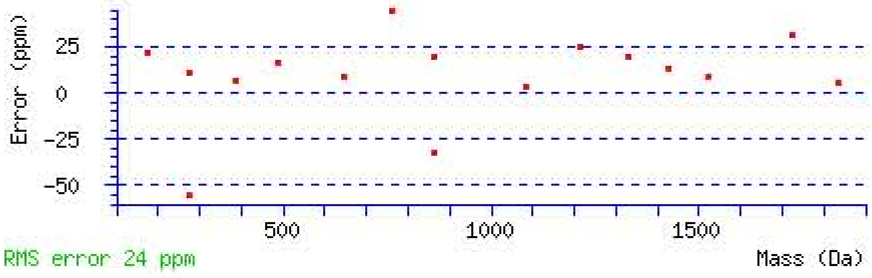
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2381.135529
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 94 **Expect:** 8.6e-009
Matches : 16/202 fragment ions using 17 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							19
2	217.081897	109.044586			199.071332	100.039304	E	2295.110779	1148.059027	2278.084230	1139.545753	2277.100214	1139.053745	18
3	**274.103361**	137.555319			256.092796	128.550036	G	2166.068186	1083.537731	2149.041637	1075.024456	2148.057621	1074.532448	17
4	361.135389	181.071332			343.124824	172.066050	S	2109.046722	1055.026999	2092.020173	1046.513724	2091.036157	1046.021716	16
5	448.167417	224.587346			430.156852	215.582064	S	2022.014694	1011.510985	2004.988145	1002.997711	2004.004129	1002.505703	15
6	547.235831	274.121554			529.225266	265.116271	V	1934.982666	967.994971	1917.956117	959.481697	1916.972101	958.989689	14
7	661.278758	331.143017	644.252209	322.629742	643.268193	322.137734	N	***1835.914252***	918.460764	1818.887703	909.947490	1817.903687	909.455482	13
8	774.362822	387.685049	757.336273	379.171774	756.352257	378.679766	L	***1721.871325***	861.439301	1704.844776	852.926026	1703.860760	852.434018	12
9	**861.394850**	431.201063	844.368301	422.687788	843.384285	422.195780	S	1608.787261	804.897269	1591.760712	796.383994	1590.776696	795.891986	11
10	958.447614	479.727445	941.421065	471.214170	940.437049	470.722162	P	***1521.755233***	761.381255	1504.728684	752.867980	1503.744668	752.375972	10
11	1055.500378	528.253827	1038.473829	519.740553	1037.489813	519.248544	P	***1424.702469***	712.854873	1407.675920	704.341598	1406.691904	703.849590	9
12	1168.584442	584.795859	1151.557893	576.282584	1150.573877	575.790576	L	***1327.649705***	664.328491	1310.623156	655.815216	1309.639140	655.323208	8
13	1297.627035	649.317155	1280.600486	640.803881	1279.616470	640.311873	E	***1214.565641***	607.786459	1197.539092	599.273184	1196.555076	598.781176	7
14	1736.852361	868.929819	1719.825812	860.416544	1718.841796	859.924536	Q	***1085.523048***	543.265162	1068.496499	534.751888	1067.512483	534.259880	6
15	1896.883010	948.945143	1879.856461	940.431869	1878.872445	939.939861	C	***646.297722***	323.652499	629.271173	315.139225	628.287157	314.647217	5
16	1995.951424	998.479350	1978.924875	989.966076	1977.940859	989.474068	V	***486.267073***	243.637174	469.240524	235.123900	468.256508	234.631892	4
17	2093.004188	1047.005732	2075.977639	1038.492457	2074.993623	1038.000449	P	***387.198659***	194.102967	370.172110	185.589693	369.188094	185.097685	3
18	2208.031131	1104.519203	2191.004582	1096.005929	2190.020566	1095.513921	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
94.2	2381.135529	0.029133	SEGSSVNLSPPLEQCVPDR
7.9	2381.168564	-0.003902	GNAVVGYLQCFDLEGESGLVVR
3.6	2381.158005	0.006657	HPKPSTVKDCPTLCKQTDNR

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

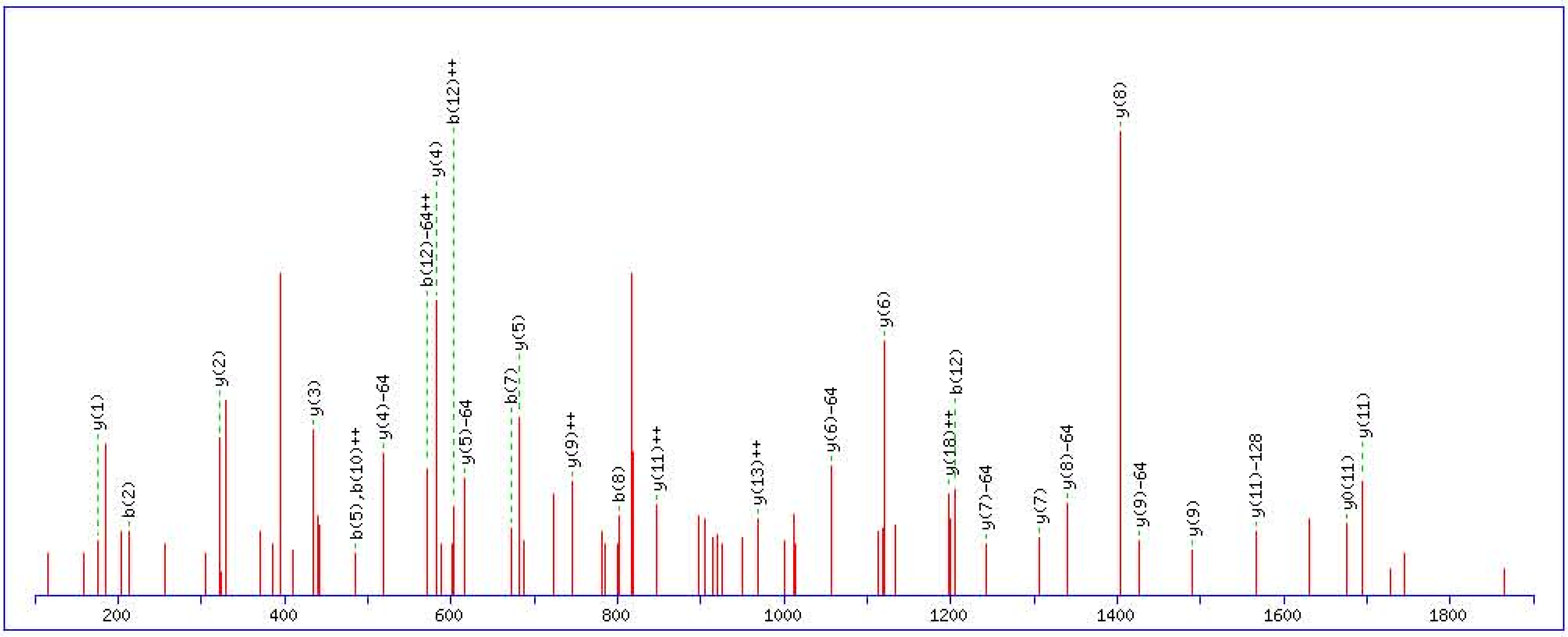
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVEGSDAEIGMSPWQVMLFR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

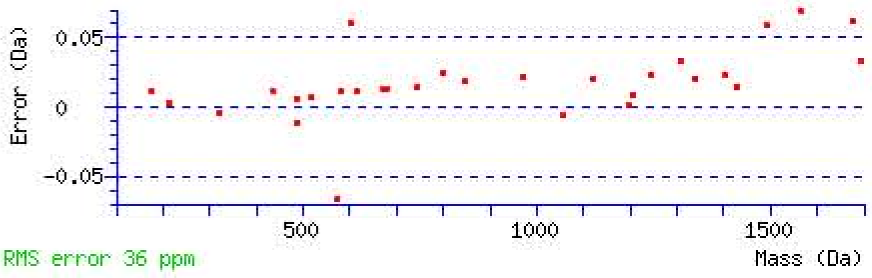
Match to Query 66681: 2607.269022 from(870.096950,3+) rtinseconds(2703) index(65321)
Title: Locus:1.1.1.3245.20 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

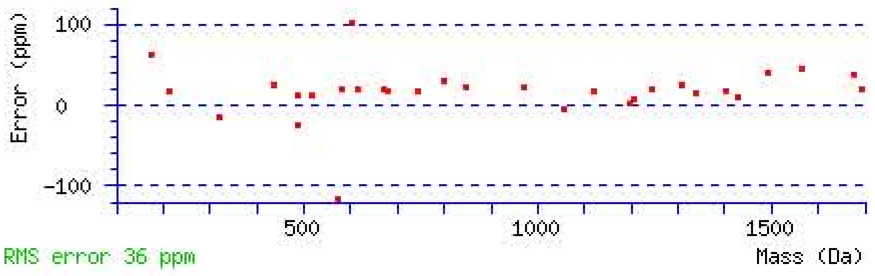
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2607.253540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11    : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q15    : Biotin:Thermo-21345 (Q)
M17    : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 46  Expect: 0.00055
Matches : 30/312 fragment ions using 54 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							20
2	**213.159754**	107.083515					V	2495.176752	1248.092014	2478.150203	1239.578739	2477.166187	1239.086731	19
3	342.202347	171.604811			324.191782	162.599529	E	2396.108338	1198.557807	2379.081789	1190.044532	2378.097773	1189.552524	18
4	399.223811	200.115543			381.213246	191.110261	G	2267.065745	1134.036510	2250.039196	1125.523236	2249.055180	1125.031228	17
5	**486.255839**	243.631557			468.245274	234.626275	S	2210.044281	1105.525778	2193.017732	1097.012504	2192.033716	1096.520496	16
6	601.282782	301.145029			583.272217	292.139747	D	2123.012253	1062.009764	2105.985704	1053.496490	2105.001688	1053.004482	15
7	**672.319896**	336.663586			654.309331	327.658303	A	2007.985310	1004.496293	1990.958761	995.983019	1989.974745	995.491011	14
8	**801.362489**	401.184883			783.351924	392.179600	E	1936.948196	968.977736	1919.921647	960.464462	1918.937631	959.972454	13
9	914.446553	457.726915			896.435988	448.721632	I	1807.905603	904.456440	1790.879054	895.943165	1789.895038	895.451157	12
10	971.468017	**486.237647**			953.457452	477.232364	G	***1694.821539***	847.914408	1677.794990	839.401133	1676.810974	838.909125	11
11	1118.503417	559.755346			1100.492852	550.750064	M	1637.800075	819.403676	1620.773526	810.890401	1619.789510	810.398393	10
12	**1205.535445**	**603.271361**			1187.524880	594.266078	S	***1490.764675***	745.885976	1473.738126	737.372701	1472.754110	736.880693	9
13	1302.588209	651.797743			1284.577644	642.792460	P	***1403.732647***	702.369962	1386.706098	693.856687			8
14	1488.667522	744.837399			1470.656957	735.832116	W	***1306.679883***	653.843580	1289.653334	645.330305			7
15	1927.892848	964.450062	1910.866299	955.936788	1909.882283	955.444780	Q	***1120.600570***	560.803923	1103.574021	552.290649			6
16	2026.961262	1013.984269	2009.934713	1005.470995	2008.950697	1004.978987	V	***681.375244***	341.191260	664.348695	332.677986			5
17	2173.996662	1087.501969	2156.970113	1078.988694	2155.986097	1078.496686	M	***582.306830***	291.657053	565.280281	283.143779			4
18	2287.080726	1144.044001	2270.054177	1135.530726	2269.070161	1135.038719	L	***435.271430***	218.139353	418.244881	209.626078			3
19	2434.149140	1217.578208	2417.122591	1209.064933	2416.138575	1208.572925	F	***322.187366***	161.597321	305.160817	153.084046			2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.4	2607.253540	0.015482	IVEGSDAEIGMSPWQVMLFR

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

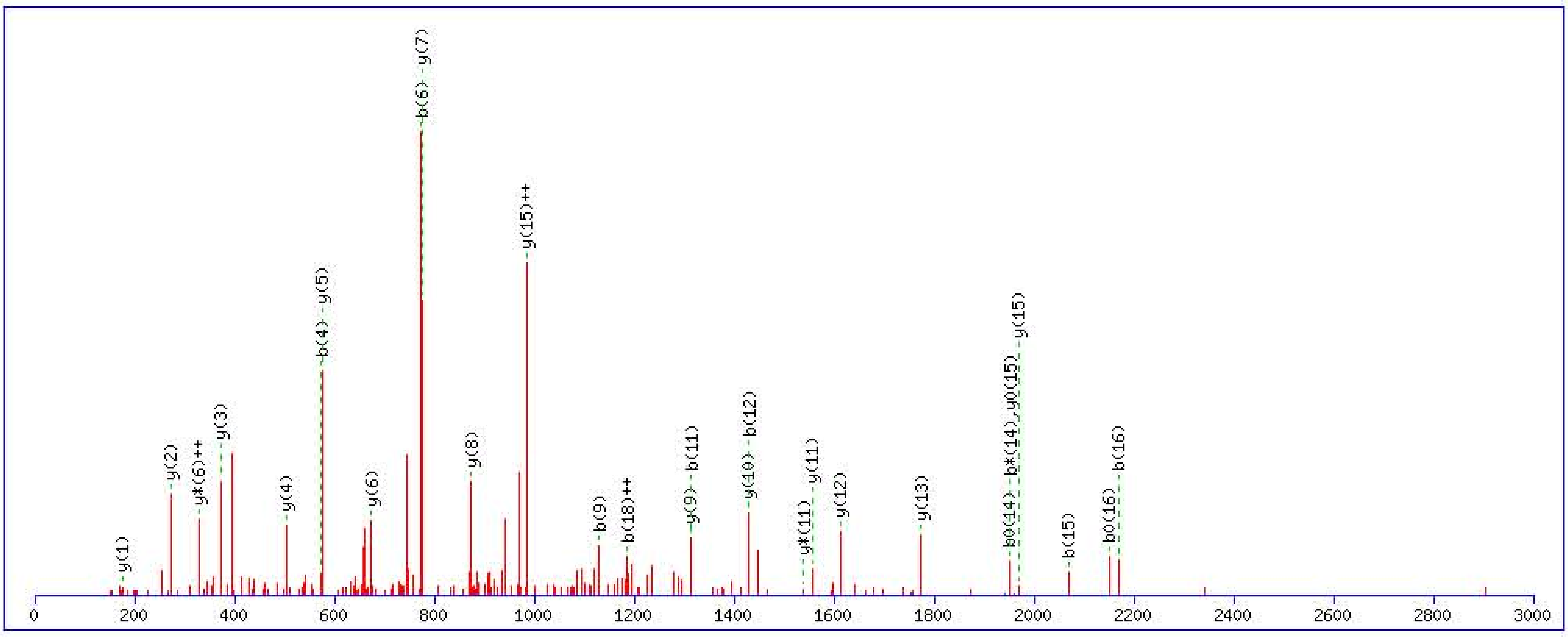
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RQECSIPVCGQDQVTVAMTPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

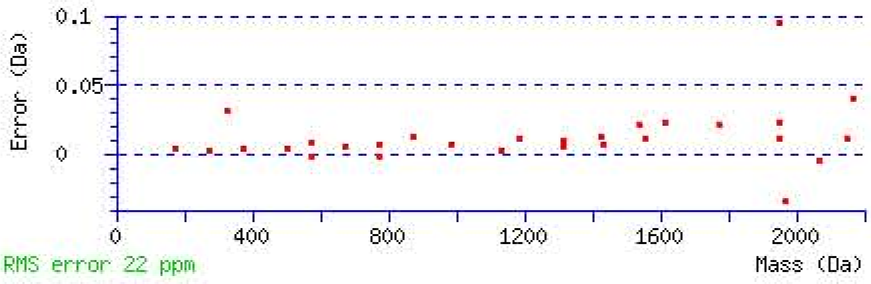
Match to Query 68027: 2742.330012 from(915.117280,3+) rtinseconds(2000) index(78518)
Title: Locus:1.1.1.2910.14 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

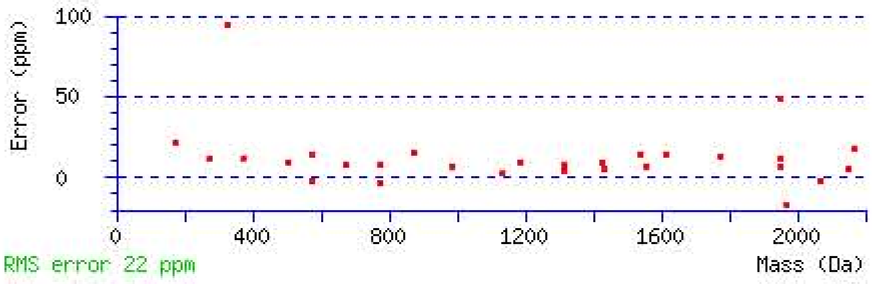
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2742.307404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 94 **Expect:** 9.6e-009
Matches : 29/232 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							21
2	285.166965	143.087121	268.140416	134.573846			Q	2587.213551	1294.110413	2570.187002	1285.597139	2569.202986	1285.105131	20
3	414.209558	207.608417	397.183009	199.095143	396.198993	198.603135	E	2459.154973	1230.081124	2442.128424	1221.567850	2441.144408	1221.075842	19
4	**574.240207**	287.623742	557.213658	279.110467	556.229642	278.618459	C	2330.112380	1165.559828	2313.085831	1157.046553	2312.101815	1156.554545	18
5	661.272235	331.139756	644.245686	322.626481	643.261670	322.134473	S	2170.081731	1085.544503	2153.055182	1077.031229	2152.071166	1076.539221	17
6	**774.356299**	387.681788	757.329750	379.168513	756.345734	378.676505	I	2083.049703	1042.028489	2066.023154	1033.515215	2065.039138	1033.023207	16
7	871.409063	436.208170	854.382514	427.694895	853.398498	427.202887	P	***1969.965639***	985.486458	1952.939090	976.973183	1951.955074	976.481175	15
8	970.477477	485.742377	953.450928	477.229102	952.466912	476.737094	V	1872.912875	936.960076	1855.886326	928.446801	1854.902310	927.954793	14
9	**1130.508126**	565.757701	1113.481577	557.244427	1112.497561	556.752418	C	***1773.844461***	887.425868	1756.817912	878.912594	1755.833896	878.420586	13
10	1187.529590	594.268433	1170.503041	585.755158	1169.519025	585.263150	G	***1613.813812***	807.410544	1596.787263	798.897270	1595.803247	798.405262	12
11	**1315.588168**	658.297722	1298.561619	649.784448	1297.577603	649.292440	Q	***1556.792348***	778.899812	1539.765799	770.386538	1538.781783	769.894530	11
12	**1430.615111**	715.811194	1413.588562	707.297919	1412.604546	706.805911	D	***1428.733770***	714.870523	1411.707221	706.357249	1410.723205	705.865241	10
13	1869.840437	935.423857	1852.813888	926.910582	1851.829872	926.418574	Q	***1313.706827***	657.357052	1296.680278	648.843777	1295.696262	648.351769	9
14	1968.908851	984.958064	1951.882302	976.444789	1950.898286	975.952781	V	***874.481501***	437.744389	857.454952	429.231114	856.470936	428.739106	8
15	**2069.956530**	1035.481903	2052.929981	1026.968628	2051.945965	1026.476620	T	***775.413087***	388.210181	758.386538	379.696907	757.402522	379.204899	7
16	**2169.024944**	1085.016110	2151.998395	1076.502835	2151.014379	1076.010827	V	***674.365408***	337.686342	657.338859	329.173067	656.354843	328.681059	6
17	2240.062058	1120.534667	2223.035509	1112.021392	2222.051493	1111.529384	A	***575.296994***	288.152135	558.270445	279.638861	557.286429	279.146853	5
18	2371.102543	1186.054909	2354.075994	1177.541635	2353.091978	1177.049627	M	***504.259880***	252.633578	487.233331	244.120303	486.249315	243.628295	4
19	2472.150222	1236.578749	2455.123673	1228.065474	2454.139657	1227.573466	T	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
20	2569.202986	1285.105131	2552.176437	1276.591856	2551.192421	1276.099848	P	***272.171716***	136.589496	255.145167	128.076221			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
94.4	2742.307404	0.022608	RQECSIPVCGQDQVTVAMTPR
68.3	2742.307404	0.022608	RQECSIPVCGQDQVTVAMTPR
22.9	2742.307404	0.022608	RQECSIPVCGQDQVTVAMTPR

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

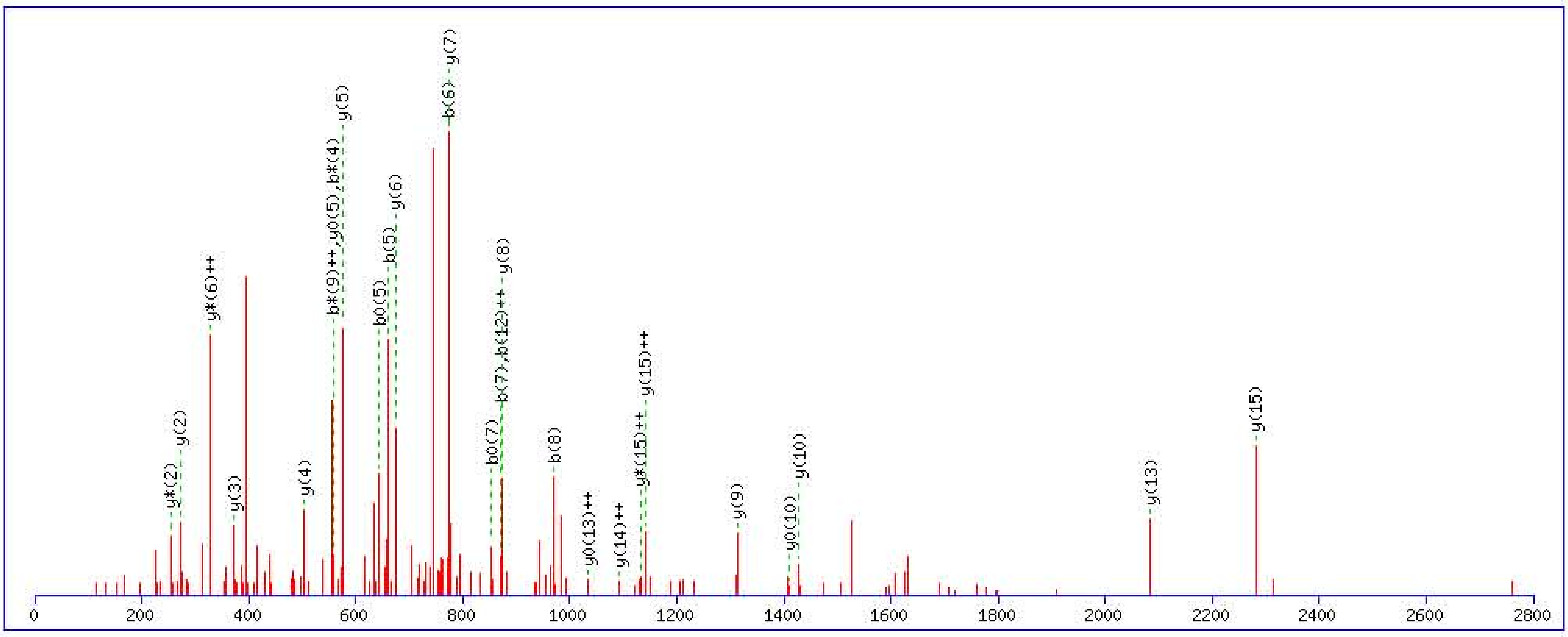
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RQECSIPVCGQDQVTVAMTPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

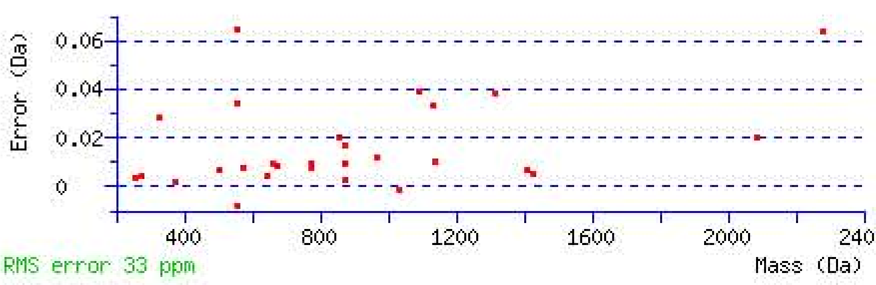
Match to Query 72078: 3053.509416 from(764.384630,4+) rtinseconds(2167) index(61713)
Title: Locus:1.1.1.3059.18 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

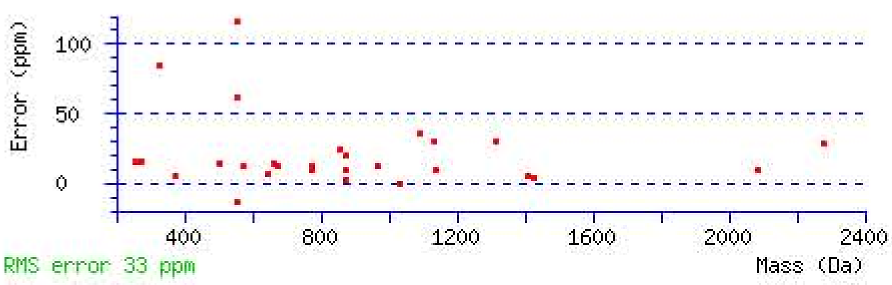
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3053.474152
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00077
Matches : 28/232 fragment ions using 55 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							21
2	285.166965	143.087121	268.140416	134.573846			Q	2898.380299	1449.693787	2881.353750	1441.180513	2880.369734	1440.688505	20
3	414.209558	207.608417	397.183009	199.095143	396.198993	198.603135	E	2770.321721	1385.664498	2753.295172	1377.151224	2752.311156	1376.659216	19
4	574.240207	287.623742	557.213658	279.110467	556.229642	278.618459	C	2641.279128	1321.143202	2624.252579	1312.629927	2623.268563	1312.137919	18
5	**661.272235**	331.139756	644.245686	322.626481	643.261670	322.134473	S	2481.248479	1241.127877	2464.221930	1232.614603	2463.237914	1232.122595	17
6	**774.356299**	387.681788	757.329750	379.168513	756.345734	378.676505	I	2394.216451	1197.611863	2377.189902	1189.098589	2376.205886	1188.606581	16
7	**871.409063**	436.208170	854.382514	427.694895	853.398498	427.202887	P	***2281.132387***	1141.069831	2264.105838	1132.556557	2263.121822	1132.064549	15
8	**970.477477**	485.742377	953.450928	477.229102	952.466912	476.737094	V	2184.079623	1092.543449	2167.053074	1084.030175	2166.069058	1083.538167	14
9	1130.508126	565.757701	1113.481577	557.244427	1112.497561	556.752418	C	***2085.011209***	1043.009242	2067.984660	1034.495968	2067.000644	1034.003960	13
10	1187.529590	594.268433	1170.503041	585.755158	1169.519025	585.263150	G	1924.980560	962.993918	1907.954011	954.480643	1906.969995	953.988635	12
11	1626.754916	813.881096	1609.728367	805.367822	1608.744351	804.875814	Q	1867.959096	934.483186	1850.932547	925.969911	1849.948531	925.477903	11
12	1741.781859	871.394568	1724.755310	862.881293	1723.771294	862.389285	D	***1428.733770***	714.870523	1411.707221	706.357248	1410.723205	705.865240	10
13	2181.007185	1091.007230	2163.980636	1082.493956	2162.996620	1082.001948	Q	***1313.706827***	657.357051	1296.680278	648.843777	1295.696262	648.351769	9
14	2280.075599	1140.541437	2263.049050	1132.028163	2262.065034	1131.536155	V	***874.481501***	437.744388	857.454952	429.231114	856.470936	428.739106	8
15	2381.123278	1191.065277	2364.096729	1182.552002	2363.112713	1182.059994	T	***775.413087***	388.210181	758.386538	379.696907	757.402522	379.204899	7
16	2480.191692	1240.599484	2463.165143	1232.086209	2462.181127	1231.594201	V	***674.365408***	337.686342	657.338859	329.173067	656.354843	328.681059	6
17	2551.228806	1276.118041	2534.202257	1267.604766	2533.218241	1267.112758	A	***575.296994***	288.152135	558.270445	279.638861	557.286429	279.146853	5
18	2682.269291	1341.638283	2665.242742	1333.125009	2664.258726	1332.633001	M	***504.259880***	252.633578	487.233331	244.120303	486.249315	243.628295	4
19	2783.316970	1392.162123	2766.290421	1383.648848	2765.306405	1383.156840	T	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
20	2880.369734	1440.688505	2863.343185	1432.175230	2862.359169	1431.683222	P	***272.171716***	136.589496	255.145167	128.076221			2
21							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.9	3053.474152	0.035264	RQECSIPVCGQDQVTVAMTPR
17.3	3053.474152	0.035264	RQECSIPVCGQDQVTVAMTPR
4.5	3053.474152	0.035264	RQECSIPVCGQDQVTVAMTPR

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

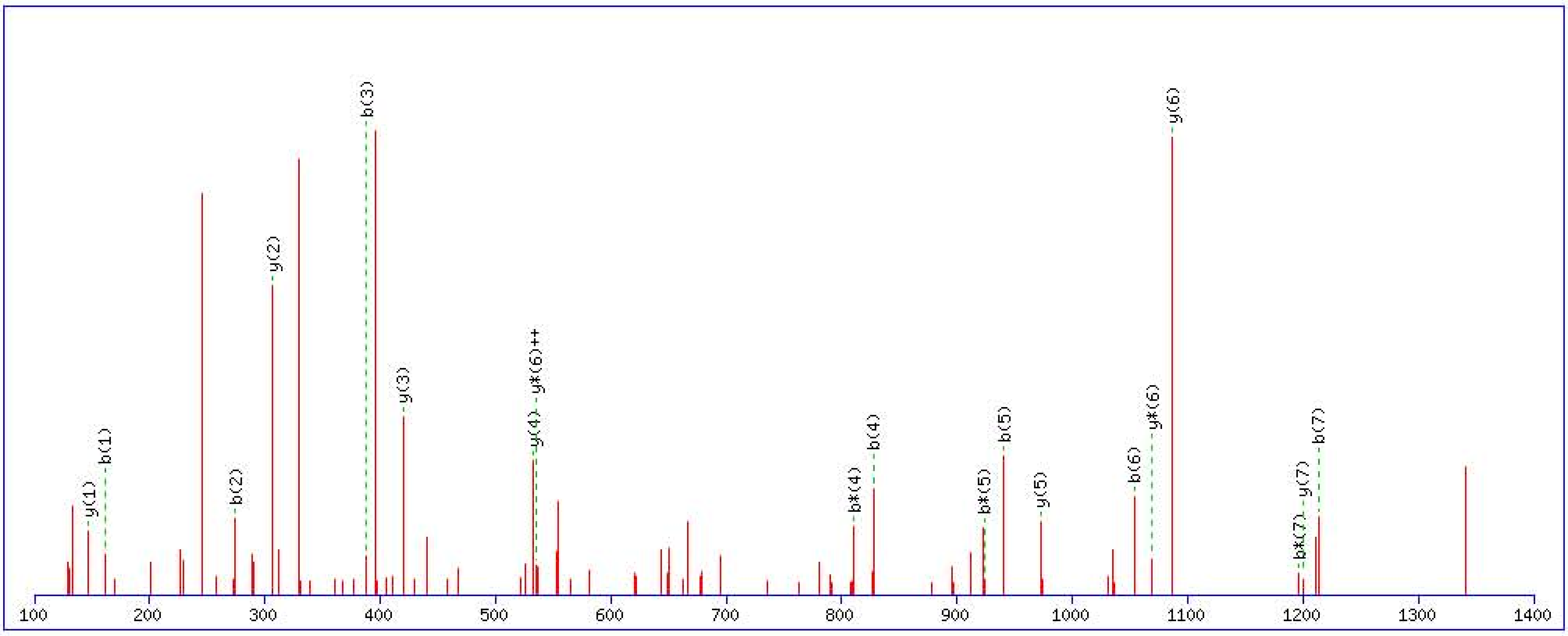
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CINQLLCK**
Found in **SEPP1_HUMAN**, Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3

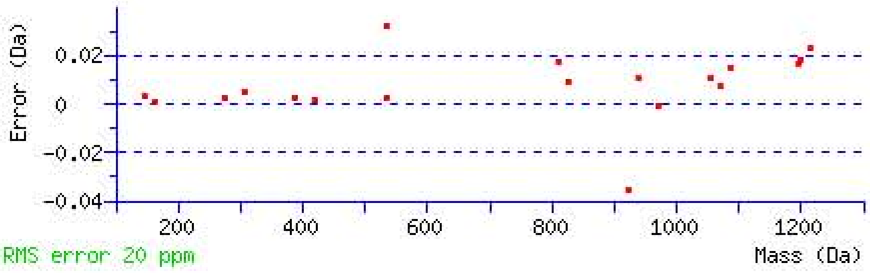
Match to Query 32959: 1358.697608 from(680.356080,2+) rtinseconds(1979) index(78348)
Title: Locus:1.1.1.2903.17 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

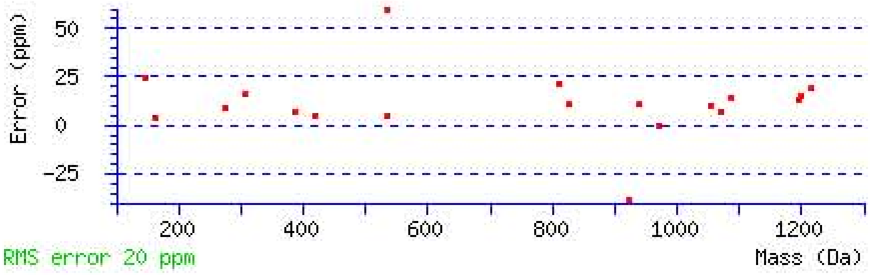
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1358.687256
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0031
Matches : 19/52 fragment ions using 44 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	*161.037925*	81.022600			C					8
2	*274.121989*	137.564632			I	**1199.663898**	600.335587	1182.637349	591.822313	7
3	*388.164916*	194.586096	371.138367	186.072822	N	**1086.579834**	543.793555	1069.553285	535.280281	6
4	*827.390242*	414.198759	810.363693	405.685485	Q	**972.536907**	486.772092	955.510358	478.258817	5
5	*940.474306*	470.740791	923.447757	462.227517	L	**533.311581**	267.159429	516.285032	258.646154	4
6	*1053.558370*	527.282823	1036.531821	518.769549	L	**420.227517**	210.617396	403.200968	202.104122	3
7	*1213.589019*	607.298148	1196.562470	598.784873	C	**307.143453**	154.075365	290.116904	145.562090	2
8					K	**147.112804**	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.0	1358.687256	0.010352	CINQLLCK
4.0	1358.701630	-0.004022	KKIYAMGGGSYGK
2.3	1358.705017	-0.007409	CLLNVQSSK
0.2	1358.679855	0.017753	AMAGQRVELPCK

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

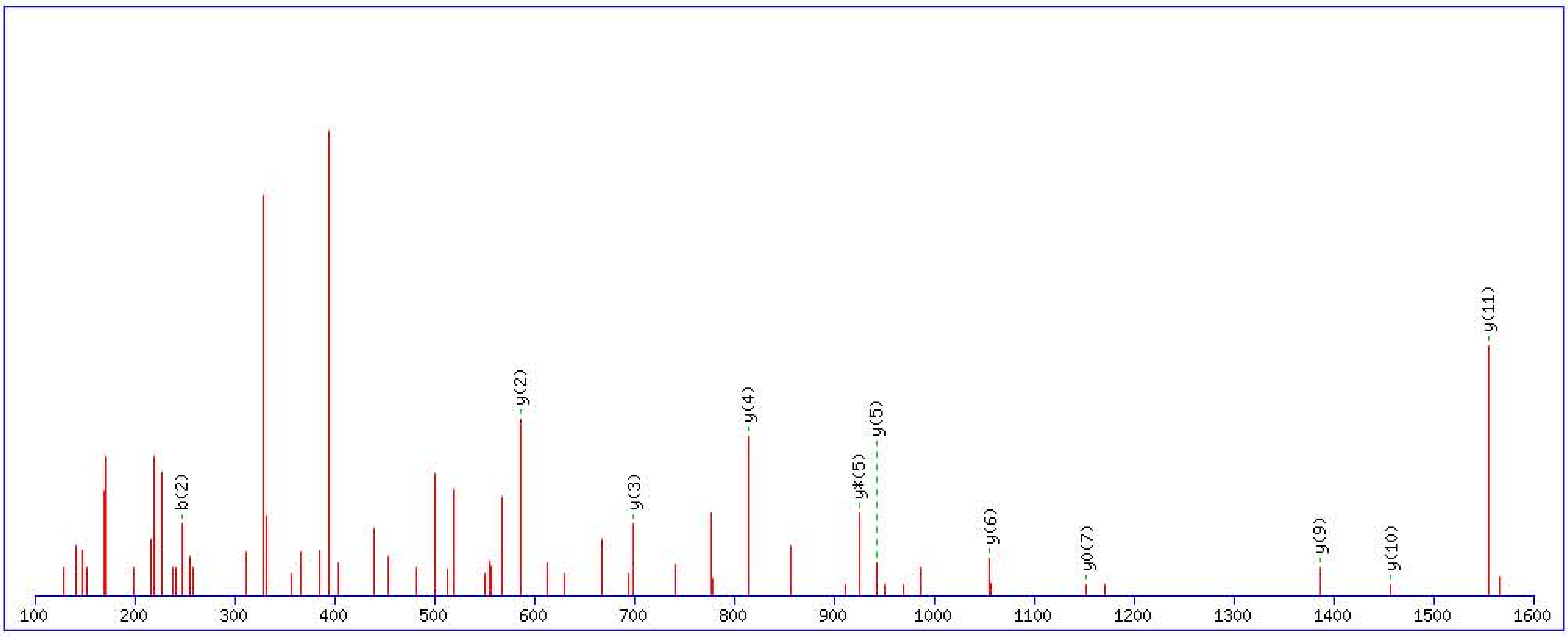
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DMPASEDLQDLQK**
Found in **SEPP1_HUMAN**, Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3

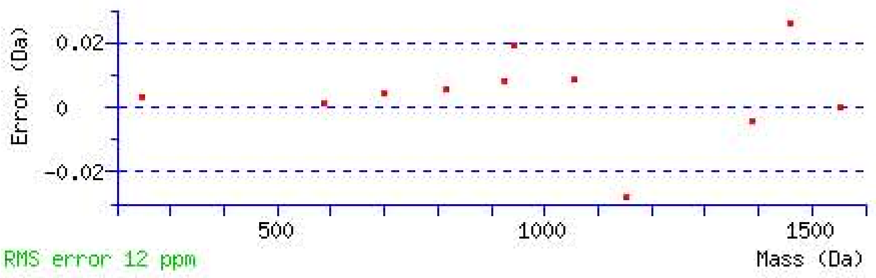
Match to Query 48409: 1799.854362 from(600.958730,3+) rtinseconds(2161) index(43162)
Title: Locus:1.1.1.3036.12 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

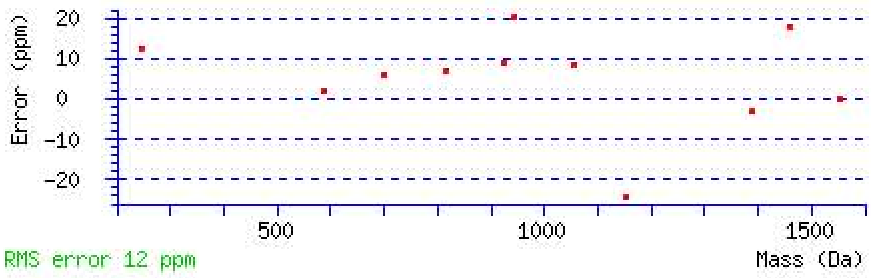
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1799.843353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 62 **Expect:** 1e-005
Matches : 11/122 fragment ions using 14 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							13
2	**247.074704**	124.040990			229.064139	115.035708	M	1685.823706	843.415491	1668.797157	834.902217	1667.813141	834.410209	12
3	344.127468	172.567372			326.116903	163.562089	P	***1554.783221***	777.895249	1537.756672	769.381974	1536.772656	768.889966	11
4	415.164582	208.085929			397.154017	199.080646	A	***1457.730457***	729.368867	1440.703908	720.855592	1439.719892	720.363584	10
5	502.196610	251.601943			484.186045	242.596660	S	***1386.693343***	693.850310	1369.666794	685.337035	1368.682778	684.845027	9
6	631.239203	316.123240			613.228638	307.117957	E	1299.661315	650.334296	1282.634766	641.821021	1281.650750	641.329013	8
7	746.266146	373.636711			728.255581	364.631428	D	1170.618722	585.812999	1153.592173	577.299725	1152.608157	576.807717	7
8	859.350210	430.178743			841.339645	421.173460	L	***1055.591779***	528.299528	1038.565230	519.786253	1037.581214	519.294245	6
9	987.408788	494.208032	970.382239	485.694757	969.398223	485.202749	Q	***942.507715***	471.757496	925.481166	463.244221	924.497150	462.752213	5
10	1102.435731	551.721504	1085.409182	543.208229	1084.425166	542.716221	D	***814.449137***	407.728207	797.422588	399.214932	796.438572	398.722924	4
11	1215.519795	608.263535	1198.493246	599.750261	1197.509230	599.258253	L	***699.422194***	350.214735	682.395645	341.701461			3
12	1654.745121	827.876199	1637.718572	819.362924	1636.734556	818.870916	Q	***586.338130***	293.672703	569.311581	285.159429			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.2	1799.843353	0.011009	DMPASEDLQDLQK
20.9	1799.843353	0.011009	DMPASEDLQDLQK

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

{MATRIX}
{SCIENCE}

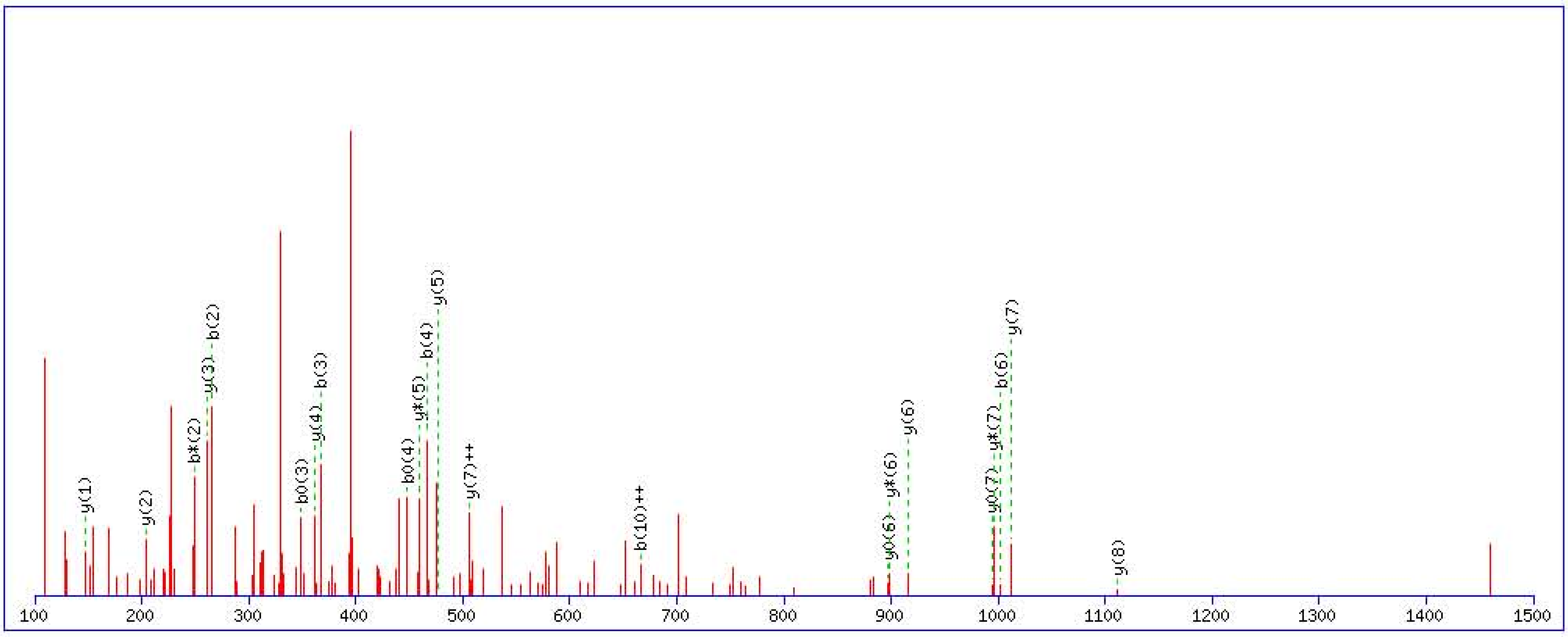
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

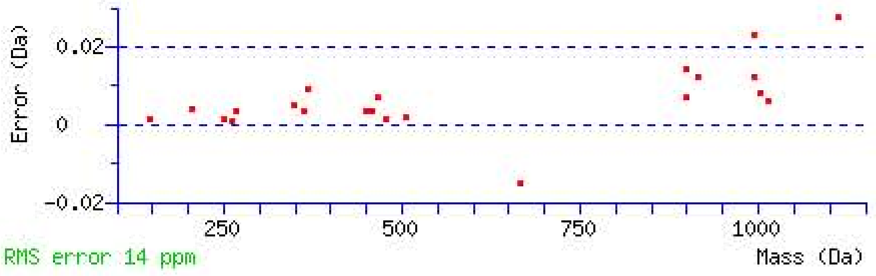
Match to Query 37895: 1476.754602 from(493.258810,3+) rtinseconds(1186) index(73073)
Title: Locus:1.1.1.2627.15 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

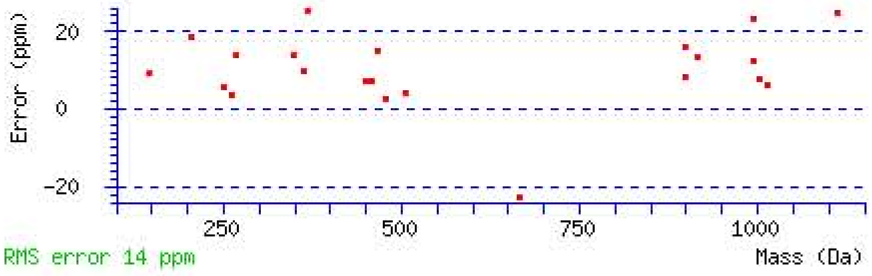
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1476.750748
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.019
Matches : 22/108 fragment ions using 54 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							11
2	**266.124766**	133.566021	249.098217	125.052746			Q	1340.699099	670.853187	1323.672550	662.339913	1322.688534	661.847905	10
3	**367.172445**	184.089860	350.145896	175.576586	349.161880	175.084578	T	1212.640521	606.823899	1195.613972	598.310624	1194.629956	597.818616	9
4	**466.240859**	233.624068	449.214310	225.110793	448.230294	224.618785	V	***1111.592842***	556.300059	1094.566293	547.786784	1093.582277	547.294776	8
5	563.293623	282.150450	546.267074	273.637175	545.283058	273.145167	P	***1012.524428***	506.765852	995.497879	498.252577	994.513863	497.760569	7
6	**1002.518949**	501.763113	985.492400	493.249838	984.508384	492.757830	Q	***915.471664***	458.239470	898.445115	449.726195	897.461099	449.234187	6
7	1116.561876	558.784576	1099.535327	550.271302	1098.551311	549.779293	N	***476.246338***	238.626807	459.219789	230.113532	458.235773	229.621524	5
8	1217.609555	609.308416	1200.583006	600.795141	1199.598990	600.303133	T	***362.203411***	181.605343	345.176862	173.092069	344.192846	172.600061	4
9	1274.631019	637.819147	1257.604470	629.305873	1256.620454	628.813865	G	***261.155732***	131.081504	244.129183	122.568229			3
10	1331.652483	666.329879	1314.625934	657.816605	1313.641918	657.324597	G	***204.134268***	102.570772	187.107719	94.057497			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.3	1476.750748	0.003854	HQTVPQNTGGK
17.5	1476.736115	0.018487	HQEALIGQSFYGK
11.8	1476.750748	0.003854	HQTVPQNTGGK
3.3	1476.739487	0.015115	GPEVMAFIEQGKR
2.2	1476.775864	-0.021262	AGPEPQALAGQK

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

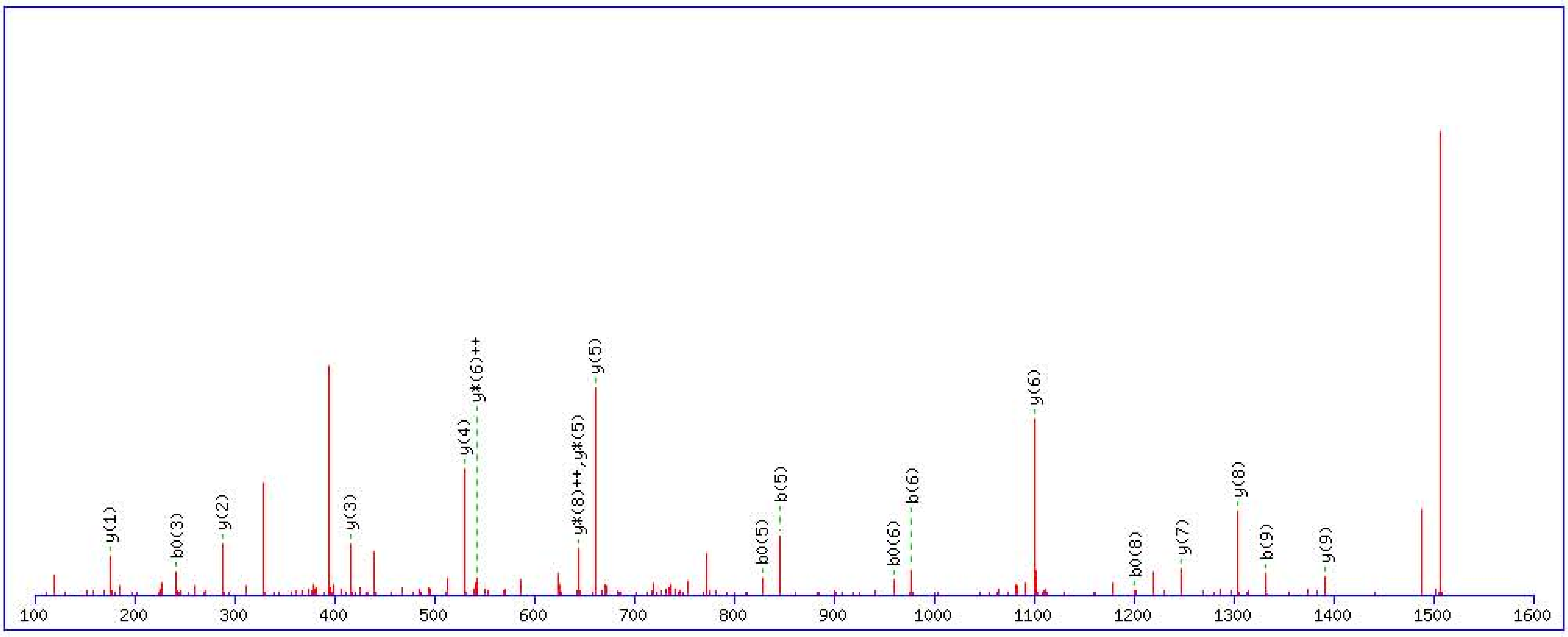
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

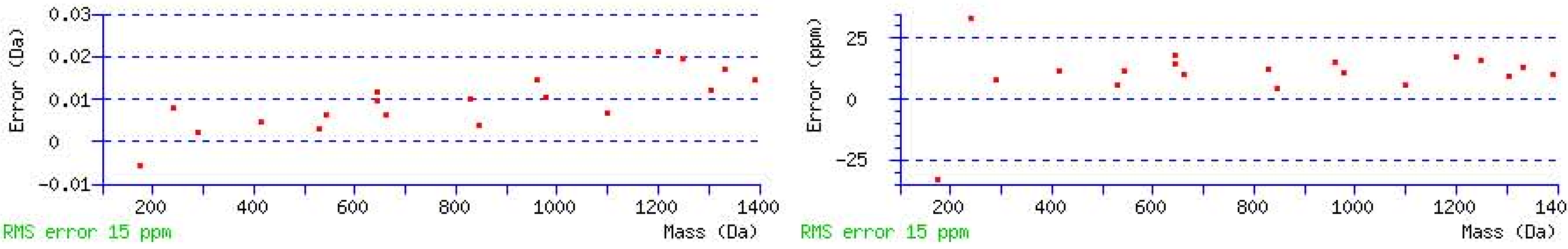
Match to Query 38767: 1505.722768 from(753.868660,2+) rtinseconds(2039) index(78778)
Title: Locus:1.1.1.2924.18 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1505.711899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 2.7e-006
Matches : 19/84 fragment ions using 28 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	***1391.692238***	696.349757	1374.665689	687.836482	1373.681673	687.344474	9
3	260.087711	130.547493			242.077146	121.542211	G	***1304.660210***	652.833743	1287.633661	644.320469			8
4	407.156125	204.081700			389.145560	195.076418	F	***1247.638746***	624.323011	1230.612197	615.809736			7
5	**846.381451**	423.694364	829.354902	415.181089	828.370886	414.689081	Q	***1100.570332***	550.788804	1083.543783	542.275530			6
6	**977.421936**	489.214606	960.395387	480.701331	959.411371	480.209323	M	***661.345006***	331.176141	644.318457	322.662867			5
7	1091.464863	546.236069	1074.438314	537.722795	1073.454298	537.230787	N	***530.304521***	265.655899	513.277972	257.142624			4
8	1219.523441	610.265359	1202.496892	601.752084	1201.512876	601.260076	Q	***416.261594***	208.634435	399.235045	200.121160			3
9	**1332.607505**	666.807391	1315.580956	658.294116	1314.596940	657.802108	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of DSGFQMNQLR
(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	1505.711899	0.010869	DSGFQMNQLR
19.1	1505.703140	0.019628	DETMEEQDIKLR
19.0	1505.711899	0.010869	DSGFQMNQLR
17.7	1505.740891	-0.018123	VQTSNFPRECIR
5.8	1505.704025	0.018743	MQMEIDQLR
5.5	1505.744232	-0.021464	QAKMAPSRMDSLR
4.3	1505.739548	-0.016780	TVQSLEIDLDSMR
3.0	1505.736862	-0.014094	EVMSPTGSARGRSR
3.0	1505.740875	-0.018107	ECGKAFSHSSKLR
3.0	1505.700653	0.022115	FMEDEQQLR

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

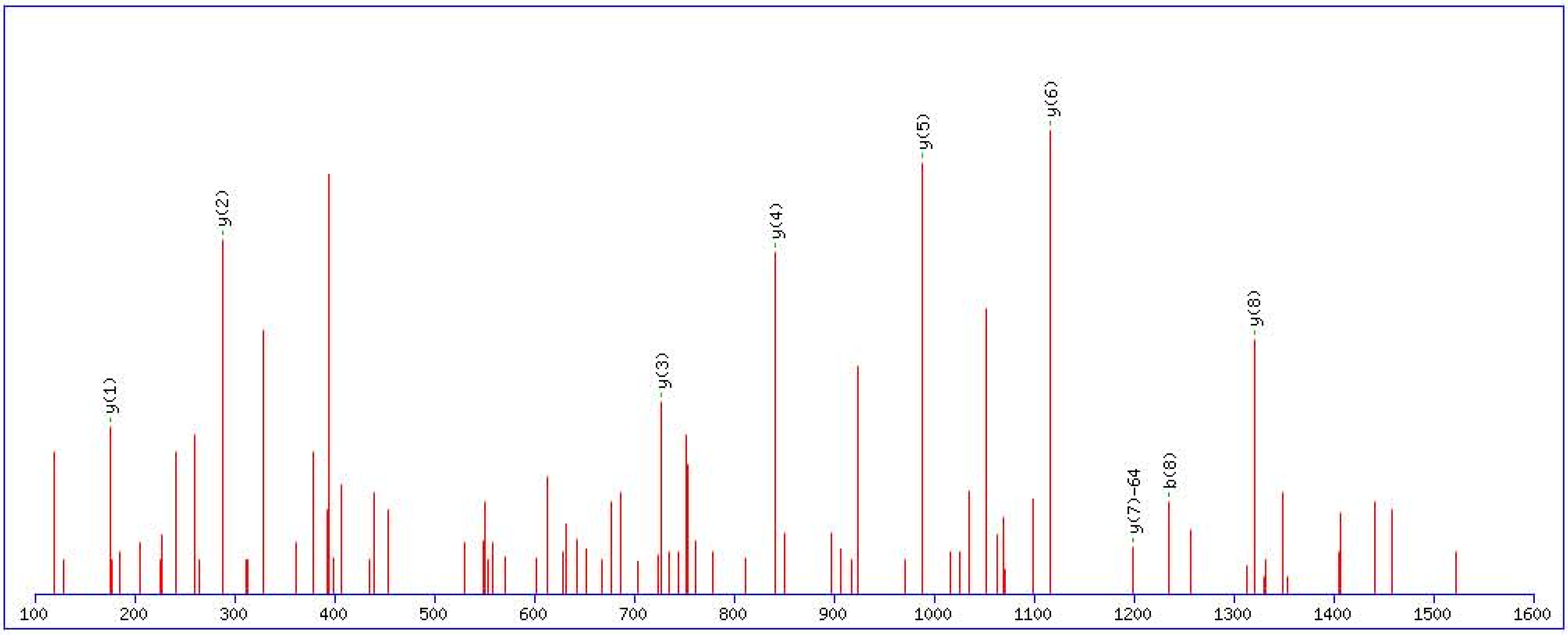
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

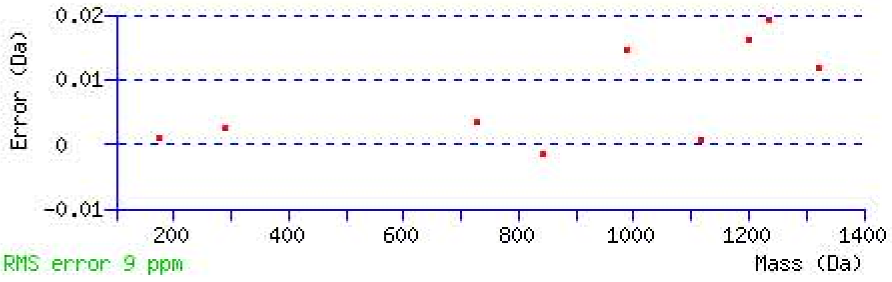
Match to Query 39303: 1521.712348 from(761.863450,2+) rtinseconds(1798) index(77138)
Title: Locus:1.1.1.2840.16 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

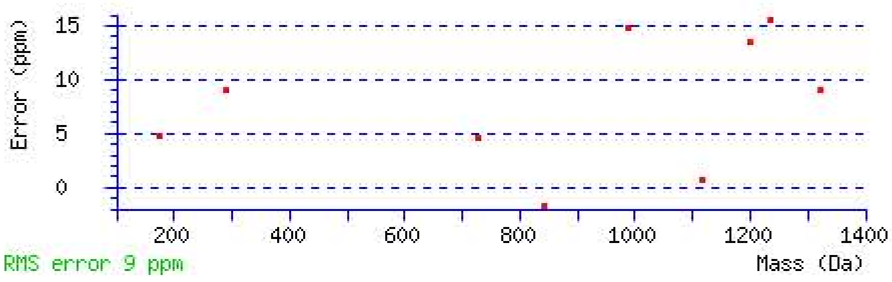
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1521.706818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 2.5e-005
Matches : 9/130 fragment ions using 14 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	1407.687153	704.347214	1390.660604	695.833940	1389.676588	695.341932	9
3	260.087711	130.547493			242.077146	121.542211	G	***1320.655125***	660.831200	1303.628576	652.317926			8
4	407.156125	204.081700			389.145560	195.076418	F	1263.633661	632.320468	1246.607112	623.807194			7
5	535.214703	268.110990	518.188154	259.597715	517.204138	259.105707	Q	***1116.565247***	558.786261	1099.538698	550.272987			6
6	682.250103	341.628690	665.223554	333.115415	664.239538	332.623407	M	***988.506669***	494.756972	971.480120	486.243698			5
7	796.293030	398.650153	779.266481	390.136878	778.282465	389.644870	N	***841.471269***	421.239272	824.444720	412.725998			4
8	**1235.518356**	618.262816	1218.491807	609.749541	1217.507791	609.257533	Q	***727.428342***	364.217809	710.401793	355.704534			3
9	1348.602420	674.804848	1331.575871	666.291573	1330.591855	665.799565	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.1	1521.706818	0.005530	DSGFQMNQLR
28.9	1521.706818	0.005530	DSGFQMNQLR
3.0	1521.695572	0.016776	FMEDEQQLR

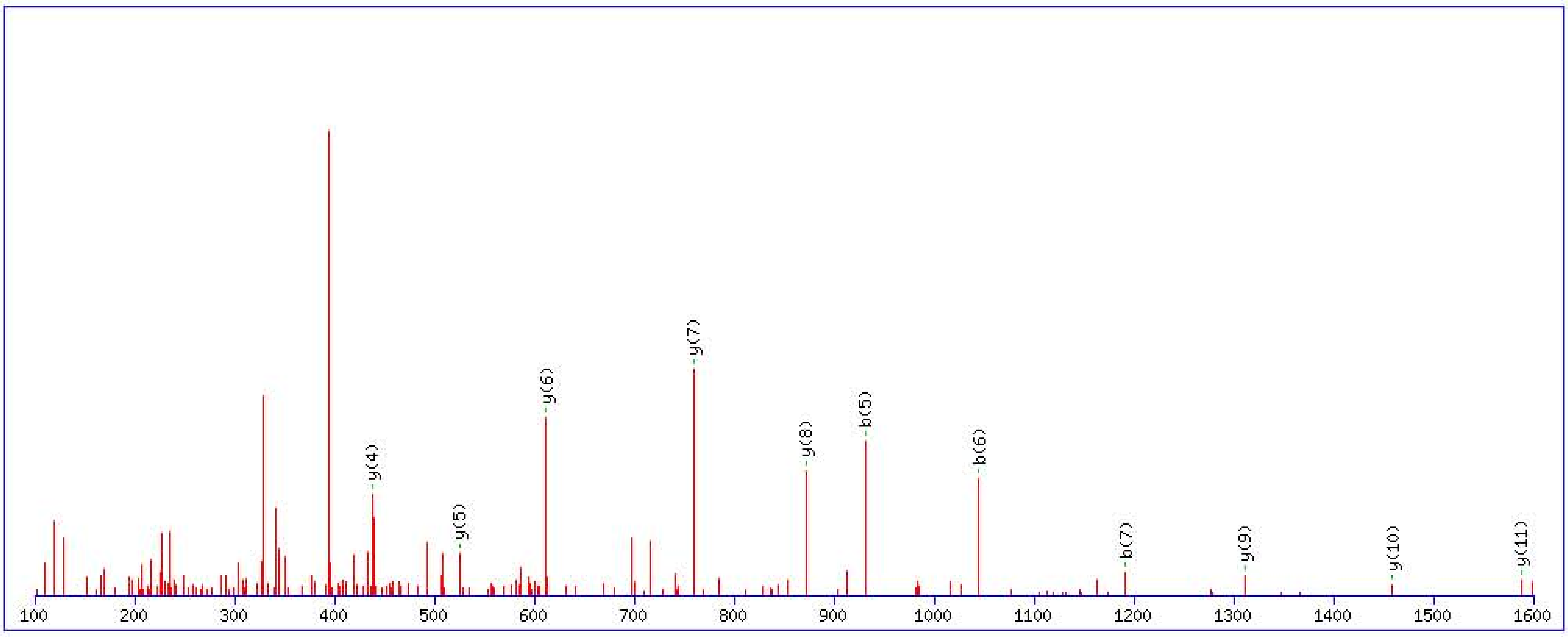
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SKEFQLFSSPHGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

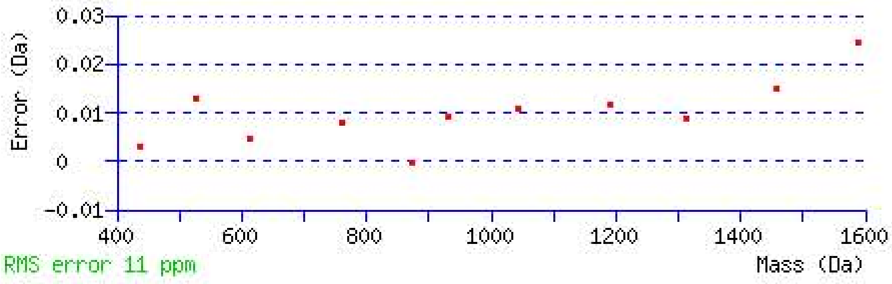
Match to Query 48441: 1801.925712 from(601.649180,3+) rtinseconds(1757) index(76876)
Title: Locus:1.1.1.2826.15 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

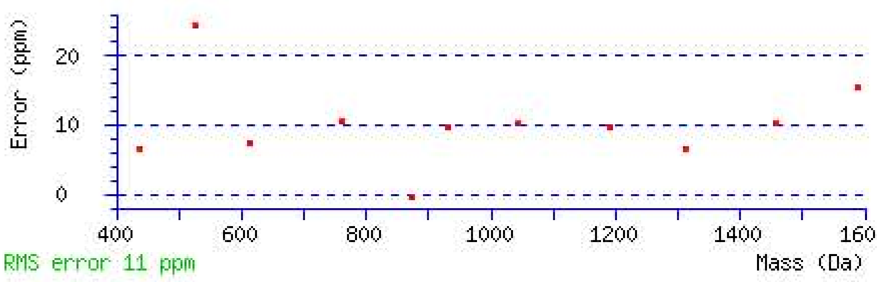
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1801.918518
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 4.3e-006
Matches : 11/134 fragment ions using 15 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							13
2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	K	1715.893774	858.450525	1698.867225	849.937251	1697.883209	849.445243	12
3	345.176860	173.092068	328.150311	164.578793	327.166295	164.086785	E	***1587.798811***	794.403044	1570.772262	785.889769	1569.788246	785.397761	11
4	492.245274	246.626275	475.218725	238.113000	474.234709	237.620992	F	***1458.756218***	729.881747	1441.729669	721.368473	1440.745653	720.876465	10
5	**931.470600**	466.238938	914.444051	457.725664	913.460035	457.233656	Q	***1311.687804***	656.347540	1294.661255	647.834266	1293.677239	647.342258	9
6	**1044.554664**	522.780970	1027.528115	514.267696	1026.544099	513.775688	L	***872.462478***	436.734877	855.435929	428.221603	854.451913	427.729595	8
7	**1191.623078**	596.315177	1174.596529	587.801903	1173.612513	587.309895	F	***759.378414***	380.192845	742.351865	371.679571	741.367849	371.187563	7
8	1278.655106	639.831191	1261.628557	631.317917	1260.644541	630.825909	S	***612.310000***	306.658638	595.283451	298.145364	594.299435	297.653356	6
9	1365.687134	683.347205	1348.660585	674.833931	1347.676569	674.341923	S	***525.277972***	263.142624	508.251423	254.629350	507.267407	254.137342	5
10	1462.739898	731.873587	1445.713349	723.360313	1444.729333	722.868305	P	***438.245944***	219.626610	421.219395	211.113335			4
11	1599.798810	800.403043	1582.772261	791.889769	1581.788245	791.397761	H	341.193180	171.100228	324.166631	162.586953			3
12	1656.820274	828.913775	1639.793725	820.400501	1638.809709	819.908493	G	204.134268	102.570772	187.107719	94.057497			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.6	1801.918518	0.007194	SKEFQLFSSPHGK
2.2	1801.914536	0.011176	QTVMTVVYGVTRYGGR
0.3	1801.924332	0.001380	MIQQEEIRKLEEEK

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

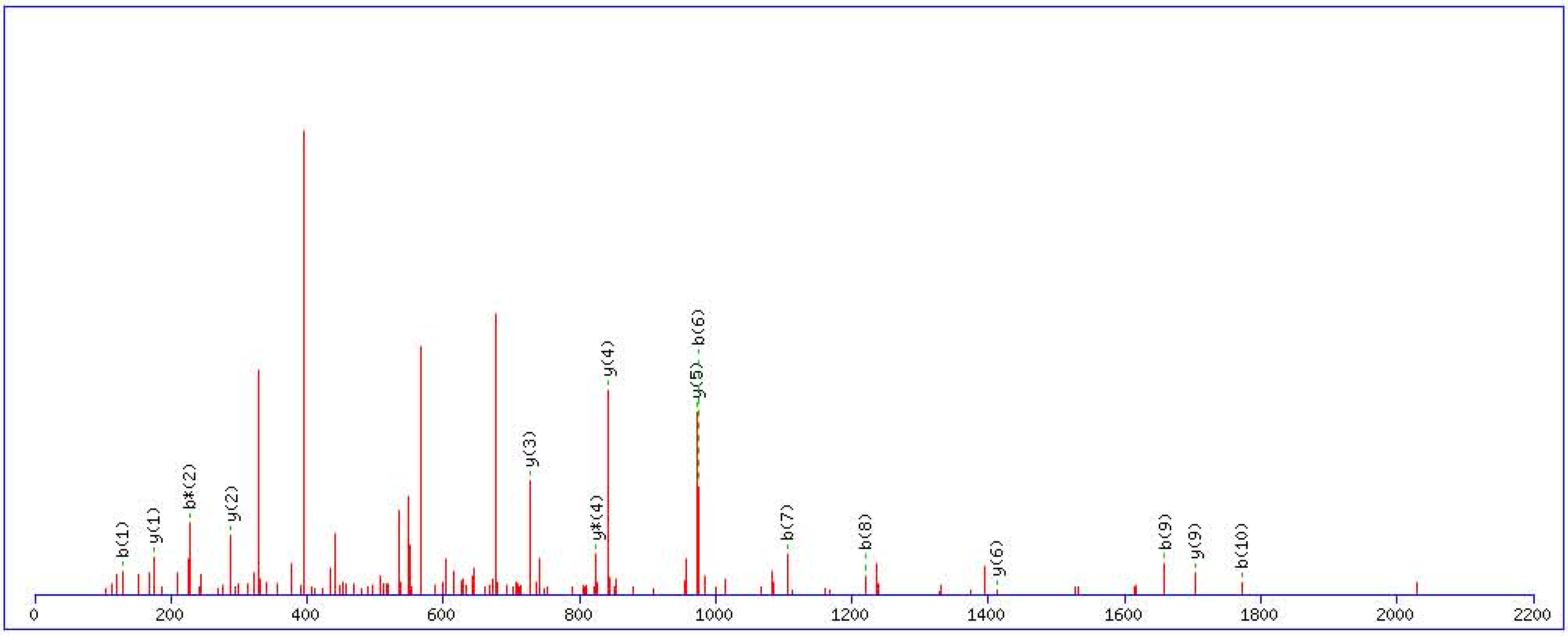
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

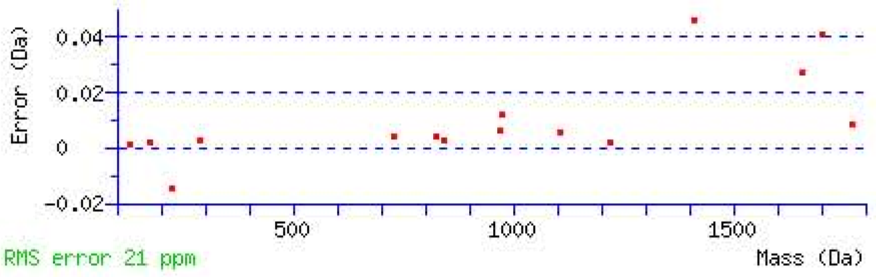
Match to Query 51630: 1944.988932 from(649.336920,3+) rtinseconds(2065) index(78963)
Title: Locus:1.1.1.2933.10 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

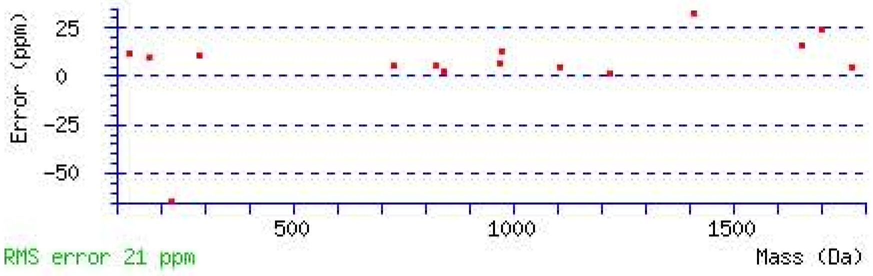
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1944.973602
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0073
Matches : 15/102 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	*129.102239*	65.054757	112.075690	56.541483			K							11
2	244.129182	122.568229	227.102633	114.054955	226.118617	113.562947	D	1817.885929	909.446603	1800.859380	900.933328	1799.875364	900.441320	10
3	331.161210	166.084243	314.134661	157.570969	313.150645	157.078961	S	*1702.858986*	851.933131	1685.832437	843.419857	1684.848421	842.927848	9
4	388.182674	194.594975	371.156125	186.081701	370.172109	185.589693	G	1615.826958	808.417117	1598.800409	799.903843			8
5	535.251088	268.129182	518.224539	259.615908	517.240523	259.123900	F	1558.805494	779.906385	1541.778945	771.393111			7
6	*974.476414*	487.741845	957.449865	479.228571	956.465849	478.736563	Q	*1411.737080*	706.372178	1394.710531	697.858904			6
7	*1105.516899*	553.262088	1088.490350	544.748813	1087.506334	544.256805	M	*972.511754*	486.759515	955.485205	478.246241			5
8	*1219.559826*	610.283551	1202.533277	601.770277	1201.549261	601.278268	N	*841.471269*	421.239273	824.444720	412.725998			4
9	*1658.785152*	829.896214	1641.758603	821.382940	1640.774587	820.890932	Q	*727.428342*	364.217809	710.401793	355.704535			3
10	*1771.869216*	886.438246	1754.842667	877.924972	1753.858651	877.432964	L	*288.203016*	144.605146	271.176467	136.091871			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.9	1944.973602	0.015330	KDSGFQMNQLR
6.7	1945.012939	-0.024007	LEQHKDLLQNTDAHKR
3.3	1945.013123	-0.024191	DKPVPEQILNYYR
0.9	1944.969574	0.019358	VDMLRDIMDAQRR

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

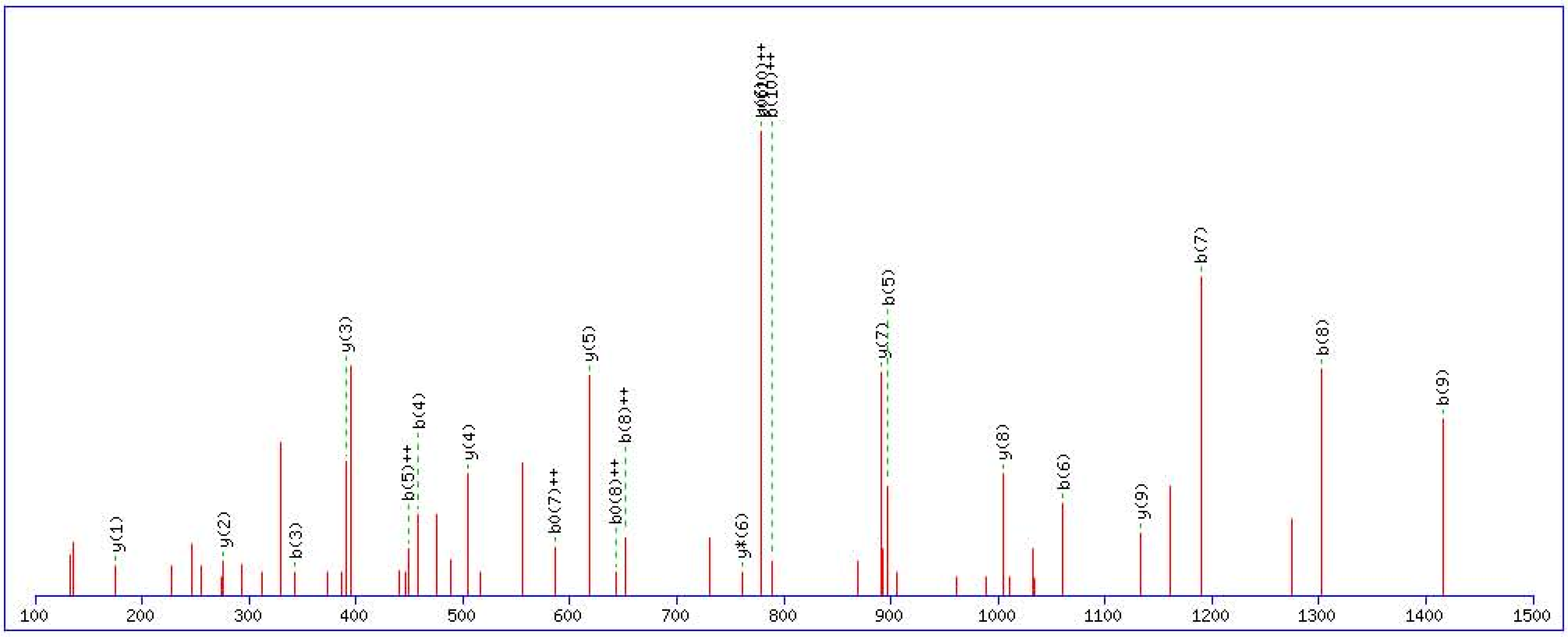
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADRDQYELLCLDNTR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

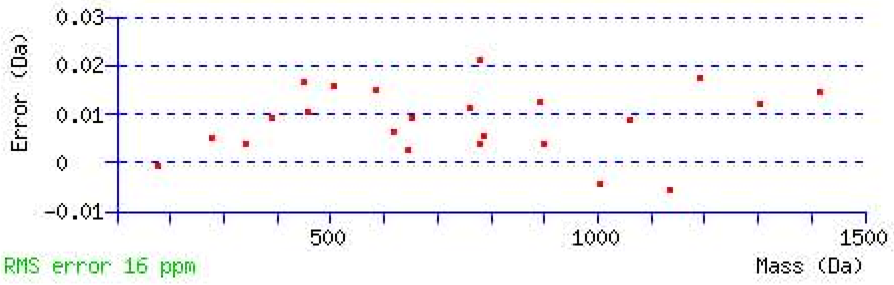
Match to Query 58001: 2192.054592 from(731.692140,3+) rtinseconds(2200) index(79935)
Title: Locus:1.1.1.2980.11 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

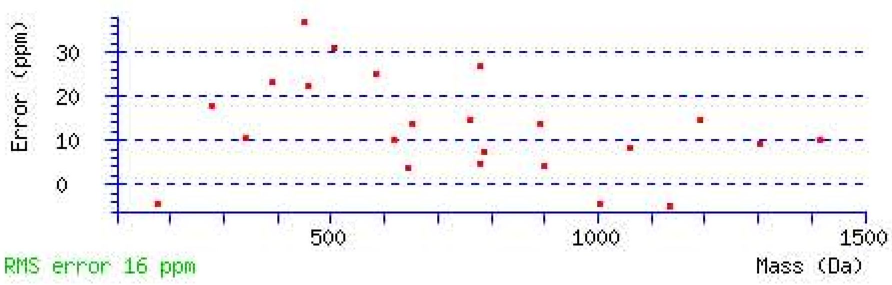
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2192.035400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 1.4e-005
Matches : 23/160 fragment ions using 43 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							15
2	187.071333	94.039304			169.060768	85.034022	D	2122.005587	1061.506431	2104.979038	1052.993157	2103.995022	1052.501149	14
3	***343.172444***	172.089860	326.145895	163.576585	325.161879	163.084577	R	2006.978644	1003.992960	1989.952095	995.479685	1988.968079	994.987677	13
4	***458.199387***	229.603332	441.172838	221.090057	440.188822	220.598049	D	1850.877533	925.942404	1833.850984	917.429130	1832.866968	916.937122	12
5	***897.424713***	**449.215995**	880.398164	440.702720	879.414148	440.210712	Q	1735.850590	868.428933	1718.824041	859.915658	1717.840025	859.423650	11
6	***1060.488042***	530.747659	1043.461493	522.234385	1042.477477	521.742376	Y	1296.625264	648.816270	1279.598715	640.302995	1278.614699	639.810987	10
7	***1189.530635***	595.268955	1172.504086	586.755681	1171.520070	586.263673	E	***1133.561935***	567.284605	1116.535386	558.771331	1115.551370	558.279323	9
8	***1302.614699***	**651.810987**	1285.588150	643.297713	1284.604134	642.805705	L	***1004.519342***	502.763309	987.492793	494.250034	986.508777	493.758026	8
9	***1415.698763***	708.353019	1398.672214	699.839745	1397.688198	699.347737	L	***891.435278***	446.221277	874.408729	437.708002	873.424713	437.215994	7
10	1575.729412	**788.368344**	1558.702863	779.855069	1557.718847	779.363061	C	***778.351214***	389.679245	761.324665	381.165971	760.340649	380.673963	6
11	1688.813476	844.910376	1671.786927	836.397101	1670.802911	835.905093	L	***618.320565***	309.663921	601.294016	301.150646	600.310000	300.658638	5
12	1803.840419	902.423847	1786.813870	893.910573	1785.829854	893.418565	D	***505.236501***	253.121888	488.209952	244.608614	487.225936	244.116606	4
13	1917.883346	959.445311	1900.856797	950.932036	1899.872781	950.440028	N	***390.209558***	195.608417	373.183009	187.095142	372.198993	186.603134	3
14	2018.931025	1009.969150	2001.904476	1001.455876	2000.920460	1000.963868	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.4	2192.035400	0.019192	ADRDQYELLCLDNTR
0.6	2192.049133	0.005459	GQETSMSPGRREQLSDASLK

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

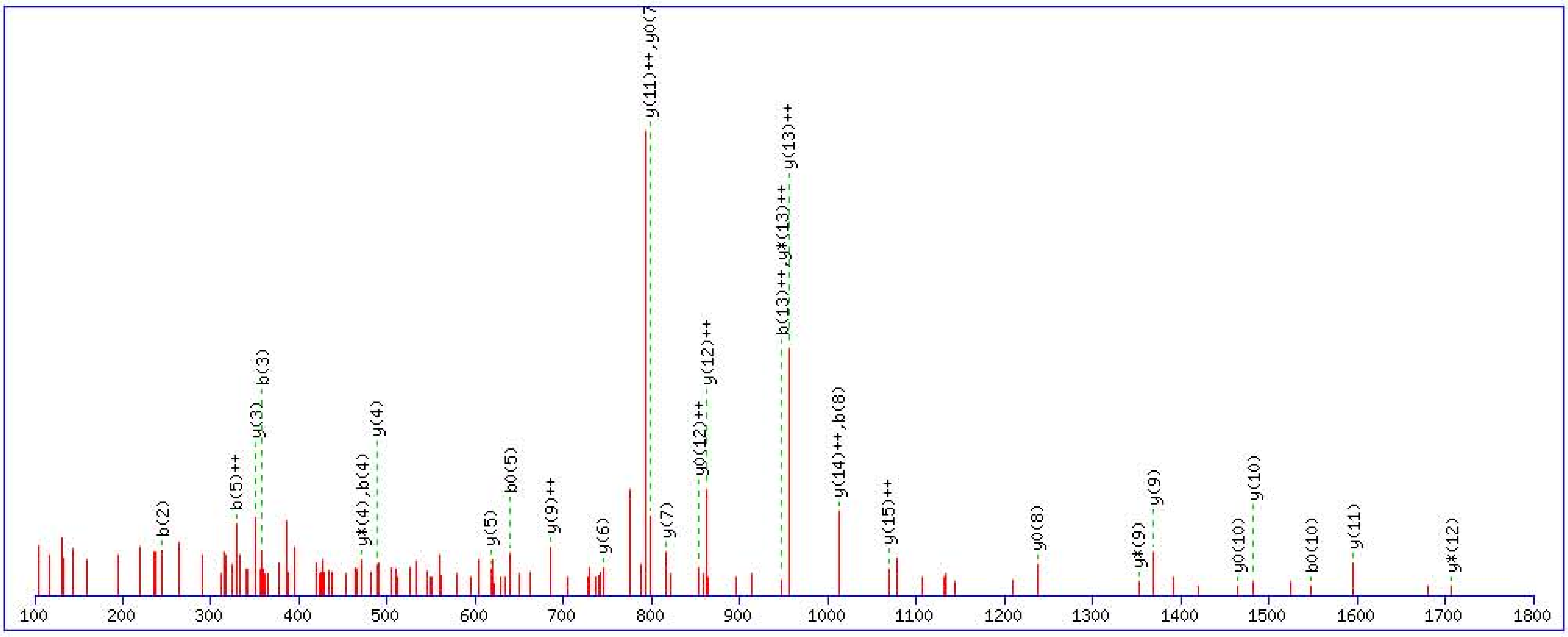
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDLIWELLNQAQEHFGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

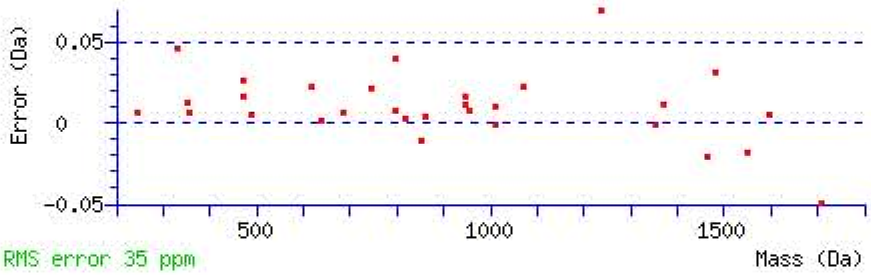
Match to Query 62025: 2380.215252 from(794.412360,3+) rtinseconds(3218) index(86894)
Title: Locus:1.1.1.3329.19 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

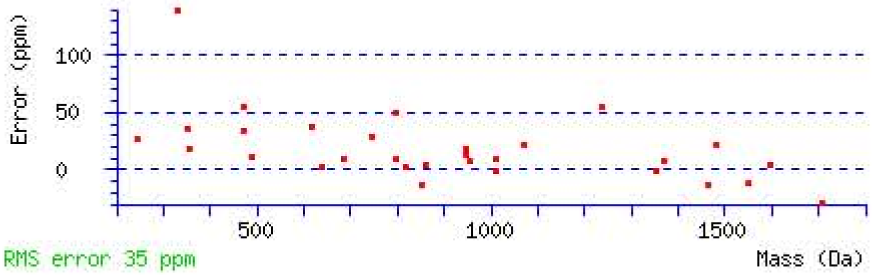
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2380.188522
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.033
Matches : 30/168 fragment ions using 64 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**							**17**
2	**245.076812**	123.042044			227.066247	114.036762	**D**	2252.153237	1126.580256	2235.126688	1118.066982	2234.142672	1117.574974	**16**
3	**358.160876**	179.584076			340.150311	170.578794	**L**	2137.126294	1069.066785	2120.099745	1060.553510	2119.115729	1060.061502	**15**
4	**471.244940**	236.126108			453.234375	227.120826	**I**	2024.042230	1012.524753	2007.015681	1004.011479	2006.031665	1003.519470	**14**
5	657.324253	**329.165765**			639.313688	320.160482	**W**	1910.958166	955.982721	1893.931617	947.469447	1892.947601	946.977438	**13**
6	786.366846	393.687061			768.356281	384.681779	**E**	1724.878853	862.943064	1707.852304	854.429790	1706.868288	853.937782	**12**
7	899.450910	450.229093			881.440345	441.223811	**L**	***1595.836260***	798.421768	1578.809711	789.908493	1577.825695	789.416485	**11**
8	**1012.534974**	506.771125			994.524409	497.765843	**L**	***1482.752196***	741.879736	1465.725647	733.366461	1464.741631	732.874453	**10**
9	1126.577901	563.792589	1109.551352	555.279314	1108.567336	554.787306	**N**	***1369.668132***	685.337704	1352.641583	676.824429	1351.657567	676.332421	**9**
10	1565.803227	783.405252	1548.776678	774.891977	1547.792662	774.399969	**Q**	1255.625205	628.316240	1238.598656	619.802966	1237.614640	619.310958	**8**
11	1636.840341	818.923809	1619.813792	810.410534	1618.829776	809.918526	**A**	***816.399879***	408.703577	799.373330	400.190303	798.389314	399.698295	**7**
12	1764.898919	882.953098	1747.872370	874.439823	1746.888354	873.947815	**Q**	***745.362765***	373.185020	728.336216	364.671746	727.352200	364.179738	**6**
13	1893.941512	**947.474394**	1876.914963	938.961120	1875.930947	938.469112	**E**	***617.304187***	309.155732	600.277638	300.642457	599.293622	300.150449	**5**
14	2031.000424	1016.003850	2013.973875	1007.490576	2012.989859	1006.998568	**H**	***488.261594***	244.634435	471.235045	236.121160			**4**
15	2178.068838	1089.538057	2161.042289	1081.024782	2160.058273	1080.532774	**F**	***351.202682***	176.104979	334.176133	167.591704			**3**
16	2235.090302	1118.048789	2218.063753	1109.535514	2217.079737	1109.043506	**G**	204.134268	102.570772	187.107719	94.057497			**2**
17							**K**	147.112804	74.060040	130.086255	65.546765			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.5	2380.188522	0.026730	EDLIWELLNQAQEHFGK
21.1	2380.188522	0.026730	EDLIWELLNQAQEHFGK

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

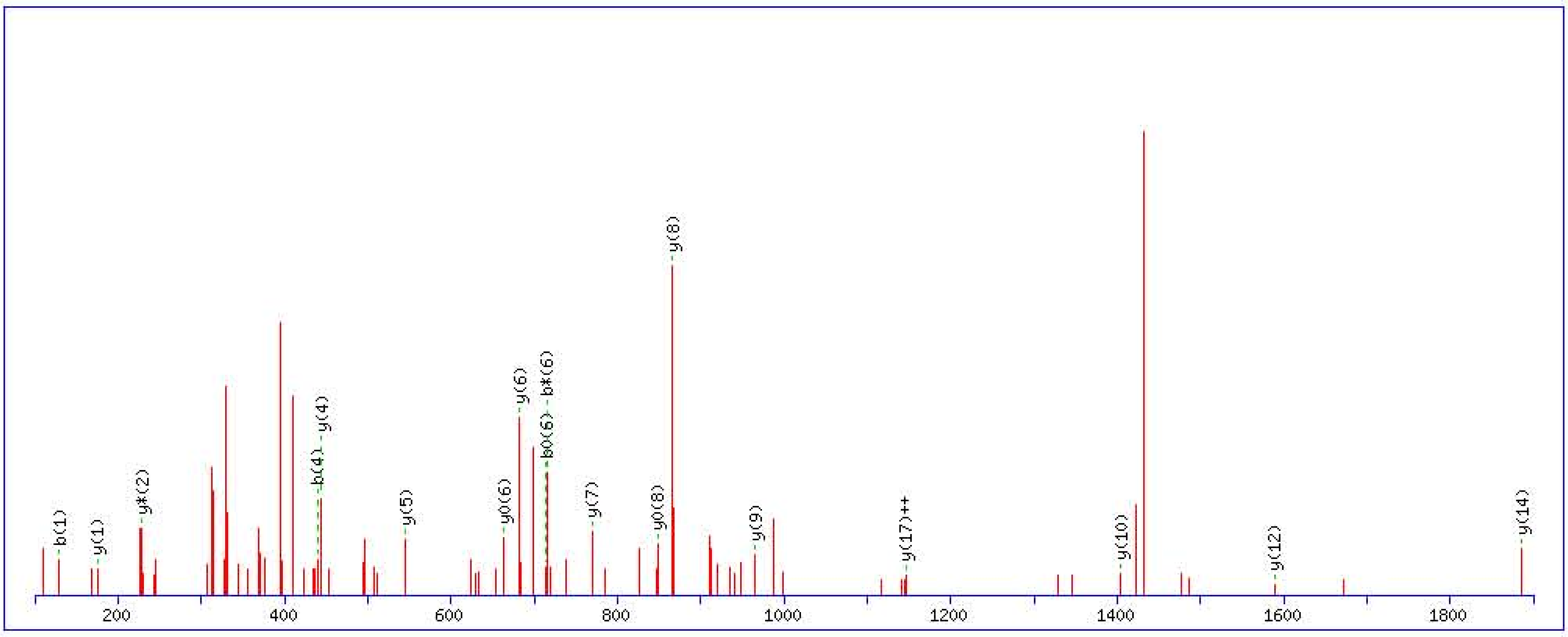
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVDEYKDCHLAQVPSHTVVAR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

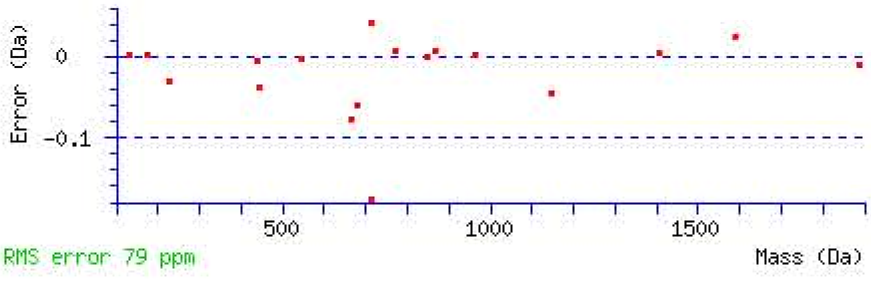
Match to Query 69961: 2859.469576 from(715.874670,4+) rtinseconds(1525) index(75422)
Title: Locus:1.1.1.2745.12 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

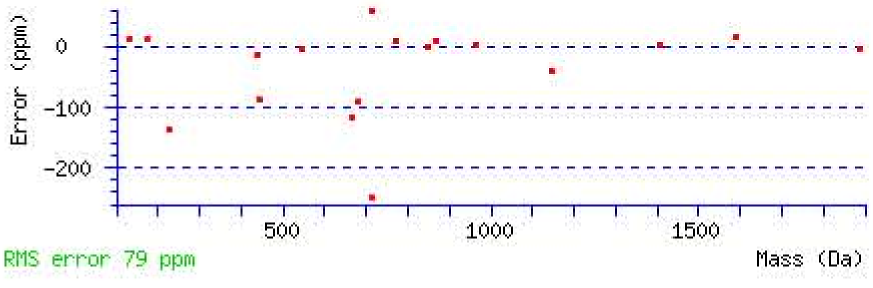
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2859.452393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.013
Matches : 18/238 fragment ions using 48 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**129.102239**	65.054757	112.075690	56.541483			K							22
2	226.155003	113.581139	209.128454	105.067865			P	2732.364705	1366.685990	2715.338156	1358.172716	2714.354140	1357.680708	21
3	325.223417	163.115346	308.196868	154.602072			V	2635.311941	1318.159608	2618.285392	1309.646334	2617.301376	1309.154326	20
4	**440.250360**	220.628818	423.223811	212.115544	422.239795	211.623536	D	2536.243527	1268.625401	2519.216978	1260.112127	2518.232962	1259.620119	19
5	569.292953	285.150115	552.266404	276.636840	551.282388	276.144832	E	2421.216584	1211.111930	2404.190035	1202.598655	2403.206019	1202.106647	18
6	732.356282	366.681779	715.329733	358.168505	714.345717	357.676497	Y	2292.173991	1146.590633	2275.147442	1138.077359	2274.163426	1137.585351	17
7	860.451245	430.729261	843.424696	422.215986	842.440680	421.723978	K	2129.110662	1065.058969	2112.084113	1056.545694	2111.100097	1056.053686	16
8	975.478188	488.242732	958.451639	479.729458	957.467623	479.237450	D	2001.015699	1001.011487	1983.989150	992.498213	1983.005134	992.006205	15
9	1135.508837	568.258057	1118.482288	559.744782	1117.498272	559.252774	C	***1885.988756***	943.498016	1868.962207	934.984741	1867.978191	934.492733	14
10	1272.567749	636.787513	1255.541200	628.274238	1254.557184	627.782230	H	1725.958107	863.482691	1708.931558	854.969417	1707.947542	854.477409	13
11	1385.651813	693.329545	1368.625264	684.816270	1367.641248	684.324262	L	***1588.899195***	794.953235	1571.872646	786.439961	1570.888630	785.947953	12
12	1456.688927	728.848101	1439.662378	720.334827	1438.678362	719.842819	A	1475.815131	738.411203	1458.788582	729.897929	1457.804566	729.405921	11
13	1895.914253	948.460765	1878.887704	939.947490	1877.903688	939.455482	Q	***1404.778017***	702.892646	1387.751468	694.379372	1386.767452	693.887364	10
14	1994.982667	997.994972	1977.956118	989.481697	1976.972102	988.989689	V	***965.552691***	483.279983	948.526142	474.766709	947.542126	474.274701	9
15	2092.035431	1046.521353	2075.008882	1038.008079	2074.024866	1037.516071	P	***866.484277***	433.745776	849.457728	425.232502	848.473712	424.740494	8
16	2179.067459	1090.037367	2162.040910	1081.524093	2161.056894	1081.032085	S	***769.431513***	385.219394	752.404964	376.706120	751.420948	376.214112	7
17	2316.126371	1158.566823	2299.099822	1150.053549	2298.115806	1149.561541	H	***682.399485***	341.703380	665.372936	333.190106	664.388920	332.698098	6
18	2417.174050	1209.090663	2400.147501	1200.577388	2399.163485	1200.085380	T	***545.340573***	273.173924	528.314024	264.660650	527.330008	264.168642	5
19	2516.242464	1258.624870	2499.215915	1250.111595	2498.231899	1249.619587	V	***444.292894***	222.650085	427.266345	214.136810			4
20	2615.310878	1308.159077	2598.284329	1299.645802	2597.300313	1299.153794	V	345.224480	173.115878	328.197931	164.602603			3
21	2686.347992	1343.677634	2669.321443	1335.164359	2668.337427	1334.672351	A	246.156066	123.581671	229.129517	115.068397			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	2859.452393	0.017183	KPVDEYKDCHLAQVPSHTVVAR

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

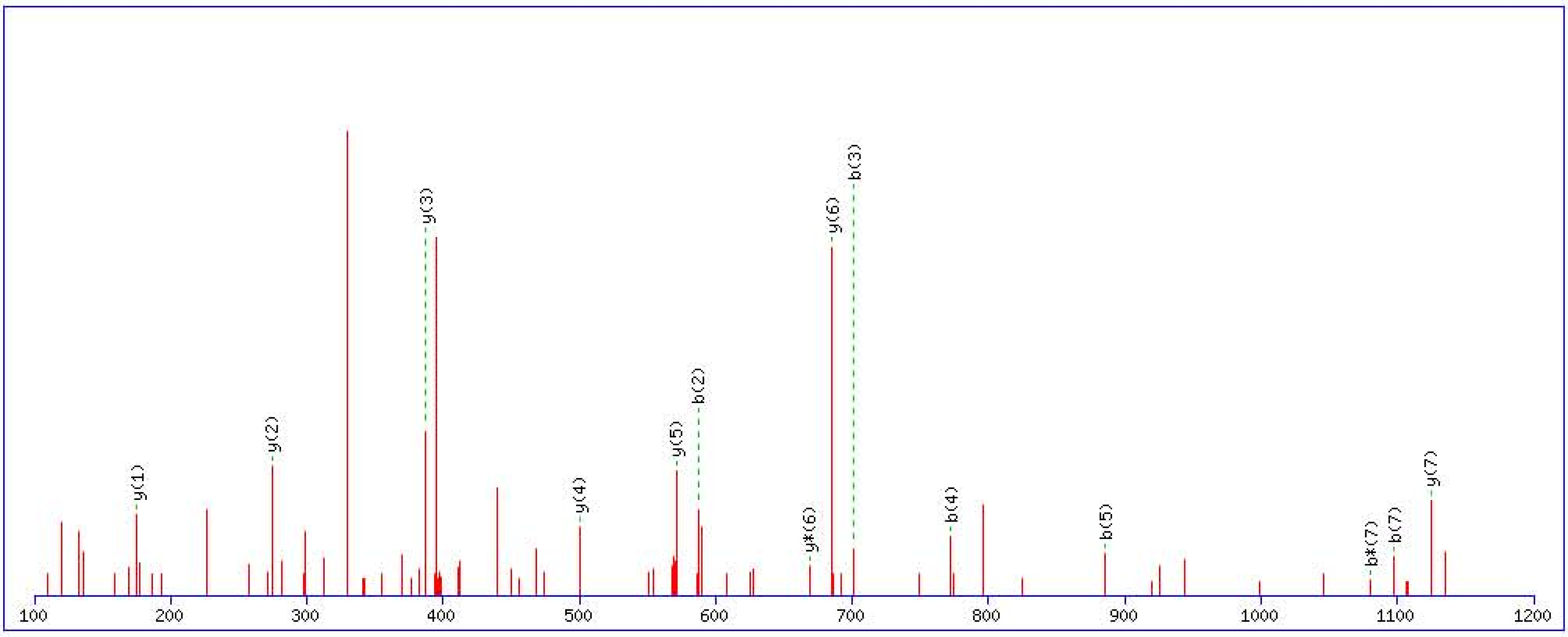
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQNALLVR**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

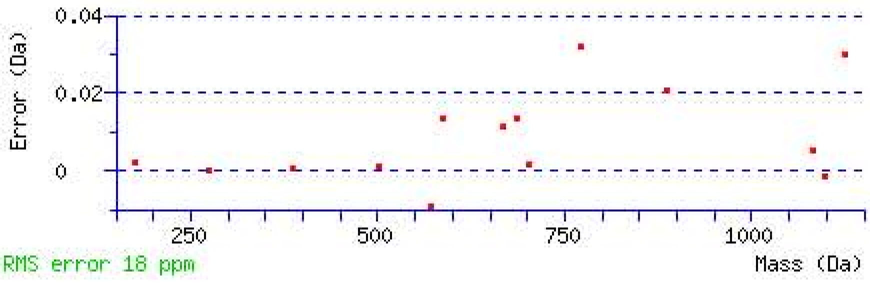
Match to Query 29984: 1270.706208 from(636.360380,2+) rtinseconds(2091) index(42693)
Title: Locus:1.1.1.3012.7 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

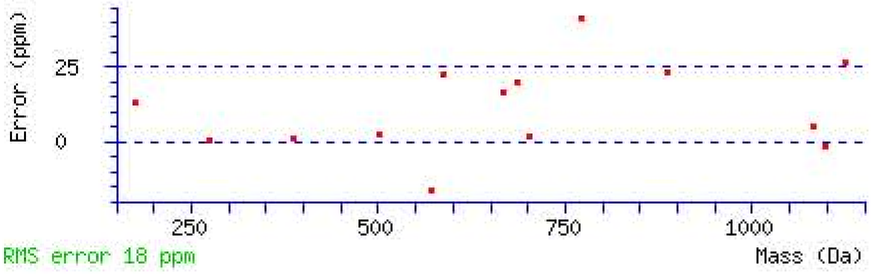
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1270.721985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0076
Matches : 14/54 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	148.075690	74.541483			F					8
2	**587.301016**	294.154146	570.274467	285.640872	Q	***1124.660861***	562.834068	1107.634312	554.320794	7
3	**701.343943**	351.175610	684.317394	342.662335	N	***685.435535***	343.221406	668.408986	334.708131	6
4	**772.381057**	386.694166	755.354508	378.180892	A	***571.392608***	286.199942	554.366059	277.686668	5
5	**885.465121**	443.236199	868.438572	434.722924	L	***500.355494***	250.681385	483.328945	242.168110	4
6	998.549185	499.778231	981.522636	491.264956	L	***387.271430***	194.139353	370.244881	185.626078	3
7	**1097.617599**	549.312437	1080.591050	540.799163	V	***274.187366***	137.597321	257.160817	129.084046	2
8					R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.2	1270.721985	-0.015777	FQNALLVR
15.2	1270.722000	-0.015792	FQIAQVVR
13.4	1270.699295	0.006913	QEAEERKLLR
8.9	1270.706696	-0.000488	LPALLEKNAMR
8.4	1270.699341	0.006867	AVTLRSGSEPVR
8.3	1270.699295	0.006913	AEKLERELQR
7.1	1270.699326	0.006882	ANGTPKSAASLVR
6.1	1270.689438	0.016770	LIQRFNSTHR
4.7	1270.700195	0.006013	SQAMRIVR
4.3	1270.688065	0.018143	LLEESIANLNR

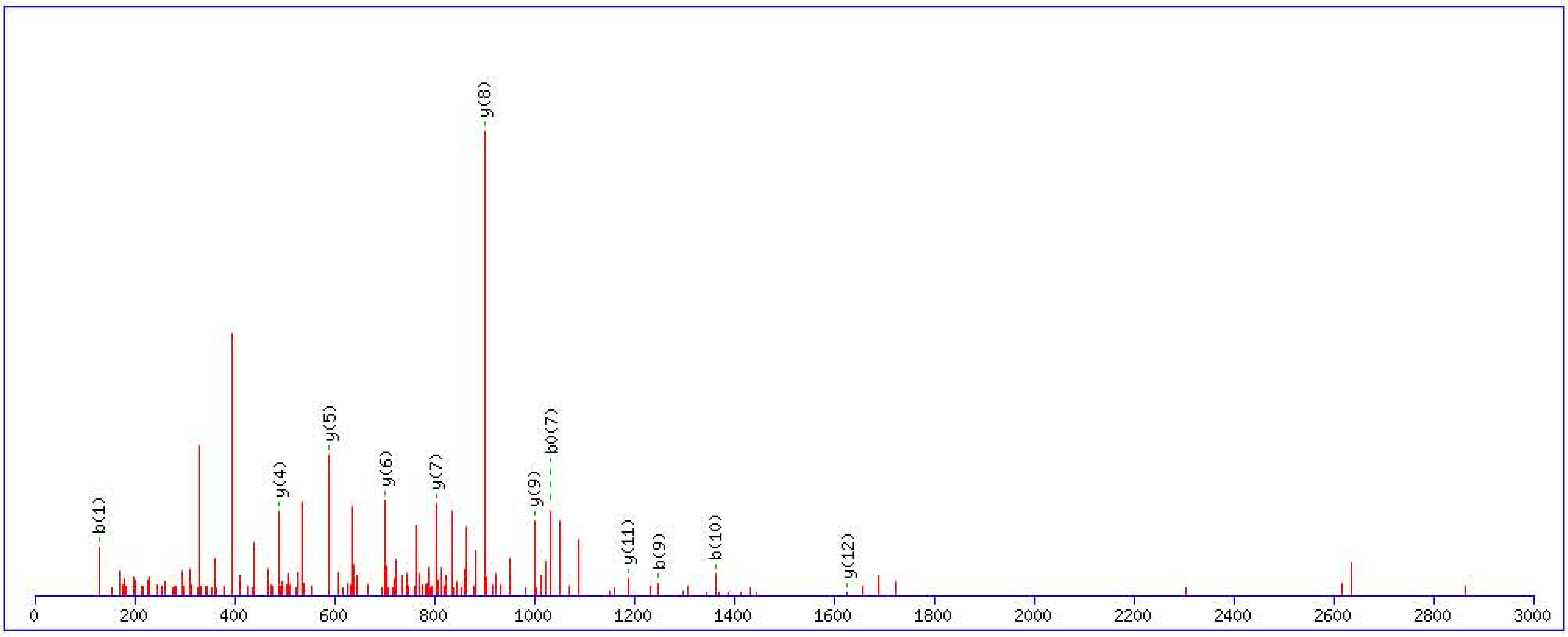
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVPQVSTPTLVEVSR**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

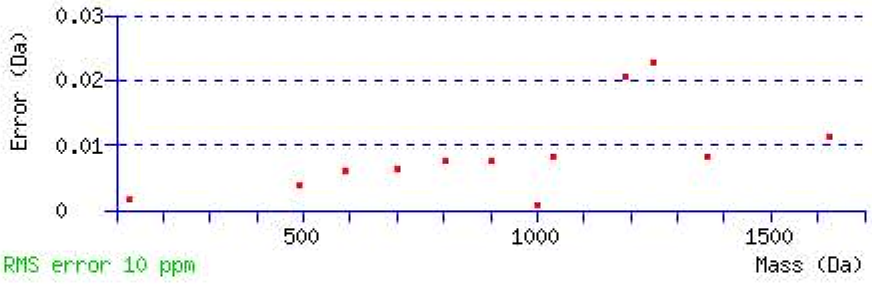
Match to Query 51751: 1950.106662 from(651.042830,3+) rtinseconds(1982) index(78370)
Title: Locus:1.1.1.2904.14 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

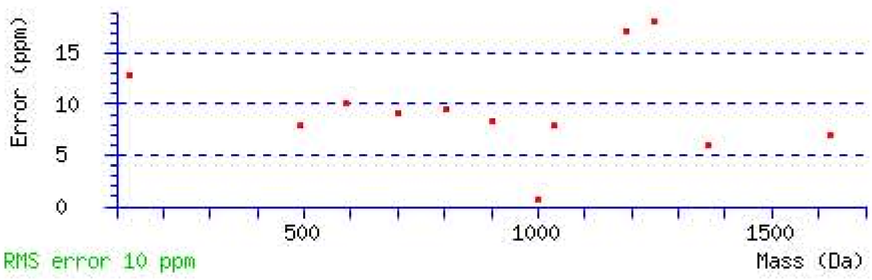
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1950.097229
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 1.1e-005
Matches : 12/156 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.102239**	65.054757	112.075690	56.541483			K							15
2	228.170653	114.588965	211.144104	106.075690			V	1823.009533	912.008404	1805.982984	903.495130	1804.998968	903.003122	14
3	325.223417	163.115346	308.196868	154.602072			P	1723.941119	862.474197	1706.914570	853.960923	1705.930554	853.468915	13
4	764.448743	382.728010	747.422194	374.214735			Q	***1626.888355***	813.947815	1609.861806	805.434541	1608.877790	804.942533	12
5	863.517157	432.262217	846.490608	423.748942			V	***1187.663029***	594.335153	1170.636480	585.821878	1169.652464	585.329870	11
6	950.549185	475.778231	933.522636	467.264956	932.538620	466.772948	S	1088.594615	544.800946	1071.568066	536.287671	1070.584050	535.795663	10
7	1051.596864	526.302070	1034.570315	517.788795	1033.586299	517.296787	T	***1001.562587***	501.284932	984.536038	492.771657	983.552022	492.279649	9
8	1148.649628	574.828452	1131.623079	566.315178	1130.639063	565.823169	P	***900.514908***	450.761092	883.488359	442.247818	882.504343	441.755810	8
9	**1249.697307**	625.352291	1232.670758	616.839017	1231.686742	616.347009	T	***803.462144***	402.234710	786.435595	393.721436	785.451579	393.229428	7
10	**1362.781371**	681.894323	1345.754822	673.381049	1344.770806	672.889041	L	***702.414465***	351.710871	685.387916	343.197596	684.403900	342.705588	6
11	1461.849785	731.428530	1444.823236	722.915256	1443.839220	722.423248	V	***589.330401***	295.168839	572.303852	286.655564	571.319836	286.163556	5
12	1590.892378	795.949827	1573.865829	787.436552	1572.881813	786.944544	E	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
13	1689.960792	845.484034	1672.934243	836.970759	1671.950227	836.478751	V	361.219394	181.113335	344.192845	172.600061	343.208829	172.108053	3
14	1776.992820	889.000048	1759.966271	880.486774	1758.982255	879.994765	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
15							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.4	1950.097229	0.009433	KVPQVSTPTLVEVSR

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

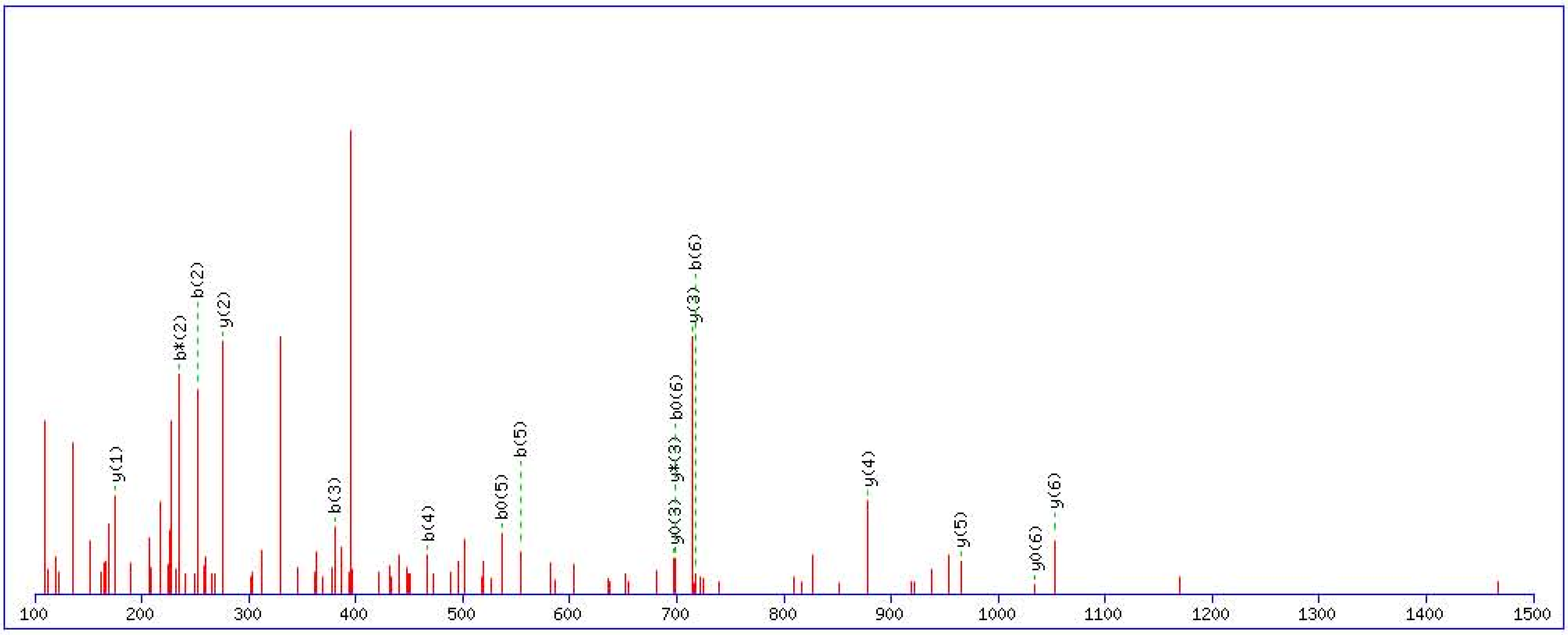
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NHQSSYQTR**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

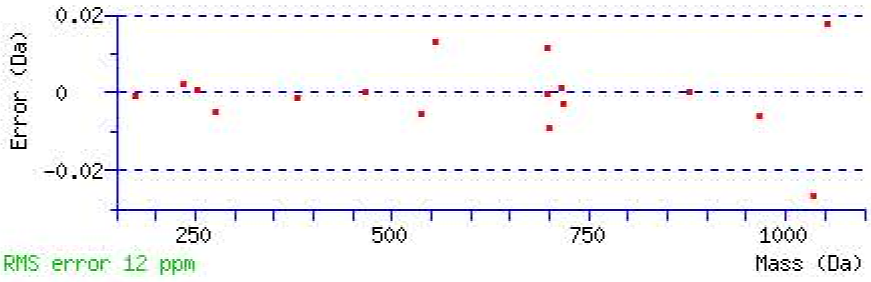
Match to Query 36345: 1430.672532 from(477.898120,3+) rtinseconds(1108) index(36230)
Title: Locus:1.1.1.2669.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

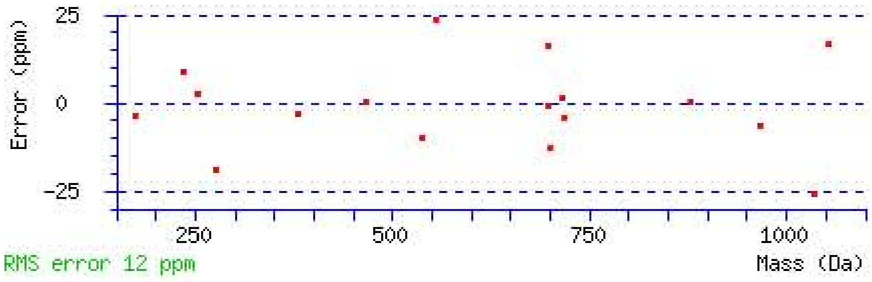
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1430.672470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0093
Matches : 17/88 fragment ions using 30 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							9
2	***252.109115***	126.558195	235.082566	118.044921			H	1317.636832	659.322054	1300.610283	650.808780	1299.626267	650.316772	8
3	***380.167693***	190.587484	363.141144	182.074210			Q	1180.577920	590.792598	1163.551371	582.279324	1162.567355	581.787316	7
4	***467.199721***	234.103499	450.173172	225.590224	449.189156	225.098216	S	***1052.519342***	526.763309	1035.492793	518.250035	1034.508777	517.758027	6
5	***554.231749***	277.619513	537.205200	269.106238	536.221184	268.614230	S	***965.487314***	483.247295	948.460765	474.734021	947.476749	474.242013	5
6	***717.295078***	359.151177	700.268529	350.637903	699.284513	350.145895	Y	***878.455286***	439.731281	861.428737	431.218007	860.444721	430.725999	4
7	1156.520404	578.763840	1139.493855	570.250566	1138.509839	569.758558	Q	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
8	1257.568083	629.287680	1240.541534	620.774405	1239.557518	620.282397	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.9	1430.672470	0.000062	NHQSSYQTR

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

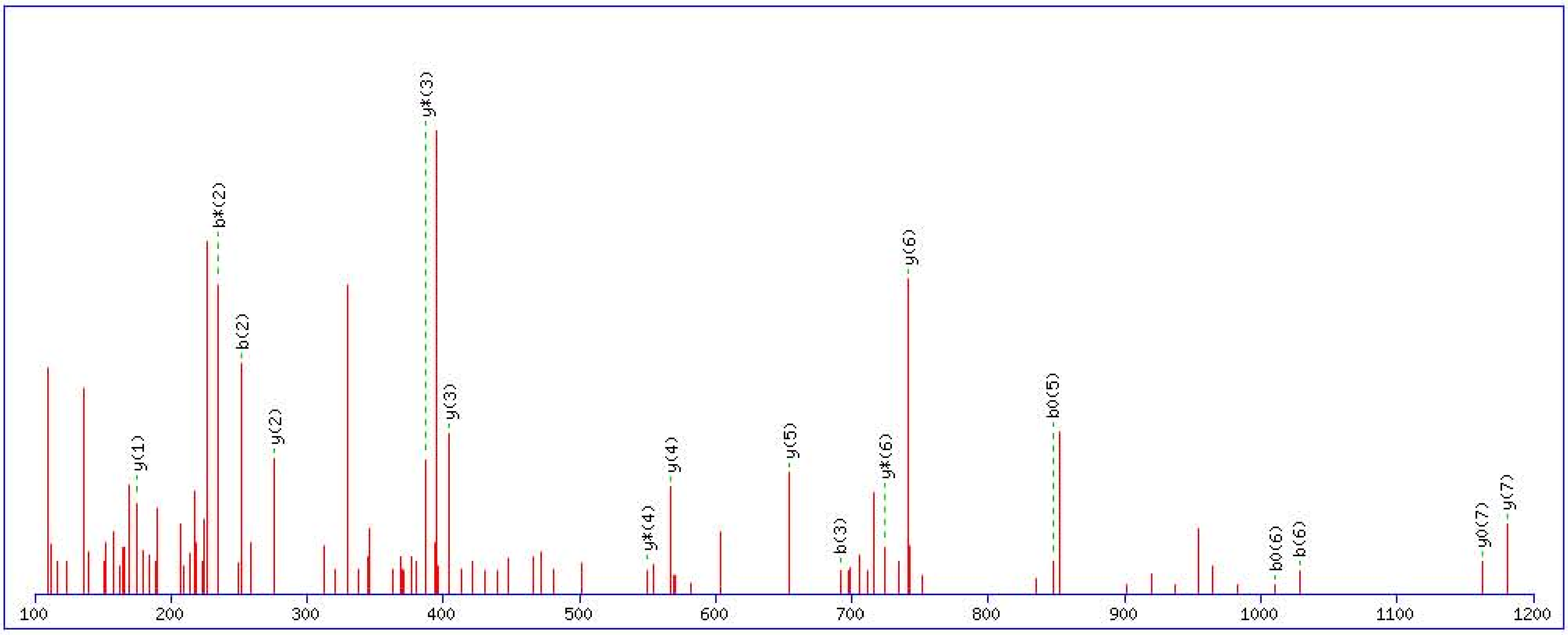
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NHQSSYQTR**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

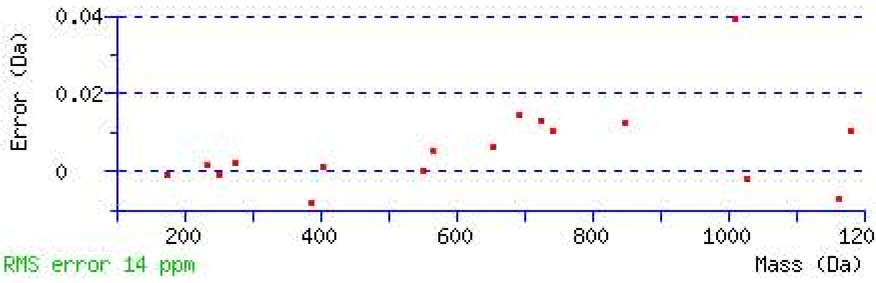
Match to Query 36349: 1430.673792 from(477.898540,3+) rtinseconds(1111) index(54218)
Title: Locus:1.1.1.2693.13 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

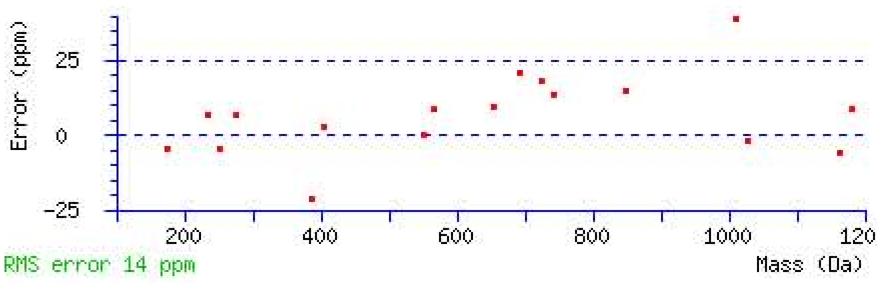
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1430.672470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.012
Matches : 17/88 fragment ions using 40 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							9
2	**252.109115**	126.558195	235.082566	118.044921			H	1317.636832	659.322054	1300.610283	650.808780	1299.626267	650.316772	8
3	**691.334441**	346.170859	674.307892	337.657584			Q	***1180.577920***	590.792598	1163.551371	582.279324	1162.567355	581.787316	7
4	778.366469	389.686872	761.339920	381.173598	760.355904	380.681590	S	***741.352594***	371.179935	724.326045	362.666661	723.342029	362.174653	6
5	865.398497	433.202886	848.371948	424.689612	847.387932	424.197604	S	***654.320566***	327.663921	637.294017	319.150647	636.310001	318.658639	5
6	**1028.461826**	514.734551	1011.435277	506.221276	1010.451261	505.729268	Y	***567.288538***	284.147907	550.261989	275.634633	549.277973	275.142625	4
7	1156.520404	578.763840	1139.493855	570.250566	1138.509839	569.758558	Q	***404.225209***	202.616243	387.198660	194.102968	386.214644	193.610960	3
8	1257.568083	629.287680	1240.541534	620.774405	1239.557518	620.282397	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.9	1430.672470	0.001322	NHQSSYQTR
2.1	1430.672470	0.001322	NHQSSYQTR

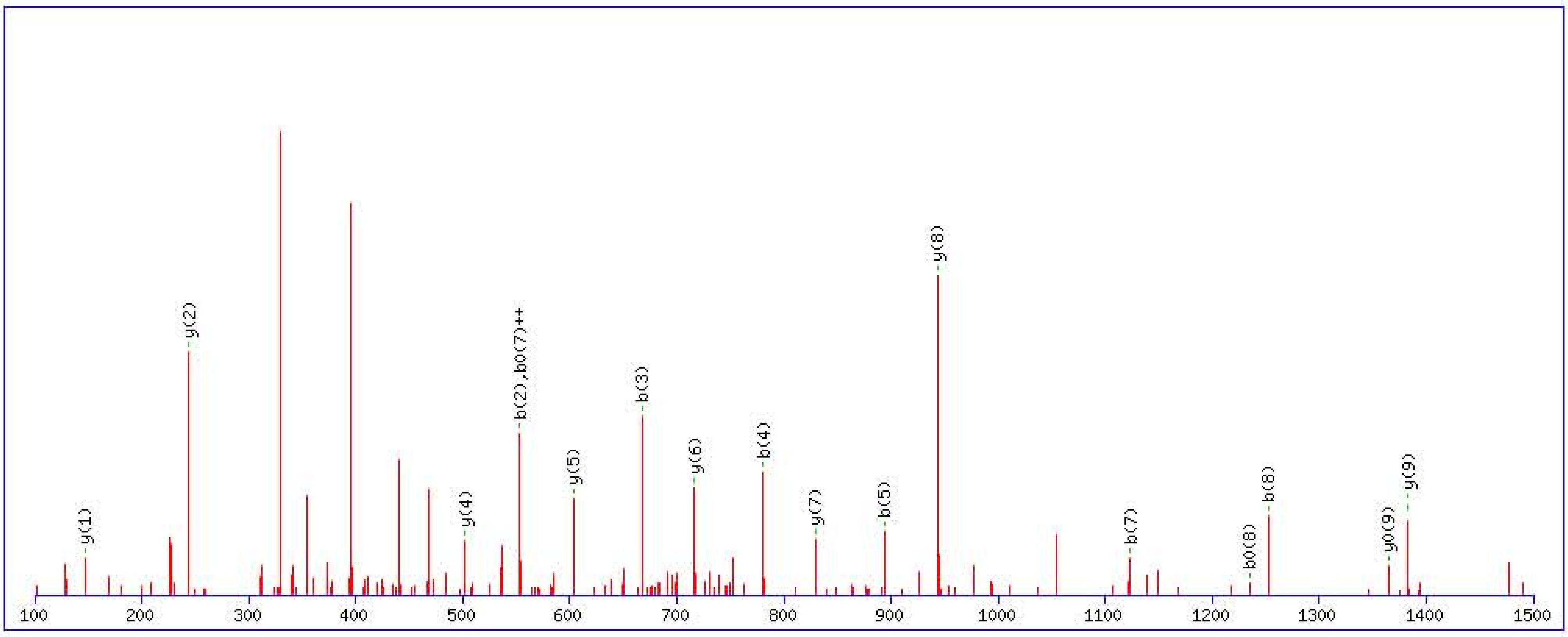
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQNILTEEPK**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

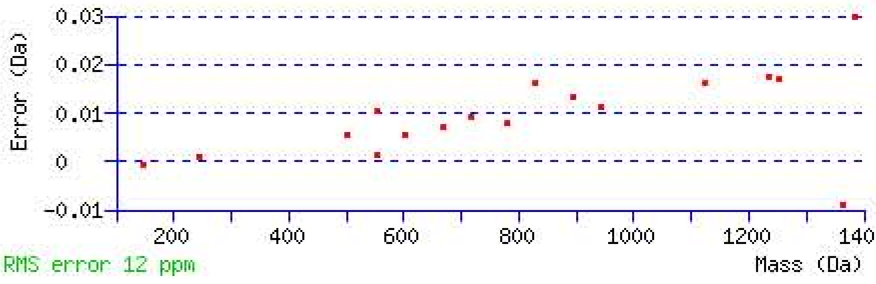
Match to Query 38459: 1494.827648 from(748.421100,2+) rtinseconds(2003) index(60553)
Title: Locus:1.1.1.3002.18 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

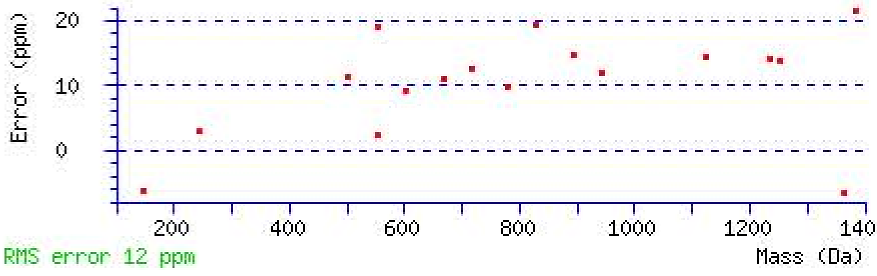
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1494.811569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 8.2e-005
Matches : 17/92 fragment ions using 28 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	**553.316666**	277.161971	536.290117	268.648697			Q	***1382.734814***	691.871045	1365.708265	683.357771	1364.724249	682.865763	9
3	**667.359593**	334.183435	650.333044	325.670160			N	***943.509488***	472.258382	926.482939	463.745108	925.498923	463.253100	8
4	**780.443657**	390.725467	763.417108	382.212192			I	***829.466561***	415.236919	812.440012	406.723644	811.455996	406.231636	7
5	**893.527721**	447.267499	876.501172	438.754224			L	***716.382497***	358.694887	699.355948	350.181612	698.371932	349.689604	6
6	994.575400	497.791338	977.548851	489.278064	976.564835	488.786056	T	***603.298433***	302.152855	586.271884	293.639580	585.287868	293.147572	5
7	**1123.617993**	562.312635	1106.591444	553.799360	1105.607428	553.307352	E	***502.250754***	251.629015	485.224205	243.115741	484.240189	242.623733	4
8	**1252.660586**	626.833931	1235.634037	618.320657	1234.650021	617.828649	E	373.208161	187.107719	356.181612	178.594444	355.197596	178.102436	3
9	1349.713350	675.360313	1332.686801	666.847039	1331.702785	666.355031	P	***244.165568***	122.586422	227.139019	114.073148			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.8	1494.811569	0.016079	IQNILTEEPK
7.7	1494.834030	-0.006382	QLLRALEEGR
7.1	1494.834030	-0.006382	QLNAIRDNIK
6.6	1494.809097	0.018551	LQLYVFVMR
6.4	1494.822800	0.004848	LQQIAAAVENK
6.3	1494.815430	0.012218	KGSTKDSGHLQIPK
4.3	1494.824142	0.003506	QIRSYPHRK
4.2	1494.820129	0.007519	LQSLCRGHLQRK
4.2	1494.822800	0.004848	LSLKNDAPQAK
3.9	1494.834030	-0.006382	LQAEAQQLRK

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

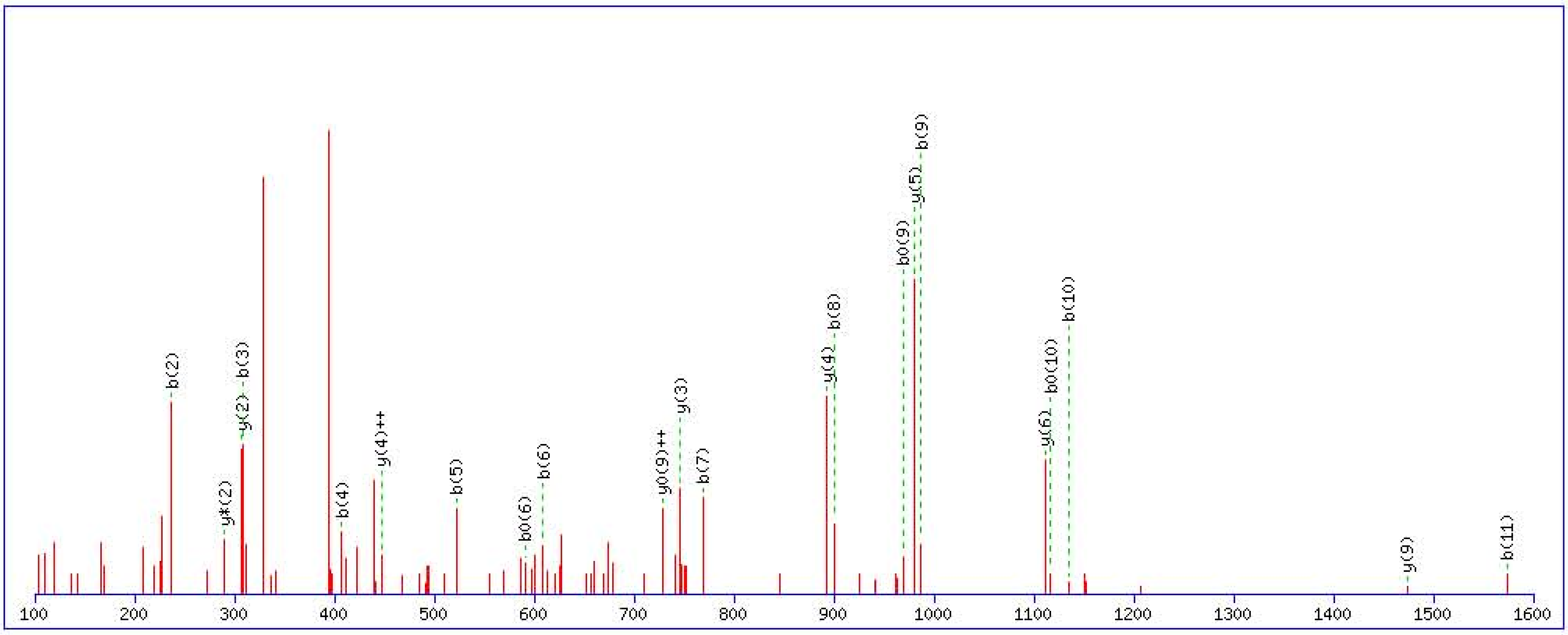
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VHAVDSCMSFQCK**
Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

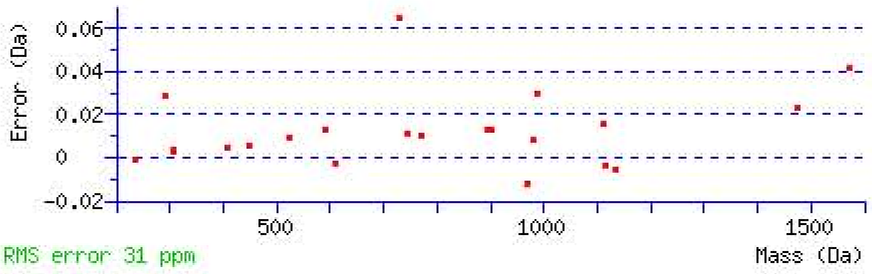
Match to Query 50262: 1878.842412 from(627.288080,3+) rtinseconds(1692) index(58251)
Title: Locus:1.1.1.2895.11 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

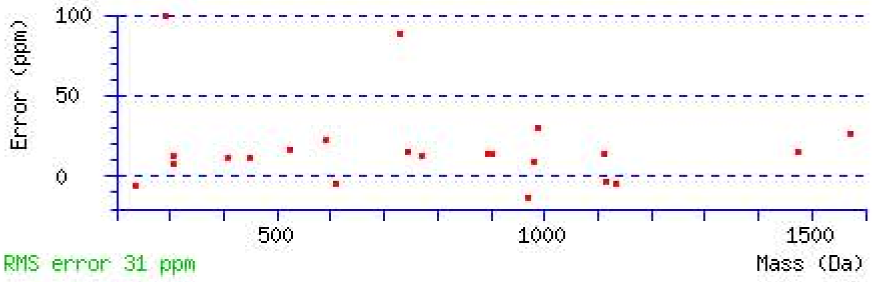
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1878.824921
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 2.5e-005
Matches : 22/108 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							13
2	***237.134602***	119.070939					H	1780.763766	890.885521	1763.737217	882.372247	1762.753201	881.880239	12
3	***308.171716***	154.589496					A	1643.704854	822.356065	1626.678305	813.842791	1625.694289	813.350783	11
4	***407.240130***	204.123703					V	1572.667740	786.837508	1555.641191	778.324234	1554.657175	777.832226	10
5	***522.267073***	261.637175			504.256508	252.631892	D	**1473.599326**	737.303301	1456.572777	728.790027	1455.588761	728.298019	9
6	***609.299101***	305.153189			591.288536	296.147906	S	1358.572383	679.789830	1341.545834	671.276555	1340.561818	670.784547	8
7	***769.329750***	385.168513			751.319185	376.163231	C	1271.540355	636.273816	1254.513806	627.760541	1253.529790	627.268533	7
8	***900.370235***	450.688756			882.359670	441.683473	M	**1111.509706**	556.258491	1094.483157	547.745217	1093.499141	547.253209	6
9	***987.402263***	494.204770			969.391698	485.199487	S	**980.469221**	490.738249	963.442672	482.224974	962.458656	481.732966	5
10	***1134.470677***	567.738977			1116.460112	558.733694	F	**893.437193**	447.222235	876.410644	438.708960			4
11	***1573.696003***	787.351640	1556.669454	778.838365	1555.685438	778.346357	Q	**746.368779**	373.688028	729.342230	365.174753			3
12	1733.726652	867.366964	1716.700103	858.853690	1715.716087	858.361682	C	**307.143453**	154.075365	290.116904	145.562090			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.6	1878.824921	0.017491	VHAVDSCMSFQCK

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

{MATRIX} {SCIENCE}

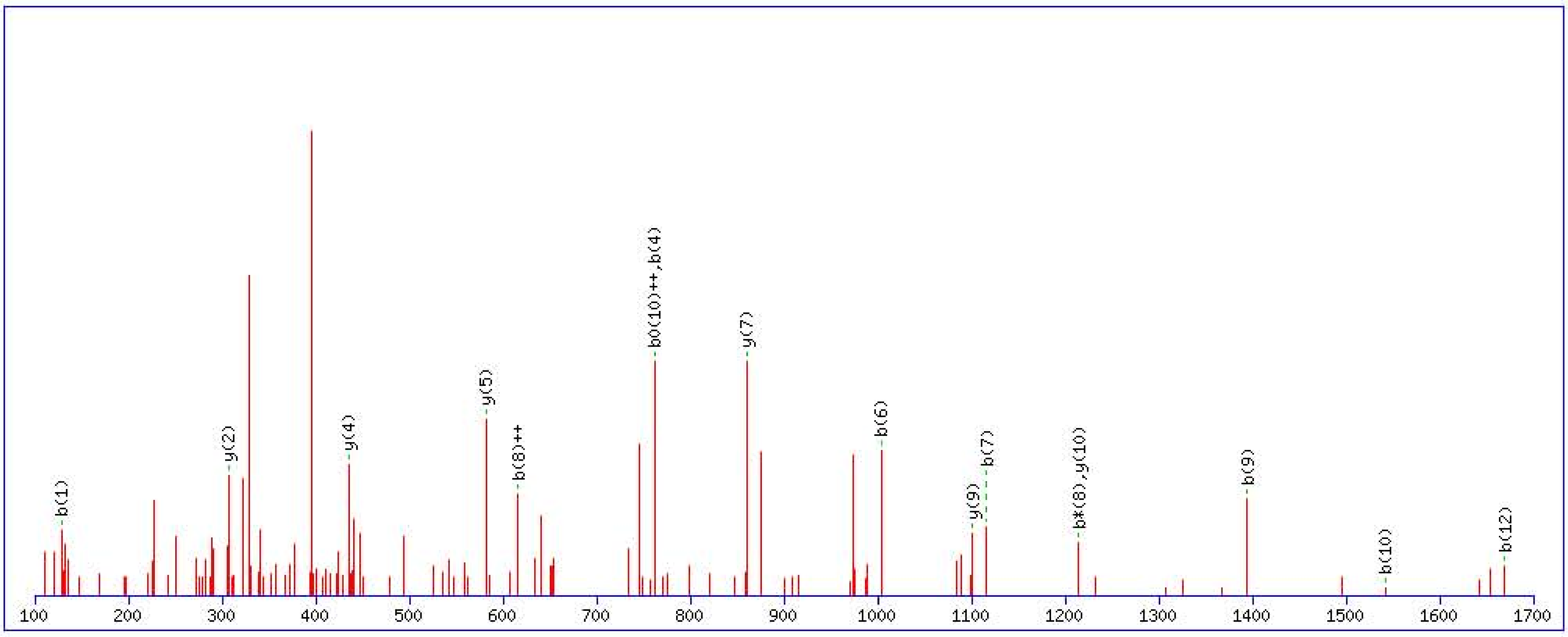
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGHQLQLDYFGACK**
Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

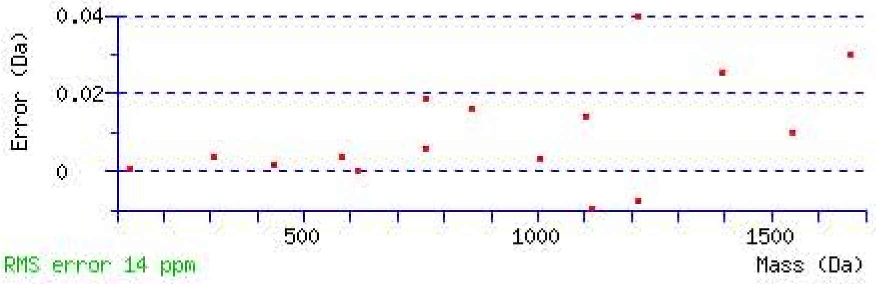
Match to Query 52362: 1974.997782 from(659.339870,3+) rtinseconds(1921) index(59942)
Title: Locus:1.1.1.2974.13 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

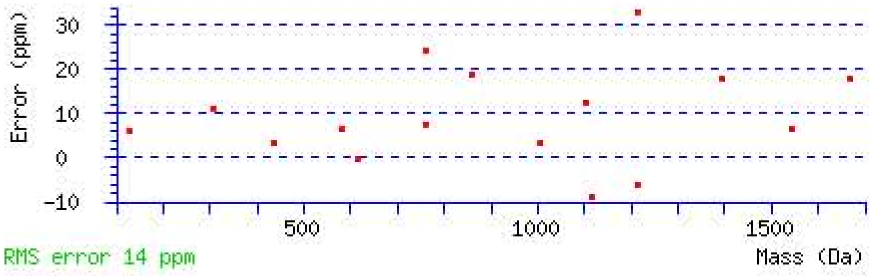
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1974.980804
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 7e-005
Matches : 16/130 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							14
2	186.123703	93.565489	169.097154	85.052215			G	1847.893125	924.450201	1830.866576	915.936926	1829.882560	915.444918	13
3	323.182615	162.094945	306.156066	153.581671			H	1790.871661	895.939469	1773.845112	887.426194	1772.861096	886.934186	12
4	***762.407941***	381.707609	745.381392	373.194334			Q	1653.812749	827.410013	1636.786200	818.896738	1635.802184	818.404730	11
5	875.492005	438.249641	858.465456	429.736366			L	***1214.587423***	607.797350	1197.560874	599.284075	1196.576858	598.792067	10
6	***1003.550583***	502.278930	986.524034	493.765655			Q	***1101.503359***	551.255318	1084.476810	542.742043	1083.492794	542.250035	9
7	***1116.634647***	558.820962	1099.608098	550.307687			L	973.444781	487.226029	956.418232	478.712754	955.434216	478.220746	8
8	1231.661590	616.334433	1214.635041	607.821159	1213.651025	607.329151	D	***860.360717***	430.683997	843.334168	422.170722	842.350152	421.678714	7
9	***1394.724919***	697.866098	1377.698370	689.352823	1376.714354	688.860815	Y	745.333774	373.170525	728.307225	364.657251			6
10	***1541.793333***	771.400305	1524.766784	762.887030	1523.782768	762.395022	F	***582.270445***	291.638861	565.243896	283.125586			5
11	1598.814797	799.911037	1581.788248	791.397762	1580.804232	790.905754	G	***435.202031***	218.104653	418.175482	209.591379			4
12	***1669.851911***	835.429594	1652.825362	826.916319	1651.841346	826.424311	A	378.180567	189.593921	361.154018	181.080647			3
13	1829.882560	915.444918	1812.856011	906.931644	1811.871995	906.439636	C	***307.143453***	154.075365	290.116904	145.562090			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.8	1974.980804	0.016978	KGHQLQLDYFGACK
38.0	1974.980804	0.016978	KGHQLQLDYFGACK

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

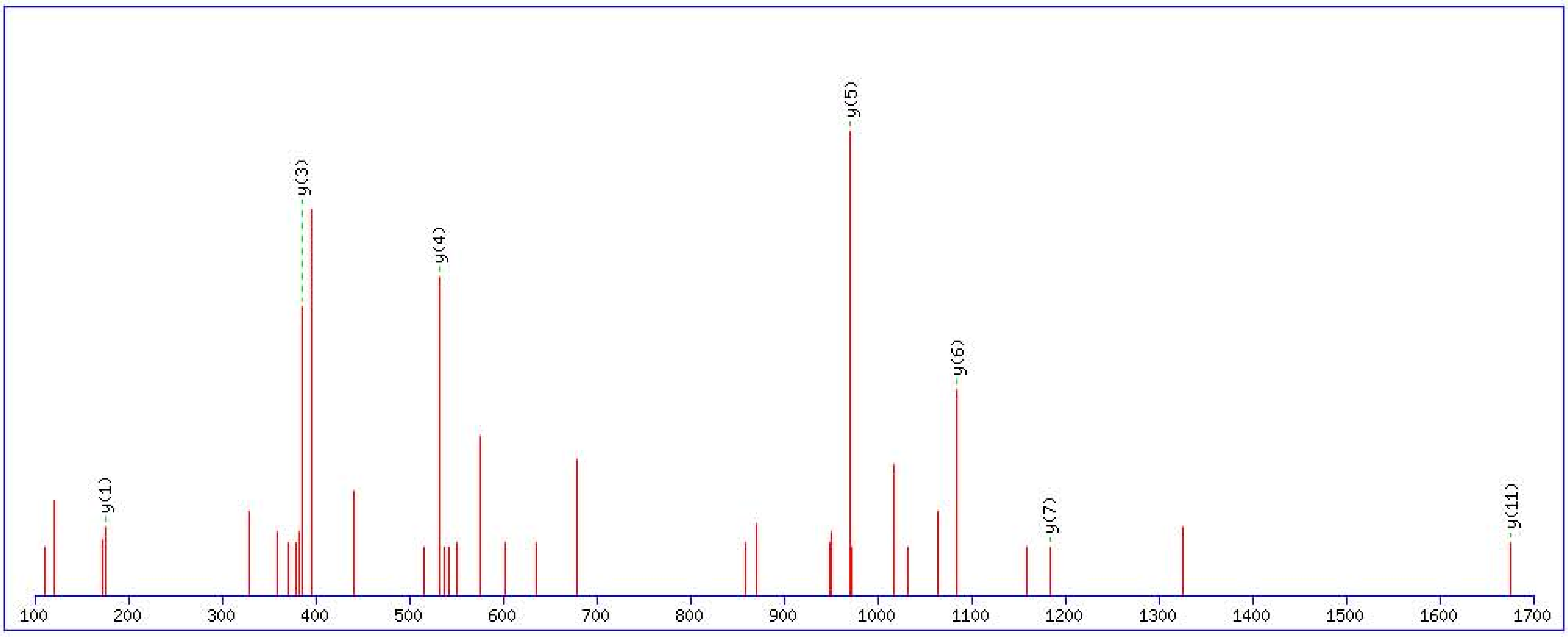
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIPTCTDFEVIQFPLR**
Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

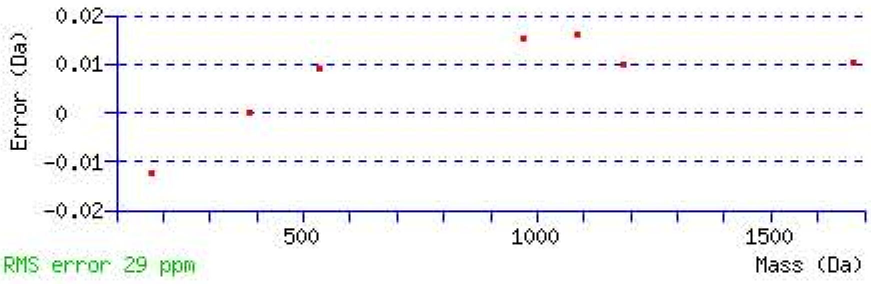
Match to Query 58987: 2233.156812 from(745.392880,3+) rtinseconds(2795) index(66092)
Title: Locus:1.1.1.3276.17 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

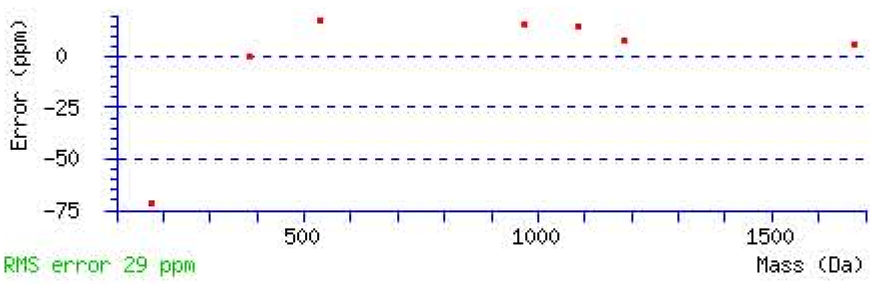
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2233.127548
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.041
Matches : 7/144 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							16
2	201.123368	101.065322			183.112803	92.060039	I	2147.102783	1074.055029	2130.076234	1065.541755	2129.092218	1065.049747	15
3	298.176132	149.591704			280.165567	140.586422	P	2034.018719	1017.512998	2016.992170	1008.999723	2016.008154	1008.507715	14
4	399.223811	200.115544			381.213246	191.110261	T	1936.965955	968.986616	1919.939406	960.473341	1918.955390	959.981333	13
5	559.254460	280.130868			541.243895	271.125586	C	1835.918276	918.462776	1818.891727	909.949502	1817.907711	909.457494	12
6	660.302139	330.654708			642.291574	321.649425	T	***1675.887627***	838.447452	1658.861078	829.934177	1657.877062	829.442169	11
7	775.329082	388.168179			757.318517	379.162897	D	1574.839948	787.923612	1557.813399	779.410338	1556.829383	778.918330	10
8	922.397496	461.702386			904.386931	452.697104	F	1459.813005	730.410141	1442.786456	721.896866	1441.802440	721.404858	9
9	1051.440089	526.223683			1033.429524	517.218400	E	1312.744591	656.875934	1295.718042	648.362659	1294.734026	647.870651	8
10	1150.508503	575.757890			1132.497938	566.752607	V	***1183.701998***	592.354637	1166.675449	583.841363			7
11	1263.592567	632.299921			1245.582002	623.294639	I	***1084.633584***	542.820430	1067.607035	534.307156			6
12	1702.817893	851.912585	1685.791344	843.399310	1684.807328	842.907302	Q	***971.549520***	486.278398	954.522971	477.765124			5
13	1849.886307	925.446792	1832.859758	916.933517	1831.875742	916.441509	F	***532.324194***	266.665735	515.297645	258.152461			4
14	1946.939071	973.973174	1929.912522	965.459899	1928.928506	964.967891	P	***385.255780***	193.131528	368.229231	184.618253			3
15	2060.023135	1030.515205	2042.996586	1022.001931	2042.012570	1021.509923	L	288.203016	144.605146	271.176467	136.091871			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	2233.127548	0.029264	SIPTCTDFEVIQFPLR

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

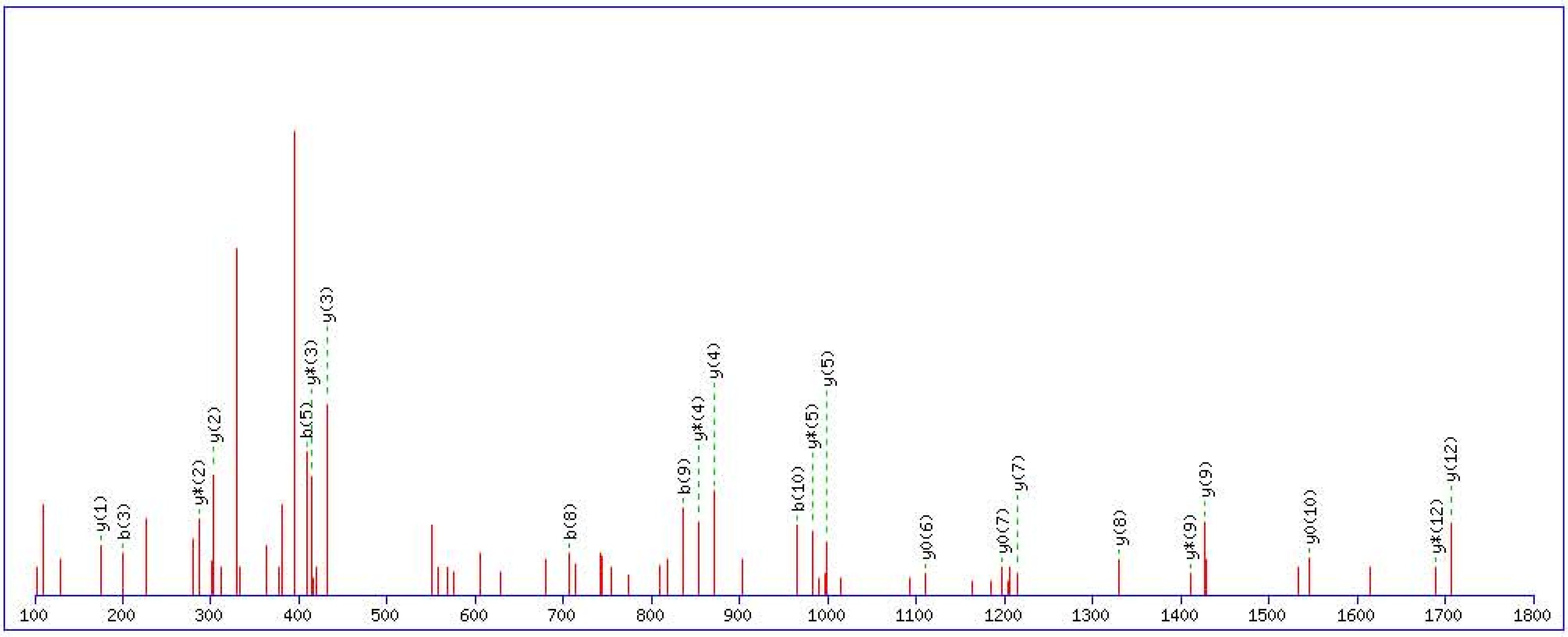
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAAAHPDSEEQQQR**
Found in **TLN1_HUMAN**, Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3

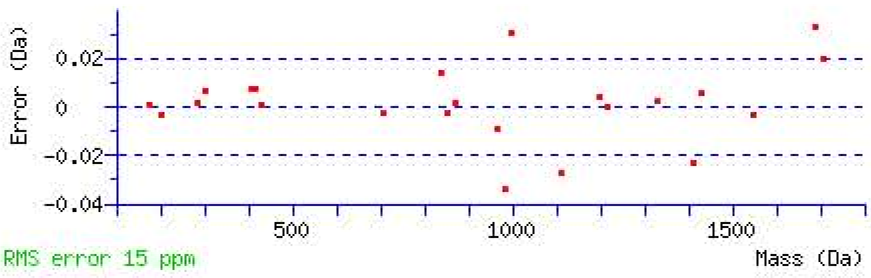
Match to Query 49146: 1833.851262 from(612.291030,3+) rtinseconds(1107) index(54182)
Title: Locus:1.1.1.2691.15 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

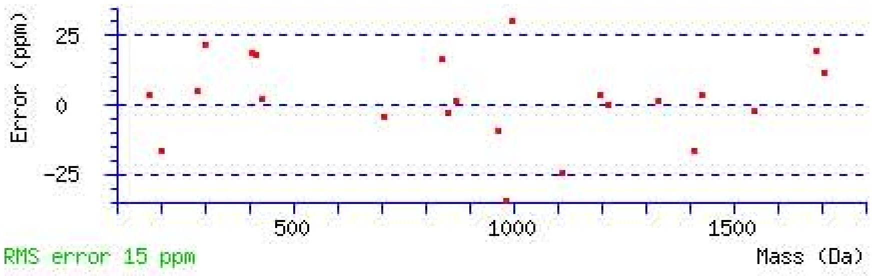
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1833.842773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00018
Matches : 23/116 fragment ions using 44 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							14
2	129.065854	65.036565					A	1777.828609	889.417943	1760.802060	880.904668	1759.818044	880.412660	13
3	**200.102968**	100.555122					A	***1706.791495***	853.899386	1689.764946	845.386111	1688.780930	844.894103	12
4	271.140082	136.073679					A	1635.754381	818.380829	1618.727832	809.867554	1617.743816	809.375546	11
5	**408.198994**	204.603135					H	1564.717267	782.862272	1547.690718	774.348997	1546.706702	773.856989	10
6	505.251758	253.129517					P	***1427.658355***	714.332816	1410.631806	705.819541	1409.647790	705.327533	9
7	620.278701	310.642989			602.268136	301.637706	D	***1330.605591***	665.806434	1313.579042	657.293159	1312.595026	656.801151	8
8	**707.310729**	354.159003			689.300164	345.153720	S	***1215.578648***	608.292962	1198.552099	599.779688	1197.568083	599.287680	7
9	**836.353322**	418.680299			818.342757	409.675017	E	1128.546620	564.776948	1111.520071	556.263674	1110.536055	555.771666	6
10	**965.395915**	483.201596			947.385350	474.196313	E	***999.504027***	500.255652	982.477478	491.742377	981.493462	491.250369	5
11	1404.621241	702.814259	1387.594692	694.300984	1386.610676	693.808976	Q	***870.461434***	435.734355	853.434885	427.221081			4
12	1532.679819	766.843548	1515.653270	758.330273	1514.669254	757.838265	Q	***431.236108***	216.121692	414.209559	207.608418			3
13	1660.738397	830.872837	1643.711848	822.359562	1642.727832	821.867554	Q	***303.177530***	152.092403	286.150981	143.579129			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.9	1833.842773	0.008489	GAAAHPDSEEQQQR
44.7	1833.842773	0.008489	GAAAHPDSEEQQQR
34.3	1833.842773	0.008489	GAAAHPDSEEQQQR
6.8	1833.864761	-0.013499	QREQMEQMKQR
5.1	1833.864761	-0.013499	QREQMEQMKQR
5.0	1833.867935	-0.016673	QPSFPANKGTEDSLMGR

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

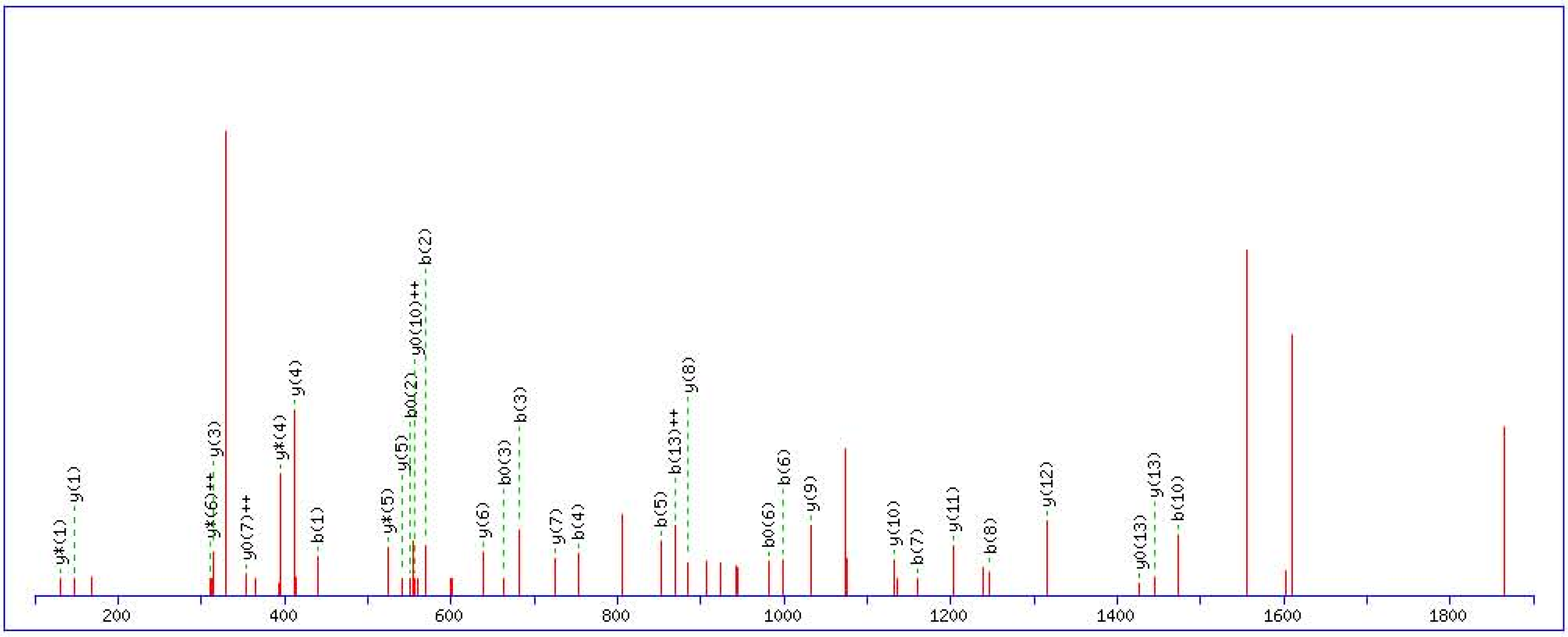
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QELAVFCSPEPPAK**
Found in **TLN1_HUMAN**, Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3

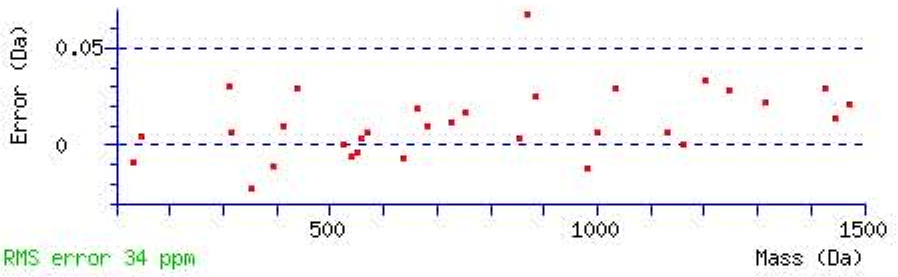
Match to Query 50310: 1882.955668 from(942.485110,2+) rtinseconds(2216) index(62102)
Title: Locus:1.1.1.3076.25 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●

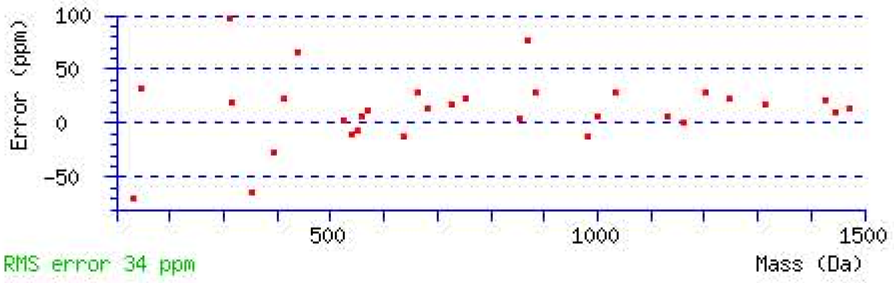


Monoisotopic mass of neutral peptide Mr(calc): 1882.932114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 73 **Expect:** 5.1e-007
Matches : 32/146 fragment ions using 61 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**440.232602**	220.619939	423.206053	212.106664			Q							14
2	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	E	***1444.714079***	722.860678	1427.687530	714.347403	1426.703514	713.855395	13
3	**682.359259**	341.683268	665.332710	333.169993	664.348694	332.677985	L	***1315.671486***	658.339381	1298.644937	649.826107	1297.660921	649.334098	12
4	**753.396373**	377.201825	736.369824	368.688550	735.385808	368.196542	A	***1202.587422***	601.797349	1185.560873	593.284075	1184.576857	592.792067	11
5	**852.464787**	426.736032	835.438238	418.222757	834.454222	417.730749	V	***1131.550308***	566.278792	1114.523759	557.765518	1113.539743	557.273510	10
6	**999.533201**	500.270239	982.506652	491.756964	981.522636	491.264956	F	***1032.481894***	516.744585	1015.455345	508.231311	1014.471329	507.739303	9
7	**1159.563850**	580.285563	1142.537301	571.772289	1141.553285	571.280281	C	***885.413480***	443.210378	868.386931	434.697104	867.402915	434.205096	8
8	**1246.595878**	623.801577	1229.569329	615.288303	1228.585313	614.796295	S	***725.382831***	363.195054	708.356282	354.681779	707.372266	354.189771	7
9	1343.648642	672.327959	1326.622093	663.814685	1325.638077	663.322677	P	***638.350803***	319.679040	621.324254	311.165765	620.340238	310.673757	6
10	**1472.691235**	736.849256	1455.664686	728.335981	1454.680670	727.843973	E	***541.298039***	271.152658	524.271490	262.639383	523.287474	262.147375	5
11	1569.743999	785.375638	1552.717450	776.862363	1551.733434	776.370355	P	***412.255446***	206.631361	395.228897	198.118087			4
12	1666.796763	833.902020	1649.770214	825.388745	1648.786198	824.896737	P	***315.202682***	158.104979	298.176133	149.591704			3
13	1737.833877	869.420577	1720.807328	860.907302	1719.823312	860.415294	A	218.149918	109.578597	201.123369	101.065322			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 34 ppm



RMS error 34 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.5	1882.932114	0.023554	QELAVFCSPEPPAK
5.2	1882.975693	-0.020025	EQLQADLLRCQAK
2.2	1882.949661	0.006007	AAGEELEKGQHLGSSSRK
1.2	1882.928070	0.027598	QELSEAEQATR
0.8	1882.932602	0.023066	GSSPWDRFLVGGYLSSR

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

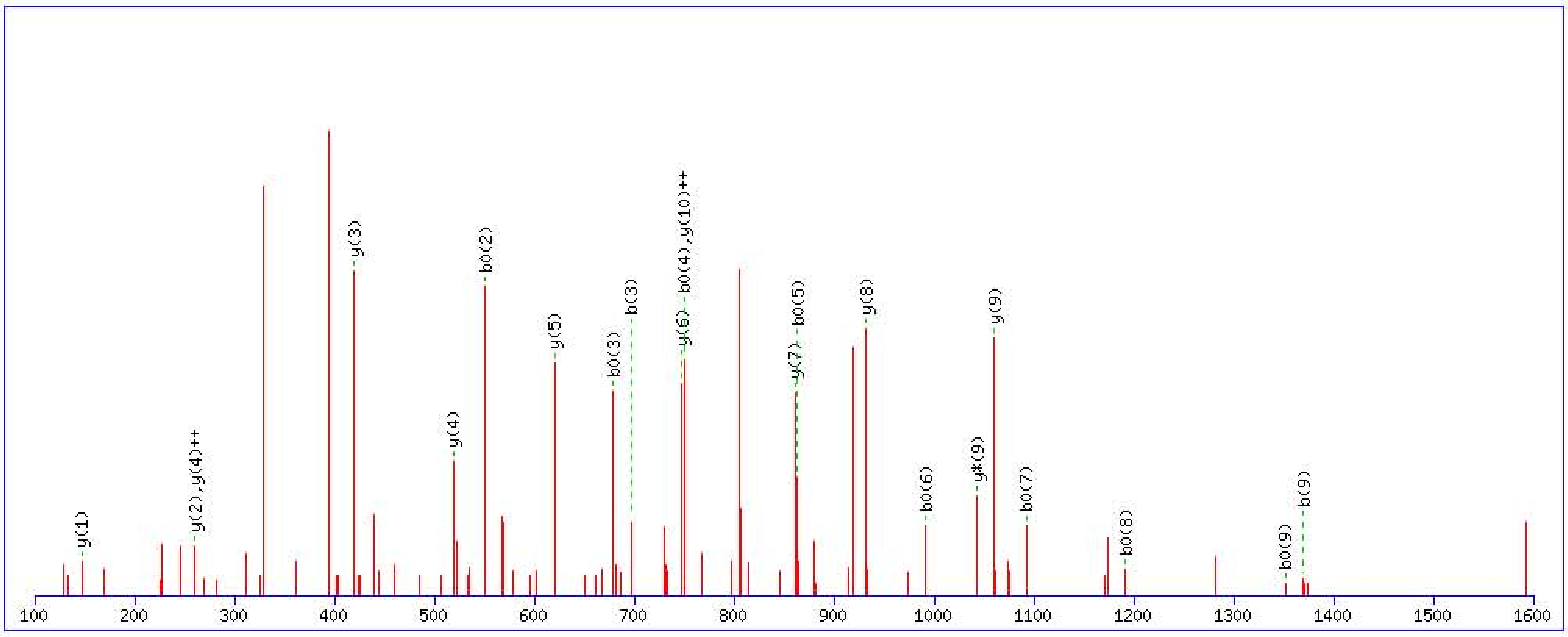
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQALQTVCLK**
Found in **TETN_HUMAN**, Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3

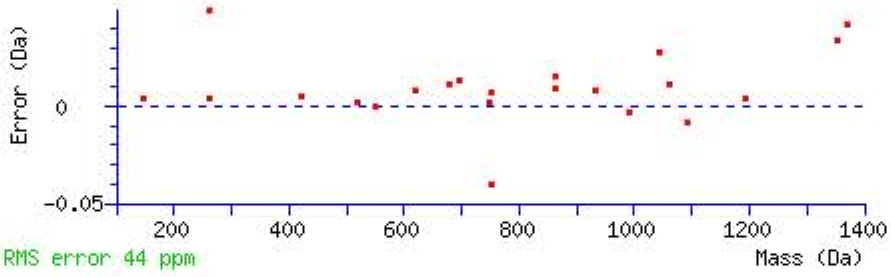
Match to Query 43913: 1627.860308 from(814.937430,2+) rtinseconds(1951) index(6732)
Title: Locus:1.1.1.2811.18 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

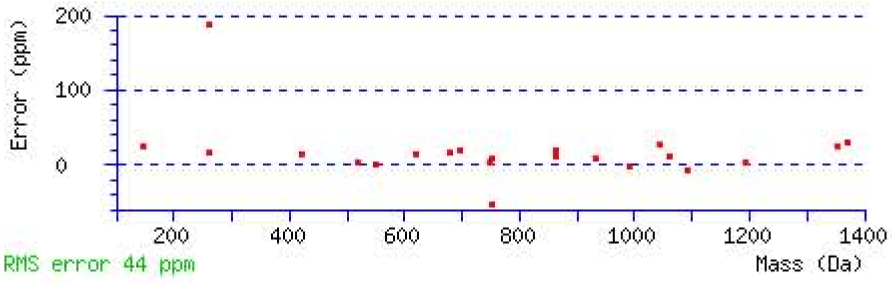
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1627.842575
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 3.5e-005
Matches : 22/110 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	130.049869	65.528572			112.039304	56.523290	E							11
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1499.807270	750.407273	1482.780721	741.893999	1481.796705	741.401991	10
3	**697.333773**	349.170525	680.307224	340.657250	679.323208	340.165242	Q	***1060.581944***	530.794610	1043.555395	522.281336	1042.571379	521.789328	9
4	768.370887	384.689082	751.344338	376.175807	750.360322	375.683799	A	***932.523366***	466.765321	915.496817	458.252047	914.512801	457.760039	8
5	881.454951	441.231114	864.428402	432.717839	863.444386	432.225831	L	***861.486252***	431.246764	844.459703	422.733490	843.475687	422.241482	7
6	1009.513529	505.260403	992.486980	496.747128	991.502964	496.255120	Q	***748.402188***	374.704732	731.375639	366.191458	730.391623	365.699450	6
7	1110.561208	555.784242	1093.534659	547.270968	1092.550643	546.778960	T	***620.343610***	310.675443	603.317061	302.162169	602.333045	301.670161	5
8	1209.629622	605.318449	1192.603073	596.805175	1191.619057	596.313167	V	***519.295931***	260.151604	502.269382	251.638329			4
9	**1369.660271**	685.333774	1352.633722	676.820499	1351.649706	676.328491	C	***420.227517***	210.617396	403.200968	202.104122			3
10	1482.744335	741.875806	1465.717786	733.362531	1464.733770	732.870523	L	***260.196868***	130.602072	243.170319	122.088797			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.5	1627.842575	0.017733	EQQALQTVCLK
52.2	1627.842575	0.017733	EQQALQTVCLK
10.7	1627.842575	0.017733	EQQALQTVCLK
8.5	1627.846390	0.013918	GAQAARGSSNASLK
4.8	1627.853775	0.006533	QEKMQQLREK
2.6	1627.879395	-0.019087	VALWARAQAERTEK
2.6	1627.846588	0.013720	QPTNPFLEMIK

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

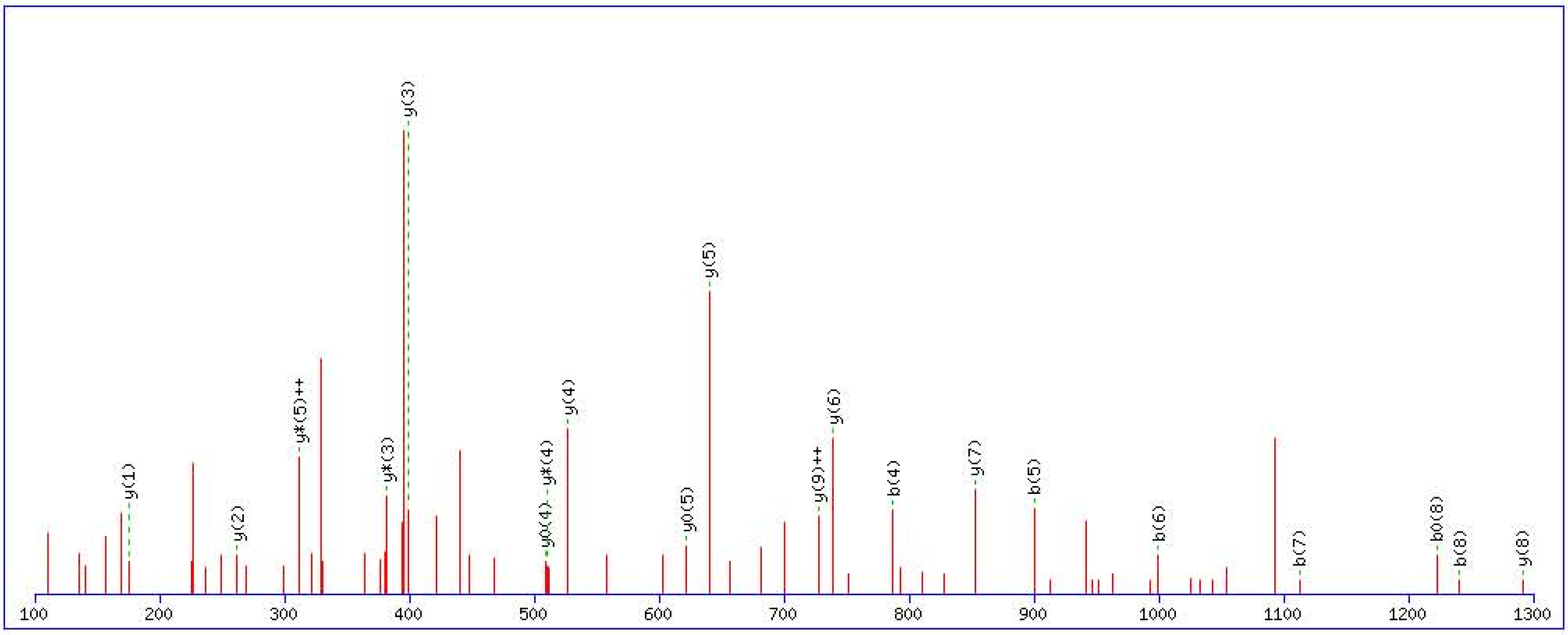
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPYQLVLQHSR**
Found in **BGH3_HUMAN**, Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1

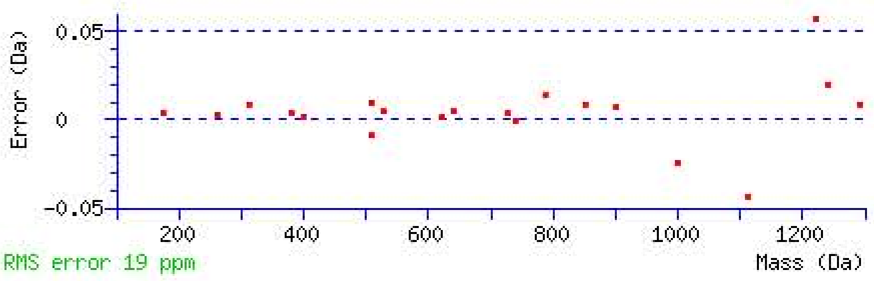
Match to Query 44266: 1637.876142 from(546.965990,3+) rtinseconds(1879) index(41233)
Title: Locus:1.1.1.2938.17 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

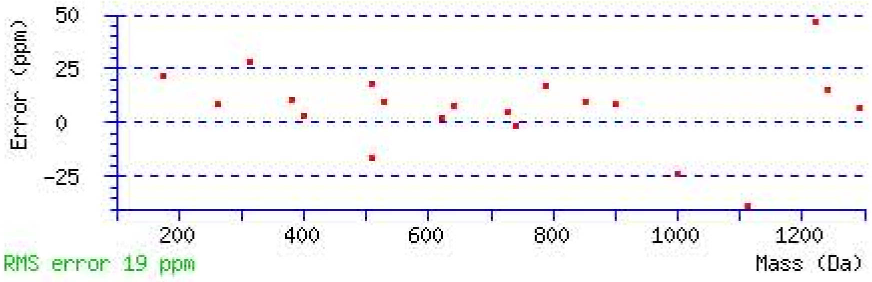
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1637.871170
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.0021
Matches : 20/112 fragment ions using 53 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							11
2	185.092068	93.049672			167.081503	84.044389	P	1551.846431	776.426853	1534.819882	767.913579	1533.835866	767.421571	10
3	348.155397	174.581336			330.144832	165.576054	Y	1454.793667	727.900471	1437.767118	719.387197	1436.783102	718.895189	9
4	**787.380723**	394.194000	770.354174	385.680725	769.370158	385.188717	Q	***1291.730338***	646.368807	1274.703789	637.855532	1273.719773	637.363524	8
5	**900.464787**	450.736032	883.438238	442.222757	882.454222	441.730749	L	***852.505012***	426.756144	835.478463	418.242869	834.494447	417.750861	7
6	**999.533201**	500.270239	982.506652	491.756964	981.522636	491.264956	V	***739.420948***	370.214112	722.394399	361.700837	721.410383	361.208829	6
7	**1112.617265**	556.812270	1095.590716	548.298996	1094.606700	547.806988	L	***640.352534***	320.679905	623.325985	312.166630	622.341969	311.674622	5
8	**1240.675843**	620.841559	1223.649294	612.328285	1222.665278	611.836277	Q	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	4
9	1377.734755	689.371015	1360.708206	680.857741	1359.724190	680.365733	H	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	3
10	1464.766783	732.887029	1447.740234	724.373755	1446.756218	723.881747	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.6	1637.871170	0.004972	SPYQLVLQHSR
0.0	1637.888916	-0.012774	APAPPPAGALLPEPGQR

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

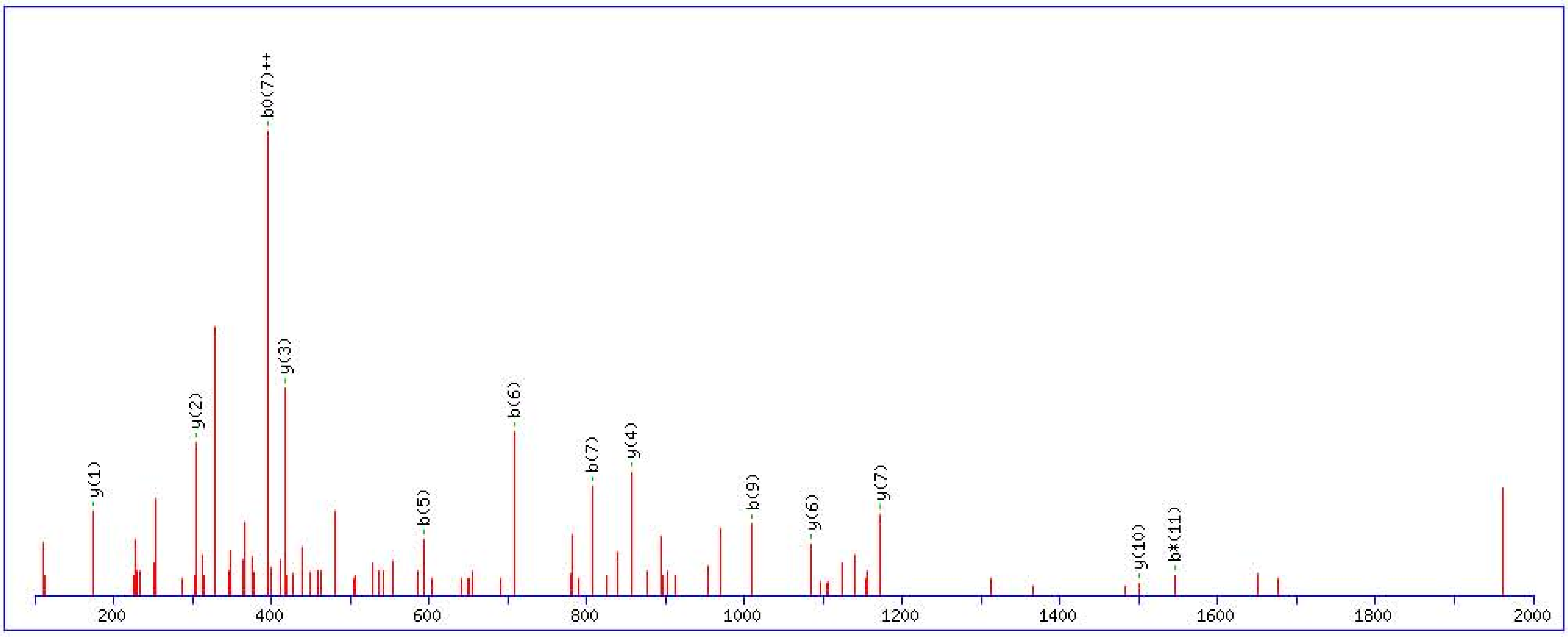
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLHDLDVSDNQLER**
Found in **VASN_HUMAN**, Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

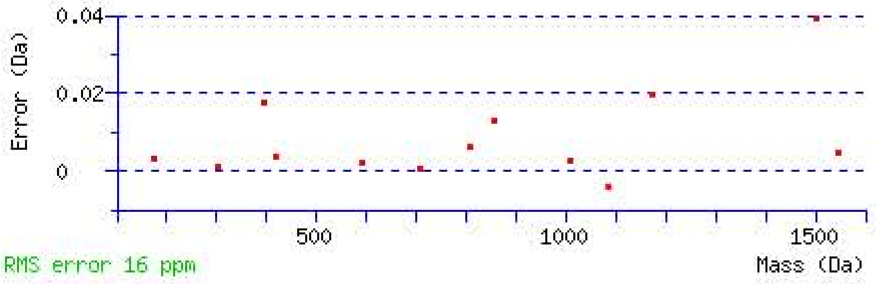
Match to Query 52397: 1977.966402 from(660.329410,3+) rtinseconds(1920) index(41576)
Title: Locus:1.1.1.2952.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

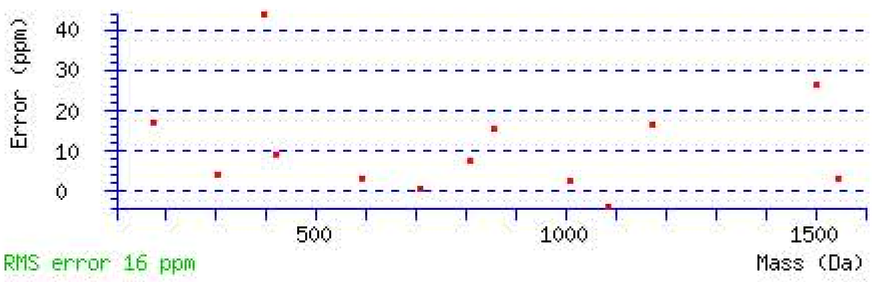
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1977.957809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 4.3e-006
Matches : 13/148 fragment ions using 16 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							14
2	228.134267	114.570771	211.107718	106.057497			L	1864.922173	932.964724	1847.895624	924.451450	1846.911608	923.959442	13
3	365.193179	183.100227	348.166630	174.586953			H	1751.838109	876.422692	1734.811560	867.909418	1733.827544	867.417410	12
4	480.220122	240.613699	463.193573	232.100425	462.209557	231.608417	D	1614.779197	807.893236	1597.752648	799.379962	1596.768632	798.887954	11
5	***593.304186***	297.155731	576.277637	288.642457	575.293621	288.150449	L	***1499.752254***	750.379765	1482.725705	741.866490	1481.741689	741.374482	10
6	***708.331129***	354.669203	691.304580	346.155928	690.320564	345.663920	D	1386.668190	693.837733	1369.641641	685.324458	1368.657625	684.832450	9
7	***807.399543***	404.203410	790.372994	395.690135	789.388978	395.198127	V	1271.641247	636.324261	1254.614698	627.810987	1253.630682	627.318979	8
8	894.431571	447.719424	877.405022	439.206149	876.421006	438.714141	S	***1172.572833***	586.790054	1155.546284	578.276780	1154.562268	577.784772	7
9	***1009.458514***	505.232895	992.431965	496.719620	991.447949	496.227612	D	***1085.540805***	543.274040	1068.514256	534.760766	1067.530240	534.268758	6
10	1123.501441	562.254358	1106.474892	553.741084	1105.490876	553.249076	N	970.513862	485.760569	953.487313	477.247294	952.503297	476.755286	5
11	1562.726767	781.867021	1545.700218	773.353747	1544.716202	772.861739	Q	***856.470935***	428.739105	839.444386	420.225831	838.460370	419.733823	4
12	1675.810831	838.409053	1658.784282	829.895779	1657.800266	829.403771	L	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
13	1804.853424	902.930350	1787.826875	894.417075	1786.842859	893.925067	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.8	1977.957809	0.008593	NLHDLDVSDNQLER
4.5	1977.969009	-0.002607	HLDMEHERLQLEKER

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

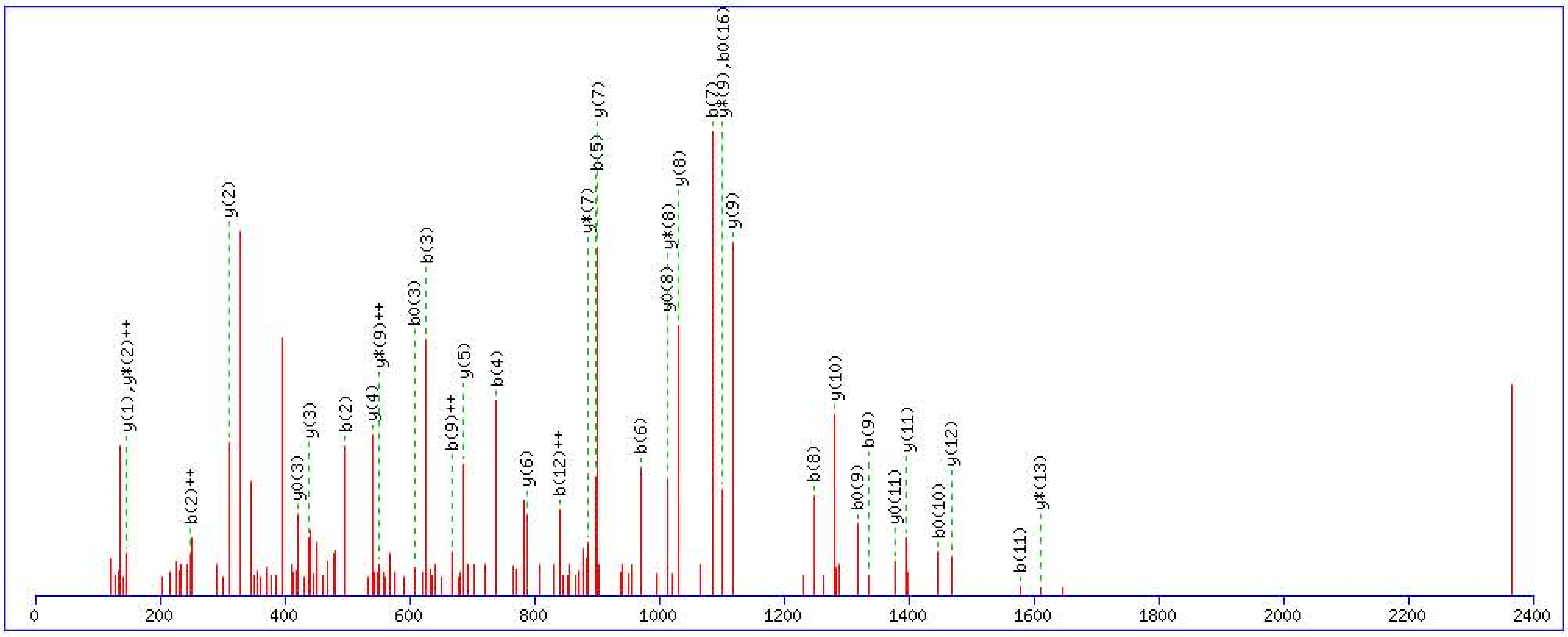
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQELCADYSENTFTEYK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

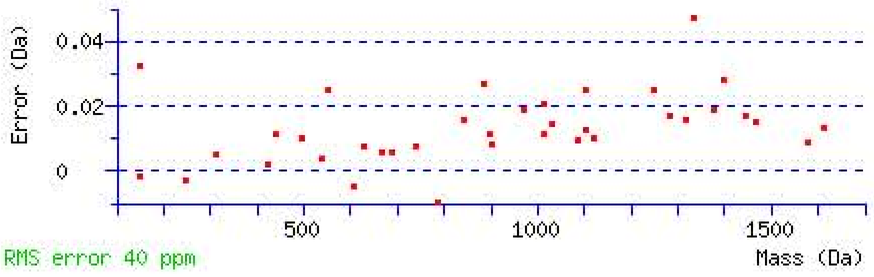
Match to Query 61874: 2365.049292 from(789.357040,3+) rtinseconds(2140) index(79477)
Title: Locus:1.1.1.2959.24 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

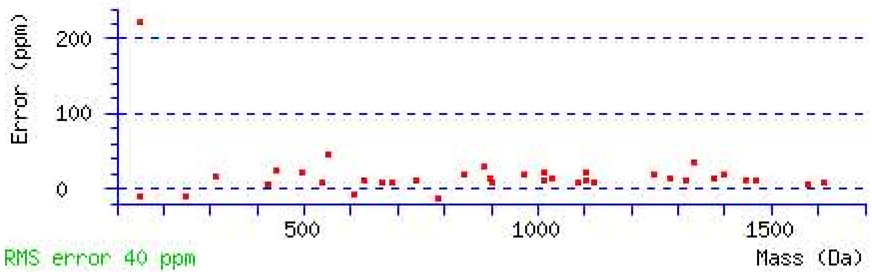
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2365.024231
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 80  Expect: 5.8e-008
Matches : 37/182 fragment ions using 54 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							17
2	***497.254066***	**249.130671**	480.227517	240.617397			Q	2309.010064	1155.008670	2291.983515	1146.495395	2290.999499	1146.003387	16
3	***626.296659***	313.651968	609.270110	305.138693	608.286094	304.646685	E	1869.784738	935.396007	1852.758189	926.882733	1851.774173	926.390725	15
4	***739.380723***	370.194000	722.354174	361.680725	721.370158	361.188717	L	1740.742145	870.874711	1723.715596	862.361436	1722.731580	861.869428	14
5	***899.411372***	450.209324	882.384823	441.696050	881.400807	441.204042	C	1627.658081	814.332679	1610.631532	805.819404	1609.647516	805.327396	13
6	***970.448486***	485.727881	953.421937	477.214607	952.437921	476.722599	A	***1467.627432***	734.317354	1450.600883	725.804080	1449.616867	725.312072	12
7	***1085.475429***	543.241353	1068.448880	534.728078	1067.464864	534.236070	D	***1396.590318***	698.798797	1379.563769	690.285523	1378.579753	689.793515	11
8	***1248.538758***	624.773017	1231.512209	616.259743	1230.528193	615.767735	Y	***1281.563375***	641.285326	1264.536826	632.772051	1263.552810	632.280043	10
9	***1335.570786***	**668.289031**	1318.544237	659.775757	1317.560221	659.283749	S	***1118.500046***	559.753661	1101.473497	551.240387	1100.489481	550.748379	9
10	1464.613379	732.810328	1447.586830	724.297053	1446.602814	723.805045	E	***1031.468018***	516.237647	1014.441469	507.724373	1013.457453	507.232365	8
11	***1578.656306***	789.831791	1561.629757	781.318517	1560.645741	780.826509	N	***902.425425***	451.716351	885.398876	443.203076	884.414860	442.711068	7
12	1679.703985	**840.355631**	1662.677436	831.842356	1661.693420	831.350348	T	***788.382498***	394.694887	771.355949	386.181613	770.371933	385.689605	6
13	1826.772399	913.889838	1809.745850	905.376563	1808.761834	904.884555	F	***687.334819***	344.171048	670.308270	335.657773	669.324254	335.165765	5
14	1927.820078	964.413677	1910.793529	955.900403	1909.809513	955.408395	T	***540.266405***	270.636841	523.239856	262.123566	522.255840	261.631558	4
15	2056.862671	1028.934973	2039.836122	1020.421699	2038.852106	1019.929691	E	***439.218726***	220.113001	422.192177	211.599726	421.208161	211.107718	3
16	2219.926000	1110.466638	2202.899451	1101.953363	2201.915435	1101.461355	Y	***310.176133***	155.591705	293.149584	147.078430			2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.4	2365.024231	0.025061	GQELCADYSENTFTEYK

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

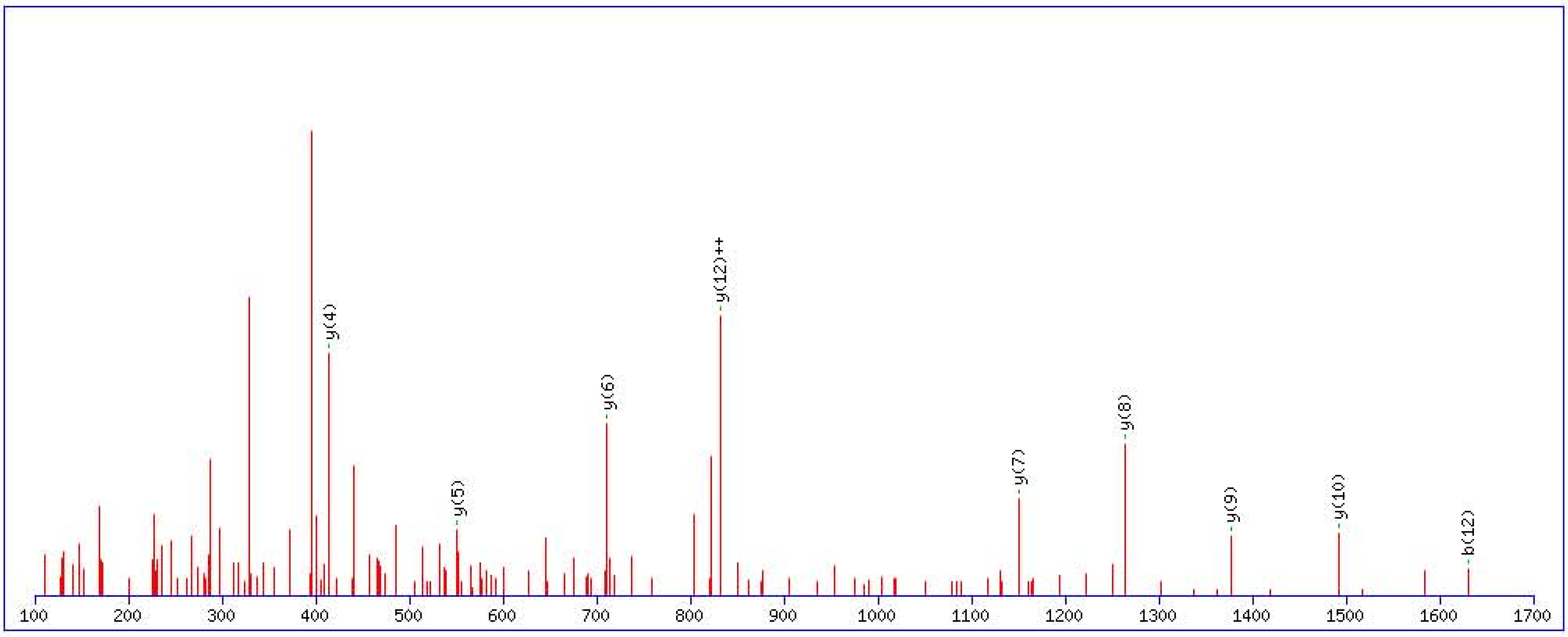
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGDDLLQCHPAVK**
Found in **PROC_HUMAN**, Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1

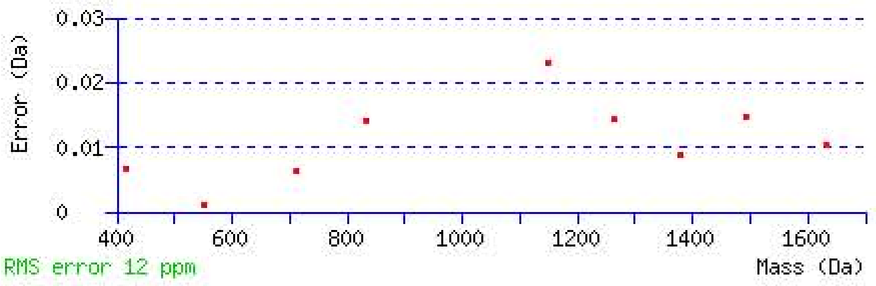
Match to Query 47910: 1775.918172 from(592.980000,3+) rtinseconds(1938) index(60089)
Title: Locus:1.1.1.2980.10 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

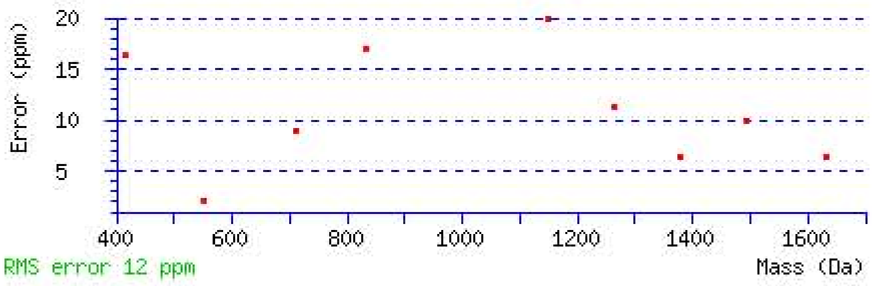
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1775.906250
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.00082
Matches : 9/110 fragment ions using 16 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							13
2	171.112804	86.060040					G	1663.829461	832.418369	1646.802912	823.905094	1645.818896	823.413086	12
3	286.139747	143.573512			268.129182	134.568229	D	1606.807997	803.907637	1589.781448	795.394362	1588.797432	794.902354	11
4	401.166690	201.086983			383.156125	192.081701	D	***1491.781054***	746.394165	1474.754505	737.880891	1473.770489	737.388883	10
5	514.250754	257.629015			496.240189	248.623733	L	***1376.754111***	688.880694	1359.727562	680.367419			9
6	627.334818	314.171047			609.324253	305.165765	L	***1263.670047***	632.338662	1246.643498	623.825387			8
7	1066.560144	533.783710	1049.533595	525.270436	1048.549579	524.778428	Q	***1150.585983***	575.796630	1133.559434	567.283355			7
8	1226.590793	613.799035	1209.564244	605.285760	1208.580228	604.793752	C	***711.360657***	356.183967	694.334108	347.670692			6
9	1363.649705	682.328491	1346.623156	673.815216	1345.639140	673.323208	H	***551.330008***	276.168642	534.303459	267.655368			5
10	1460.702469	730.854873	1443.675920	722.341598	1442.691904	721.849590	P	***414.271096***	207.639186	397.244547	199.125912			4
11	1531.739583	766.373430	1514.713034	757.860155	1513.729018	757.368147	A	317.218332	159.112804	300.191783	150.599530			3
12	1630.807997	815.907637	1613.781448	807.394362	1612.797432	806.902354	V	246.181218	123.594247	229.154669	115.080973			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.7	1775.906250	0.011922	LGDDLLQCHPAVK
1.8	1775.919952	-0.001780	NVDSSGNKSVLMERLK

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

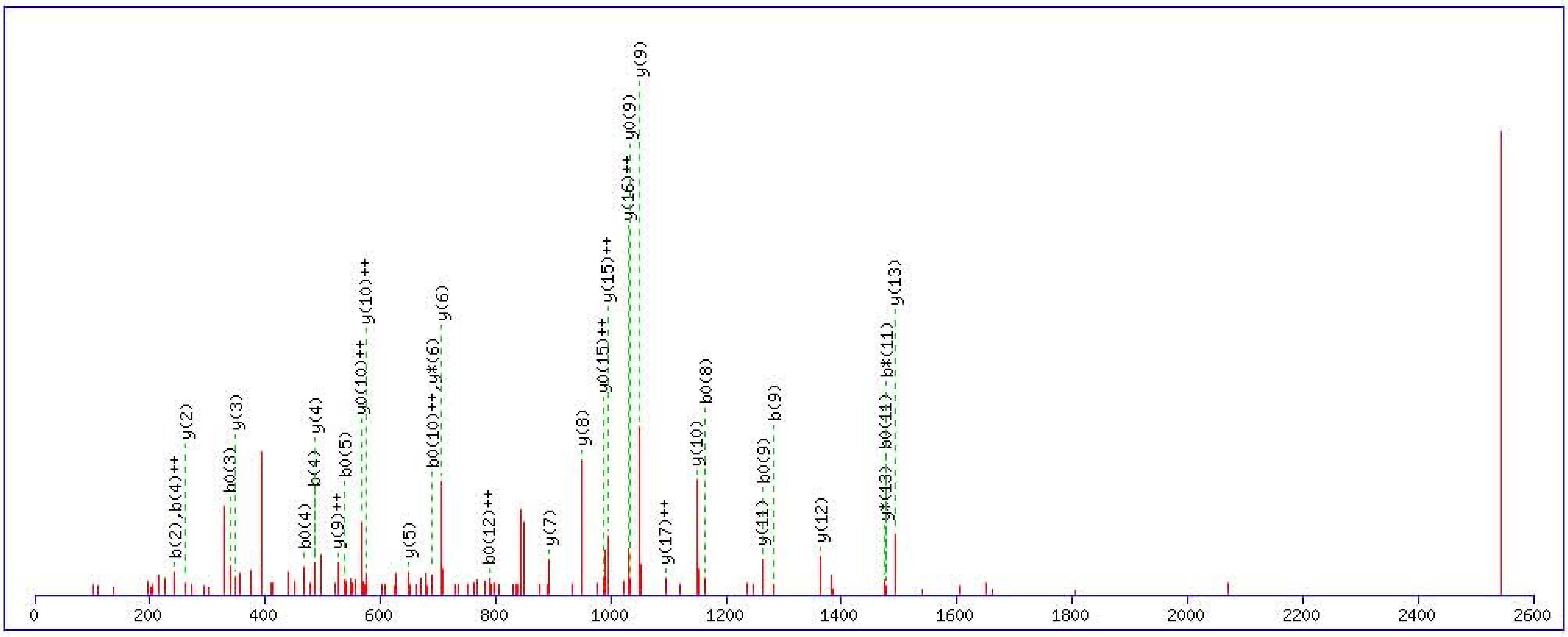
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELNQAGQETLVTGWGYHSSR**
Found in **PROC_HUMAN**, Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1

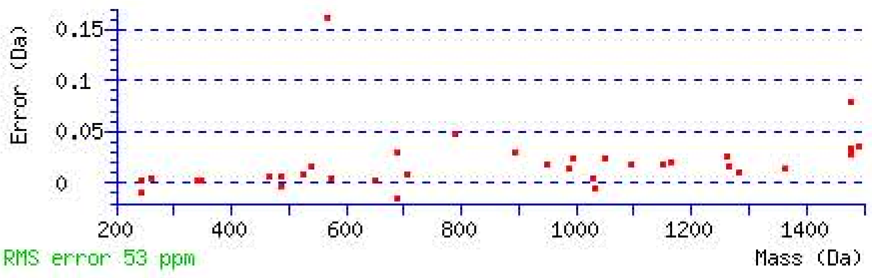
Match to Query 66019: 2543.257482 from(848.759770,3+) rtinseconds(2141) index(61494)
Title: Locus:1.1.1.3050.24 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

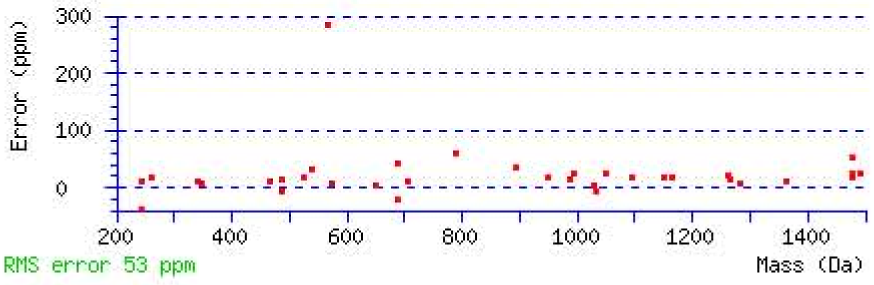


```
Monoisotopic mass of neutral peptide Mr(calc): 2543.222702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00077
Matches : 35/222 fragment ions using 82 most intense peaks   (help)
```

#	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							20
2	**243.133933**	122.070605			225.123368	113.065322	L	2415.187392	1208.097334	2398.160843	1199.584059	2397.176827	1199.092051	19
3	357.176860	179.092068	340.150311	170.578794	339.166295	170.086786	N	2302.103328	1151.555302	2285.076779	1143.042027	2284.092763	1142.550019	18
4	**485.235438**	243.121357	468.208889	234.608083	467.224873	234.116075	Q	2188.060401	1094.533838	2171.033852	1086.020564	2170.049836	1085.528556	17
5	556.272552	278.639914	539.246003	270.126640	538.261987	269.634632	A	2060.001823	1030.504549	2042.975274	1021.991275	2041.991258	1021.499267	16
6	613.294016	307.150646	596.267467	298.637372	595.283451	298.145364	G	1988.964709	994.985993	1971.938160	986.472718	1970.954144	985.980710	15
7	1052.519342	526.763309	1035.492793	518.250035	1034.508777	517.758027	Q	1931.943245	966.475261	1914.916696	957.961986	1913.932680	957.469978	14
8	1181.561935	591.284606	1164.535386	582.771331	1163.551370	582.279323	E	***1492.717919***	746.862597	1475.691370	738.349323	1474.707354	737.857315	13
9	**1282.609614**	641.808445	1265.583065	633.295171	1264.599049	632.803163	T	***1363.675326***	682.341301	1346.648777	673.828026	1345.664761	673.336018	12
10	1395.693678	698.350477	1378.667129	689.837203	1377.683113	689.345195	L	***1262.627647***	631.817461	1245.601098	623.304187	1244.617082	622.812179	11
11	1494.762092	747.884684	1477.735543	739.371410	1476.751527	738.879402	V	***1149.543583***	575.275429	1132.517034	566.762155	1131.533018	566.270147	10
12	1595.809771	798.408524	1578.783222	789.895249	1577.799206	789.403241	T	***1050.475169***	525.741222	1033.448620	517.227948	1032.464604	516.735940	9
13	1652.831235	826.919256	1635.804686	818.405981	1634.820670	817.913973	G	***949.427490***	475.217383	932.400941	466.704108	931.416925	466.212100	8
14	1838.910548	919.958912	1821.883999	911.445638	1820.899983	910.953630	W	***892.406026***	446.706651	875.379477	438.193376	874.395461	437.701368	7
15	1895.932012	948.469644	1878.905463	939.956370	1877.921447	939.464362	G	***706.326713***	353.666994	689.300164	345.153720	688.316148	344.661712	6
16	2058.995341	1030.001308	2041.968792	1021.488034	2040.984776	1020.996026	Y	***649.305249***	325.156263	632.278700	316.642988	631.294684	316.150980	5
17	2196.054253	1098.530764	2179.027704	1090.017490	2178.043688	1089.525482	H	***486.241920***	243.624598	469.215371	235.111324	468.231355	234.619316	4
18	2283.086281	1142.046778	2266.059732	1133.533504	2265.075716	1133.041496	S	***349.183008***	175.095142	332.156459	166.581868	331.172443	166.089860	3
19	2370.118309	1185.562792	2353.091760	1177.049518	2352.107744	1176.557510	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
20							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 53 ppm



RMS error 53 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.7	2543.222702	0.034780	ELNQAGQETLVTGWGYHSSR
39.7	2543.222702	0.034780	ELNQAGQETLVTGWGYHSSR

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

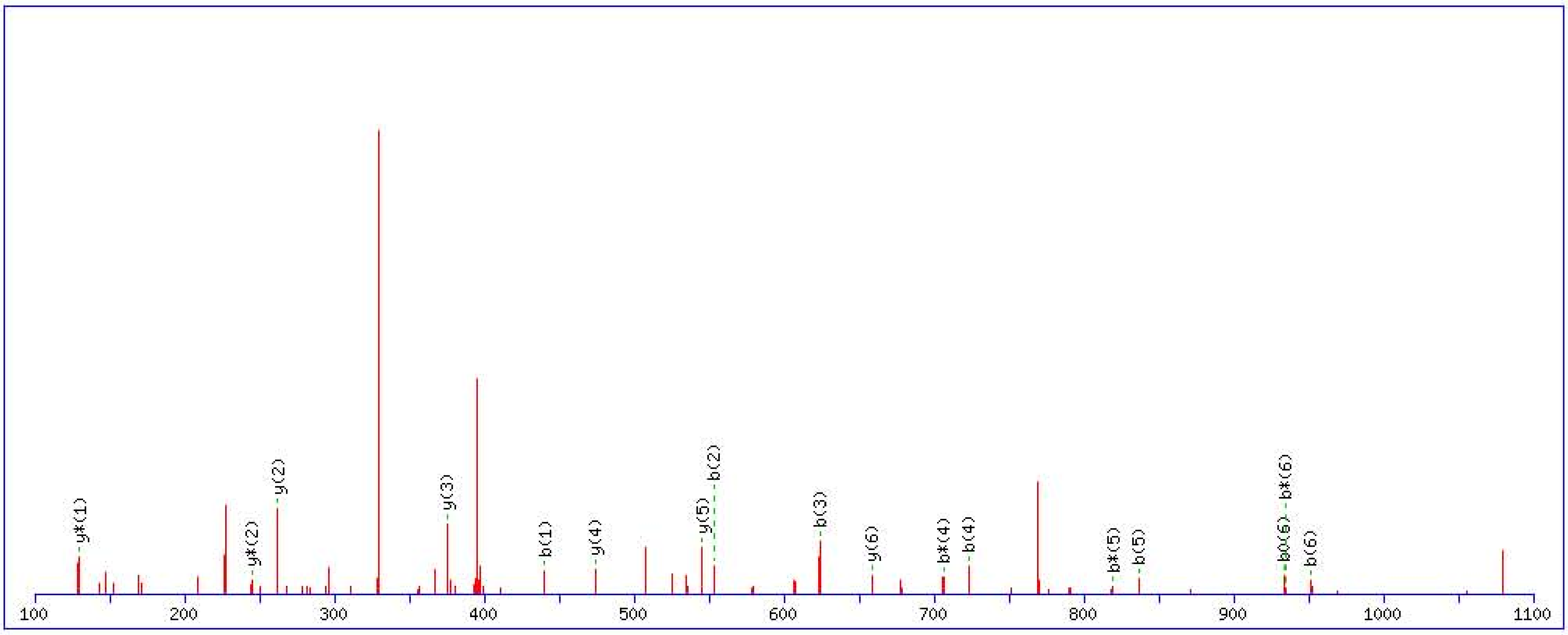
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLAVLDK**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

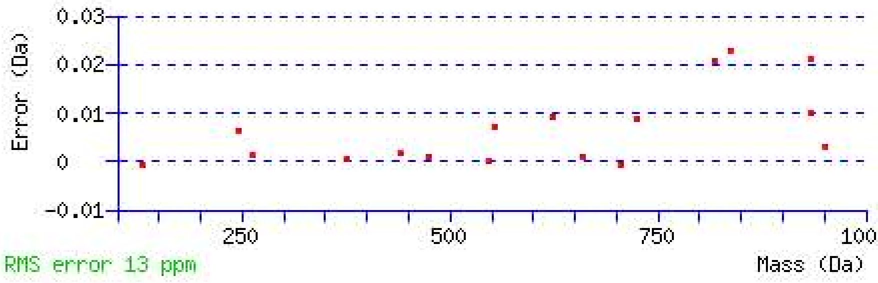
Match to Query 22436: 1096.637388 from(549.325970,2+) rtinseconds(1941) index(60113)
Title: Locus:1.1.1.2981.9 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

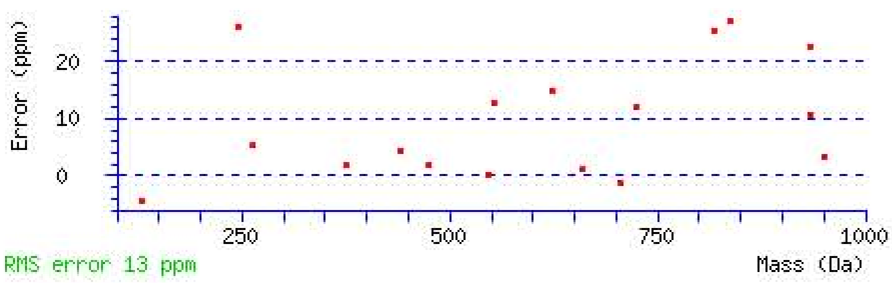
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1096.631439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.019
Matches : 17/60 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***440.232602***	220.619939	423.206053	212.106664			Q							7
2	***553.316666***	277.161971	536.290117	268.648697			L	**658.413403**	329.710340	641.386854	321.197065	640.402838	320.705057	6
3	***624.353780***	312.680528	607.327231	304.167254			A	**545.329339**	273.168308	528.302790	264.655033	527.318774	264.163025	5
4	***723.422194***	362.214735	706.395645	353.701461			V	**474.292225**	237.649750	457.265676	229.136476	456.281660	228.644468	4
5	***836.506258***	418.756767	819.479709	410.243493			L	**375.223811**	188.115543	358.197262	179.602269	357.213246	179.110261	3
6	***951.533201***	476.270239	934.506652	467.756964	933.522636	467.264956	D	**262.139747**	131.573511	245.113198	123.060237	244.129182	122.568229	2
7							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.8	1096.631439	0.005949	QLAVLDK
17.5	1096.624054	0.013334	KPVDSVPLSR
7.9	1096.635269	0.002119	SSSLVIHKAR
7.0	1096.624023	0.013365	IPRENLLDK
2.7	1096.631439	0.005949	GILQLDK
1.9	1096.628067	0.009321	YIFVSLLSR
0.0	1096.631439	0.005949	QIDVAIK

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

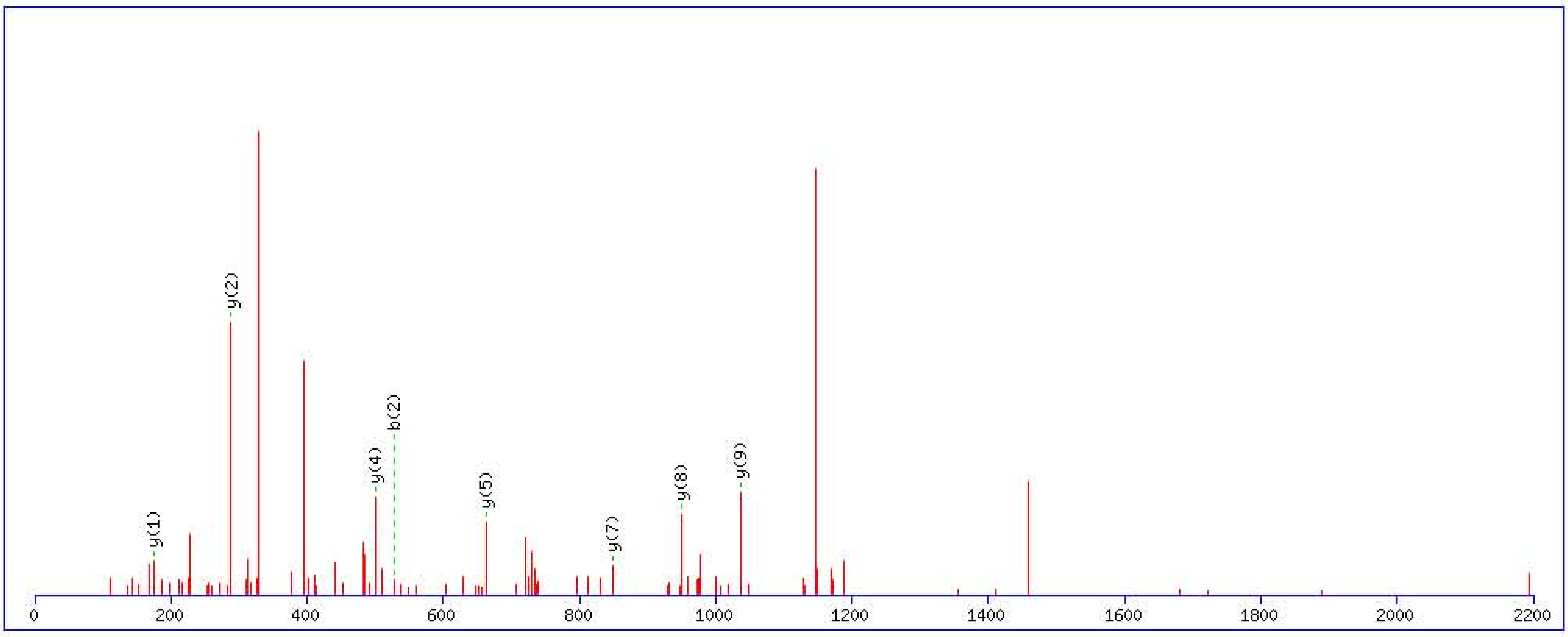
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSTNAYPDLR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

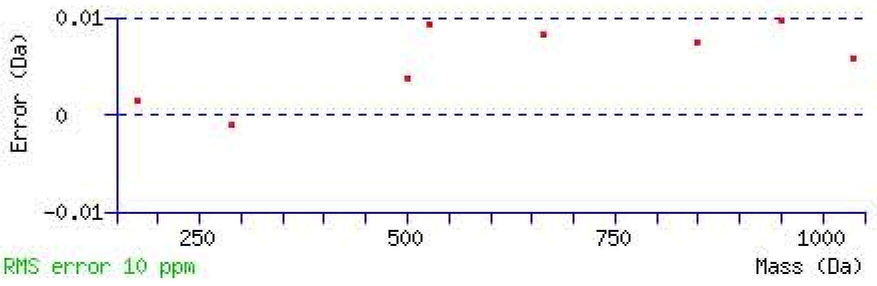
Match to Query 37809: 1474.739688 from(738.377120,2+) rtinseconds(1739) index(58642)
Title: Locus:1.1.1.2911.19 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

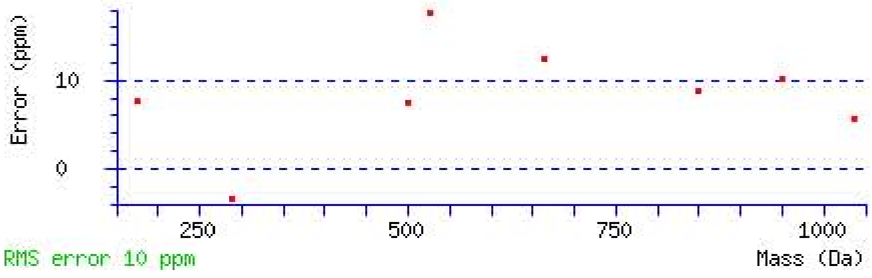
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1474.723831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00021
Matches : 8/102 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							10
2	**527.264630**	264.135953	510.238081	255.622679	509.254065	255.130671	S	***1036.505800***	518.756538	1019.479251	510.243263	1018.495235	509.751255	9
3	628.312309	314.659793	611.285760	306.146518	610.301744	305.654510	T	***949.473772***	475.240524	932.447223	466.727249	931.463207	466.235241	8
4	742.355236	371.681256	725.328687	363.167982	724.344671	362.675974	N	***848.426093***	424.716684	831.399544	416.203410	830.415528	415.711402	7
5	813.392350	407.199813	796.365801	398.686538	795.381785	398.194530	A	734.383166	367.695221	717.356617	359.181946	716.372601	358.689938	6
6	976.455679	488.731477	959.429130	480.218203	958.445114	479.726195	Y	***663.346052***	332.176664	646.319503	323.663389	645.335487	323.171382	5
7	1073.508443	537.257860	1056.481894	528.744585	1055.497878	528.252577	P	***500.282723***	250.644999	483.256174	242.131725	482.272158	241.639717	4
8	1188.535386	594.771331	1171.508837	586.258057	1170.524821	585.766049	D	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
9	1301.619450	651.313363	1284.592901	642.800089	1283.608885	642.308080	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.7	1474.723831	0.015857	QSTNAYPDLR
16.7	1474.721161	0.018527	QSTHGERGHR
8.9	1474.741592	-0.001904	SSLEHGSDVYLLR
8.4	1474.744934	-0.005246	LSKEELIQNMDR
5.8	1474.760239	-0.020551	TWTKQPDLTMVR
5.2	1474.757523	-0.017835	MGLQARRWASGSR
4.6	1474.719788	0.019900	QQEELEQMRLR
3.9	1474.748779	-0.009091	LQSESTNNGKNKR
0.8	1474.742462	-0.002774	QCKSEFPIR
0.8	1474.753708	-0.014020	QRPSFTCLR

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

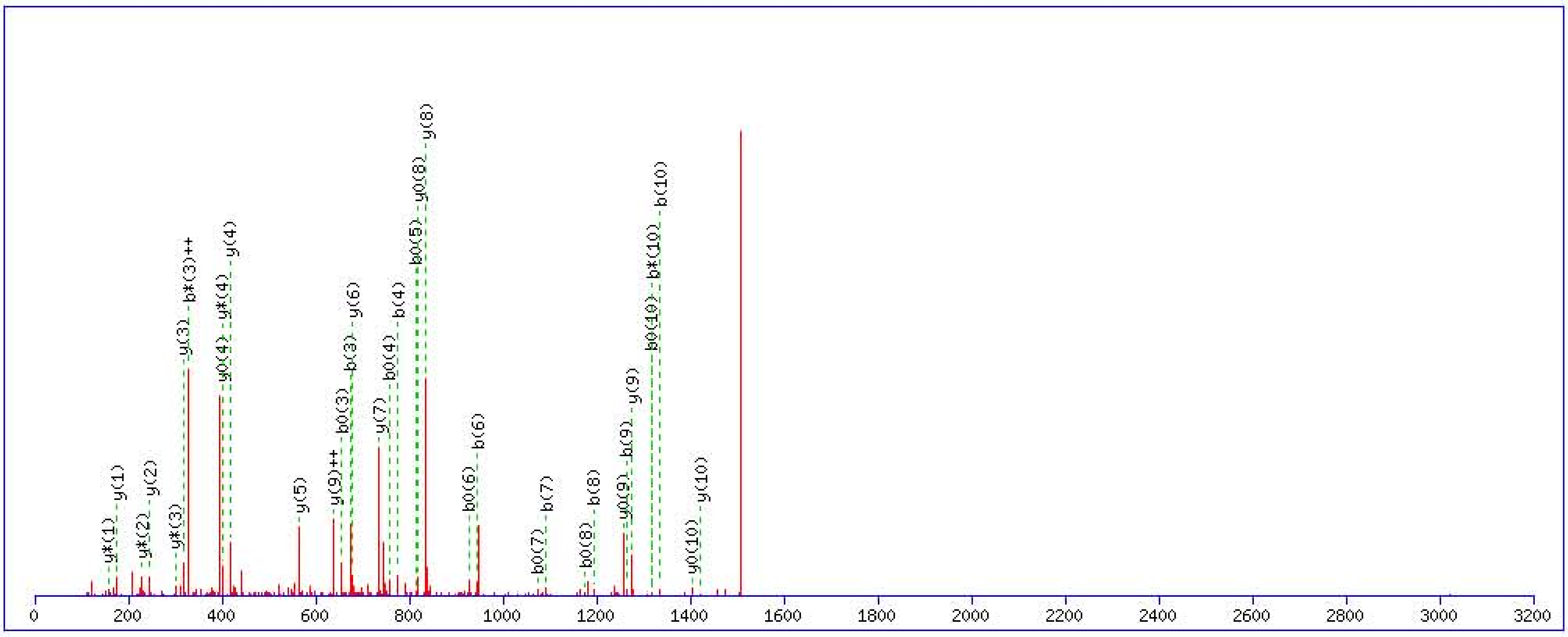
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFQTGLFTAAR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

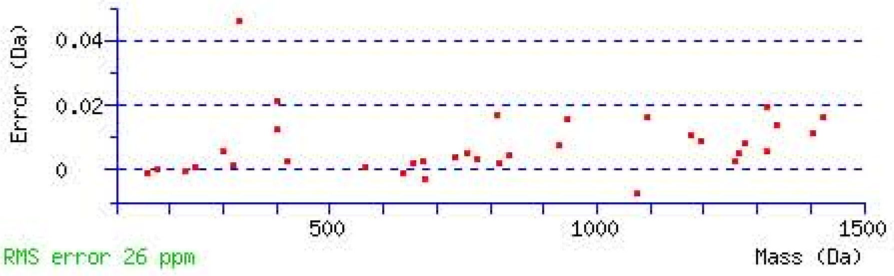
Match to Query 38959: 1508.795228 from(755.404890,2+) rtinseconds(2277) index(43923)
Title: Locus:1.1.1.3076.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

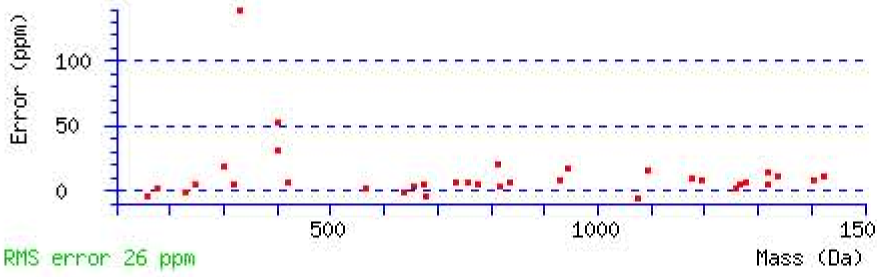


```
Monoisotopic mass of neutral peptide Mr(calc): 1508.780975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 2e-005
Matches : 35/110 fragment ions using 70 most intense peaks   (help)
```

#	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							11
2	235.107718	118.057497			217.097153	109.052214	F	***1422.756220***	711.881748	1405.729671	703.368474	1404.745655	702.876465	10
3	**674.333044**	337.670160	657.306495	329.156885	656.322479	328.664877	Q	***1275.687806***	638.347541	1258.661257	629.834267	1257.677241	629.342259	9
4	**775.380723**	388.194000	758.354174	379.680725	757.370158	379.188717	T	***836.462480***	418.734878	819.435931	410.221604	818.451915	409.729596	8
5	832.402187	416.704732	815.375638	408.191457	814.391622	407.699449	G	***735.414801***	368.211039	718.388252	359.697764	717.404236	359.205756	7
6	**945.486251**	473.246764	928.459702	464.733489	927.475686	464.241481	L	***678.393337***	339.700307	661.366788	331.187032	660.382772	330.695024	6
7	**1092.554665**	546.780971	1075.528116	538.267696	1074.544100	537.775688	F	***565.309273***	283.158275	548.282724	274.645000	547.298708	274.152992	5
8	**1193.602344**	597.304810	1176.575795	588.791536	1175.591779	588.299528	T	***418.240859***	209.624067	401.214310	201.110793	400.230294	200.618785	4
9	**1264.639458**	632.823367	1247.612909	624.310093	1246.628893	623.818085	A	***317.193180***	159.100228	300.166631	150.586953			3
10	**1335.676572**	668.341924	1318.650023	659.828650	1317.666007	659.336642	A	***246.156066***	123.581671	229.129517	115.068396			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 26 ppm



RMS error 26 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.3	1508.780975	0.014253	SFQTGLFTAAR
5.9	1508.805893	-0.010665	RLELPRASDAEPR
3.3	1508.798721	-0.003493	SSYGVAAPVDFLRK
3.0	1508.776932	0.018296	LMGADSLQLFRSR

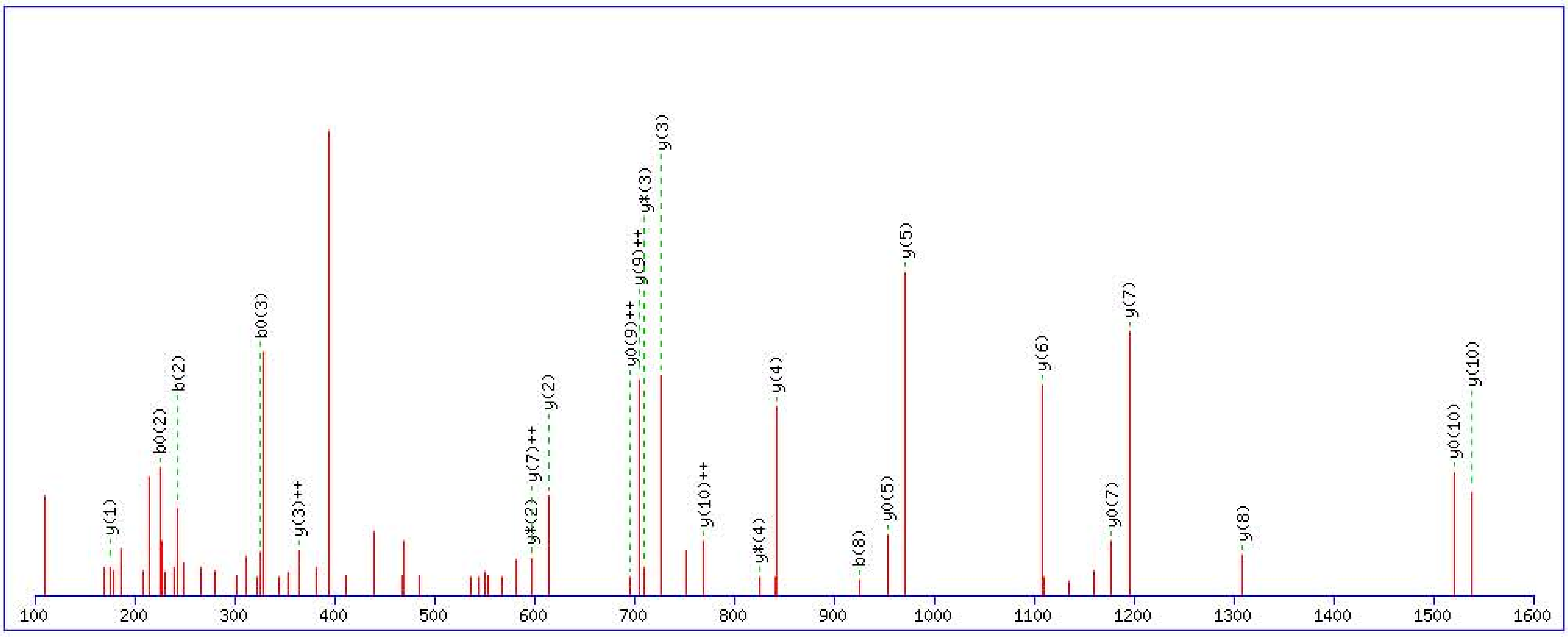
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IETISHEDLQR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

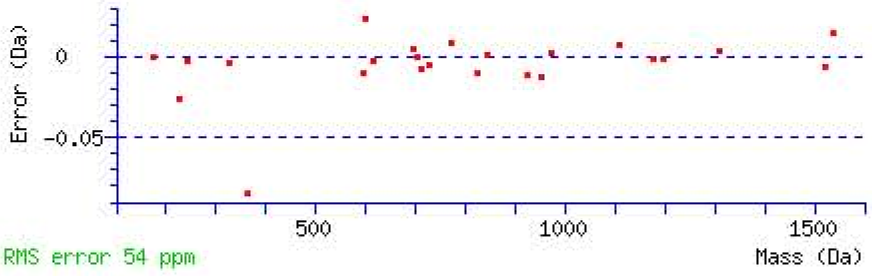
Match to Query 44635: 1650.837372 from(551.286400,3+) rtinseconds(1603) index(39521)
Title: Locus:1.1.1.2842.9 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

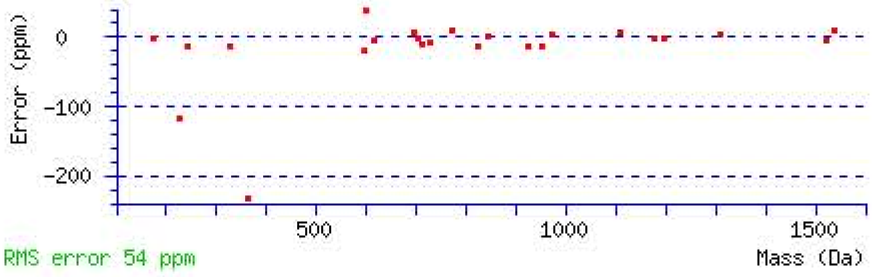
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1650.839920
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 9.7e-005
Matches : 24/94 fragment ions using 43 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	114.091340	57.549308					I							11
2	**243.133933**	122.070605			225.123368	113.065322	E	***1538.763154***	769.885215	1521.736605	761.371941	1520.752589	760.879933	10
3	344.181612	172.594444			326.171047	163.589162	T	1409.720561	705.363919	1392.694012	696.850644	1391.709996	696.358636	9
4	457.265676	229.136476			439.255111	220.131194	I	***1308.672882***	654.840079	1291.646333	646.326805	1290.662317	645.834797	8
5	544.297704	272.652490			526.287139	263.647208	S	***1195.588818***	598.298047	1178.562269	589.784773	1177.578253	589.292764	7
6	681.356616	341.181946			663.346051	332.176664	H	***1108.556790***	554.782033	1091.530241	546.268759	1090.546225	545.776751	6
7	810.399209	405.703243			792.388644	396.697960	E	***971.497878***	486.252577	954.471329	477.739303	953.487313	477.247295	5
8	**925.426152**	463.216714			907.415587	454.211432	D	***842.455285***	421.731281	825.428736	413.218006	824.444720	412.725998	4
9	1038.510216	519.758746			1020.499651	510.753463	L	***727.428342***	364.217809	710.401793	355.704535			3
10	1477.735542	739.371409	1460.708993	730.858135	1459.724977	730.366127	Q	***614.344278***	307.675777	597.317729	299.162503			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.7	1650.839920	-0.002548	IETISHEDLQR
13.6	1650.855881	-0.018509	MQRTGGGAPRPGR
8.0	1650.833389	0.003983	QQLEHIMATNR
0.6	1650.833389	0.003983	QQLEHIMATNR
0.3	1650.822144	0.015228	QSALNTEKMYR

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

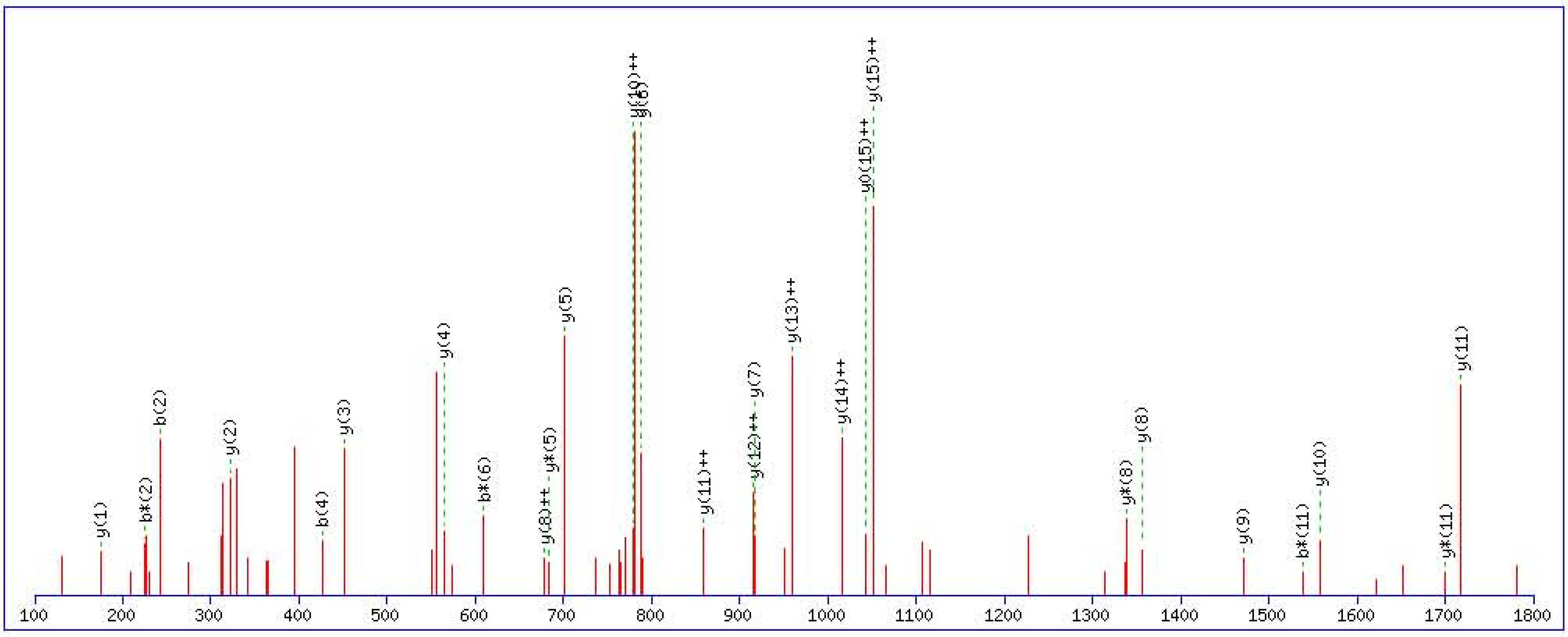
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQALSLCSDQQSHLEFR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

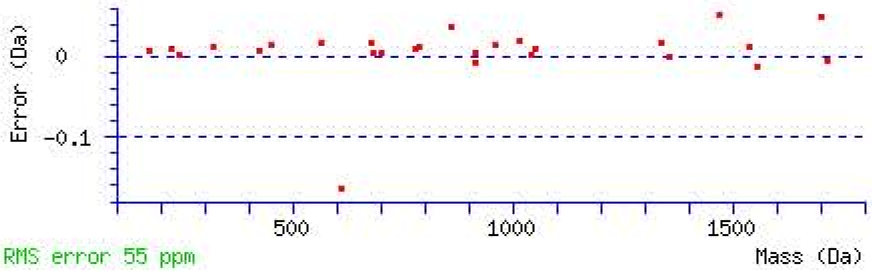
Match to Query 61547: 2342.170932 from(781.730920,3+) rtinseconds(2175) index(79768)
Title: Locus:1.1.1.2971.22 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

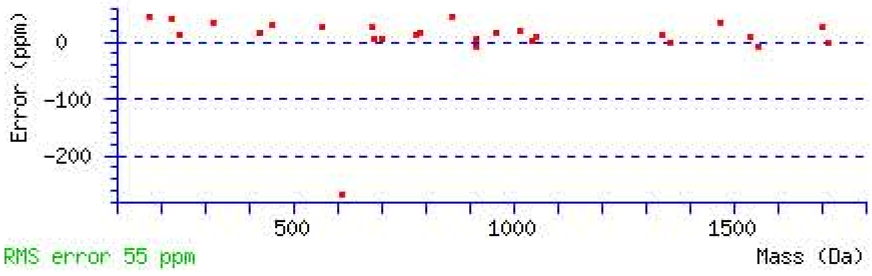
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2342.151108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 76  Expect: 8.6e-007
Matches : 27/178 fragment ions using 42 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							17
2	**242.149918**	121.578597	225.123369	113.065323			Q	2230.074335	1115.540805	2213.047786	1107.027531	2212.063770	1106.535523	16
3	313.187032	157.097154	296.160483	148.583879			A	2102.015757	1051.511516	2084.989208	1042.998242	2084.005192	1042.506234	15
4	**426.271096**	213.639186	409.244547	205.125912			L	2030.978643	1015.992959	2013.952094	1007.479685	2012.968078	1006.987677	14
5	513.303124	257.155200	496.276575	248.641926	495.292559	248.149918	S	1917.894579	959.450927	1900.868030	950.937653	1899.884014	950.445645	13
6	626.387188	313.697232	609.360639	305.183958	608.376623	304.691950	L	1830.862551	915.934913	1813.836002	907.421639	1812.851986	906.929631	12
7	786.417837	393.712557	769.391288	385.199282	768.407272	384.707274	C	***1717.778487***	859.392881	1700.751938	850.879607	1699.767922	850.387599	11
8	873.449865	437.228571	856.423316	428.715296	855.439300	428.223288	S	***1557.747838***	779.377557	1540.721289	770.864282	1539.737273	770.372274	10
9	988.476808	494.742042	971.450259	486.228768	970.466243	485.736760	D	***1470.715810***	735.861543	1453.689261	727.348268	1452.705245	726.856260	9
10	1427.702134	714.354705	1410.675585	705.841431	1409.691569	705.349422	Q	***1355.688867***	678.348071	1338.662318	669.834797	1337.678302	669.342789	8
11	1555.760712	778.383994	1538.734163	769.870720	1537.750147	769.378712	Q	***916.463541***	458.735408	899.436992	450.222134	898.452976	449.730126	7
12	1642.792740	821.900008	1625.766191	813.386734	1624.782175	812.894726	S	***788.404963***	394.706119	771.378414	386.192845	770.394398	385.700837	6
13	1779.851652	890.429464	1762.825103	881.916190	1761.841087	881.424182	H	***701.372935***	351.190105	684.346386	342.676831	683.362370	342.184823	5
14	1892.935716	946.971496	1875.909167	938.458222	1874.925151	937.966213	L	***564.314023***	282.660649	547.287474	274.147375	546.303458	273.655367	4
15	2021.978309	1011.492793	2004.951760	1002.979518	2003.967744	1002.487510	E	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	3
16	2169.046723	1085.026999	2152.020174	1076.513725	2151.036158	1076.021717	F	***322.187366***	161.597321	305.160817	153.084046			2
17							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.6	2342.151108	0.019824	IQALSLCSDQQSHLEFR
75.6	2342.151108	0.019824	IQALSLCSDQQSHLEFR
8.5	2342.151108	0.019824	IQALSLCSDQQSHLEFR

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

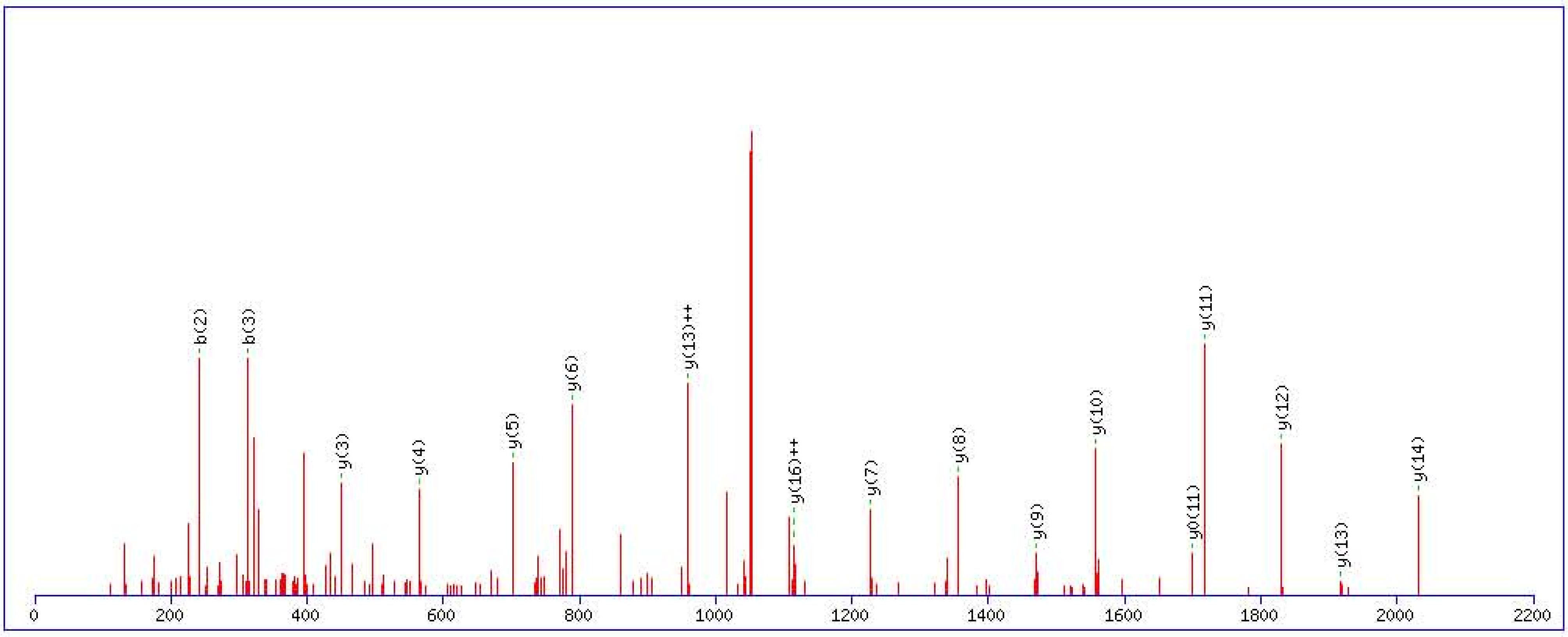
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQALSLCSDQQSHLEFR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

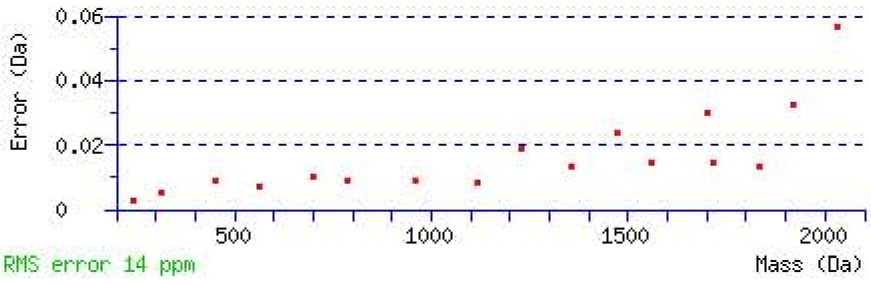
Match to Query 61548: 2342.170932 from(781.730920,3+) rtinseconds(2166) index(79695)
Title: Locus:1.1.1.2968.24 File:"2013-07-02 CLN FXIII 60 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

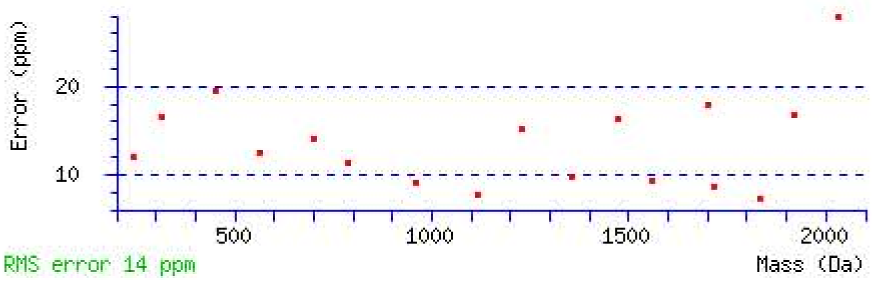
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2342.151108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 107  Expect: 1.8e-010
Matches : 17/178 fragment ions using 20 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							17
2	**242.149918**	121.578597	225.123369	113.065323			Q	2230.074335	1115.540805	2213.047786	1107.027531	2212.063770	1106.535523	16
3	**313.187032**	157.097154	296.160483	148.583879			A	2102.015757	1051.511516	2084.989208	1042.998242	2084.005192	1042.506234	15
4	426.271096	213.639186	409.244547	205.125912			L	***2030.978643***	1015.992959	2013.952094	1007.479685	2012.968078	1006.987677	14
5	513.303124	257.155200	496.276575	248.641926	495.292559	248.149918	S	***1917.894579***	959.450927	1900.868030	950.937653	1899.884014	950.445645	13
6	626.387188	313.697232	609.360639	305.183958	608.376623	304.691950	L	***1830.862551***	915.934913	1813.836002	907.421639	1812.851986	906.929631	12
7	786.417837	393.712557	769.391288	385.199282	768.407272	384.707274	C	***1717.778487***	859.392881	1700.751938	850.879607	1699.767922	850.387599	11
8	873.449865	437.228571	856.423316	428.715296	855.439300	428.223288	S	***1557.747838***	779.377557	1540.721289	770.864282	1539.737273	770.372274	10
9	988.476808	494.742042	971.450259	486.228768	970.466243	485.736760	D	***1470.715810***	735.861543	1453.689261	727.348268	1452.705245	726.856260	9
10	1116.535386	558.771331	1099.508837	550.258057	1098.524821	549.766049	Q	***1355.688867***	678.348071	1338.662318	669.834797	1337.678302	669.342789	8
11	1555.760712	778.383994	1538.734163	769.870720	1537.750147	769.378712	Q	***1227.630289***	614.318782	1210.603740	605.805508	1209.619724	605.313500	7
12	1642.792740	821.900008	1625.766191	813.386734	1624.782175	812.894726	S	***788.404963***	394.706119	771.378414	386.192845	770.394398	385.700837	6
13	1779.851652	890.429464	1762.825103	881.916190	1761.841087	881.424182	H	***701.372935***	351.190105	684.346386	342.676831	683.362370	342.184823	5
14	1892.935716	946.971496	1875.909167	938.458222	1874.925151	937.966213	L	***564.314023***	282.660649	547.287474	274.147375	546.303458	273.655367	4
15	2021.978309	1011.492793	2004.951760	1002.979518	2003.967744	1002.487510	E	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	3
16	2169.046723	1085.026999	2152.020174	1076.513725	2151.036158	1076.021717	F	322.187366	161.597321	305.160817	153.084046			2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
106.8	2342.151108	0.019824	IQALSLCSDQQSHLEFR
94.1	2342.151108	0.019824	IQALSLCSDQQSHLEFR
6.7	2342.151108	0.019824	IQALSLCSDQQSHLEFR
2.9	2342.197372	-0.026440	LVAAASPSAMLSQSLDLSDR

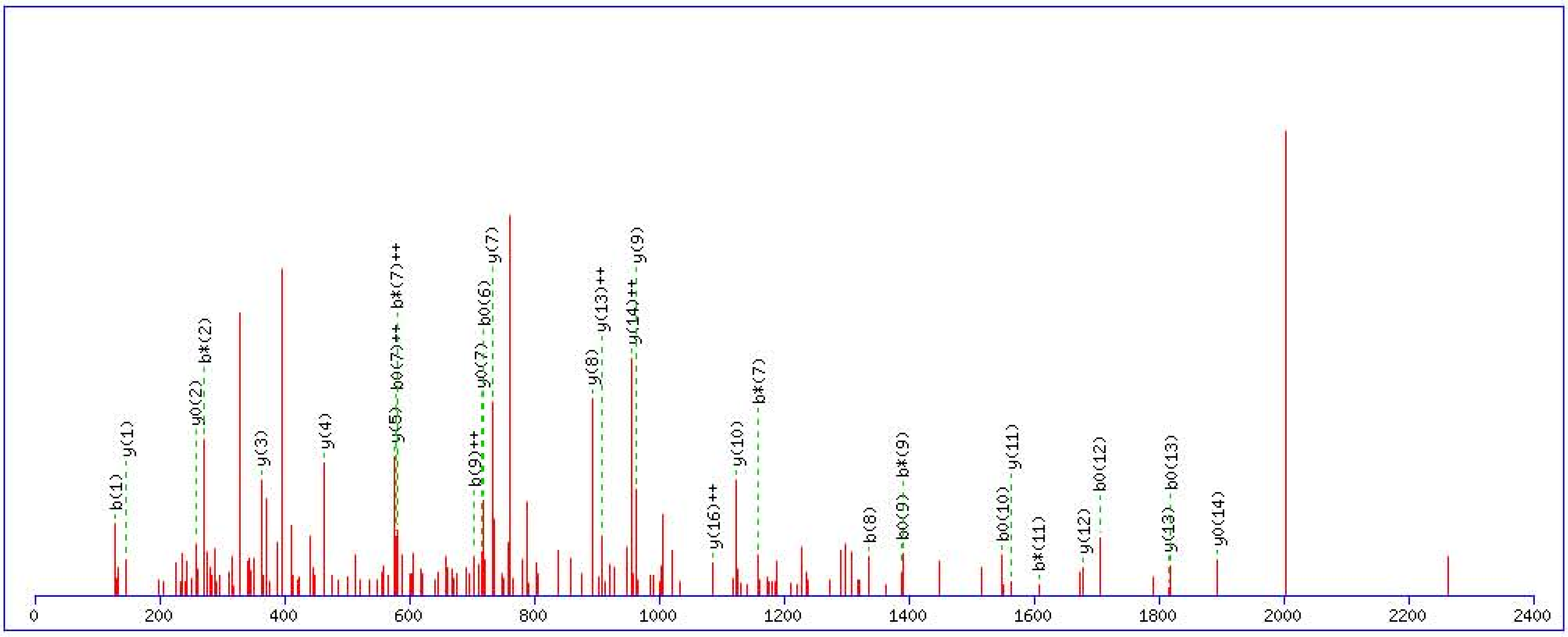
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QCVPHDQCACGVLTSEK**
Found in **PROZ_HUMAN**, Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2

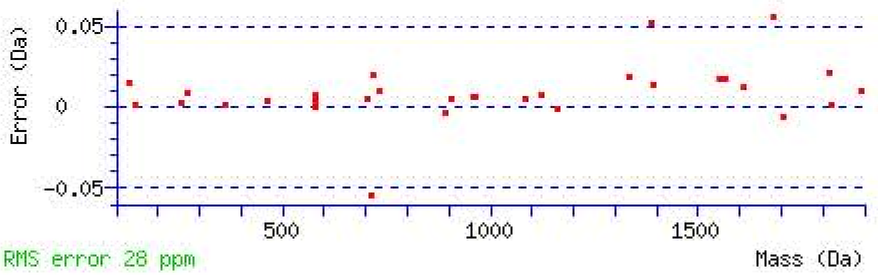
Match to Query 60653: 2299.039152 from(767.353660,3+) rtinseconds(1583) index(57512)
Title: Locus:1.1.1.2857.10 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

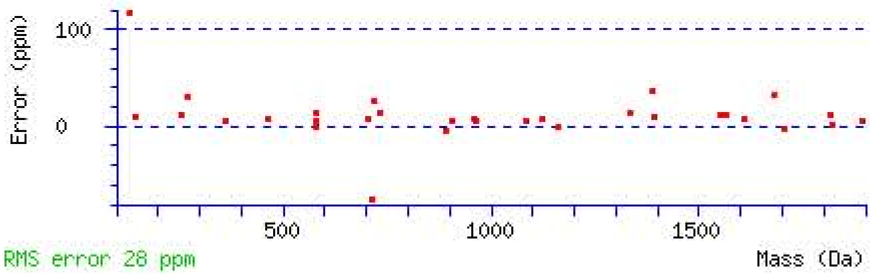
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2299.021790
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 60 **Expect:** 1e-005
Matches : 31/180 fragment ions using 53 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.065854**	65.036565	112.039305	56.523291			Q							17
2	289.096503	145.051890	272.069954	136.538615			C	2171.970466	1086.488871	2154.943917	1077.975596	2153.959901	1077.483588	16
3	388.164917	194.586097	371.138368	186.072822			V	2011.939817	1006.473547	1994.913268	997.960272	1993.929252	997.468264	15
4	485.217681	243.112479	468.191132	234.599204			P	1912.871403	956.939340	1895.844854	948.426065	1894.860838	947.934057	14
5	622.276593	311.641935	605.250044	303.128660			H	***1815.818639***	908.412958	1798.792090	899.899683	1797.808074	899.407675	13
6	737.303536	369.155406	720.276987	360.642132	719.292971	360.150124	D	***1678.759727***	839.883502	1661.733178	831.370227	1660.749162	830.878219	12
7	1176.528862	588.768069	1159.502313	580.254795	1158.518297	579.762786	Q	***1563.732784***	782.370030	1546.706235	773.856756	1545.722219	773.364748	11
8	**1336.559511**	668.783393	1319.532962	660.270119	1318.548946	659.778111	C	***1124.507458***	562.757367	1107.480909	554.244093	1106.496893	553.752085	10
9	1407.596625	704.301950	1390.570076	695.788676	1389.586060	695.296668	A	***964.476809***	482.742043	947.450260	474.228768	946.466244	473.736760	9
10	1567.627274	784.317275	1550.600725	775.804001	1549.616709	775.311992	C	***893.439695***	447.223486	876.413146	438.710211	875.429130	438.218203	8
11	1624.648738	812.828007	1607.622189	804.314732	1606.638173	803.822724	G	***733.409046***	367.208161	716.382497	358.694887	715.398481	358.202879	7
12	1723.717152	862.362214	1706.690603	853.848940	1705.706587	853.356931	V	676.387582	338.697429	659.361033	330.184155	658.377017	329.692147	6
13	1836.801216	918.904246	1819.774667	910.390971	1818.790651	909.898963	L	***577.319168***	289.163222	560.292619	280.649948	559.308603	280.157940	5
14	1937.848895	969.428085	1920.822346	960.914811	1919.838330	960.422803	T	***464.235104***	232.621190	447.208555	224.107916	446.224539	223.615908	4
15	2024.880923	1012.944100	2007.854374	1004.430825	2006.870358	1003.938817	S	***363.187425***	182.097351	346.160876	173.584076	345.176860	173.092068	3
16	2153.923516	1077.465396	2136.896967	1068.952121	2135.912951	1068.460113	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.4	2299.021790	0.017362	QCVPHDQCACGVLTSEK
25.6	2299.021790	0.017362	QCVPHDQCACGVLTSEK

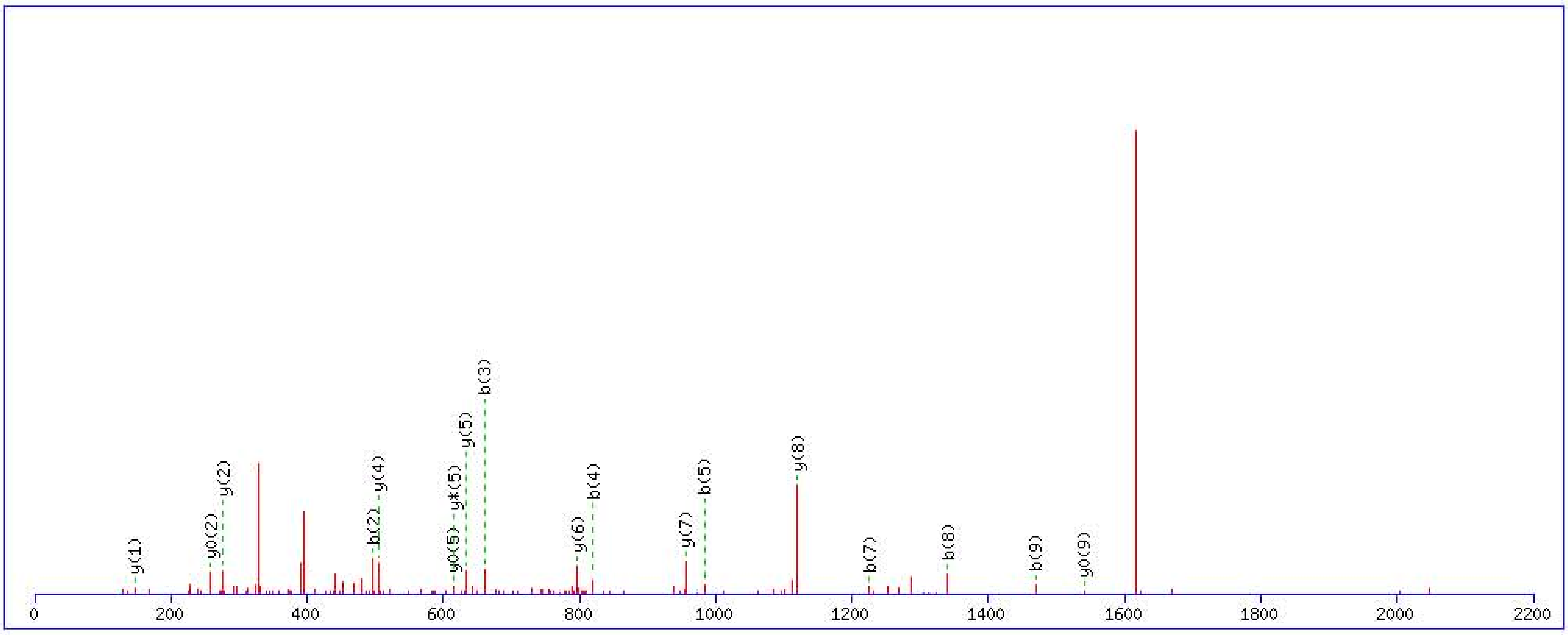
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQYCYELDEK**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

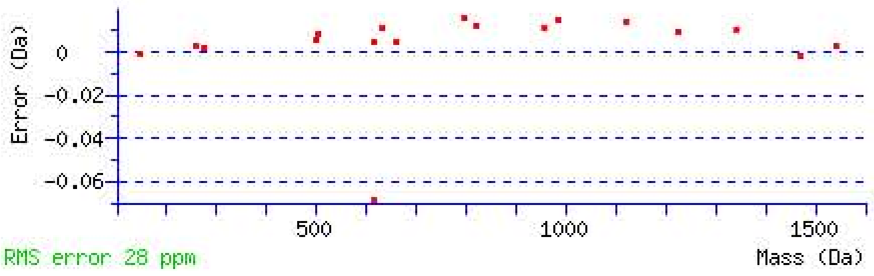
Match to Query 42765: 1614.724568 from(808.369560,2+) rtinseconds(1857) index(59425)
Title: Locus:1.1.1.2952.21 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

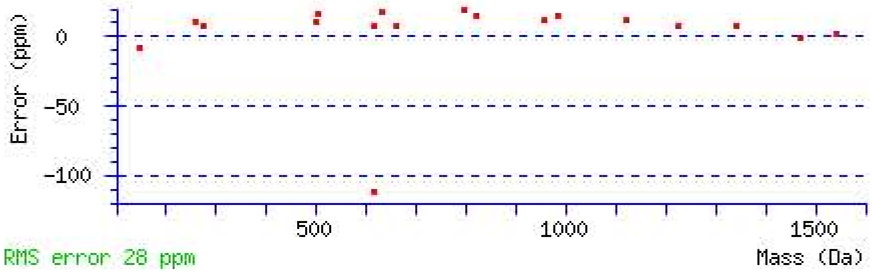
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1614.705795
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 4.6e-005
Matches : 18/94 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							10
2	***497.254066***	249.130671	480.227517	240.617397			Q	1558.691630	779.849453	1541.665081	771.336179	1540.681065	770.844171	9
3	***660.317395***	330.662336	643.290846	322.149061			Y	***1119.466304***	560.236790	1102.439755	551.723516	1101.455739	551.231508	8
4	***820.348044***	410.677660	803.321495	402.164386			C	***956.402975***	478.705126	939.376426	470.191851	938.392410	469.699843	7
5	***983.411373***	492.209325	966.384824	483.696050			Y	***796.372326***	398.689801	779.345777	390.176527	778.361761	389.684519	6
6	1112.453966	556.730621	1095.427417	548.217347	1094.443401	547.725339	E	***633.308997***	317.158137	616.282448	308.644862	615.298432	308.152854	5
7	***1225.538030***	613.272653	1208.511481	604.759379	1207.527465	604.267371	L	***504.266404***	252.636840	487.239855	244.123566	486.255839	243.631558	4
8	***1340.564973***	670.786125	1323.538424	662.272850	1322.554408	661.780842	D	391.182340	196.094808	374.155791	187.581534	373.171775	187.089526	3
9	***1469.607566***	735.307421	1452.581017	726.794147	1451.597001	726.302139	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.0	1614.705795	0.018773	GQYCYELDEK
13.9	1614.748520	-0.023952	TRAPAEEGAEGPSDTK
5.3	1614.717010	0.007558	EYFRMELMHAEK
1.0	1614.748535	-0.023967	VDNSSLTGESEPQPR

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

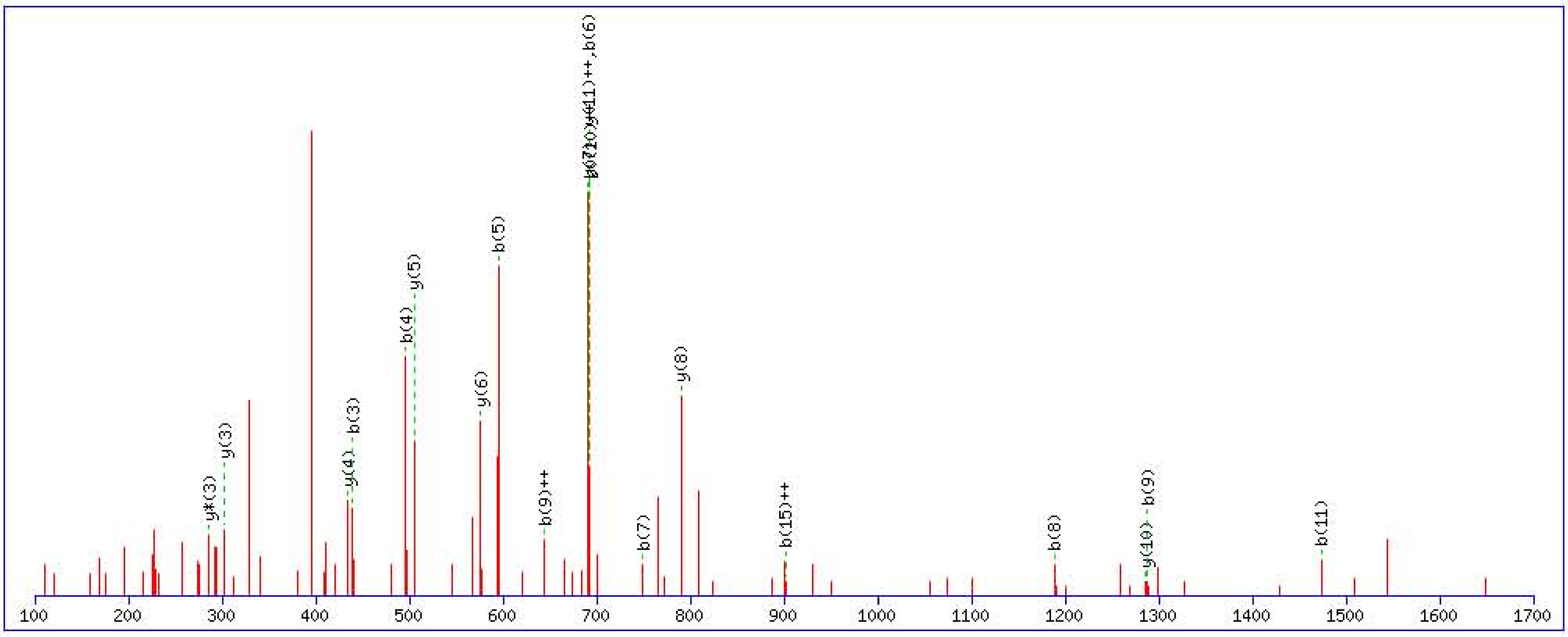
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DWHGVPGQVDAAMAGR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

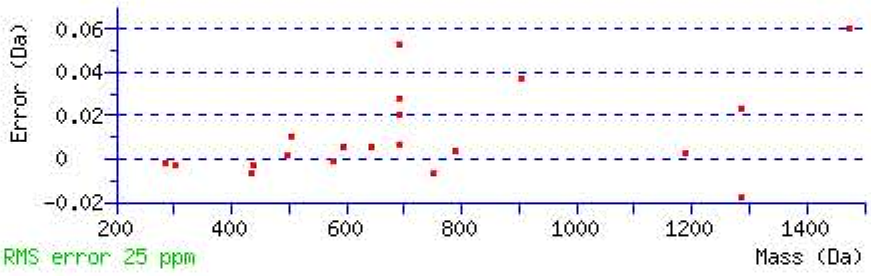
Match to Query 52383: 1976.948952 from(659.990260,3+) rtinseconds(2147) index(43046)
Title: Locus:1.1.1.3031.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

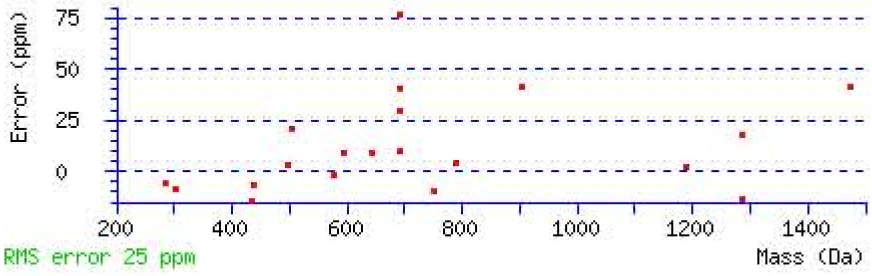
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1976.934937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.0077
Matches : 20/154 fragment ions using 51 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							16
2	302.113532	151.560404			284.102967	142.555122	W	1862.915257	931.961266	1845.888708	923.447992	1844.904692	922.955984	15
3	***439.172444***	220.089860			421.161879	211.084577	H	1676.835944	838.921610	1659.809395	830.408336	1658.825379	829.916327	14
4	***496.193908***	248.600592			478.183343	239.595309	G	1539.777032	770.392154	1522.750483	761.878880	1521.766467	761.386871	13
5	***595.262322***	298.134799			577.251757	289.129517	V	1482.755568	741.881422	1465.729019	733.368148	1464.745003	732.876140	12
6	***692.315086***	346.661181			674.304521	337.655899	P	1383.687154	692.347215	1366.660605	683.833941	1365.676589	683.341932	11
7	***749.336550***	375.171913			731.325985	366.166631	G	***1286.634390***	643.820833	1269.607841	635.307559	1268.623825	634.815550	10
8	***1188.561876***	594.784576	1171.535327	586.271302	1170.551311	585.779293	Q	1229.612926	615.310101	1212.586377	606.796827	1211.602361	606.304819	9
9	***1287.630290***	**644.318783**	1270.603741	635.805509	1269.619725	635.313501	V	***790.387600***	395.697438	773.361051	387.184164	772.377035	386.692156	8
10	1402.657233	701.832255	1385.630684	693.318980	1384.646668	692.826972	D	***691.319186***	346.163231	674.292637	337.649956	673.308621	337.157948	7
11	***1473.694347***	737.350812	1456.667798	728.837537	1455.683782	728.345529	A	***576.292243***	288.649759	559.265694	280.136485			6
12	1544.731461	772.869369	1527.704912	764.356094	1526.720896	763.864086	A	***505.255129***	253.131202	488.228580	244.617928			5
13	1675.771946	838.389611	1658.745397	829.876337	1657.761381	829.384329	M	***434.218015***	217.612645	417.191466	209.099371			4
14	1746.809060	873.908168	1729.782511	865.394894	1728.798495	864.902886	A	***303.177530***	152.092403	286.150981	143.579128			3
15	1803.830524	**902.418900**	1786.803975	893.905626	1785.819959	893.413617	G	232.140416	116.573846	215.113867	108.060571			2
16							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.4	1976.934937	0.014015	DWHGVPGQVDAAMAGR

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

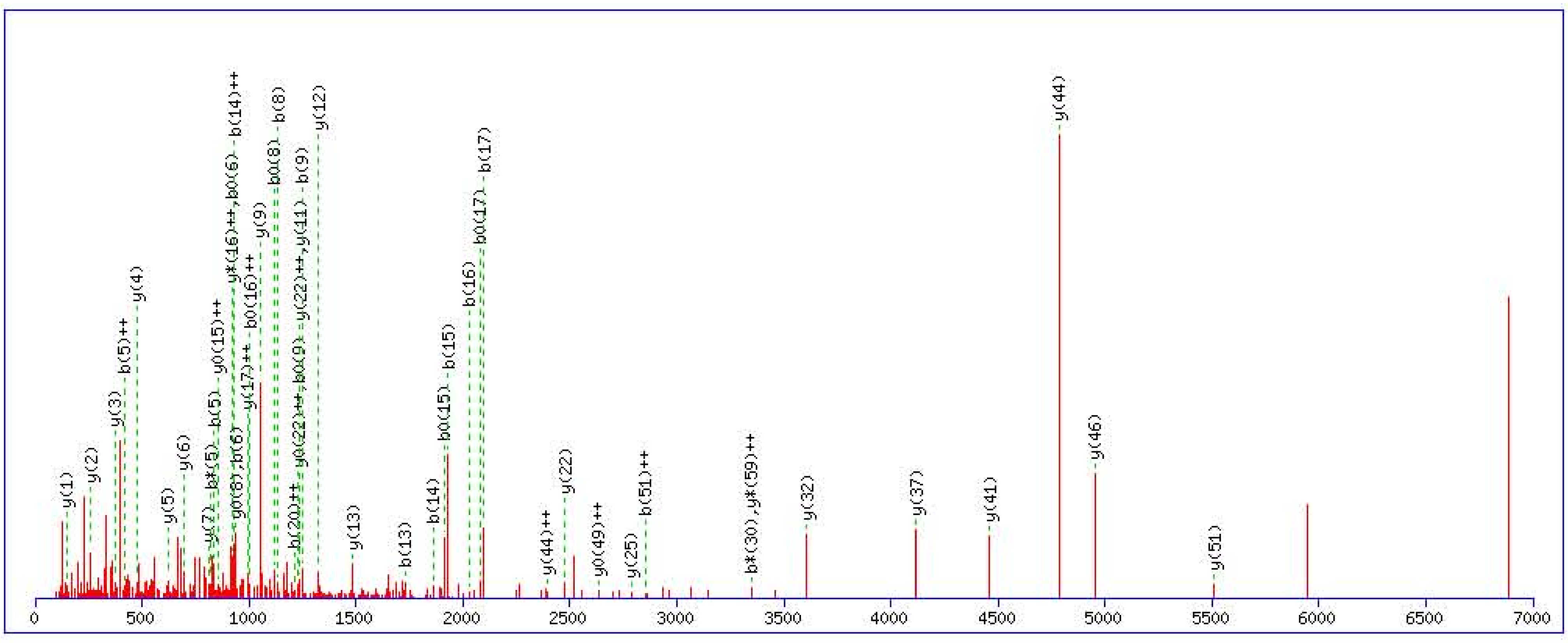
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

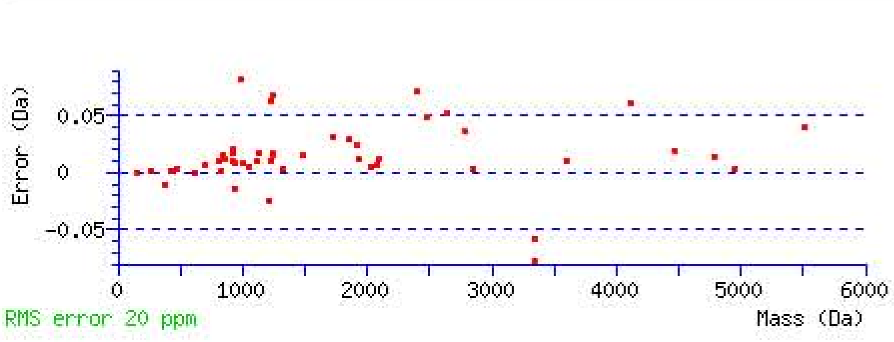
Match to Query 89465: 6883.449392 from(861.438450,8+) rtinseconds(2078) index(42613)
Title: Locus:1.1.1.3007.10 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

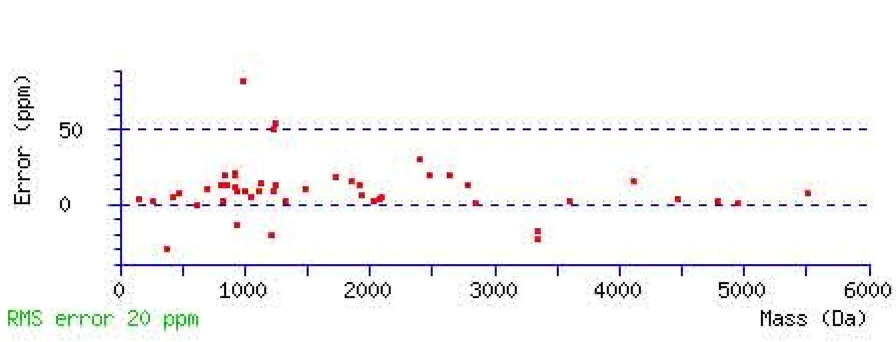
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 7000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 6883.374893
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0051
Matches : 49/708 fragment ions using 149 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							61
2	172.071667	86.539471	155.045118	78.026197			N	6827.360757	3414.184017	6810.334208	3405.670742	6809.350192	3405.178734	60
3	269.124431	135.065854	252.097882	126.552579			P	6713.317830	3357.162553	6696.291281	3348.649279	6695.307265	3348.157271	59
4	398.167024	199.587150	381.140475	191.073876	380.156459	190.581868	E	6616.265066	3308.636171	6599.238517	3300.122897	6598.254501	3299.630889	58
5	***837.392350***	**419.199813**	820.365801	410.686539	819.381785	410.194531	Q	6487.222473	3244.114875	6470.195924	3235.601600	6469.211908	3235.109592	57
6	***938.440029***	469.723653	921.413480	461.210378	920.429464	460.718370	T	6047.997147	3024.502212	6030.970598	3015.988937	6029.986582	3015.496929	56
7	1035.492793	518.250035	1018.466244	509.736760	1017.482228	509.244752	P	5946.949468	2973.978372	5929.922919	2965.465098	5928.938903	2964.973090	55
8	***1134.561207***	567.784242	1117.534658	559.270967	1116.550642	558.778959	V	5849.896704	2925.451990	5832.870155	2916.938716	5831.886139	2916.446708	54
9	***1247.645271***	624.326274	1230.618722	615.812999	1229.634706	615.320991	L	5750.828290	2875.917783	5733.801741	2867.404509	5732.817725	2866.912501	53
10	1375.740234	688.373755	1358.713685	679.860481	1357.729669	679.368473	K	5637.744226	2819.375751	5620.717677	2810.862477	5619.733661	2810.370469	52
11	1472.792998	736.900137	1455.766449	728.386863	1454.782433	727.894855	P	***5509.649263***	2755.328270	5492.622714	2746.814995	5491.638698	2746.322987	51
12	1601.835591	801.421434	1584.809042	792.908159	1583.825026	792.416151	E	5412.596499	2706.801888	5395.569950	2698.288613	5394.585934	2697.796605	50
13	***1730.878184***	865.942730	1713.851635	857.429456	1712.867619	856.937448	E	5283.553906	2642.280591	5266.527357	2633.767317	5265.543341	2633.275309	49
14	***1859.920777***	**930.464027**	1842.894228	921.950752	1841.910212	921.458744	E	5154.511313	2577.759295	5137.484764	2569.246020	5136.500748	2568.754012	48
15	***1930.957891***	965.982584	1913.931342	957.469309	1912.947326	956.977301	A	5025.468720	2513.237998	5008.442171	2504.724724	5007.458155	2504.232716	47
16	***2028.010655***	1014.508966	2010.984106	1005.995691	2010.000090	1005.503683	P	***4954.431606***	2477.719441	4937.405057	2469.206167	4936.421041	2468.714159	46
17	***2099.047769***	1050.027523	2082.021220	1041.514248	2081.037204	1041.022240	A	4857.378842	2429.193059	4840.352293	2420.679785	4839.368277	2420.187777	45
18	2196.100533	1098.553905	2179.073984	1090.040630	2178.089968	1089.548622	P	***4786.341728***	2393.674502	4769.315179	2385.161228	4768.331163	2384.669220	44
19	2325.143126	1163.075201	2308.116577	1154.561927	2307.132561	1154.069919	E	4689.288964	2345.148120	4672.262415	2336.634846	4671.278399	2336.142838	43
20	2424.211540	**1212.609408**	2407.184991	1204.096134	2406.200975	1203.604126	V	4560.246371	2280.626824	4543.219822	2272.113549	4542.235806	2271.621541	42
21	2481.233004	1241.120140	2464.206455	1232.606865	2463.222439	1232.114858	G	***4461.177957***	2231.092617	4444.151408	2222.579342	4443.167392	2222.087334	41
22	2552.270118	1276.638697	2535.243569	1268.125423	2534.259553	1267.633415	A	4404.156493	2202.581885	4387.129944	2194.068610	4386.145928	2193.576602	40
23	2639.302146	1320.154711	2622.275597	1311.641437	2621.291581	1311.149429	S	4333.119379	2167.063328	4316.092830	2158.550053	4315.108814	2158.058045	39
24	2767.397109	1384.202193	2750.370560	1375.688918	2749.386544	1375.196910	K	4246.087351	2123.547314	4229.060802	2115.034039	4228.076786	2114.542031	38
25	2864.449873	1432.728575	2847.423324	1424.215300	2846.439308	1423.723292	P	***4117.992388***	2059.499832	4100.965839	2050.986558	4099.981823	2050.494550	37
26	2993.492466	1497.249871	2976.465917	1488.736597	2975.481901	1488.244589	E	4020.939624	2010.973450	4003.913075	2002.460176	4002.929059	2001.968168	36
27	3050.513930	1525.760603	3033.487381	1517.247329	3032.503365	1516.755321	G	3891.897031	1946.452154	3874.870482	1937.938879	3873.886466	1937.446871	35
28	3163.597994	1582.302635	3146.571445	1573.789361	3145.587429	1573.297353	I	3834.875567	1917.941422	3817.849018	1909.428147	3816.865002	1908.936139	34
29	3278.624937	1639.816107	3261.598388	1631.302832	3260.614372	1630.810824	D	3721.791503	1861.399390	3704.764954	1852.886115	3703.780938	1852.394107	33
30	3365.656965	1683.332121	3348.630416	1674.818846	3347.646400	1674.326838	S	***3606.764560***	1803.885918	3589.738011	1795.372644	3588.753995	1794.880636	32
31	3521.758076	1761.382676	3504.731527	1752.869402	3503.747511	1752.377394	R	3519.732532	1760.369904	3502.705983	1751.856630	3501.721967	1751.364622	31
32	3618.810840	1809.909058	3601.784291	1801.395784	3600.800275	1800.903776	P	3363.631421	1682.319349	3346.604872	1673.806074	3345.620856	1673.314066	30
33	3747.853433	1874.430355	3730.826884	1865.917080	3729.842868	1865.425072	E	3266.578657	1633.792967	3249.552108	1625.279692	3248.568092	1624.787684	29
34	3848.901112	1924.954194	3831.874563	1916.440920	3830.890547	1915.948912	T	3137.536064	1569.271670	3120.509515	1560.758396	3119.525499	1560.266388	28
35	3961.985176	1981.496226	3944.958627	1972.982952	3943.974611	1972.490944	L	3036.488385	1518.747831	3019.461836	1510.234556	3018.477820	1509.742548	27
36	4099.044088	2050.025682	4082.017539	2041.512408	4081.033523	2041.020400	H	2923.404321	1462.205799	2906.377772	1453.692524	2905.393756	1453.200516	26
37	4196.096852	2098.552064	4179.070303	2090.038790	4178.086287	2089.546782	P	***2786.345409***	1393.676343	2769.318860	1385.163068	2768.334844	1384.671060	25
38	4253.118316	2127.062796	4236.091767	2118.549522	4235.107751	2118.057514	G	2689.292645	1345.149961	2672.266096	1336.636686	2671.282080	1336.144678	24
39	4409.219427	2205.113352	4392.192878	2196.600077	4391.208862	2196.108069	R	2632.271181	1316.639229	2615.244632	1308.125954	2614.260616	1307.633946	23
40	4506.272191	2253.639734	4489.245642	2245.126459	4488.261626	2244.634451	P	***2476.170070***	1238.588673	2459.143521	1230.075399	2458.159505	1229.583391	22
41	4634.330769	2317.669023	4617.304220	2309.155748	4616.320204	2308.663740	Q	2379.117306	1190.062291	2362.090757	1181.549017	2361.106741	1181.057009	21
42	4731.383533	2366.195405	4714.356984	2357.682130	4713.372968	2357.190122	P	2251.058728	1126.033002	2234.032179	1117.519728	2233.048163	1117.027720	20
43	4828.436297	2414.721787	4811.409748	2406.208512	4810.425732	2405.716504	P	2154.005964	1077.506620	2136.979415	1068.993346	2135.995399	1068.501338	19
44	4899.473411	2450.240344	4882.446862	2441.727069	4881.462846	2441.235061	A	2056.953200	1028.980238	2039.926651	1020.466964	2038.942635	1019.974956	18
45	5028.516004	2514.761640	5011.489455	2506.248366	5010.505439	2505.756358	E	1985.916086	993.461681	1968.889537	984.948407	1967.905521	984.456399	17
46	5157.558597	2579.282937	5140.532048	2570.769662	5139.548032	2570.277654	E	1856.873493	928.940385	1839.846944	920.427110	1838.862928	919.935102	16
47	5286.601190	2643.804233	5269.574641	2635.290959	5268.590625	2634.798951	E	1727.830900	864.419088	1710.804351	855.905814	1709.820335	855.413806	15
48	5399.685254	2700.346265	5382.658705	2691.832991	5381.674689	2691.340983	L	1598.788307	799.897792	1581.761758	791.384517	1580.777742	790.892509	14
49	5559.715903	2780.361590	5542.689354	2771.848315	5541.705338	2771.356307	C	***1485.704243***	743.355760	1468.677694	734.842485	1467.693678	734.350477	13
50	5646.747931	2823.877604	5629.721382	2815.364329	5628.737366	2814.872321	S	***1325.673594***	663.340435	1308.647045	654.827161	1307.663029	654.335153	12
51	5703.769395	**2852.388336**	5686.742846	2843.875061	5685.758830	2843.383053	G	***1238.641566***	619.824421	1221.615017	611.311147	1220.631001	610.819139	11
52	5831.864358	2916.435817	5814.837809	2907.922543	5813.853793	2907.430535	K	1181.620102	591.313689	1164.593553	582.800415	1163.609537	582.308407	10
53	5928.917122	2964.962199	5911.890573	2956.448925	5910.906557	2955.956917	P	***1053.525139***	527.266208	1036.498590	518.752933	1035.514574	518.260925	9
54	6075.985536	3038.496406	6058.958987	3029.983132	6057.974971	3029.491124	F	956.472375	478.739826	939.445826	470.226551	938.461810	469.734543	8
55	6191.012479	3096.009878	6173.985930	3087.496603	6173.001914	3087.004595	D	***809.403961***	405.205619	792.377412	396.692344	791.393396	396.200336	7
56	6262.049593	3131.528435	6245.023044	3123.015160	6244.039028	3122.523152	A	***694.377018***	347.692147	677.350469	339.178873	676.366453	338.686865	6
57	6409.118007	3205.062642	6392.091458	3196.549367	6391.107442	3196.057359	F	***623.339904***	312.173590	606.313355	303.660316	605.329339	303.168308	5
58	6510.165686	3255.586481	6493.139137	3247.073207	6492.155121	3246.581199	T	***476.271490***	238.639383	459.244941	230.126109	458.260925	229.634101	4
59	6625.192629	3313.099953	6608.166080	3304.586678	6607.182064	3304.094670	D	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
60	6738.276693	3369.641985	6721.250144	3361.128710	6720.266128	3360.636702	L	***260.196868***	130.602072	243.170319	122.088798			2
61							K	***147.112804***	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.5	6883.374893	0.074499	GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK

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

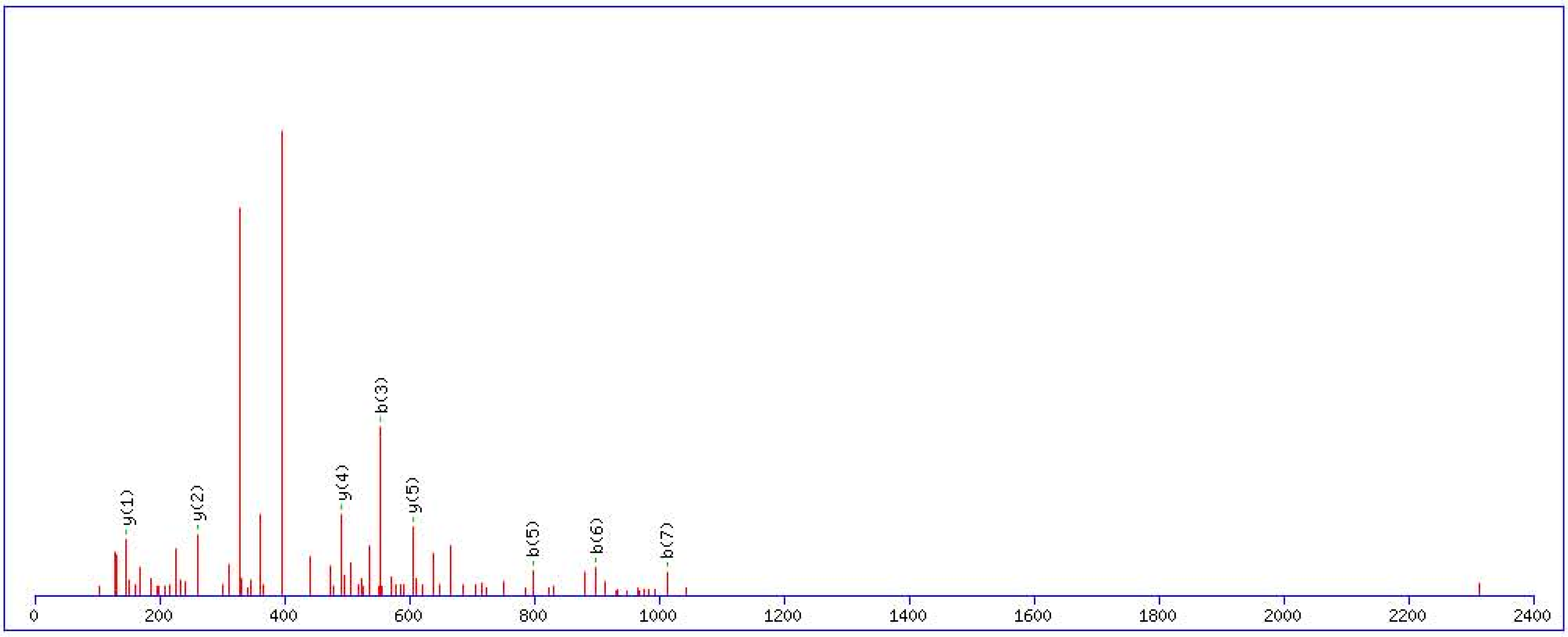
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGQIMTLK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

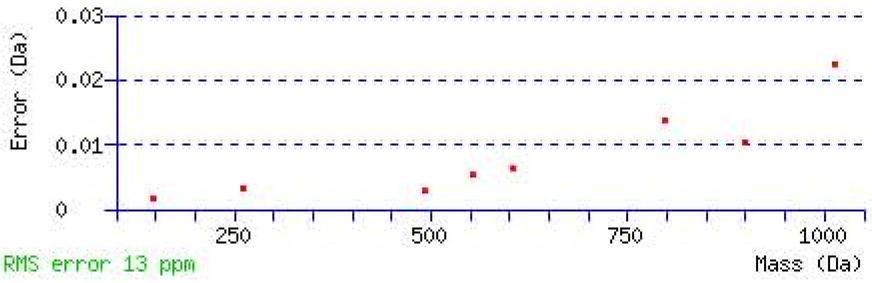
Match to Query 25993: 1157.632688 from(579.823620,2+) rtinseconds(1888) index(41306)
Title: Locus:1.1.1.2941.15 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

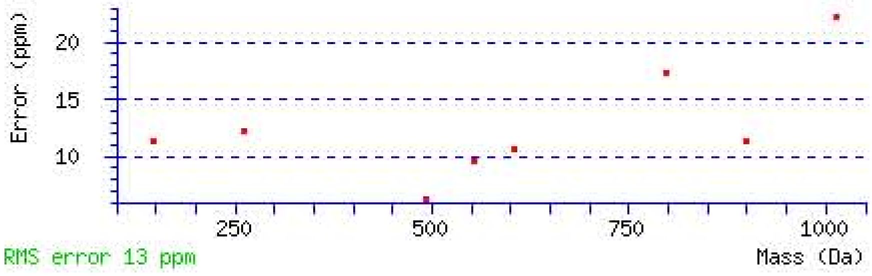
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1157.630066
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.015
Matches : 8/66 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	58.028740	29.518008					G							8
2	115.050204	58.028740					G	1101.615886	551.311581	1084.589337	542.798307	1083.605321	542.306299	7
3	***554.275530***	277.641403	537.248981	269.128129			Q	1044.594422	522.800849	1027.567873	514.287575	1026.583857	513.795567	6
4	667.359594	334.183435	650.333045	325.670161			I	***605.369096***	303.188186	588.342547	294.674912	587.358531	294.182904	5
5	***798.400079***	399.703678	781.373530	391.190403			M	***492.285032***	246.646154	475.258483	238.132880	474.274467	237.640872	4
6	***899.447758***	450.227517	882.421209	441.714243	881.437193	441.222235	T	361.244547	181.125912	344.217998	172.612637	343.233982	172.120629	3
7	***1012.531822***	506.769549	995.505273	498.256275	994.521257	497.764267	L	***260.196868***	130.602072	243.170319	122.088798			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.0	1157.630066	0.002622	GGQIMTLK
13.1	1157.647827	-0.015139	ALVGGTAPMTIK
12.8	1157.640411	-0.007723	AQQLLSSGNLK
12.6	1157.630051	0.002637	QLSQMLK
10.4	1157.647827	-0.015139	IMVPINGSVTK
9.0	1157.640411	-0.007723	SPGKNSSIQLK
7.0	1157.619293	0.013395	TNFEGPPRLK
5.9	1157.630081	0.002607	CVTLVQK
5.9	1157.629196	0.003492	VTGKPDAETLK
5.6	1157.630051	0.002637	MLQTNLK

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

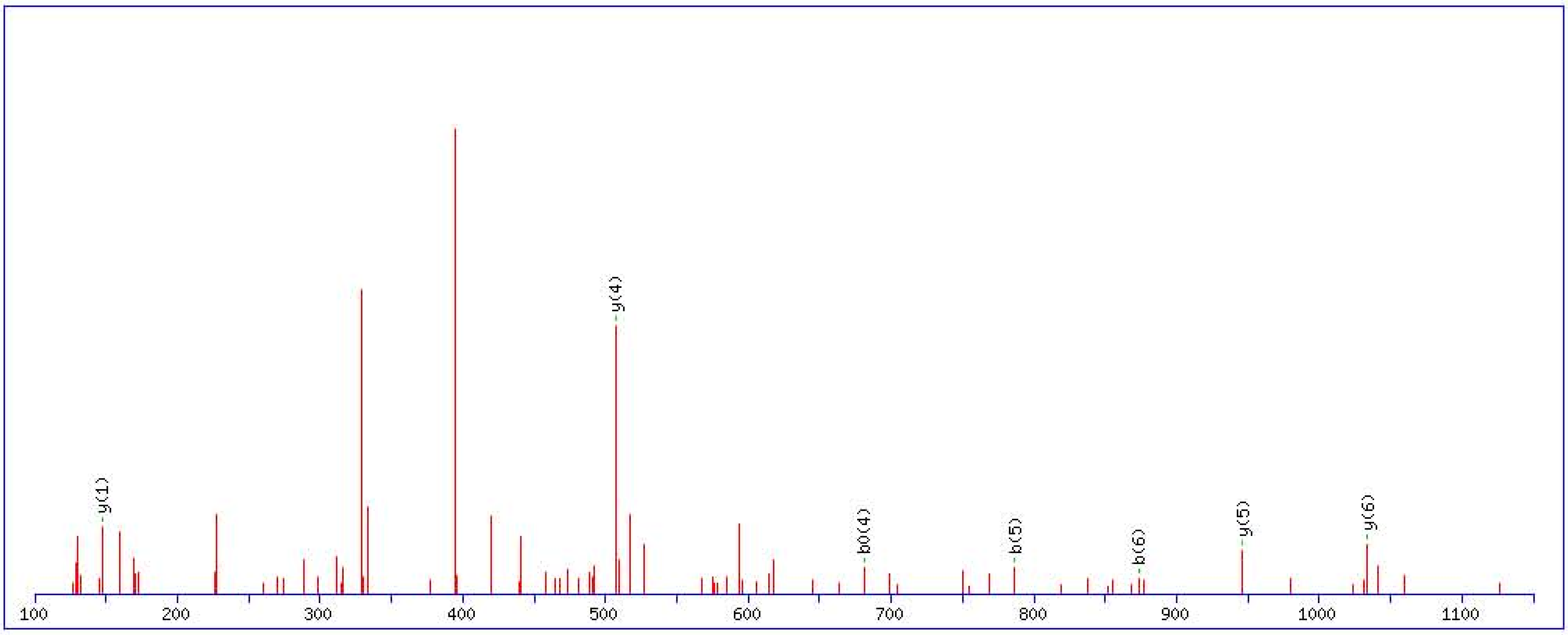
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDSQSSWK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

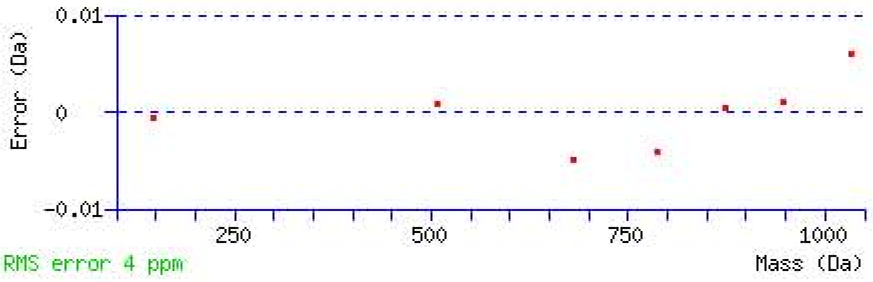
Match to Query 27798: 1204.556168 from(603.285360,2+) rtinseconds(1521) index(39013)
Title: Locus:1.1.1.2813.18 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●

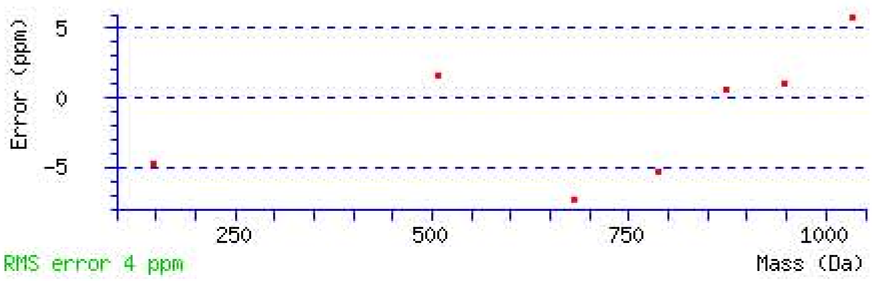


```
Monoisotopic mass of neutral peptide Mr(calc): 1204.554657
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.011
Matches : 7/72 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							8
2	173.055683	87.031479			155.045118	78.026197	D	1148.540470	574.773873	1131.513921	566.260599	1130.529905	565.768591	7
3	260.087711	130.547493			242.077146	121.542211	S	***1033.513527***	517.260402	1016.486978	508.747127	1015.502962	508.255119	6
4	699.313037	350.160157	682.286488	341.646882	681.302472	341.154874	Q	***946.481499***	473.744388	929.454950	465.231113	928.470934	464.739105	5
5	***786.345065***	393.676171	769.318516	385.162896	768.334500	384.670888	S	***507.256173***	254.131724	490.229624	245.618450	489.245608	245.126442	4
6	***873.377093***	437.192185	856.350544	428.678910	855.366528	428.186902	S	420.224145	210.615711	403.197596	202.102436	402.213580	201.610428	3
7	1059.456406	530.231841	1042.429857	521.718567	1041.445841	521.226559	W	333.192117	167.099697	316.165568	158.586422			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 4 ppm



RMS error 4 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.4	1204.554657	0.001511	GDSQSSWK
7.3	1204.540253	0.015915	QMQECAK
3.6	1204.565872	-0.009704	QAKQACDAWK
2.4	1204.540253	0.015915	QMQECAK

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

{MATRIX SCIENCE}

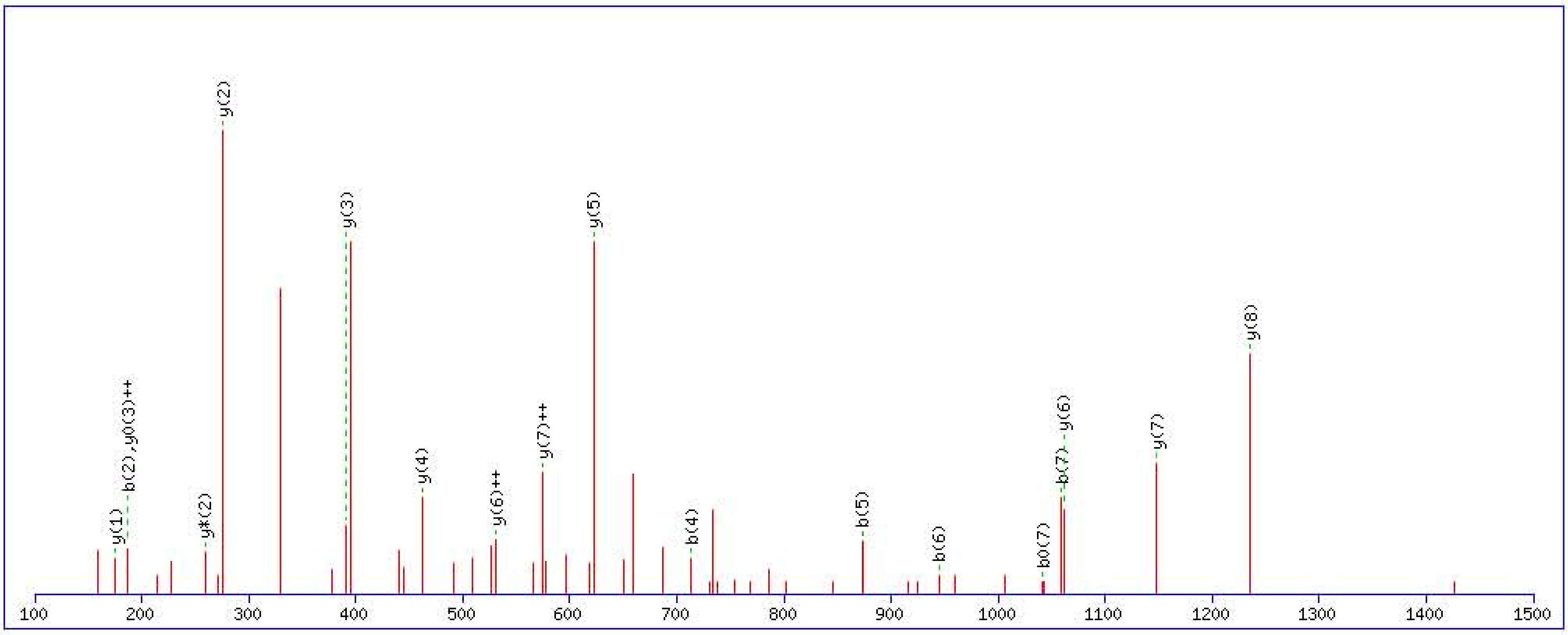
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSQCADTR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

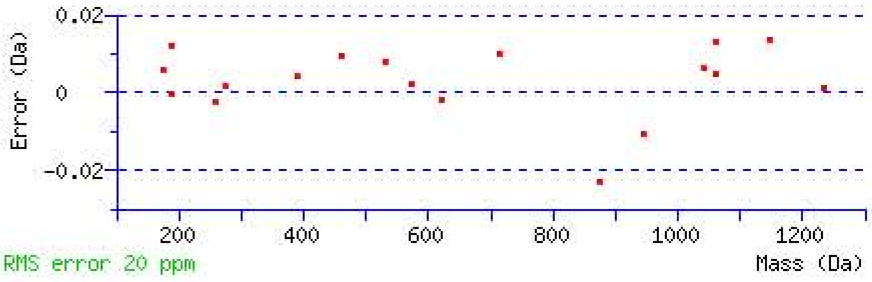
Match to Query 31611: 1333.616868 from(667.815710,2+) rtinseconds(1223) index(36953)
Title: Locus:1.1.1.2709.21 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

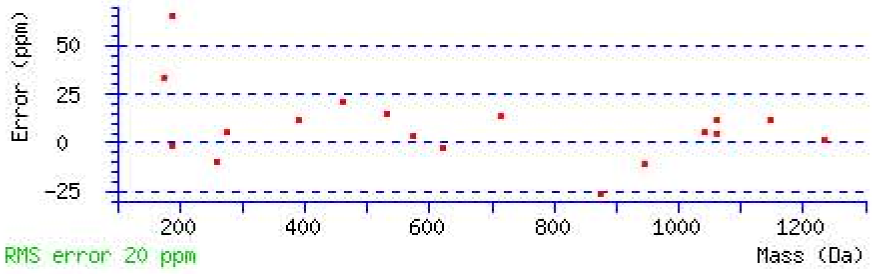
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1333.611862
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 6.5e-005
Matches : 18/86 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							9
2	**187.107718**	94.057497			169.097153	85.052214	S	***1235.550719***	618.278998	1218.524170	609.765723	1217.540154	609.273715	8
3	274.139746	137.573511			256.129181	128.568229	S	***1148.518691***	574.762984	1131.492142	566.249709	1130.508126	565.757701	7
4	**713.365072**	357.186174	696.338523	348.672900	695.354507	348.180892	Q	***1061.486663***	531.246970	1044.460114	522.733695	1043.476098	522.241687	6
5	**873.395721**	437.201499	856.369172	428.688224	855.385156	428.196216	C	***622.261337***	311.634307	605.234788	303.121032	604.250772	302.629024	5
6	**944.432835**	472.720056	927.406286	464.206781	926.422270	463.714773	A	***462.230688***	231.618982	445.204139	223.105707	444.220123	222.613700	4
7	**1059.459778**	530.233527	1042.433229	521.720253	1041.449213	521.228245	D	***391.193574***	196.100425	374.167025	187.587151	373.183009	187.095143	3
8	1160.507457	580.757367	1143.480908	572.244092	1142.496892	571.752084	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.5	1333.611862	0.005006	VSSQCADTR
8.3	1333.633606	-0.016738	LIYNTHMADEK
4.2	1333.607117	0.009751	GEIEIESDAPMK
3.4	1333.615005	0.001863	DVQNFPAATDEK
2.5	1333.601105	0.015763	VDNRPDGFGDSR

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

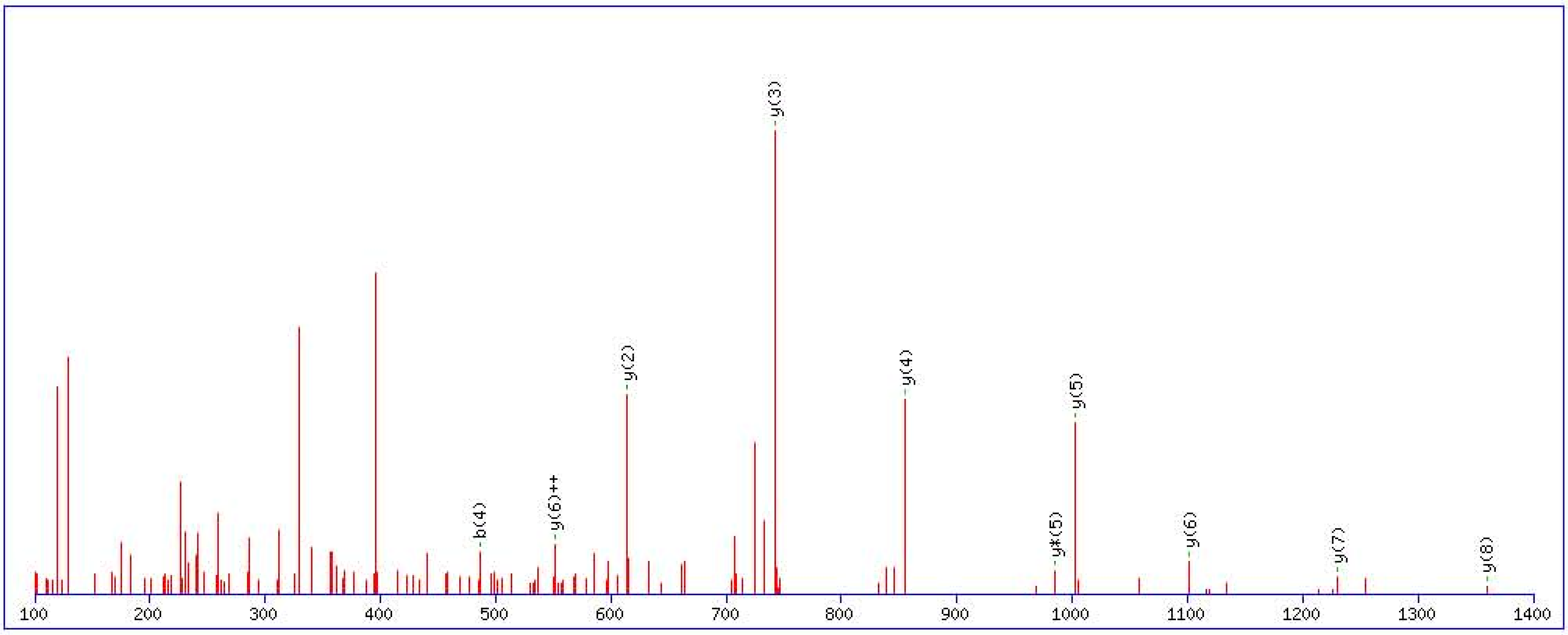
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VKEEVFIQQR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

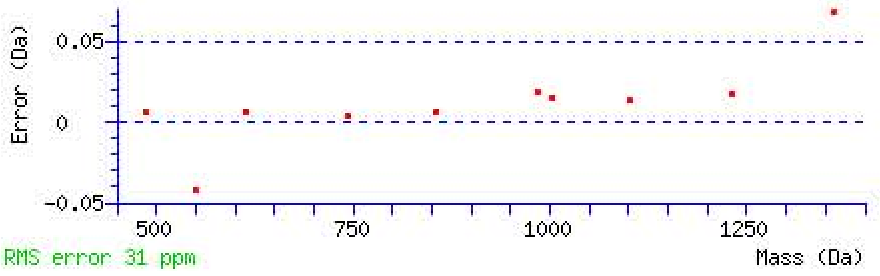
Match to Query 41492: 1585.874262 from(529.632030,3+) rtinseconds(1741) index(58656)
Title: Locus:1.1.1.2912.8 File:"2013-07-02 CLN FXIII 60 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

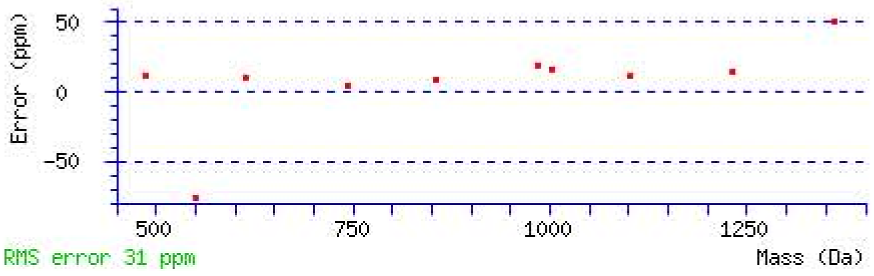
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1585.865021
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 2.4e-005
Matches : 10/90 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							10
2	228.170653	114.588965	211.144104	106.075690			K	1487.803897	744.405587	1470.777348	735.892312	1469.793332	735.400304	9
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	E	***1359.708934***	680.358105	1342.682385	671.844831	1341.698369	671.352823	8
4	**486.255839**	243.631558	469.229290	235.118283	468.245274	234.626275	E	***1230.666341***	615.836809	1213.639792	607.323534	1212.655776	606.831526	7
5	585.324253	293.165765	568.297704	284.652490	567.313688	284.160482	V	***1101.623748***	551.315512	1084.597199	542.802238			6
6	732.392667	366.699972	715.366118	358.186697	714.382102	357.694689	F	***1002.555334***	501.781305	985.528785	493.268031			5
7	845.476731	423.242004	828.450182	414.728729	827.466166	414.236721	I	***855.486920***	428.247098	838.460371	419.733824			4
8	973.535309	487.271293	956.508760	478.758018	955.524744	478.266010	Q	***742.402856***	371.705066	725.376307	363.191792			3
9	1412.760635	706.883956	1395.734086	698.370681	1394.750070	697.878673	Q	***614.344278***	307.675777	597.317729	299.162503			2
10							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.5	1585.865021	0.009241	VKEEVFIQQR
38.6	1585.865021	0.009241	VKEEVFIQQR
4.0	1585.857605	0.016657	QEEVAGIRAKFPNK
2.0	1585.893524	-0.019262	QDLIKSLAMLK

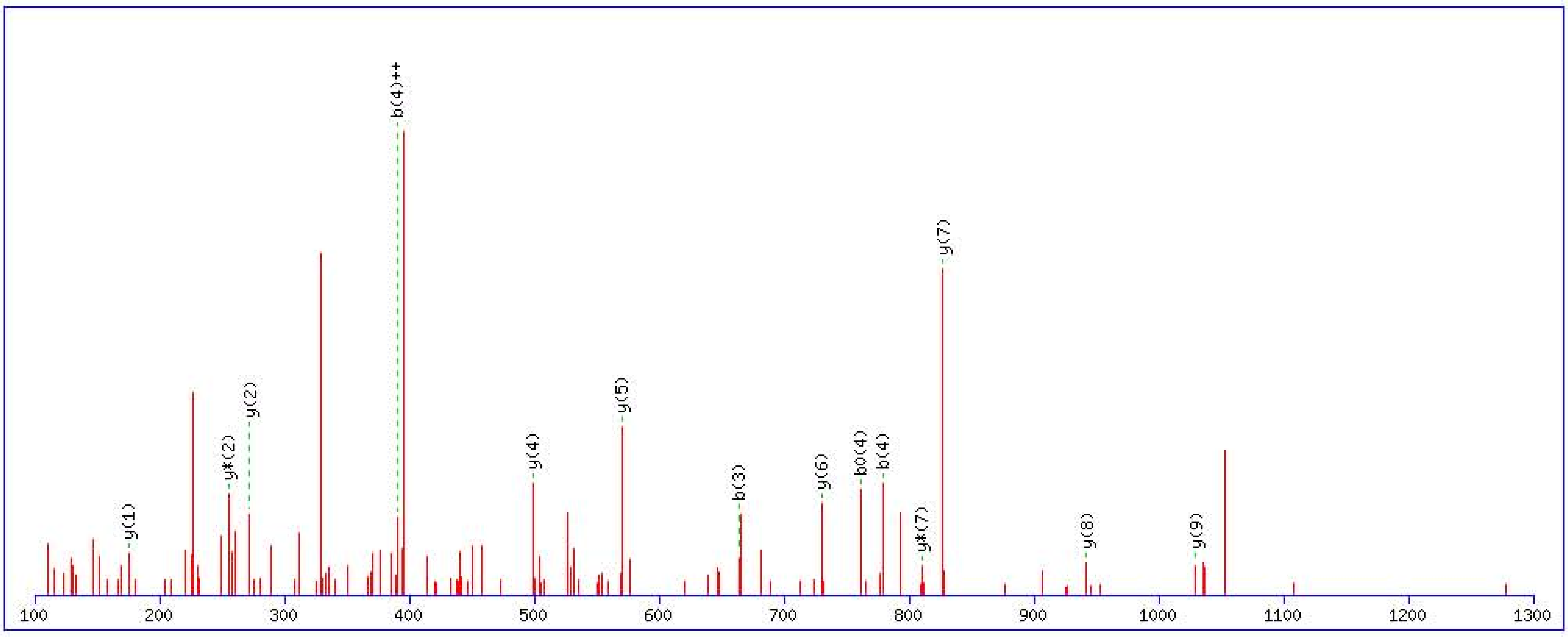
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QHSDPCALNPR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

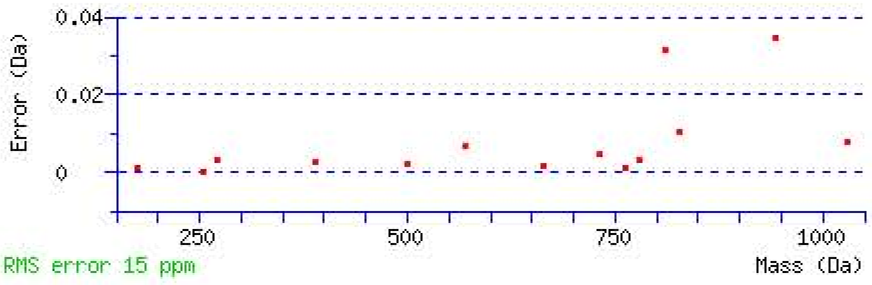
Match to Query 42313: 1604.754072 from(535.925300,3+) rtinseconds(1383) index(37970)
Title: Locus:1.1.1.2765.12 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

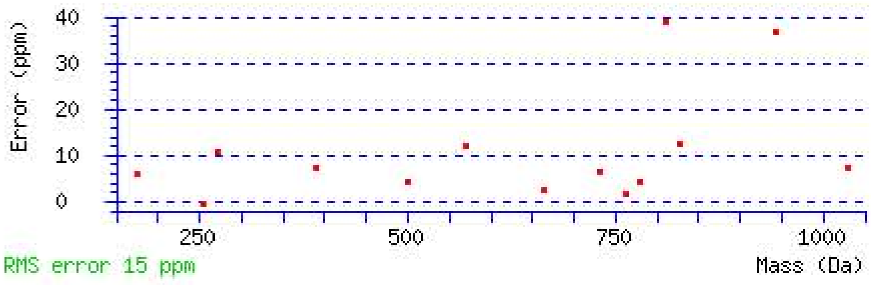
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1604.755157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0013
Matches : 14/102 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							11
2	577.291514	289.149395	560.264965	280.636121			H	1166.537117	583.772196	1149.510568	575.258922	1148.526552	574.766914	10
3	**664.323542**	332.665409	647.296993	324.152134	646.312977	323.660126	S	***1029.478205***	515.242740	1012.451656	506.729466	1011.467640	506.237458	9
4	**779.350485**	390.178880	762.323936	381.665606	761.339920	381.173598	D	***942.446177***	471.726726	925.419628	463.213452	924.435612	462.721444	8
5	876.403249	438.705263	859.376700	430.191988	858.392684	429.699980	P	***827.419234***	414.213255	810.392685	405.699980			7
6	1036.433898	518.720587	1019.407349	510.207313	1018.423333	509.715305	C	***730.366470***	365.686873	713.339921	357.173598			6
7	1107.471012	554.239144	1090.444463	545.725870	1089.460447	545.233861	A	***570.335821***	285.671548	553.309272	277.158274			5
8	1220.555076	610.781176	1203.528527	602.267901	1202.544511	601.775893	L	***499.298707***	250.152991	482.272158	241.639717			4
9	1334.598003	667.802639	1317.571454	659.289365	1316.587438	658.797357	N	386.214643	193.610959	369.188094	185.097685			3
10	1431.650767	716.329021	1414.624218	707.815747	1413.640202	707.323739	P	***272.171716***	136.589496	255.145167	128.076221			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.5	1604.755157	-0.001085	QHSDPCALNPR
6.3	1604.743912	0.010160	QMIMKDKNWHDK
4.8	1604.736725	0.017347	EGMGWSYLVFCLK
4.7	1604.772247	-0.018175	TDDIPVWDQEFLK
3.2	1604.771530	-0.017458	LTNELKEEQEMNK
2.9	1604.747070	0.007002	NGYAEFPPSPSNPTK
2.7	1604.765030	-0.010958	KEASPPSNKLCCSK
2.3	1604.757828	-0.003756	AEKTFSVYEIMCK
1.6	1604.761200	-0.007128	QCDLEIMEIK
0.9	1604.769043	-0.014971	KEIMYYQQALMR

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

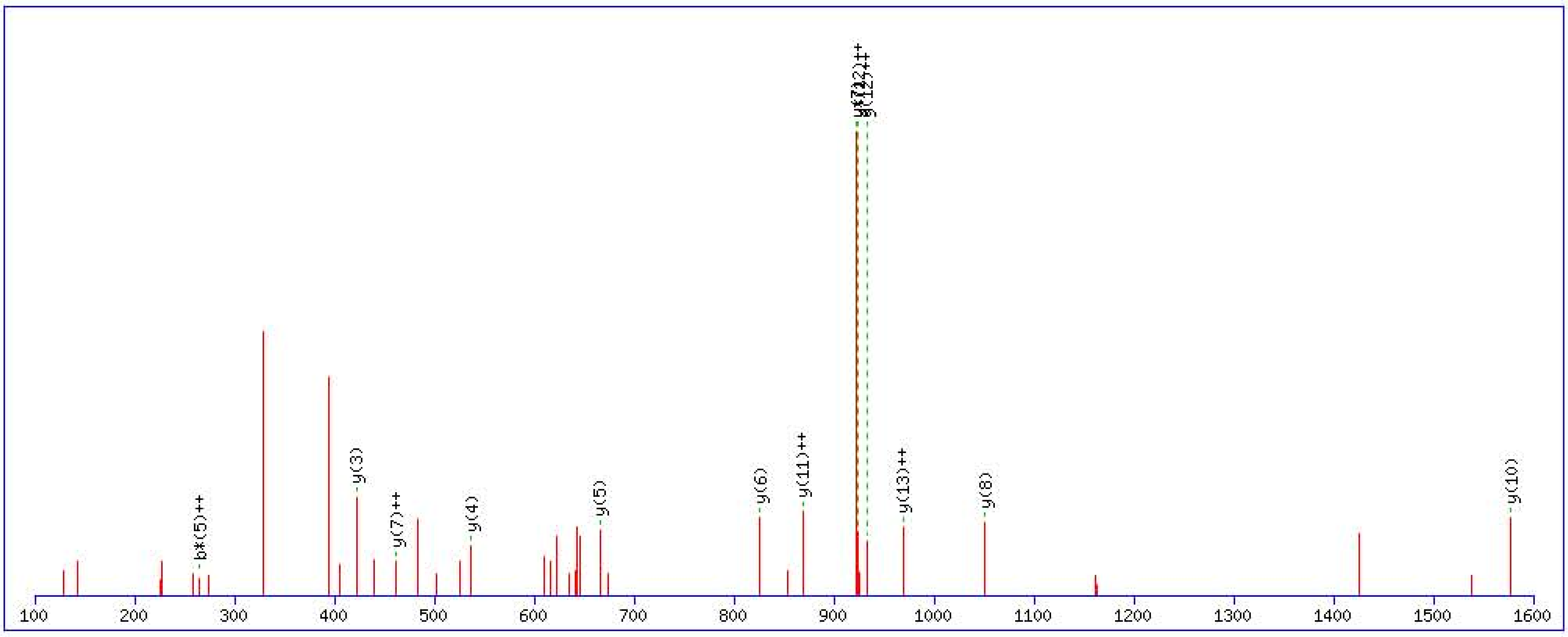
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAQCSQKPCEDSCR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

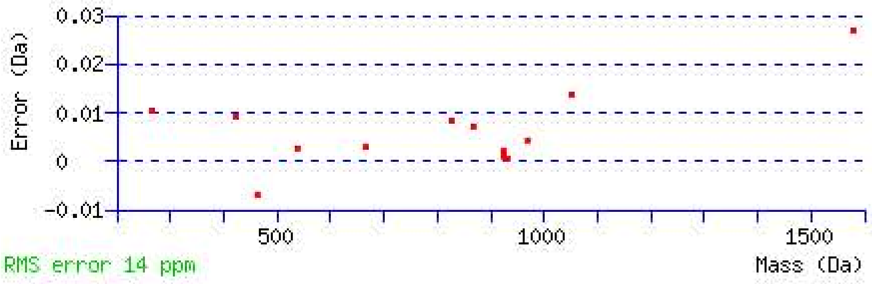
Match to Query 54585: 2034.881172 from(679.301000,3+) rtinseconds(1140) index(36435)
Title: Locus:1.1.1.2680.23 File:"2013-07-02 CLN FXIII 60 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

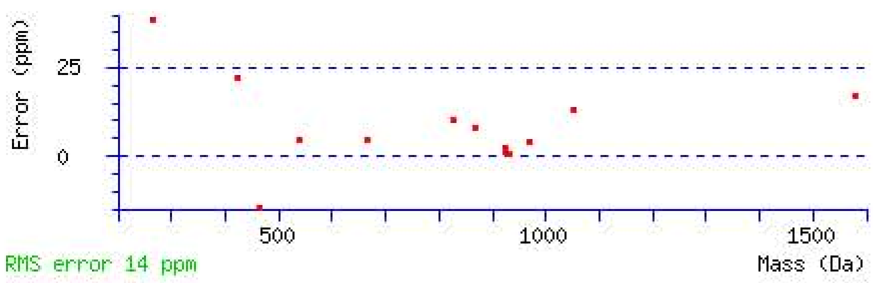
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2034.874374
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.0051
Matches : 13/140 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							14
2	171.112804	86.060040					A	1936.813236	968.910256	1919.786687	960.396982	1918.802671	959.904973	13
3	299.171382	150.089329	282.144833	141.576055			Q	1865.776122	933.391699	1848.749573	924.878425	1847.765557	924.386417	12
4	459.202031	230.104653	442.175482	221.591379			C	1737.717544	869.362410	1720.690995	860.849136	1719.706979	860.357128	11
5	546.234059	273.620668	529.207510	265.107393	528.223494	264.615385	S	***1577.686895***	789.347086	1560.660346	780.833811	1559.676330	780.341803	10
6	985.459385	493.233331	968.432836	484.720056	967.448820	484.228048	Q	1490.654867	745.831072	1473.628318	737.317797	1472.644302	736.825789	9
7	1113.554348	557.280812	1096.527799	548.767538	1095.543783	548.275529	K	***1051.429541***	526.218409	1034.402992	517.705134	1033.418976	517.213126	8
8	1210.607112	605.807194	1193.580563	597.293920	1192.596547	596.801911	P	***923.334578***	462.170927	906.308029	453.657653	905.324013	453.165645	7
9	1370.637761	685.822519	1353.611212	677.309244	1352.627196	676.817236	C	***826.281814***	413.644545	809.255265	405.131271	808.271249	404.639263	6
10	1499.680354	750.343815	1482.653805	741.830540	1481.669789	741.338532	E	***666.251165***	333.629221	649.224616	325.115946	648.240600	324.623938	5
11	1614.707297	807.857286	1597.680748	799.344012	1596.696732	798.852004	D	***537.208572***	269.107924	520.182023	260.594650	519.198007	260.102642	4
12	1701.739325	851.373301	1684.712776	842.860026	1683.728760	842.368018	S	***422.181629***	211.594453	405.155080	203.081178	404.171064	202.589170	3
13	1861.769974	931.388625	1844.743425	922.875351	1843.759409	922.383343	C	335.149601	168.078438	318.123052	159.565164			2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.4	2034.874374	0.006798	VAQCSQKPCEDSCR
26.1	2034.874374	0.006798	VAQCSQKPCEDSCR

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

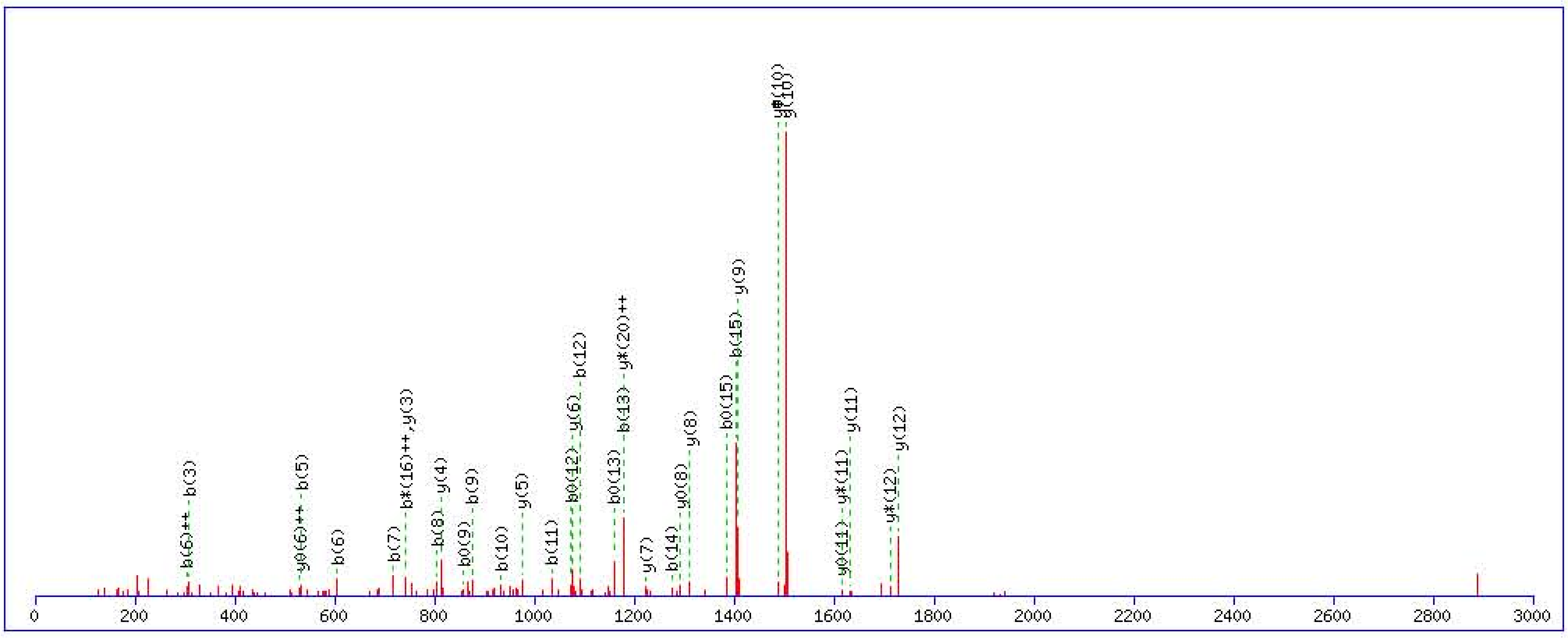
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGHPEALSAGTGSPQPPSFTYAQQR**
Found in **ZYX_HUMAN**, Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1

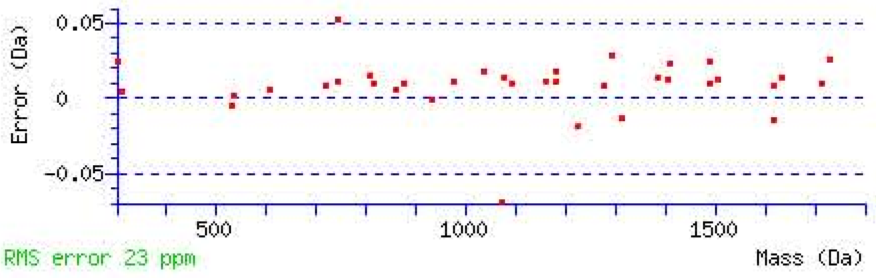
Match to Query 70642: 2907.473352 from(970.165060,3+) rtinseconds(1983) index(6907)
Title: Locus:1.1.1.2822.14 File:"2013-07-02 CLN FXIII 60 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\4 FXIII 60 min 1st\mascot_daemon_merge.mgf

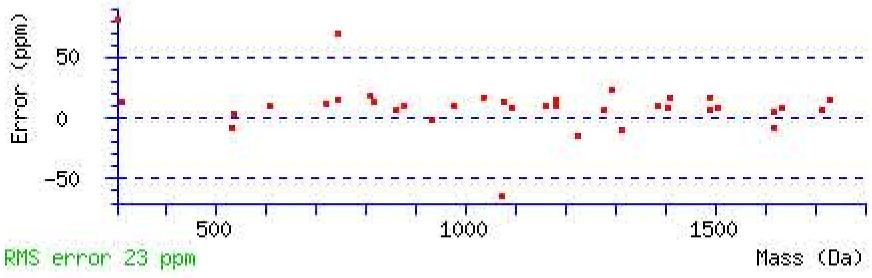
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2907.433762
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q24    : Biotin:Thermo-21345 (Q)
Ions Score: 78  Expect: 4.7e-007
Matches : 36/242 fragment ions using 67 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							25
2	171.112804	86.060040					G	2795.356978	1398.182127	2778.330429	1389.668853	2777.346413	1389.176845	24
3	***308.171716***	154.589496					H	2738.335514	1369.671395	2721.308965	1361.158121	2720.324949	1360.666113	23
4	405.224480	203.115878					P	2601.276602	1301.141939	2584.250053	1292.628665	2583.266037	1292.136657	22
5	***534.267073***	267.637175			516.256508	258.631892	E	2504.223838	1252.615557	2487.197289	1244.102283	2486.213273	1243.610275	21
6	***605.304187***	303.155732			587.293622	294.150449	A	2375.181245	1188.094261	2358.154696	1179.580986	2357.170680	1179.088978	20
7	***718.388251***	359.697764			700.377686	350.692481	L	2304.144131	1152.575704	2287.117582	1144.062429	2286.133566	1143.570421	19
8	***805.420279***	403.213778			787.409714	394.208495	S	2191.060067	1096.033672	2174.033518	1087.520397	2173.049502	1087.028389	18
9	***876.457393***	438.732335			858.446828	429.727052	A	2104.028039	1052.517658	2087.001490	1044.004383	2086.017474	1043.512375	17
10	***933.478857***	467.243067			915.468292	458.237784	G	2032.990925	1016.999101	2015.964376	1008.485826	2014.980360	1007.993818	16
11	***1034.526536***	517.766906			1016.515971	508.761624	T	1975.969461	988.488369	1958.942912	979.975094	1957.958896	979.483086	15
12	***1091.548000***	546.277638			1073.537435	537.272356	G	1874.921782	937.964529	1857.895233	929.451255	1856.911217	928.959247	14
13	***1178.580028***	589.793652			1160.569463	580.788370	S	1817.900318	909.453797	1800.873769	900.940523	1799.889753	900.448515	13
14	***1275.632792***	638.320034			1257.622227	629.314752	P	***1730.868290***	865.937783	1713.841741	857.424509	1712.857725	856.932501	12
15	***1403.691370***	702.349323	1386.664821	693.836049	1385.680805	693.344041	Q	***1633.815526***	817.411401	1616.788977	808.898127	1615.804961	808.406119	11
16	1500.744134	750.875705	1483.717585	742.362431	1482.733569	741.870423	P	***1505.756948***	753.382112	1488.730399	744.868838	1487.746383	744.376830	10
17	1597.796898	799.402087	1580.770349	790.888813	1579.786333	790.396805	P	***1408.704184***	704.855730	1391.677635	696.342456	1390.693619	695.850448	9
18	1684.828926	842.918101	1667.802377	834.404827	1666.818361	833.912819	S	***1311.651420***	656.329348	1294.624871	647.816074	1293.640855	647.324066	8
19	1831.897340	916.452308	1814.870791	907.939034	1813.886775	907.447026	F	***1224.619392***	612.813334	1207.592843	604.300060	1206.608827	603.808052	7
20	1932.945019	966.976148	1915.918470	958.462873	1914.934454	957.970865	T	***1077.550978***	539.279127	1060.524429	530.765853	1059.540413	530.273845	6
21	2096.008348	1048.507812	2078.981799	1039.994538	2077.997783	1039.502530	Y	***976.503299***	488.755288	959.476750	480.242013			5
22	2167.045462	1084.026369	2150.018913	1075.513095	2149.034897	1075.021087	A	***813.439970***	407.223623	796.413421	398.710349			4
23	2295.104040	1148.055658	2278.077491	1139.542384	2277.093475	1139.050376	Q	***742.402856***	371.705066	725.376307	363.191792			3
24	2734.329366	1367.668321	2717.302817	1359.155047	2716.318801	1358.663039	Q	614.344278	307.675777	597.317729	299.162503			2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.0	2907.433762	0.039590	LGHPEALSAGTGSPQPPSFTYAQQR
77.5	2907.433762	0.039590	LGHPEALSAGTGSPQPPSFTYAQQR
36.0	2907.433762	0.039590	LGHPEALSAGTGSPQPPSFTYAQQR

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