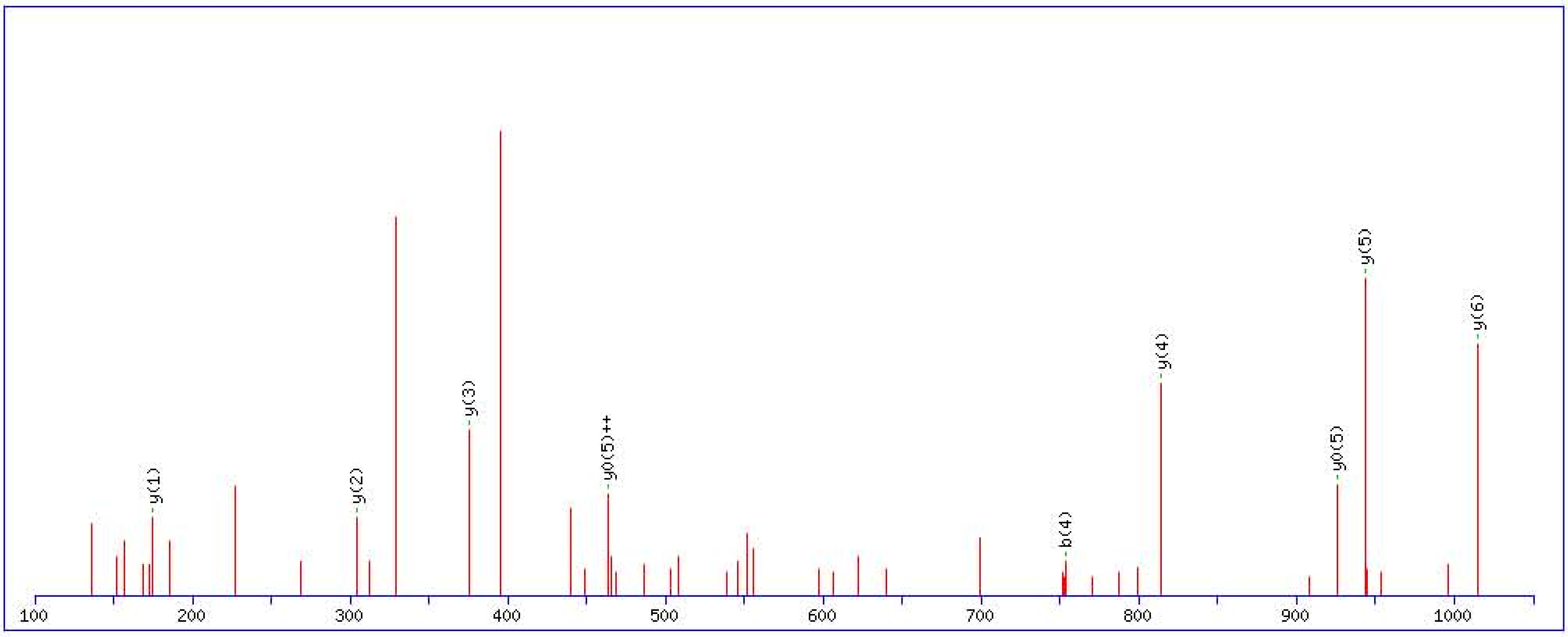
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAEQAER**
Found in **1433B_HUMAN**, 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3

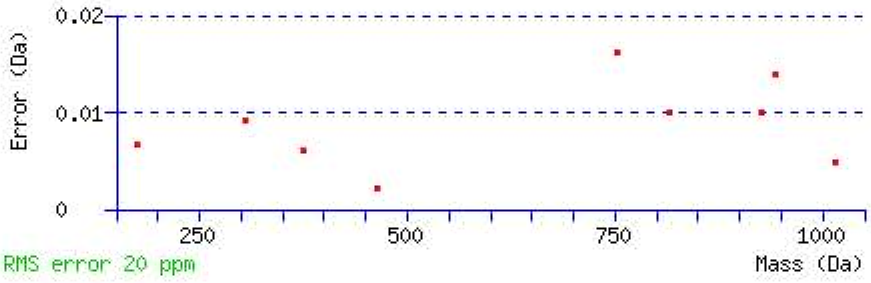
Match to Query 20271: 1126.592068 from(564.303310,2+) rtinseconds(1407) index(56577)
Title: Locus:1.1.1.2913.17 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

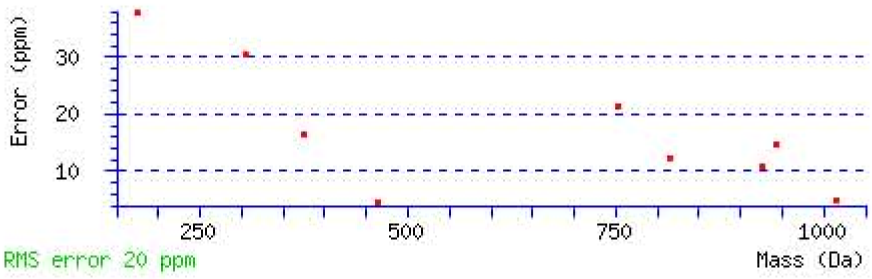
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1126.580444
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0057
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					L							7
2	185.128454	93.067865					A	***1014.503692***	507.755484	997.477143	499.242210	996.493127	498.750202	6
3	314.171047	157.589161			296.160482	148.583879	E	***943.466578***	472.236927	926.440029	463.723653	925.456013	463.231645	5
4	753.396373	377.201825	736.369824	368.688550	735.385808	368.196542	Q	***814.423985***	407.715631	797.397436	399.202356	796.413420	398.710348	4
5	824.433487	412.720382	807.406938	404.207107	806.422922	403.715099	A	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
6	953.476080	477.241678	936.449531	468.728404	935.465515	468.236396	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
7							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.4	1126.580444	0.011624	LAEQAER
13.4	1126.580444	0.011624	LAQAEER
12.1	1126.605606	-0.013538	AIEDQLK
11.2	1126.599075	-0.007007	MAMFKKSLR
9.6	1126.598221	-0.006153	LISDPAGELGR
7.0	1126.605621	-0.013553	LAQESGLV
4.9	1126.580444	0.011624	AIQAEER
4.2	1126.577789	0.014279	MRGAGGPRGPR
2.2	1126.585648	0.006420	RLSGGHAHHR
0.6	1126.602280	-0.010212	QLSFTGVTFK

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

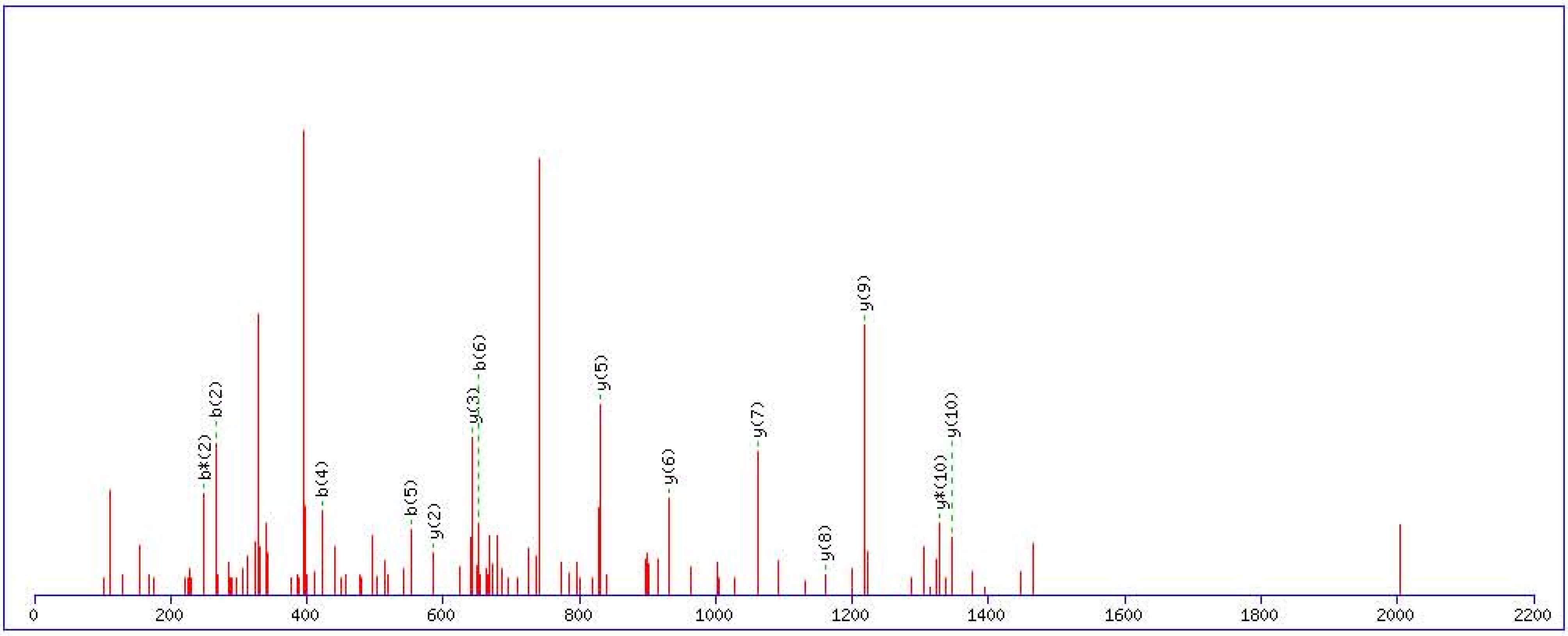
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

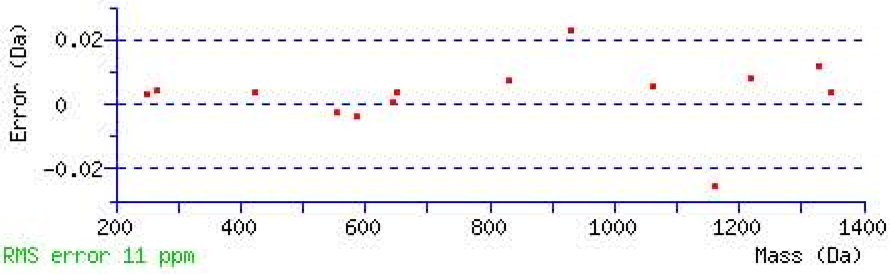
Match to Query 34437: 1481.752028 from(741.883290,2+) rtinseconds(1560) index(39236)
Title: Locus:1.1.1.2992.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

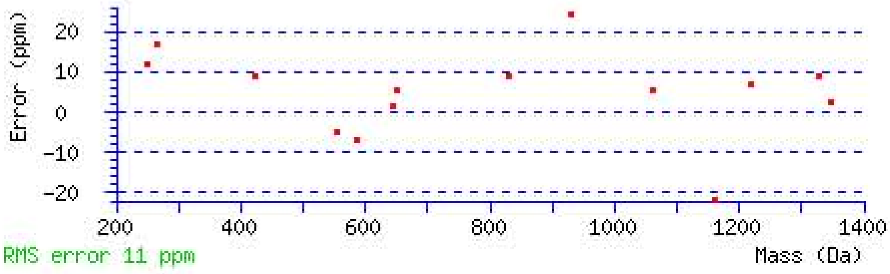
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1481.730545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00017
Matches : 14/78 fragment ions using 28 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
48.7	1481.730545	0.021483	HQGVMVGMGQK
8.2	1481.747391	0.004637	SLQADAKDLEQHK
2.1	1481.772568	-0.020540	TLVVQDEEITAHK

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

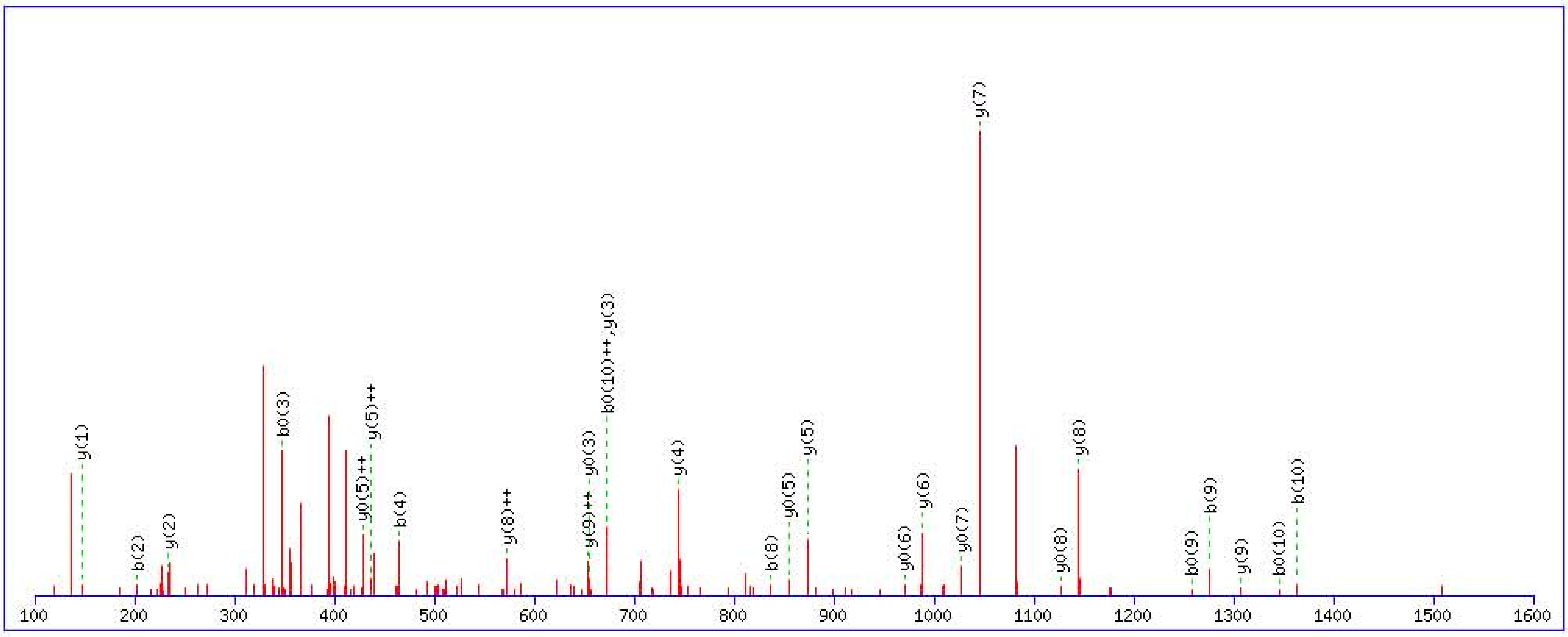
Mascot Search Results

Peptide View

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

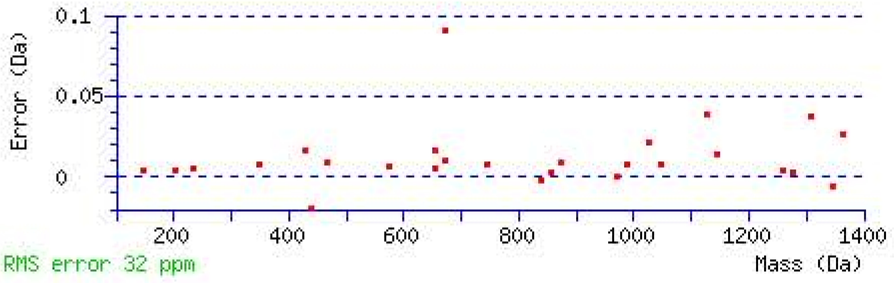
Match to Query 35324: 1508.693908 from(755.354230,2+) rtinseconds(1579) index(57856)
Title: Locus:1.1.1.2973.17 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

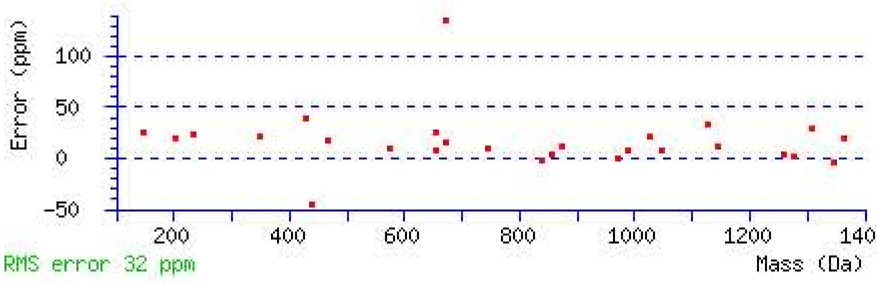
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1508.681702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 3.7e-005
Matches : 27/102 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	116.034219	58.520748			98.023654	49.515465	D							11
2	**203.066247**	102.036761			185.055682	93.031479	S	1394.662043	697.834660	1377.635494	689.321385	1376.651478	688.829377	10
3	366.129576	183.568426			348.119011	174.563144	Y	***1307.630015***	654.318646	1290.603466	645.805371	1289.619450	645.313363	9
4	**465.197990**	233.102633			447.187425	224.097351	V	***1144.566686***	572.786981	1127.540137	564.273707	1126.556121	563.781699	8
5	522.219454	261.613365			504.208889	252.608083	G	***1045.498272***	523.252774	1028.471723	514.739500	1027.487707	514.247492	7
6	637.246397	319.126837			619.235832	310.121554	D	***988.476808***	494.742042	971.450259	486.228768	970.466243	485.736760	6
7	766.288990	383.648133			748.278425	374.642851	E	***873.449865***	437.228571	856.423316	428.715296	855.439300	428.223288	5
8	**837.326104**	419.166690			819.315539	410.161408	A	***744.407272***	372.707274	727.380723	364.194000	726.396707	363.701992	4
9	**1276.551430**	638.779353	1259.524881	630.266079	1258.540865	629.774070	Q	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
10	**1363.583458**	682.295367	1346.556909	673.782093	1345.572893	673.290085	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.8	1508.681702	0.012206	DSYVGDEAQSK
6.2	1508.703461	-0.009553	LKSFTYEYEDSK
4.8	1508.690277	0.003631	GGRGGMGGSDRGGFNK
2.0	1508.714066	-0.020158	EGTQLSSQQSVMSK

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

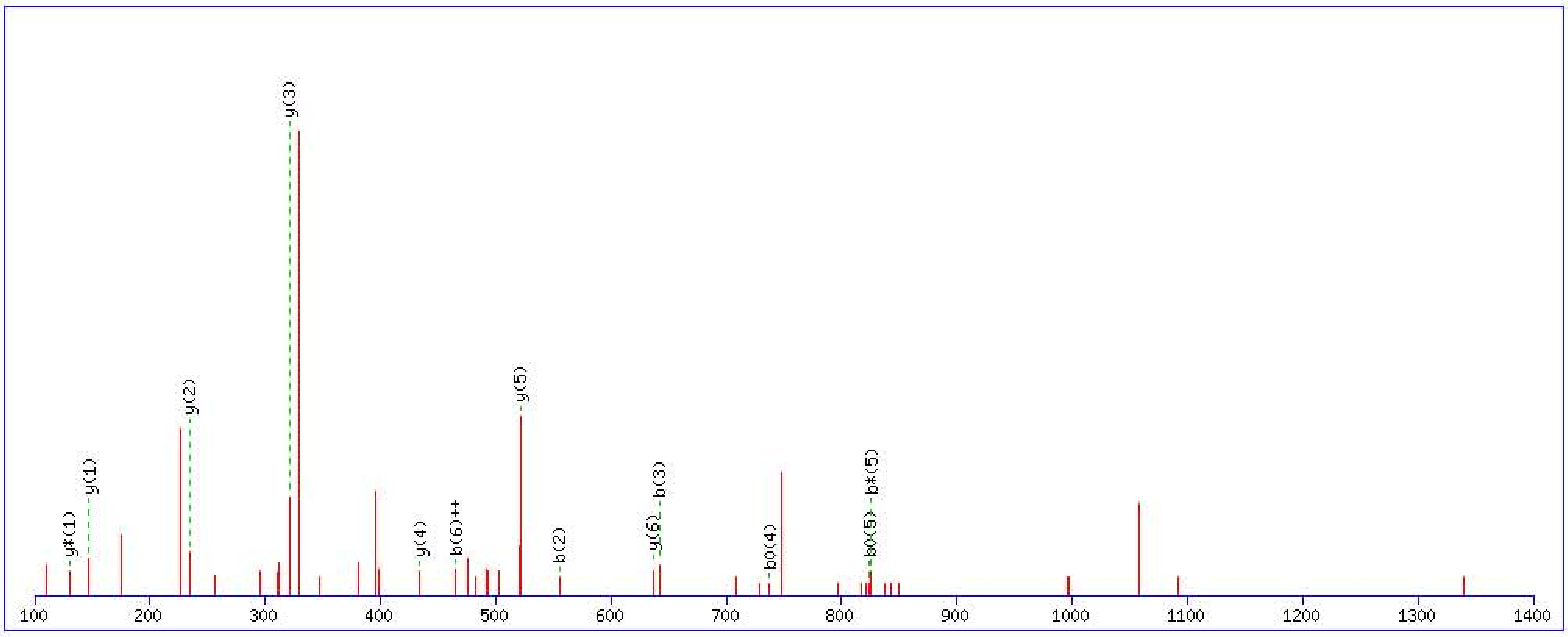
Mascot Search Results

Peptide View

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

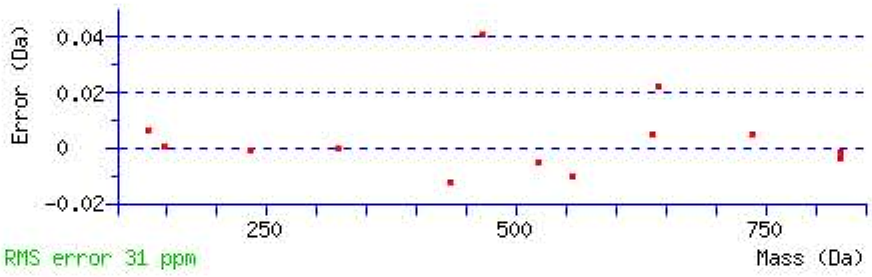
Match to Query 18298: 1074.538328 from(538.276440,2+) rtinseconds(1377) index(20095)
Title: Locus:1.1.1.2622.19 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

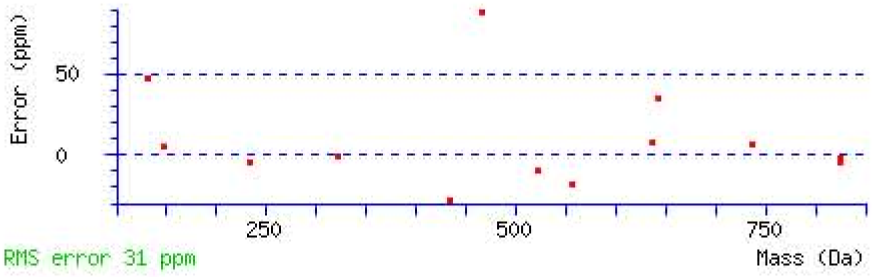
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1074.537933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.037
Matches : 13/68 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	440.232602	220.619939	423.206053	212.106664			Q							7
2	**555.259545**	278.133411	538.232996	269.620136	537.248980	269.128128	D	***636.319895***	318.663586	619.293346	310.150311	618.309330	309.658303	6
3	**642.291573**	321.649425	625.265024	313.136150	624.281008	312.644142	S	***521.292952***	261.150114	504.266403	252.636840	503.282387	252.144832	5
4	755.375637	378.191457	738.349088	369.678182	737.365072	369.186174	I	***434.260924***	217.634100	417.234375	209.120826	416.250359	208.628818	4
5	842.407665	421.707471	825.381116	413.194196	824.397100	412.702188	S	***321.176860***	161.092068	304.150311	152.578794	303.166295	152.086786	3
6	929.439693	465.223484	912.413144	456.710210	911.429128	456.218202	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
7							K	***147.112804***	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of QDSISSK
(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	1074.537933	0.000395	QDSISSK
13.8	1074.530548	0.007780	QVTEPTSSAR
9.7	1074.531418	0.006910	LLACPSVCR
7.8	1074.537933	0.000395	QDSSKSI
1.8	1074.549179	-0.010851	AQEVVMSGVR
1.2	1074.531891	0.006437	HLHTPGSNGR
0.3	1074.530518	0.007810	VDNAASEKNK
0.3	1074.541763	-0.003435	DKRLESGDR

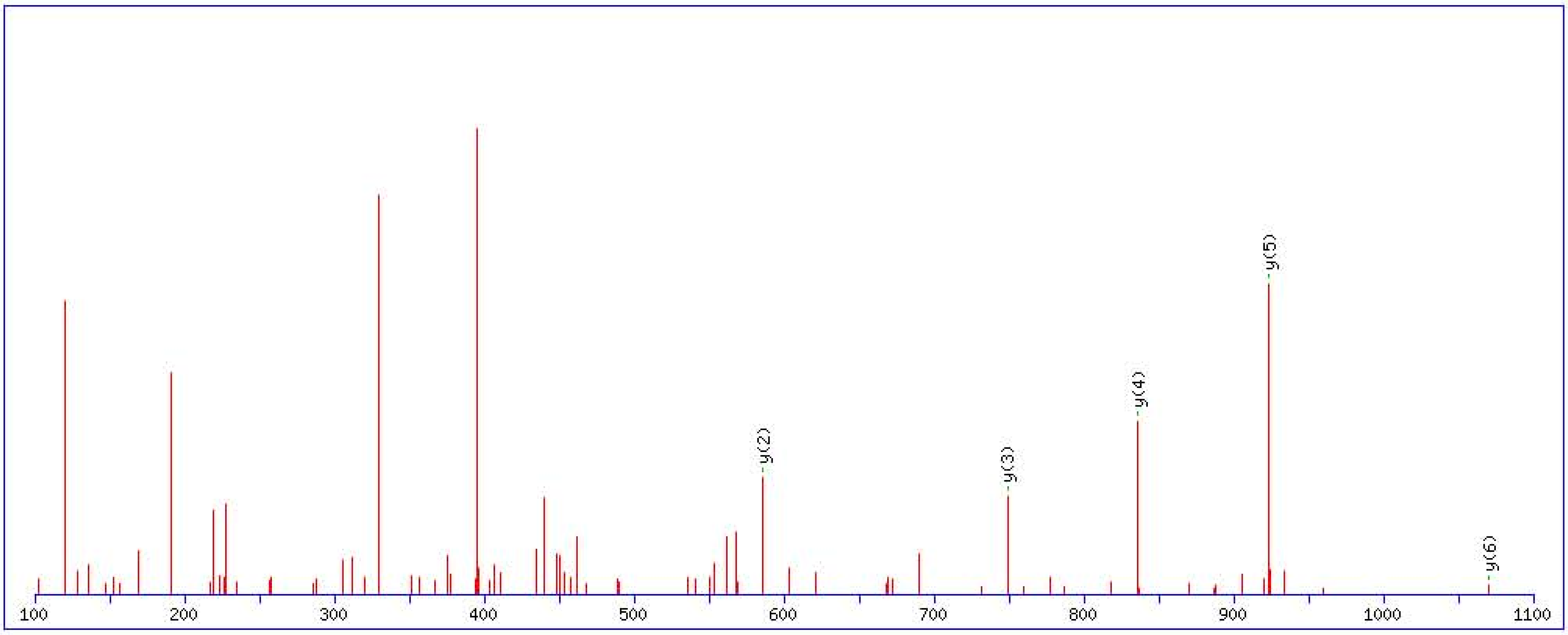
Mascot Search Results

Peptide View

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

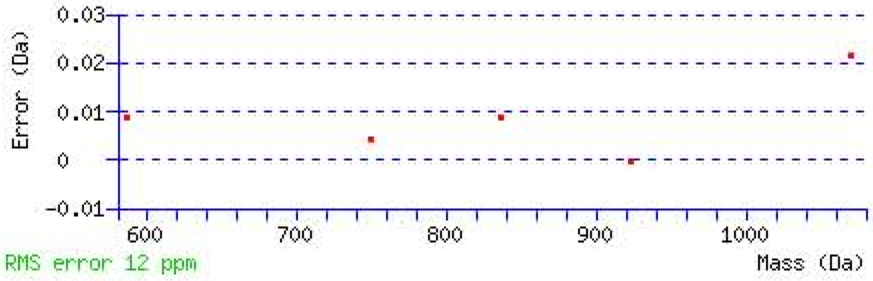
Match to Query 21517: 1140.568748 from(571.291650,2+) rtinseconds(1566) index(3794)
Title: Locus:1.1.1.2799.14 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

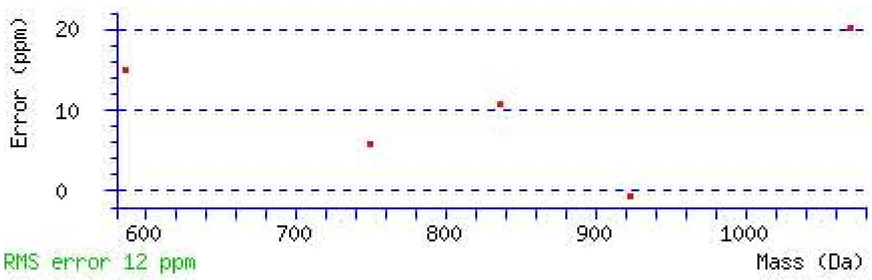
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1140.563751
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0086
Matches : 5/52 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	72.044390	36.525833					A							7
2	219.112804	110.060040					F	***1070.533929***	535.770603	1053.507380	527.257328	1052.523364	526.765320	6
3	306.144832	153.576054			288.134267	144.570772	S	***923.465515***	462.236396	906.438966	453.723121	905.454950	453.231113	5
4	393.176860	197.092068			375.166295	188.086785	S	***836.433487***	418.720382	819.406938	410.207107	818.422922	409.715099	4
5	556.240189	278.623733			538.229624	269.618450	Y	***749.401459***	375.204368	732.374910	366.691093			3
6	995.465515	498.236396	978.438966	489.723121	977.454950	489.231113	Q	***586.338130***	293.672703	569.311581	285.159429			2
7							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AFSSYQK
(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	1140.563751	0.004997	AFSSYQK
5.0	1140.559723	0.009025	AFSRSSDLMK

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

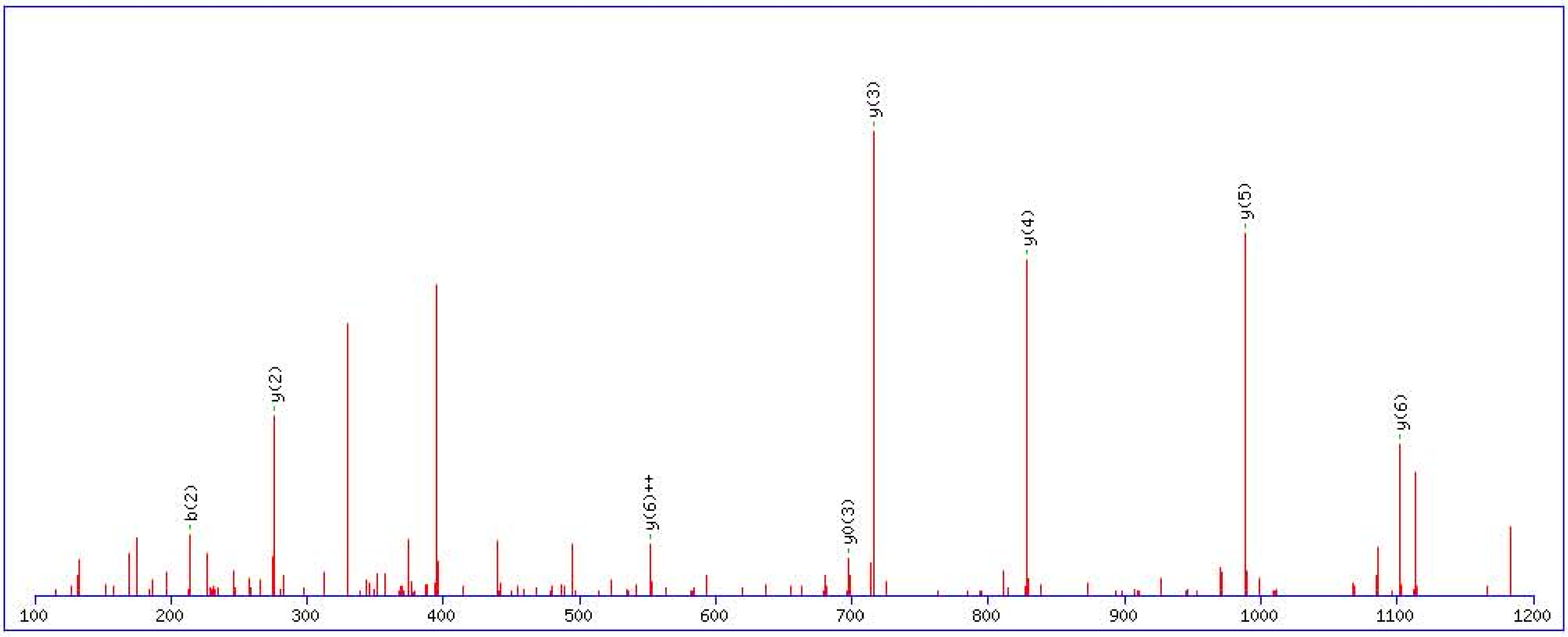
Mascot Search Results

Peptide View

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

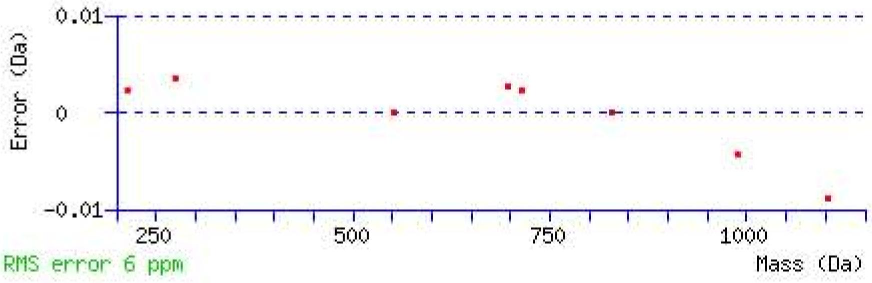
Match to Query 23706: 1200.611908 from(601.313230,2+) rtinseconds(1483) index(20869)
Title: Locus:1.1.1.2659.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

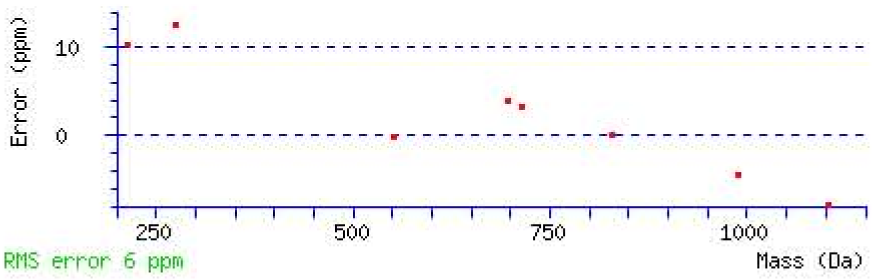
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1200.610733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.00076
Matches : 8/58 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	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
40.5	1200.610733	0.001175	VNCLQTR
6.8	1200.603333	0.008575	GRIAEPSVCGR
5.9	1200.628479	-0.016571	MVAALLGGGGEAR
1.9	1200.607361	0.004547	RGDYVHVMPK
1.3	1200.609848	0.002060	ERAPVSGTQEK
0.2	1200.621948	-0.010040	VNMLKHCKR
0.1	1200.617233	-0.005325	VMEETPNILR
0.1	1200.621094	-0.009186	ESRPVQQTTR

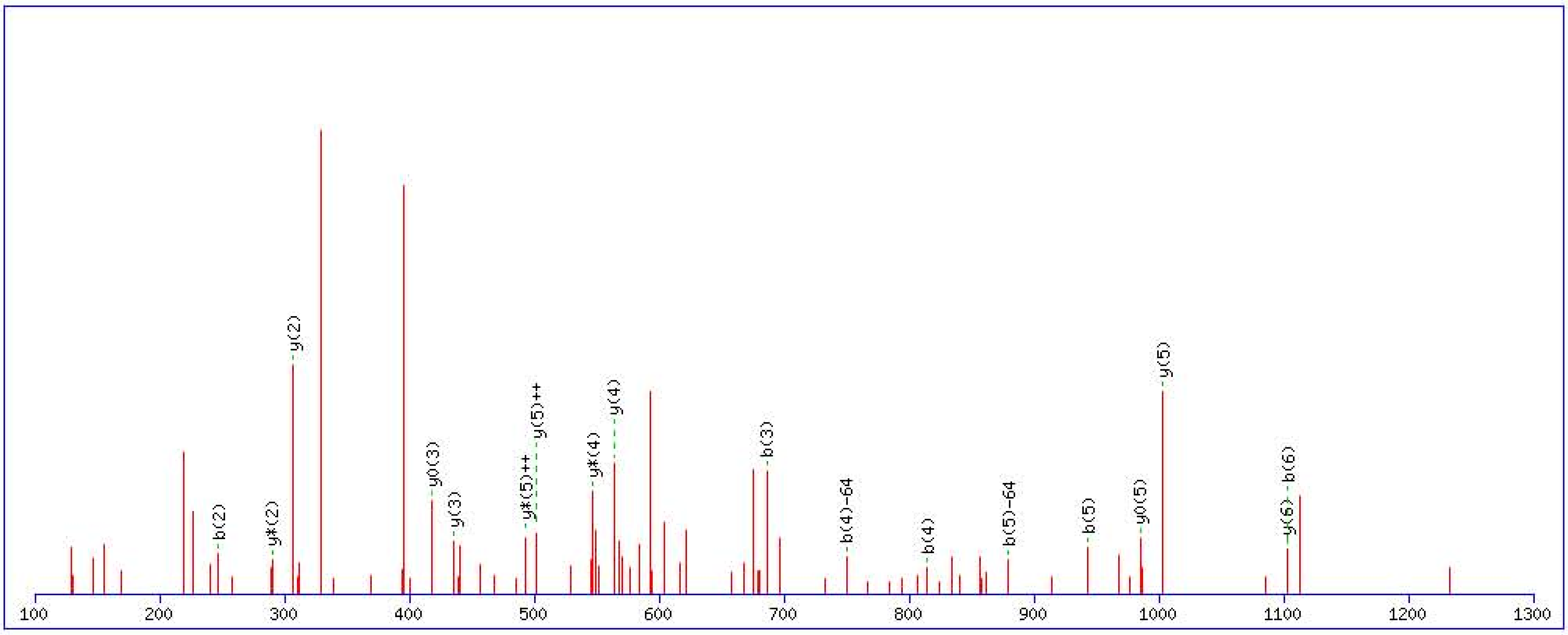
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

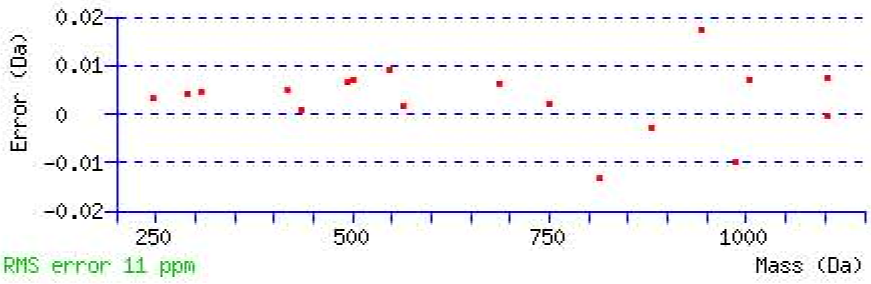
Match to Query 25188: 1248.571008 from(625.292780,2+) rtinseconds(1179) index(1166)
Title: Locus:1.1.1.2664.23 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

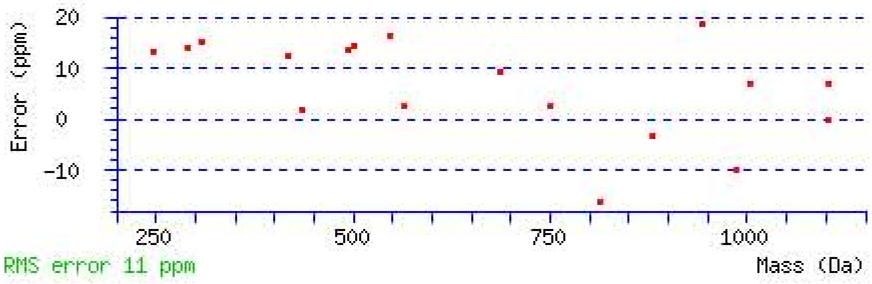
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1248.566483
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
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.015
Matches : 18/80 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	148.042676	74.524976					M							7
2	***247.111090***	124.059183					V	***1102.538364***	551.772820	1085.511815	543.259546	1084.527799	542.767538	6
3	***686.336416***	343.671846	669.309867	335.158572			Q	***1003.469950***	502.238613	986.443401	493.725339	985.459385	493.233331	5
4	***814.394994***	407.701135	797.368445	399.187861			Q	***564.244624***	282.625950	547.218075	274.112676	546.234059	273.620668	4
5	***943.437587***	472.222432	926.411038	463.709157	925.427022	463.217149	E	***436.186046***	218.596661	419.159497	210.083387	418.175481	209.591379	3
6	***1103.468236***	552.237756	1086.441687	543.724482	1085.457671	543.232474	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 MVQQECK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.2	1248.566483	0.004525	MVQQECK
16.9	1248.566483	0.004525	MVQQECK
11.4	1248.588089	-0.017081	MVDVGGQRSER

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

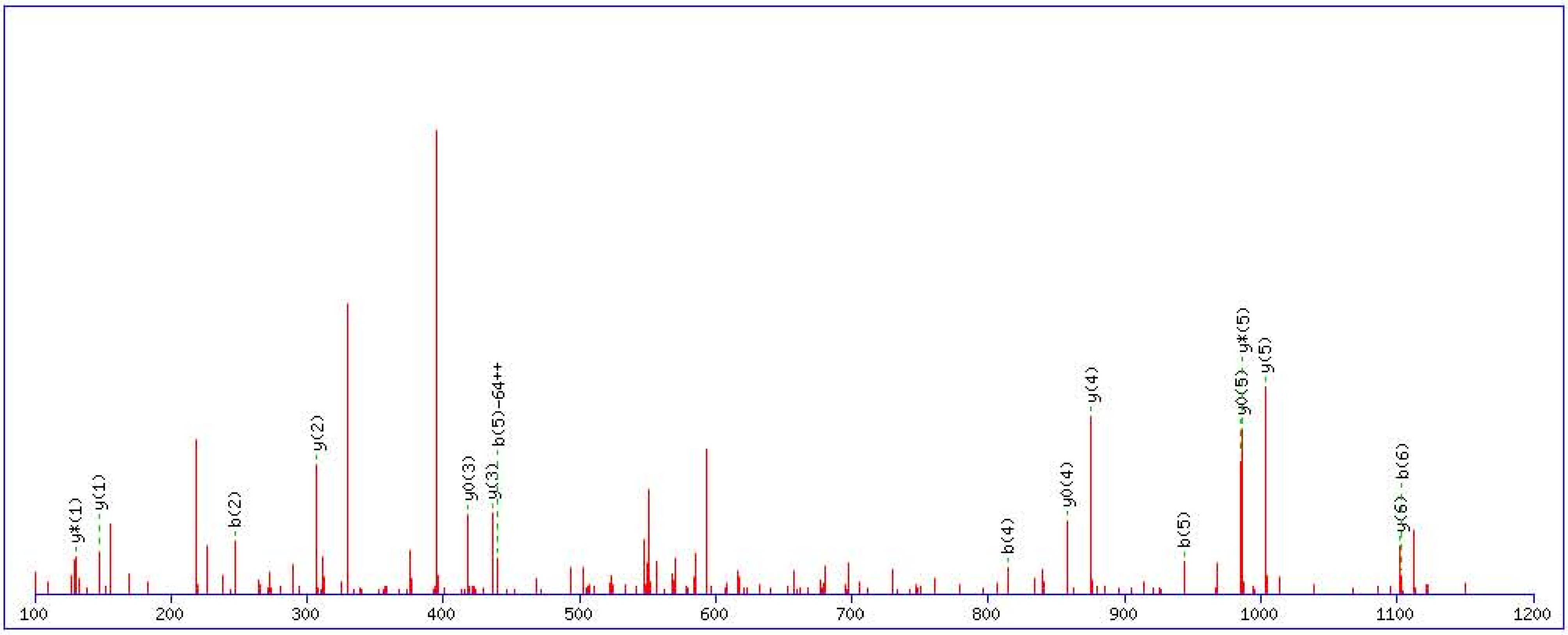
Mascot Search Results

Peptide View

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

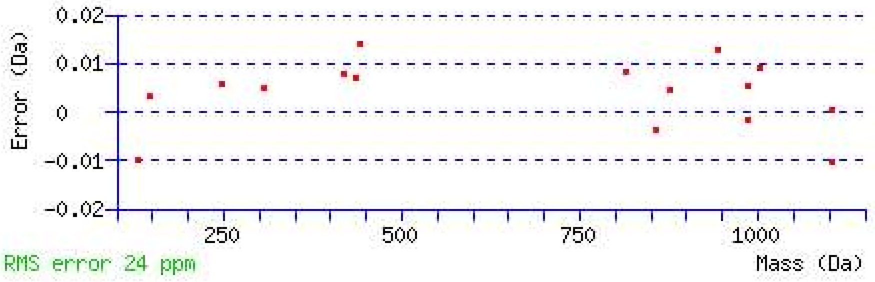
Match to Query 25192: 1248.571748 from(625.293150,2+) rtinseconds(1205) index(1333)
Title: Locus:1.1.1.2673.8 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

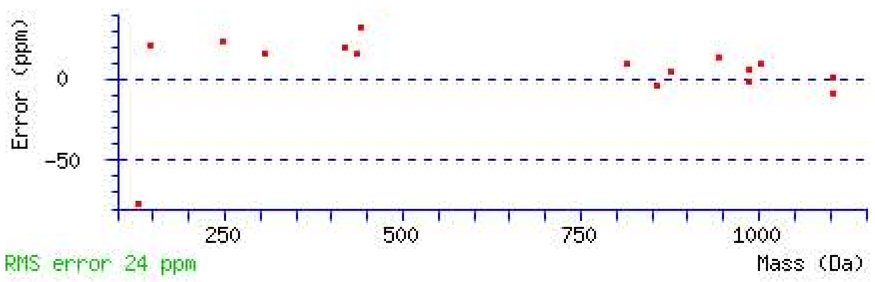
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1248.566483
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)
Ions Score: 29 **Expect:** 0.012
Matches : 16/80 fragment ions using 33 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.042676	74.524976					M							7
2	**247.111090**	124.059183					V	***1102.538364***	551.772820	1085.511815	543.259546	1084.527799	542.767538	6
3	375.169668	188.088472	358.143119	179.575198			Q	***1003.469950***	502.238613	986.443401	493.725338	985.459385	493.233330	5
4	**814.394994**	407.701135	797.368445	399.187861			Q	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
5	**943.437587**	472.222432	926.411038	463.709157	925.427022	463.217149	E	***436.186046***	218.596661	419.159497	210.083386	418.175481	209.591378	3
6	**1103.468236**	552.237756	1086.441687	543.724482	1085.457671	543.232473	C	***307.143453***	154.075364	290.116904	145.562090			2
7							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of MVQQECK
(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	1248.566483	0.005265	MVQQECK
19.2	1248.566483	0.005265	MVQQECK
13.2	1248.576813	-0.005065	KCESLEQEAR
6.9	1248.584244	-0.012496	MHSMISSVDVK
3.8	1248.584244	-0.012496	MHSMISSVDVK
1.1	1248.588089	-0.016341	MVDVGGQRSER

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

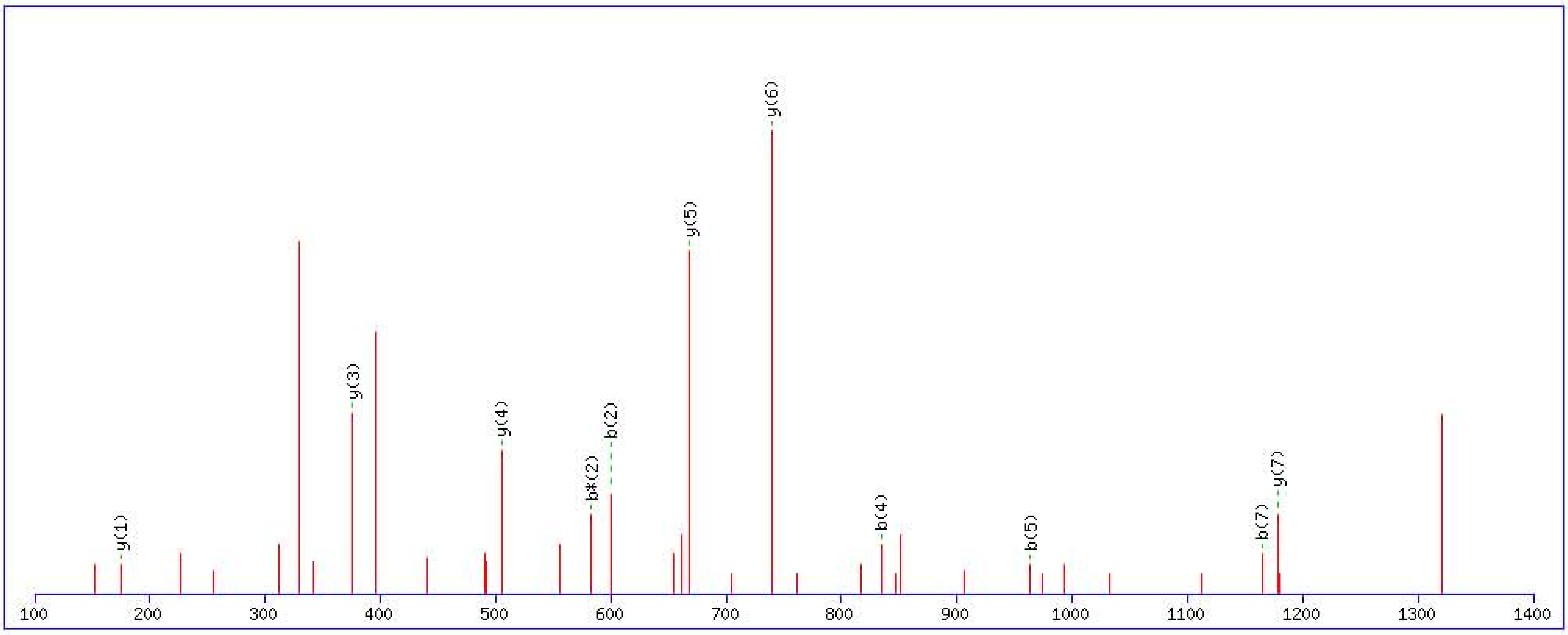
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

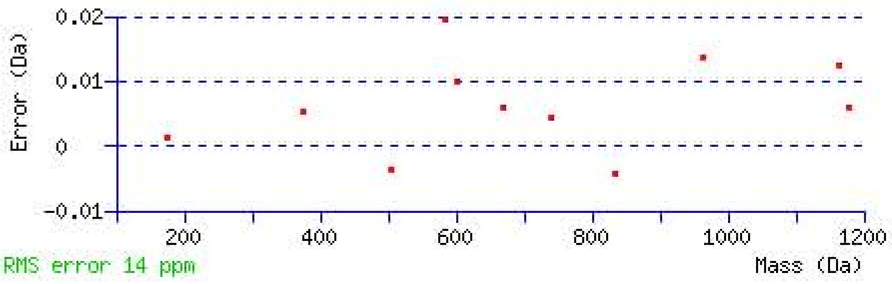
Match to Query 27794: 1337.594548 from(669.804550,2+) rtinseconds(1369) index(2344)
Title: Locus:1.1.1.2730.25 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

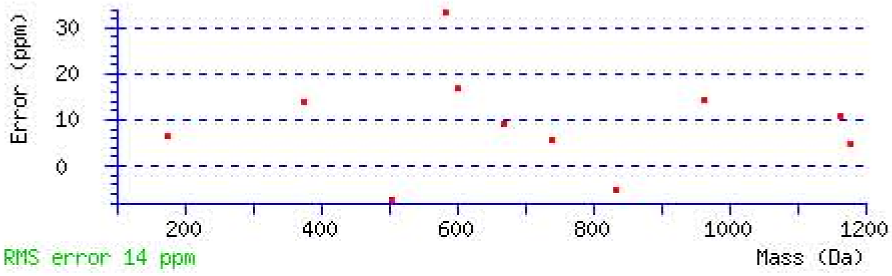
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1337.585617
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.011
Matches : 11/70 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	161.037925	81.022600					C							8
2	**600.263251**	300.635264	583.236702	292.121989			Q	***1178.562269***	589.784773	1161.535720	581.271498	1160.551704	580.779490	7
3	671.300365	336.153821	654.273816	327.640546			A	***739.336943***	370.172110	722.310394	361.658835	721.326378	361.166827	6
4	**834.363694**	417.685485	817.337145	409.172211			Y	***668.299829***	334.653553	651.273280	326.140278	650.289264	325.648270	5
5	**963.406287**	482.206782	946.379738	473.693507	945.395722	473.201499	E	***505.236500***	253.121888	488.209951	244.608613	487.225935	244.116605	4
6	1050.438315	525.722796	1033.411766	517.209521	1032.427750	516.717513	S	***376.193907***	188.600591	359.167358	180.087317	358.183342	179.595309	3
7	**1164.481242**	582.744259	1147.454693	574.230985	1146.470677	573.738977	N	289.161879	145.084577	272.135330	136.571303			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.2	1337.585617	0.008931	CQAYESNR
8.2	1337.596848	-0.002300	CYEMASHLRR
3.6	1337.592148	0.002400	ELDFAACVEER

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

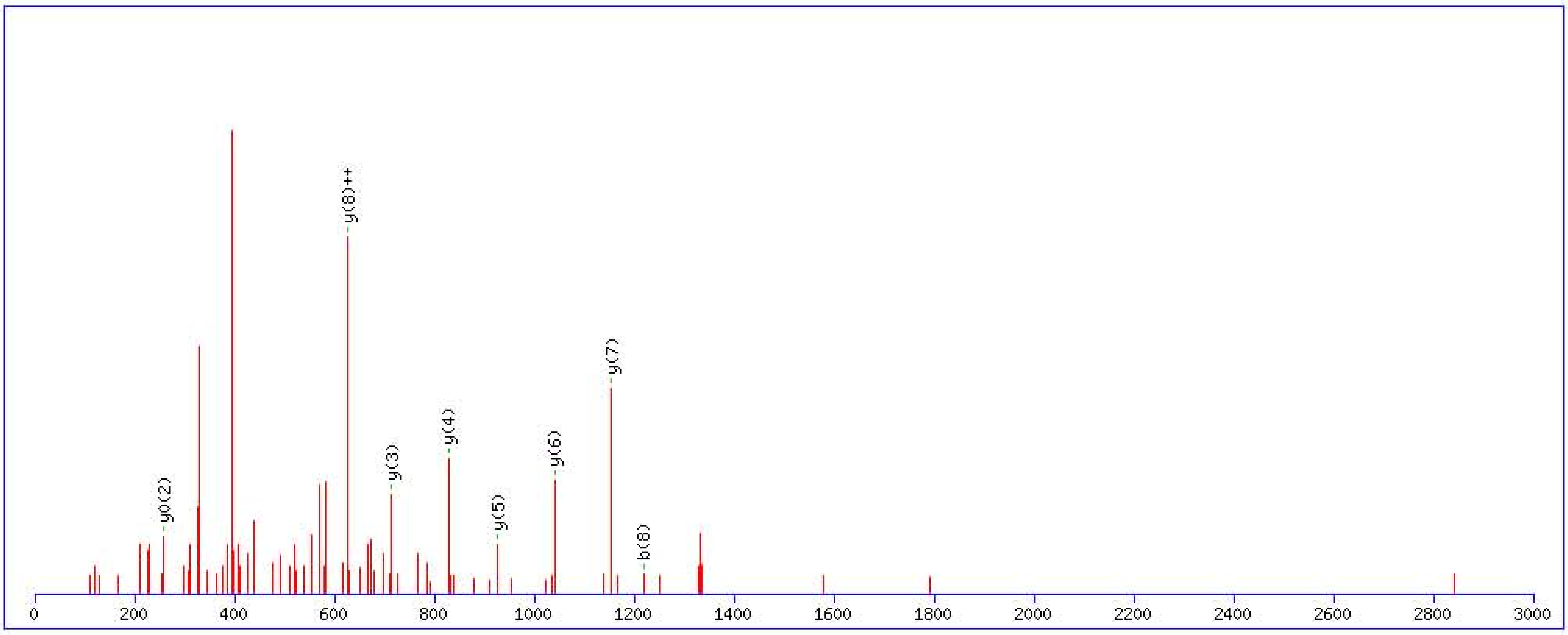
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

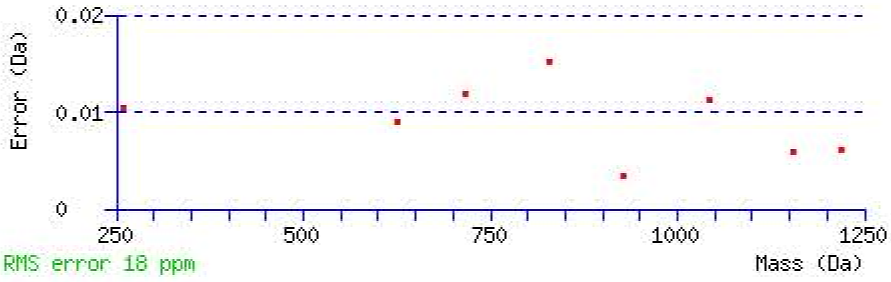
Match to Query 29392: 1364.760848 from(683.387700,2+) rtinseconds(1787) index(5137)
Title: Locus:1.1.1.2876.23 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

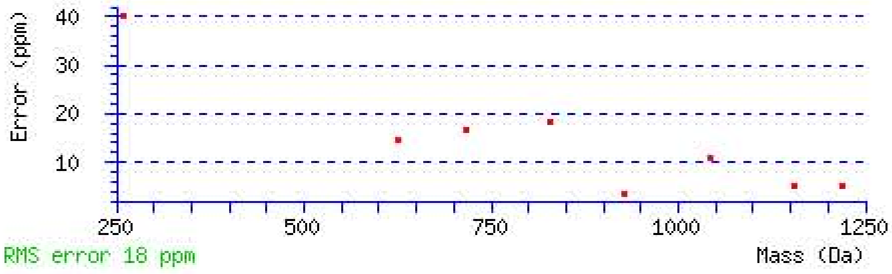
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1364.748581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0027
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	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
28.4	1364.748581	0.012267	LPNNVLQEK
0.9	1364.745239	0.015609	KVVSWIDVYTR

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

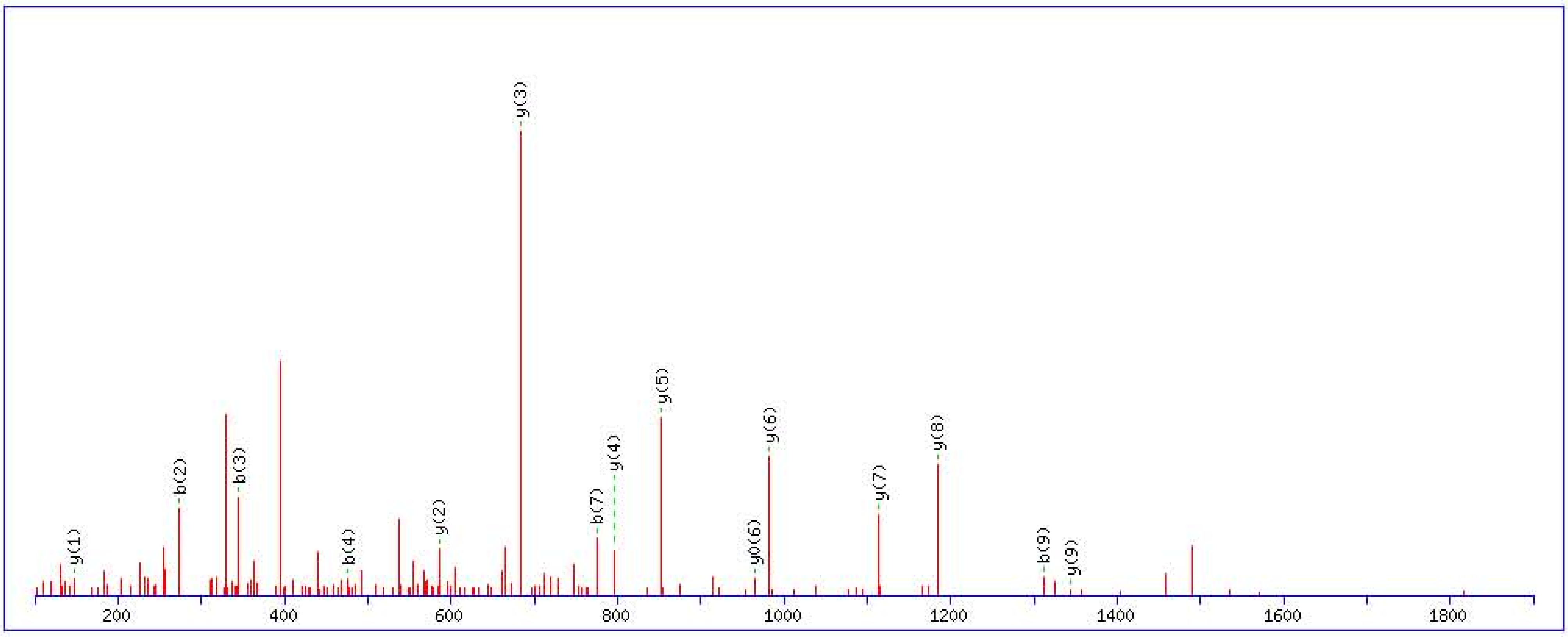
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

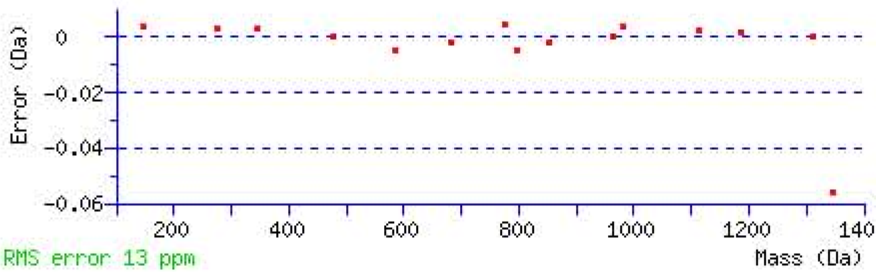
Match to Query 33613: 1456.739288 from(729.376920,2+) rtinseconds(1916) index(24097)
Title: Locus:1.1.1.2809.17 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

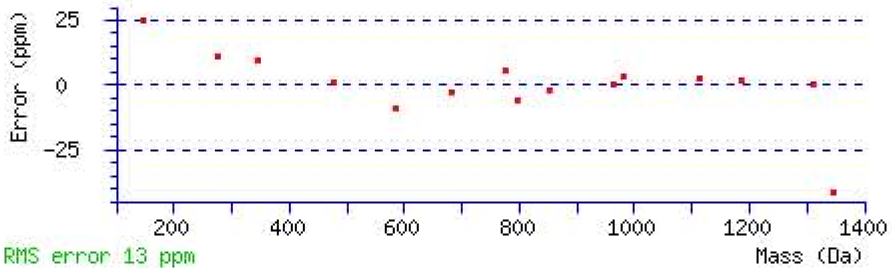
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1456.724030
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 47 **Expect:** 0.00055
Matches : 15/74 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	114.091340	57.549308					I							10
2	**274.121989**	137.564632					C	***1344.647263***	672.827270	1327.620714	664.313995	1326.636698	663.821987	9
3	**345.159103**	173.083190					A	***1184.616614***	592.811945	1167.590065	584.298671	1166.606049	583.806663	8
4	**476.199588**	238.603432					M	***1113.579500***	557.293388	1096.552951	548.780114	1095.568935	548.288106	7
5	605.242181	303.124729			587.231616	294.119446	E	***982.539015***	491.773146	965.512466	483.259871	964.528450	482.767863	6
6	662.263645	331.635461			644.253080	322.630178	G	***853.496422***	427.251849	836.469873	418.738575			5
7	**775.347709**	388.177493			757.337144	379.172210	L	***796.474958***	398.741117	779.448409	390.227843			4
8	872.400473	436.703875			854.389908	427.698592	P	***683.390894***	342.199085	666.364345	333.685811			3
9	**1311.625799**	656.316538	1294.599250	647.803263	1293.615234	647.311255	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 ICAMEGLPQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.7	1456.724030	0.015258	ICAMEGLPQK
12.4	1456.740921	-0.001633	ATVPAGEGVSLEEAK
7.8	1456.723145	0.016143	QQTLEAEEAK
6.4	1456.745605	-0.006317	QNENTRKEK
4.3	1456.723160	0.016128	ALAVMVDHLESEK
4.2	1456.745621	-0.006333	LKEPHTMSRSQK
3.8	1456.742279	-0.002991	LSGSHSQGVAYPVR
2.0	1456.723145	0.016143	QQTLEAEEAK
0.5	1456.759521	-0.020233	SKMIYASSKDAIK

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

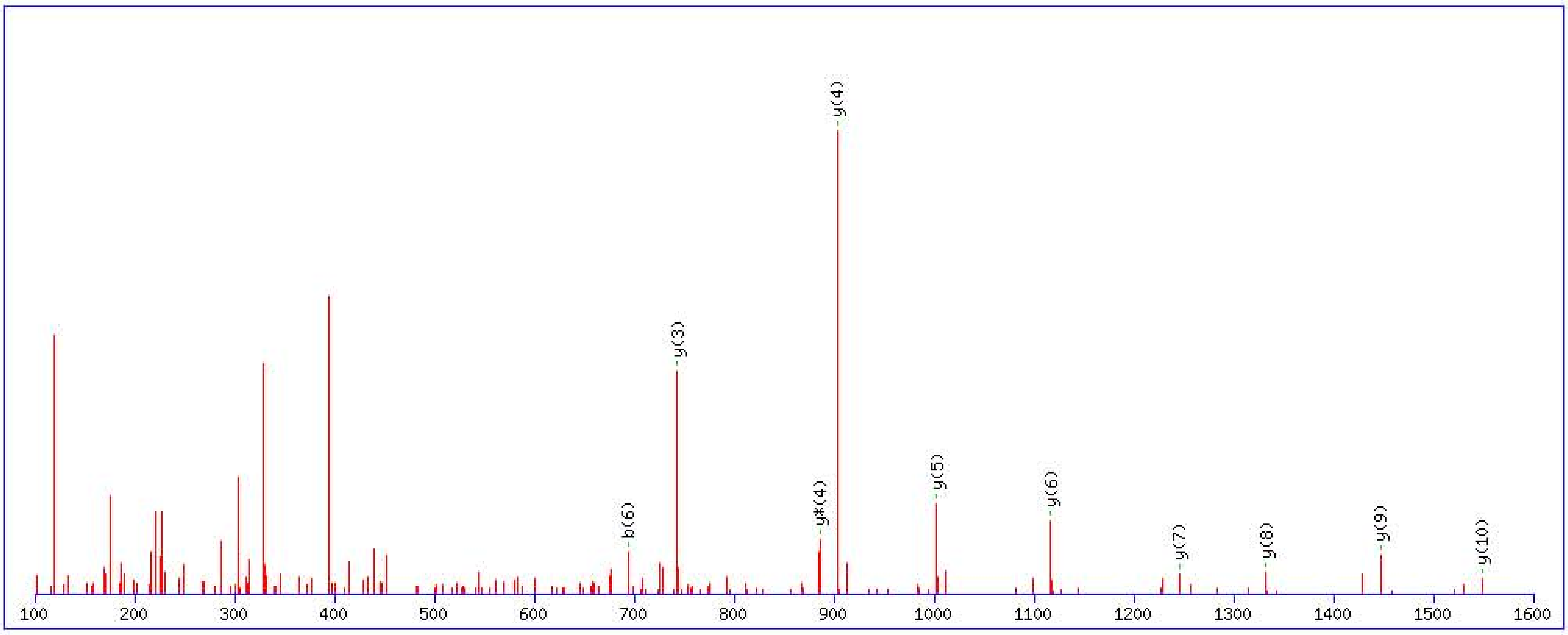
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

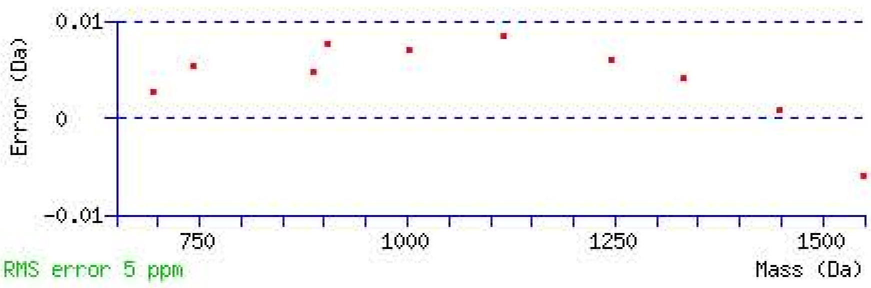
Match to Query 42317: 1694.747232 from(565.923020,3+) rtinseconds(1540) index(3596)
Title: Locus:1.1.1.2790.11 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

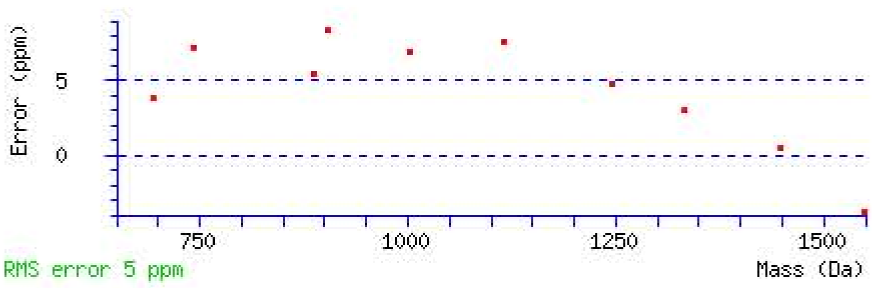
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1694.739243
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 2.2e-005
Matches : 10/106 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	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
53.9	1694.739243	0.007989	FTDSENVCQER

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

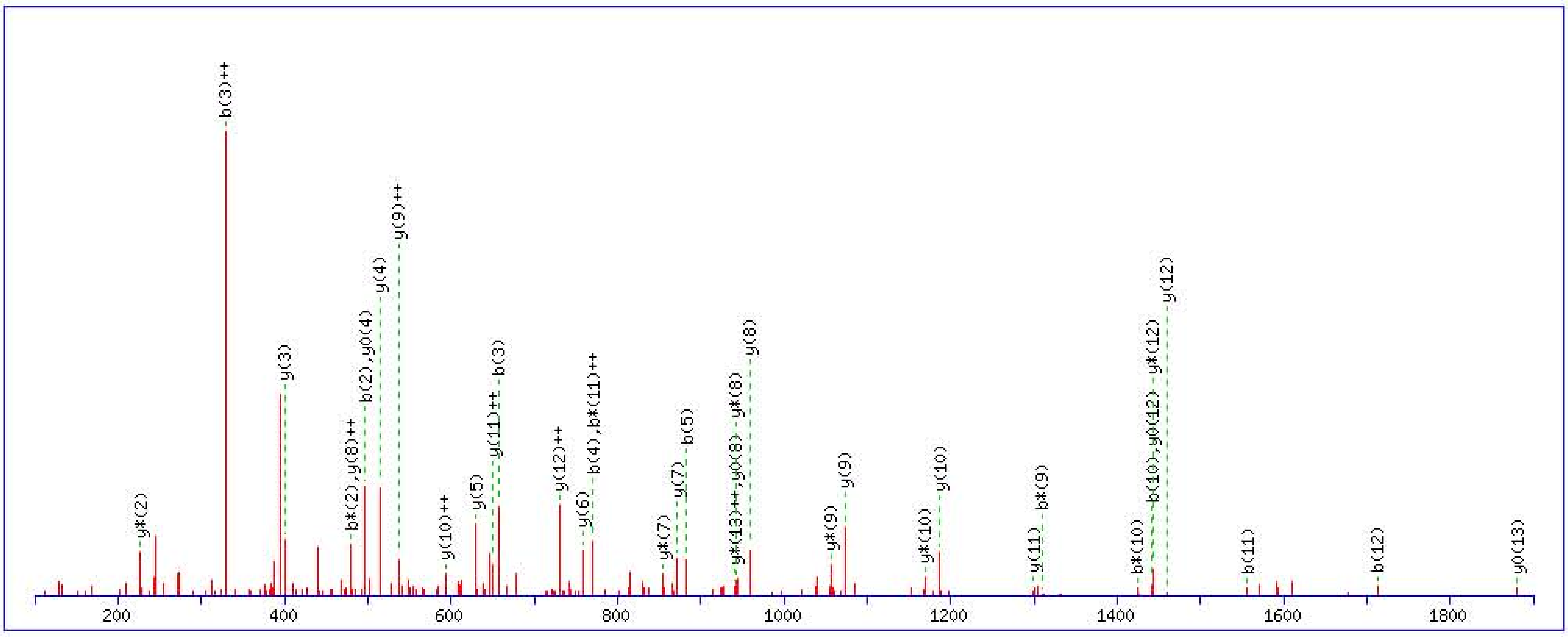
Mascot Search Results

Peptide View

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

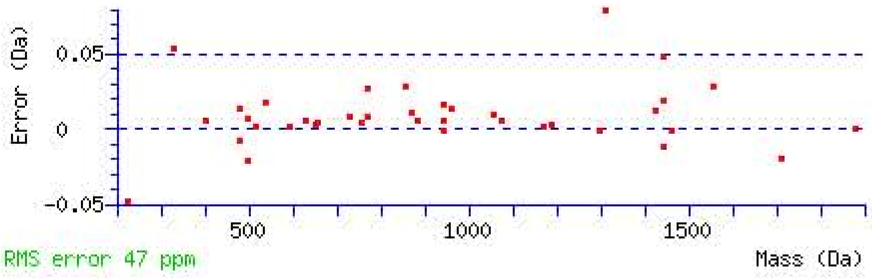
Match to Query 48807: 1954.979472 from(652.667100,3+) rtinseconds(1351) index(2211)
Title: Locus:1.1.1.2724.13 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

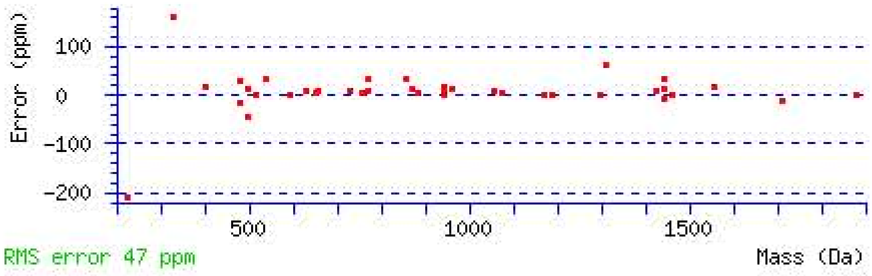
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1954.971680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.0002
Matches : 38/136 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	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
51.2	1954.971680	0.007792	GQCIINSNKDDRPK

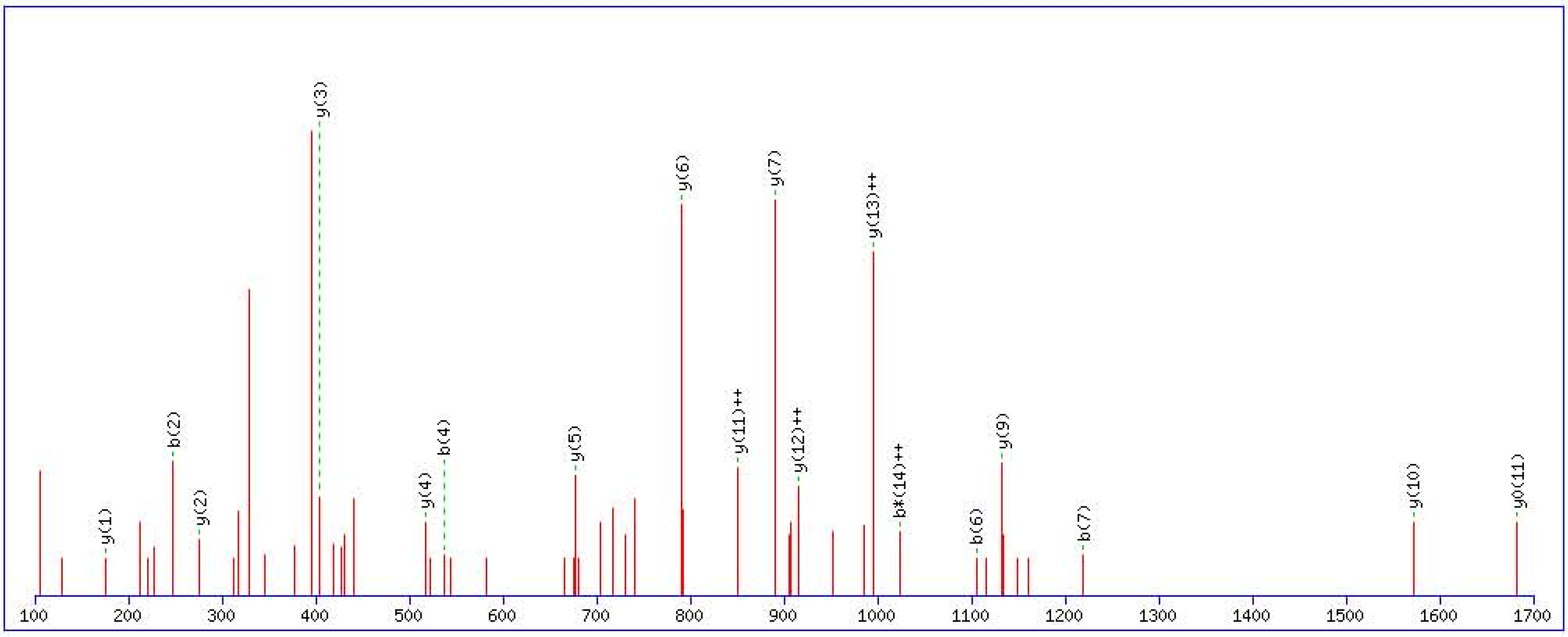
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

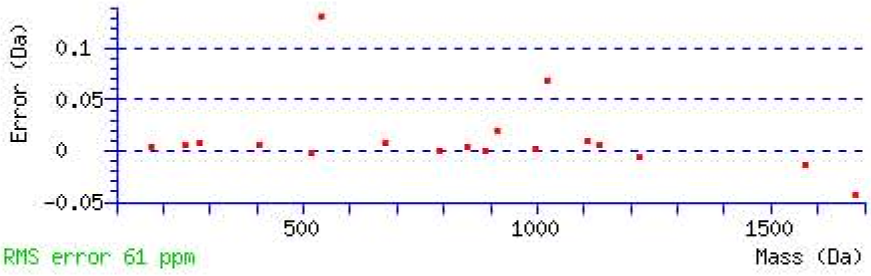
Match to Query 56323: 2235.987612 from(746.336480,3+) rtinseconds(1432) index(2804)
Title: Locus:1.1.1.2752.25 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

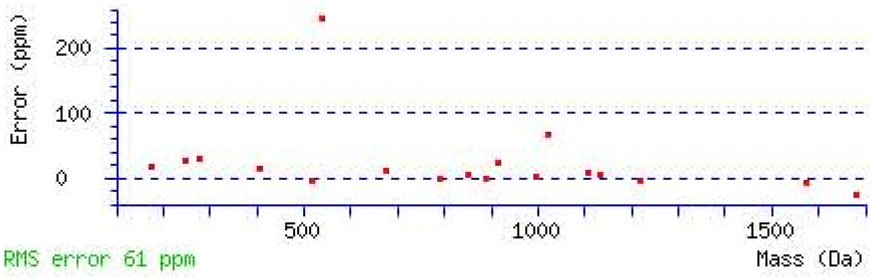
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 46  Expect: 0.00013
Matches : 18/156 fragment ions using 34 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							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
46.4	2235.985703	0.001909	SCCEEQNKVNCLQTR
5.8	2235.985703	0.001909	SCCEEQNKVNCLQTR

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

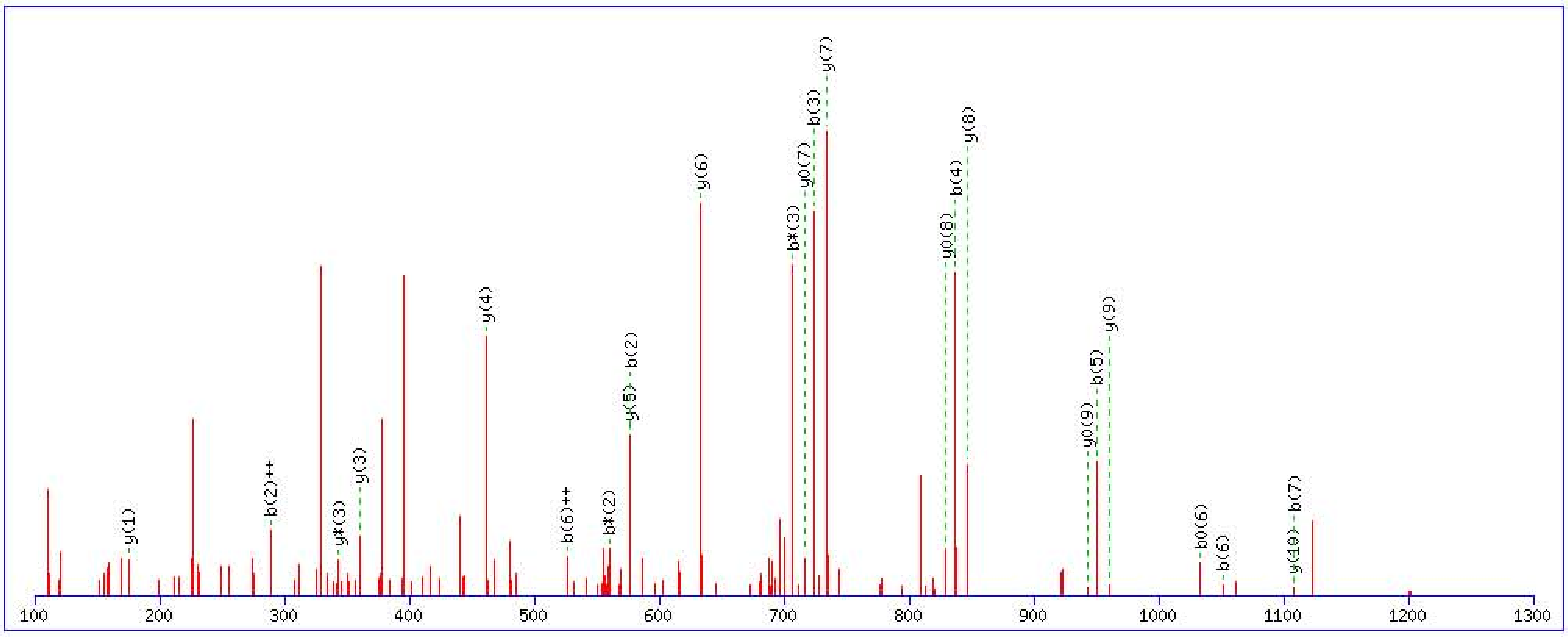
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQFLLTGDTQGR**
Found in **A1BG_HUMAN**, Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4

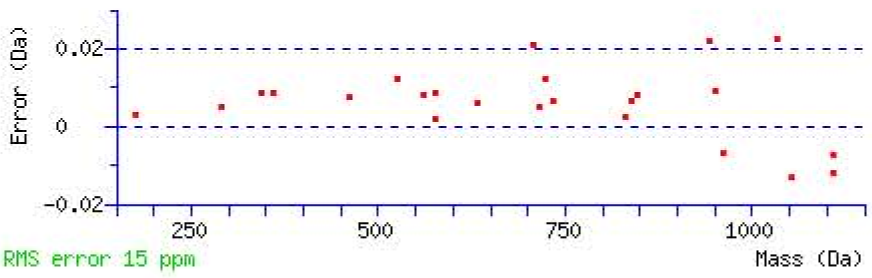
Match to Query 42068: 1682.867202 from(561.963010,3+) rtinseconds(1921) index(6025)
Title: Locus:1.1.1.2923.10 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

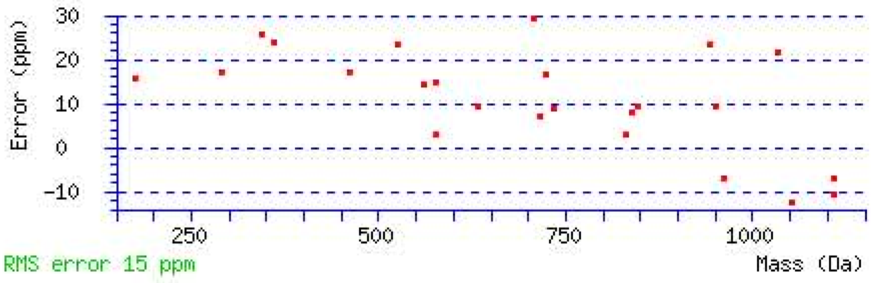
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1682.856277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00028
Matches : 24/114 fragment ions using 53 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	138.066188	69.536732					H							12
2	**577.291514**	**289.149395**	560.264965	280.636121			Q	1546.804627	773.905951	1529.778078	765.392677	1528.794062	764.900669	11
3	**724.359928**	362.683602	707.333379	354.170327			F	***1107.579301***	554.293288	1090.552752	545.780014	1089.568736	545.288006	10
4	**837.443992**	419.225634	820.417443	410.712359			L	***960.510887***	480.759081	943.484338	472.245807	942.500322	471.753799	9
5	**950.528056**	475.767666	933.501507	467.254392			L	***847.426823***	424.217049	830.400274	415.703775	829.416258	415.211767	8
6	**1051.575735**	**526.291505**	1034.549186	517.778231	1033.565170	517.286223	T	***734.342759***	367.675017	717.316210	359.161743	716.332194	358.669735	7
7	**1108.597199**	554.802237	1091.570650	546.288963	1090.586634	545.796955	G	***633.295080***	317.151178	616.268531	308.637903	615.284515	308.145895	6
8	1223.624142	612.315709	1206.597593	603.802435	1205.613577	603.310426	D	***576.273616***	288.640446	559.247067	280.127171	558.263051	279.635163	5
9	1324.671821	662.839548	1307.645272	654.326274	1306.661256	653.834266	T	***461.246673***	231.126974	444.220124	222.613700	443.236108	222.121692	4
10	1452.730399	726.868837	1435.703850	718.355563	1434.719834	717.863555	Q	***360.198994***	180.603135	343.172445	172.089860			3
11	1509.751863	755.379569	1492.725314	746.866295	1491.741298	746.374287	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 HQFLLTGDTQGR
(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	1682.856277	0.010925	HQFLLTGDTQGR
3.7	1682.845032	0.022170	APEHCELVVDLFVR
0.8	1682.845032	0.022170	QFHLTDDDLLR
0.5	1682.848389	0.018813	AMMQQKVVTSEIFR

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

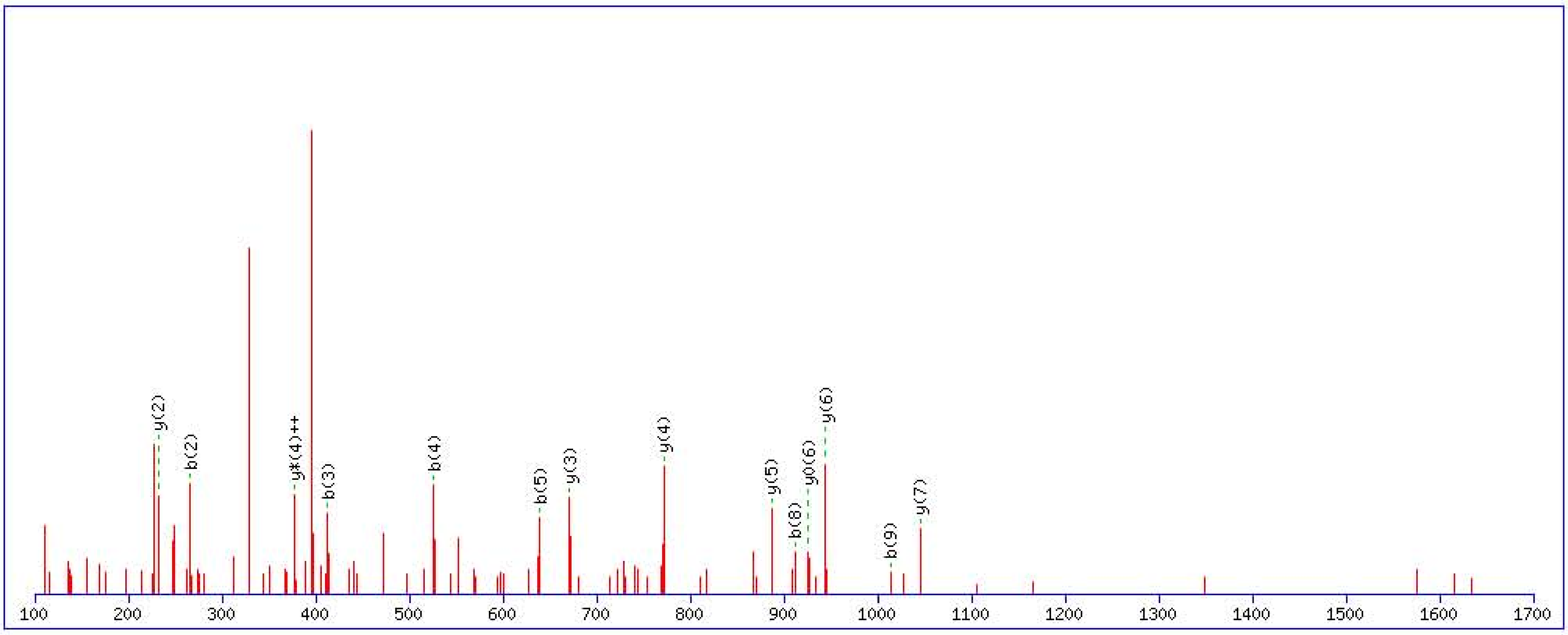
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQFLLTGDTQGR**
Found in **A1BG_HUMAN**, Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4

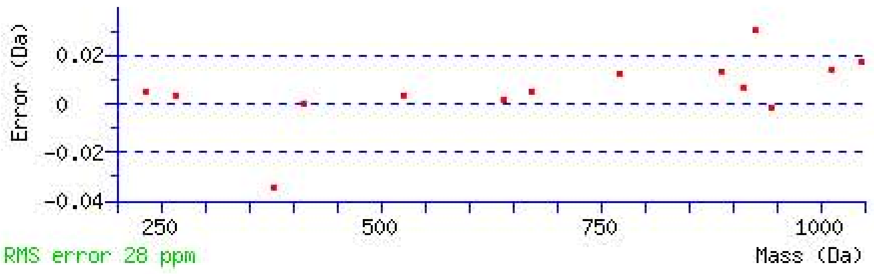
Match to Query 42070: 1682.873652 from(561.965160,3+) rtinseconds(1869) index(5585)
Title: Locus:1.1.1.2905.11 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

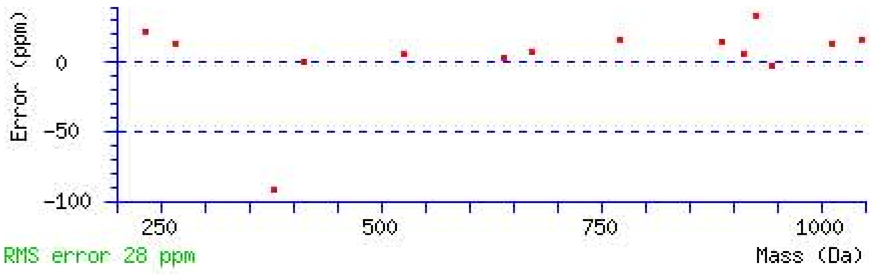
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1682.856277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.039
Matches : 14/114 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	138.066188	69.536732					H							12
2	***266.124766***	133.566021	249.098217	125.052746			Q	1546.804627	773.905952	1529.778078	765.392677	1528.794062	764.900669	11
3	***413.193180***	207.100228	396.166631	198.586953			F	1418.746049	709.876663	1401.719500	701.363388	1400.735484	700.871380	10
4	***526.277244***	263.642260	509.250695	255.128986			L	1271.677635	636.342456	1254.651086	627.829181	1253.667070	627.337173	9
5	***639.361308***	320.184292	622.334759	311.671018			L	1158.593571	579.800424	1141.567022	571.287149	1140.583006	570.795141	8
6	740.408987	370.708132	723.382438	362.194857	722.398422	361.702849	T	***1045.509507***	523.258392	1028.482958	514.745117	1027.498942	514.253109	7
7	797.430451	399.218864	780.403902	390.705589	779.419886	390.213581	G	***944.461828***	472.734552	927.435279	464.221278	926.451263	463.729270	6
8	***912.457394***	456.732335	895.430845	448.219061	894.446829	447.727053	D	***887.440364***	444.223820	870.413815	435.710546	869.429799	435.218538	5
9	***1013.505073***	507.256175	996.478524	498.742900	995.494508	498.250892	T	***772.413421***	386.710349	755.386872	378.197074	754.402856	377.705066	4
10	1452.730399	726.868838	1435.703850	718.355563	1434.719834	717.863555	Q	***671.365742***	336.186509	654.339193	327.673235			3
11	1509.751863	755.379570	1492.725314	746.866295	1491.741298	746.374287	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 HQFLLTGDTQGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.0	1682.856277	0.017375	HQFLLTGDTQGR

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

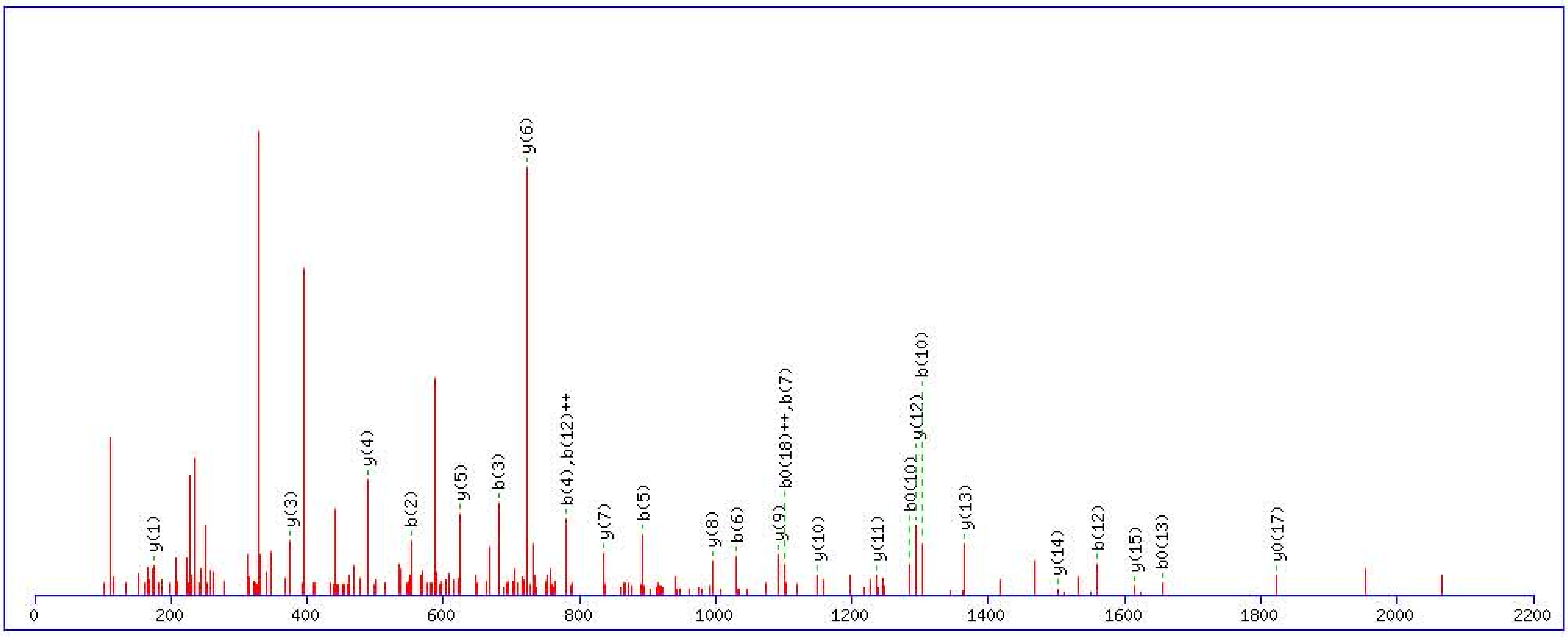
Mascot Search Results

Peptide View

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

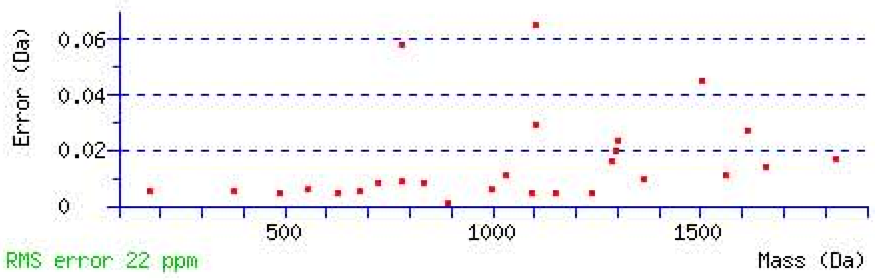
Match to Query 23625: 2393.316936 from(599.336510,4+) rtinseconds(2088) index(7056)
Title: Locus:1.1.1.2981.9 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

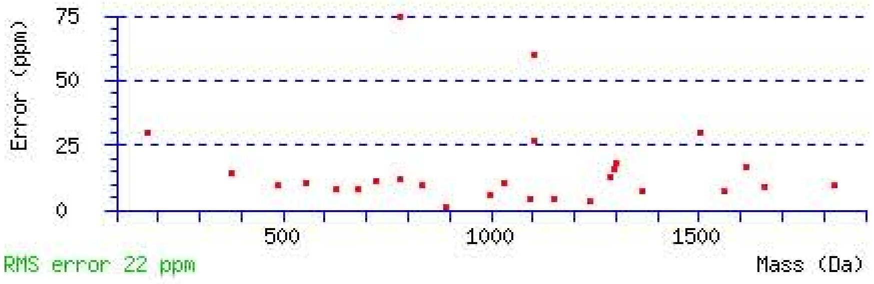
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2393.282410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 82  Expect: 3.3e-007
Matches : 27/196 fragment ions using 50 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	**553.316666**	277.161971	536.290117	268.648697			Q	2281.205625	1141.106450	2264.179076	1132.593176	2263.195060	1132.101168	18
3	**681.375244**	341.191260	664.348695	332.677986			Q	1841.980299	921.493788	1824.953750	912.980513	1823.969734	912.488505	17
4	**780.443658**	390.725467	763.417109	382.212193			V	1713.921721	857.464498	1696.895172	848.951224	1695.911156	848.459216	16
5	**893.527722**	447.267499	876.501173	438.754225			L	***1614.853307***	807.930292	1597.826758	799.417017	1596.842742	798.925009	15
6	**1030.586634**	515.796955	1013.560085	507.283681			H	***1501.769243***	751.388260	1484.742694	742.874985	1483.758678	742.382977	14
7	**1101.623748**	551.315512	1084.597199	542.802238			A	***1364.710331***	682.858804	1347.683782	674.345529	1346.699766	673.853521	13
8	1158.645212	579.826244	1141.618663	571.312970			G	***1293.673217***	647.340247	1276.646668	638.826972	1275.662652	638.334964	12
9	1245.677240	623.342258	1228.650691	614.828984	1227.666675	614.336975	S	***1236.651753***	618.829515	1219.625204	610.316240	1218.641188	609.824232	11
10	**1302.698704**	651.852990	1285.672155	643.339716	1284.688139	642.847707	G	***1149.619725***	575.313501	1132.593176	566.800226	1131.609160	566.308218	10
11	1399.751468	700.379372	1382.724919	691.866098	1381.740903	691.374089	P	***1092.598261***	546.802769	1075.571712	538.289494	1074.587696	537.797486	9
12	**1559.782117**	780.394697	1542.755568	771.881422	1541.771552	771.389414	C	***995.545497***	498.276387	978.518948	489.763112	977.534932	489.271104	8
13	1672.866181	836.936728	1655.839632	828.423454	1654.855616	827.931446	L	***835.514848***	418.261062	818.488299	409.747788	817.504283	409.255780	7
14	1769.918945	885.463110	1752.892396	876.949836	1751.908380	876.457828	P	***722.430784***	361.719030	705.404235	353.205756	704.420219	352.713748	6
15	1906.977857	953.992566	1889.951308	945.479292	1888.967292	944.987284	H	***625.378020***	313.192648	608.351471	304.679374	607.367455	304.187366	5
16	2020.061921	1010.534598	2003.035372	1002.021324	2002.051356	1001.529316	L	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
17	2133.145985	1067.076630	2116.119436	1058.563356	2115.135420	1058.071348	L	***375.235044***	188.121160	358.208495	179.607886	357.224479	179.115878	3
18	2220.178013	1110.592644	2203.151464	1102.079370	2202.167448	1101.587362	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 LQQVLHAGSGPCLPHLLSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.1	2393.282410	0.034526	LQQVLHAGSGPCLPHLLSR
77.9	2393.282410	0.034526	LQQVLHAGSGPCLPHLLSR

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

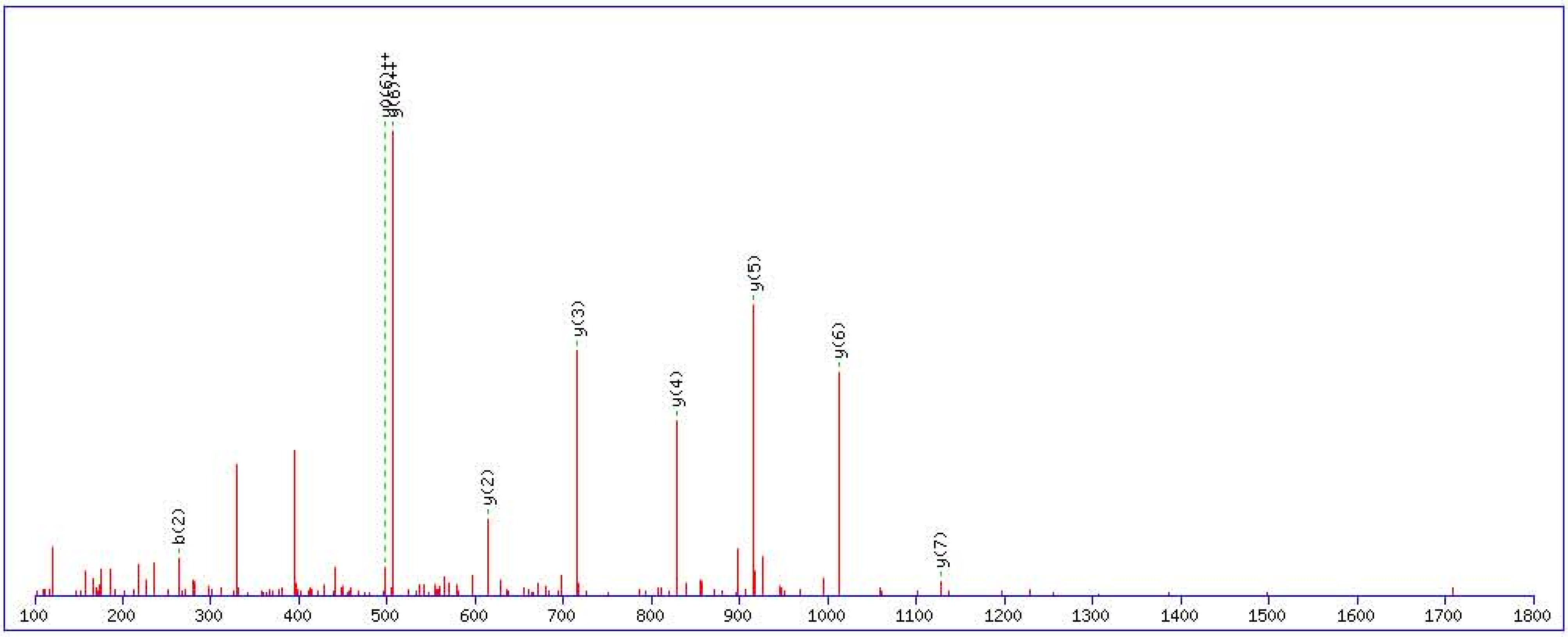
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

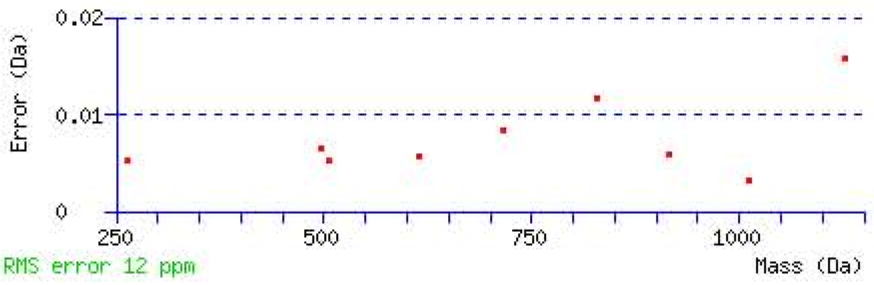
Match to Query 26038: 1273.658628 from(637.836590,2+) rtinseconds(1882) index(5684)
Title: Locus:1.1.1.2909.19 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

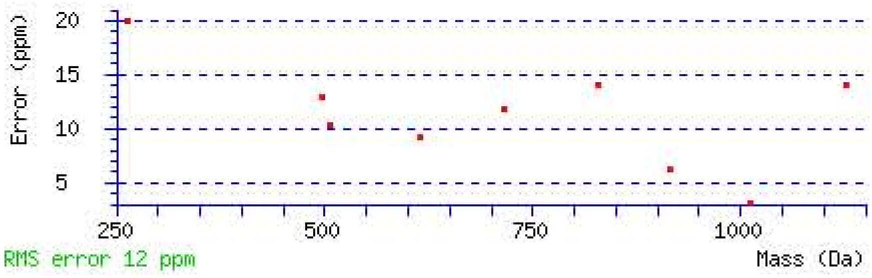
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1273.648895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 48 **Expect:** 0.00037
Matches : 9/66 fragment ions using 12 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.075690	74.541483					F							8
2	**263.102633**	132.054954			245.092068	123.049672	D	***1127.587756***	564.297516	1110.561207	555.784242	1109.577191	555.292233	7
3	360.155397	180.581336			342.144832	171.576054	P	***1012.560813***	506.784045	995.534264	498.270770	994.550248	497.778762	6
4	447.187425	224.097350			429.176860	215.092068	S	***915.508049***	458.257663	898.481500	449.744388	897.497484	449.252380	5
5	560.271489	280.639383			542.260924	271.634100	L	***828.476021***	414.741649	811.449472	406.228374	810.465456	405.736366	4
6	661.319168	331.163222			643.308603	322.157940	T	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
7	1100.544494	550.775885	1083.517945	542.262611	1082.533929	541.770603	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 FDPSLTQR
(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	1273.648895	0.009733	FDPSLTQR
21.7	1273.670654	-0.012026	FDIAIIYYTR
2.6	1273.671356	-0.012728	LLCARTFHTR
1.1	1273.652695	0.005933	EHQAHLEALAR
0.7	1273.677399	-0.018771	MVSLLQEK
0.5	1273.667984	-0.009356	RGSYLTVHWR
0.1	1273.670013	-0.011385	DLVTMVEQLAR

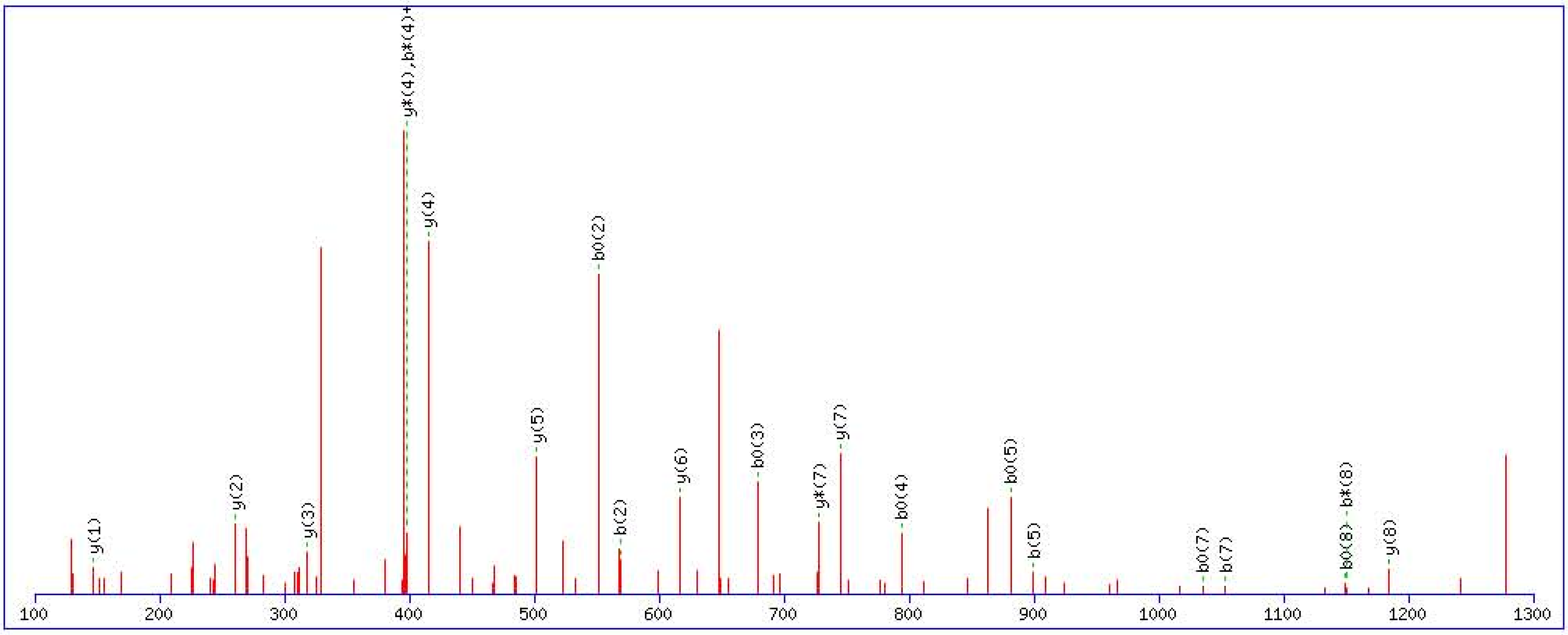
Mascot Search Results

Peptide View

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

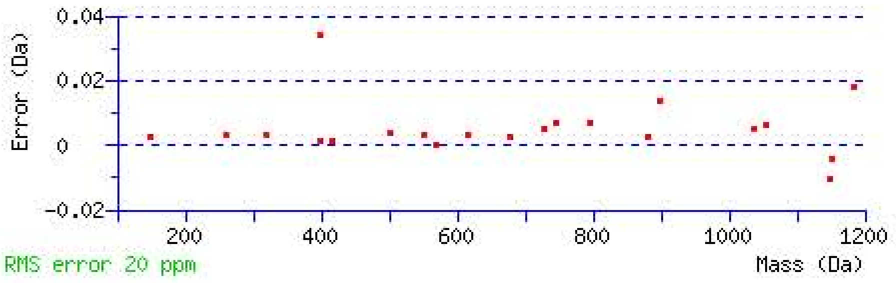
Match to Query 27204: 1312.597368 from(657.305960,2+) rtinseconds(1151) index(18676)
Title: Locus:1.1.1.2543.11 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

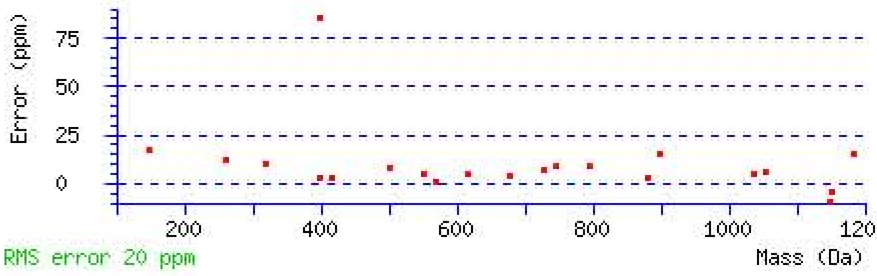
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 46 **Expect:** 0.00071
Matches : 21/86 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	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
46.0	1312.608139	-0.010771	EQQDSPGNK
30.5	1312.608139	-0.010771	EQQDSPGNK

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

{MATRIX}
{SCIENCE}

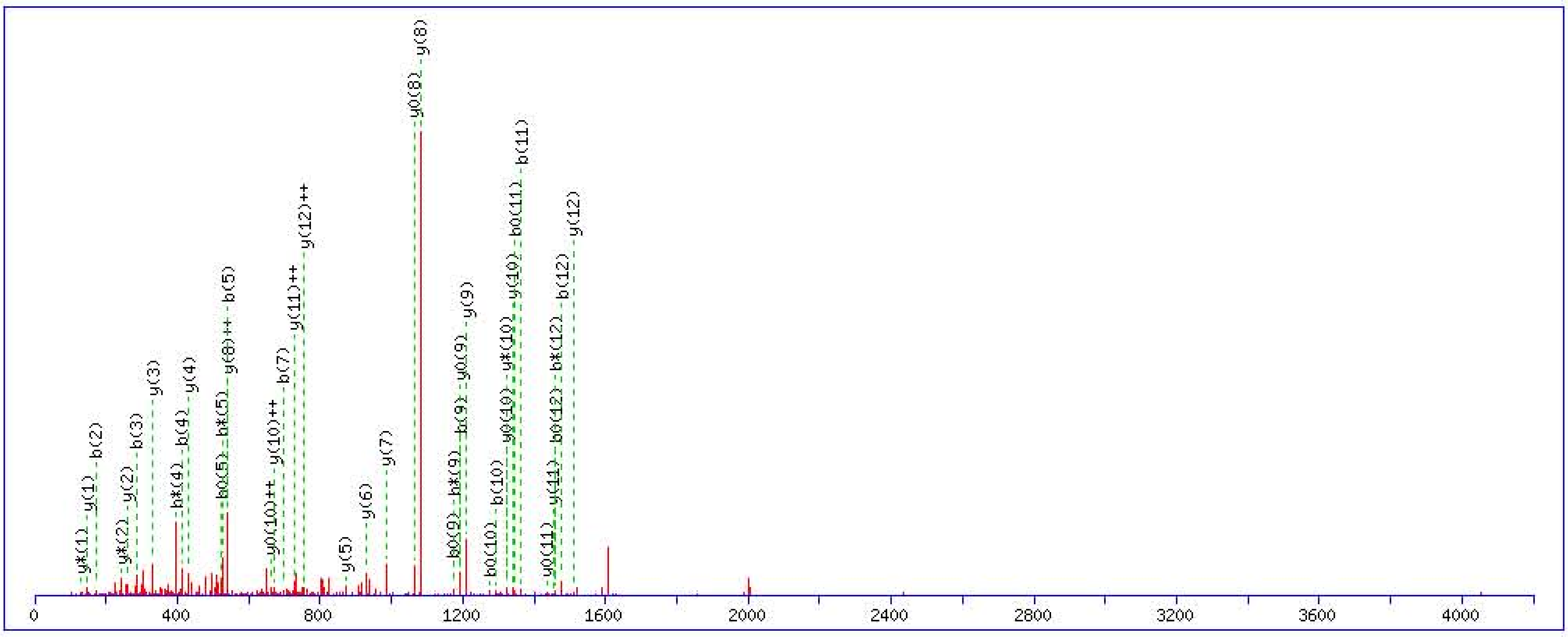
Mascot Search Results

Peptide View

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

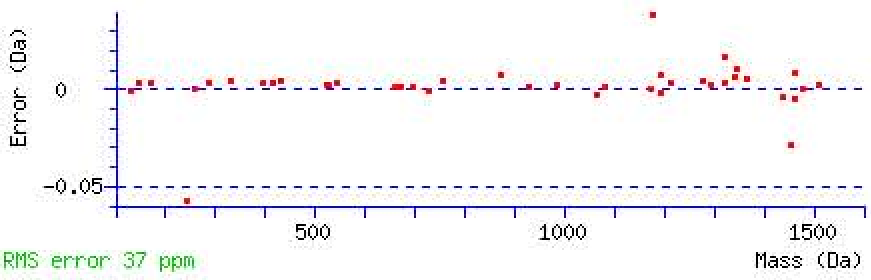
Match to Query 39839: 1622.853288 from(812.433920,2+) rtinseconds(1598) index(3977)
Title: Locus:1.1.1.2810.18 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

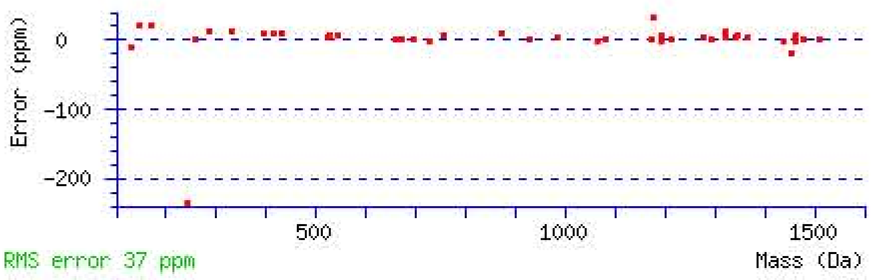
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 69 **Expect:** 2.5e-006
Matches : 42/126 fragment ions using 92 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
68.8	1622.845016	0.008272	LGNQEPGGQTALK
28.8	1622.845016	0.008272	LGNQEPGGQTALK
8.5	1622.831085	0.022203	GLNPNPSHQMTKRK
5.2	1622.858917	-0.005629	SVLLMELEVNYGLK
3.7	1622.837601	0.015687	SQSEKQTYLEVRR
2.7	1622.864288	-0.011000	FPLPSMYRALVWK
2.3	1622.860260	-0.006972	EHSAFQAPAVKK
2.3	1622.849045	0.004243	IPMPDFDLHLKGPK
0.7	1622.863632	-0.010344	KRMILSTISWMGGK
0.2	1622.833771	0.019517	LDLAGRDLTDYLMK

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

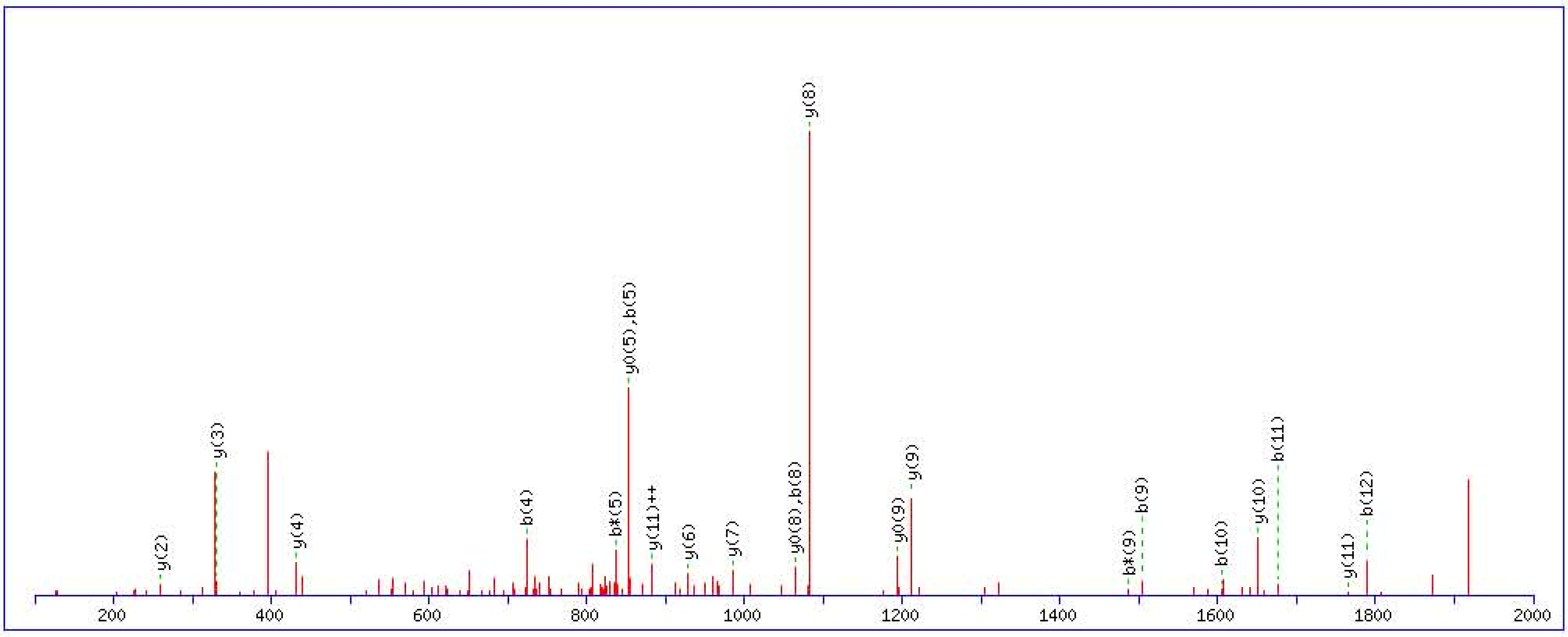
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

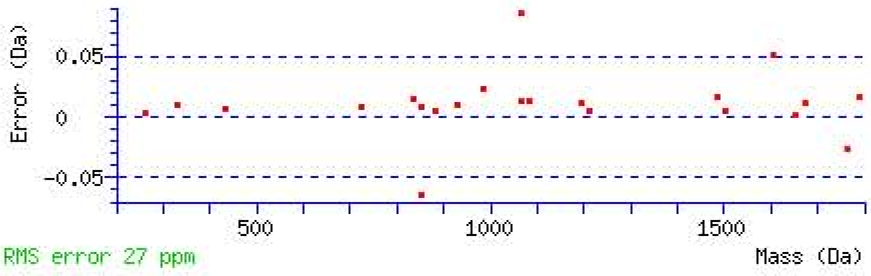
Match to Query 48369: 1934.030968 from(968.022760,2+) rtinseconds(1958) index(6285)
Title: Locus:1.1.1.2935.26 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

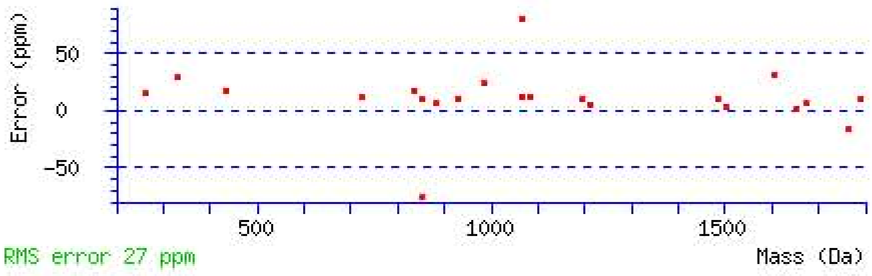
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 43  Expect: 0.0013
Matches : 22/126 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					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
42.6	1934.011765	0.019203	LGNQEPGGQTALK
11.3	1934.032867	-0.001899	KSRPLTGLMDLAKEMTK
5.6	1934.032867	-0.001899	KSRPLTGLMDLAKEMTK
4.7	1934.004349	0.026619	SQSEKQTYLEVRR
2.7	1934.015594	0.015374	RCRTTYSASQLHTLIK
1.5	1934.037369	-0.006401	NYLEGIYNVPVAAVRTR
1.1	1934.034225	-0.003257	QVQSQAHGLQMRLK
0.3	1934.027008	0.003960	VSFRLHITEPKMMFAK

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

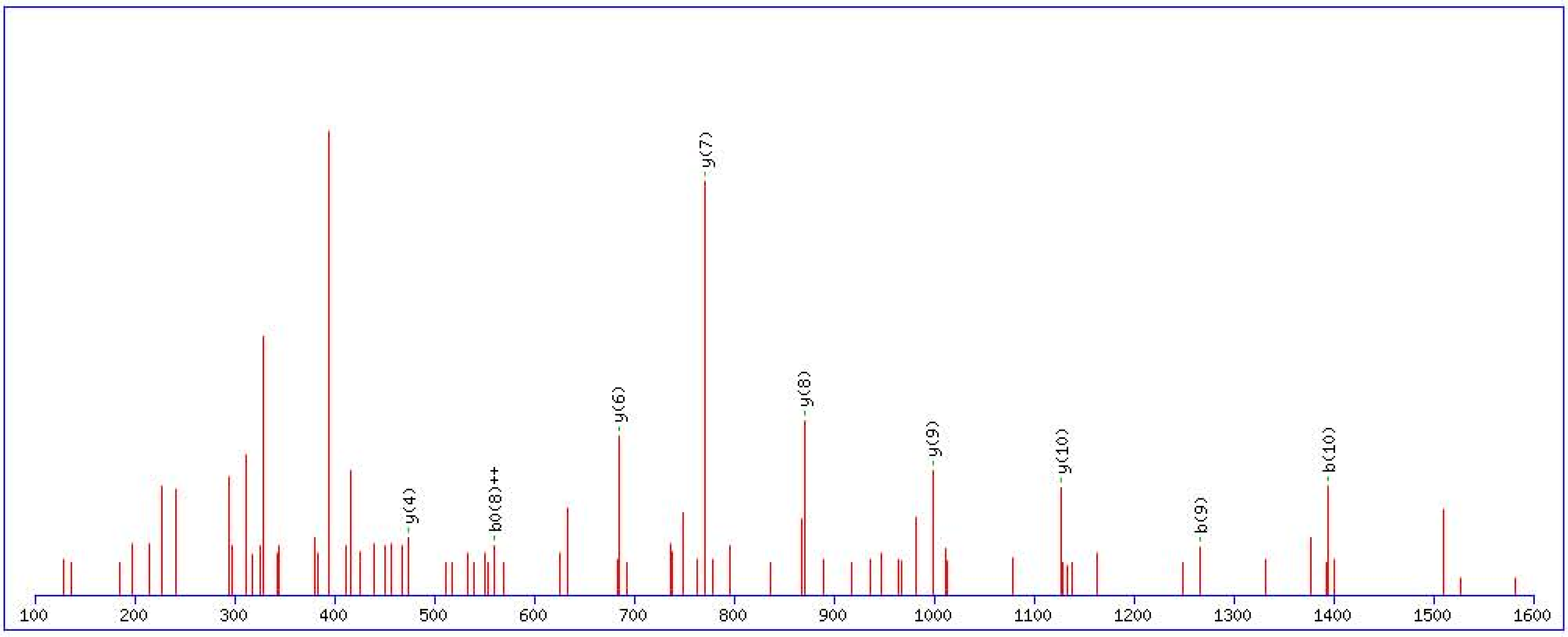
Mascot Search Results

Peptide View

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

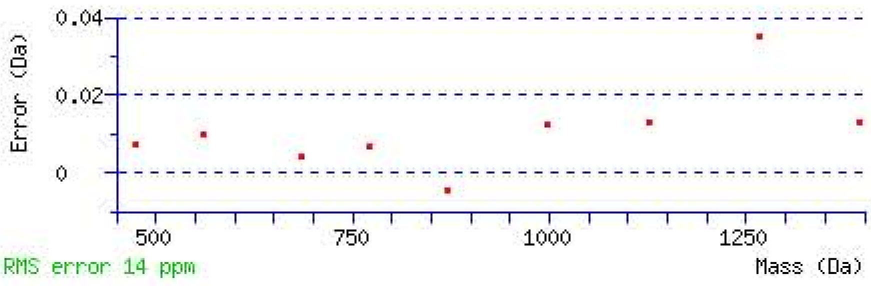
Match to Query 57027: 2263.248342 from(755.423390,3+) rtinseconds(2508) index(28121)
Title: Locus:1.1.1.3015.11 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

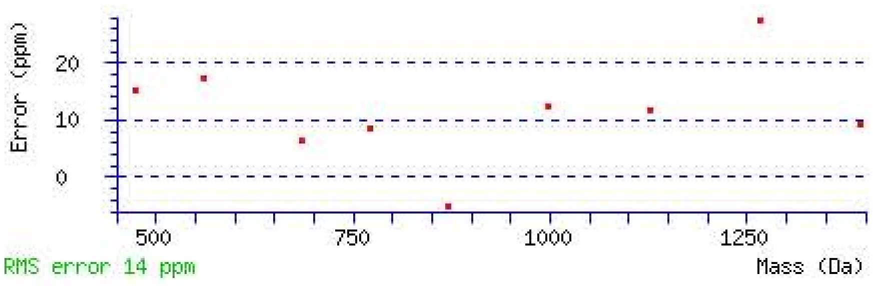
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2263.224594
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0036
Matches : 9/194 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	129.065854	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
30.0	2263.224594	0.023748	QLTSGPNQEQVSPLTLLK
30.0	2263.224594	0.023748	QLTSGPNQEQVSPLTLLK
5.6	2263.224594	0.023748	QLTSGPNQEQVSPLTLLK
4.0	2263.224594	0.023748	GLALSSNKVKSVVMVVFDNEK

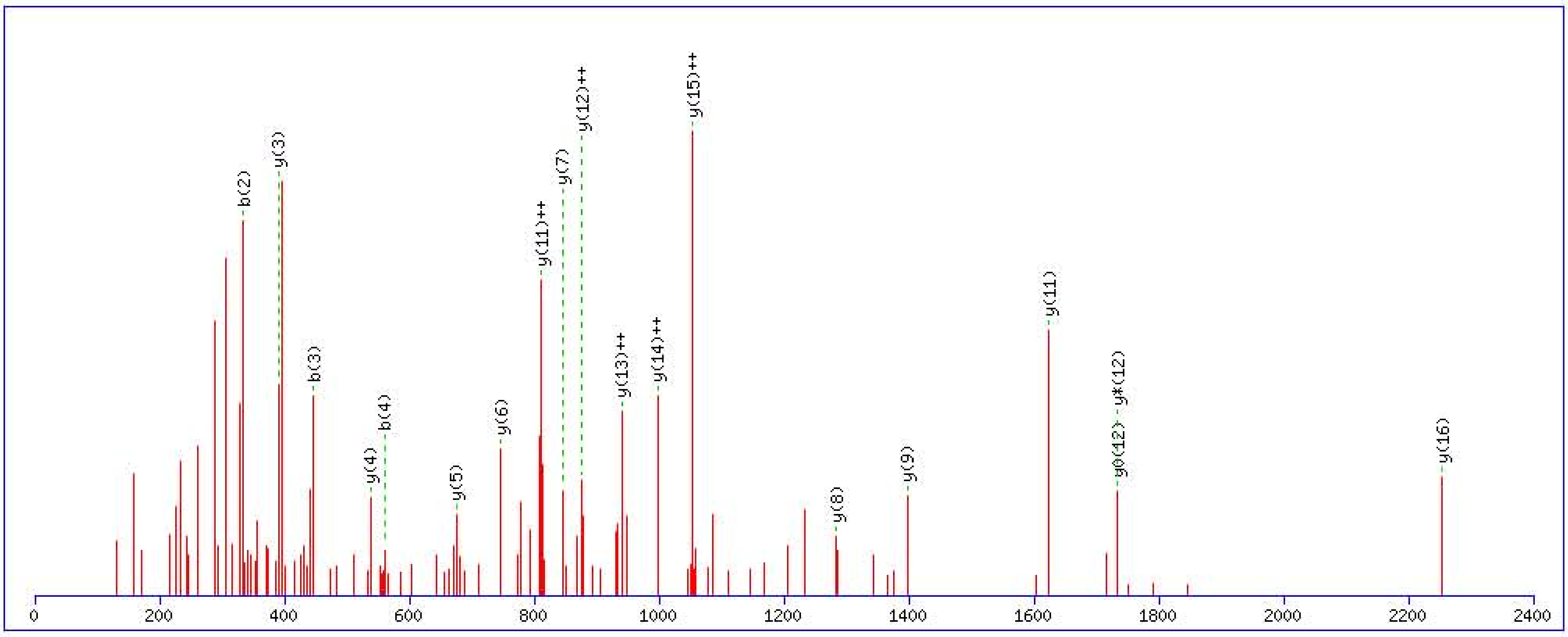
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

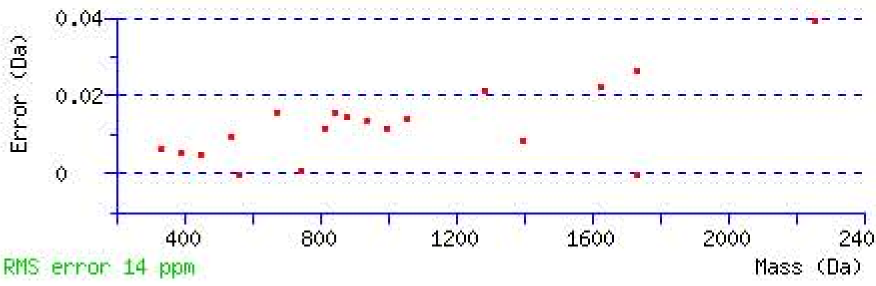
Match to Query 61171: 2439.311442 from(814.111090,3+) rtinseconds(2904) index(12378)
Title: Locus:1.1.1.3263.14 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

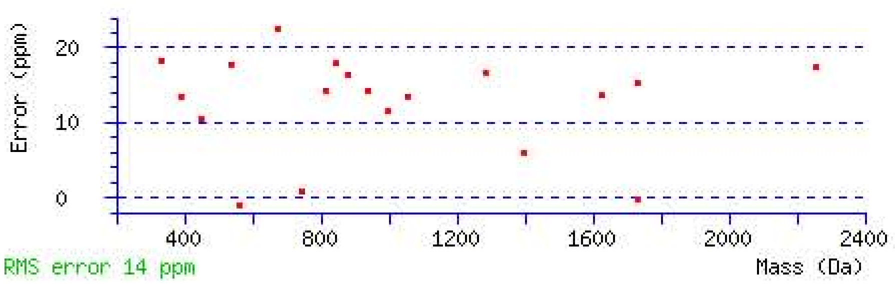
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2439.281326
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0042
Matches : 19/156 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	187.086589	94.046932					W							17
2	**334.155003**	167.581140					F	***2254.209296***	1127.608286	2237.182747	1119.095011	2236.198731	1118.603003	16
3	**447.239067**	224.123172					L	2107.140882	1054.074079	2090.114333	1045.560804	2089.130317	1045.068796	15
4	**560.323131**	280.665204					L	1994.056818	997.532047	1977.030269	989.018772	1976.046253	988.526764	14
5	689.365724	345.186500			671.355159	336.181218	E	1880.972754	940.990015	1863.946205	932.476741	1862.962189	931.984732	13
6	817.424302	409.215789	800.397753	400.702515	799.413737	400.210507	Q	1751.930161	876.468719	1734.903612	867.955444	1733.919596	867.463436	12
7	914.477066	457.742171	897.450517	449.228897	896.466501	448.736889	P	***1623.871583***	812.439429	1606.845034	803.926155	1605.861018	803.434147	11
8	1043.519659	522.263468	1026.493110	513.750193	1025.509094	513.258185	E	1526.818819	763.913047	1509.792270	755.399773	1508.808254	754.907765	10
9	1156.603723	578.805500	1139.577174	570.292225	1138.593158	569.800217	I	***1397.776226***	699.391751	1380.749677	690.878476			9
10	1595.829049	798.418163	1578.802500	789.904888	1577.818484	789.412880	Q	***1284.692162***	642.849719	1267.665613	634.336444			8
11	1694.897463	847.952370	1677.870914	839.439095	1676.886898	838.947087	V	***845.466836***	423.237056	828.440287	414.723781			7
12	1765.934577	883.470927	1748.908028	874.957652	1747.924012	874.465644	A	***746.398422***	373.702849	729.371873	365.189574			6
13	1902.993489	952.000383	1885.966940	943.487108	1884.982924	942.995100	H	***675.361308***	338.184292	658.334759	329.671017			5
14	2050.061903	1025.534589	2033.035354	1017.021315	2032.051338	1016.529307	F	***538.302396***	269.654836	521.275847	261.141561			4
15	2147.114667	1074.060971	2130.088118	1065.547697	2129.104102	1065.055689	P	***391.233982***	196.120629	374.207433	187.607354			3
16	2294.183081	1147.595178	2277.156532	1139.081904	2276.172516	1138.589896	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 WFLLEQPEIQVAHFPFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.6	2439.281326	0.030116	WFLLEQPEIQVAHFPFK
15.0	2439.281326	0.030116	WFLLEQPEIQVAHFPFK

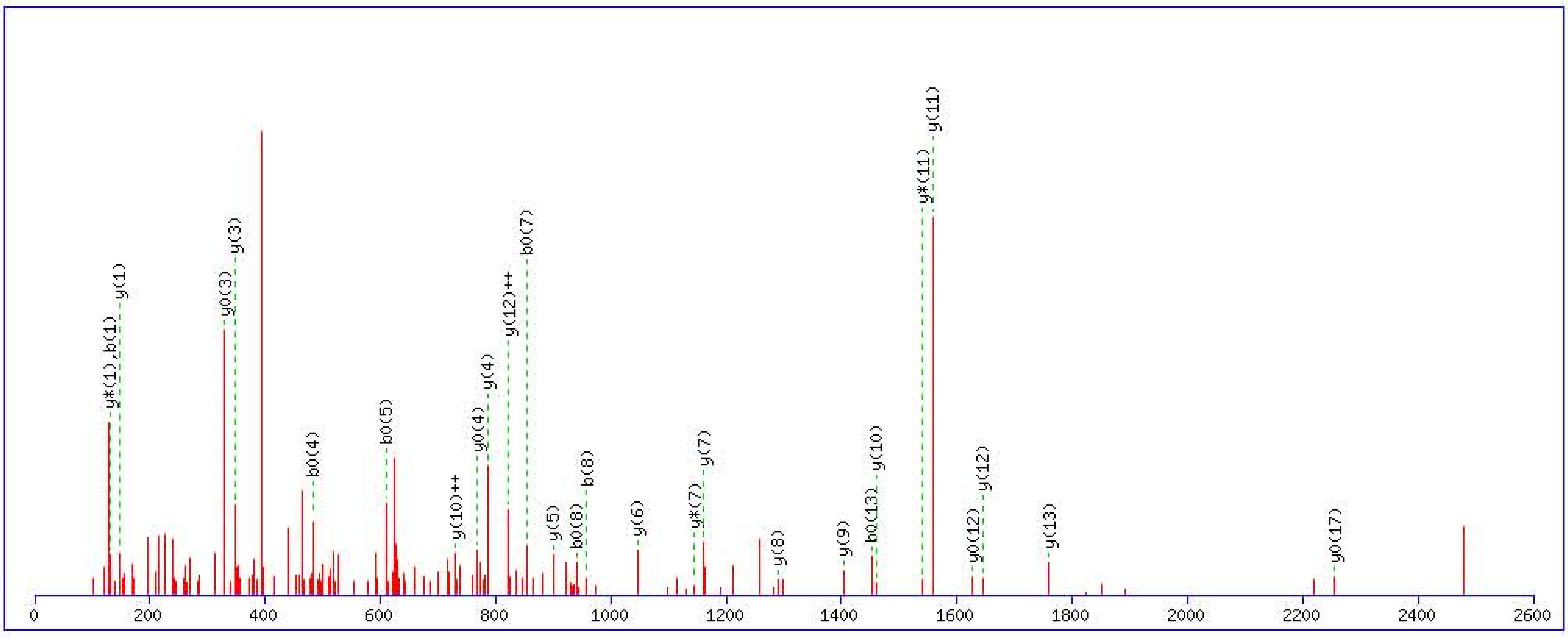
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

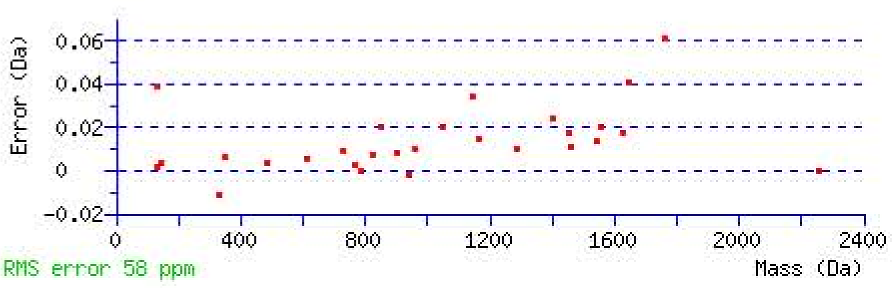
Match to Query 63379: 2514.299056 from(629.582040,4+) rtinseconds(1896) index(5807)
Title: Locus:1.1.1.2914.17 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

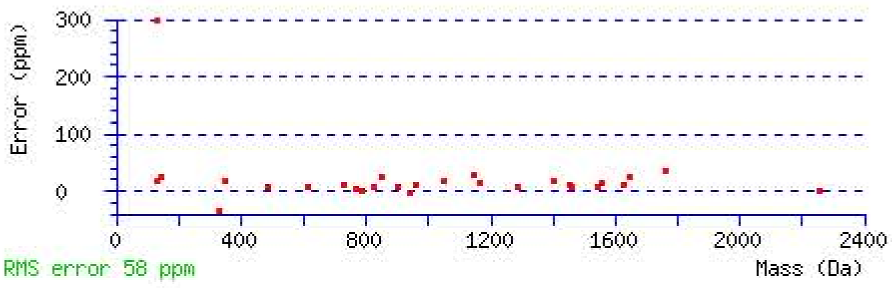
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2514.278793
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 0.00011
Matches : 28/208 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	**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
54.0	2514.278793	0.020263	ELKEQQDSPGNKDFLQSLK

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

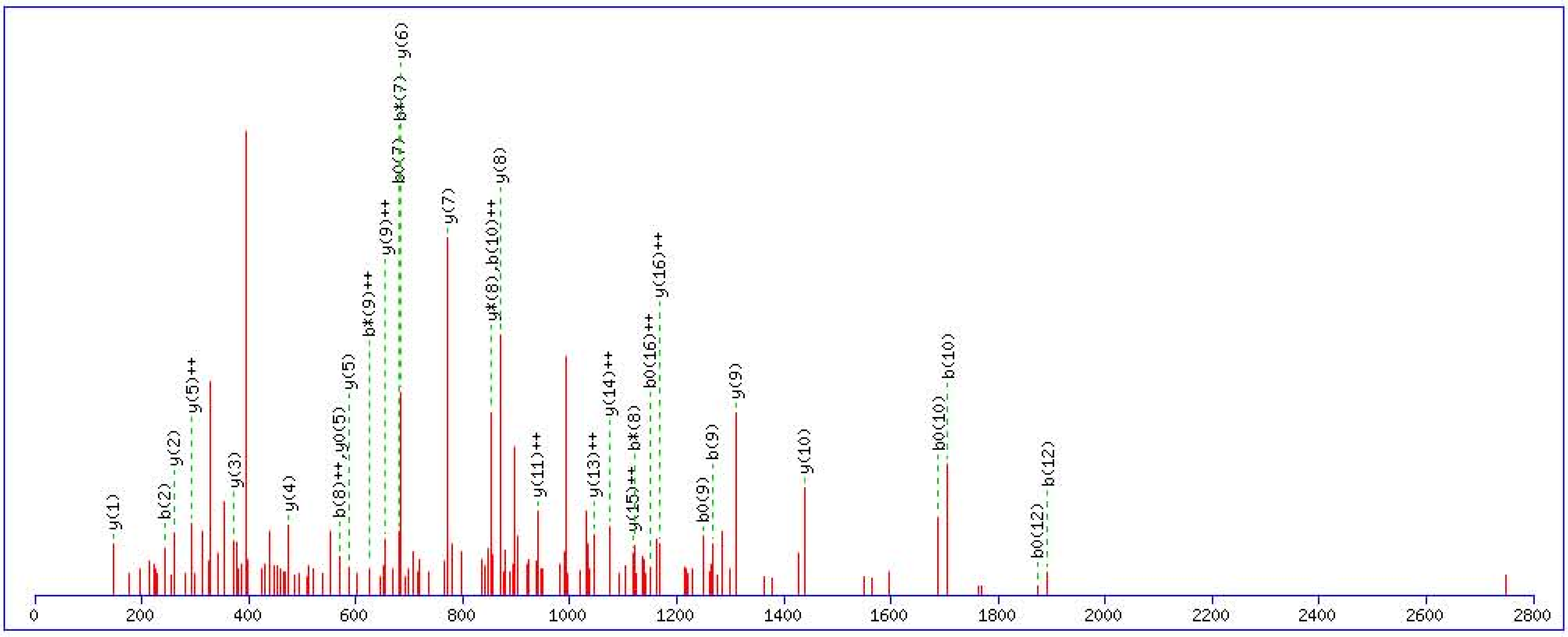
Mascot Search Results

Peptide View

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

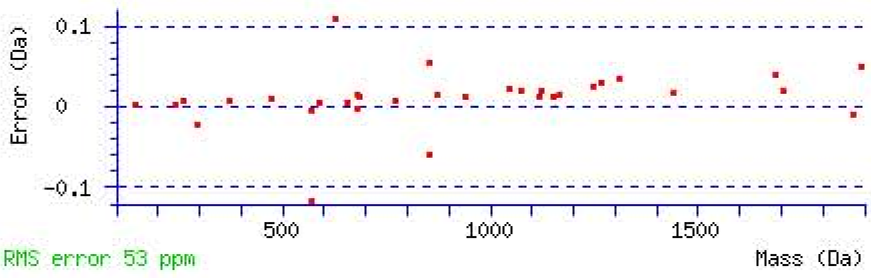
Match to Query 64174: 2574.423792 from(859.148540,3+) rtinseconds(2676) index(10838)
Title: Locus:1.1.1.3185.24 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

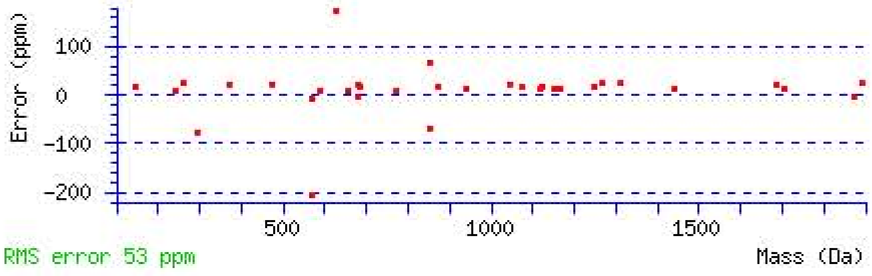
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 51  Expect: 8.1e-005
Matches : 33/194 fragment ions using 62 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	**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
51.3	2574.391342	0.032450	QLTSGPNQEQVSPLTLLK
34.9	2574.391342	0.032450	QLTSGPNQEQVSPLTLLK
14.5	2574.391342	0.032450	QLTSGPNQEQVSPLTLLK

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

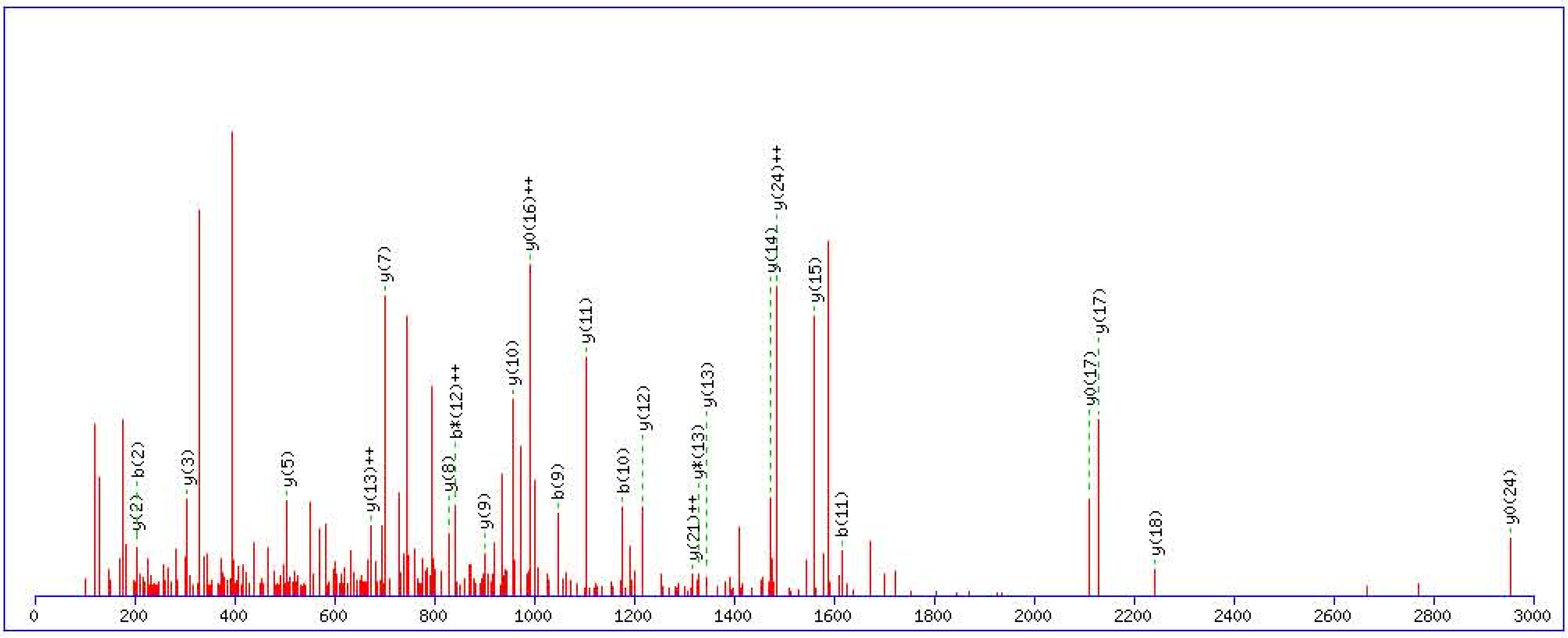
Mascot Search Results

Peptide View

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

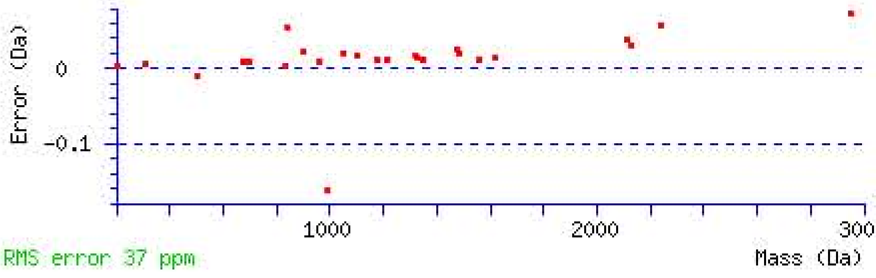
Match to Query 72124: 3175.708696 from(794.934450,4+) rtinseconds(2737) index(11178)
Title: Locus:1.1.1.3206.8 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

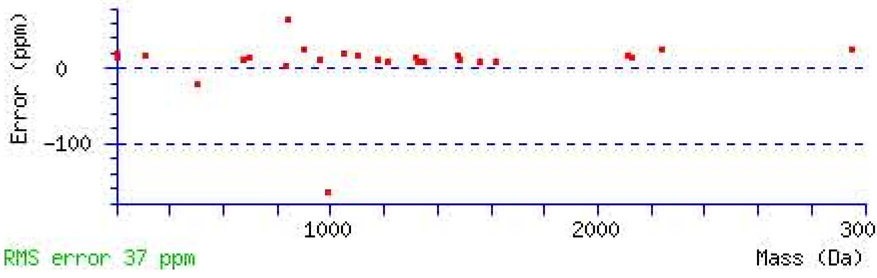
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3175.662750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 7.2e-006
Matches : 26/278 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	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





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
63.2	3175.662750	0.045946	GFPIKEDFLEQSEQLFGAKPVSLTGK
33.6	3175.662750	0.045946	GFPIKEDFLEQSEQLFGAKPVSLTGK

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

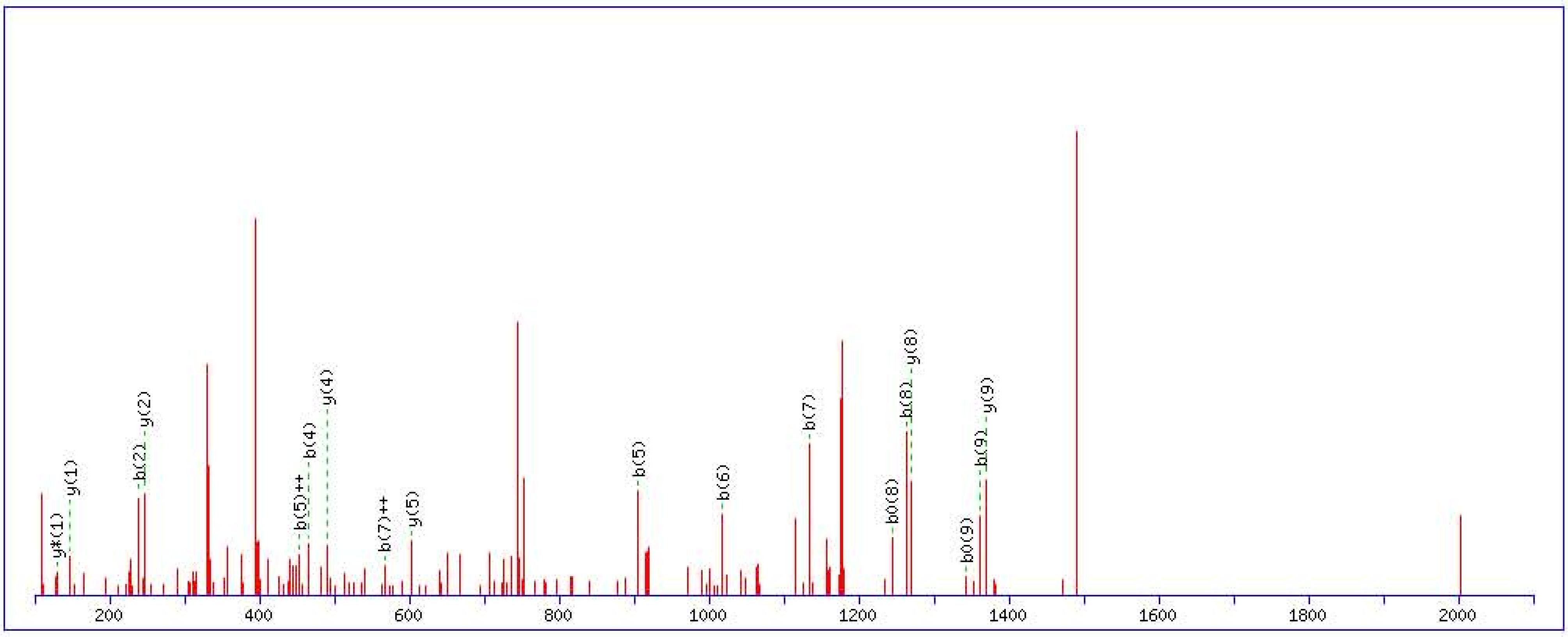
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

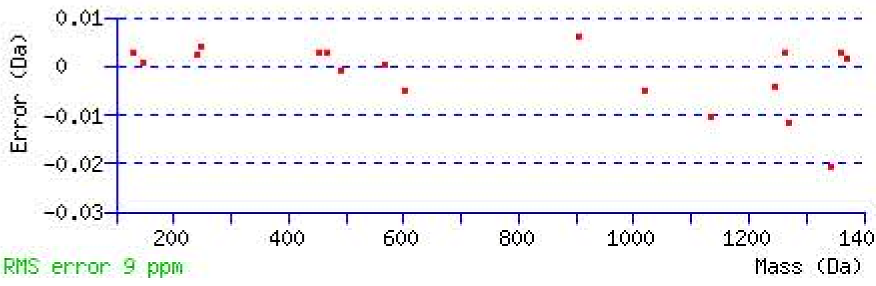
Match to Query 35225: 1506.790428 from(754.402490,2+) rtinseconds(1566) index(21511)
Title: Locus:1.1.1.2688.8 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

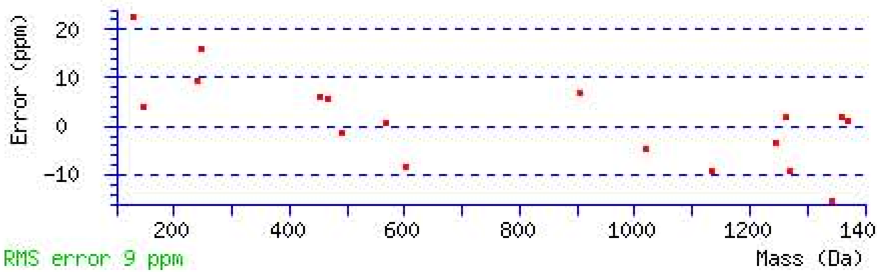
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1506.786438
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0044
Matches : 18/96 fragment ions using 41 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	138.066188	69.536732					H							10
2	***239.113867***	120.060571			221.103302	111.055289	T	***1370.734814***	685.871045	1353.708265	677.357771	1352.724249	676.865763	9
3	352.197931	176.602603			334.187366	167.597321	L	***1269.687135***	635.347206	1252.660586	626.833931	1251.676570	626.341923	8
4	***466.240858***	233.624067	449.214309	225.110793	448.230293	224.618785	N	1156.603071	578.805174	1139.576522	570.291899	1138.592506	569.799891	7
5	***905.466184***	**453.236730**	888.439635	444.723456	887.455619	444.231448	Q	1042.560144	521.783710	1025.533595	513.270436	1024.549579	512.778428	6
6	***1018.550248***	509.778762	1001.523699	501.265488	1000.539683	500.773480	I	***603.334818***	302.171047	586.308269	293.657773	585.324253	293.165765	5
7	***1133.577191***	**567.292234**	1116.550642	558.778959	1115.566626	558.286951	D	***490.250754***	245.629015	473.224205	237.115741	472.240189	236.623733	4
8	***1262.619784***	631.813530	1245.593235	623.300256	1244.609219	622.808248	E	375.223811	188.115544	358.197262	179.602269	357.213246	179.110261	3
9	***1361.688198***	681.347737	1344.661649	672.834463	1343.677633	672.342455	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 HTLNQIDEVK
(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	1506.786438	0.003990	HTLNQIDEVK
8.9	1506.794983	-0.004555	HRATQSGQRR
7.3	1506.779037	0.011391	EHQALQDLVDLAR
6.5	1506.790253	0.000175	SSRFLKEGNNLSR
4.4	1506.783081	0.007347	SPKFQLFGSPSGQK
3.8	1506.771149	0.019279	GEKSSMERLLTEK
2.8	1506.792953	-0.002525	DIDYLIGKESQVK
2.7	1506.772507	0.017921	QHISRNAQDK
2.5	1506.790482	-0.000054	EGQKDFVFVK
0.5	1506.792969	-0.002541	IGDFGLTKAIETDK

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

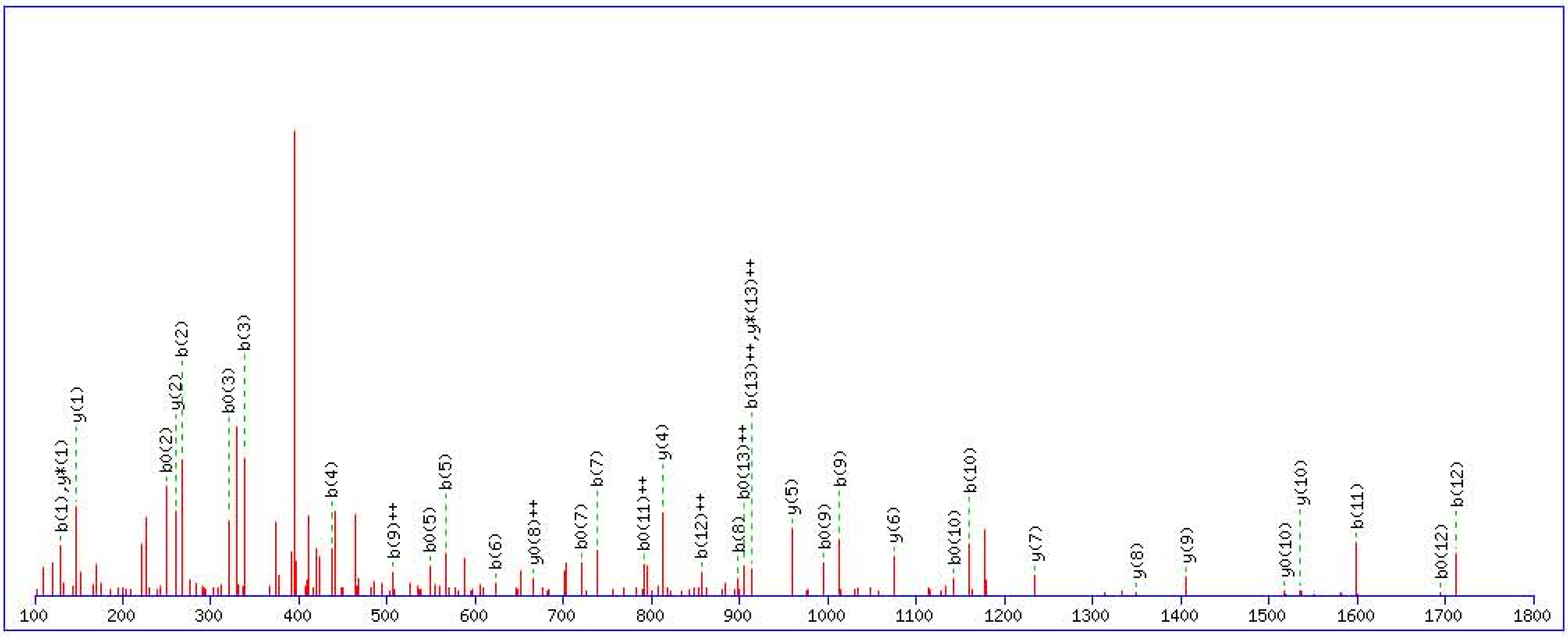
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

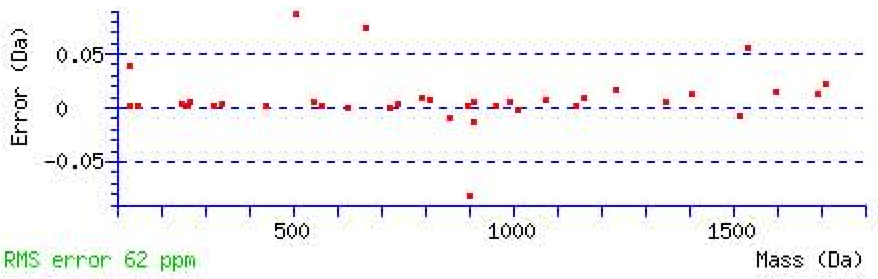
Match to Query 49286: 1970.935452 from(657.985760,3+) rtinseconds(2029) index(24899)
Title: Locus:1.1.1.2849.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

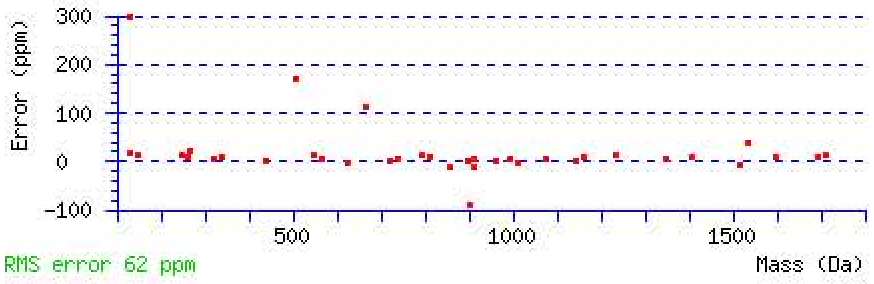
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1970.923019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 81  Expect: 9.9e-008
Matches : 37/126 fragment ions using 55 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							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
80.6	1970.923019	0.012433	EHAVEGDCDFQLLK
5.7	1970.959396	-0.023944	DVQSAMDRYTAFLK
3.2	1970.959381	-0.023929	NEEKPVQMMFKQSTFK

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

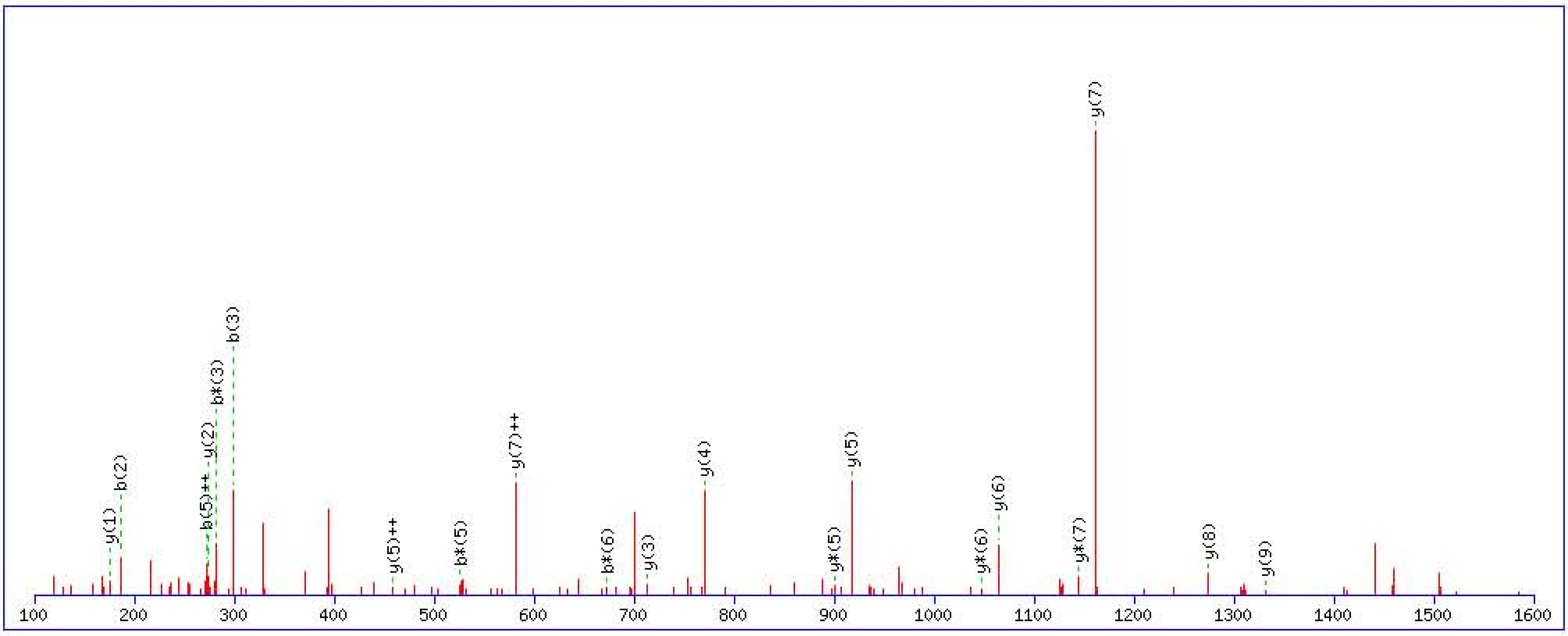
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

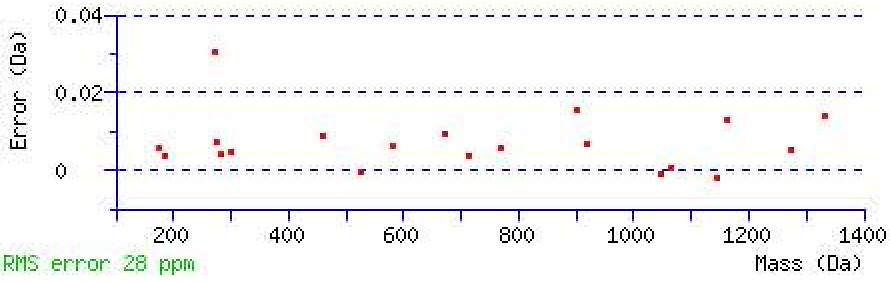
Match to Query 33661: 1458.795568 from(730.405060,2+) rtinseconds(2502) index(28074)
Title: Locus:1.1.1.3013.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

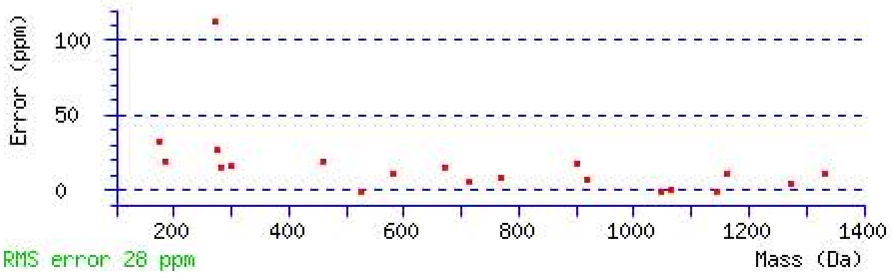
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1458.780594
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.00071
Matches : 20/72 fragment ions using 63 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	129.065854	65.036565	112.039305	56.523291	Q					10
2	**186.087318**	93.547297	169.060769	85.034023	G	***1331.729276***	666.368276	1314.702727	657.855002	9
3	**299.171382**	150.089329	282.144833	141.576055	I	***1274.707812***	637.857544	1257.681263	629.344270	8
4	396.224146	198.615711	379.197597	190.102436	P	***1161.623748***	581.315512	1144.597199	572.802238	7
5	543.292560	272.149918	526.266011	263.636643	F	***1064.570984***	532.789130	1047.544435	524.275856	6
6	690.360974	345.684125	673.334425	337.170850	F	***917.502570***	459.254923	900.476021	450.741649	5
7	747.382438	374.194857	730.355889	365.681582	G	***770.434156***	385.720716	753.407607	377.207442	4
8	1186.607764	593.807520	1169.581215	585.294246	Q	***713.412692***	357.209984	696.386143	348.696710	3
9	1285.676178	643.341727	1268.649629	634.828453	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 QGIPFFGQVR
(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	1458.780594	0.014974	QGIPFFGQVR
0.9	1458.805054	-0.009486	AVQPLLKVSMSMR
0.6	1458.775177	0.020391	SEMDKQALIPIAK

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

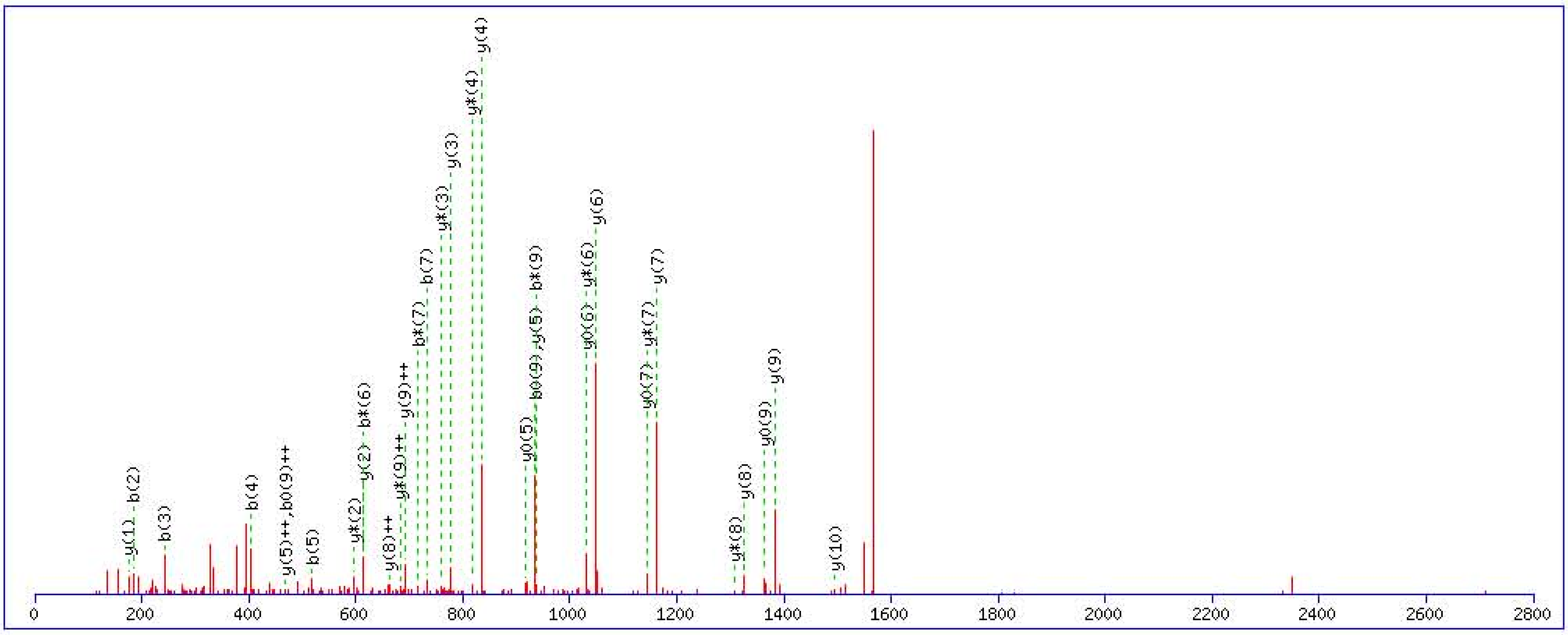
Mascot Search Results

Peptide View

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

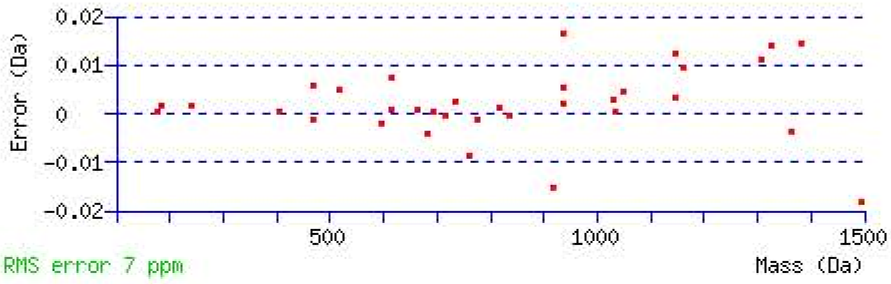
Match to Query 36976: 1565.814748 from(783.914650,2+) rtinseconds(1973) index(24489)
Title: Locus:1.1.1.2829.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

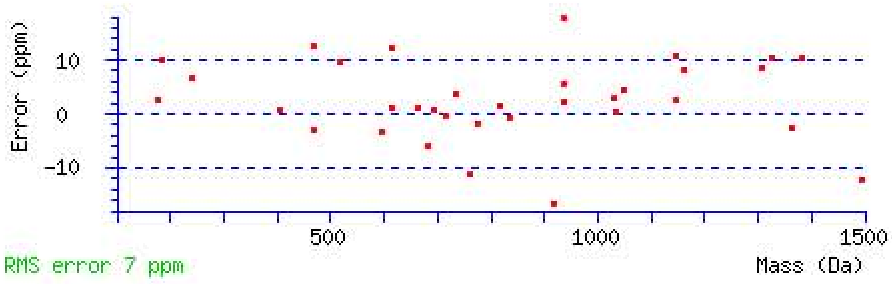


Monoisotopic mass of neutral peptide Mr(calc): 1565.802414
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 63 **Expect:** 9.8e-006
Matches : 34/90 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					**A**							**11**
2	**185.128454**	93.067865					**I**	***1495.772598***	748.389937	1478.746049	739.876663	1477.762033	739.384655	**10**
3	**242.149918**	121.578597					**G**	***1382.688534***	691.847905	1365.661985	683.334631	1364.677969	682.842623	**9**
4	**405.213247**	203.110261					**Y**	***1325.667070***	663.337173	1308.640521	654.823899	1307.656505	654.331890	**8**
5	**518.297311**	259.652294					**L**	***1162.603741***	581.805509	1145.577192	573.292234	1144.593176	572.800226	**7**
6	632.340238	316.673757	615.313689	308.160483			**N**	***1049.519677***	525.263477	1032.493128	516.750202	1031.509112	516.258194	**6**
7	**733.387917**	367.197597	716.361368	358.684322	715.377352	358.192314	**T**	***935.476750***	468.242013	918.450201	459.728739	917.466185	459.236731	**5**
8	790.409381	395.708329	773.382832	387.195054	772.398816	386.703046	**G**	***834.429071***	417.718174	817.402522	409.204899			**4**
9	953.472710	477.239993	936.446161	468.726719	935.462145	468.234711	**Y**	***777.407607***	389.207442	760.381058	380.694167			**3**
10	1392.698036	696.852656	1375.671487	688.339382	1374.687471	687.847374	**Q**	***614.344278***	307.675777	597.317729	299.162503			**2**
11							**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



RMS error 7 ppm



RMS error 7 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.9	1565.802414	0.012334	AIGYLNTGYQR
9.1	1565.827393	-0.012645	VHPALNVSTRTSER
2.8	1565.816132	-0.001384	SQIEKEGLEHQLR

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

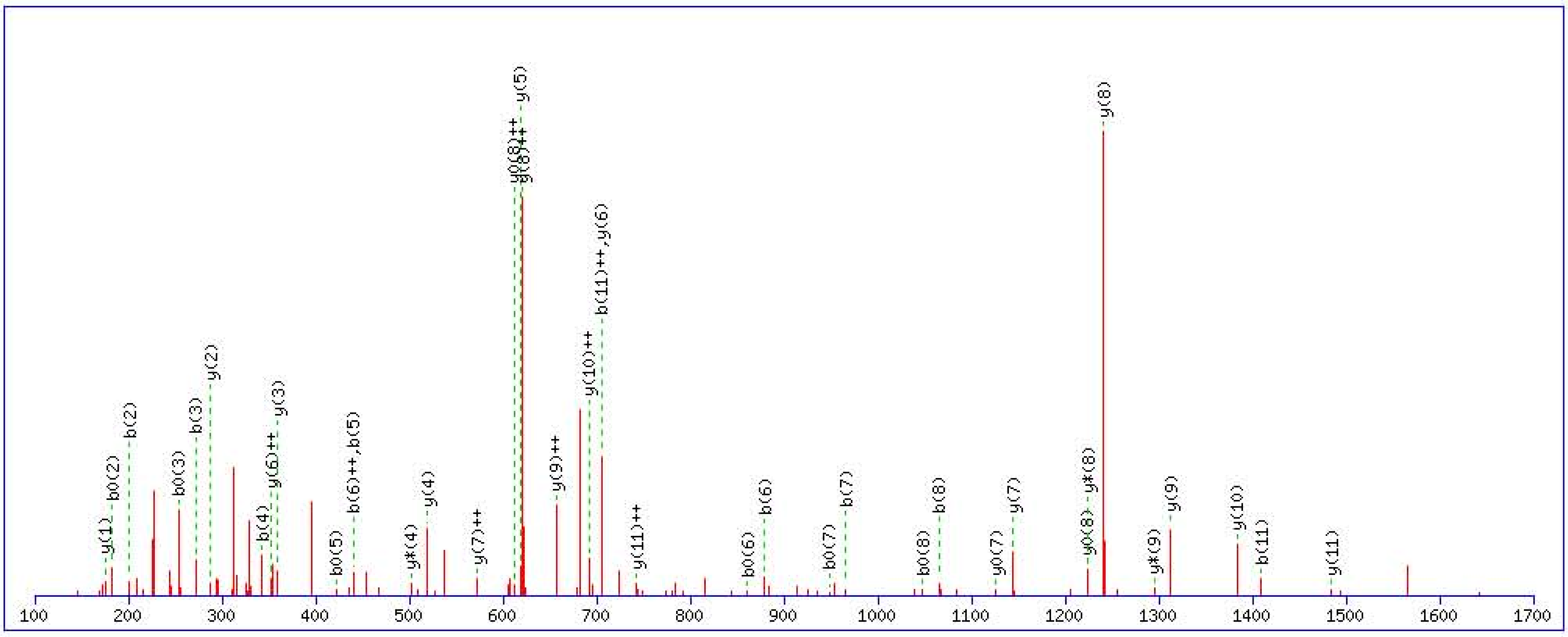
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

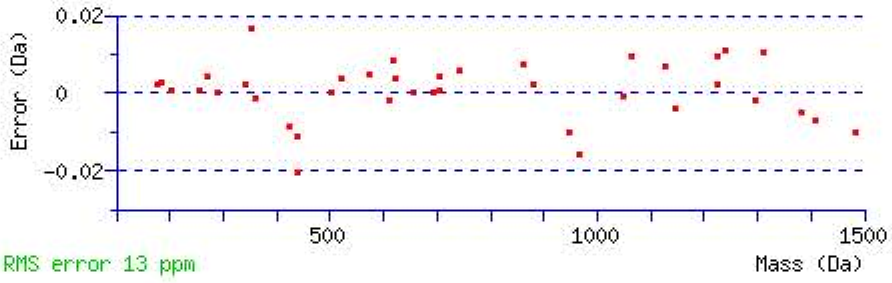
Match to Query 37721: 1582.843088 from(792.428820,2+) rtinseconds(1791) index(23162)
Title: Locus:1.1.1.2766.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

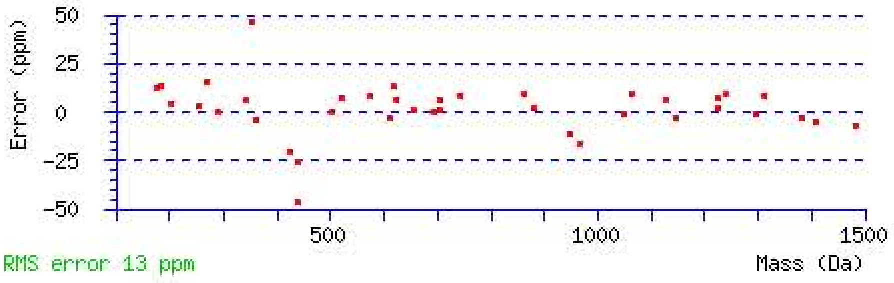
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1582.832352
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 9.8e-005
Matches : 39/110 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	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
52.4	1582.832352	0.010736	VTAAPQSVCALR
9.1	1582.865356	-0.022268	QPAPGPVEKPPR
5.7	1582.821579	0.021509	IGGHGPTLKAYQEGR
1.5	1582.821564	0.021524	LSKAVATWHANTER
1.3	1582.850128	-0.007040	GLTPTGMLPSGVLAGGR
1.1	1582.853912	-0.010824	RKPASGGLAASSSAPAR
0.2	1582.836868	0.006220	LHTVDGHWVAPVPR

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

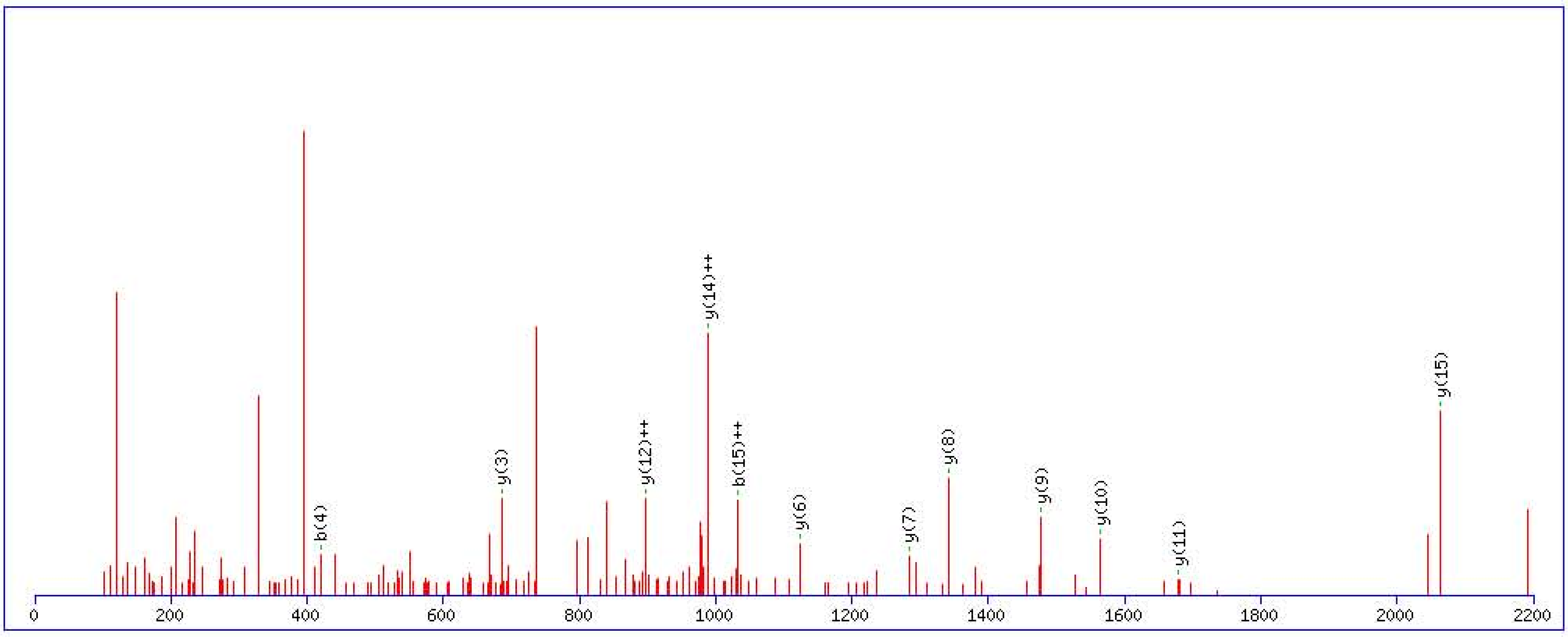
Mascot Search Results

Peptide View

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

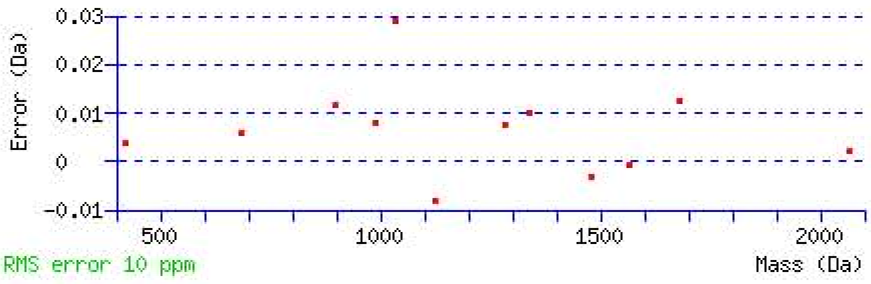
Match to Query 55593: 2210.056812 from(737.692880,3+) rtinseconds(1852) index(23581)
Title: Locus:1.1.1.2787.21 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

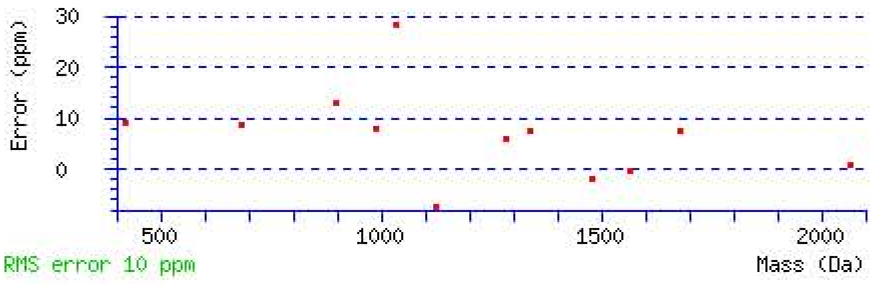
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 42  Expect: 0.00023
Matches : 12/154 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	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
42.4	2210.040131	0.016681	FSGQLNSHGCFYQQVK
31.1	2210.040131	0.016681	FSGQLNSHGCFYQQVK
3.4	2210.058075	-0.001263	FSHLSRNMTMQRTMK
3.4	2210.058075	-0.001263	FSHLSRNMTMQRTMK
0.0	2210.045486	0.011326	MSMKEVDEQMLAIQSK

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

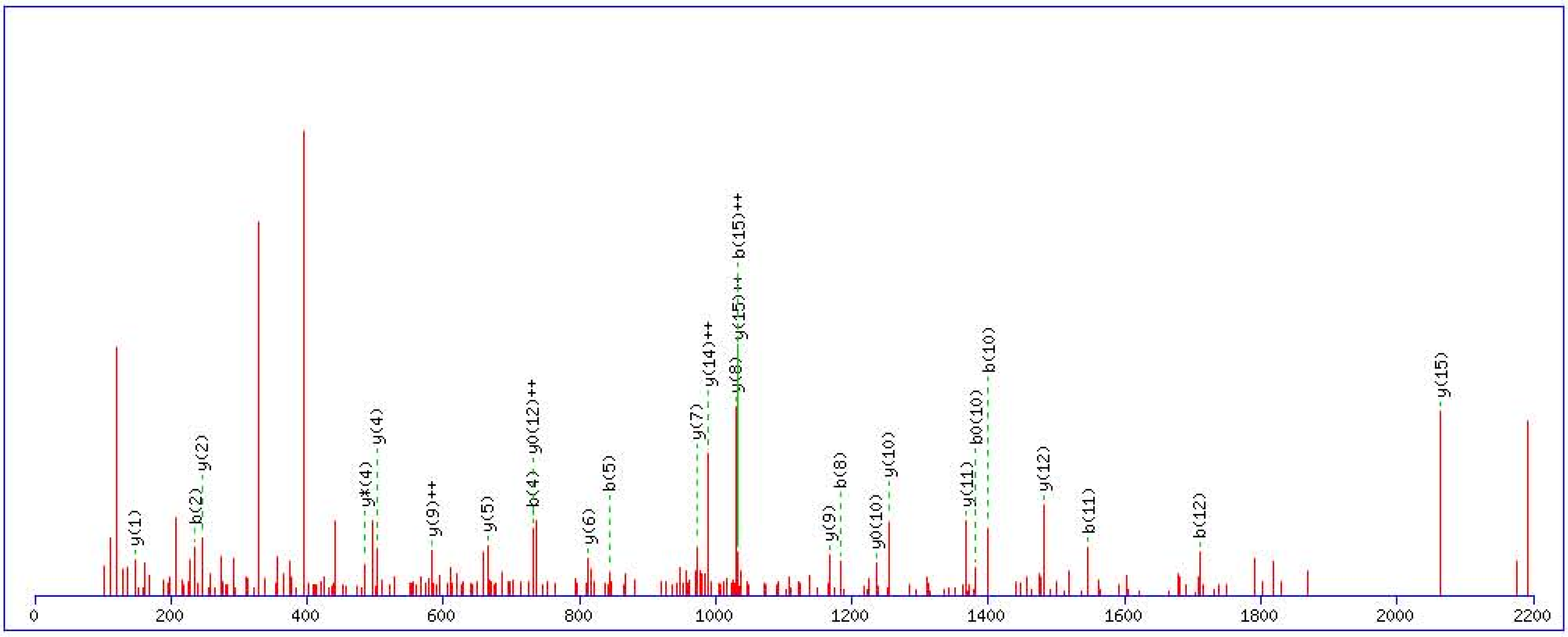
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

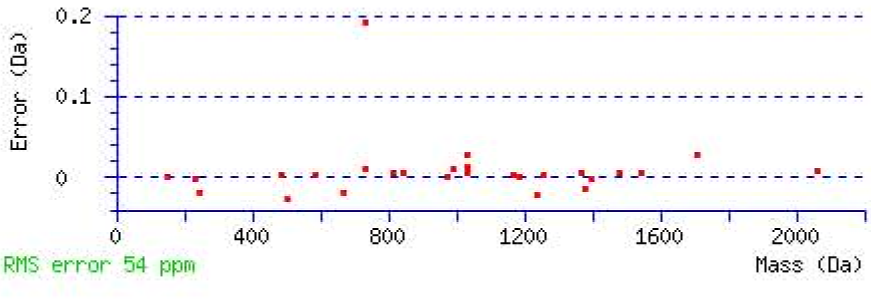
Match to Query 55597: 2210.057082 from(737.692970,3+) rtinseconds(1826) index(23382)
Title: Locus:1.1.1.2778.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

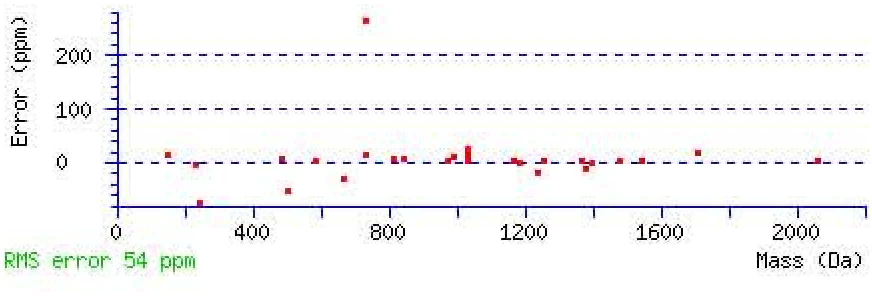
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2210.040131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 1.3e-006
Matches : 27/154 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	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	**731.354508**	366.180892	714.327959	357.667618	713.343943	357.175610	Q	1919.925487	960.466382	1902.898938	951.953107	1901.914922	951.461099	13
5	**844.438572**	422.722924	827.412023	414.209650	826.428007	413.717642	L	***1480.700161***	740.853719	1463.673612	732.340444	1462.689596	731.848436	12
6	958.481499	479.744388	941.454950	471.231113	940.470934	470.739105	N	***1367.616097***	684.311687	1350.589548	675.798412	1349.605532	675.306404	11
7	1045.513527	523.260402	1028.486978	514.747127	1027.502962	514.255119	S	***1253.573170***	627.290223	1236.546621	618.776949	1235.562605	618.284941	10
8	**1182.572439**	591.789858	1165.545890	583.276583	1164.561874	582.784575	H	***1166.541142***	583.774209	1149.514593	575.260935			9
9	1239.593903	620.300590	1222.567354	611.787315	1221.583338	611.295307	G	***1029.482230***	515.244753	1012.455681	506.731479			8
10	**1399.624552**	700.315914	1382.598003	691.802640	1381.613987	691.310632	C	***972.460766***	486.734021	955.434217	478.220747			7
11	**1546.692966**	773.850121	1529.666417	765.336847	1528.682401	764.844839	F	***812.430117***	406.718697	795.403568	398.205422			6
12	**1709.756295**	855.381786	1692.729746	846.868511	1691.745730	846.376503	Y	***665.361703***	333.184490	648.335154	324.671215			5
13	1837.814873	919.411075	1820.788324	910.897800	1819.804308	910.405792	Q	***502.298374***	251.652825	485.271825	243.139550			4
14	1965.873451	983.440364	1948.846902	974.927089	1947.862886	974.435081	Q	374.239796	187.623536	357.213247	179.110261			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
62.7	2210.040131	0.016951	FSGQLNSHGCFYQQVK
4.3	2210.040131	0.016951	FSGQLNSHGCFYQQVK
0.1	2210.037872	0.019210	RDKPSVEPVEEYDYEDLK

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

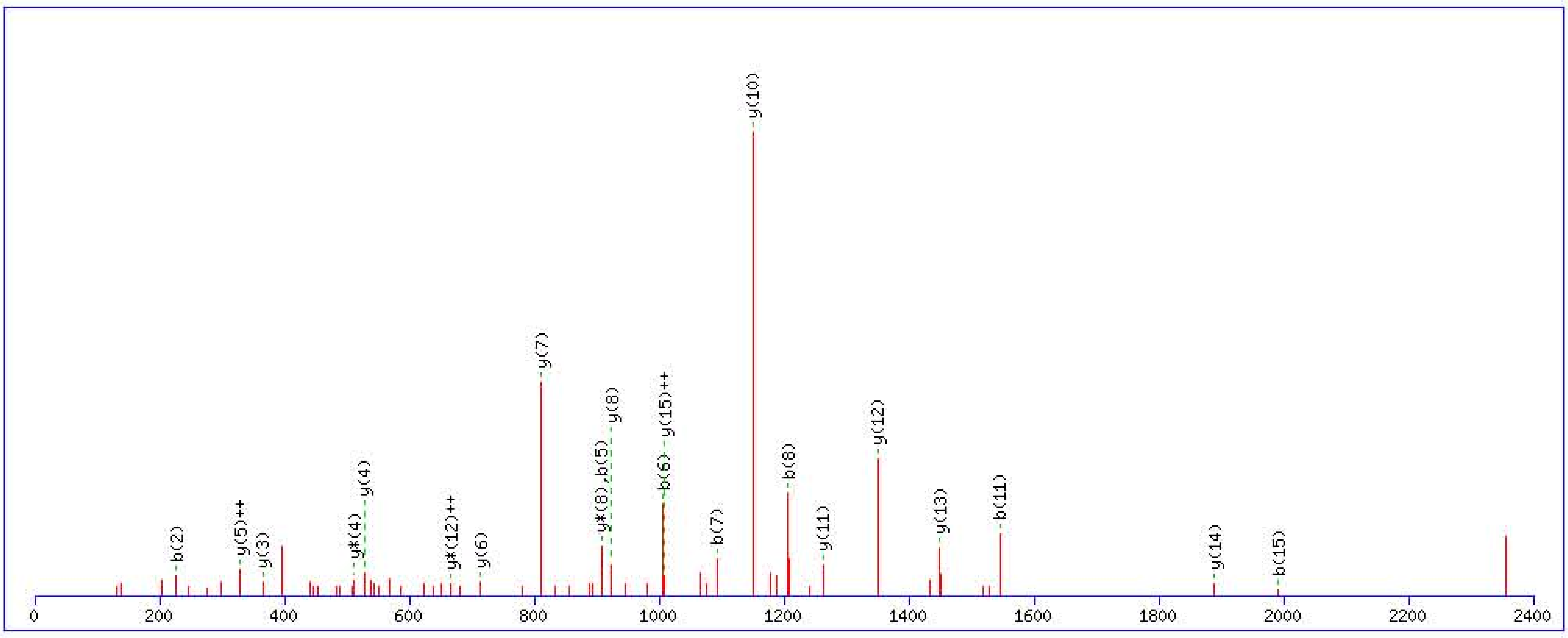
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

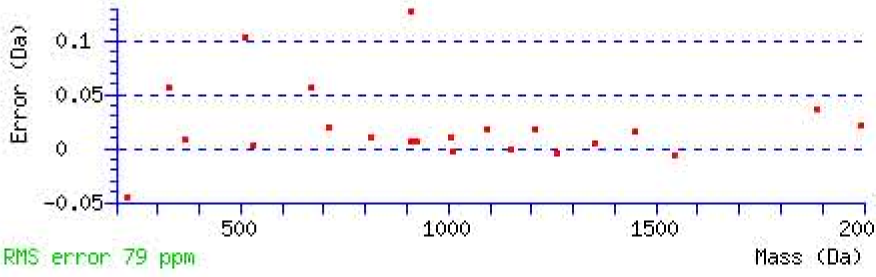
Match to Query 59167: 2355.257148 from(1178.635850,2+) rtinseconds(2815) index(30158)
Title: Locus:1.1.1.3121.23 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

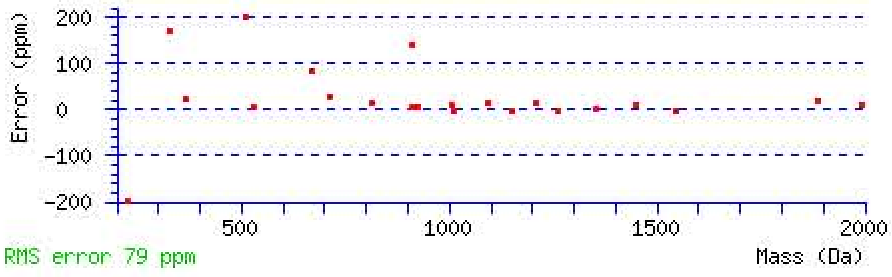
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2355.258179
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 6.6e-007
Matches : 22/182 fragment ions using 31 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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	468.318046	234.662661	451.291497	226.149386			Q	2017.013298	1009.010287	1999.986749	1000.497013	1999.002733	1000.005005	15
5	**907.543372**	454.275324	890.516823	445.762049			Q	***1888.954720***	944.980998	1871.928171	936.467724	1870.944155	935.975715	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
67.7	2355.258179	-0.001031	LLLQQVSLPELPGEYSMK
58.1	2355.258179	-0.001031	LLLQQVSLPELPGEYSMK
1.7	2355.288498	-0.031350	LIQQERALLNFTEWKR
1.7	2355.288498	-0.031350	LIQQERALLNFTEWKR
1.2	2355.229019	0.028129	QKMELEQNVVLVQQQSK
0.7	2355.248795	0.008353	FYEQVVQAIQRHIHFDVVK
0.3	2355.259354	-0.002206	SQPRASGPPRSIQPQVSPR

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

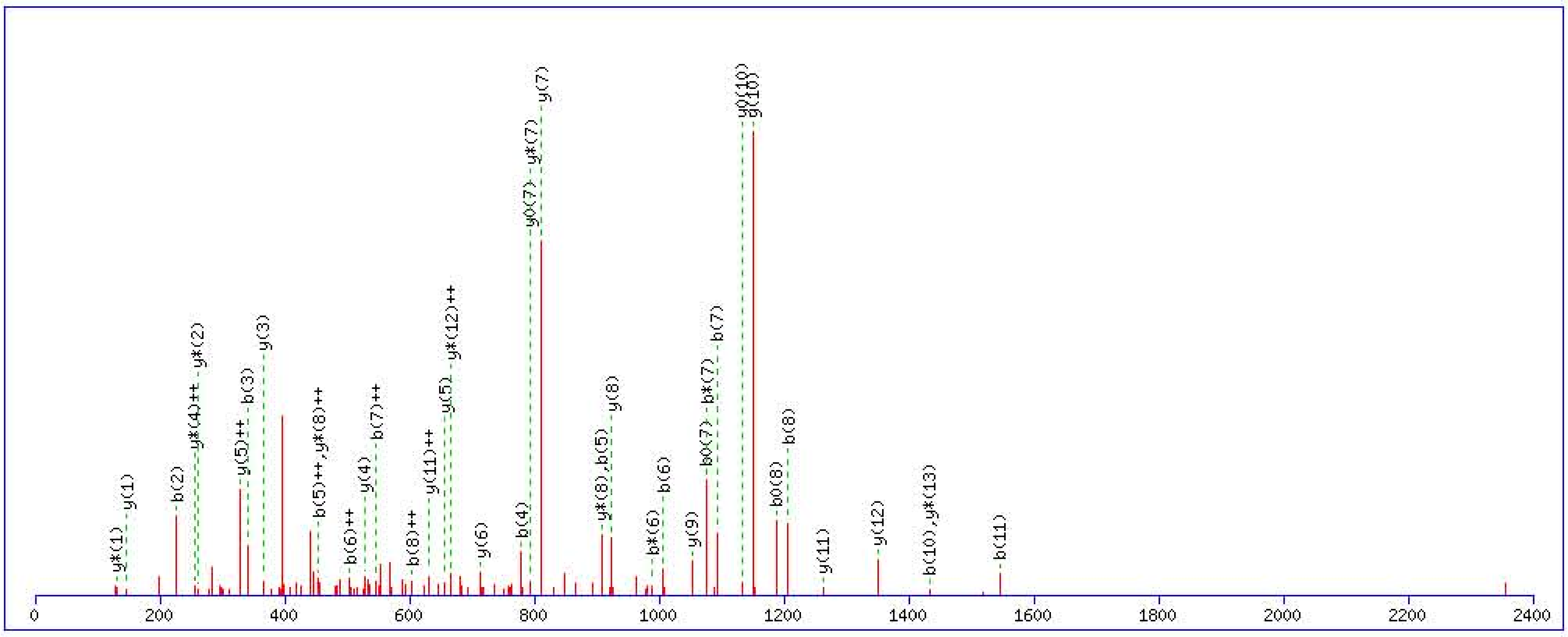
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

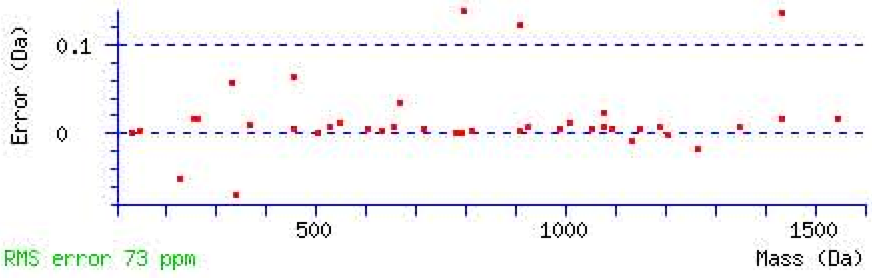
Match to Query 59174: 2355.285072 from(786.102300,3+) rtinseconds(2838) index(30349)
Title: Locus:1.1.1.3129.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

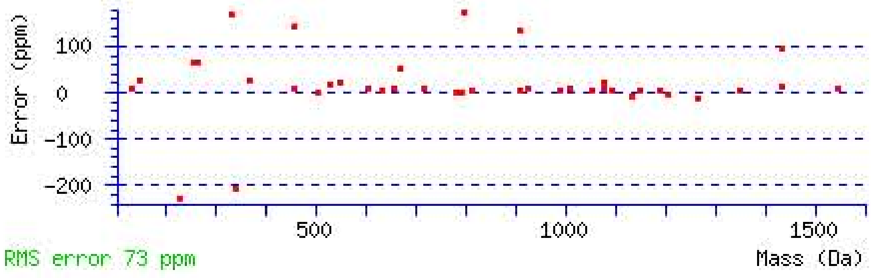


Monoisotopic mass of neutral peptide Mr(calc): 2355.258179
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 5e-006
Matches : 40/182 fragment ions using 69 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 73 ppm



RMS error 73 ppm

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
63.7	2355.258179	0.026893	LLLQQVSLPELPGEYSMK
56.2	2355.258179	0.026893	LLLQQVSLPELPGEYSMK
6.8	2355.288498	-0.003426	LIQQERALLNFTEWKR
1.4	2355.288498	-0.003426	LIQQERALLNFTEWKR
1.2	2355.259354	0.025718	SQPRASGPPRSIQPQVSPR

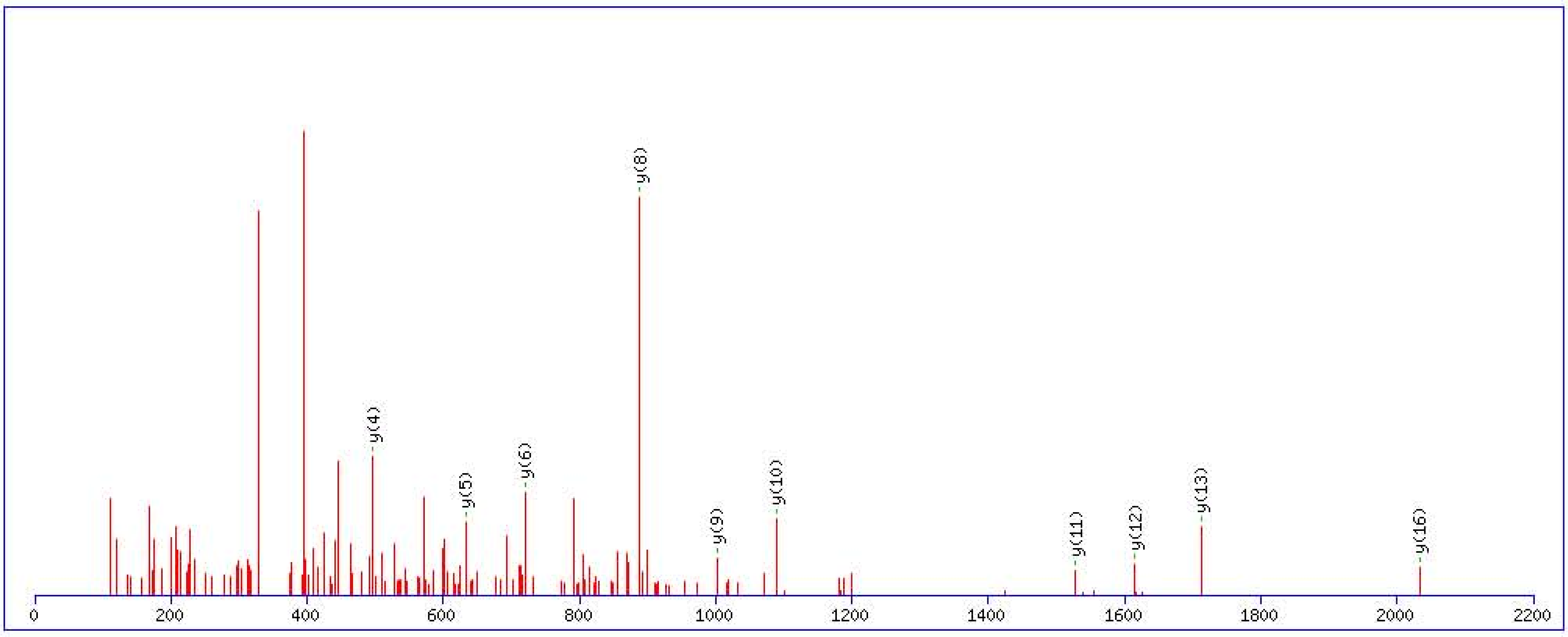
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

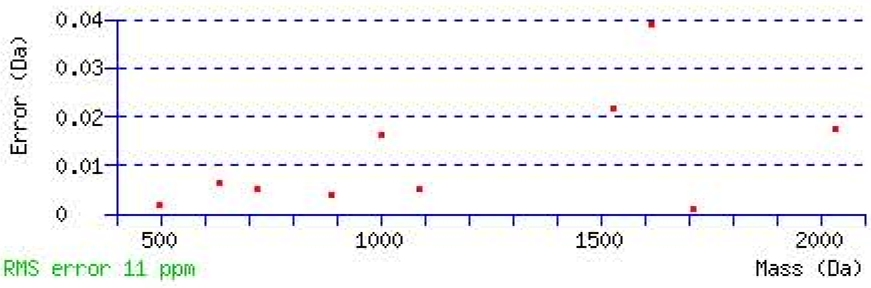
Match to Query 59248: 2359.220216 from(590.812330,4+) rtinseconds(1975) index(24502)
Title: Locus:1.1.1.2830.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

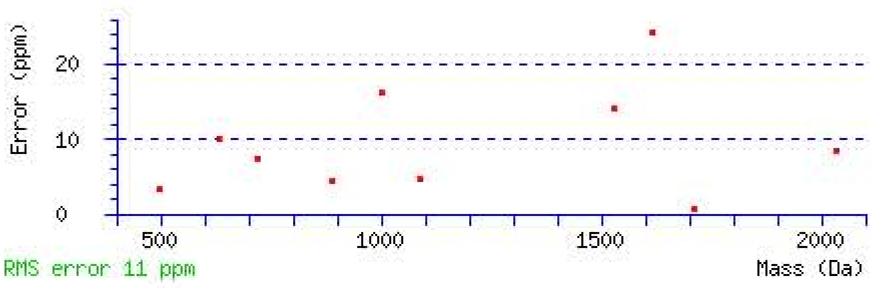
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2359.210678
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 67 **Expect:** 6.2e-006
Matches : 10/188 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	100.075690	50.541483					V							19
2	215.102633	108.054954			197.092068	99.049672	D	2261.149547	1131.078411	2244.122998	1122.565137	2243.138982	1122.073129	18
3	328.186697	164.596986			310.176132	155.591704	L	2146.122604	1073.564940	2129.096055	1065.051665	2128.112039	1064.559657	17
4	415.218725	208.113001			397.208160	199.107718	S	***2033.038540***	1017.022908	2016.011991	1008.509634	2015.027975	1008.017626	16
5	562.287139	281.647208			544.276574	272.641925	F	1946.006512	973.506894	1928.979963	964.993620	1927.995947	964.501612	15
6	649.319167	325.163222			631.308602	316.157939	S	1798.938098	899.972687	1781.911549	891.459413	1780.927533	890.967405	14
7	746.371931	373.689604			728.361366	364.684321	P	***1711.906070***	856.456673	1694.879521	847.943399	1693.895505	847.451391	13
8	833.403959	417.205618			815.393394	408.200335	S	***1614.853306***	807.930291	1597.826757	799.417017	1596.842741	798.925009	12
9	1272.629285	636.818281	1255.602736	628.305006	1254.618720	627.812998	Q	***1527.821278***	764.414277	1510.794729	755.901003	1509.810713	755.408995	11
10	1359.661313	680.334295	1342.634764	671.821020	1341.650748	671.329012	S	***1088.595952***	544.801614	1071.569403	536.288340	1070.585387	535.796332	10
11	1472.745377	736.876327	1455.718828	728.363052	1454.734812	727.871044	L	***1001.563924***	501.285600	984.537375	492.772326	983.553359	492.280318	9
12	1569.798141	785.402709	1552.771592	776.889434	1551.787576	776.397426	P	***888.479860***	444.743568	871.453311	436.230294	870.469295	435.738286	8
13	1640.835255	820.921266	1623.808706	812.407991	1622.824690	811.915983	A	791.427096	396.217186	774.400547	387.703912	773.416531	387.211904	7
14	1727.867283	864.437280	1710.840734	855.924005	1709.856718	855.431997	S	***720.389982***	360.698629	703.363433	352.185355	702.379417	351.693347	6
15	1864.926195	932.966736	1847.899646	924.453461	1846.915630	923.961453	H	***633.357954***	317.182615	616.331405	308.669341			5
16	1935.963309	968.485293	1918.936760	959.972018	1917.952744	959.480010	A	***496.299042***	248.653159	479.272493	240.139884			4
17	2073.022221	1037.014748	2055.995672	1028.501474	2055.011656	1028.009466	H	425.261928	213.134602	408.235379	204.621328			3
18	2186.106285	1093.556780	2169.079736	1085.043506	2168.095720	1084.551498	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 VDLSFSPSQSLPASHAHLR
(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	2359.210678	0.009538	VDLSFSPSQSLPASHAHLR

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

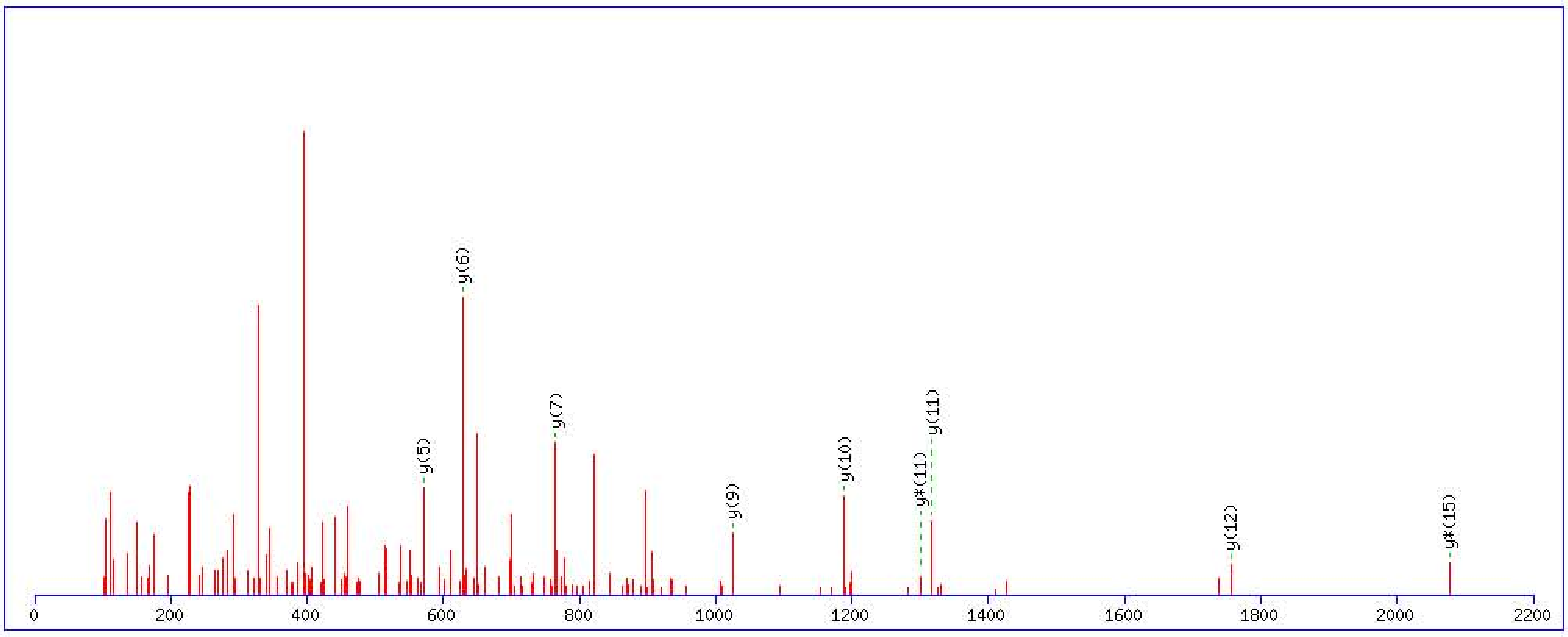
Mascot Search Results

Peptide View

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

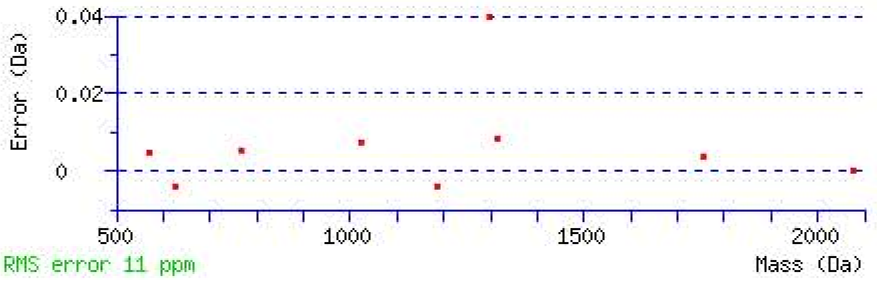
Match to Query 59563: 2384.099776 from(597.032220,4+) rtinseconds(1972) index(24481)
Title: Locus:1.1.1.2829.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

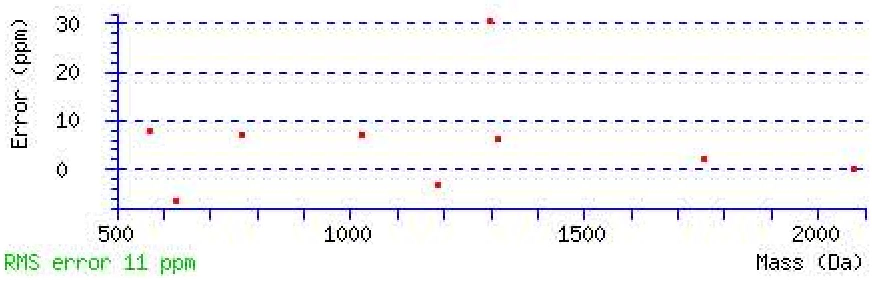
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2384.089767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0043
Matches : 9/164 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	132.047761	66.527518					M							17
2	292.078410	146.542843					C	2254.056579	1127.531927	2237.030030	1119.018653	2236.046014	1118.526645	16
3	389.131174	195.069225					P	2094.025930	1047.516603	2076.999381	1039.003328	2076.015365	1038.511320	15
4	517.189752	259.098514	500.163203	250.585240			Q	1996.973166	998.990221	1979.946617	990.476947	1978.962601	989.984939	14
5	630.273816	315.640546	613.247267	307.127272			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	1197.557720	599.282498	1180.531171	590.769224			Q	***1316.605198***	658.806237	1299.578649	650.292963	1298.594633	649.800955	11
8	1360.621049	680.814163	1343.594500	672.300888			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1489.663642	745.335459	1472.637093	736.822185	1471.653077	736.330177	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1620.704127	810.855702	1603.677578	802.342427	1602.693562	801.850419	M	896.440698	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	1757.763039	879.385158	1740.736490	870.871883	1739.752474	870.379875	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	1814.784503	907.895890	1797.757954	899.382615	1796.773938	898.890607	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	1911.837267	956.422272	1894.810718	947.908997	1893.826702	947.416989	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2040.879860	1020.943568	2023.853311	1012.430294	2022.869295	1011.938286	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2097.901324	1049.454300	2080.874775	1040.941025	2079.890759	1040.449017	G	345.224480	173.115878	328.197931	164.602603			3
16	2210.985388	1105.996332	2193.958839	1097.483057	2192.974823	1096.991049	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
34.9	2384.089767	0.010009	MCPQLQQYEMHGPEGLR
26.5	2384.089767	0.010009	MCPQLQQYEMHGPEGLR
22.9	2384.089767	0.010009	MCPQLQQYEMHGPEGLR

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

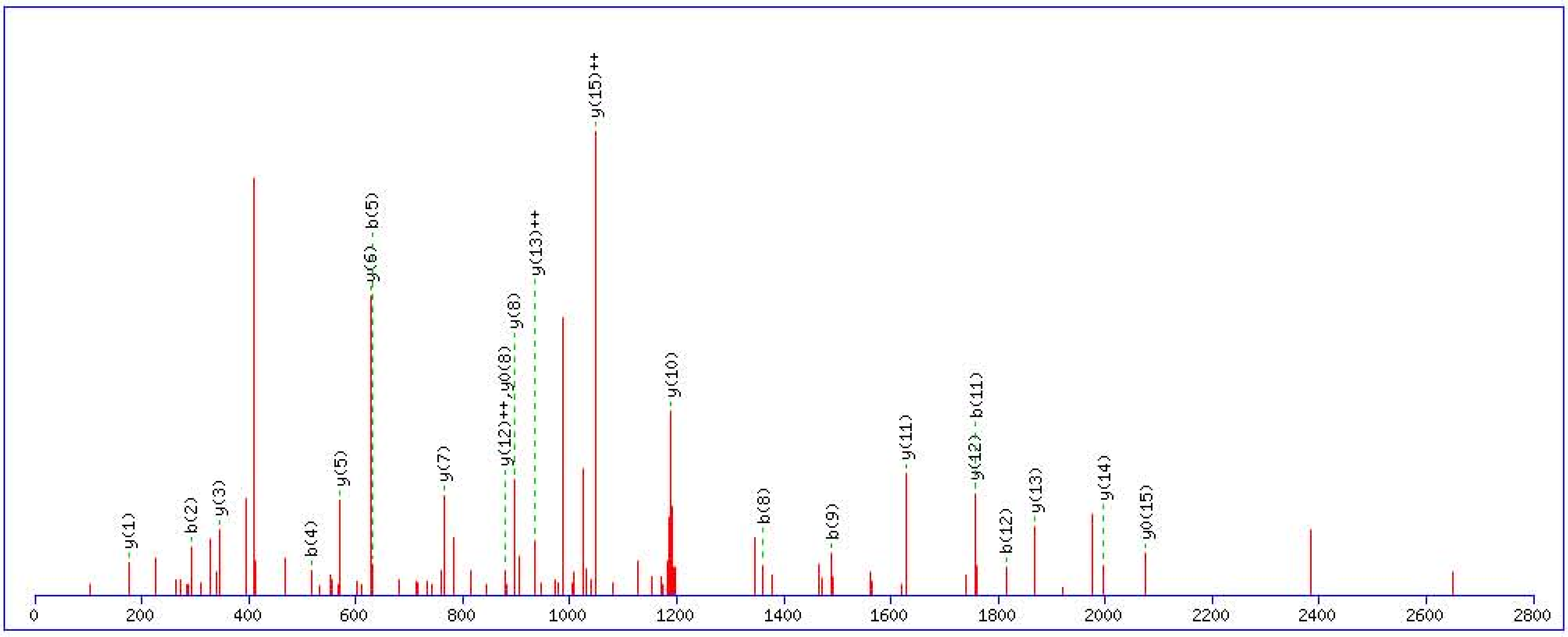
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

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

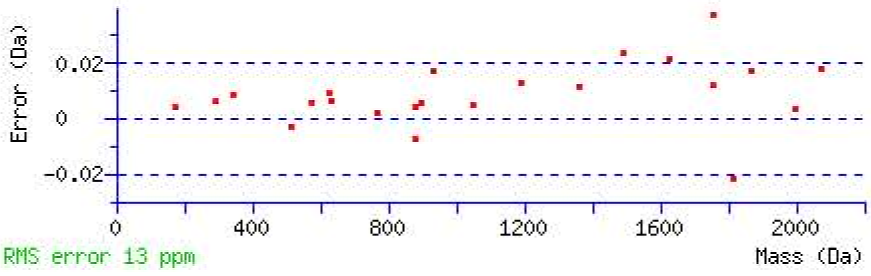
Match to Query 59577: 2384.112168 from(1193.063360,2+) rtinseconds(2018) index(6609)
Title: Locus:1.1.1.2956.14 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

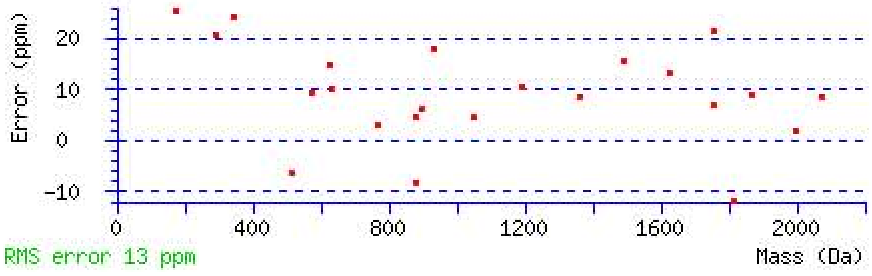
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2384.089767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 67 **Expect:** 5.4e-007
Matches : 23/164 fragment ions using 37 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.047761	66.527518					M							17
2	**292.078410**	146.542843					C	2254.056579	1127.531927	2237.030030	1119.018653	2236.046014	1118.526645	16
3	389.131174	195.069225					P	2094.025930	1047.516603	2076.999381	1039.003328	2076.015365	1038.511320	15
4	**517.189752**	259.098514	500.163203	250.585240			Q	***1996.973166***	998.990221	1979.946617	990.476947	1978.962601	989.984939	14
5	**630.273816**	315.640546	613.247267	307.127272			L	***1868.914588***	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	758.332394	379.669835	741.305845	371.156561			Q	***1755.830524***	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1197.557720	599.282498	1180.531171	590.769224			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	**1360.621049**	680.814163	1343.594500	672.300888			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	**1489.663642**	745.335459	1472.637093	736.822185	1471.653077	736.330177	E	1025.483291	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1620.704127	810.855702	1603.677578	802.342427	1602.693562	801.850419	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	**1757.763039**	879.385158	1740.736490	870.871883	1739.752474	870.379875	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	**1814.784503**	907.895890	1797.757954	899.382615	1796.773938	898.890607	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	1911.837267	956.422272	1894.810718	947.908997	1893.826702	947.416989	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2040.879860	1020.943568	2023.853311	1012.430294	2022.869295	1011.938286	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2097.901324	1049.454300	2080.874775	1040.941025	2079.890759	1040.449017	G	***345.224480***	173.115878	328.197931	164.602603			3
16	2210.985388	1105.996332	2193.958839	1097.483057	2192.974823	1096.991049	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
67.0	2384.089767	0.022401	MCPQLQQYEMHGPEGLR
55.8	2384.089767	0.022401	MCPQLQQYEMHGPEGLR
29.3	2384.089767	0.022401	MCPQLQQYEMHGPEGLR
0.1	2384.111389	0.000779	HPGDAAATLGPSAQDMVAVHMHR

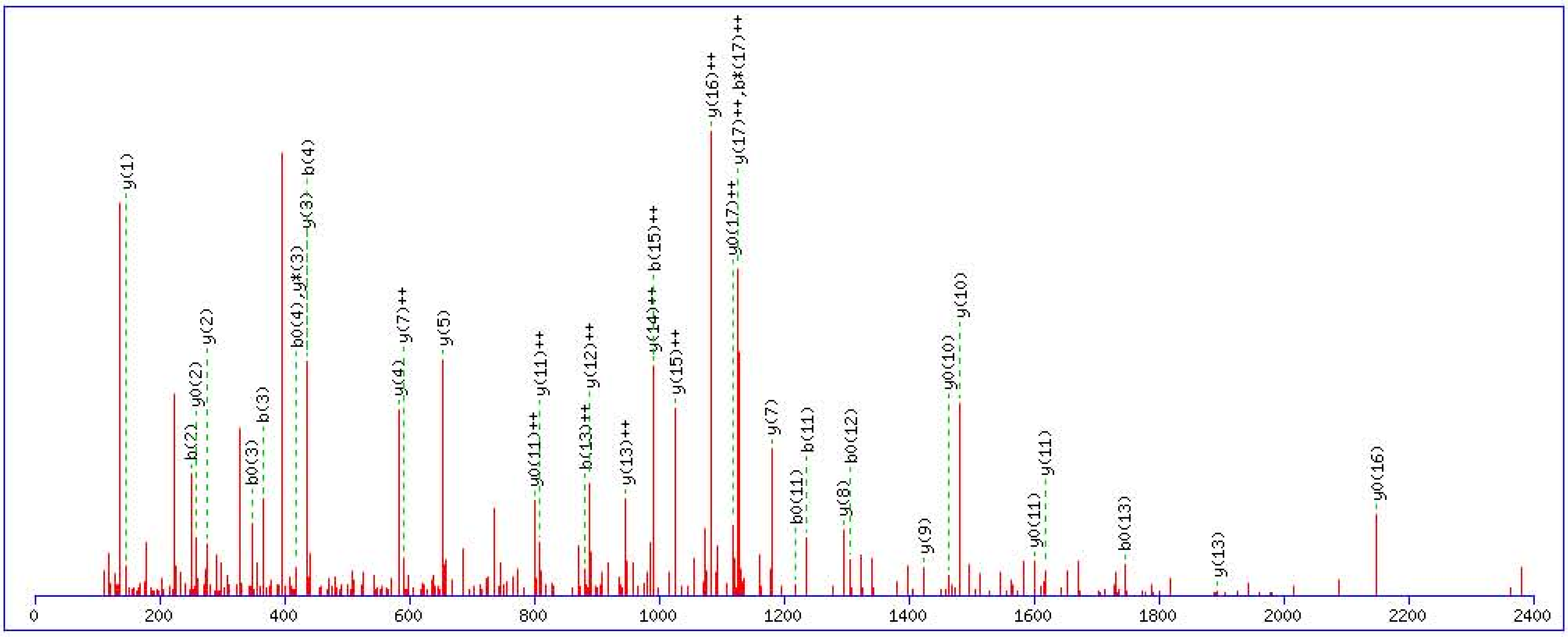
Mascot Search Results

Peptide View

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

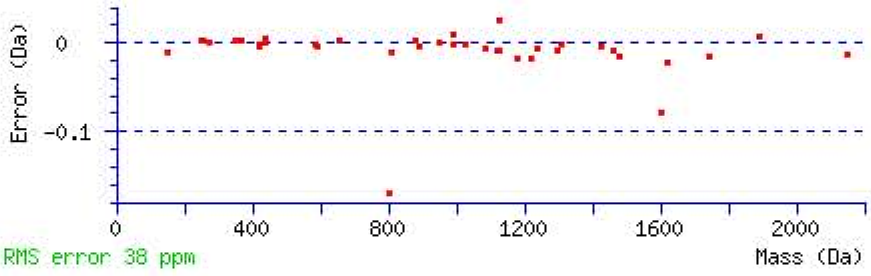
Match to Query 60416: 2415.946512 from(806.322780,3+) rtinseconds(1521) index(21150)
Title: Locus:1.1.1.2672.19 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

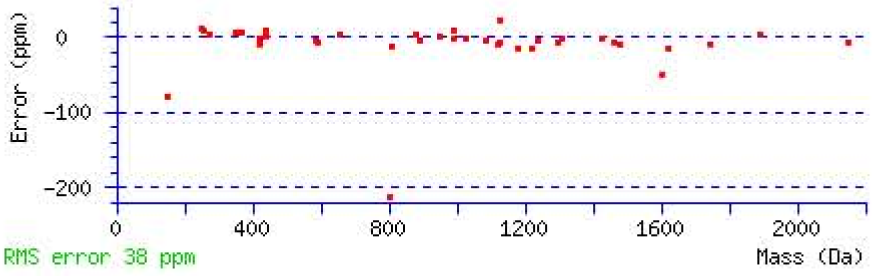
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2415.940598
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 55 **Expect:** 3.2e-006
Matches : 38/176 fragment ions using 81 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	**251.102633**	126.054954			233.092068	117.049672	S	2253.884545	1127.445910	2236.857996	1118.932636	2235.873980	1118.440628	17
3	**366.129576**	183.568426			348.119011	174.563144	D	2166.852517	1083.929896	2149.825968	1075.416622	2148.841952	1074.924614	16
4	**437.166690**	219.086983			419.156125	210.081700	A	2051.825574	1026.416425	2034.799025	1017.903150	2033.815009	1017.411142	15
5	524.198718	262.602997			506.188153	253.597715	S	1980.788460	990.897868	1963.761911	982.384594	1962.777895	981.892586	14
6	639.225661	320.116469			621.215096	311.111186	D	***1893.756432***	947.381854	1876.729883	938.868580	1875.745867	938.376572	13
7	799.256310	400.131793			781.245745	391.126510	C	1778.729489	889.868383	1761.702940	881.355108	1760.718924	880.863100	12
8	936.315222	468.661249			918.304657	459.655966	H	***1618.698840***	809.853058	1601.672291	801.339784	1600.688275	800.847776	11
9	993.336686	497.171981			975.326121	488.166699	G	***1481.639928***	741.323602	1464.613379	732.810328	1463.629363	732.318320	10
10	1122.379279	561.693278			1104.368714	552.687995	E	***1424.618464***	712.812870	1407.591915	704.299596	1406.607899	703.807588	9
11	**1237.406222**	619.206749			1219.395657	610.201467	D	***1295.575871***	648.291574	1278.549322	639.778299	1277.565306	639.286291	8
12	1324.438250	662.722763			1306.427685	653.717481	S	***1180.548928***	590.778102	1163.522379	582.264828	1162.538363	581.772820	7
13	1763.663576	**882.335426**	1746.637027	873.822152	1745.653011	873.330144	Q	1093.516900	547.262088	1076.490351	538.748814	1075.506335	538.256806	6
14	1834.700690	917.853983	1817.674141	909.340709	1816.690125	908.848701	A	***654.291574***	327.649425	637.265025	319.136151	636.281009	318.644143	5
15	1981.769104	**991.388190**	1964.742555	982.874916	1963.758539	982.382908	F	***583.254460***	292.130868	566.227911	283.617594	565.243895	283.125586	4
16	2141.799753	1071.403514	2124.773204	1062.890240	2123.789188	1062.398232	C	***436.186046***	218.596661	419.159497	210.083386	418.175481	209.591378	3
17	2270.842346	1135.924811	2253.815797	1127.411536	2252.831781	1126.919528	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.9	2415.940598	0.005914	YSDASDCHGEDSQAFCEK

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

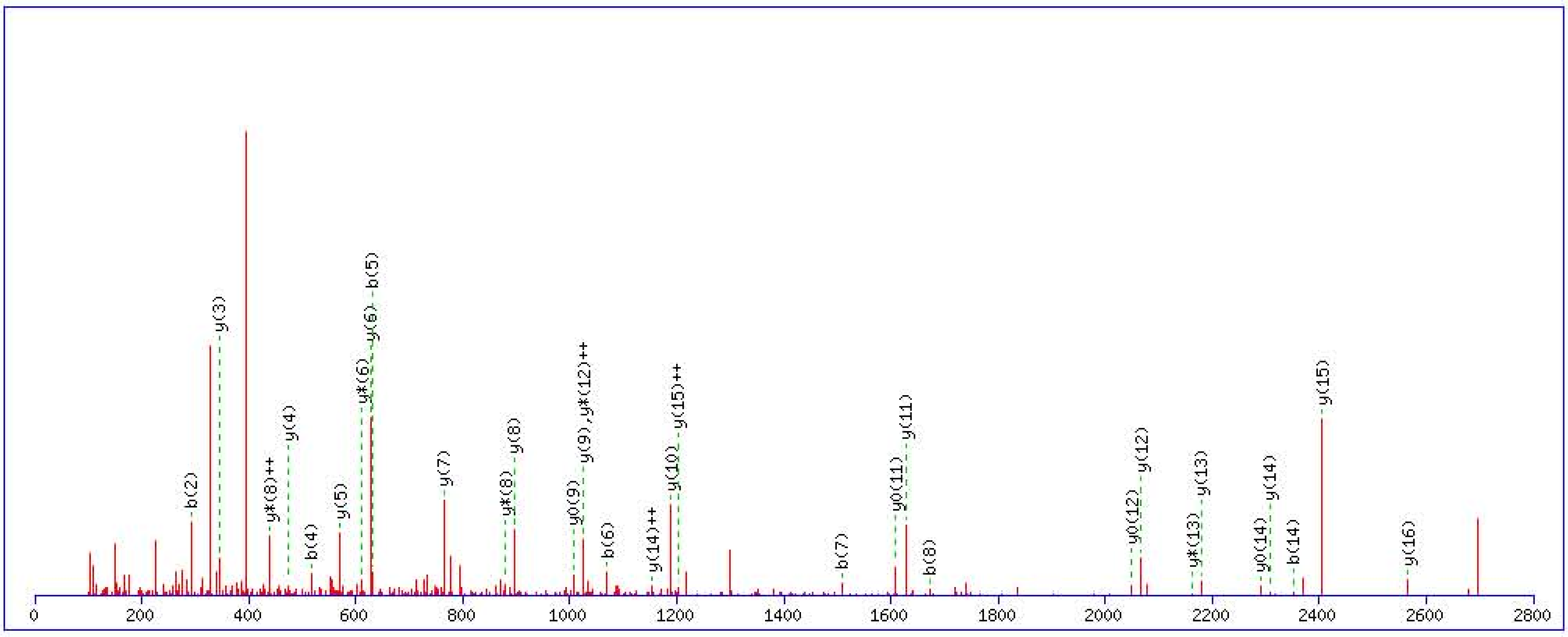
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

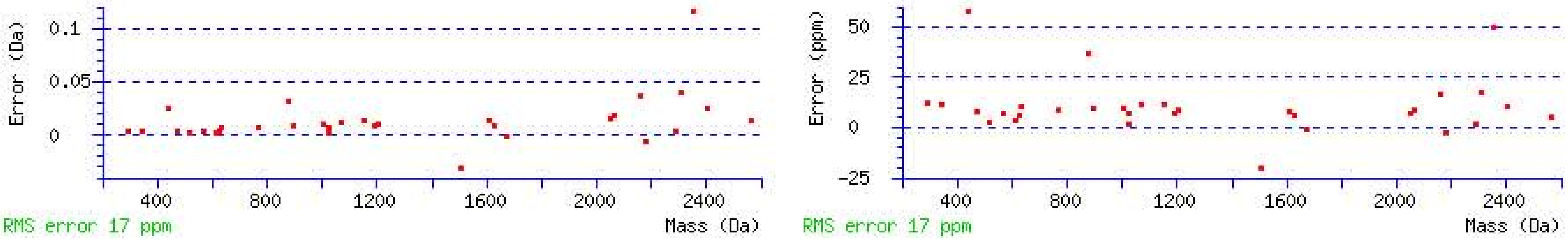
Match to Query 65613: 2695.275176 from(674.826070,4+) rtinseconds(2160) index(25839)
Title: Locus:1.1.1.2894.17 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 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: 70  Expect: 2e-006
Matches : 32/164 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	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
69.6	2695.256516	0.018660	MCPQLQQYEMHGPEGLR
47.2	2695.256516	0.018660	MCPQLQQYEMHGPEGLR
39.2	2695.256516	0.018660	MCPQLQQYEMHGPEGLR

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

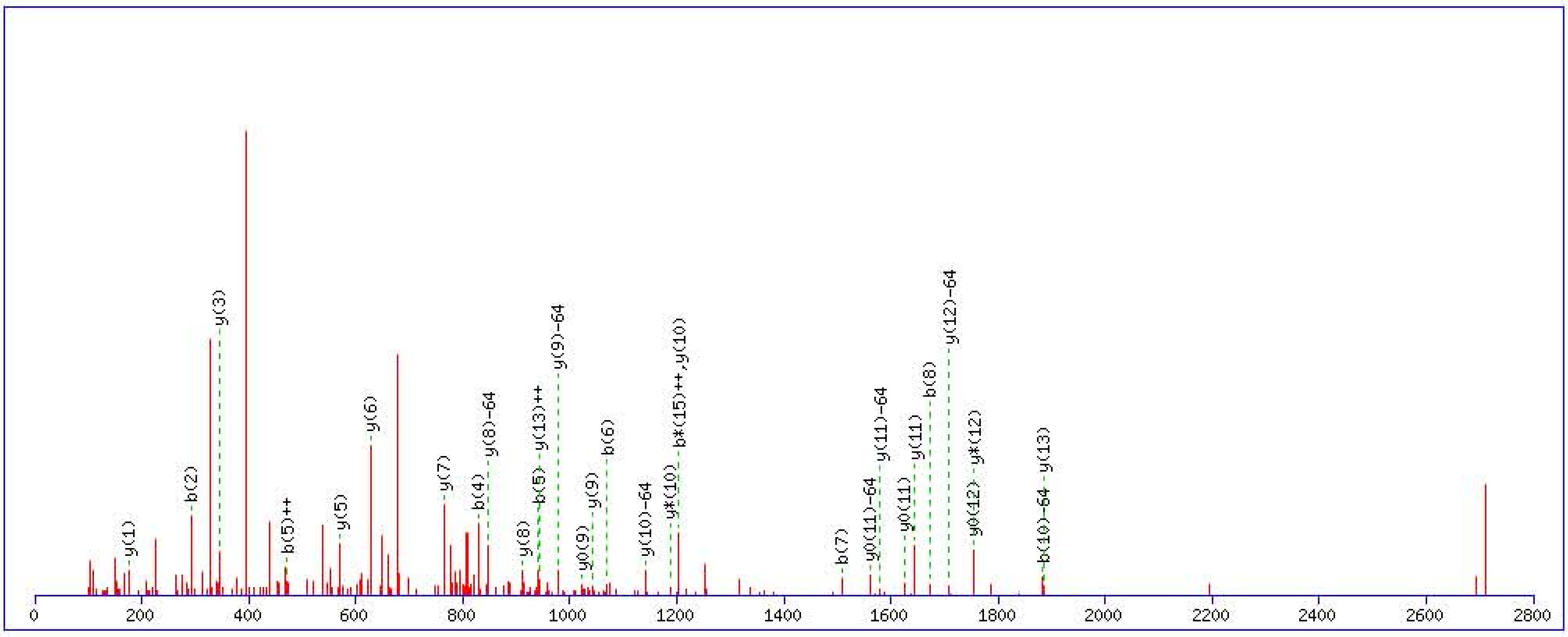
Mascot Search Results

Peptide View

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

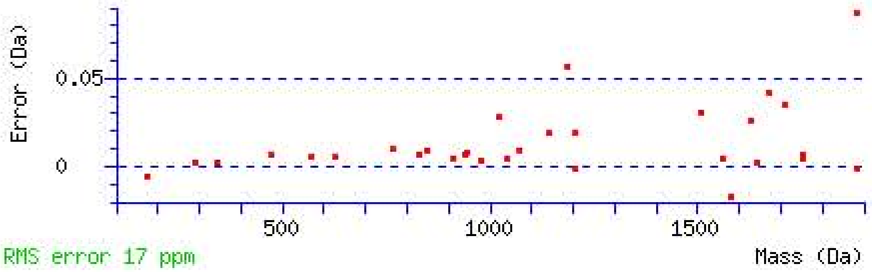
Match to Query 65805: 2711.271496 from(678.825150,4+) rtinseconds(2084) index(25281)
Title: Locus:1.1.1.2868.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

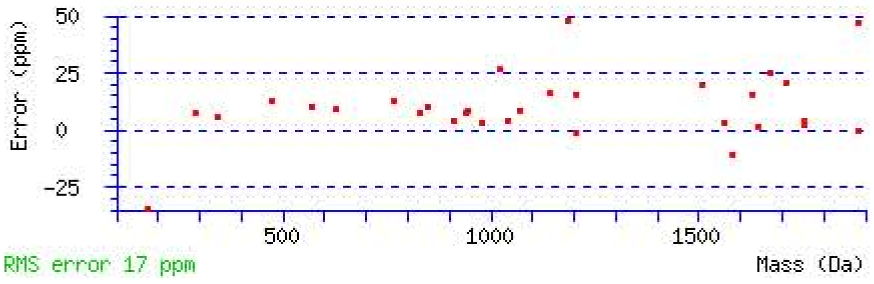
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2711.251434
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Q7      : Biotin:Thermo-21345 (Q)
M10     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 32  Expect: 0.011
Matches : 31/260 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							17
2	**292.078410**	146.542843					C	2581.218242	1291.112759	2564.191693	1282.599484	2563.207677	1282.107476	16
3	389.131174	195.069225					P	2421.187593	1211.097435	2404.161044	1202.584160	2403.177028	1202.092152	15
4	**828.356500**	414.681888	811.329951	406.168614			Q	2324.134829	1162.571053	2307.108280	1154.057778	2306.124264	1153.565770	14
5	**941.440564**	471.223920	924.414015	462.710646			L	***1884.909503***	942.958390	1867.882954	934.445115	1866.898938	933.953107	13
6	**1069.499142**	535.253209	1052.472593	526.739935			Q	1771.825439	886.416358	1754.798890	877.903083	1753.814874	877.411075	12
7	**1508.724468**	754.865872	1491.697919	746.352598			Q	***1643.766861***	822.387069	1626.740312	813.873794	1625.756296	813.381786	11
8	**1671.787797**	836.397537	1654.761248	827.884262			Y	***1204.541535***	602.774406	1187.514986	594.261131	1186.530970	593.769123	10
9	1800.830390	900.918833	1783.803841	892.405559	1782.819825	891.913551	E	***1041.478206***	521.242741	1024.451657	512.729467	1023.467641	512.237459	9
10	1947.865790	974.436533	1930.839241	965.923259	1929.855225	965.431251	M	***912.435613***	456.721445	895.409064	448.208170	894.425048	447.716162	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
32.1	2711.251434	0.020062	MCPQLQQYEMHGPEGLR
22.2	2711.251434	0.020062	MCPQLQQYEMHGPEGLR
19.7	2711.251434	0.020062	MCPQLQQYEMHGPEGLR

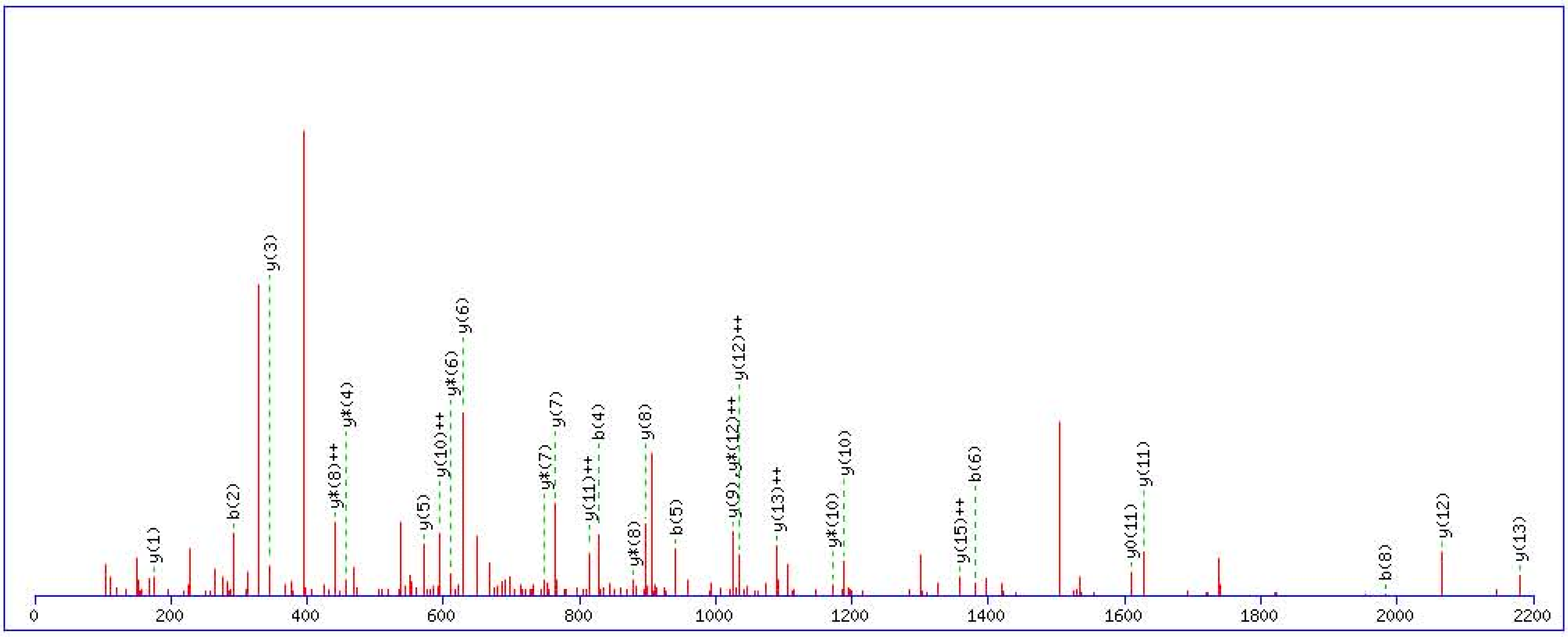
Mascot Search Results

Peptide View

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

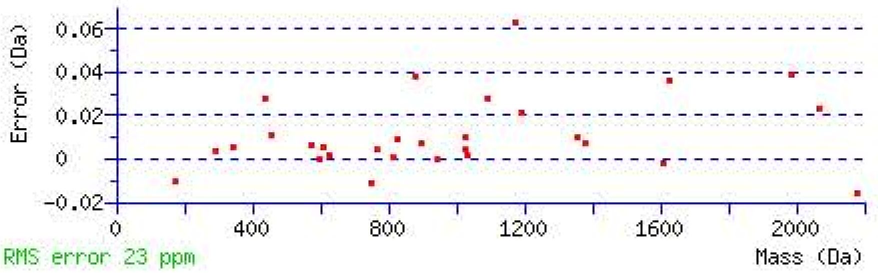
Match to Query 70478: 3006.456896 from(752.621500,4+) rtinseconds(2325) index(26978)
Title: Locus:1.1.1.2951.21 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

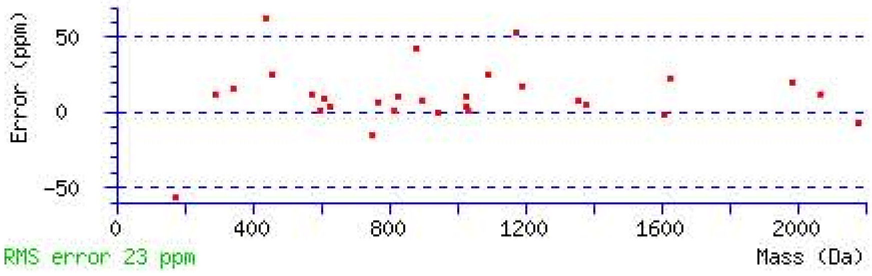
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 34  Expect: 0.012
Matches : 29/164 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	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
33.7	3006.423264	0.033632	MCPQLQQYEMHGPEGLR

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

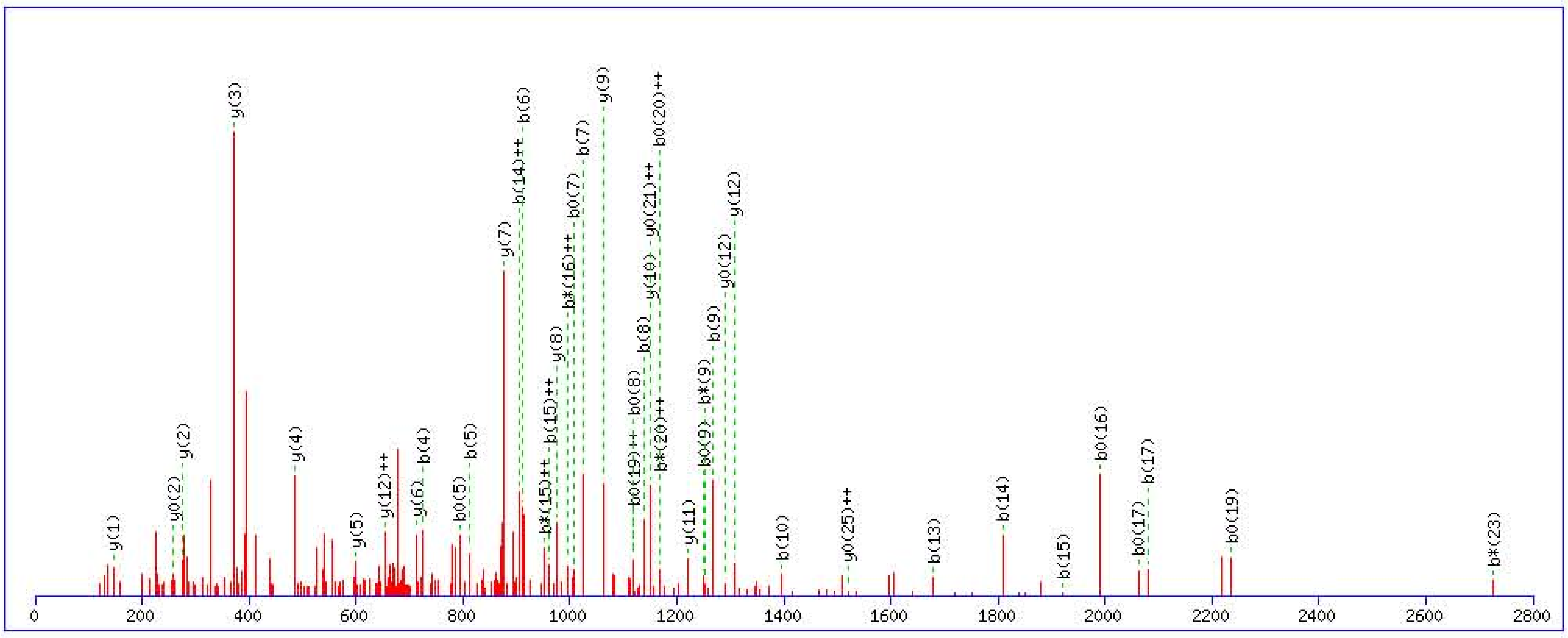
Mascot Search Results

Peptide View

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

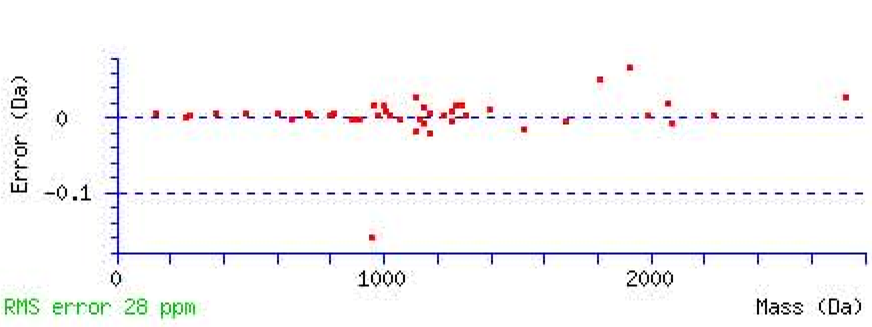
Match to Query 73321: 3227.721296 from(807.937600,4+) rtinseconds(2739) index(29724)
Title: Locus:1.1.1.3094.17 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

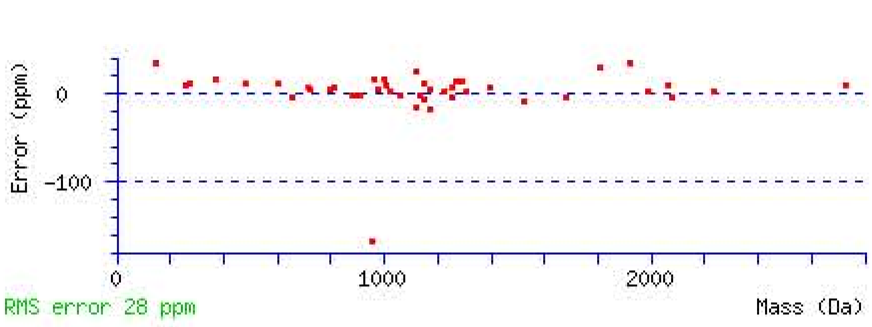
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3227.682129
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 4.5e-006
Matches : 44/300 fragment ions using 103 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
65.7	3227.682129	0.039167	AVDQSVLLMKPDAELSASSVYNLLPEK

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

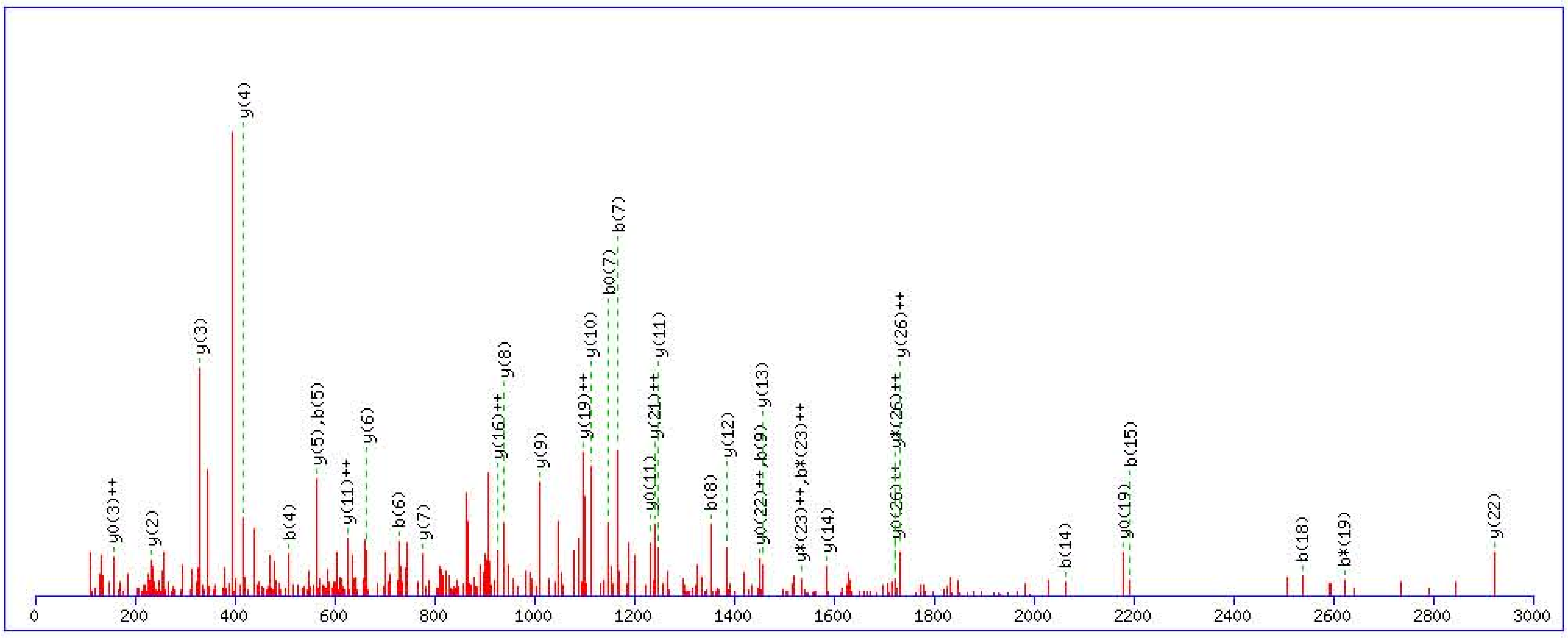
Mascot Search Results

Peptide View

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

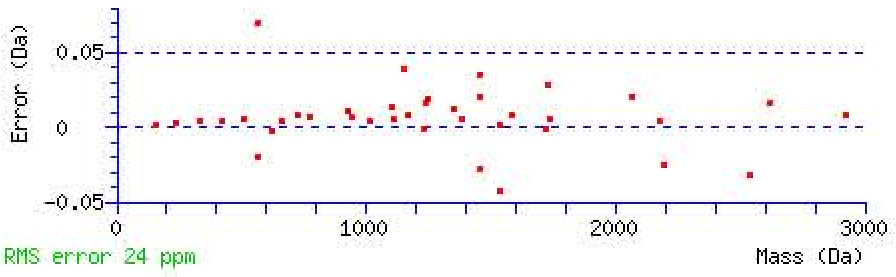
Match to Query 78975: 3648.692456 from(913.180390,4+) rtinseconds(2135) index(25623)
Title: Locus:1.1.1.2885.13 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

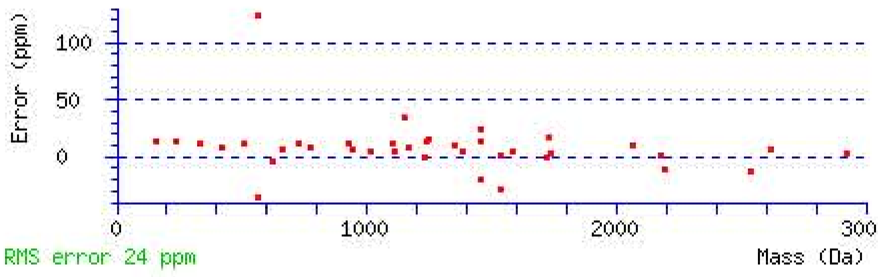
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3648.644211
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 62 **Expect:** 9.4e-006
Matches : 38/310 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	88.039304	44.523290			70.028739	35.518008	S							28
2	185.092068	93.049672			167.081503	84.044389	P	3562.619476	1781.813376	3545.592927	1773.300101	3544.608911	1772.808093	27
3	345.122717	173.064997			327.112152	164.059714	C	3465.566712	1733.286994	3448.540163	1724.773719	3447.556147	1724.281711	26
4	***508.186046***	254.596661			490.175481	245.591379	Y	3305.536063	1653.271669	3288.509514	1644.758395	3287.525498	1644.266387	25
5	***565.207510***	283.107393			547.196945	274.102111	G	3142.472734	1571.740005	3125.446185	1563.226730	3124.462169	1562.734722	24
6	***728.270839***	364.639058			710.260274	355.633775	Y	3085.451270	1543.229273	3068.424721	1534.715998	3067.440705	1534.223990	23
7	***1167.496165***	584.251721	1150.469616	575.738446	1149.485600	575.246438	Q	***2922.387941***	1461.697608	2905.361392	1453.184334	2904.377376	1452.692326	22
8	***1353.575478***	677.291377	1336.548929	668.778103	1335.564913	668.286094	W	2483.162615	1242.084945	2466.136066	1233.571671	2465.152050	1233.079663	21
9	***1452.643892***	726.825584	1435.617343	718.312310	1434.633327	717.820302	V	2297.083302	1149.045289	2280.056753	1140.532014	2279.072737	1140.040006	20
10	1539.675920	770.341598	1522.649371	761.828324	1521.665355	761.336316	S	2198.014888	1099.511082	2180.988339	1090.997807	2180.004323	1090.505800	19
11	1668.718513	834.862895	1651.691964	826.349620	1650.707948	825.857612	E	2110.982860	1055.995068	2093.956311	1047.481793	2092.972295	1046.989785	18
12	1797.761106	899.384191	1780.734557	890.870917	1779.750541	890.378909	E	1981.940267	991.473772	1964.913718	982.960497	1963.929702	982.468489	17
13	1934.820018	967.913647	1917.793469	959.400373	1916.809453	958.908365	H	1852.897674	926.952475	1835.871125	918.439201	1834.887109	917.947193	16
14	***2063.862611***	1032.434943	2046.836062	1023.921669	2045.852046	1023.429661	E	1715.838762	858.423019	1698.812213	849.909745	1697.828197	849.417737	15
15	***2192.905204***	1096.956240	2175.878655	1088.442965	2174.894639	1087.950958	E	***1586.796169***	793.901723	1569.769620	785.388448	1568.785604	784.896440	14
16	2263.942318	1132.474797	2246.915769	1123.961523	2245.931753	1123.469515	A	***1457.753576***	729.380426	1440.727027	720.867152	1439.743011	720.375144	13
17	2401.001230	1201.004253	2383.974681	1192.490979	2382.990665	1191.998971	H	***1386.716462***	693.861869	1369.689913	685.348595	1368.705897	684.856587	12
18	***2538.060142***	1269.533709	2521.033593	1261.020435	2520.049577	1260.528427	H	***1249.657550***	625.332413	1232.631001	616.819139	1231.646985	616.327131	11
19	2639.107821	1320.057548	2622.081272	1311.544274	2621.097256	1311.052266	T	***1112.598638***	556.802957	1095.572089	548.289683	1094.588073	547.797675	10
20	2710.144935	1355.576106	2693.118386	1347.062831	2692.134370	1346.570823	A	***1011.550959***	506.279118	994.524410	497.765843	993.540394	497.273835	9
21	2873.208264	1437.107770	2856.181715	1428.594496	2855.197699	1428.102488	Y	***940.513845***	470.760561	923.487296	462.247286	922.503280	461.755278	8
22	2986.292328	1493.649802	2969.265779	1485.136528	2968.281763	1484.644520	L	***777.450516***	389.228896	760.423967	380.715622	759.439951	380.223614	7
23	3085.360742	1543.184009	3068.334193	1534.670735	3067.350177	1534.178727	V	***664.366452***	332.686864	647.339903	324.173589	646.355887	323.681581	6
24	3232.429156	1616.718216	3215.402607	1608.204941	3214.418591	1607.712934	F	***565.298038***	283.152657	548.271489	274.639383	547.287473	274.147375	5
25	3319.461184	1660.234230	3302.434635	1651.720955	3301.450619	1651.228948	S	***418.229624***	209.618450	401.203075	201.105176	400.219059	200.613168	4
26	3416.513948	1708.760612	3399.487399	1700.247338	3398.503383	1699.755330	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
27	3503.545976	1752.276626	3486.519427	1743.763352	3485.535411	1743.271344	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
28							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.1	3648.644211	0.048245	SPCYGYQWVSEEHEEAHHTAYLVFSPSK

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

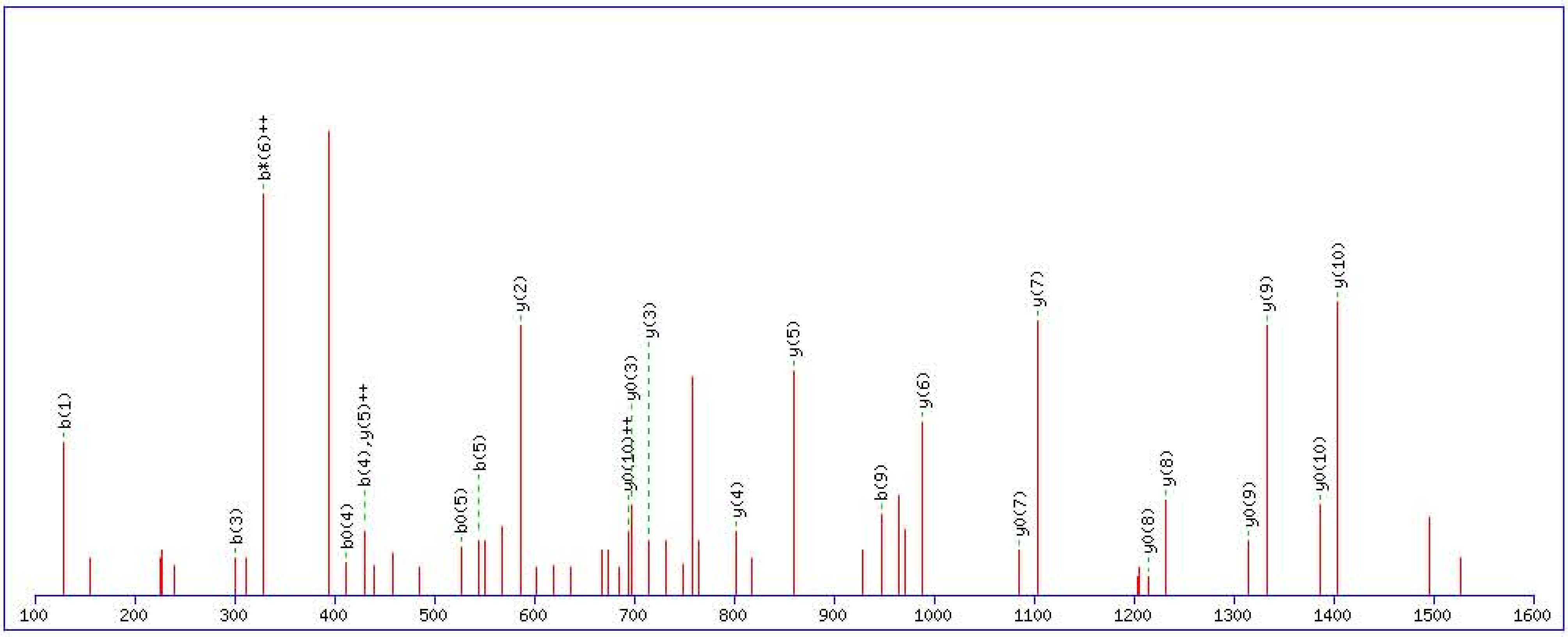
Mascot Search Results

Peptide View

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

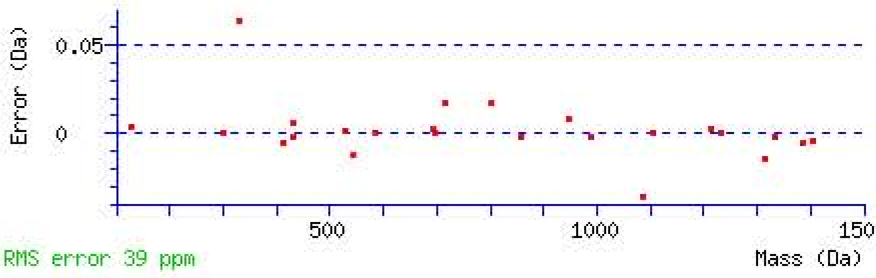
Match to Query 35996: 1531.722868 from(766.868710,2+) rtinseconds(1002) index(17999)
Title: Locus:1.1.1.2491.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

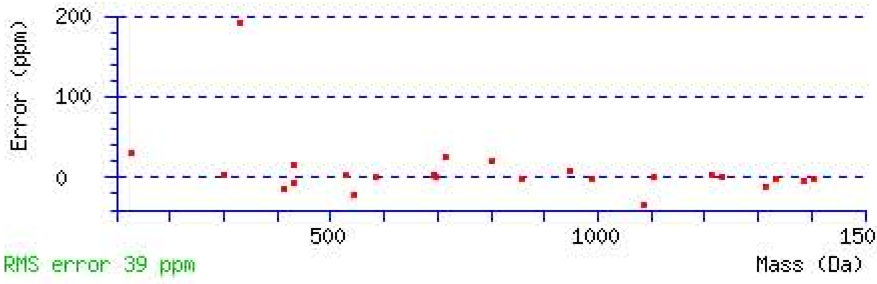
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1531.718796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 2.7e-006
Matches : 26/112 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	**129.102239**	65.054757	112.075690	56.541483			K							11
2	200.139353	100.573315	183.112804	92.060040			A	***1404.631137***	702.819207	1387.604588	694.305932	1386.620572	693.813924	10
3	**301.187032**	151.097154	284.160483	142.583879	283.176467	142.091872	T	***1333.594023***	667.300650	1316.567474	658.787375	1315.583458	658.295367	9
4	**430.229625**	215.618450	413.203076	207.105176	412.219060	206.613168	E	***1232.546344***	616.776810	1215.519795	608.263536	1214.535779	607.771528	8
5	**545.256568**	273.131922	528.230019	264.618648	527.246003	264.126640	D	***1103.503751***	552.255514	1086.477202	543.742239	1085.493186	543.250231	7
6	674.299161	337.653219	657.272612	329.139944	656.288596	328.647936	E	***988.476808***	494.742042	971.450259	486.228768	970.466243	485.736760	6
7	731.320625	366.163951	714.294076	357.650676	713.310060	357.158668	G	***859.434215***	430.220746	842.407666	421.707471	841.423650	421.215463	5
8	818.352653	409.679965	801.326104	401.166690	800.342088	400.674682	S	***802.412751***	401.710014	785.386202	393.196739	784.402186	392.704731	4
9	**947.395246**	474.201261	930.368697	465.687987	929.384681	465.195979	E	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
10	**1386.620572**	693.813924	1369.594023	685.300650	1368.610007	684.808642	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 KATEDEGSEQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.9	1531.718796	0.004072	KATEDEGSEQK
14.6	1531.715454	0.007414	EWNGVVSESDSPVK
11.9	1531.716309	0.006559	QVDSMWAEQK
7.7	1531.734055	-0.011187	VNPQEESYQK
7.0	1531.722626	0.000242	EAQQATETQRNEK
6.9	1531.730072	-0.007204	DGQQSGTVSSQK
3.2	1531.734055	-0.011187	DKGEKNFAMSYVK
0.8	1531.730698	-0.007830	AGYFGDPLAPNPADK
0.3	1531.711380	0.011488	KDSEEEAASPEGKR
0.2	1531.701523	0.021345	EGFDPQGASQLNNR

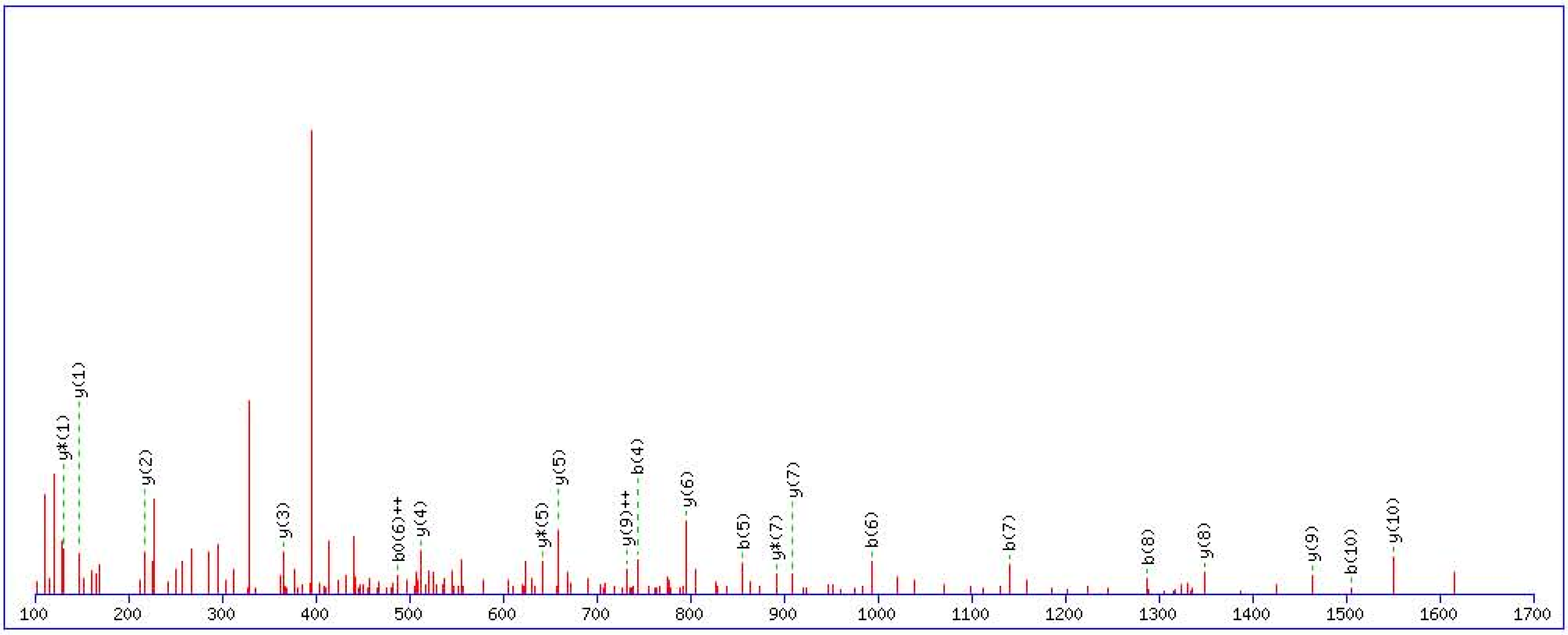
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

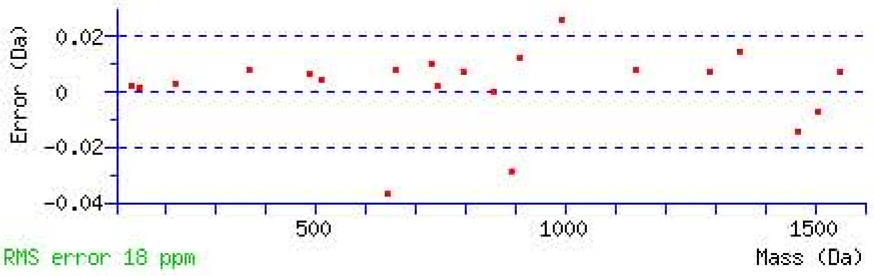
Match to Query 41203: 1650.835872 from(551.285900,3+) rtinseconds(2311) index(26886)
Title: Locus:1.1.1.2947.3 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

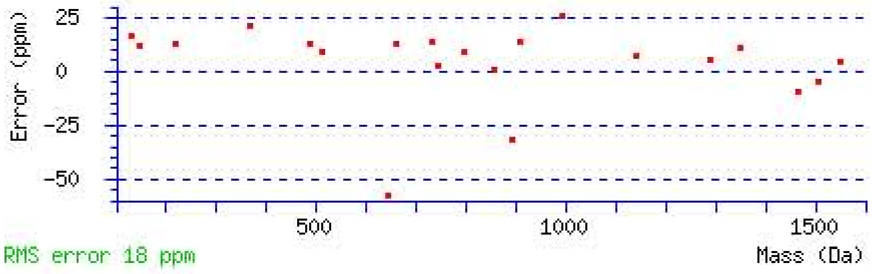
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1650.822845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.00093
Matches : 21/98 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	102.054955	51.531116			84.044390	42.525833	T							11
2	189.086983	95.047129			171.076418	86.041847	S	***1550.782433***	775.894855	1533.755884	767.381580	1532.771868	766.889572	10
3	304.113926	152.560601			286.103361	143.555319	D	***1463.750405***	732.378841	1446.723856	723.865566	1445.739840	723.373558	9
4	**743.339252**	372.173264	726.312703	363.659989	725.328687	363.167982	Q	***1348.723462***	674.865369	1331.696913	666.352095			8
5	**856.423316**	428.715296	839.396767	420.202022	838.412751	419.710014	I	***909.498136***	455.252706	892.471587	446.739432			7
6	**993.482228**	497.244752	976.455679	488.731477	975.471663	488.239469	H	***796.414072***	398.710674	779.387523	390.197400			6
7	**1140.550642**	570.778959	1123.524093	562.265685	1122.540077	561.773676	F	***659.355160***	330.181218	642.328611	321.667944			5
8	**1287.619056**	644.313166	1270.592507	635.799892	1269.608491	635.307884	F	***512.286746***	256.647011	495.260197	248.133737			4
9	1434.687470	717.847373	1417.660921	709.334099	1416.676905	708.842091	F	***365.218332***	183.112804	348.191783	174.599530			3
10	**1505.724584**	753.365930	1488.698035	744.852656	1487.714019	744.360648	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 TSDQIHFFFAK
(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	1650.822845	0.013027	TSDQIHFFFAK
2.3	1650.814789	0.021083	EVTTDLTPMHARHK

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

{MATRIX SCIENCE}

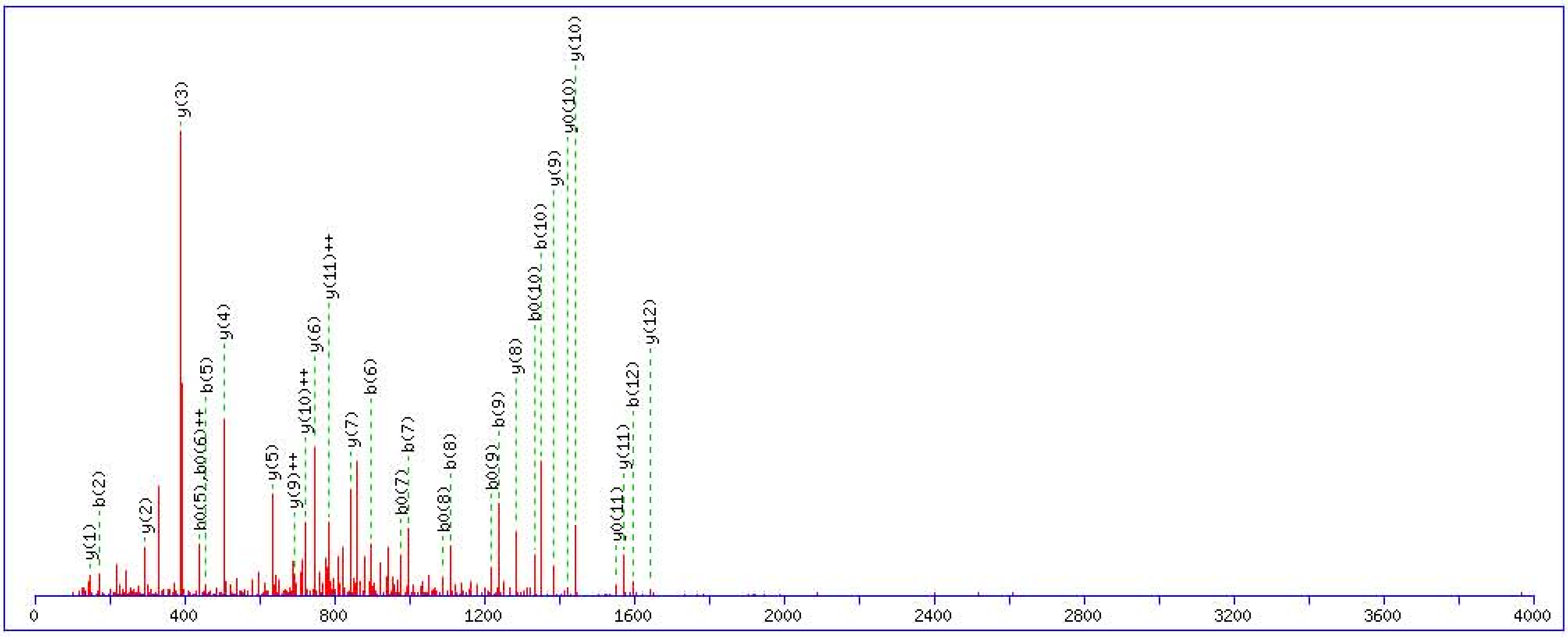
Mascot Search Results

Peptide View

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

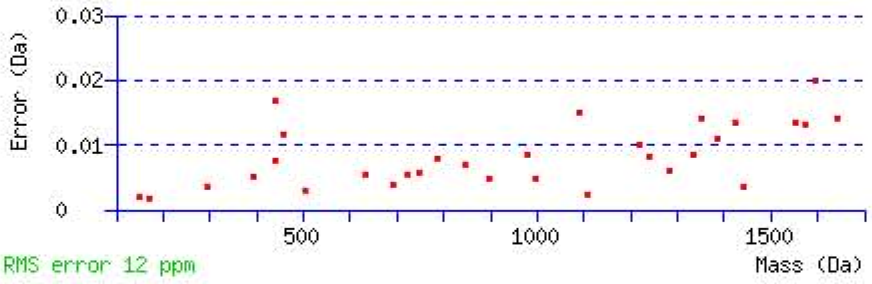
Match to Query 43495: 1740.970268 from(871.492410,2+) rtinseconds(2523) index(28244)
Title: Locus:1.1.1.3020.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

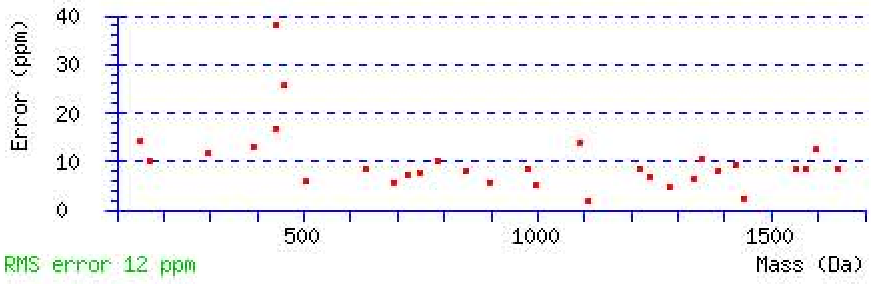
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1740.948425
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 89  Expect: 2e-008
Matches : 31/122 fragment ions using 49 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	**171.112804**	86.060040					A	***1642.887293***	821.947284	1625.860744	813.434010	1624.876728	812.942002	12
3	300.155397	150.581336			282.144832	141.576054	E	***1571.850179***	786.428727	1554.823630	777.915453	1553.839614	777.423445	11
4	357.176861	179.092068			339.166296	170.086786	G	***1442.807586***	721.907431	1425.781037	713.394157	1424.797021	712.902148	10
5	**458.224540**	229.615908			440.213975	220.610626	T	***1385.786122***	693.396699	1368.759573	684.883424	1367.775557	684.391416	9
6	**897.449866**	449.228571	880.423317	440.715297	879.439301	440.223289	Q	***1284.738443***	642.872860	1267.711894	634.359585	1266.727878	633.867577	8
7	**996.518280**	498.762778	979.491731	490.249504	978.507715	489.757496	V	***845.513117***	423.260196	828.486568	414.746922	827.502552	414.254914	7
8	**1109.602344**	555.304810	1092.575795	546.791536	1091.591779	546.299527	L	***746.444703***	373.725989	729.418154	365.212715	728.434138	364.720707	6
9	**1238.644937**	619.826106	1221.618388	611.312832	1220.634372	610.820824	E	***633.360639***	317.183958	616.334090	308.670683	615.350074	308.178675	5
10	**1351.729001**	676.368138	1334.702452	667.854864	1333.718436	667.362856	L	***504.318046***	252.662661	487.291497	244.149386			4
11	1448.781765	724.894520	1431.755216	716.381246	1430.771200	715.889238	P	***391.233982***	196.120629	374.207433	187.607355			3
12	**1595.850179**	798.428727	1578.823630	789.915453	1577.839614	789.423445	F	***294.181218***	147.594247	277.154669	139.080973			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.5	1740.948425	0.021843	VAEGTQVLELPFK
8.4	1740.962982	0.007286	ISRQLAEEILMK

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

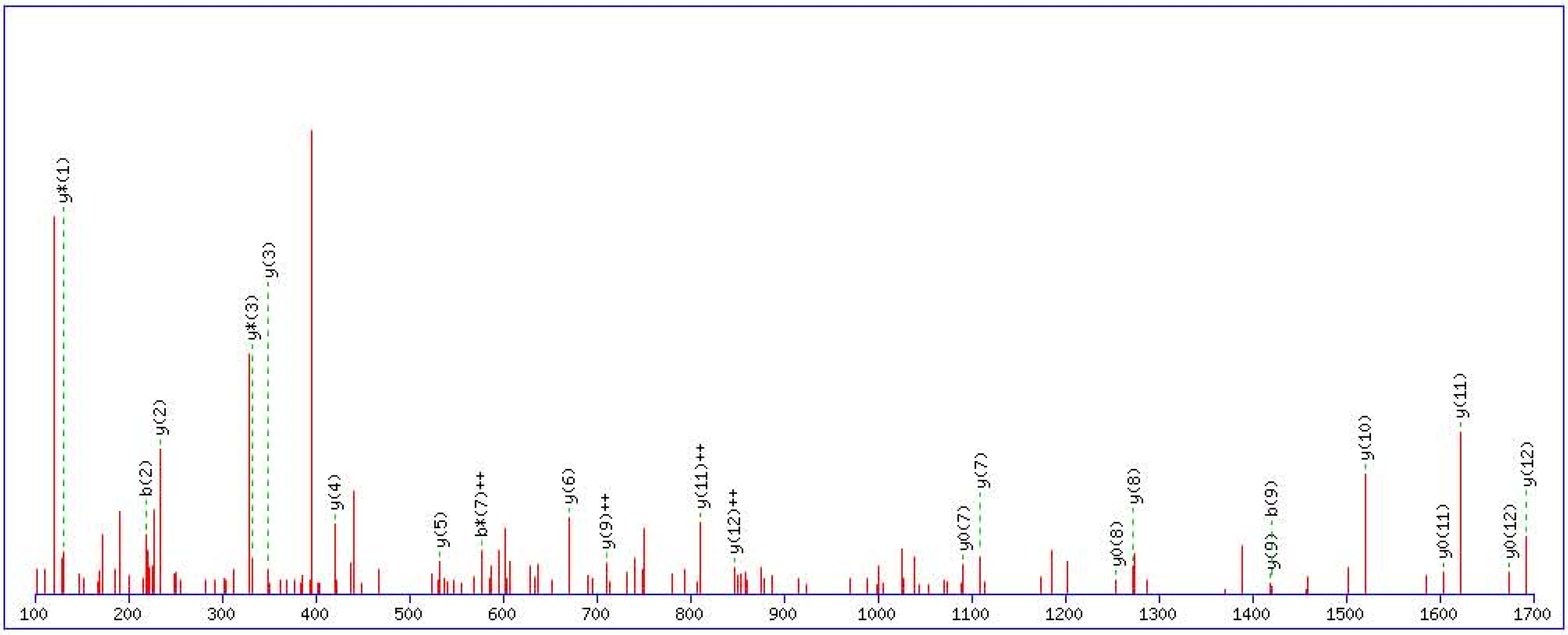
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

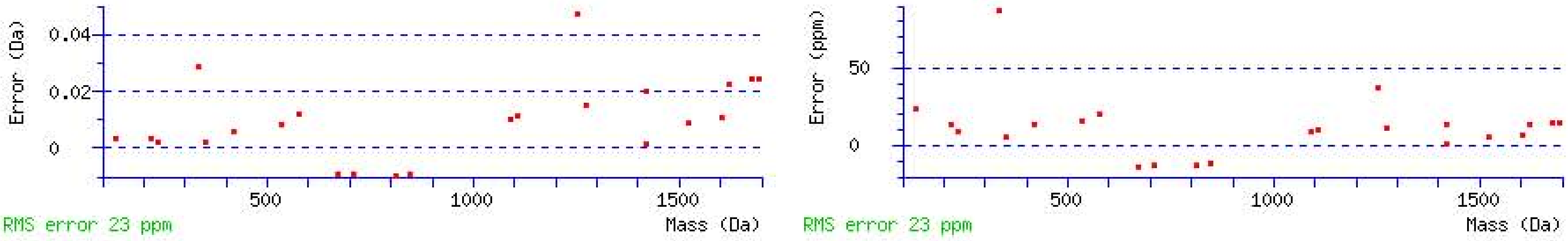
Match to Query 46199: 1838.913672 from(613.978500,3+) rtinseconds(2038) index(24966)
Title: Locus:1.1.1.2852.5 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1838.902542
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00036
Matches : 23/126 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	148.075690	74.541483					F							13
2	**219.112804**	110.060040					A	***1692.841406***	846.924341	1675.814857	838.411067	1674.830841	837.919059	12
3	320.160483	160.583879			302.149918	151.578597	T	***1621.804292***	811.405784	1604.777743	802.892510	1603.793727	802.400502	11
4	421.208162	211.107719			403.197597	202.102437	T	***1520.756613***	760.881945	1503.730064	752.368670	1502.746048	751.876662	10
5	568.276576	284.641926			550.266011	275.636644	F	***1419.708934***	710.358105	1402.682385	701.844831	1401.698369	701.352823	9
6	731.339905	366.173591			713.329340	357.168308	Y	***1272.640520***	636.823898	1255.613971	628.310624	1254.629955	627.818616	8
7	1170.565231	585.786254	1153.538682	577.272979	1152.554666	576.780971	Q	***1109.577191***	555.292234	1092.550642	546.778959	1091.566626	546.286951	7
8	1307.624143	654.315710	1290.597594	645.802435	1289.613578	645.310427	H	***670.351865***	335.679571	653.325316	327.166296	652.341300	326.674288	6
9	**1420.708207**	710.857741	1403.681658	702.344467	1402.697642	701.852459	L	***533.292953***	267.150115	516.266404	258.636840	515.282388	258.144832	5
10	1491.745321	746.376298	1474.718772	737.863024	1473.734756	737.371016	A	***420.208889***	210.608083	403.182340	202.094808	402.198324	201.602800	4
11	1606.772264	803.889770	1589.745715	795.376496	1588.761699	794.884487	D	***349.171775***	175.089526	332.145226	166.576251	331.161210	166.084243	3
12	1693.804292	847.405784	1676.777743	838.892510	1675.793727	838.400502	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 FATTFYQHLADSK
(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	1838.902542	0.011130	FATTFYQHLADSK

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

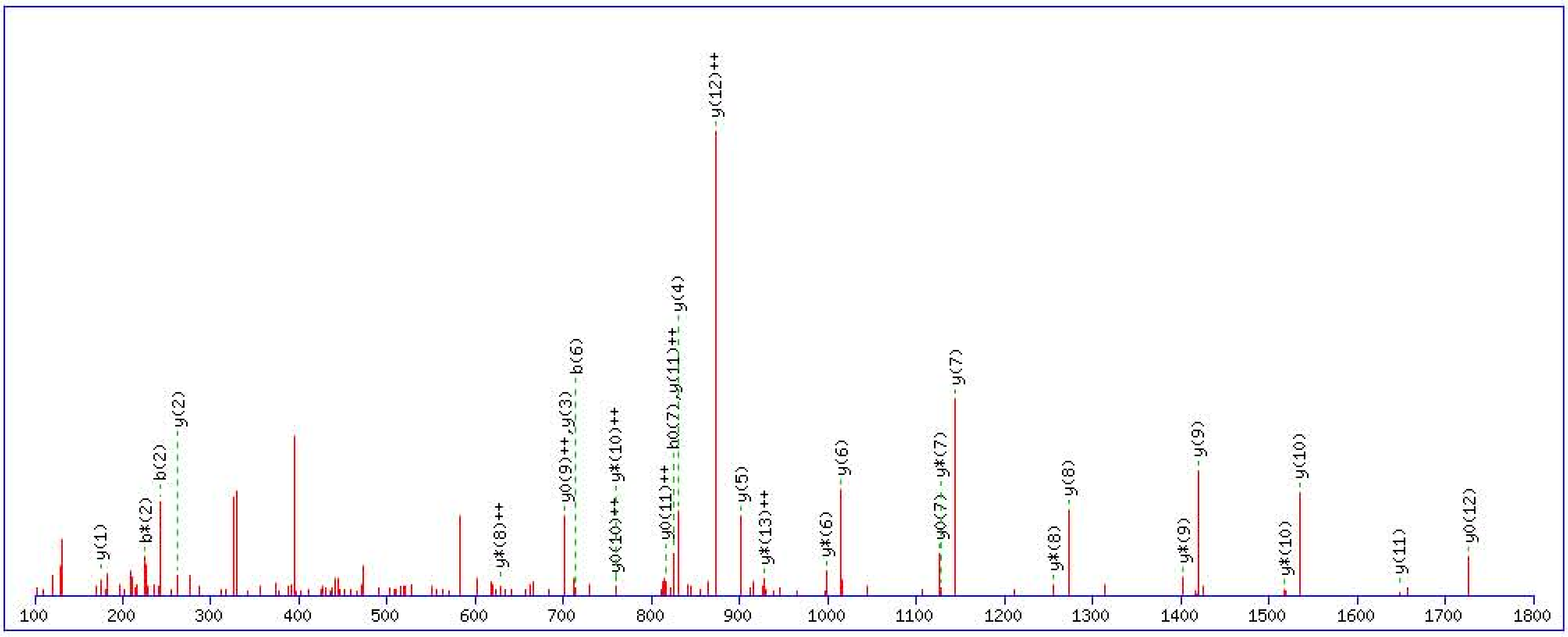
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

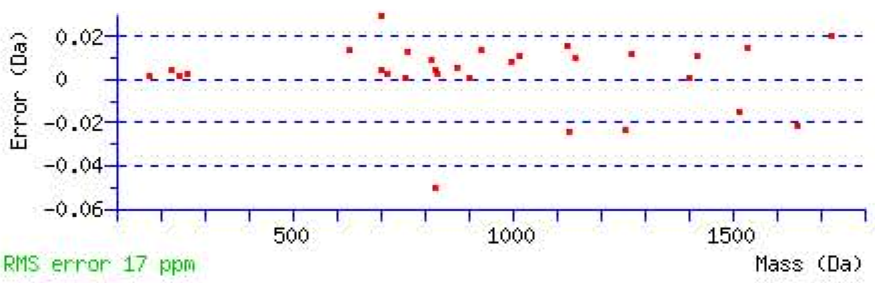
Match to Query 49569: 1985.017632 from(662.679820,3+) rtinseconds(1880) index(23812)
Title: Locus:1.1.1.2797.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

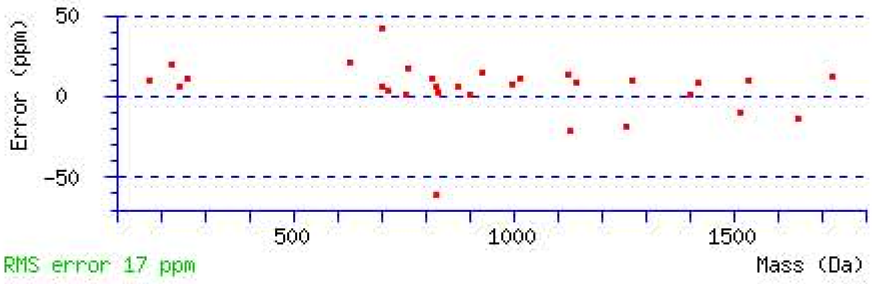
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1985.004013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 9.8e-005
Matches : 30/144 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							14
2	**242.149918**	121.578597	225.123369	113.065323			Q	1872.927259	936.967268	1855.900710	928.453993	1854.916694	927.961985	13
3	339.202682	170.104979	322.176133	161.591705			P	1744.868681	872.937979	1727.842132	864.424704	1726.858116	863.932696	12
4	452.286746	226.647011	435.260197	218.133737			L	***1647.815917***	824.411597	1630.789368	815.898322	1629.805352	815.406314	11
5	567.313689	284.160483	550.287140	275.647208	549.303124	275.155200	D	***1534.731853***	767.869565	1517.705304	759.356290	1516.721288	758.864282	10
6	**714.382103**	357.694690	697.355554	349.181415	696.371538	348.689407	F	***1419.704910***	710.356093	1402.678361	701.842819	1401.694345	701.350811	9
7	842.477066	421.742171	825.450517	413.228897	824.466501	412.736889	K	***1272.636496***	636.821886	1255.609947	628.308612	1254.625931	627.816604	8
8	971.519659	486.263468	954.493110	477.750193	953.509094	477.258185	E	***1144.541533***	572.774405	1127.514984	564.261130	1126.530968	563.769122	7
9	1085.562586	543.284931	1068.536037	534.771657	1067.552021	534.279649	N	***1015.498940***	508.253108	998.472391	499.739834	997.488375	499.247826	6
10	1156.599700	578.803488	1139.573151	570.290214	1138.589135	569.798205	A	***901.456013***	451.231645	884.429464	442.718370	883.445448	442.226362	5
11	1285.642293	643.324785	1268.615744	634.811510	1267.631728	634.319502	E	***830.418899***	415.713088	813.392350	407.199813	812.408334	406.707805	4
12	1724.867619	862.937448	1707.841070	854.424173	1706.857054	853.932165	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
13	1811.899647	906.453462	1794.873098	897.940187	1793.889082	897.448179	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.9	1985.004013	0.013619	LQPLDFKENAEQSR
2.1	1985.043762	-0.026130	QLIEKMNLSAIQDR

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

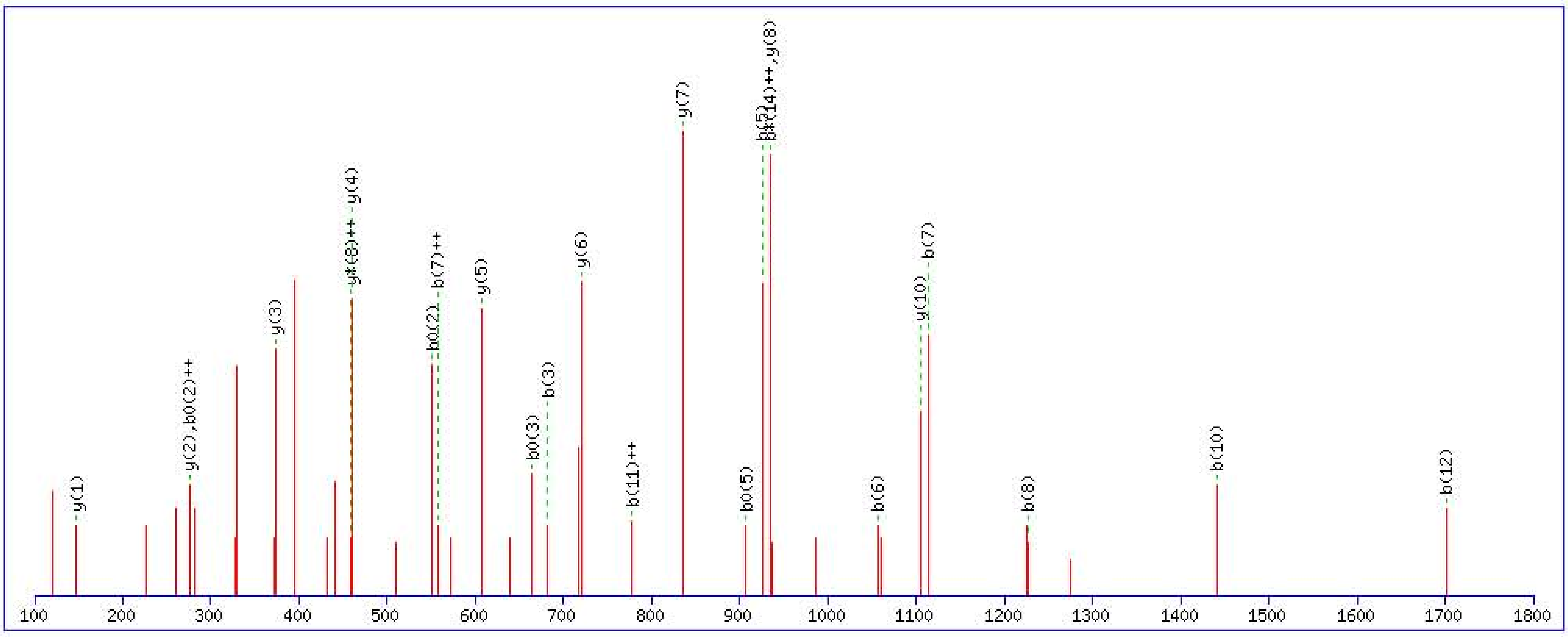
Mascot Search Results

Peptide View

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

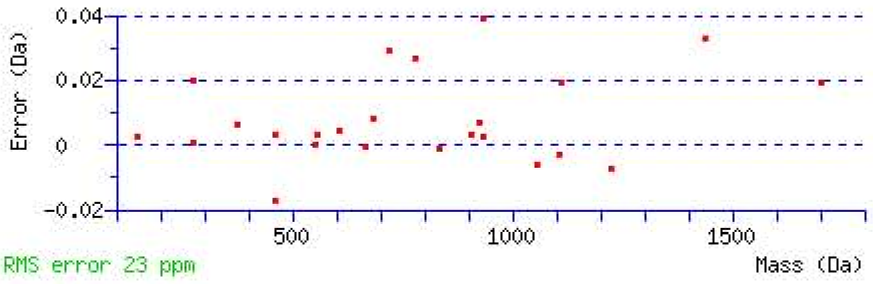
Match to Query 54347: 2159.087682 from(720.703170,3+) rtinseconds(2890) index(30706)
Title: Locus:1.1.1.3147.8 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

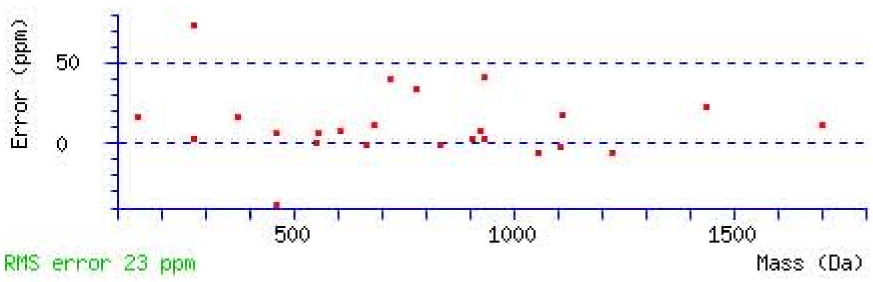
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2159.064255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 4.9e-007
Matches : 24/176 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	130.049869	65.528572			112.039304	56.523290	E							16
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	Q	2031.028948	1016.018112	2014.002399	1007.504838	2013.018383	1007.012830	15
3	***682.359259***	341.683268	665.332710	333.169993	664.348694	332.677985	L	1591.803622	796.405449	1574.777073	787.892175	1573.793057	787.400167	14
4	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	Q	1478.719558	739.863417	1461.693009	731.350143	1460.708993	730.858135	13
5	***925.444780***	463.226028	908.418231	454.712754	907.434215	454.220746	D	1350.660980	675.834128	1333.634431	667.320854	1332.650415	666.828845	12
6	***1056.485265***	528.746271	1039.458716	520.232996	1038.474700	519.740988	M	1235.634037	618.320657	1218.607488	609.807382	1217.623472	609.315374	11
7	***1113.506729***	**557.257003**	1096.480180	548.743728	1095.496164	548.251720	G	***1104.593552***	552.800414	1087.567003	544.287140	1086.582987	543.795132	10
8	***1226.590793***	613.799034	1209.564244	605.285760	1208.580228	604.793752	L	1047.572088	524.289682	1030.545539	515.776408	1029.561523	515.284400	9
9	1325.659207	663.333241	1308.632658	654.819967	1307.648642	654.327959	V	***934.488024***	467.747650	917.461475	459.234376	916.477459	458.742368	8
10	***1440.686150***	720.846713	1423.659601	712.333439	1422.675585	711.841431	D	***835.419610***	418.213443	818.393061	409.700169	817.409045	409.208161	7
11	1553.770214	**777.388745**	1536.743665	768.875471	1535.759649	768.383462	L	***720.392667***	360.699972	703.366118	352.186697	702.382102	351.694689	6
12	***1700.838628***	850.922952	1683.812079	842.409678	1682.828063	841.917669	F	***607.308603***	304.157940	590.282054	295.644665	589.298038	295.152657	5
13	1787.870656	894.438966	1770.844107	885.925692	1769.860091	885.433684	S	***460.240189***	230.623732	443.213640	222.110458	442.229624	221.618450	4
14	1884.923420	942.965348	1867.896871	934.452074	1866.912855	933.960066	P	***373.208161***	187.107718	356.181612	178.594444	355.197596	178.102436	3
15	2013.966013	1007.486645	1996.939464	998.973370	1995.955448	998.481362	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
16							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.8	2159.064255	0.023427	EQLQDMGLVDLFSPEK
58.9	2159.064255	0.023427	EQLQDMGLVDLFSPEK
0.4	2159.074600	0.013082	EKTTIAVTSRGYYGLEDEK

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

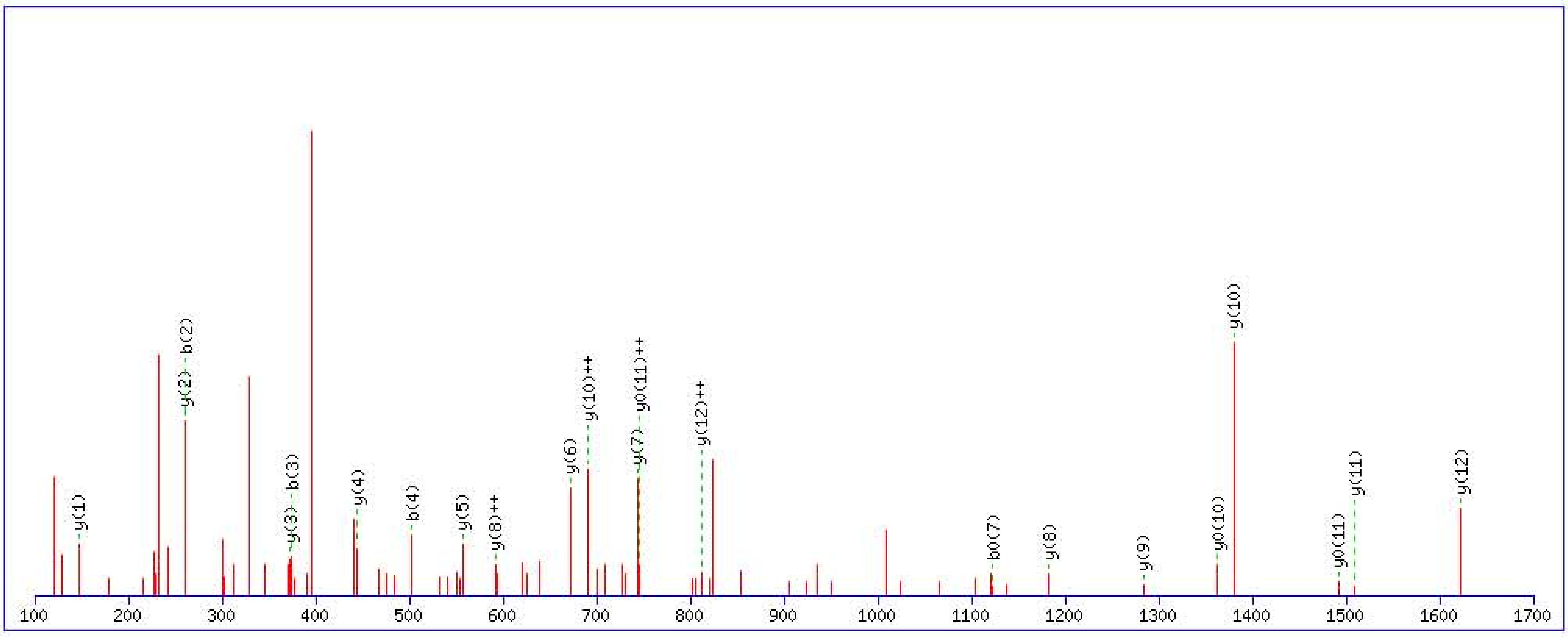
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFLEPTQADIALLK**
Found in **APOA_HUMAN**, Apolipoprotein(a) OS=Homo sapiens GN=LPA PE=1 SV=1

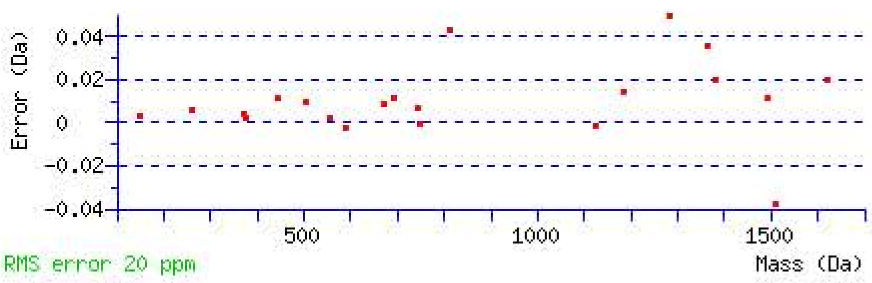
Match to Query 47194: 1882.091052 from(628.370960,3+) rtinseconds(2742) index(47337)
Title: Locus:1.1.1.3402.8 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

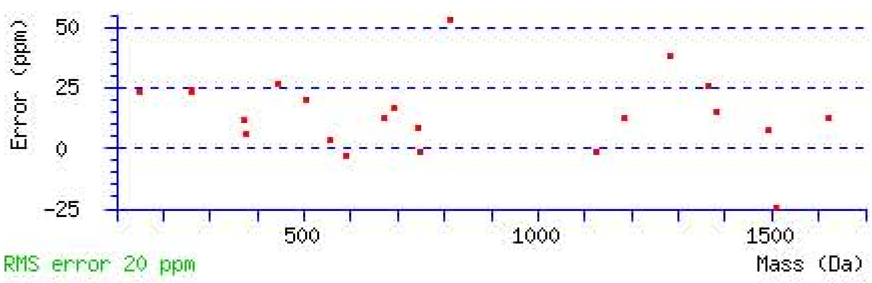
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1882.063766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 68 **Expect:** 4.5e-007
Matches : 22/128 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	114.091340	57.549308					L							14
2	**261.159754**	131.083515					F	1769.987007	885.497142	1752.960458	876.983867	1751.976442	876.491859	13
3	**374.243818**	187.625547					L	***1622.918593***	811.962934	1605.892044	803.449660	1604.908028	802.957652	12
4	**503.286411**	252.146843			485.275846	243.141561	E	***1509.834529***	755.420903	1492.807980	746.907628	1491.823964	746.415620	11
5	600.339175	300.673226			582.328610	291.667943	P	***1380.791936***	690.899606	1363.765387	682.386331	1362.781371	681.894323	10
6	701.386854	351.197065			683.376289	342.191783	T	***1283.739172***	642.373224	1266.712623	633.859949	1265.728607	633.367941	9
7	1140.612180	570.809728	1123.585631	562.296454	1122.601615	561.804446	Q	***1182.691493***	591.849384	1165.664944	583.336110	1164.680928	582.844102	8
8	1211.649294	606.328285	1194.622745	597.815011	1193.638729	597.323003	A	***743.466167***	372.236721	726.439618	363.723447	725.455602	363.231439	7
9	1326.676237	663.841757	1309.649688	655.328482	1308.665672	654.836474	D	***672.429053***	336.718164	655.402504	328.204890	654.418488	327.712882	6
10	1439.760301	720.383789	1422.733752	711.870514	1421.749736	711.378506	I	***557.402110***	279.204693	540.375561	270.691418			5
11	1510.797415	755.902346	1493.770866	747.389071	1492.786850	746.897063	A	***444.318046***	222.662661	427.291497	214.149386			4
12	1623.881479	812.444377	1606.854930	803.931103	1605.870914	803.439095	L	***373.280932***	187.144104	356.254383	178.630829			3
13	1736.965543	868.986409	1719.938994	860.473135	1718.954978	859.981127	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 LFLEPTQADIALLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.2	1882.063766	0.027286	LFLEPTQADIALLK
0.5	1882.100143	-0.009091	KMNTLLLVSLSFLYLK

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

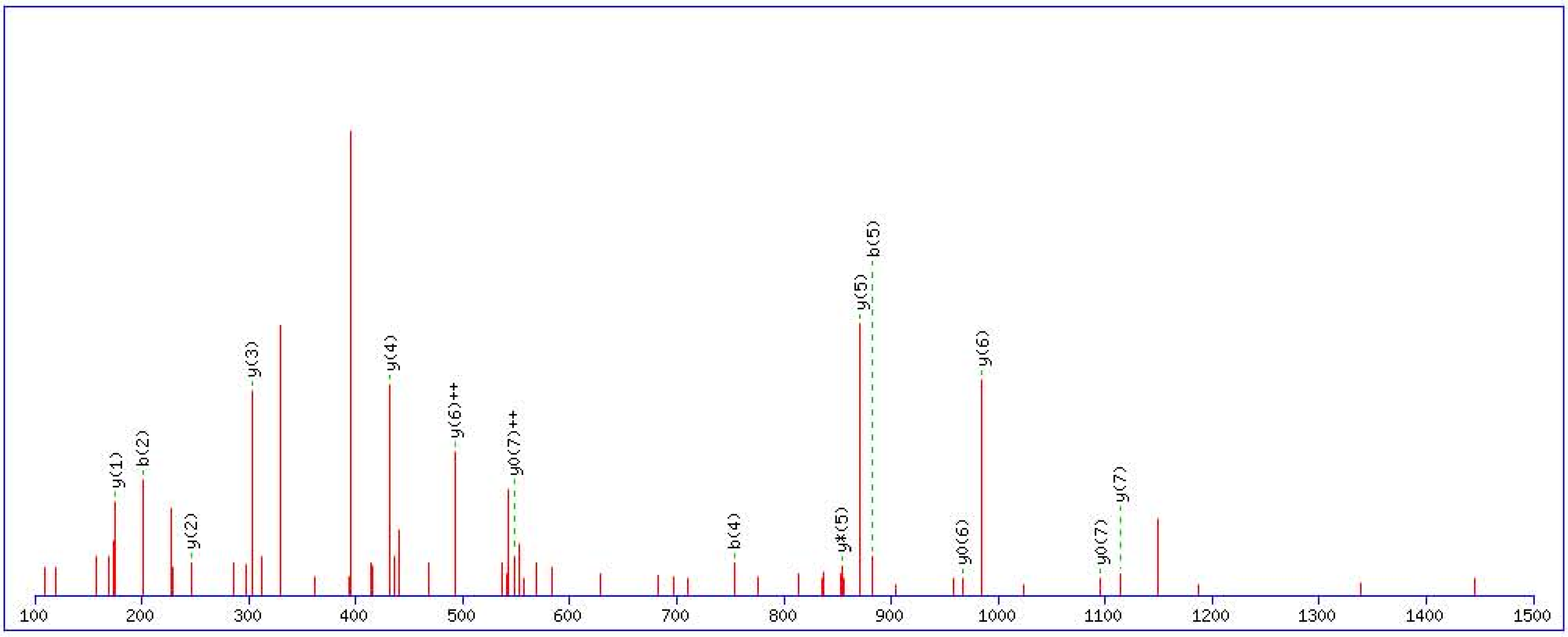
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

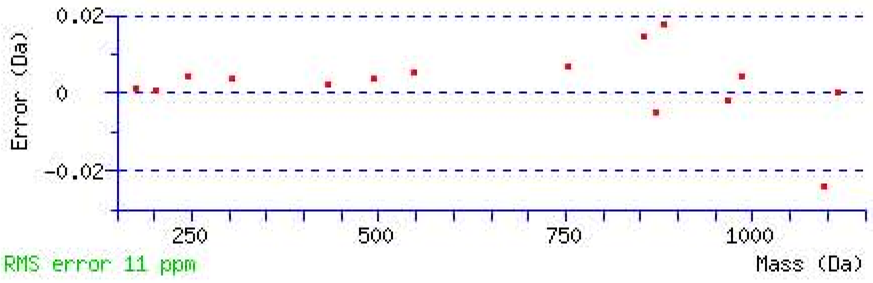
Match to Query 23209: 1183.603788 from(592.809170,2+) rtinseconds(1460) index(20695)
Title: Locus:1.1.1.2651.16 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

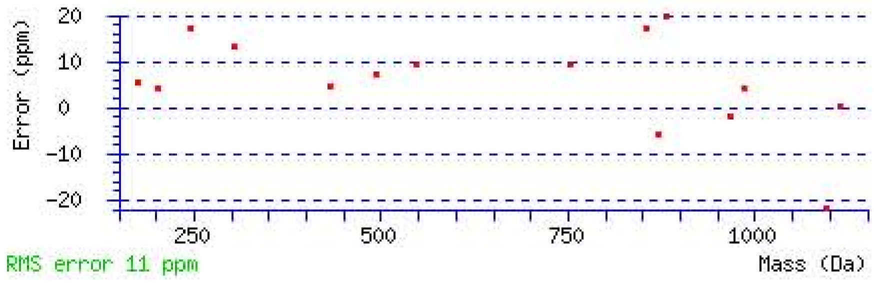
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1183.601913
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.0019
Matches : 15/70 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	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
39.7	1183.601913	0.001875	AELQEGAR
11.1	1183.601913	0.001875	EALEQQR
7.9	1183.613815	-0.010027	FHFEALPPAR
5.8	1183.601913	0.001875	ELQAEAGR
5.5	1183.587997	0.015791	EAKLDHCRR
3.7	1183.617172	-0.013384	AQLEAWR
3.0	1183.595413	0.008375	AFCRMVTRK
1.8	1183.601913	0.001875	LQEAQER
1.7	1183.617172	-0.013384	AIQEAWR
0.9	1183.609802	-0.006014	ATPHFSGLAAGR

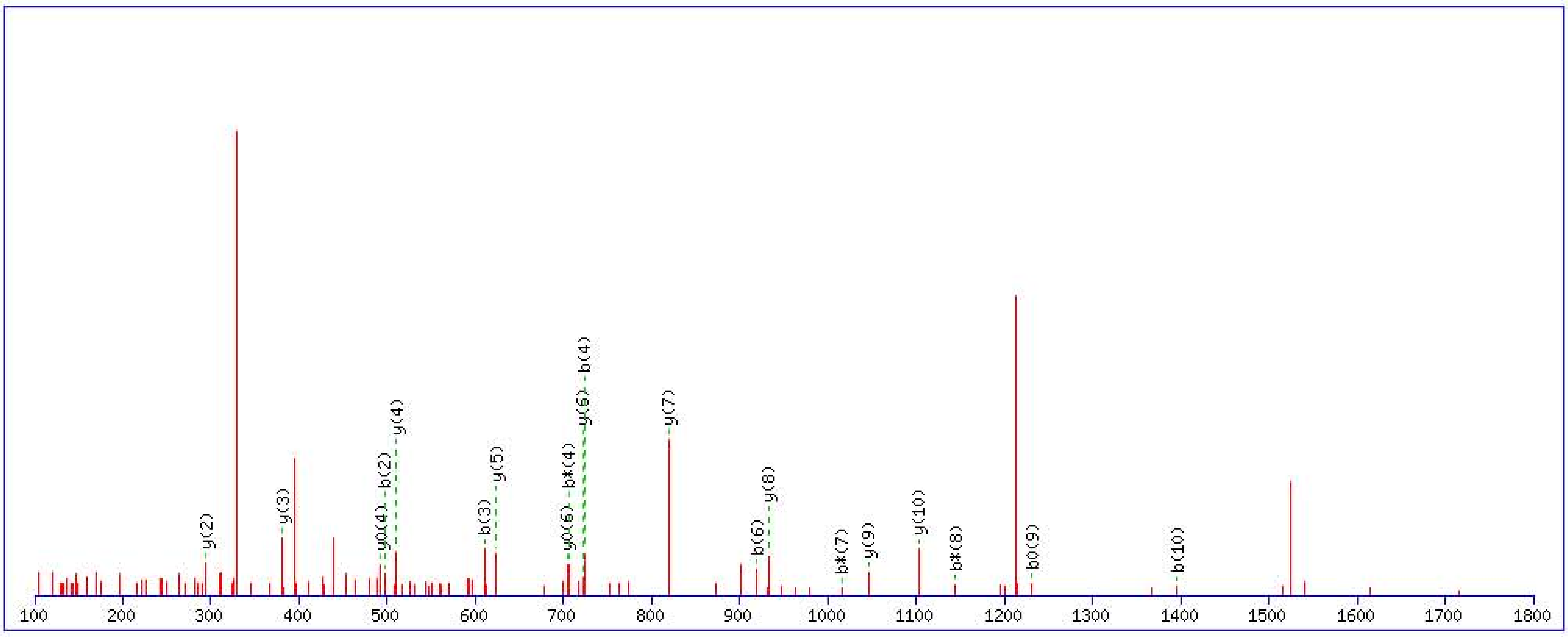
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

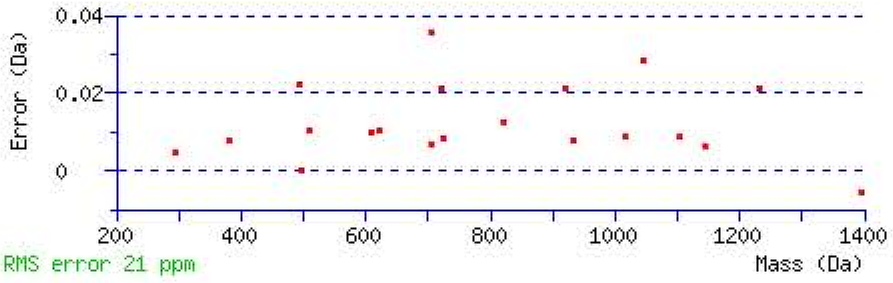
Match to Query 36238: 1540.884448 from(771.449500,2+) rtinseconds(2787) index(84185)
Title: Locus:1.1.1.2319.13 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

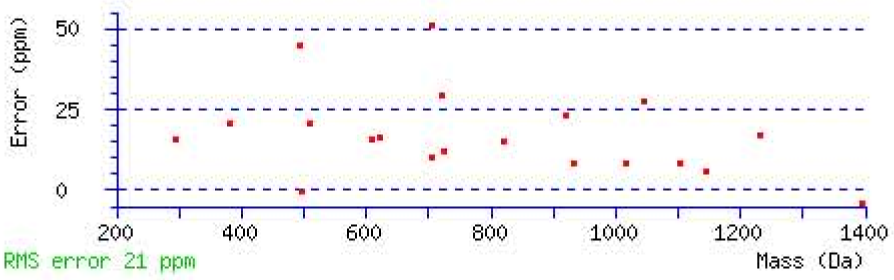
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1540.868713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 7.2e-005
Matches : 20/102 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	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
51.8	1540.868713	0.015735	QGLLPVLESFK
14.8	1540.894531	-0.010083	QAVLSMVRKAK
0.2	1540.864700	0.019748	KVTVGKDDIQK
0.2	1540.893677	-0.009229	LKSVDVGLQGLREK

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

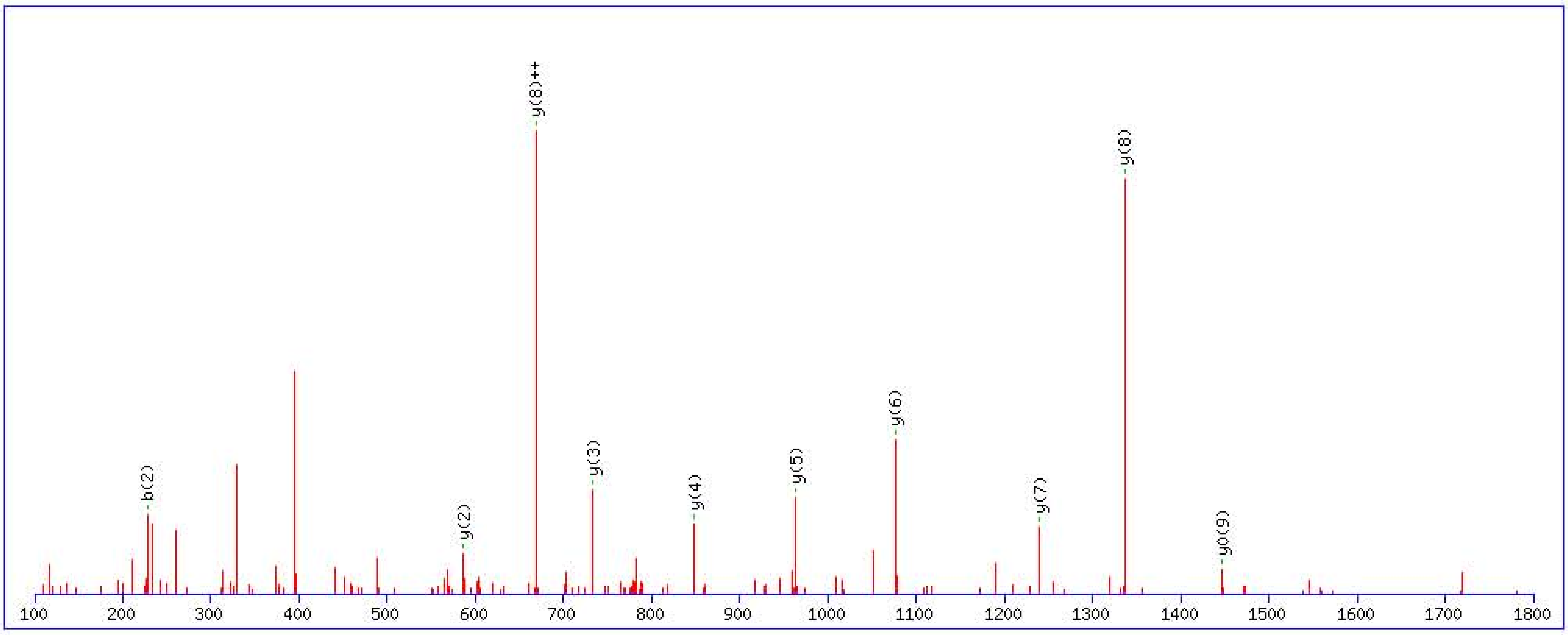
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

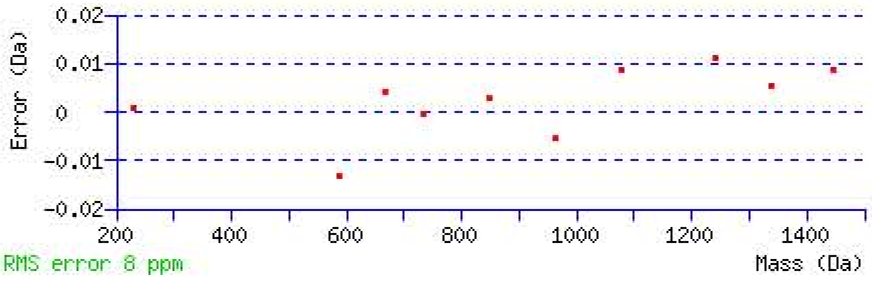
Match to Query 36860: 1562.795488 from(782.405020,2+) rtinseconds(2154) index(25787)
Title: Locus:1.1.1.2892.15 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

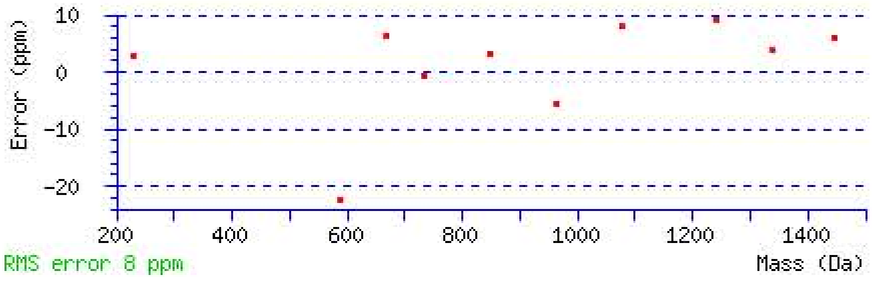
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1562.780304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00014
Matches : 10/90 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	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
46.9	1562.780304	0.015184	VQPYLDDFQK
5.4	1562.804764	-0.009276	QVEELLMAMEKVK
0.5	1562.808624	-0.013136	LNSPTTTSQIMARK
0.3	1562.795364	0.000124	KVKFTQQNYHDR

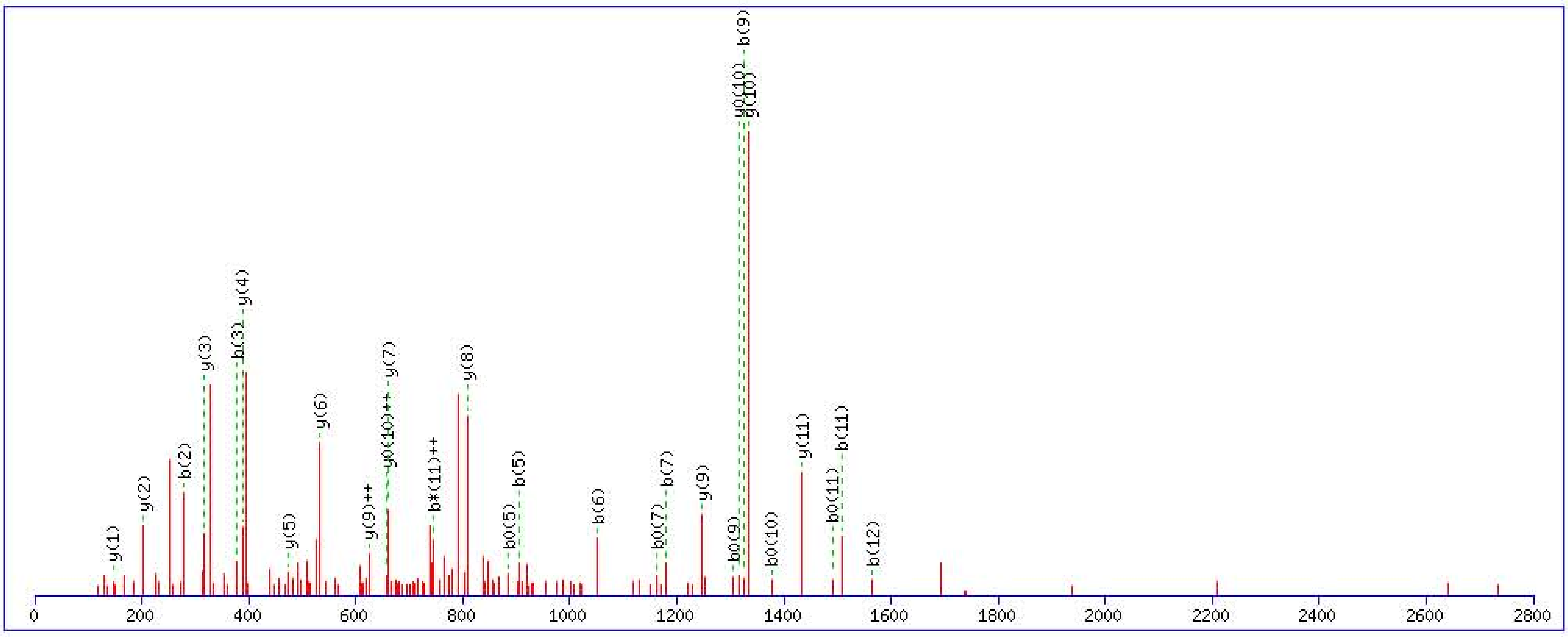
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

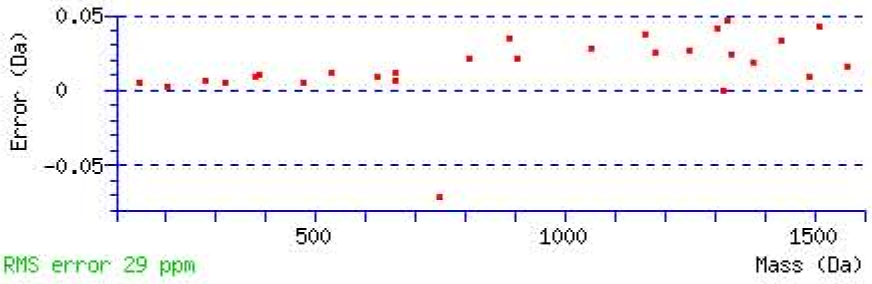
Match to Query 42761: 1710.824208 from(856.419380,2+) rtinseconds(2387) index(63520)
Title: Locus:1.1.1.3253.12 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

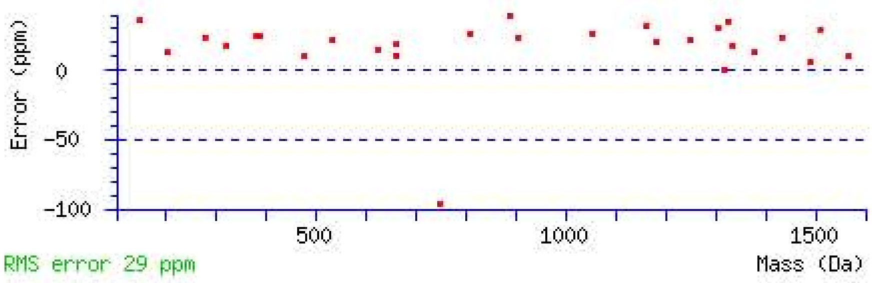
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1710.828705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 66 **Expect:** 9.8e-007
Matches : 28/128 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	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
66.2	1710.828705	-0.004497	DYVSQFEGSALGK
2.1	1710.799500	0.024708	QAYTGNNSSQIQAAMK

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

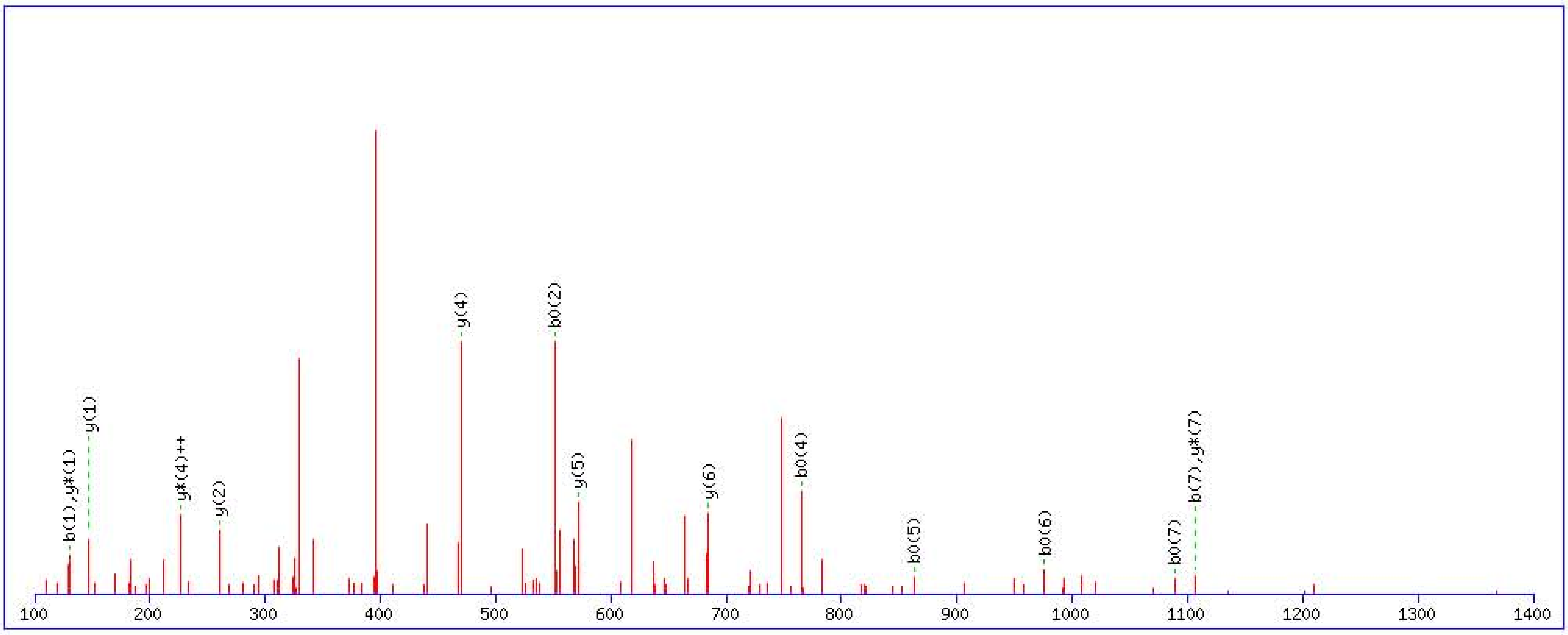
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

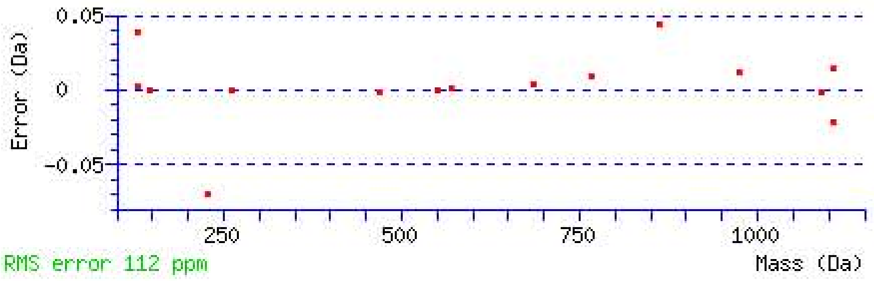
Match to Query 25365: 1251.724908 from(626.869730,2+) rtinseconds(2090) index(25310)
Title: Locus:1.1.1.2870.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

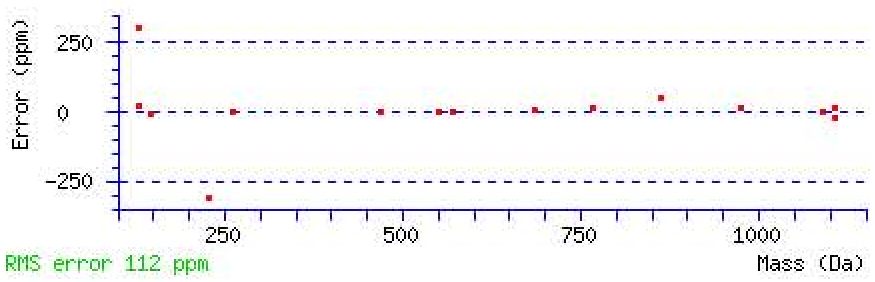
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1251.726059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.017
Matches : 15/74 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	**130.049869**	65.528572			112.039304	56.523290	E							8
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1123.690765	562.349021	1106.664216	553.835746	1105.680200	553.343738	7
3	682.359259	341.683268	665.332710	333.169993	664.348694	332.677985	L	***684.465439***	342.736358	667.438890	334.223083	666.454874	333.731075	6
4	783.406938	392.207107	766.380389	383.693833	765.396373	383.201825	T	***571.381375***	286.194326	554.354826	277.681051	553.370810	277.189043	5
5	880.459702	440.733489	863.433153	432.220215	862.449137	431.728207	P	***470.333696***	235.670486	453.307147	227.157212			4
6	993.543766	497.275521	976.517217	488.762247	975.533201	488.270239	L	373.280932	187.144104	356.254383	178.630830			3
7	**1106.627830**	553.817553	1089.601281	545.304279	1088.617265	544.812271	I	***260.196868***	130.602072	243.170319	122.088798			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EQLTPLIK
(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	1251.726059	-0.001151	EQLTPLIK
15.8	1251.722672	0.002236	NYIPYLTKLK
4.1	1251.722702	0.002206	FFKTLQDLLK
3.0	1251.729874	-0.004966	RHKLESELIK
2.8	1251.718689	0.006219	ASGVGLPGGSLPIK
1.4	1251.712143	0.012765	KMGVKLTPHNK

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

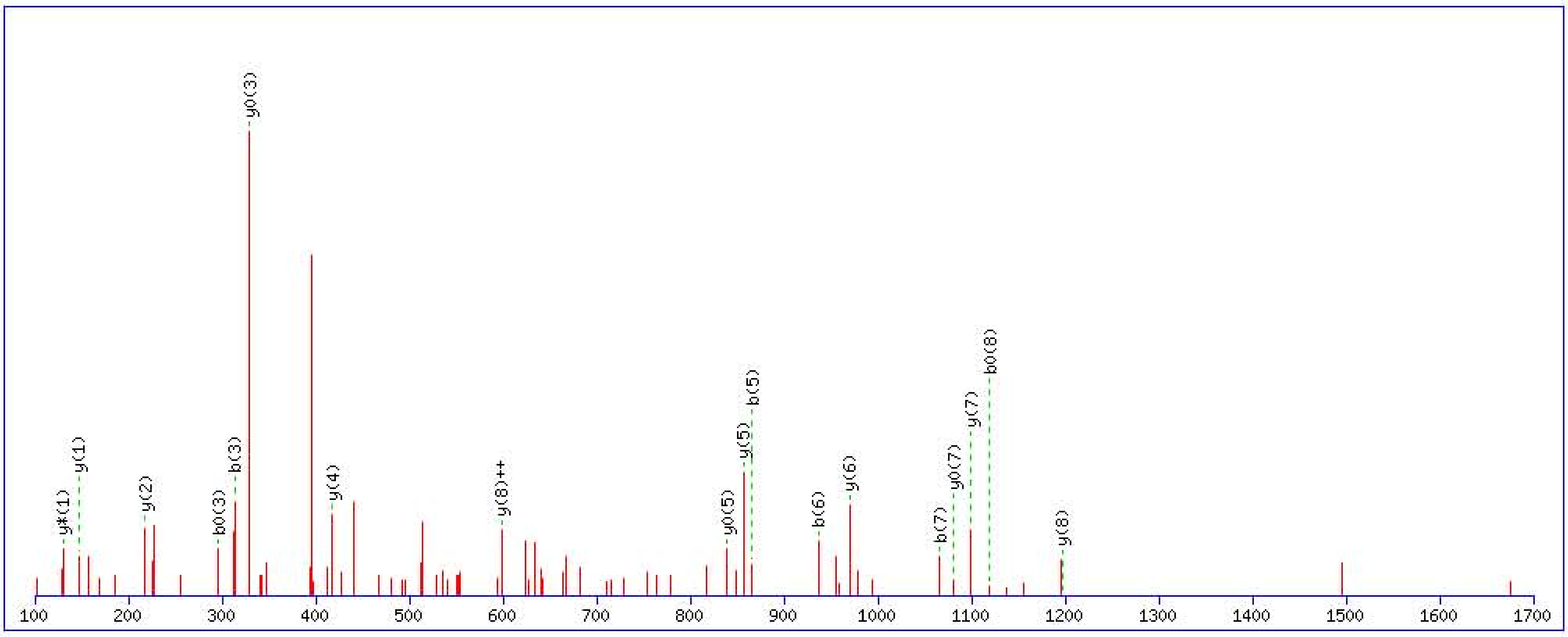
Mascot Search Results

Peptide View

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

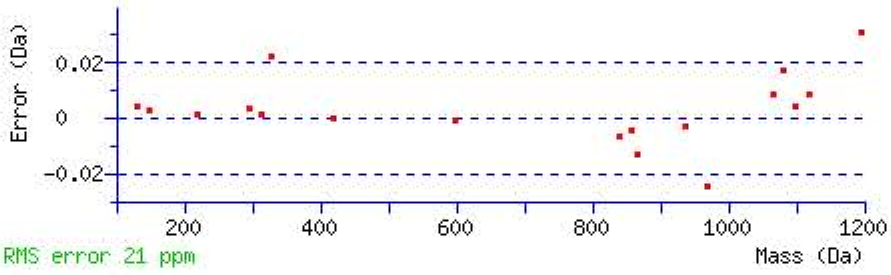
Match to Query 26441: 1282.659328 from(642.336940,2+) rtinseconds(1541) index(21322)
Title: Locus:1.1.1.2679.16 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

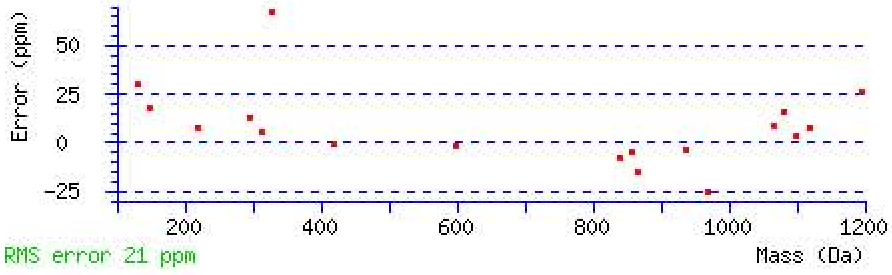
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1282.659088
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00041
Matches : 18/84 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**							9
2	185.092068	93.049672			167.081503	84.044389	**P**	***1196.634372***	598.820824	1179.607823	590.307550	1178.623807	589.815541	8
3	**314.134661**	157.570968			296.124096	148.565686	**E**	***1099.581608***	550.294442	1082.555059	541.781168	1081.571043	541.289160	7
4	427.218725	214.113001			409.208160	205.107718	**L**	***970.539015***	485.773146	953.512466	477.259871	952.528450	476.767863	6
5	**866.444051**	433.725664	849.417502	425.212389	848.433486	424.720381	**Q**	***857.454951***	429.231114	840.428402	420.717839	839.444386	420.225831	5
6	**937.481165**	469.244221	920.454616	460.730946	919.470600	460.238938	**A**	***418.229625***	209.618450	401.203076	201.105176	400.219060	200.613168	4
7	**1066.523758**	533.765517	1049.497209	525.252243	1048.513193	524.760235	**E**	347.192511	174.099893	330.165962	165.586619	329.181946	165.094611	3
8	1137.560872	569.284074	1120.534323	560.770800	1119.550307	560.278792	**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 SPELQAEAK
(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	1282.659088	0.000240	SPELQAEAK
5.7	1282.652573	0.006755	KMRAISWTMK
4.5	1282.651688	0.007640	KKQELDEHEK
3.6	1282.670334	-0.011006	QQQEQIAK
2.7	1282.655716	0.003612	ALEAEKYGFQK
2.3	1282.662949	-0.003621	DLSDTQRHLAK
0.8	1282.645203	0.014125	AAGPGLGNVAMGPR
0.7	1282.678207	-0.018879	SLQQGPPKWSR

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

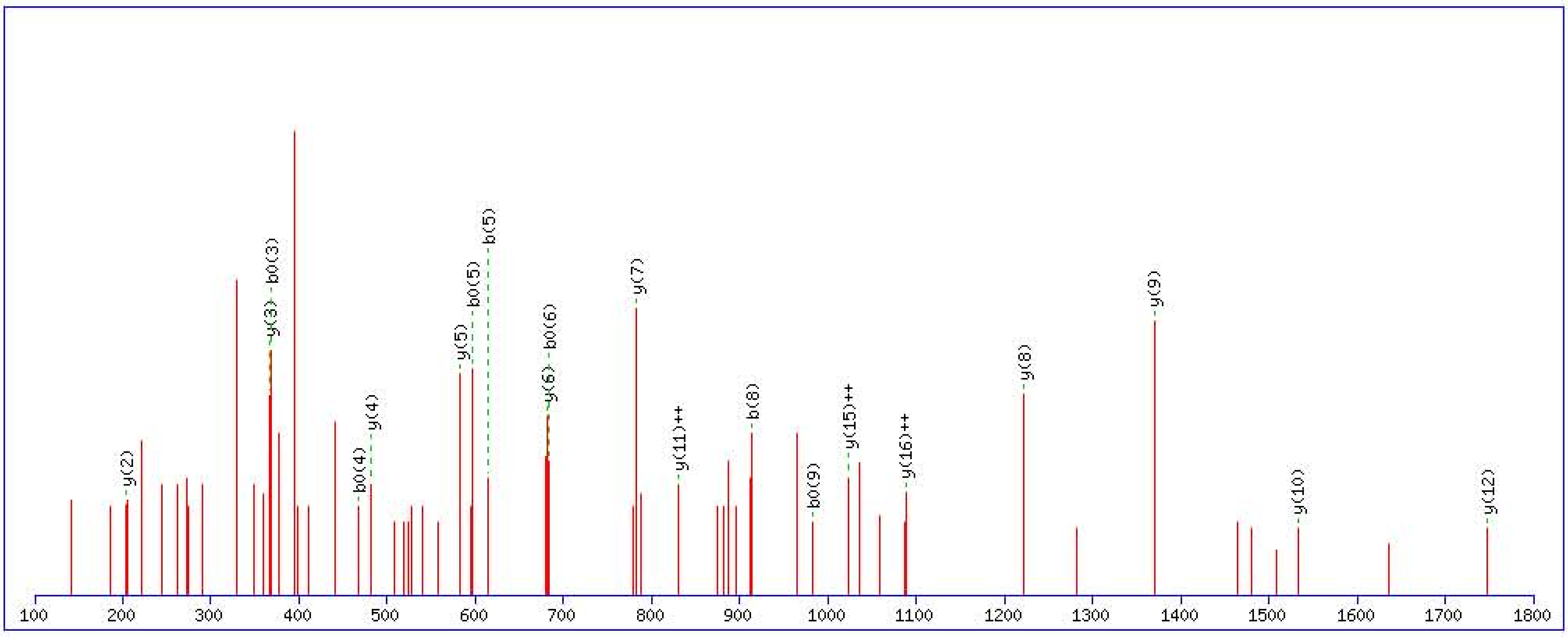
Mascot Search Results

Peptide View

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

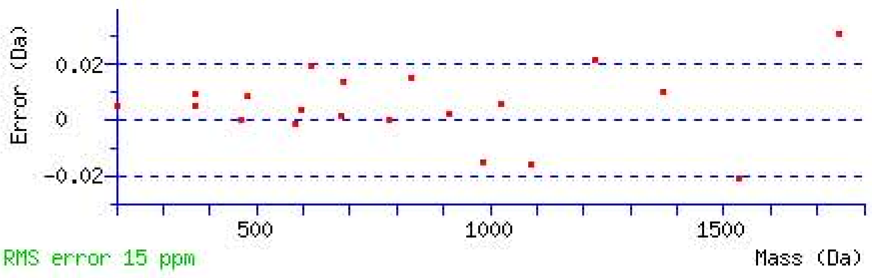
Match to Query 65203: 2660.280432 from(887.767420,3+) rtinseconds(3135) index(32335)
Title: Locus:1.1.1.3230.17 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

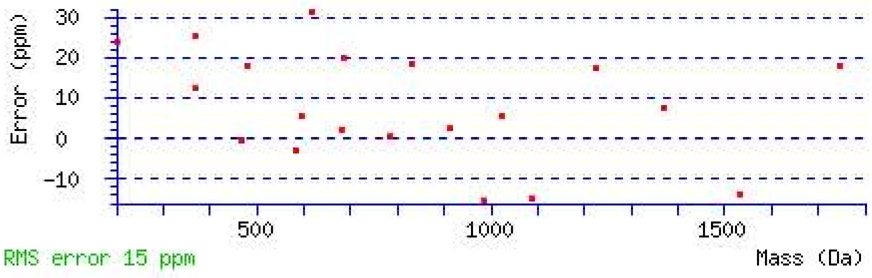
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2660.250244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.003
Matches : 20/204 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	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
39.1	2660.250244	0.030188	EPCVESLVSQYFQTVTDYGK
38.7	2660.250244	0.030188	EPCVESLVSQYFQTVTDYGK

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

{MATRIX SCIENCE}

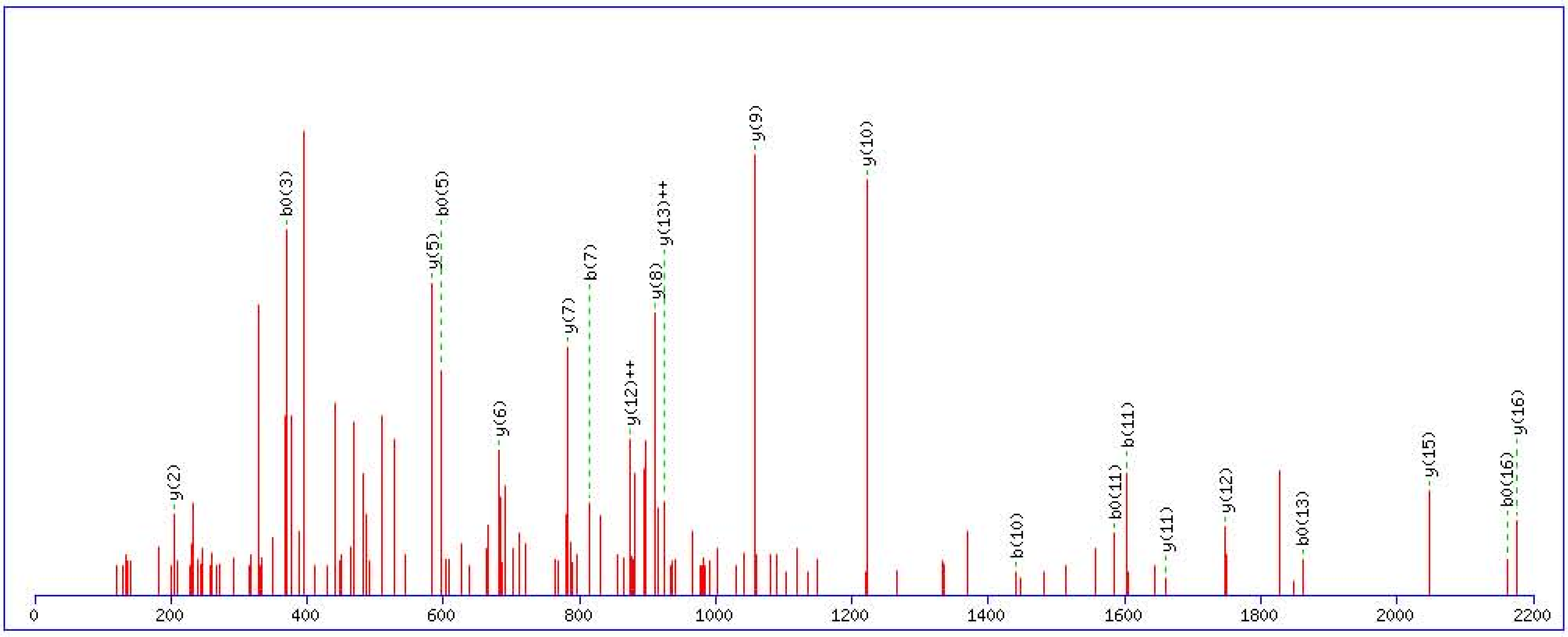
Mascot Search Results

Peptide View

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

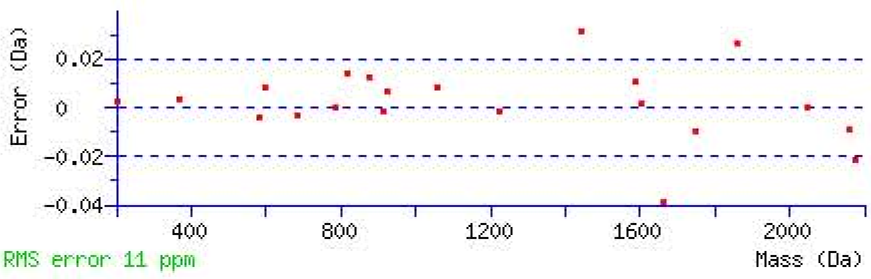
Match to Query 65204: 2660.280492 from(887.767440,3+) rtinseconds(3144) index(32410)
Title: Locus:1.1.1.3233.18 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

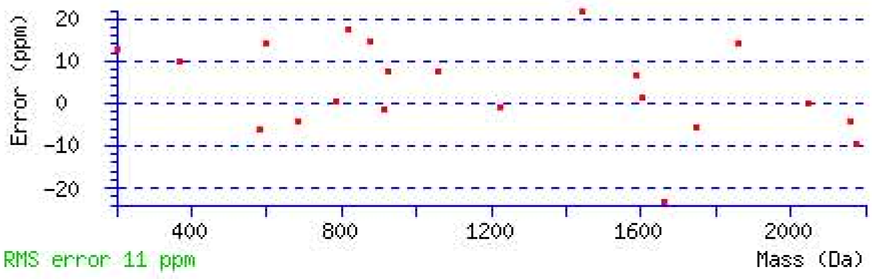
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2660.250244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 3.3e-005
Matches : 21/204 fragment ions using 39 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							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
58.7	2660.250244	0.030248	EPCVESLVSQYFQTVTDYGK
33.4	2660.250244	0.030248	EPCVESLVSQYFQTVTDYGK

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

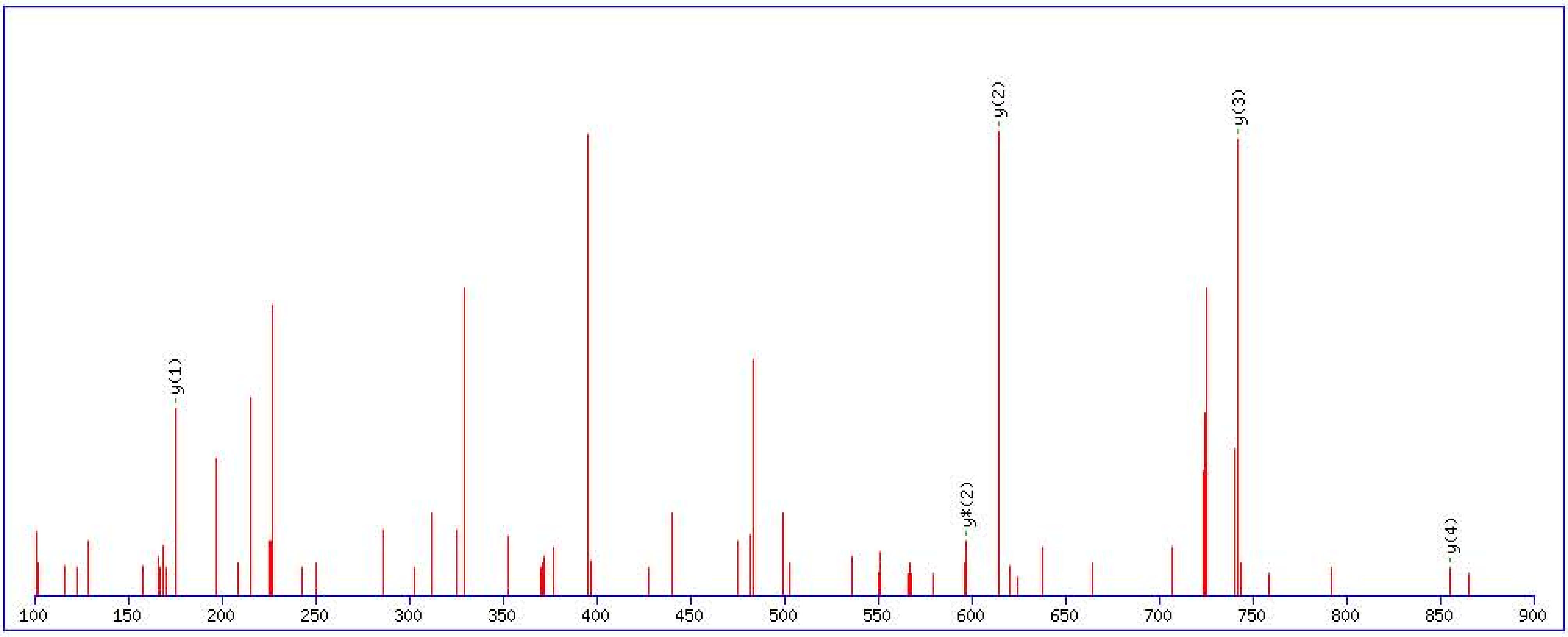
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIQQR**
Found in **T161A_HUMAN**, Transmembrane protein 161A OS=Homo sapiens GN=TMEM161A PE=2 SV=1

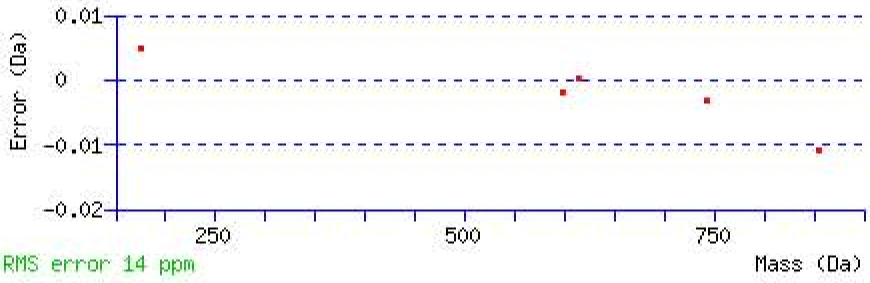
Match to Query 15332: 983.524408 from(492.769480,2+) rtinseconds(1379) index(2437)
Title: Locus:1.1.1.2734.18 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

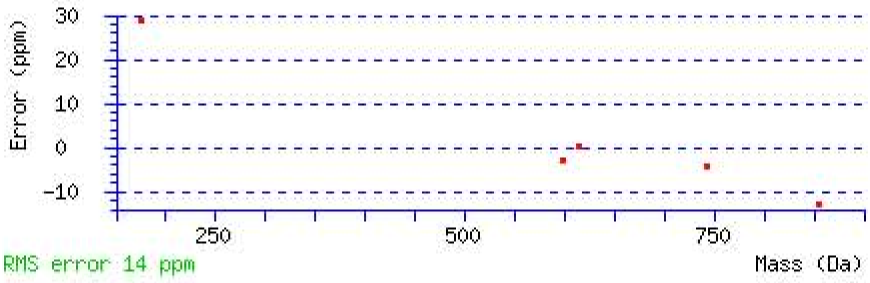
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 28 **Expect:** 0.029
Matches : 5/36 fragment ions using 8 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					5
2	243.133933	122.070605			225.123368	113.065322	I	***855.486920***	428.247098	838.460371	419.733824	4
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	Q	***742.402856***	371.705066	725.376307	363.191792	3
4	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	Q	***614.344278***	307.675777	597.317729	299.162503	2
5							R	***175.118952***	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.3	983.522217	0.002191	EIQQR
28.3	983.522217	0.002191	ELQQR
15.4	983.522217	0.002191	IEQQR
15.4	983.522217	0.002191	LEQQR
13.8	983.522217	0.002191	EAAVQR
13.8	983.522217	0.002191	EGLAQR
13.8	983.514816	0.009592	EKISHNTR
13.8	983.522217	0.002191	EQIQR
13.8	983.522217	0.002191	EQLQR
13.1	983.533447	-0.009039	NKQQR

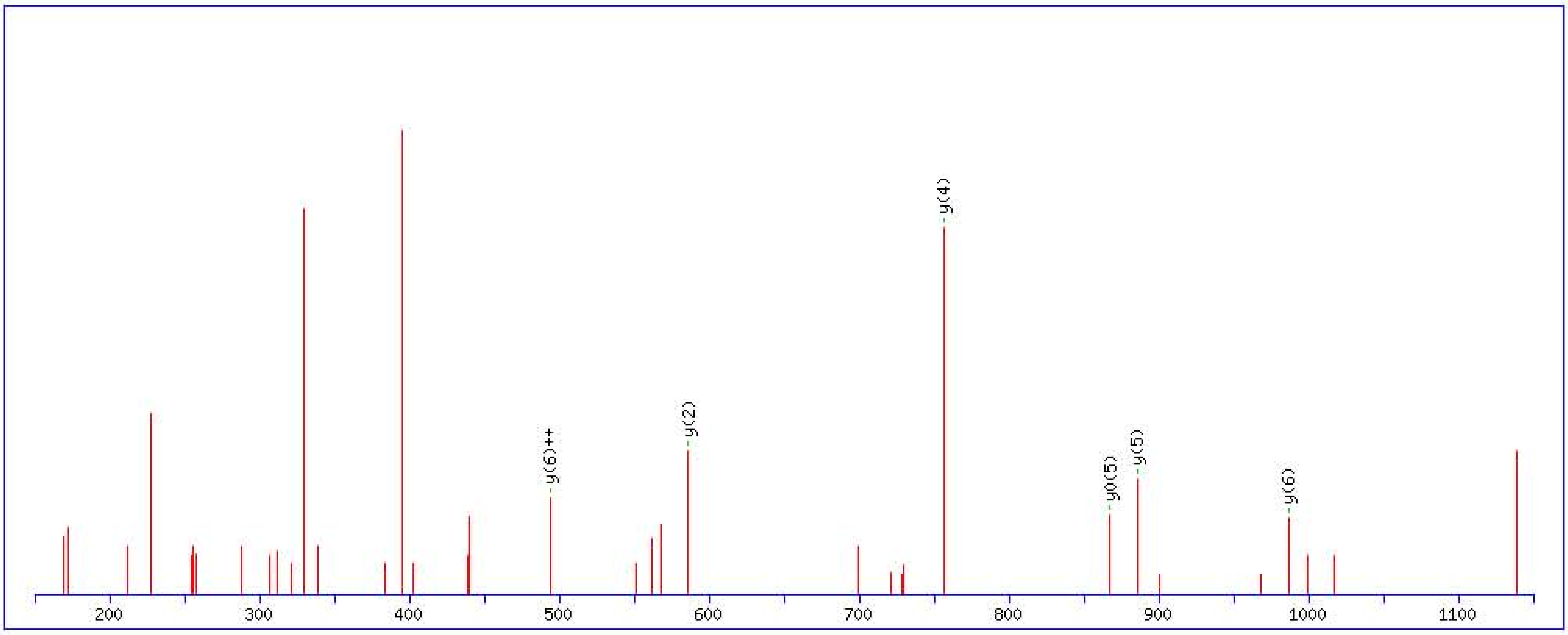
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

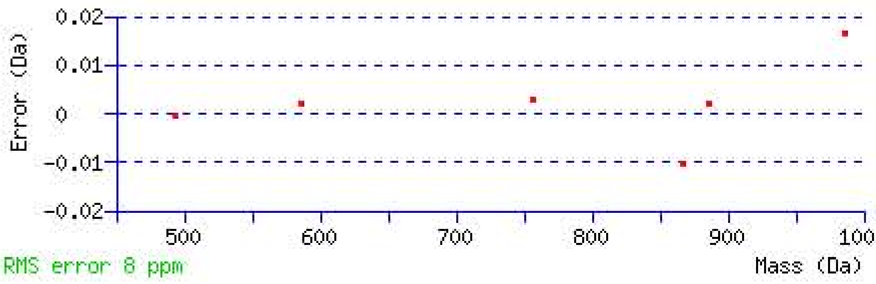
Match to Query 22066: 1156.590908 from(579.302730,2+) rtinseconds(1412) index(20337)
Title: Locus:1.1.1.2634.18 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

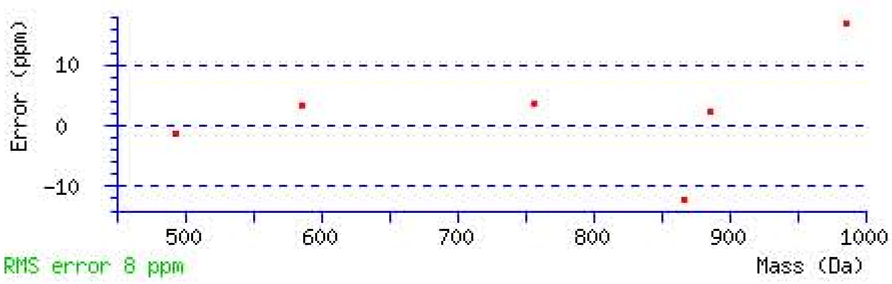
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1156.591034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.055
Matches : 6/70 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	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
25.2	1156.591034	-0.000126	GNTEGLQK

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

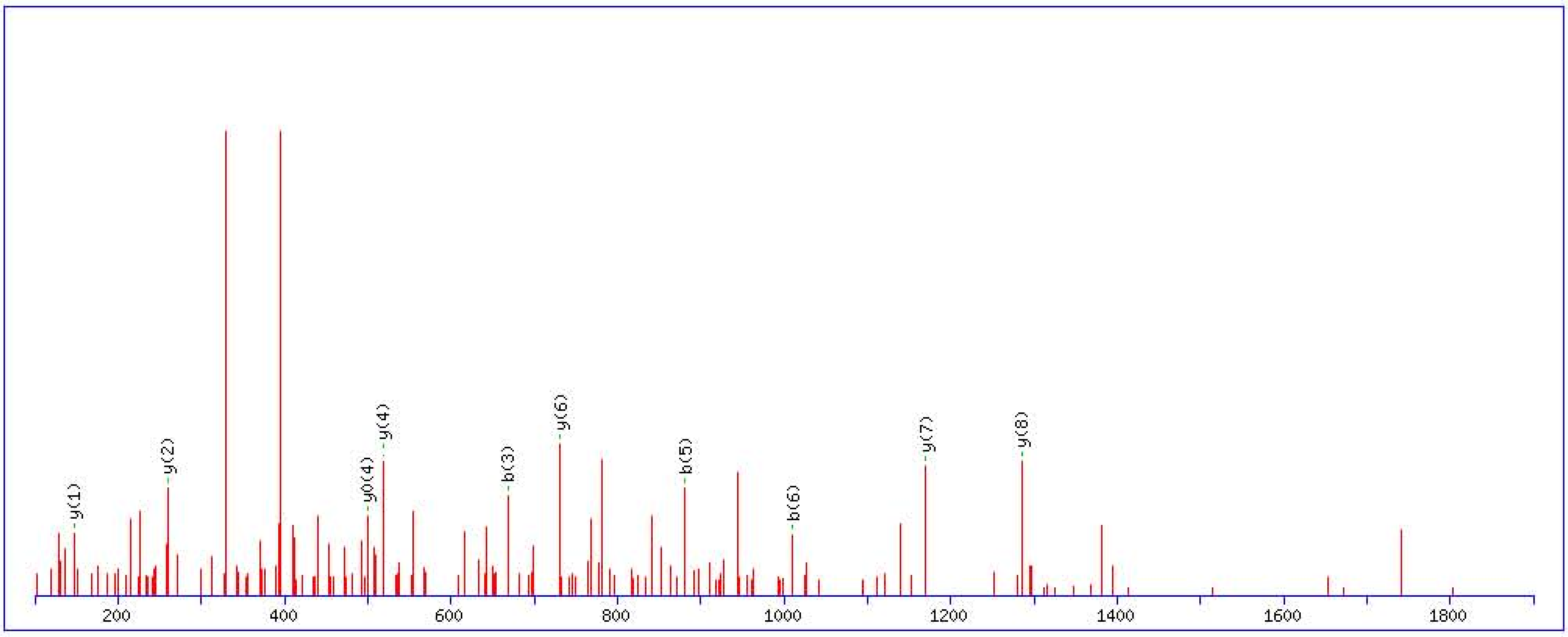
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

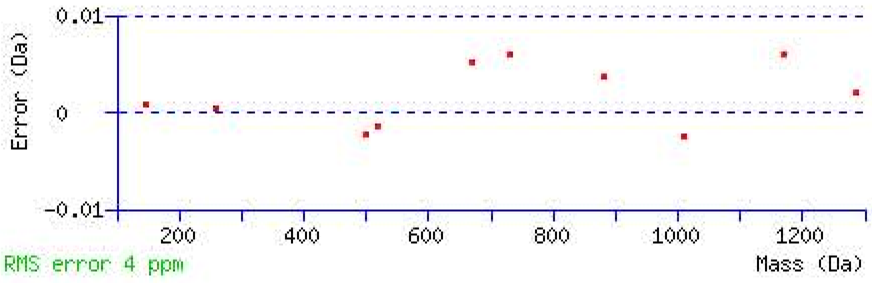
Match to Query 30688: 1397.726868 from(699.870710,2+) rtinseconds(1802) index(23227)
Title: Locus:1.1.1.2770.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

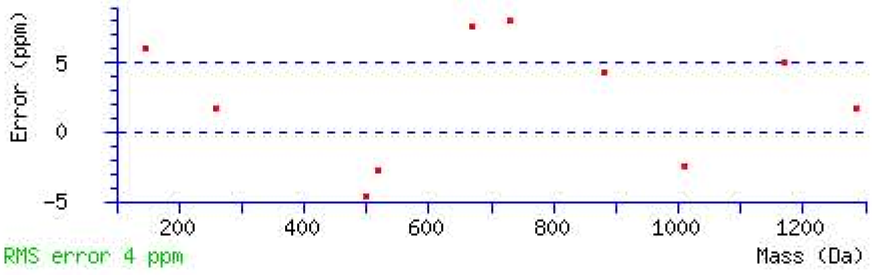
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1397.722427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00023
Matches : 10/86 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					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
46.6	1397.722427	0.004441	IDQNVEELK
7.3	1397.744873	-0.018005	MLEKARHQELK
7.3	1397.744873	-0.018005	QRREEELK
6.5	1397.737686	-0.010818	LKEFCGEFLKK
3.3	1397.744904	-0.018036	SSGPQRAGSLK
1.6	1397.708527	0.018341	EGLHGREITCVK
1.1	1397.723785	0.003083	LFVSHMIDKHR
1.1	1397.715057	0.011811	LEDGSHLTGQTLK
0.7	1397.722412	0.004456	QLEAQLEEK
0.6	1397.733688	-0.006820	LCDVTLKIGDHK

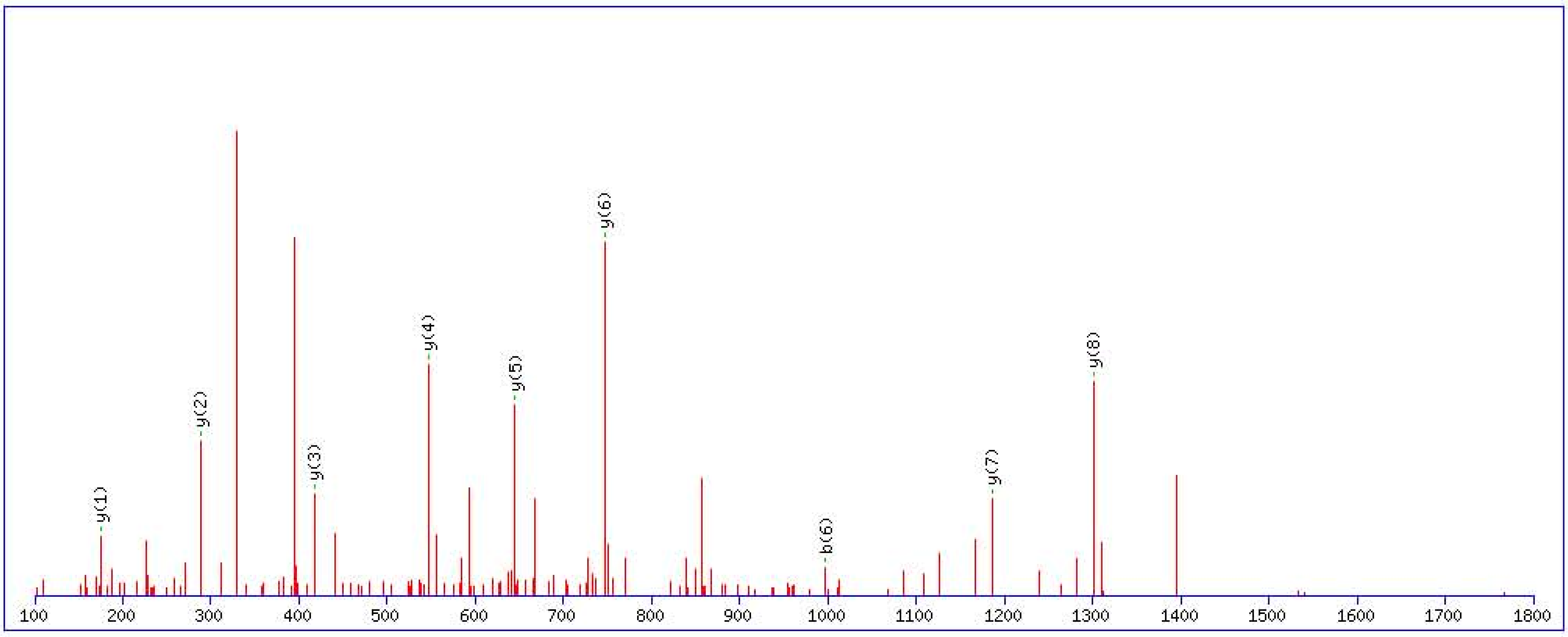
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

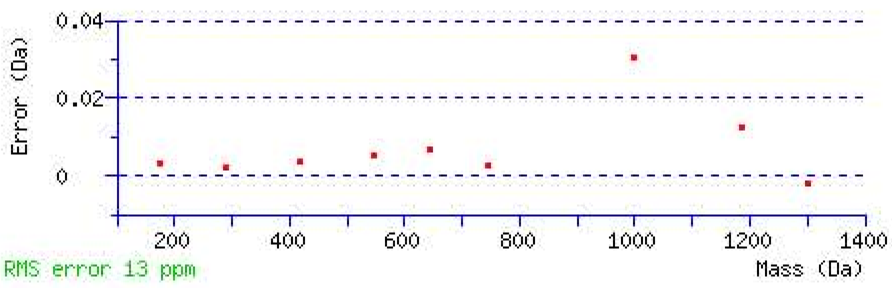
Match to Query 31784: 1412.741468 from(707.378010,2+) rtinseconds(1878) index(23791)
Title: Locus:1.1.1.2796.16 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

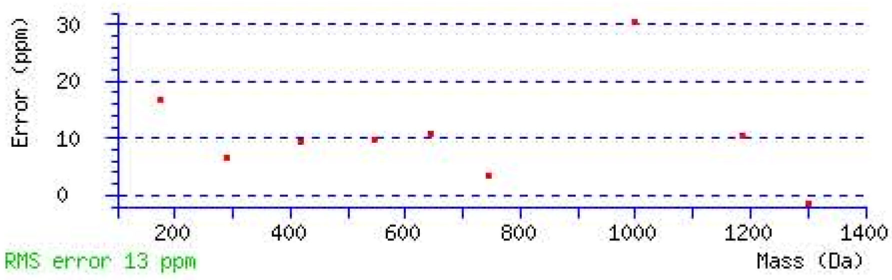
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1412.733337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 69   Expect: 2.9e-006
Matches : 9/86 fragment ions using 13 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
69.4	1412.733337	0.008131	IDQTVEELR
16.2	1412.744537	-0.003069	IPPEKMRELER
9.6	1412.734665	0.006803	MPADWRQQLLR
9.2	1412.741211	0.000257	KVTIYSFTGNQR
6.1	1412.737167	0.004301	ARPEDVISEGRGK
4.5	1412.730621	0.010847	ARMEHSRELLR
4.3	1412.741196	0.000272	SSLHYKPTPDLR
3.6	1412.752426	-0.010958	WKQSVDRPELR
3.6	1412.741180	0.000288	WQQQELIAELR
3.3	1412.762299	-0.020831	EEELRAAVEVLR

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

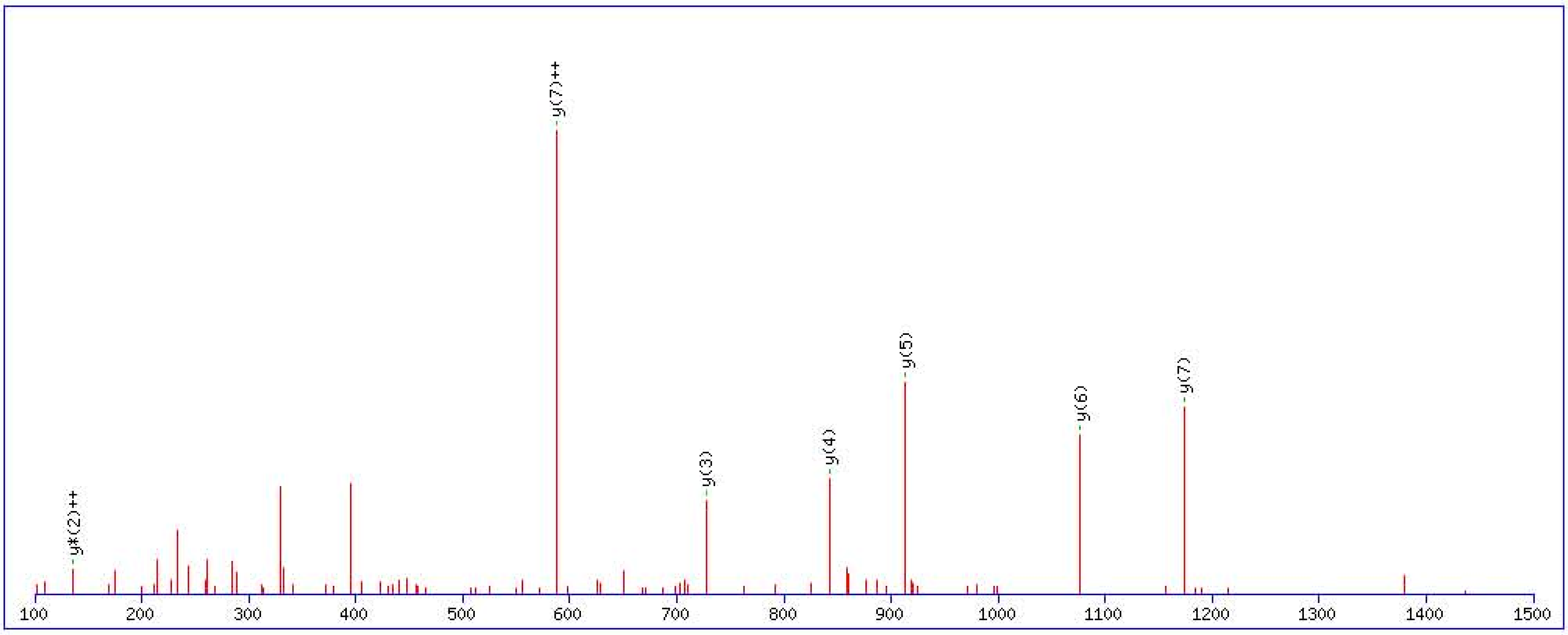
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

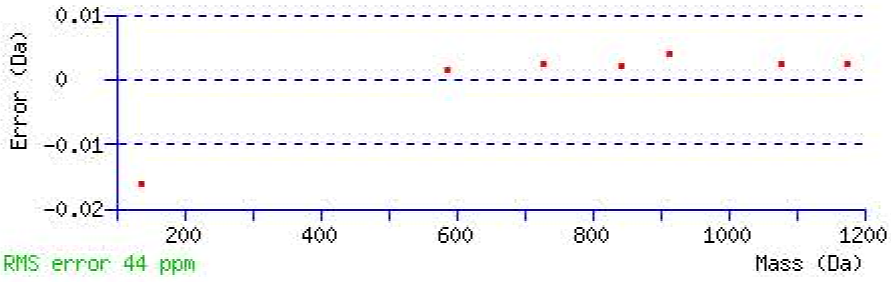
Match to Query 31821: 1414.736928 from(708.375740,2+) rtinseconds(1958) index(24409)
Title: Locus:1.1.1.2824.8 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

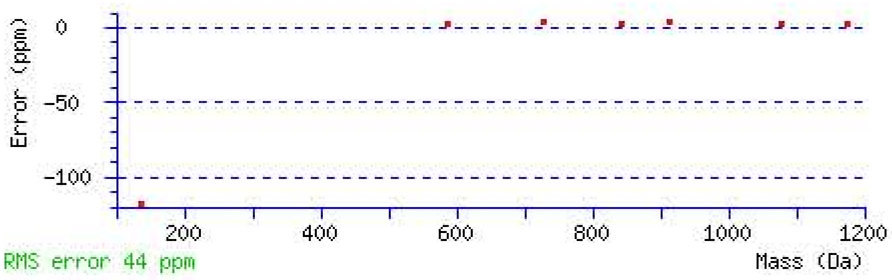
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1414.727844
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 : 7/76 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	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
28.9	1414.727844	0.009084	LEPYADQLR
9.6	1414.756821	-0.019893	QNPKNLFAINEK
2.4	1414.741592	-0.004664	TINEVENQVLTR
0.5	1414.757690	-0.020762	NKLMIMHWKAK

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

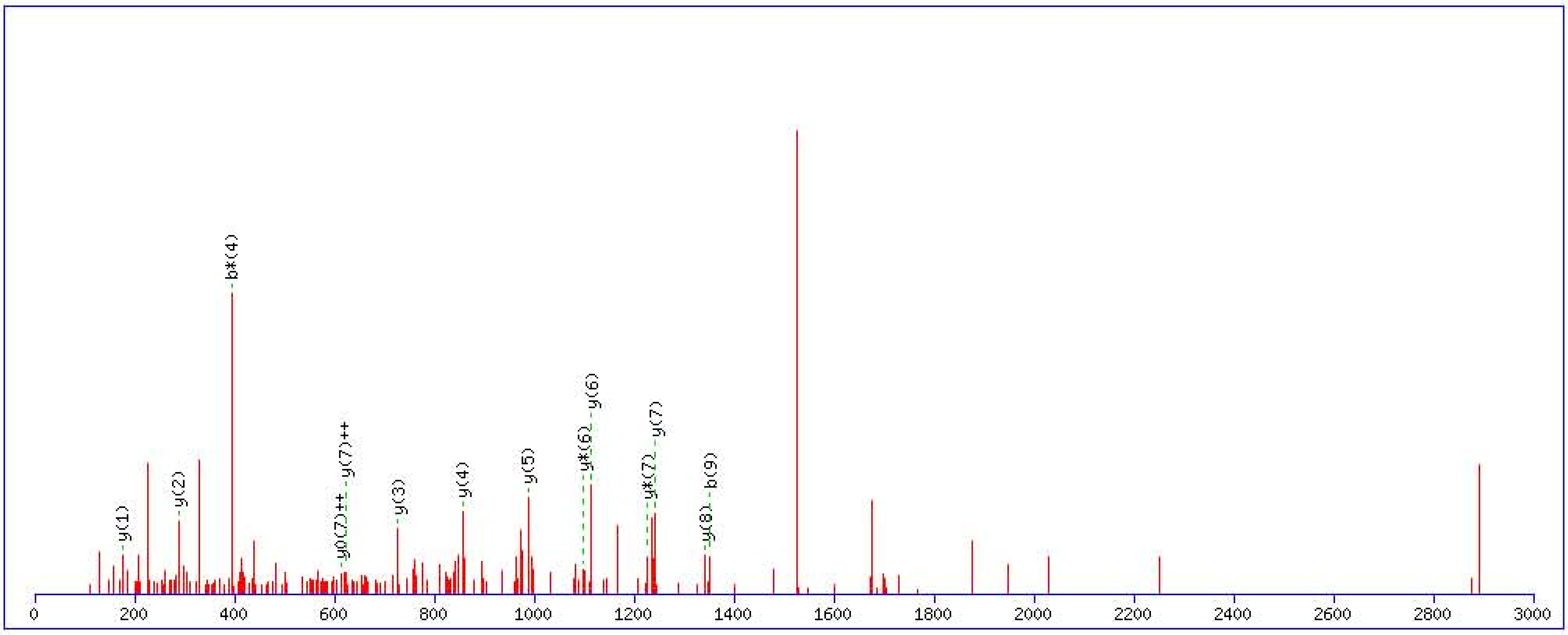
Mascot Search Results

Peptide View

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

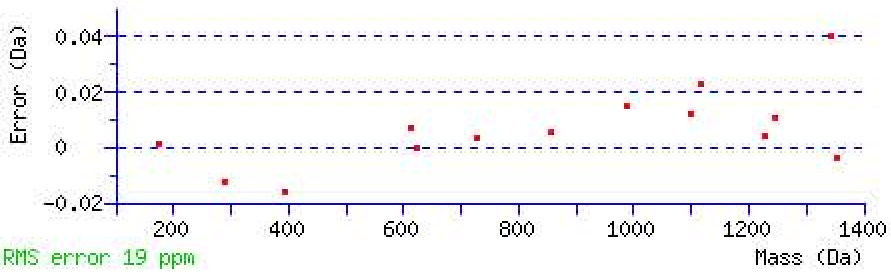
Match to Query 35866: 1525.822448 from(763.918500,2+) rtinseconds(2099) index(79533)
Title: Locus:1.1.1.2081.20 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

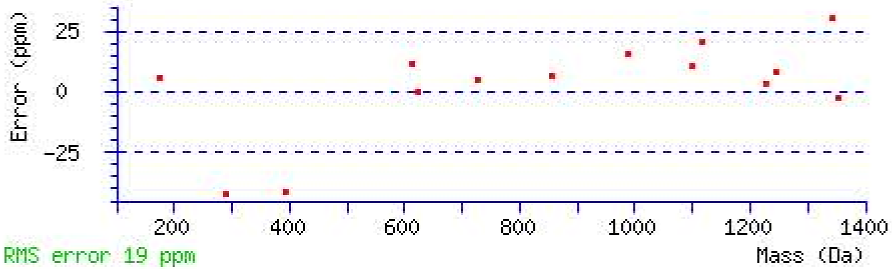
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1525.810867
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0083
Matches : 14/84 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							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
26.7	1525.810867	0.011581	ALVQQMEQLR
6.4	1525.810867	0.011581	ALVQQMEQLR
4.5	1525.807495	0.014953	WPPQQLMLSAALR

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

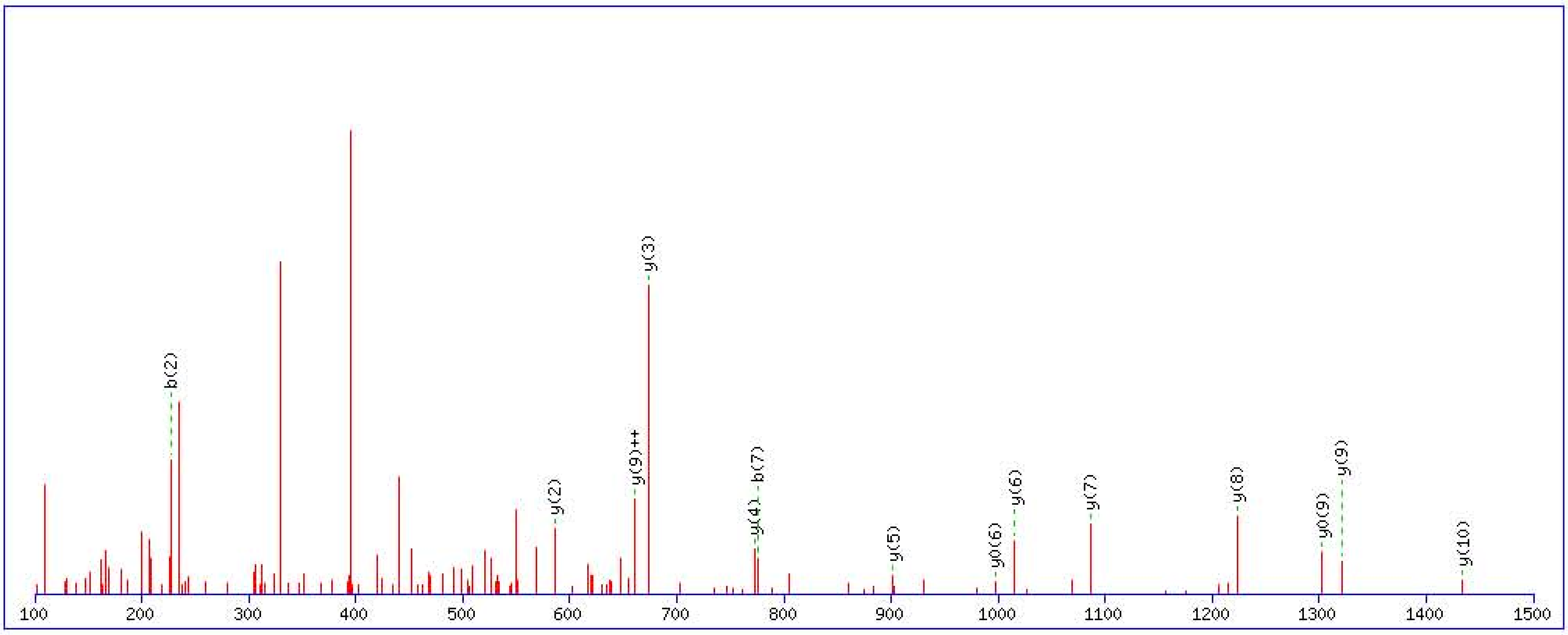
Mascot Search Results

Peptide View

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

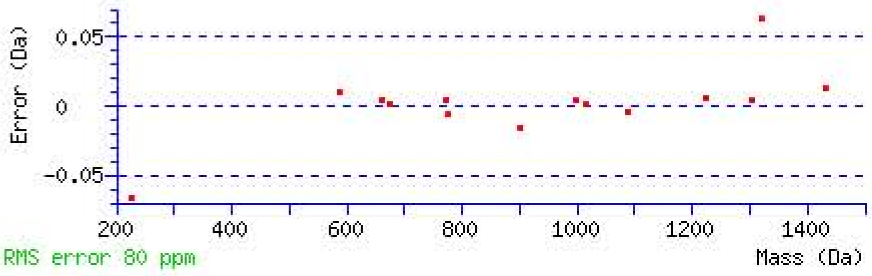
Match to Query 36371: 1545.840882 from(516.287570,3+) rtinseconds(1508) index(3381)
Title: Locus:1.1.1.2779.8 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

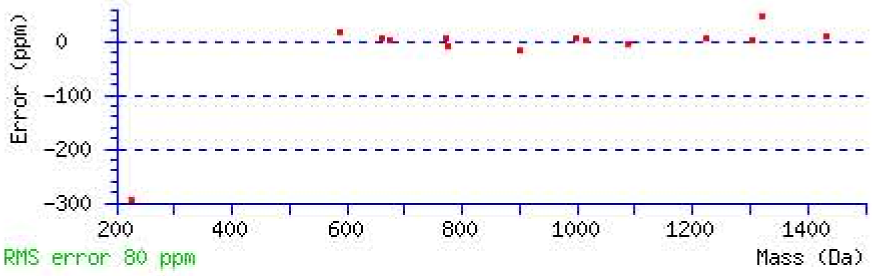
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1545.833710
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 9.5e-005
Matches : 14/94 fragment ions using 27 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
53.7	1545.833710	0.007172	LLPHANEVSQK

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

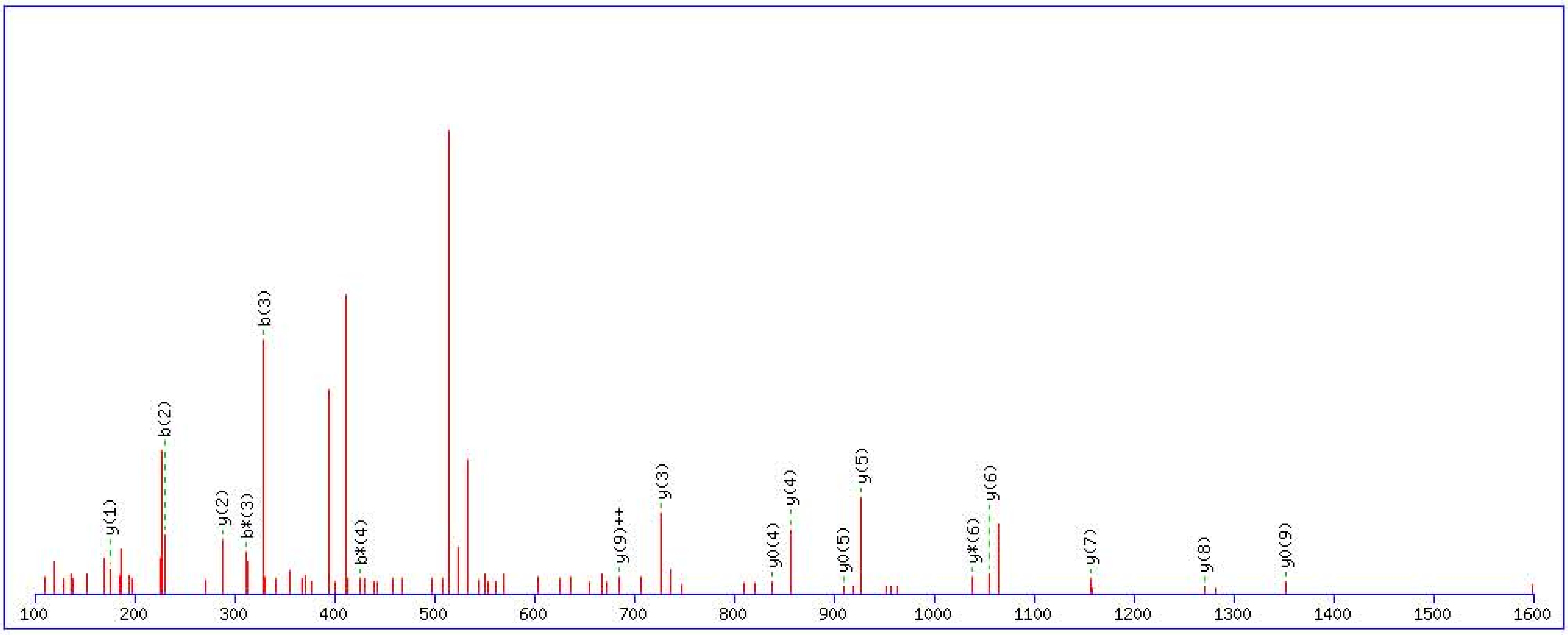
Mascot Search Results

Peptide View

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

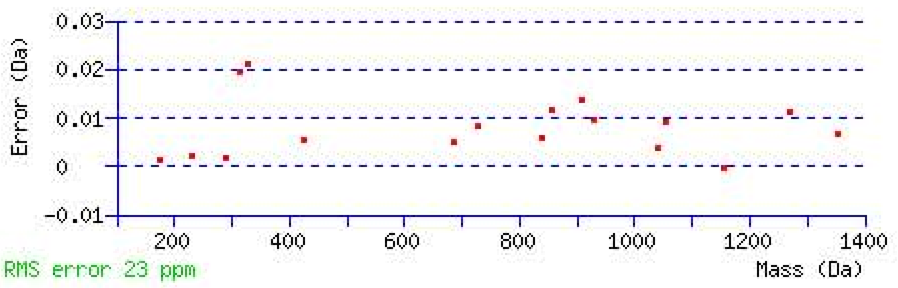
Match to Query 38685: 1597.837392 from(533.619740,3+) rtinseconds(1546) index(76051)
Title: Locus:1.1.1.1889.12 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

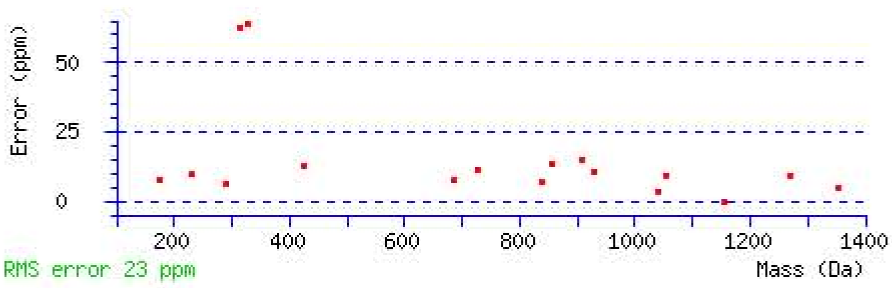
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1597.824615
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0034
Matches : 17/112 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	102.054955	51.531116			84.044390	42.525833	T							11
2	**230.113533**	115.560405	213.086984	107.047130	212.102968	106.555122	Q	1497.784225	749.395751	1480.757676	740.882476	1479.773660	740.390468	10
3	**329.181947**	165.094612	312.155398	156.581337	311.171382	156.089329	V	1369.725647	685.366462	1352.699098	676.853187	1351.715082	676.361179	9
4	443.224874	222.116075	426.198325	213.602801	425.214309	213.110793	N	***1270.657233***	635.832255	1253.630684	627.318980	1252.646668	626.826972	8
5	544.272553	272.639915	527.246004	264.126640	526.261988	263.634632	T	***1156.614306***	578.810791	1139.587757	570.297517	1138.603741	569.805509	7
6	672.331131	336.669204	655.304582	328.155929	654.320566	327.663921	Q	***1055.566627***	528.286951	1038.540078	519.773677	1037.556062	519.281669	6
7	743.368245	372.187761	726.341696	363.674486	725.357680	363.182478	A	***927.508049***	464.257663	910.481500	455.744388	909.497484	455.252380	5
8	872.410838	436.709057	855.384289	428.195783	854.400273	427.703775	E	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
9	1311.636164	656.321720	1294.609615	647.808446	1293.625599	647.316438	Q	***727.428342***	364.217809	710.401793	355.704535			3
10	1424.720228	712.863752	1407.693679	704.350478	1406.709663	703.858470	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
29.5	1597.824615	0.012777	TQVNTQAEQLR
5.0	1597.824615	0.012777	TQVNTQAEQLR
3.3	1597.846375	-0.008983	EQLPIFKAQNPDAK

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

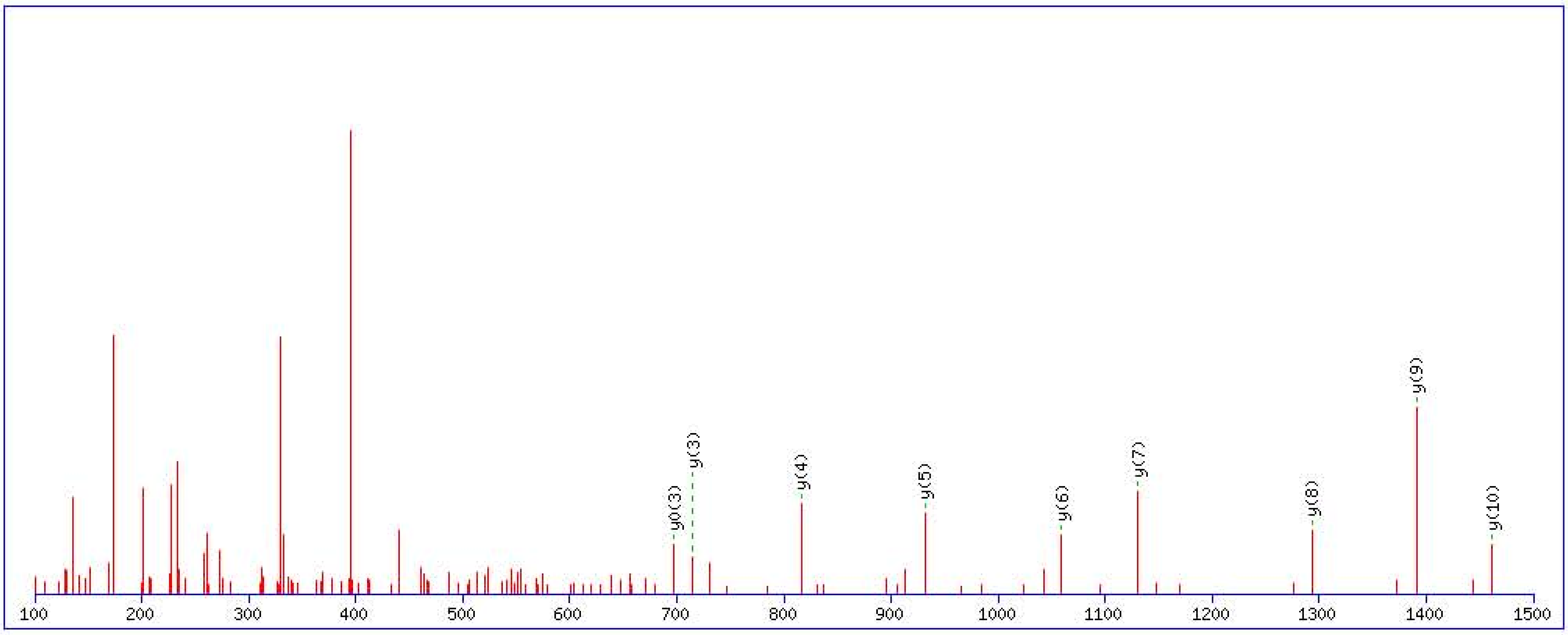
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

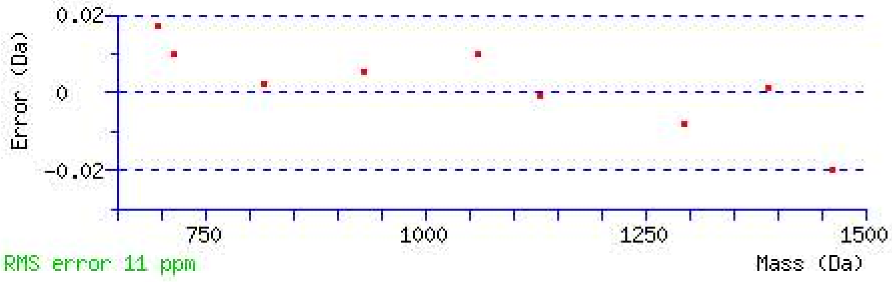
Match to Query 41490: 1660.817412 from(554.613080,3+) rtinseconds(1695) index(22418)
Title: Locus:1.1.1.2733.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

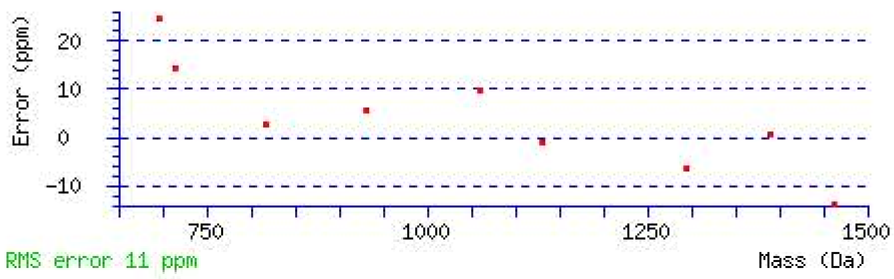


```
Monoisotopic mass of neutral peptide Mr(calc): 1660.813034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 4.8e-005
Matches : 9/118 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 11 ppm



RMS error 11 ppm

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
56.7	1660.813034	0.004378	SLAPYAQDTQEK
15.5	1660.813034	0.004378	SLAPYAQDTQEK

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

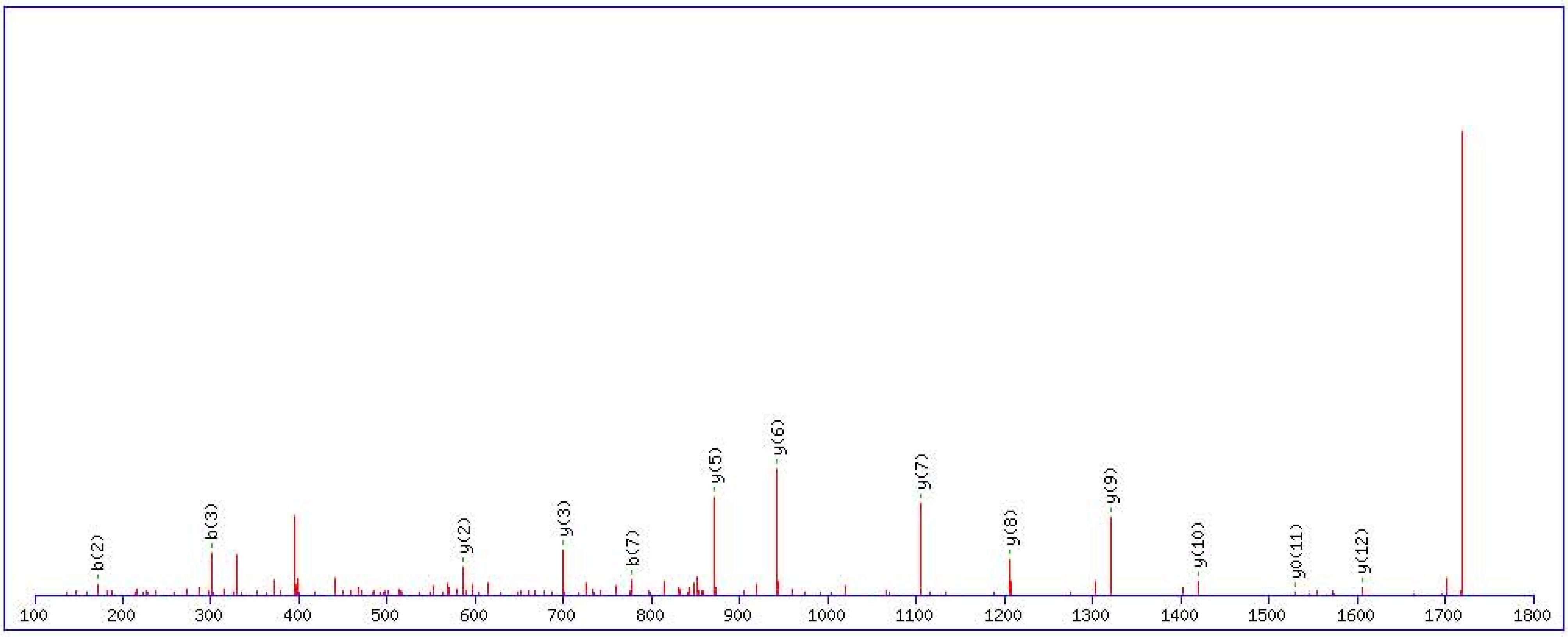
Mascot Search Results

Peptide View

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

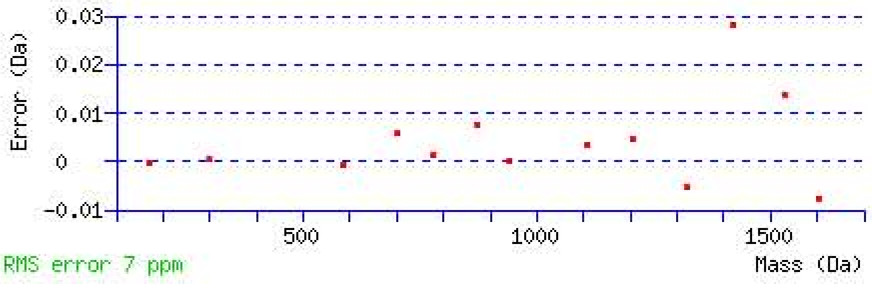
Match to Query 42957: 1717.887248 from(859.950900,2+) rtinseconds(1959) index(24419)
Title: Locus:1.1.1.2824.18 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

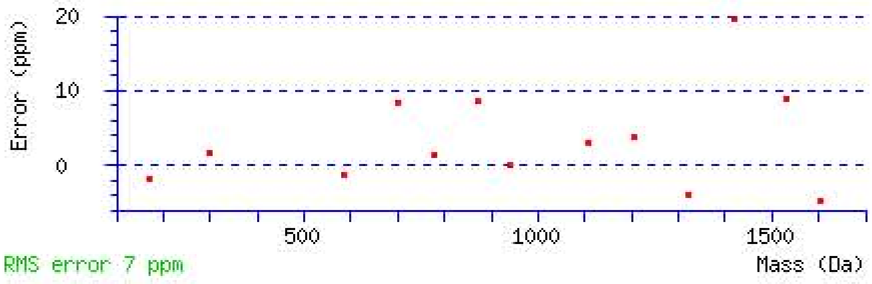
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 83 **Expect:** 1.4e-007
Matches : 13/126 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	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
83.3	1717.870895	0.016353	LGEVNTYAGDLQK
10.4	1717.866867	0.020381	IDAVNAETIREVCTK
5.2	1717.878754	0.008494	IDAVAWNTTPYQLAR
3.3	1717.878067	0.009181	RATEKEINNMGNTLK
2.4	1717.863495	0.023753	KSNISVYEVDGKDHK
1.4	1717.885956	0.001292	SLGGAVAIHLASENSHR
0.0	1717.892014	-0.004766	LSTAVNIGKMDSPIEK

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

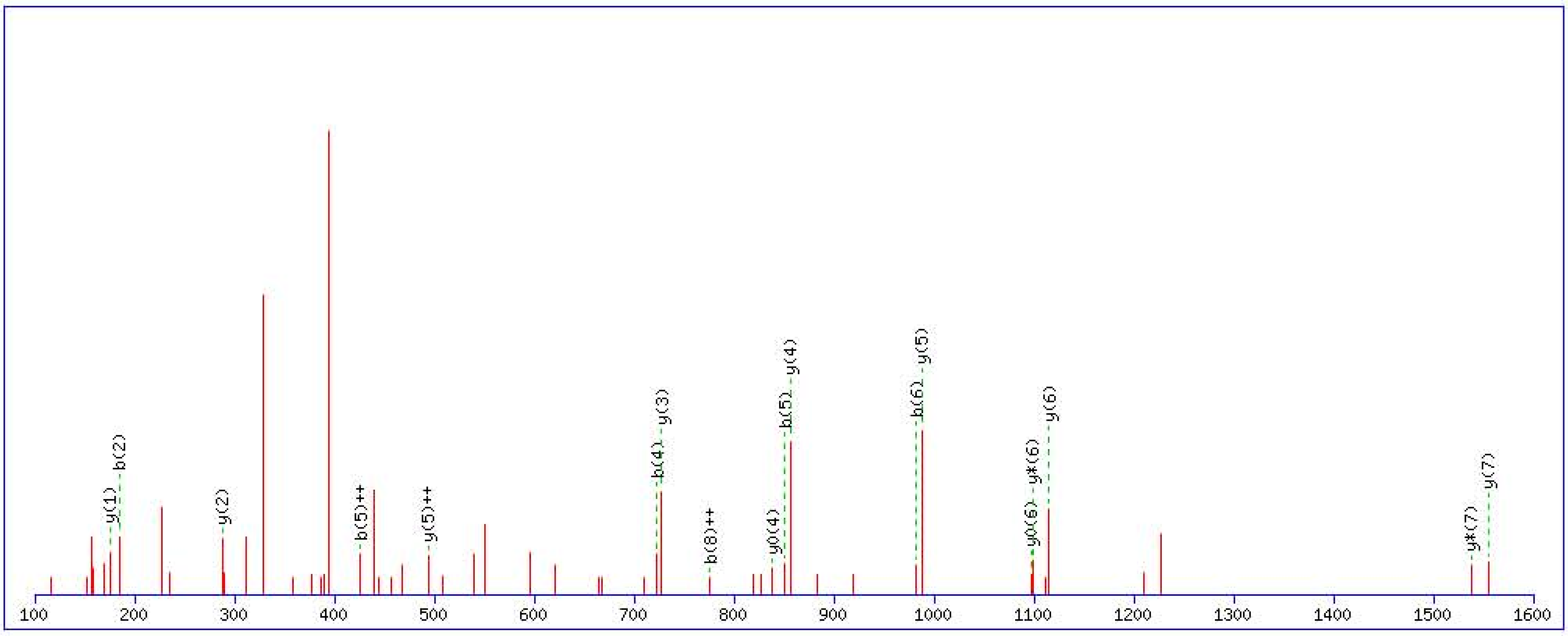
Mascot Search Results

Peptide View

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

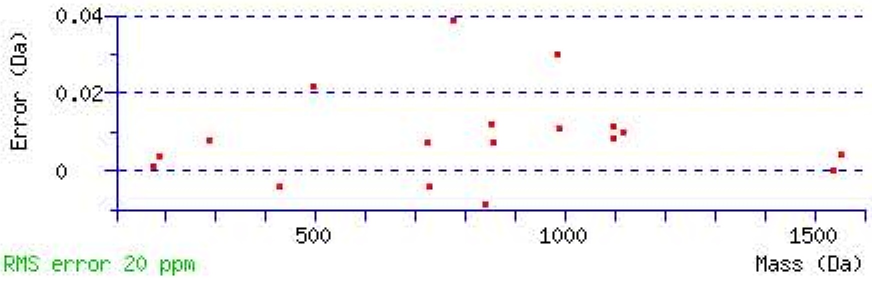
Match to Query 46166: 1837.002822 from(613.341550,3+) rtinseconds(2326) index(8654)
Title: Locus:1.1.1.3064.4 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

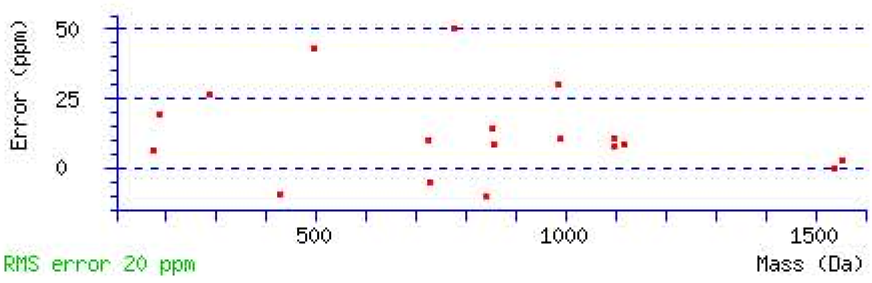
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1836.977615
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0074
Matches : 18/84 fragment ions using 35 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	1766.947802	883.977539	1749.921253	875.464265	1748.937237	874.972256	9
3	284.196868	142.602072					V	1653.863738	827.435507	1636.837189	818.922232	1635.853173	818.430224	8
4	**723.422194**	362.214735	706.395645	353.701461			Q	***1554.795324***	777.901300	1537.768775	769.388026	1536.784759	768.896017	7
5	**851.480772**	**426.244024**	834.454223	417.730750			Q	***1115.569998***	558.288637	1098.543449	549.775363	1097.559433	549.283354	6
6	**982.521257**	491.764267	965.494708	483.250992			M	***987.511420***	494.259348	970.484871	485.746073	969.500855	485.254065	5
7	1111.563850	556.285563	1094.537301	547.772289	1093.553285	547.280281	E	***856.470935***	428.739105	839.444386	420.225831	838.460370	419.733823	4
8	1550.789176	**775.898226**	1533.762627	767.384952	1532.778611	766.892944	Q	***727.428342***	364.217809	710.401793	355.704534			3
9	1663.873240	832.440258	1646.846691	823.926984	1645.862675	823.434975	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
30.1	1836.977615	0.025207	ALVQQMEQLR
20.4	1836.977615	0.025207	ALVQQMEQLR
7.2	1836.999207	0.003615	QQSLQRQLEQLR
6.4	1837.005722	-0.002900	AIVTEPKTEKPERPSR
4.5	1837.004578	-0.001756	RHSWRQQIFLR

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

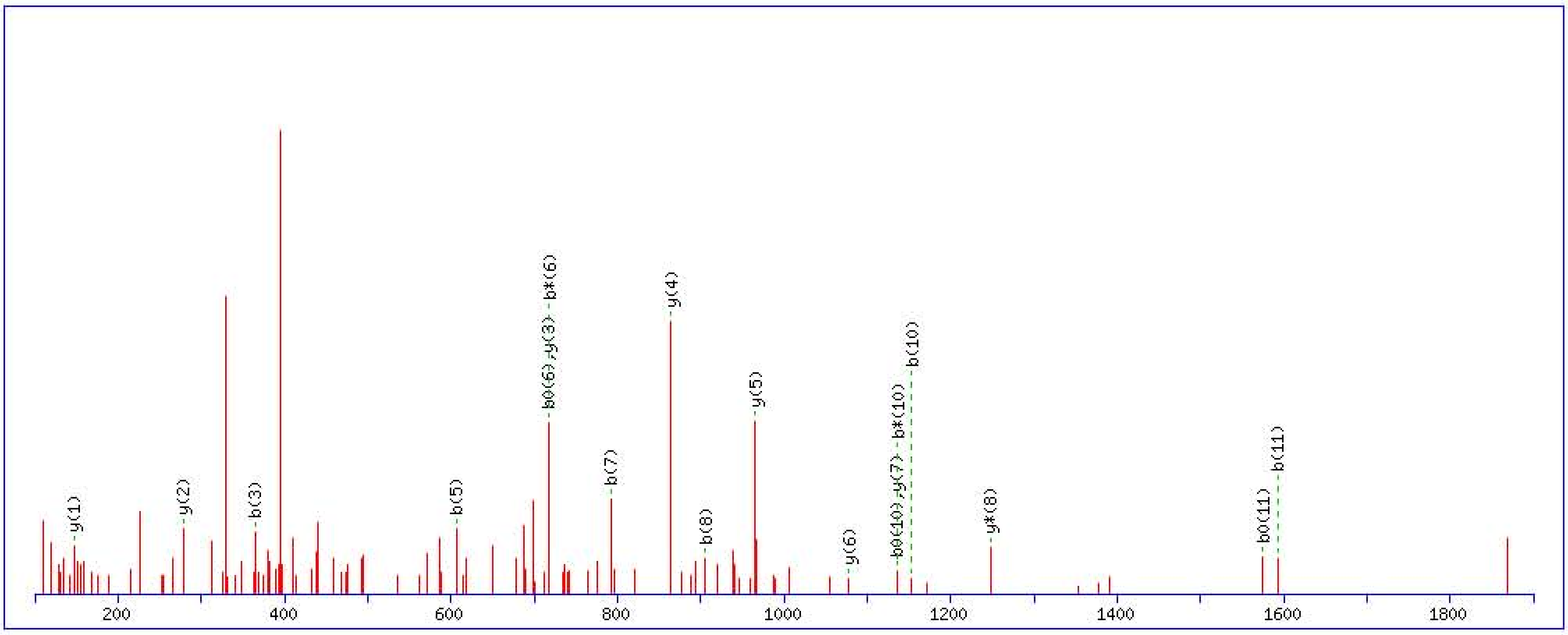
Mascot Search Results

Peptide View

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

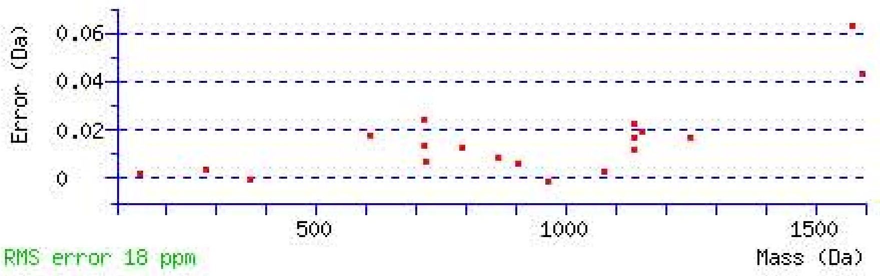
Match to Query 46937: 1868.976372 from(623.999400,3+) rtinseconds(2126) index(79694)
Title: Locus:1.1.1.2091.7 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

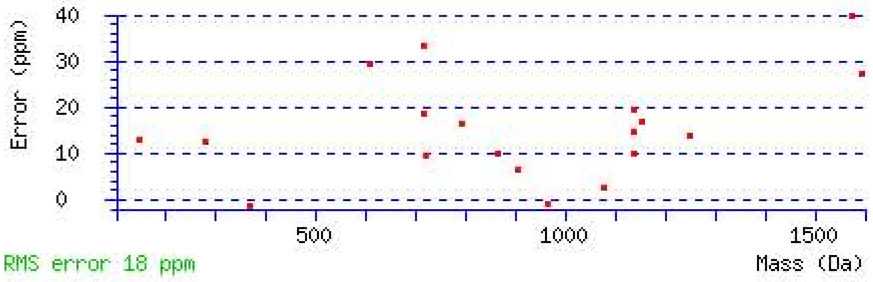
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 31 **Expect:** 0.024
Matches : 19/124 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	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
30.9	1868.964081	0.012291	LNHQLEGLTFQMK

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

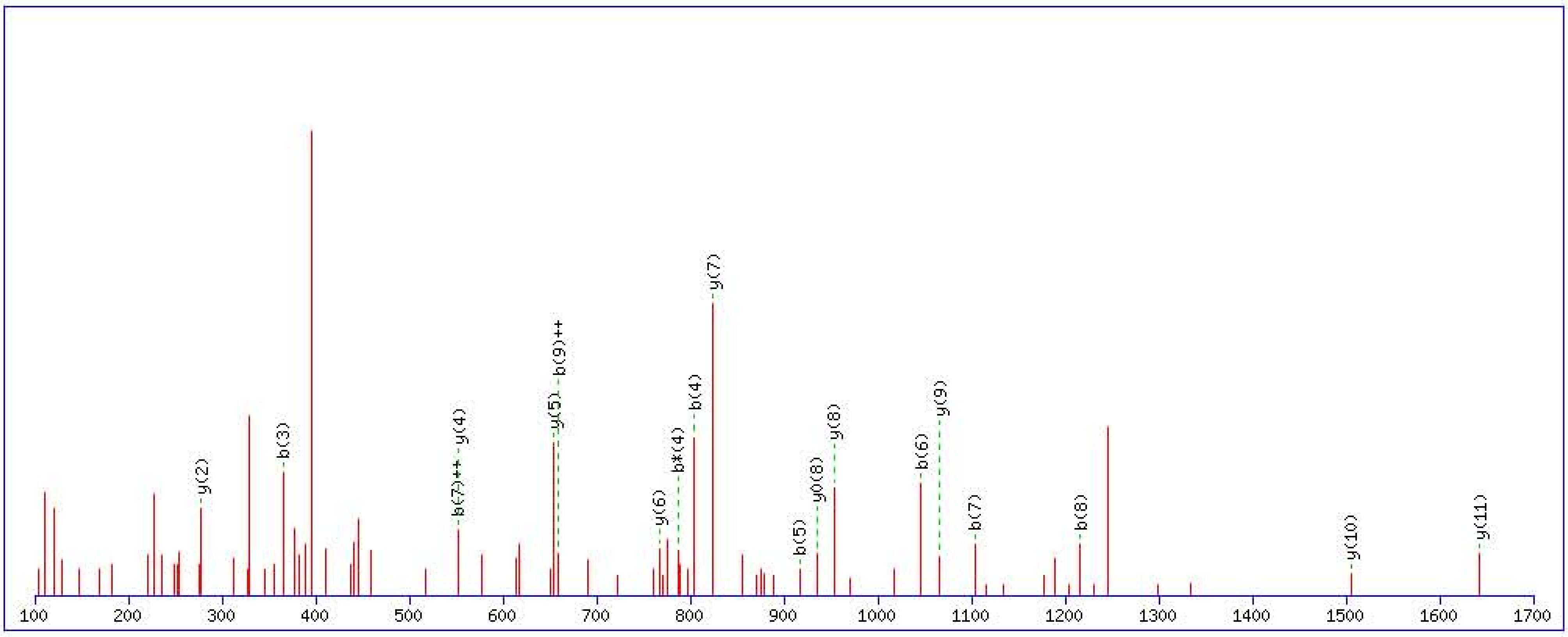
Mascot Search Results

Peptide View

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

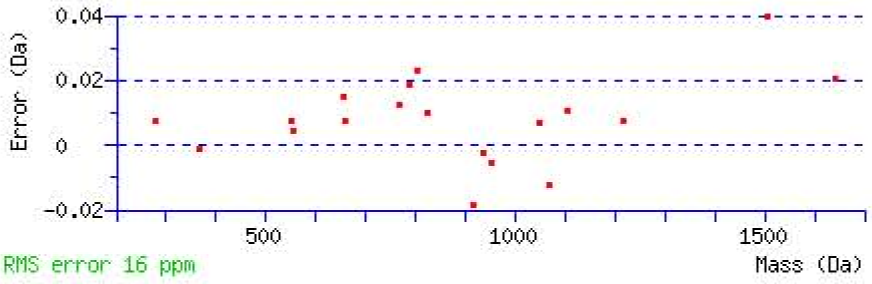
Match to Query 46939: 1868.981712 from(624.001180,3+) rtinseconds(2155) index(7491)
Title: Locus:1.1.1.3004.16 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

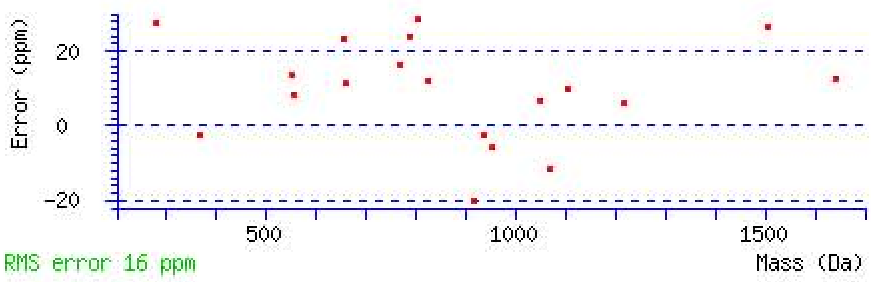
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1868.964081
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.0002
Matches : 19/124 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	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***	821.925829	1625.817834	813.412555	1624.833818	812.920547	11
4	**804.418505**	402.712891	787.391956	394.199616			Q	***1505.785471***	753.396373	1488.758922	744.883099	1487.774906	744.391091	10
5	**917.502569**	459.254923	900.476020	450.741648			L	***1066.560145***	533.783710	1049.533596	525.270436	1048.549580	524.778428	9
6	**1046.545162**	523.776219	1029.518613	515.262945	1028.534597	514.770937	E	***953.476081***	477.241678	936.449532	468.728404	935.465516	468.236396	8
7	**1103.566626**	**552.286951**	1086.540077	543.773677	1085.556061	543.281669	G	***824.433488***	412.720382	807.406939	404.207107	806.422923	403.715099	7
8	**1216.650690**	608.828983	1199.624141	600.315709	1198.640125	599.823700	L	***767.412024***	384.209650	750.385475	375.696375	749.401459	375.204367	6
9	1317.698369	**659.352823**	1300.671820	650.839548	1299.687804	650.347540	T	***654.327960***	327.667618	637.301411	319.154344	636.317395	318.662336	5
10	1464.766783	732.887030	1447.740234	724.373755	1446.756218	723.881747	F	***553.280281***	277.143779	536.253732	268.630504			4
11	1592.825361	796.916318	1575.798812	788.403044	1574.814796	787.911036	Q	406.211867	203.609571	389.185318	195.096297			3
12	1723.865846	862.436561	1706.839297	853.923287	1705.855281	853.431278	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
45.7	1868.964081	0.017631	LNHQLEGLTFQMK
6.0	1868.971970	0.009742	GFSWQSVLLTHQR
1.7	1868.989227	-0.007515	SLSPQELQAFK

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

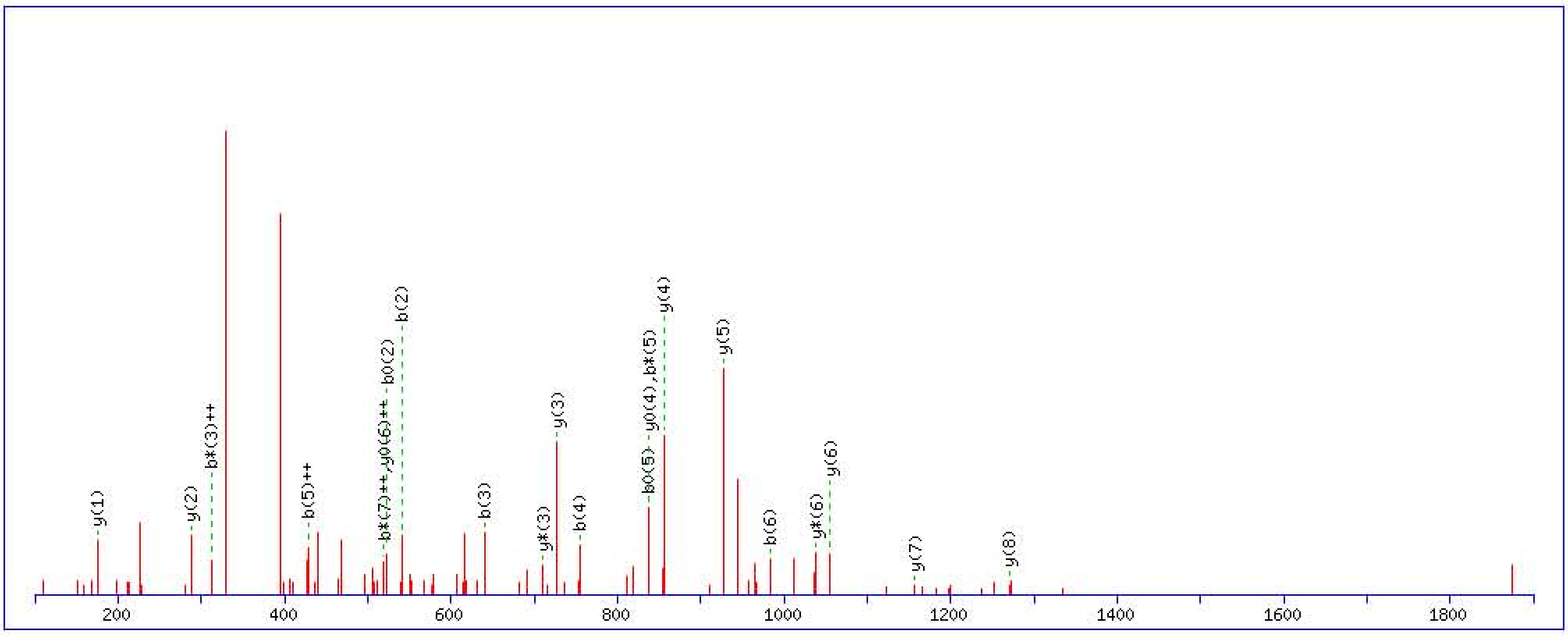
Mascot Search Results

Peptide View

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

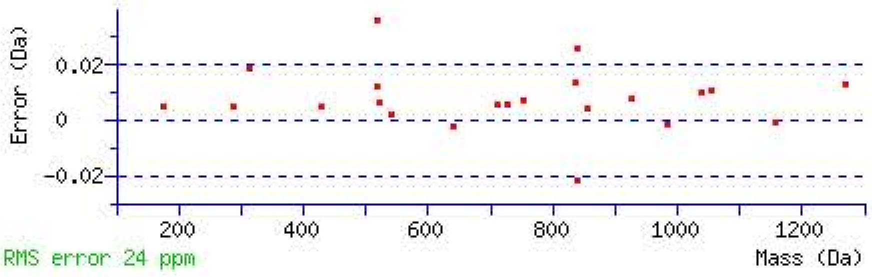
Match to Query 47731: 1909.003872 from(637.341900,3+) rtinseconds(1907) index(5901)
Title: Locus:1.1.1.2918.11 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

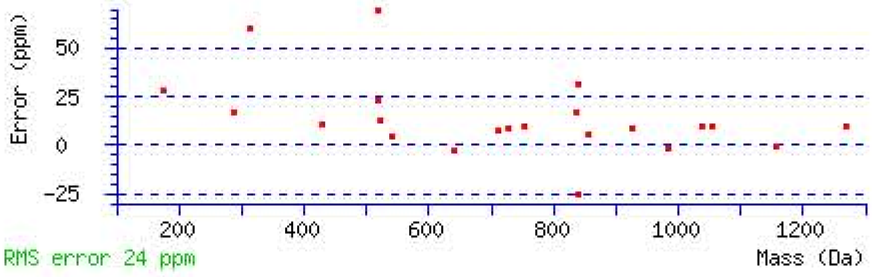
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 39  Expect: 0.00025
Matches : 22/112 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	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
38.7	1908.991364	0.012508	TQVNTQAEQLR
13.5	1908.991364	0.012508	TQVNTQAEQLR
9.9	1908.991364	0.012508	TQVNTQAEQLR
0.3	1909.015610	-0.011738	SSIALTAPDAAADPKEKPK

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

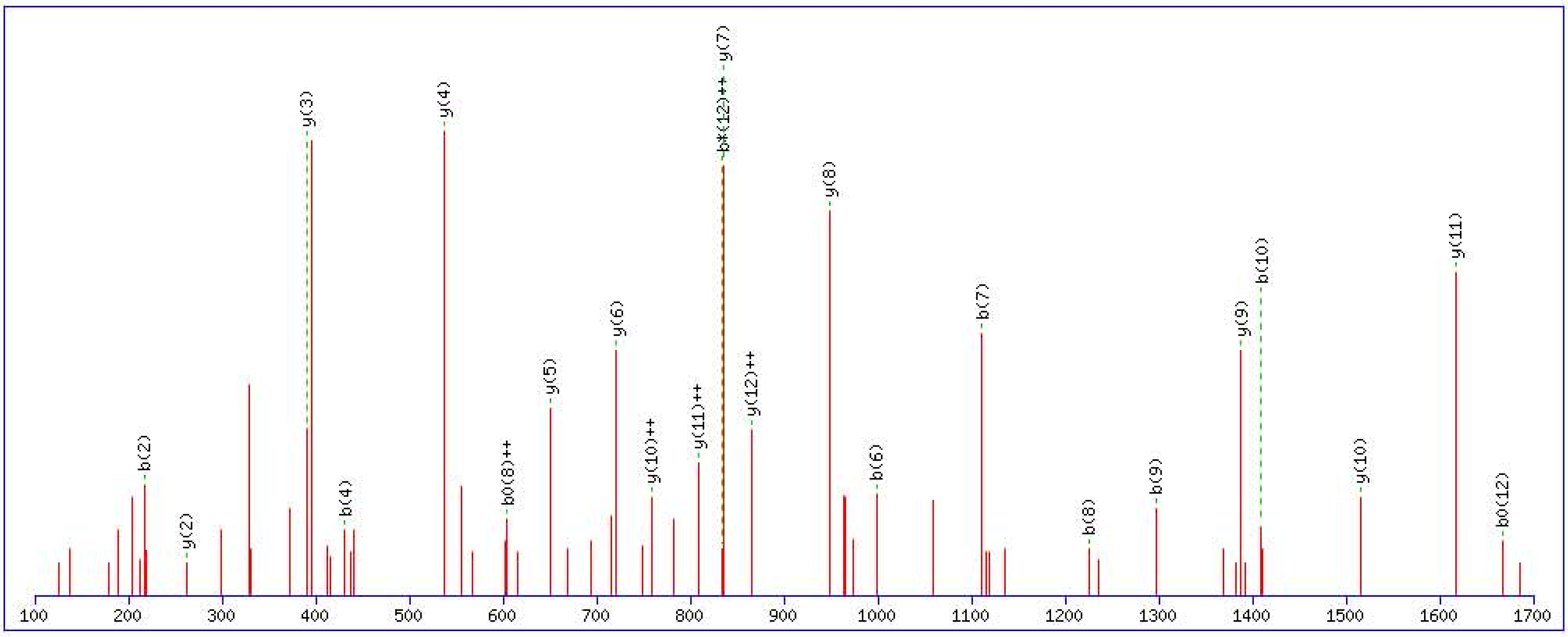
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

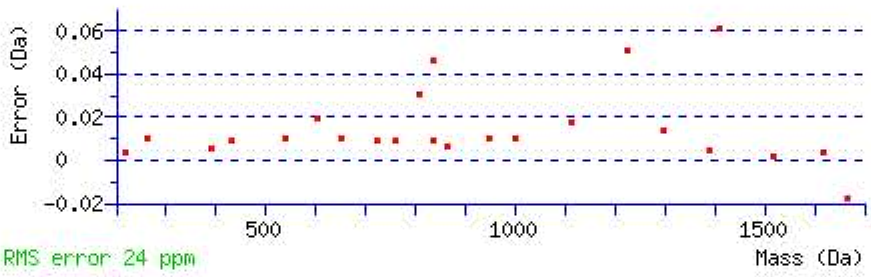
Match to Query 48576: 1945.008228 from(973.511390,2+) rtinseconds(2849) index(12025)
Title: Locus:1.1.1.3244.25 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

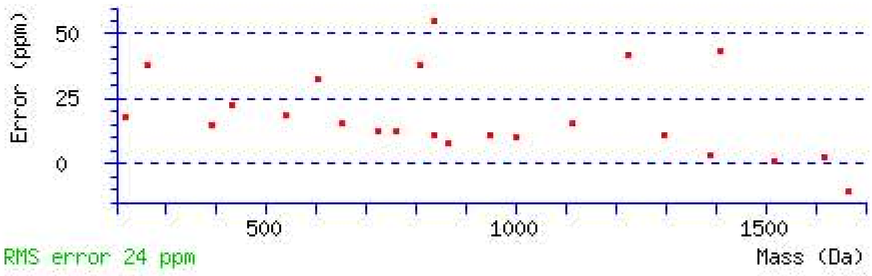
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1944.997879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 63 **Expect:** 1.4e-006
Matches : 23/146 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	88.039304	44.523290			70.028739	35.518008	S							14
2	**217.081897**	109.044586			199.071332	100.039304	E	1858.973148	929.990212	1841.946599	921.476938	1840.962583	920.984930	13
3	330.165961	165.586618			312.155396	156.581336	L	1729.930555	865.468916	1712.904006	856.955641	1711.919990	856.463633	12
4	**431.213640**	216.110458			413.203075	207.105176	T	***1616.846491***	808.926884	1599.819942	800.413609	1598.835926	799.921601	11
5	559.272218	280.139747	542.245669	271.626473	541.261653	271.134465	Q	***1515.798812***	758.403044	1498.772263	749.889770	1497.788247	749.397762	10
6	**998.497544**	499.752410	981.470995	491.239136	980.486979	490.747128	Q	***1387.740234***	694.373755	1370.713685	685.860481	1369.729669	685.368473	9
7	**1111.581608**	556.294442	1094.555059	547.781168	1093.571043	547.289159	L	***948.514908***	474.761092	931.488359	466.247818	930.504343	465.755810	8
8	**1225.624535**	613.315905	1208.597986	604.802631	1207.613970	604.310623	N	***835.430844***	418.219060	818.404295	409.705786	817.420279	409.213778	7
9	**1296.661649**	648.834462	1279.635100	640.321188	1278.651084	639.829180	A	***721.387917***	361.197597	704.361368	352.684322	703.377352	352.192314	6
10	**1409.745713**	705.376494	1392.719164	696.863220	1391.735148	696.371212	L	***650.350803***	325.679040	633.324254	317.165765	632.340238	316.673757	5
11	1556.814127	778.910701	1539.787578	770.397427	1538.803562	769.905419	F	***537.266739***	269.137008	520.240190	260.623733	519.256174	260.131725	4
12	1684.872705	842.939991	1667.846156	834.426716	1666.862140	833.934708	Q	***390.198325***	195.602801	373.171776	187.089526	372.187760	186.597518	3
13	1799.899648	900.453462	1782.873099	891.940188	1781.889083	891.448180	D	***262.139747***	131.573512	245.113198	123.060237	244.129182	122.568229	2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.1	1944.997879	0.010349	SELTQQLNALFQDK
53.0	1944.997879	0.010349	SELTQQLNALFQDK
6.0	1944.997879	0.010349	SELTQQLNALFQDK
0.5	1945.009109	-0.000881	ESQTALVANQRSLFA
0.2	1945.005280	0.002948	QPPSDAALTMLSFIK

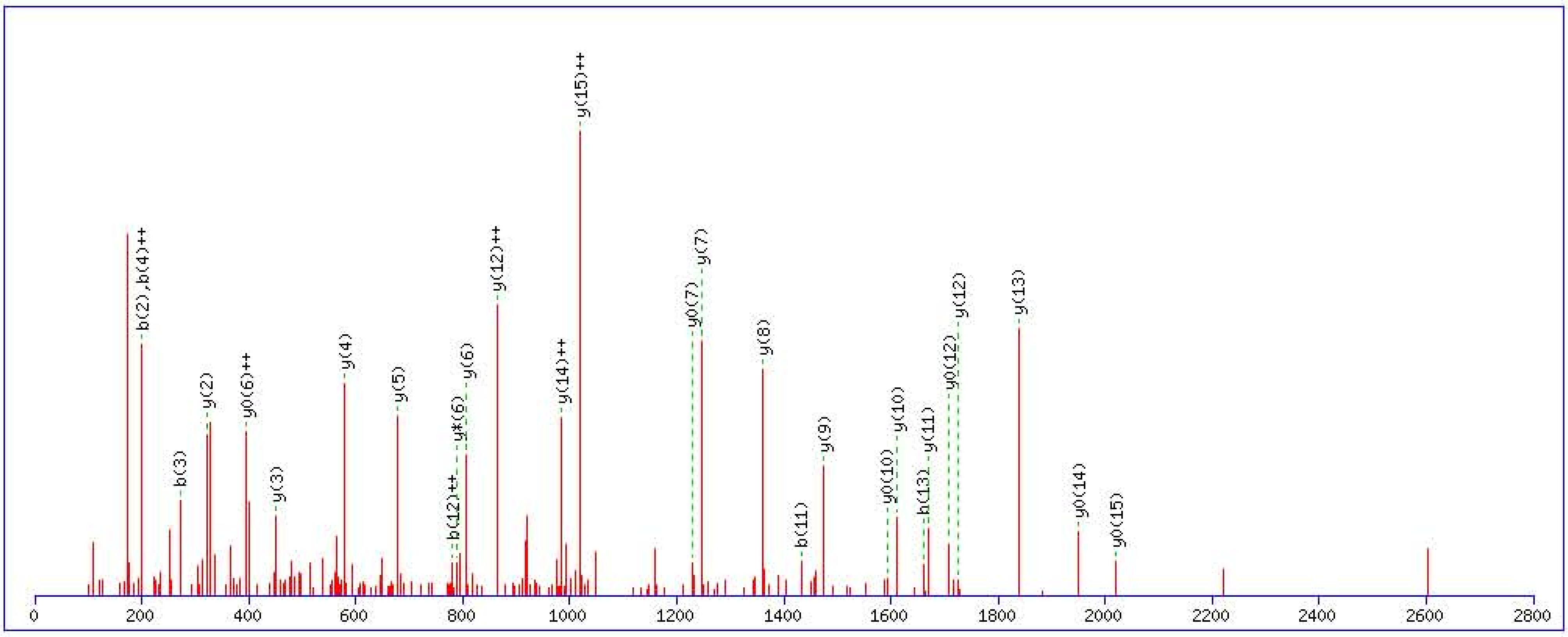
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

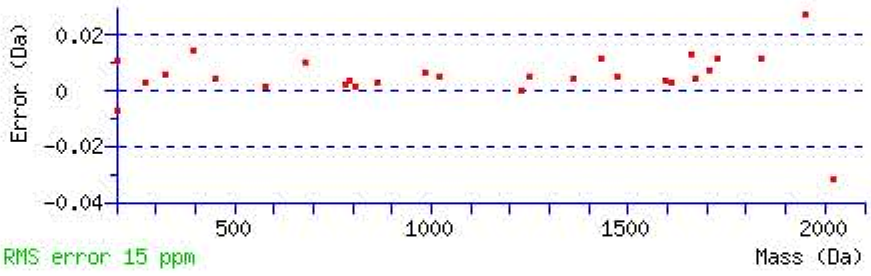
Match to Query 56359: 2238.127032 from(747.049620,3+) rtinseconds(2200) index(26150)
Title: Locus:1.1.1.2908.10 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

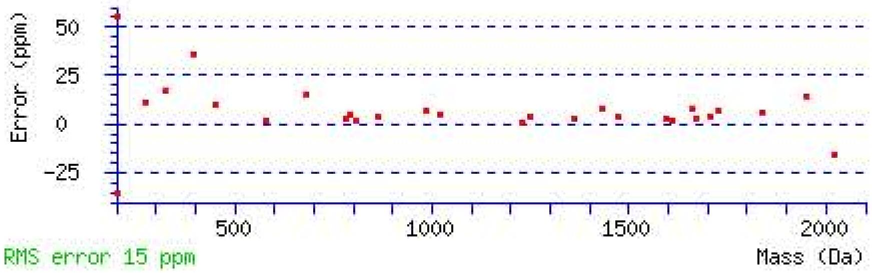
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2238.110291
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 1.1e-005
Matches : 28/168 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	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
64.1	2238.110291	0.016741	SLAELGGHLDQQVEEFR
55.4	2238.110291	0.016741	SLAELGGHLDQQVEEFR

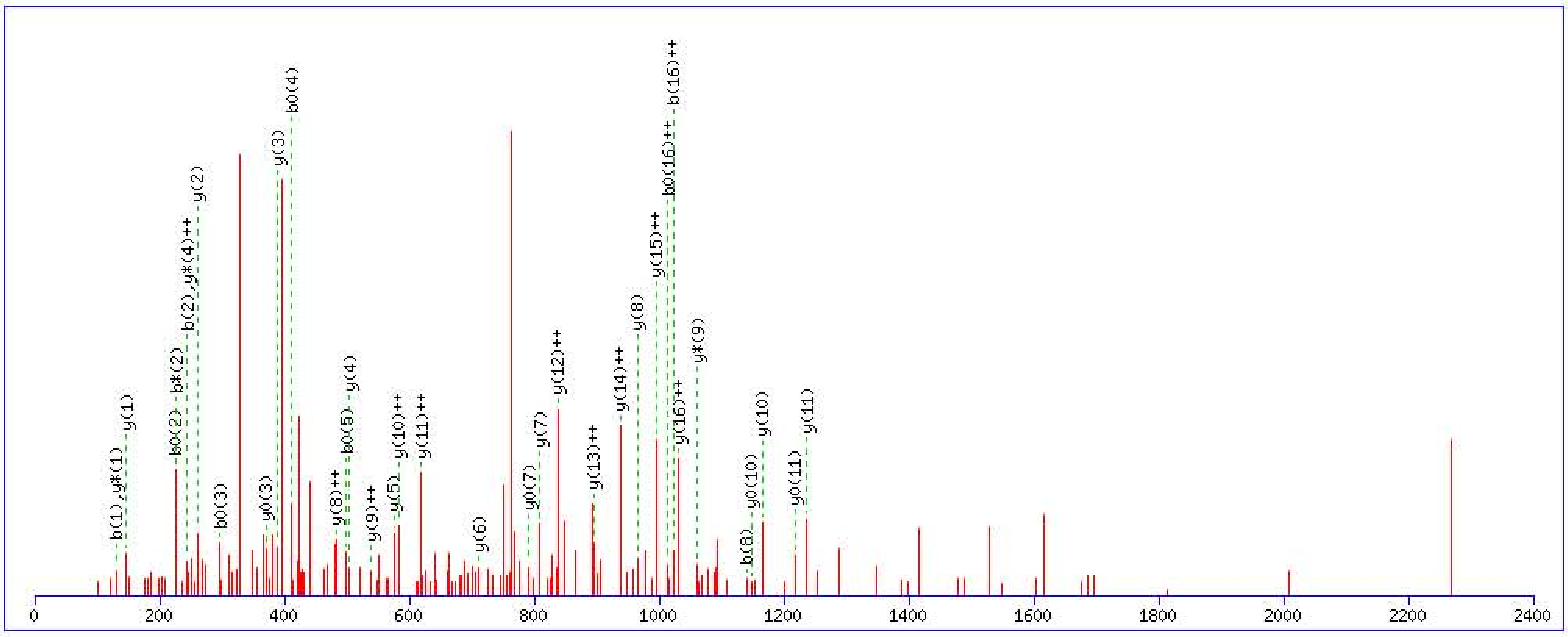
Mascot Search Results

Peptide View

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

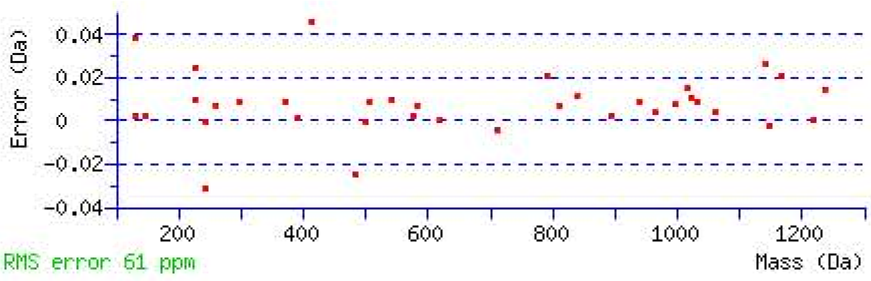
Match to Query 58142: 2304.170712 from(769.064180,3+) rtinseconds(1868) index(77883)
Title: Locus:1.1.1.2001.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

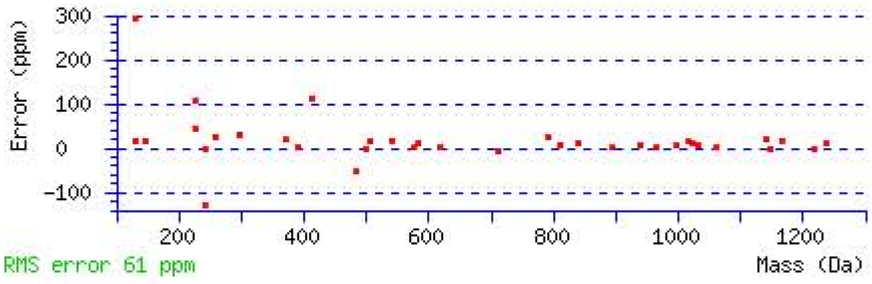
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 43  Expect: 0.0014
Matches : 36/198 fragment ions using 97 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							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
43.0	2304.153183	0.017529	ENADSLQASLRPHADELK

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

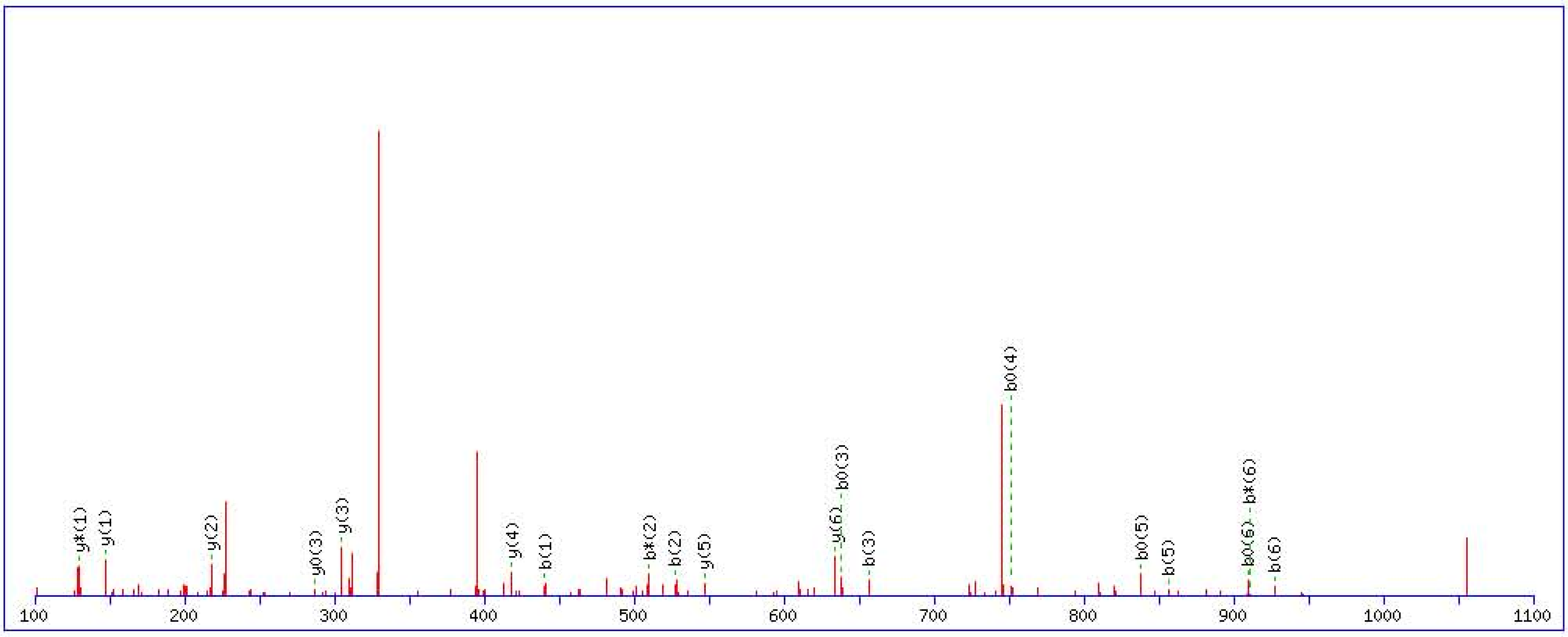
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSELSAK**
Found in **APOC1_HUMAN**, Apolipoprotein C-I OS=Homo sapiens GN=APOC1 PE=1 SV=1

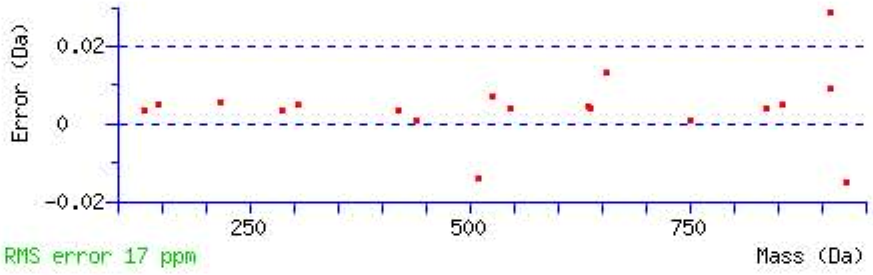
Match to Query 18251: 1072.564088 from(537.289320,2+) rtinseconds(1428) index(2771)
Title: Locus:1.1.1.2751.17 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

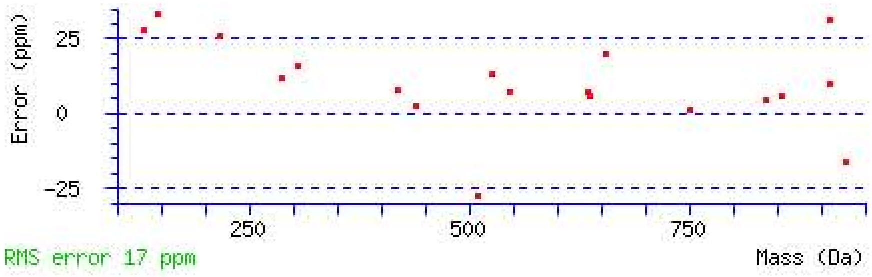
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1072.558655
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1     : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.065
Matches : 19/66 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	**440.232602**	220.619939	423.206053	212.106664			**Q**							7
2	**527.264630**	264.135953	510.238081	255.622679	509.254065	255.130671	**S**	***634.340631***	317.673954	617.314082	309.160679	616.330066	308.668671	6
3	**656.307223**	328.657250	639.280674	320.143975	638.296658	319.651967	**E**	***547.308603***	274.157940	530.282054	265.644665	529.298038	265.152657	5
4	769.391287	385.199282	752.364738	376.686007	751.380722	376.193999	**L**	***418.266010***	209.636643	401.239461	201.123368	400.255445	200.631360	4
5	**856.423315**	428.715296	839.396766	420.202021	838.412750	419.710013	**S**	***305.181946***	153.094611	288.155397	144.581336	287.171381	144.089328	3
6	**927.460429**	464.233853	910.433880	455.720578	909.449864	455.228570	**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 QSELSAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.4	1072.558655	0.005433	QSELSAK
11.9	1072.551239	0.012849	ERQEALEAK
10.6	1072.551239	0.012849	EAERELQAK
10.2	1072.562500	0.001588	KQQQQQSAK
9.6	1072.558655	0.005433	QSLSAEK
9.5	1072.551254	0.012834	KEAPRDETK
9.1	1072.562500	0.001588	HSSTSSRIAK
8.9	1072.576401	-0.012313	KEADEQLIK
7.8	1072.576401	-0.012313	QLEEEVKAK
7.4	1072.576401	-0.012313	IKEGVEEAAK

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

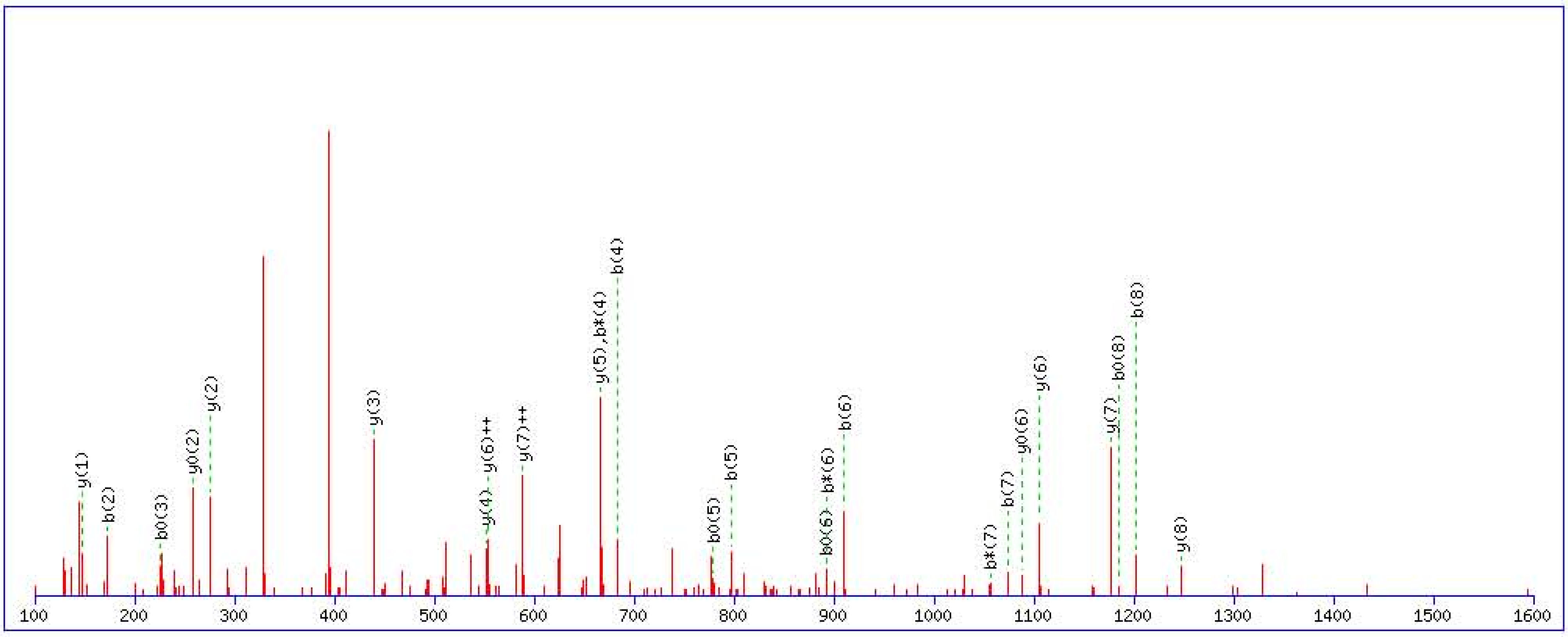
Mascot Search Results

Peptide View

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

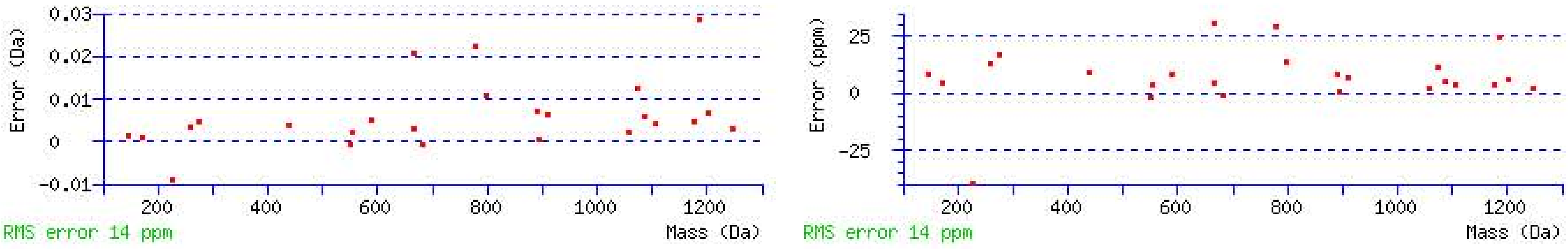
Match to Query 28041: 1347.697608 from(674.856080,2+) rtinseconds(1600) index(39504)
Title: Locus:1.1.1.3006.8 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1347.685638
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0019
Matches : 25/88 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	102.054955	51.531116			84.044390	42.525833	T							9
2	**173.092069**	87.049672			155.081504	78.044390	A	***1247.645271***	624.326273	1230.618722	615.812999	1229.634706	615.320991	8
3	244.129183	122.568229			226.118618	113.562947	A	***1176.608157***	588.807716	1159.581608	580.294442	1158.597592	579.802434	7
4	**683.354509**	342.180893	666.327960	333.667618	665.343944	333.175610	Q	***1105.571043***	553.289159	1088.544494	544.775885	1087.560478	544.283877	6
5	**797.397436**	399.202356	780.370887	390.689081	779.386871	390.197073	N	***666.345717***	333.676496	649.319168	325.163222	648.335152	324.671214	5
6	**910.481500**	455.744388	893.454951	447.231113	892.470935	446.739105	L	***552.302790***	276.655033	535.276241	268.141758	534.292225	267.649750	4
7	**1073.544829**	537.276052	1056.518280	528.762778	1055.534264	528.270770	Y	***439.218726***	220.113001	422.192177	211.599726	421.208161	211.107718	3
8	**1202.587422**	601.797349	1185.560873	593.284074	1184.576857	592.792066	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 TAAQNLYEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.4	1347.685638	0.011970	TAAQNLYEK
9.8	1347.682297	0.015311	TAYFSLDTRFK
5.0	1347.689011	0.008597	DKCMLPKSLEK
4.9	1347.714645	-0.017037	GADNVIFERLSK
4.0	1347.699371	-0.001763	EKPKSGDAKSSSK
3.4	1347.681610	0.015998	RSQISMEQLEK
3.2	1347.682480	0.015128	QSRMKMEK
2.5	1347.704086	-0.006478	KPTRSNMQRSK
1.2	1347.681625	0.015983	GLERNLAVMSDK

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

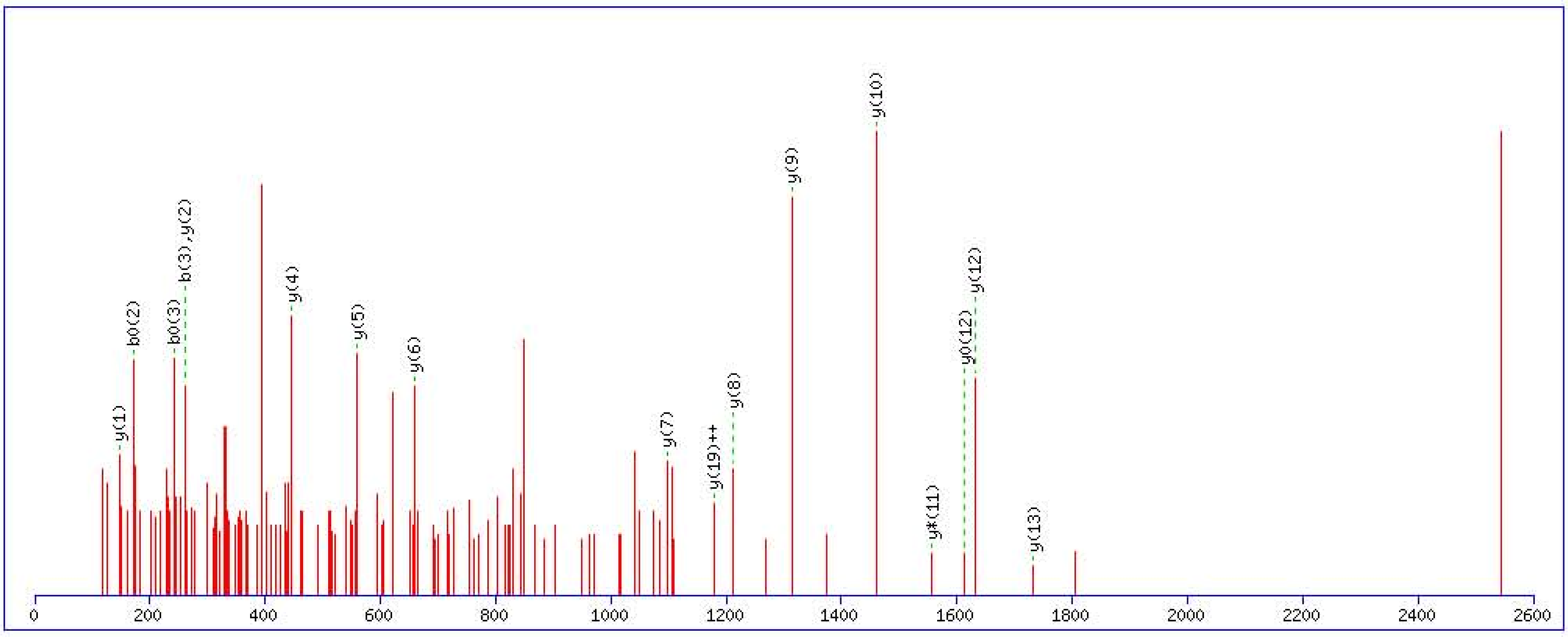
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

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

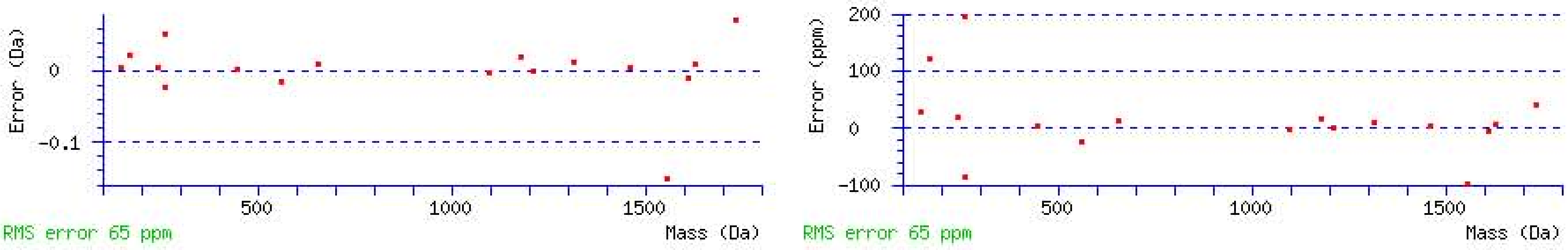
Match to Query 63785: 2543.334072 from(848.785300,3+) rtinseconds(3204) index(32852)
Title: Locus:1.1.1.3253.15 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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: 52  Expect: 0.00015
Matches : 17/206 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							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
52.2	2543.301544	0.032528	STAAMSTYTGIFTDQVLSVLK

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

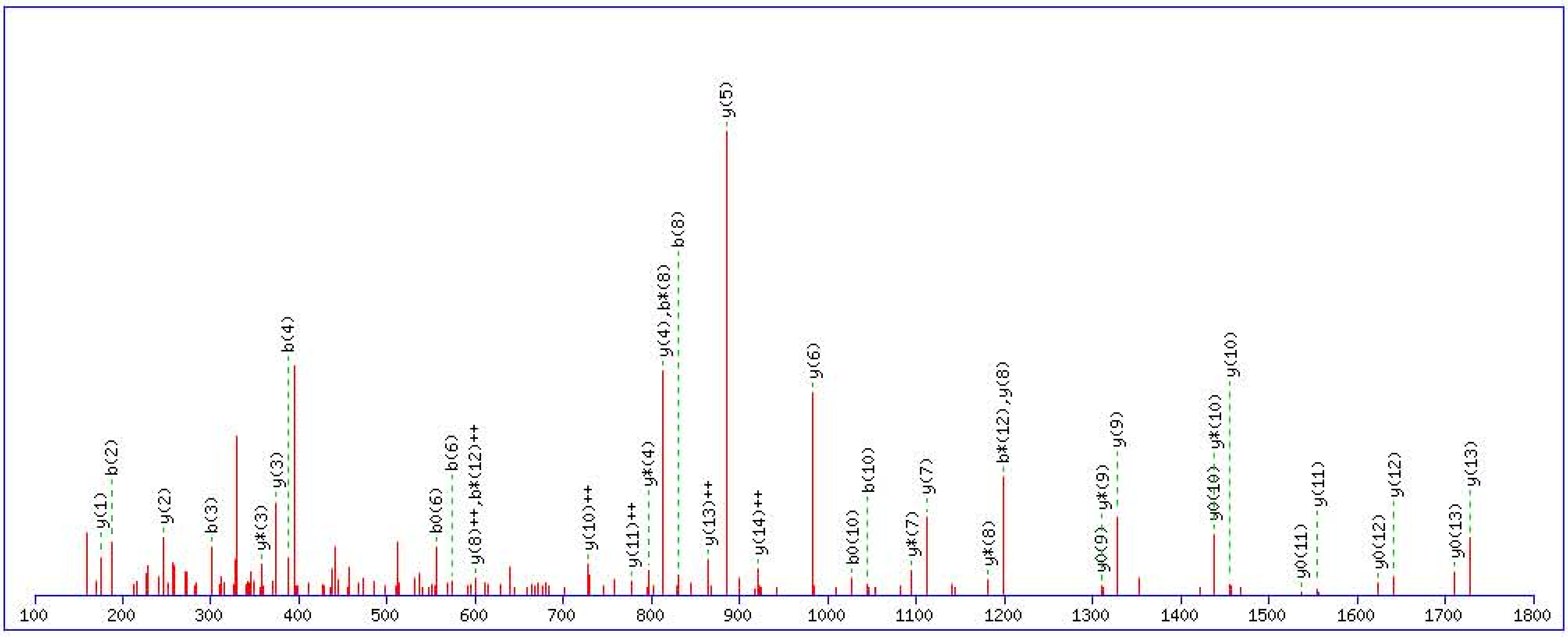
Mascot Search Results

Peptide View

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

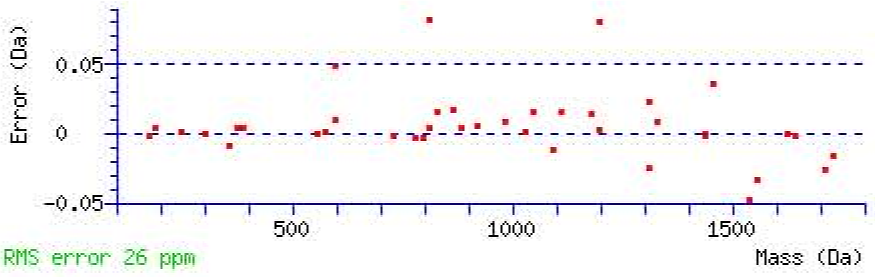
Match to Query 51431: 2027.023602 from(676.681810,3+) rtinseconds(1872) index(23745)
Title: Locus:1.1.1.2794.20 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

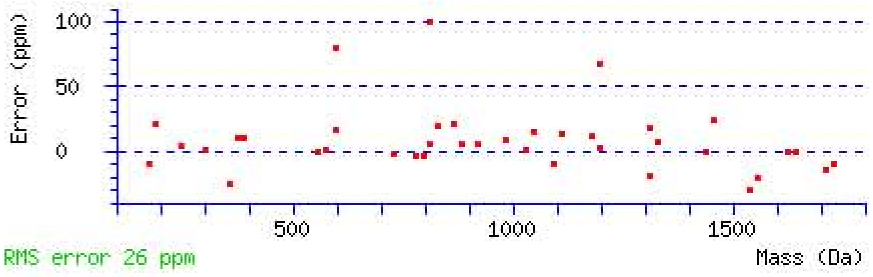
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 89  Expect: 5.3e-009
Matches : 40/154 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	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
88.9	2027.010574	0.013028	DALSSVQESQVAQQAR
74.7	2027.010574	0.013028	DALSSVQESQVAQQAR
59.0	2027.010574	0.013028	DALSSVQESQVAQQAR
21.5	2027.010574	0.013028	DALSSVQESQVAQQAR
0.6	2027.017960	0.005642	MFELTLRGMSEALVDKR

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

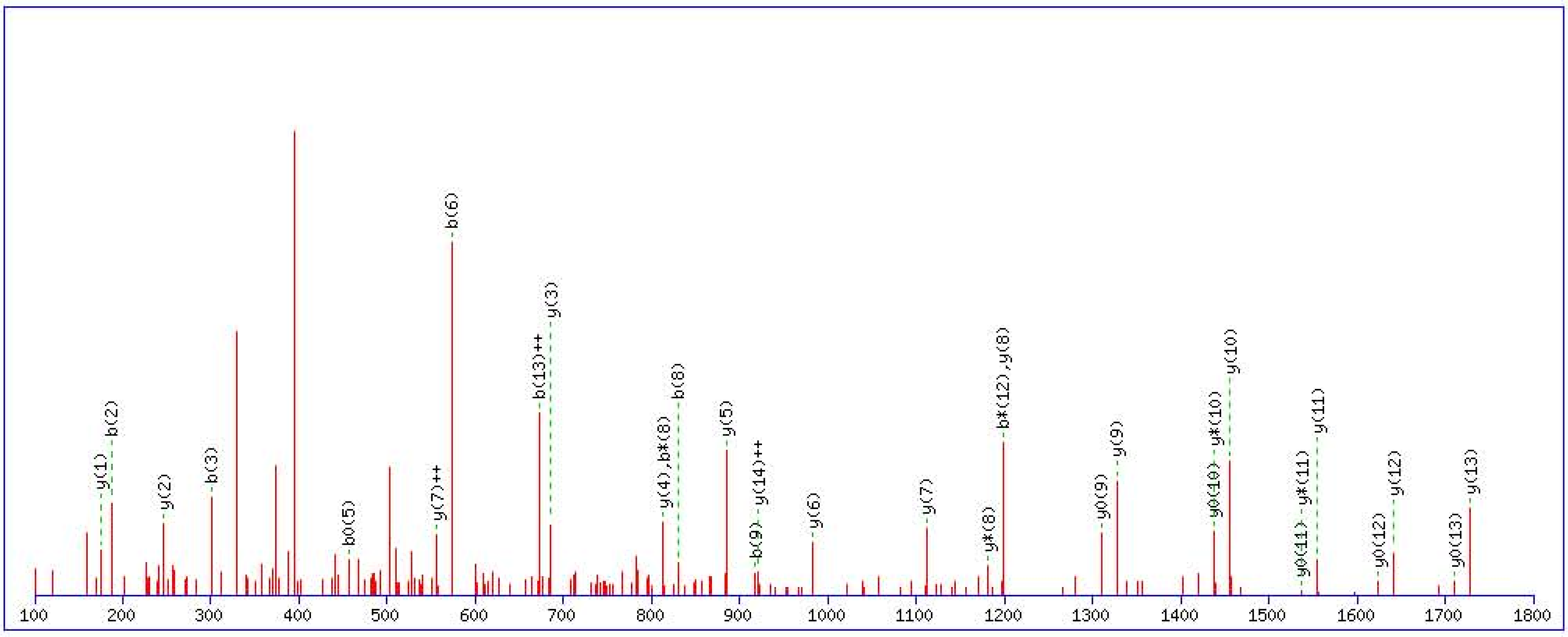
Mascot Search Results

Peptide View

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

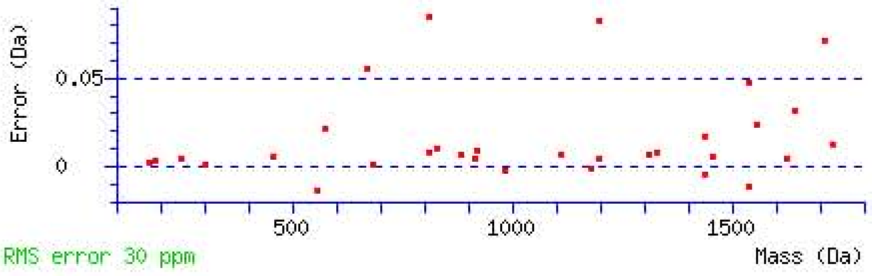
Match to Query 51432: 2027.023602 from(676.681810,3+) rtinseconds(1926) index(24169)
Title: Locus:1.1.1.2813.8 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

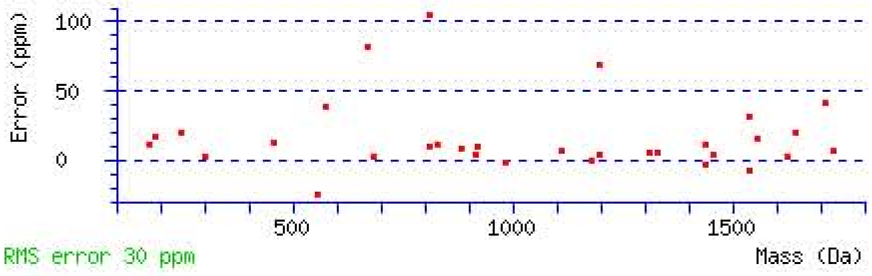
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 88  Expect: 4.2e-008
Matches : 32/154 fragment ions using 49 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	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
88.0	2027.010574	0.013028	DALSSVQESQVAQQAR
88.0	2027.010574	0.013028	DALSSVQESQVAQQAR
87.8	2027.010574	0.013028	DALSSVQESQVAQQAR
44.1	2027.010574	0.013028	DALSSVQESQVAQQAR

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

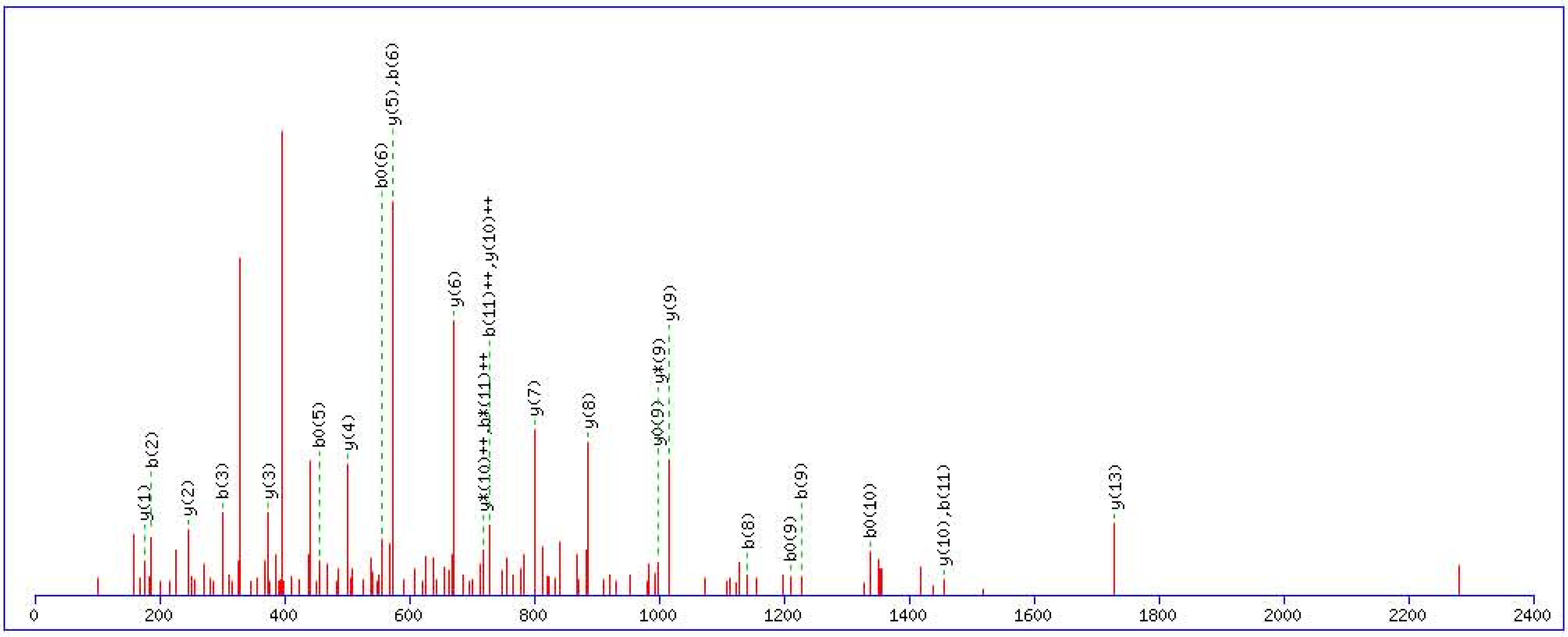
Mascot Search Results

Peptide View

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

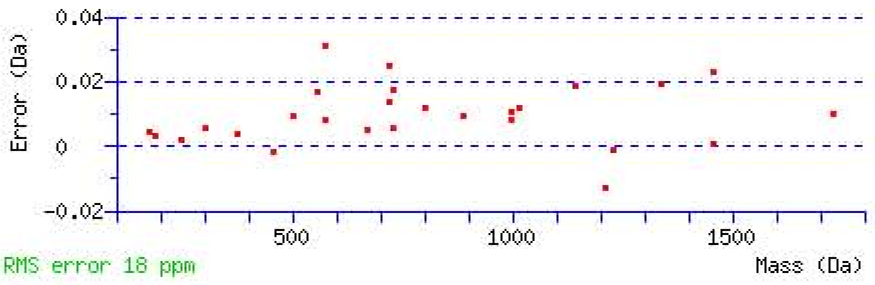
Match to Query 51436: 2027.031912 from(676.684580,3+) rtinseconds(1967) index(42009)
Title: Locus:1.1.1.3134.14 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

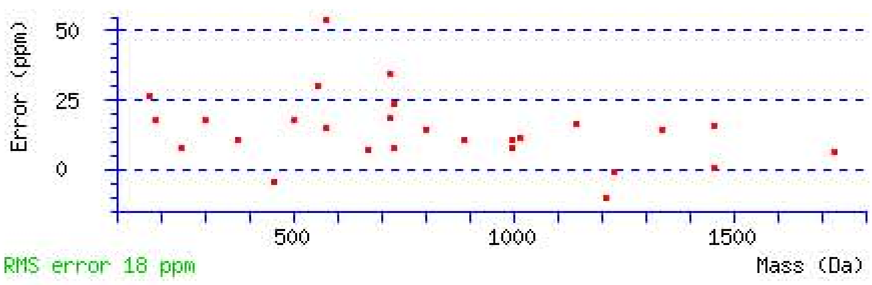
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 2.4e-006
Matches : 27/154 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	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
63.5	2027.010574	0.021338	DALSSVQESQVAQQAR
33.7	2027.010574	0.021338	DALSSVQESQVAQQAR
29.7	2027.010574	0.021338	DALSSVQESQVAQQAR
28.7	2027.010574	0.021338	DALSSVQESQVAQQAR
3.6	2027.010559	0.021353	LTGRGAEDSLADQAANK

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

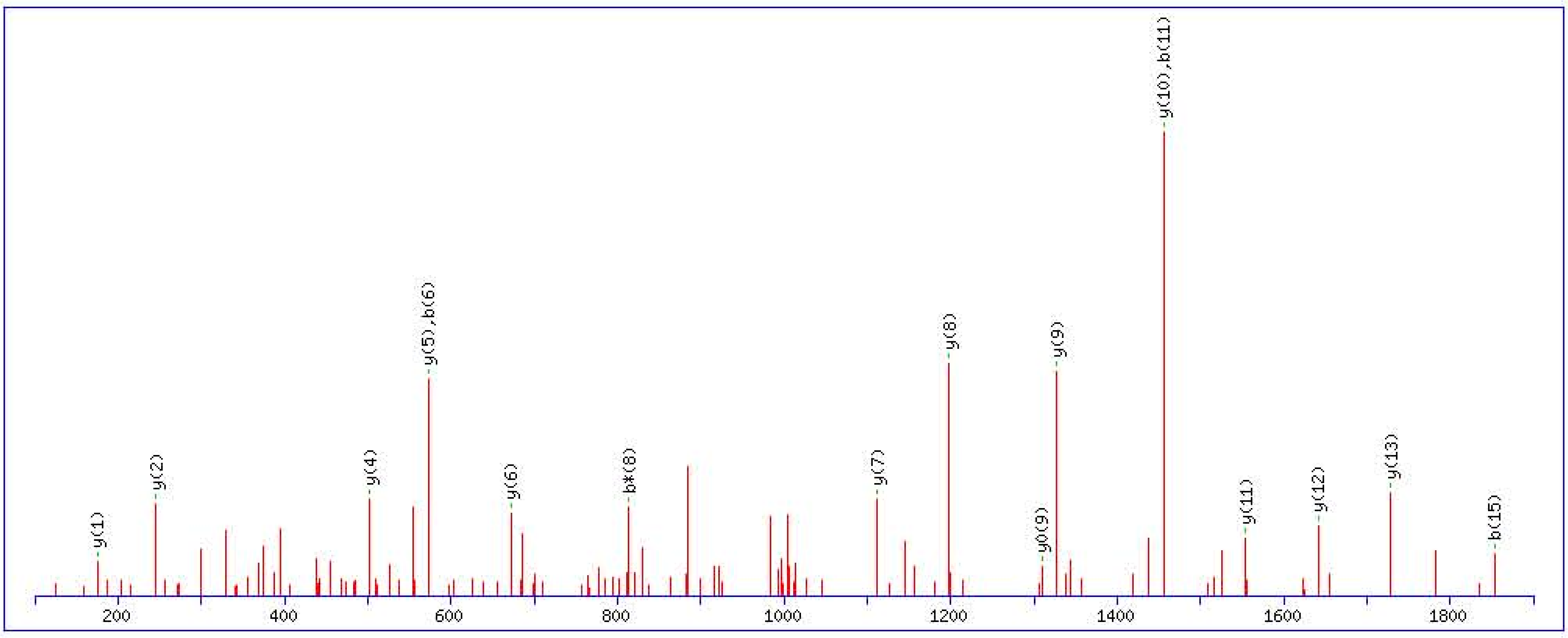
Mascot Search Results

Peptide View

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

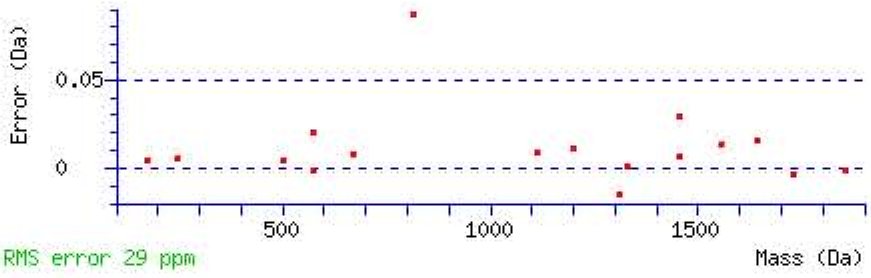
Match to Query 51441: 2027.035068 from(1014.524810,2+) rtinseconds(1925) index(24160)
Title: Locus:1.1.1.2812.24 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

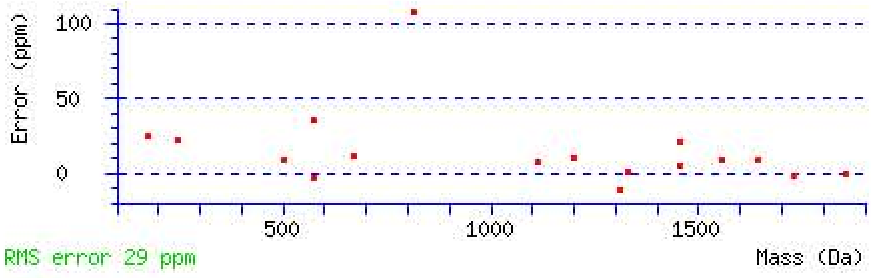
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 117  Expect: 5e-011
Matches : 17/154 fragment ions using 18 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
117.4	2027.010574	0.024494	DALSSVQESQVAQQAR
107.2	2027.010574	0.024494	DALSSVQESQVAQQAR
99.4	2027.010574	0.024494	DALSSVQESQVAQQAR
59.8	2027.010574	0.024494	DALSSVQESQVAQQAR
12.9	2027.021805	0.013263	VASVESQGQEISGNRR
9.4	2027.029633	0.005435	QEESEHSHKHLIELRR
4.3	2027.017960	0.017108	MFELTLRGMSEALVDKR
3.0	2027.039520	-0.004452	GLERALEEAANSGGLNLSAR
2.9	2027.021820	0.013248	DTDNKAAIRDCGGVPALVR
2.7	2027.021805	0.013263	VASVESQGQEISGNRR

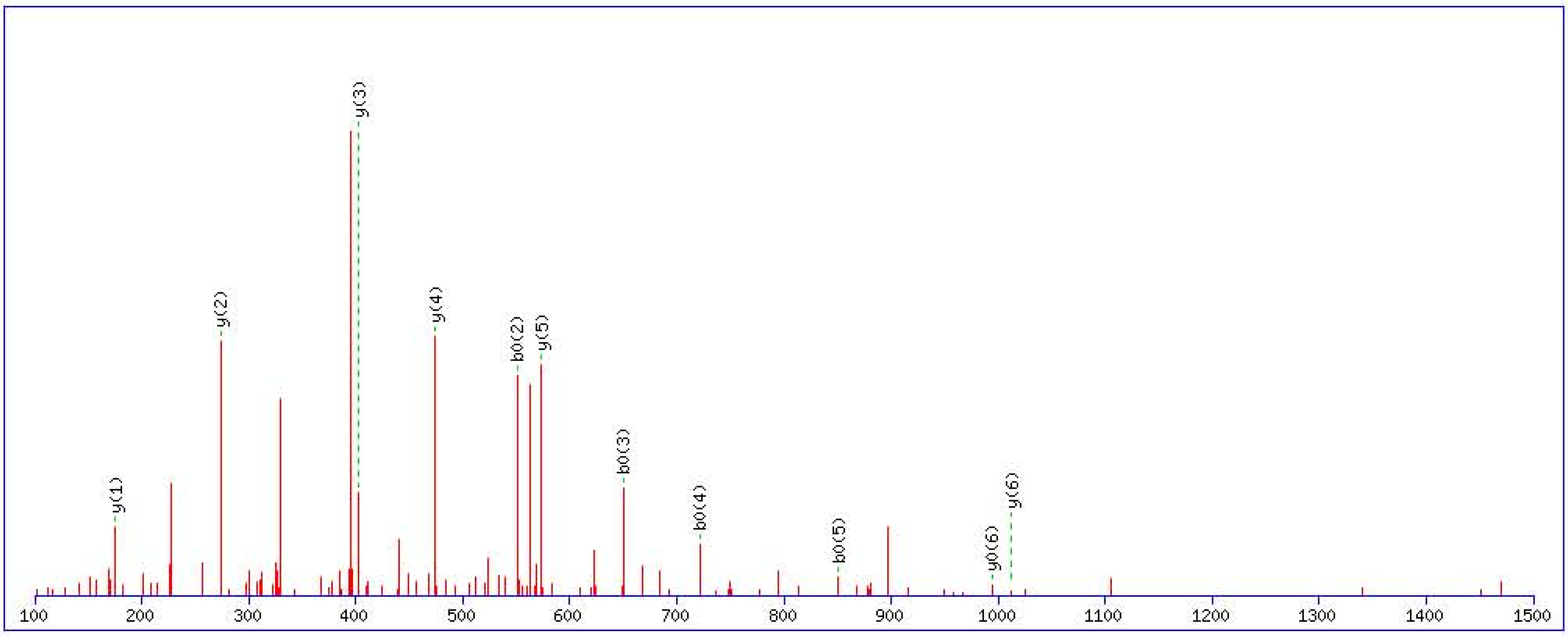
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

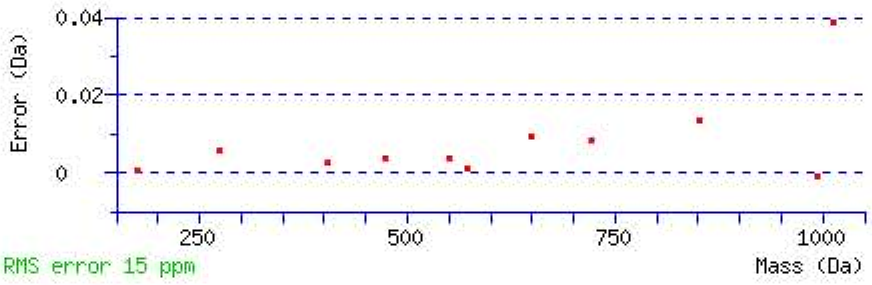
Match to Query 21525: 1140.605628 from(571.310090,2+) rtinseconds(1507) index(38824)
Title: Locus:1.1.1.2974.15 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

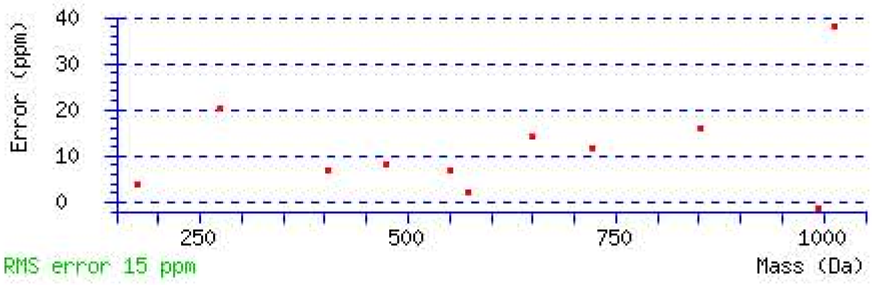
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1140.596115
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.052
Matches : 11/66 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	130.049869	65.528572			112.039304	56.523290	E							7
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	Q	***1012.560813***	506.784044	995.534264	498.270770	994.550248	497.778762	6
3	668.343609	334.675443	651.317060	326.162168	650.333044	325.670160	V	***573.335487***	287.171382	556.308938	278.658107	555.324922	278.166099	5
4	739.380723	370.194000	722.354174	361.680725	721.370158	361.188717	A	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
5	868.423316	434.715296	851.396767	426.202022	850.412751	425.710014	E	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
6	967.491730	484.249503	950.465181	475.736228	949.481165	475.244220	V	***274.187366***	137.597321	257.160817	129.084046			2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EQVAEVR
(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	1140.596115	0.009513	EQVAEVR
12.1	1140.596115	0.009513	QEVADLR
7.9	1140.596115	0.009513	EQALDVR
6.0	1140.599945	0.005683	ERVALSHSSR
4.0	1140.599945	0.005683	SSSKLAQHQR
3.3	1140.596115	0.009513	QEGLDLR
3.1	1140.588715	0.016913	RLAADDPEVR
3.1	1140.613876	-0.008248	LLQAPDTDLR
3.1	1140.592789	0.012839	IGTGSFGTVFR
2.4	1140.596115	0.009513	EQSTLPR

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

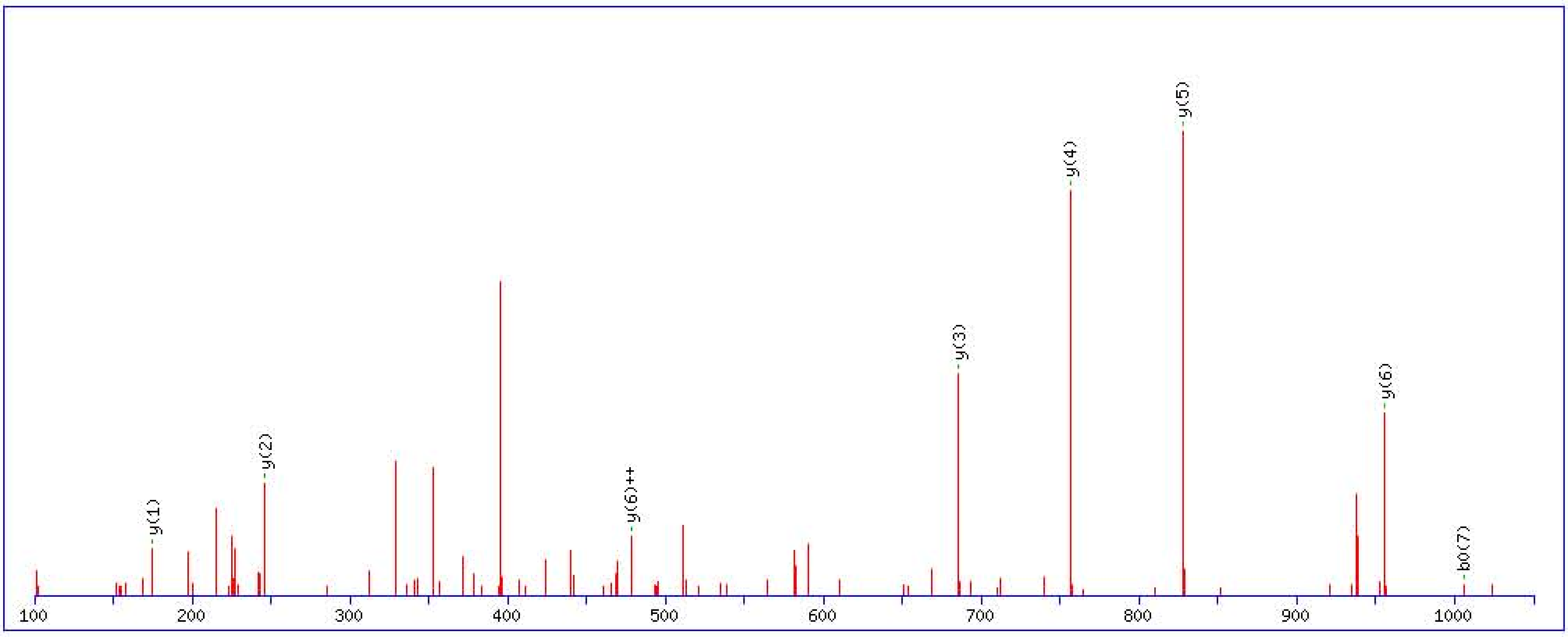
Mascot Search Results

Peptide View

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

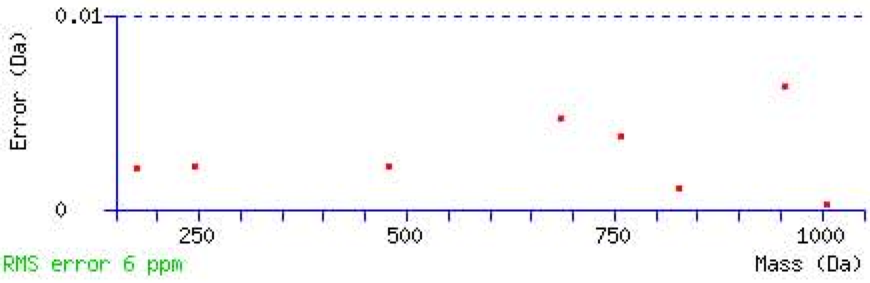
Match to Query 23620: 1196.644228 from(599.329390,2+) rtinseconds(1456) index(38425)
Title: Locus:1.1.1.2956.21 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

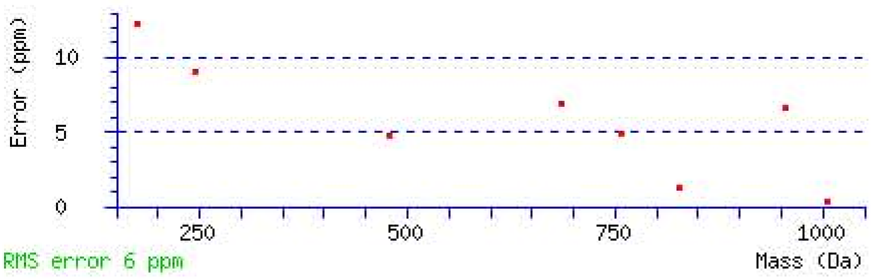
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1196.633545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00018
Matches : 8/66 fragment ions using 10 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
47.9	1196.633545	0.010683	ELQAAQAR
7.5	1196.633575	0.010653	QASTQVPR
6.0	1196.633545	0.010683	ELQAAQAR
4.0	1196.627029	0.017199	AGMPRQAR
4.0	1196.648819	-0.004591	LNVWQAR
3.2	1196.641434	0.002794	STRPQAWVPR
3.0	1196.637390	0.006838	TLRQAGAPNNR
1.1	1196.655350	-0.011122	FITEKAVFSR
1.1	1196.641418	0.002810	EAKKAGPGFHR
0.3	1196.640091	0.004137	LDIDSPPITAR

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

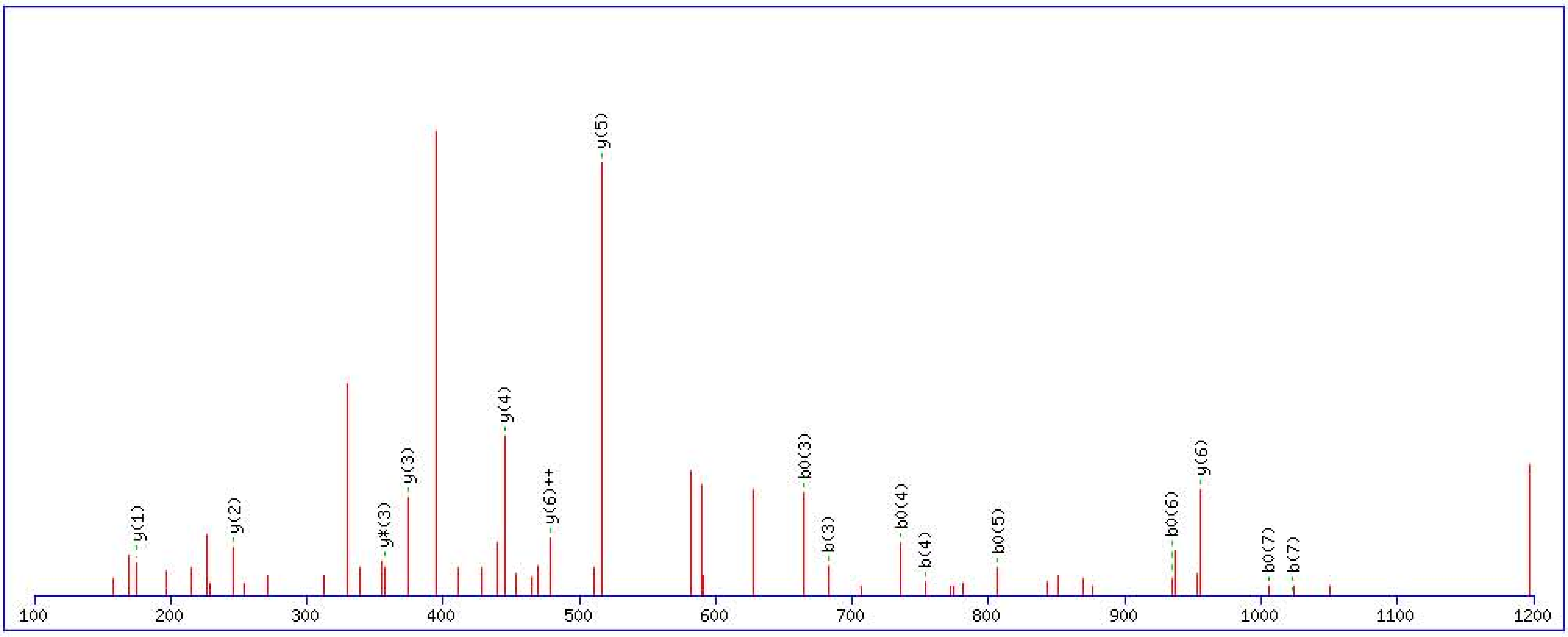
Mascot Search Results

Peptide View

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

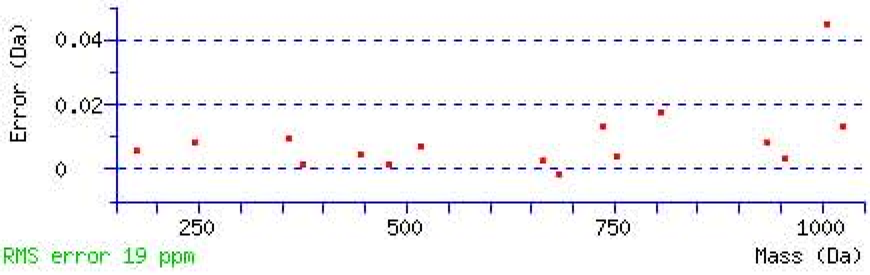
Match to Query 23622: 1196.648668 from(599.331610,2+) rtinseconds(1442) index(38317)
Title: Locus:1.1.1.2951.21 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

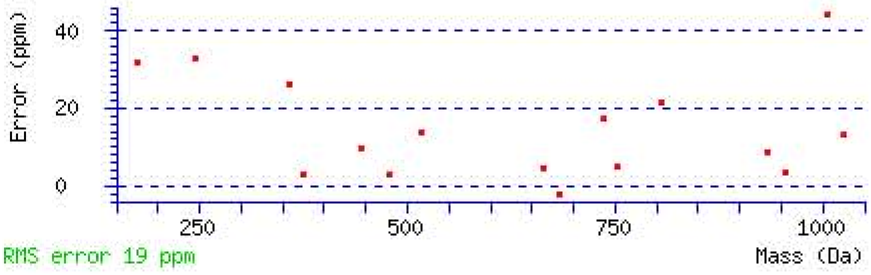
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1196.633545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.015
Matches : 16/66 fragment ions using 35 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	**682.359259**	341.683268	665.332710	333.169993	664.348694	332.677985	Q	***955.514198***	478.260737	938.487649	469.747463	6
4	**753.396373**	377.201825	736.369824	368.688550	735.385808	368.196542	A	***516.288872***	258.648074	499.262323	250.134800	5
5	824.433487	412.720382	807.406938	404.207107	806.422922	403.715099	A	***445.251758***	223.129517	428.225209	214.616243	4
6	952.492065	476.749671	935.465516	468.236396	934.481500	467.744388	Q	***374.214644***	187.610960	357.188095	179.097686	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
31.0	1196.633545	0.015123	ELQAAQAR
10.9	1196.644775	0.003893	LEQANRR
10.6	1196.658707	-0.010039	MIIAVTSYKR
7.3	1196.641418	0.007250	EAKKAGPGFHR
6.3	1196.644791	0.003877	QALEGGRR
6.1	1196.666565	-0.017897	LLLAEFAQHR
4.7	1196.666565	-0.017897	LFALQAEIHR
4.2	1196.662537	-0.013869	KSIAPANGNLGR
4.0	1196.633560	0.015108	QNQDILR
4.0	1196.658707	-0.010039	LQEVEIR

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

{MATRIX SCIENCE}

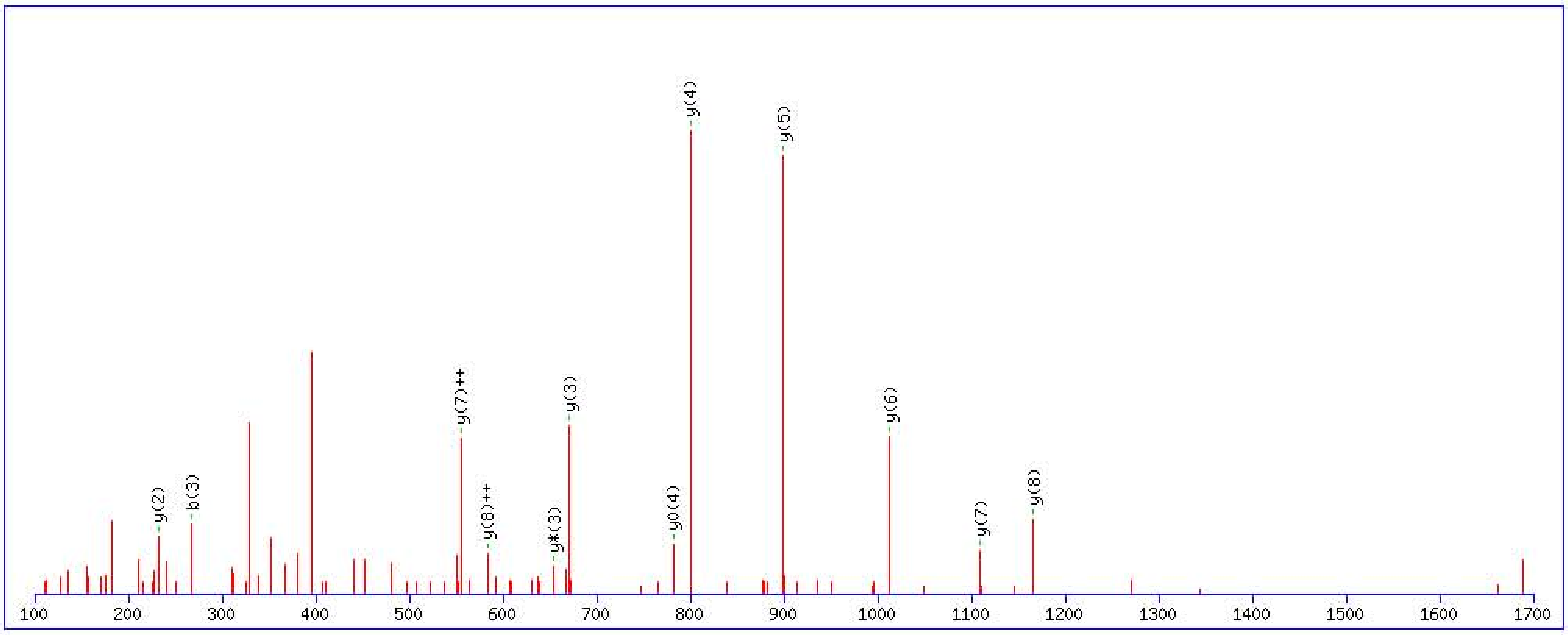
Mascot Search Results

Peptide View

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

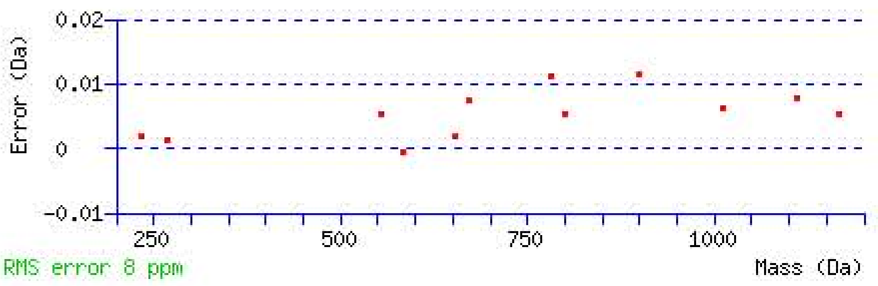
Match to Query 26176: 1278.715108 from(640.364830,2+) rtinseconds(1932) index(24223)
Title: Locus:1.1.1.2815.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

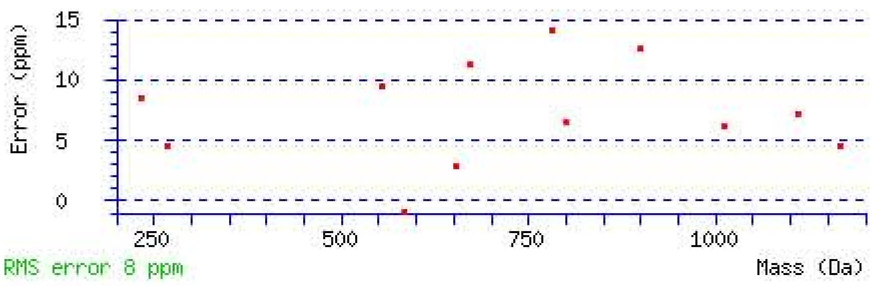
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1278.711823
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00099
Matches : 12/68 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	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
41.6	1278.711823	0.003285	LGPLVEQGR

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

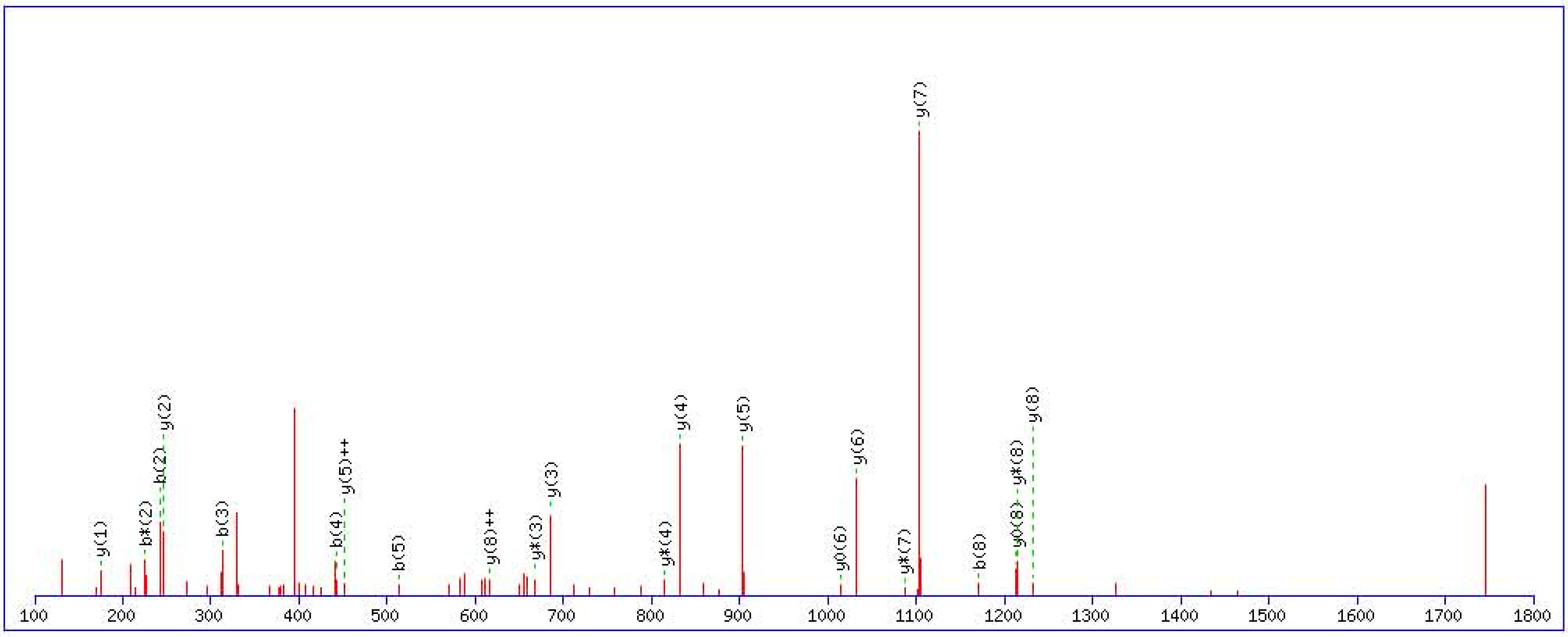
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

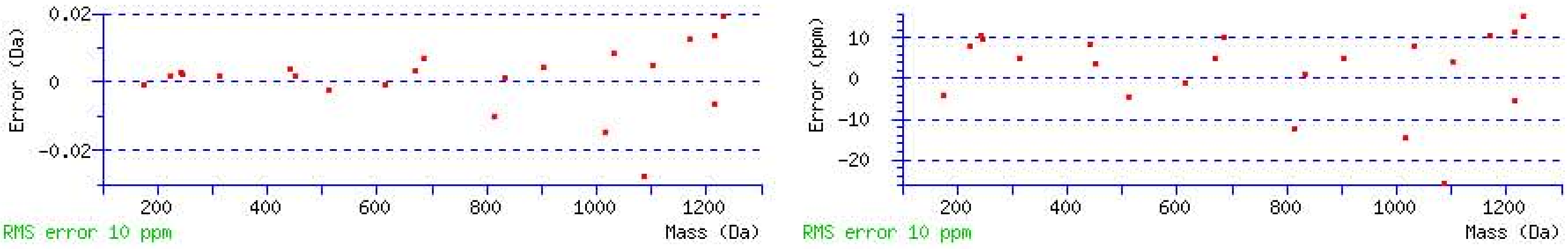
Match to Query 27956: 1343.706168 from(672.860360,2+) rtinseconds(1768) index(23005)
Title: Locus:1.1.1.2758.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1343.701965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 0.00026
Matches : 22/78 fragment ions using 41 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	**242.149918**	121.578597	225.123369	113.065323			Q	***1231.625205***	616.316241	1214.598656	607.802966	1213.614640	607.310958	8
3	**313.187032**	157.097154	296.160483	148.583879			A	***1103.566627***	552.286951	1086.540078	543.773677	1085.556062	543.281669	7
4	**442.229625**	221.618450	425.203076	213.105176	424.219060	212.613168	E	***1032.529513***	516.768395	1015.502964	508.255120	1014.518948	507.763112	6
5	**513.266739**	257.137008	496.240190	248.623733	495.256174	248.131725	A	***903.486920***	452.247098	886.460371	443.733823			5
6	660.335153	330.671215	643.308604	322.157940	642.324588	321.665932	F	***832.449806***	416.728541	815.423257	408.215266			4
7	1099.560479	550.283878	1082.533930	541.770603	1081.549914	541.278595	Q	***685.381392***	343.194334	668.354843	334.681060			3
8	**1170.597593**	585.802435	1153.571044	577.289160	1152.587028	576.797152	A	***246.156066***	123.581671	229.129517	115.068396			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.0	1343.701965	0.004203	LQAEAFQAR
12.5	1343.694107	0.012061	IQAMSEVQK
7.5	1343.715683	-0.009515	LKDSEAELQRR
7.5	1343.716583	-0.010415	LQQVMSRR
6.5	1343.704453	0.001715	IQEKKDEDIAR
6.0	1343.704453	0.001715	IKGEELSEANVR
4.1	1343.693237	0.012931	LQDLELDLETR
3.1	1343.686707	0.019461	AAVQMDPELAKR
2.9	1343.697952	0.008216	AMGTVREAAGLPR
2.3	1343.715683	-0.009515	QSLIEDARKER

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

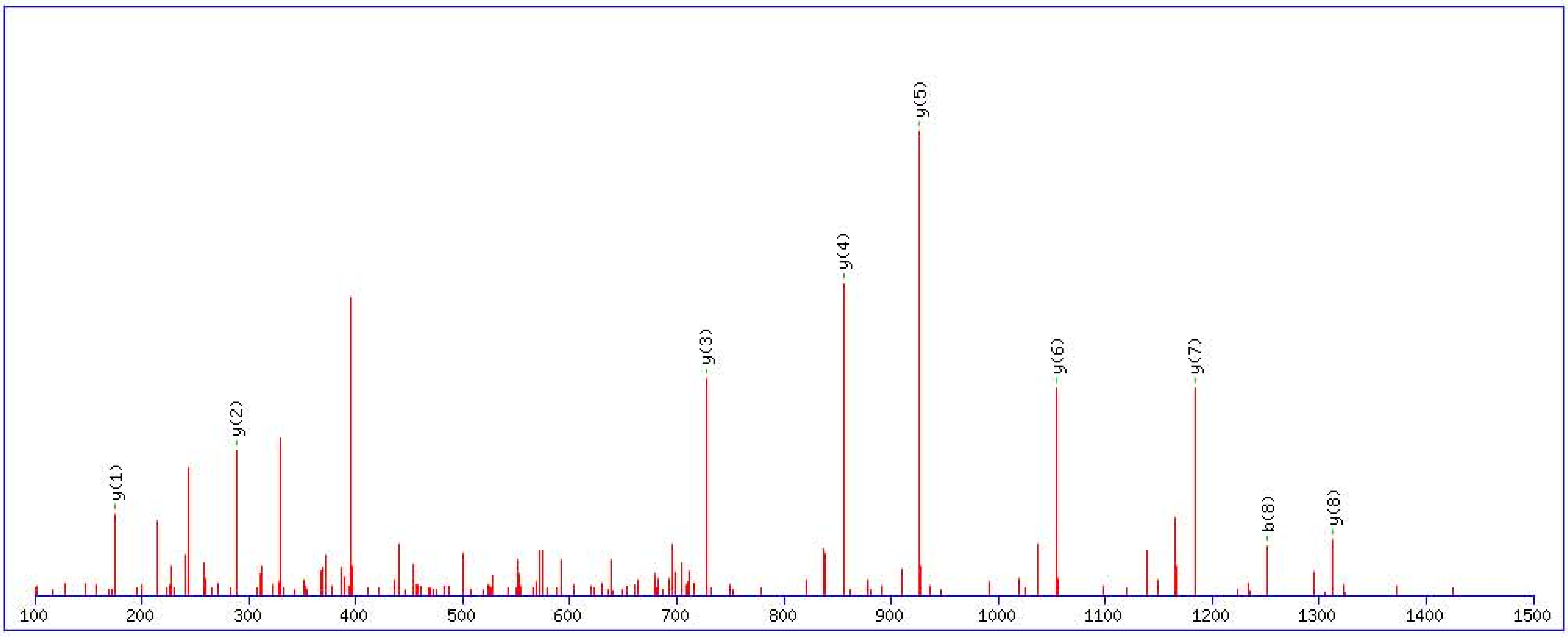
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

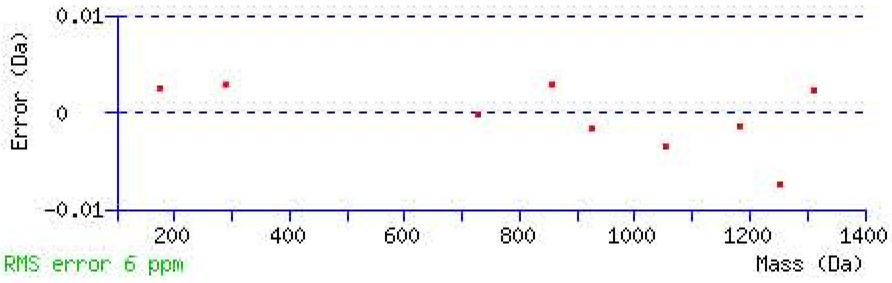
Match to Query 32443: 1424.745428 from(713.379990,2+) rtinseconds(1532) index(21248)
Title: Locus:1.1.1.2676.17 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

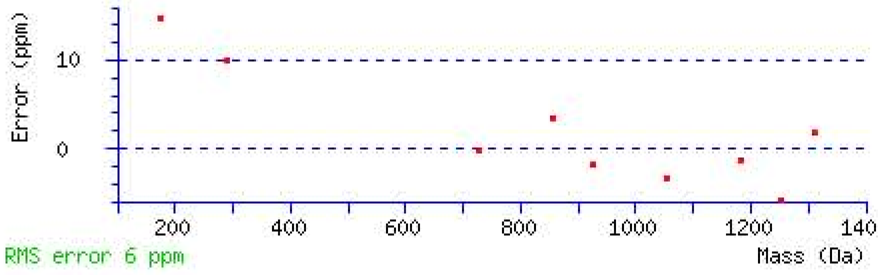
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
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: 70  Expect: 2.2e-006
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	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
70.1	1424.744553	0.000875	LEEQAQQIR
53.7	1424.744553	0.000875	LEEQAQQIR
24.4	1424.744553	0.000875	LEEQAQQIR
16.1	1424.733322	0.012106	LEQETEPLR
14.4	1424.745438	-0.000010	QMQQIR
9.3	1424.726807	0.018621	QMNLQQQPK
7.3	1424.744583	0.000845	QLSGDQPTIR
6.9	1424.744583	0.000845	QLSGDQPTIR
6.8	1424.734680	0.010748	WVLTAAHCLAQR
5.8	1424.745438	-0.000010	QMQQIR

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

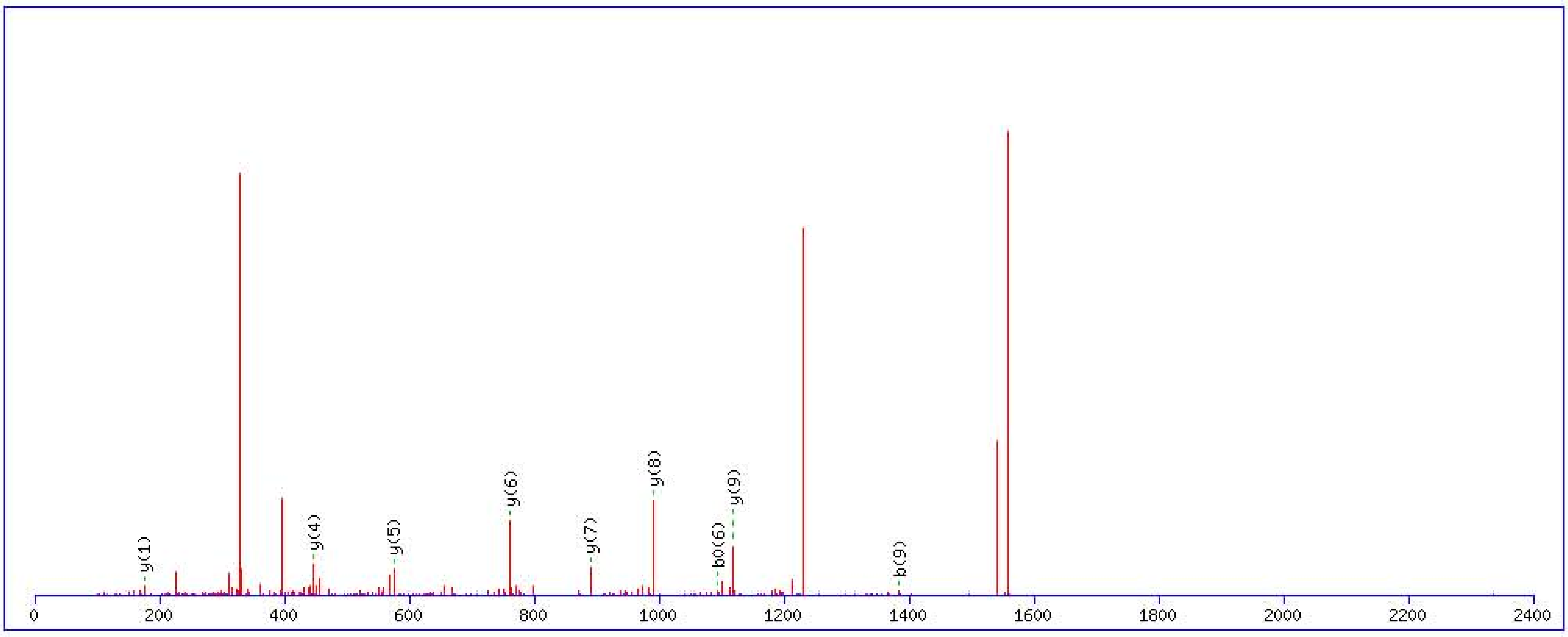
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

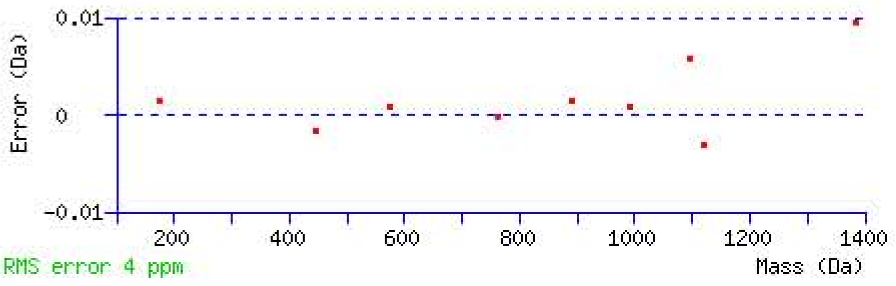
Match to Query 36604: 1557.739868 from(779.877210,2+) rtinseconds(1536) index(21280)
Title: Locus:1.1.1.2677.24 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

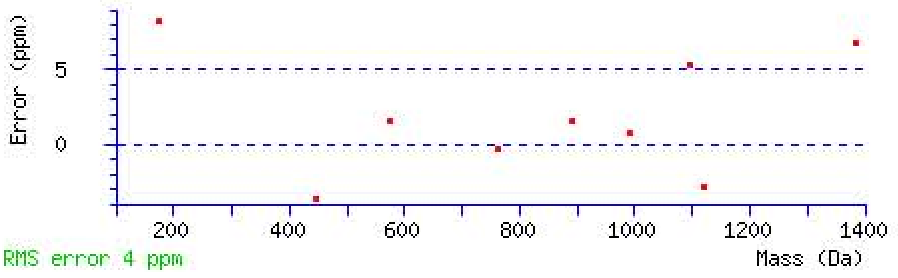
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 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



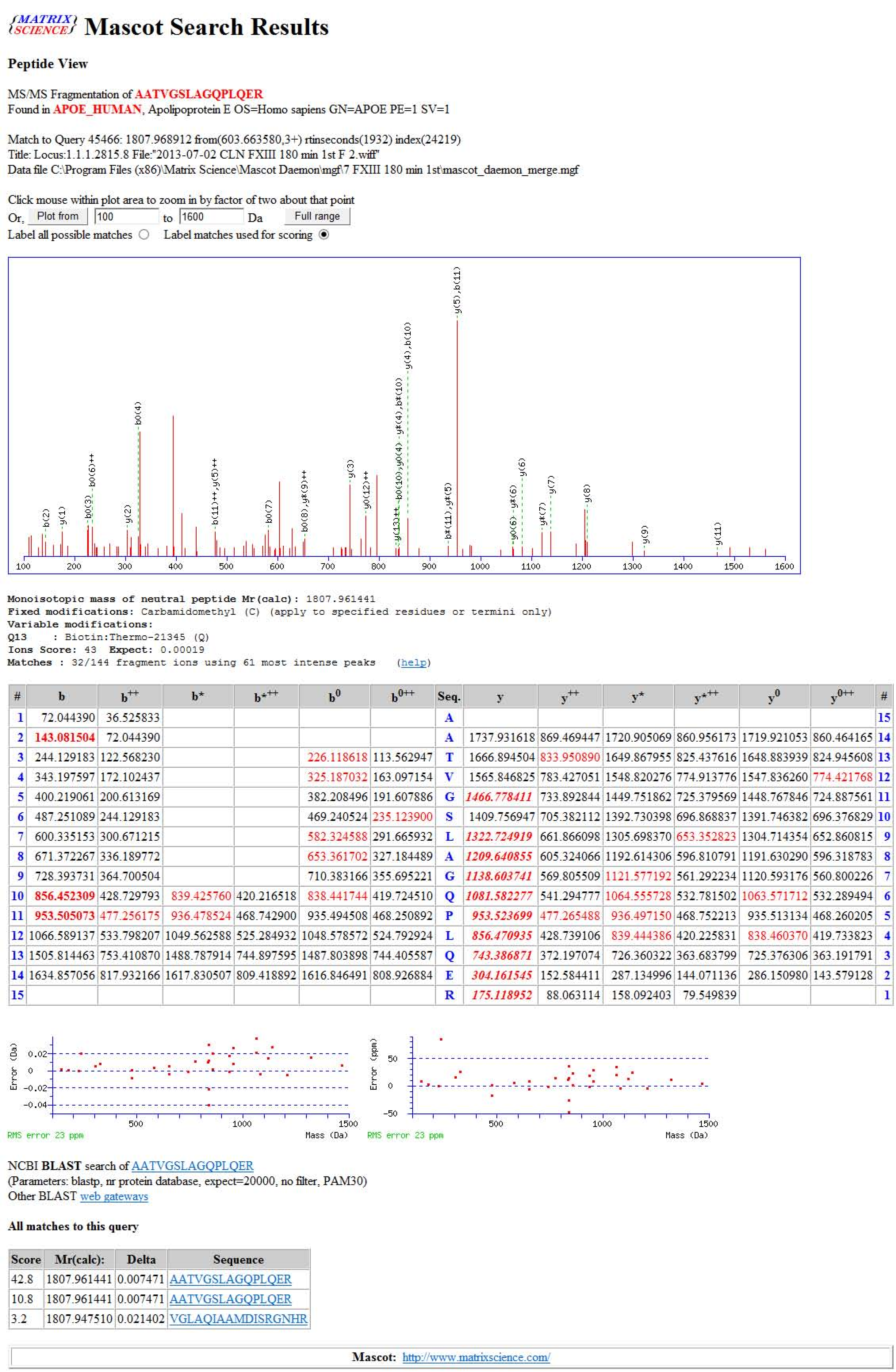


NCBI **BLAST** search of QQTEWQSGQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.1	1557.735809	0.004059	QQTEWQSGQR
28.7	1557.735809	0.004059	QQTEWQSGQR
9.2	1557.747040	-0.007172	AFSHCSSLTKHQR
6.4	1557.742340	-0.002472	TQSFEIPQPDSGPR
6.0	1557.746567	-0.006699	QMSSPQSR
3.7	1557.760925	-0.021057	AKEEAEWQTR
3.7	1557.720551	0.019317	LSQVSPEDDRPCR
3.7	1557.756897	-0.017029	MAASAAAAELQASGGPR
3.7	1557.749496	-0.009628	QAEATRQAAAQEER
3.7	1557.720566	0.019302	QEAATGVDTICTHR

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 45466: 1807.968912 from(603.663580,3+) rtinseconds(1932) index(24219)
Title: Locus:1.1.1.2815.8 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\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): 1807.961441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00019
Matches : 32/144 fragment ions using 61 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
42.8	1807.961441	0.007471	AATVGSLAGQPLQER
10.8	1807.961441	0.007471	AATVGSLAGQPLQER
3.2	1807.947510	0.021402	VGLAQIAAMDISRGNHR

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

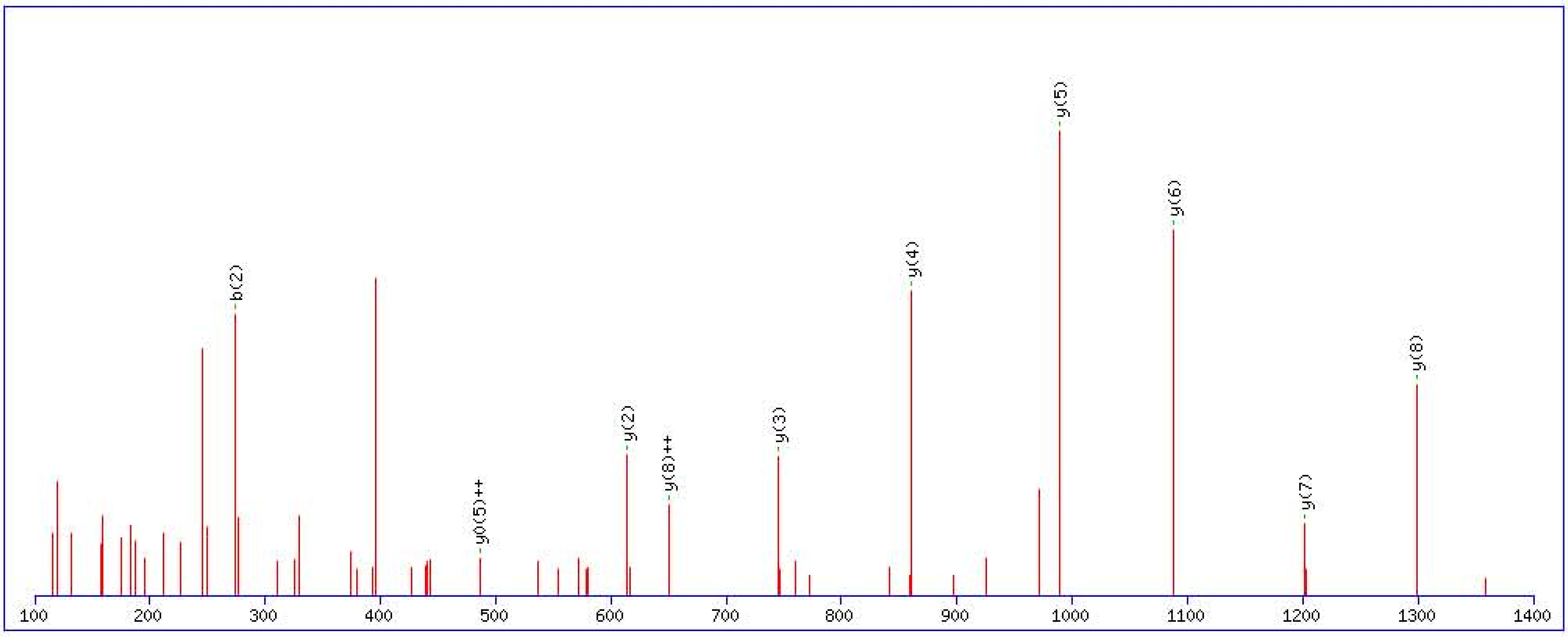
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

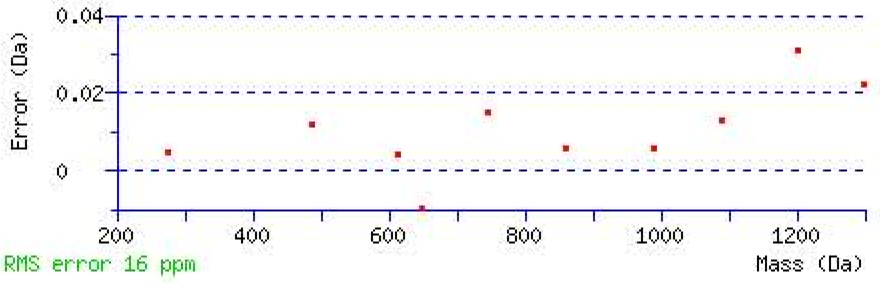
Match to Query 46399: 1846.890732 from(616.637520,3+) rtinseconds(2810) index(30114)
Title: Locus:1.1.1.3120.4 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

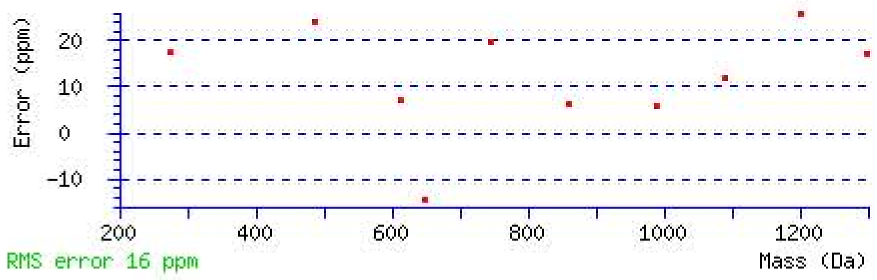
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1846.874603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 1.7e-005
Matches : 10/106 fragment ions using 13 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	**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
53.7	1846.874603	0.016129	SWFEPLVEDMQR
2.8	1846.895721	-0.004989	LQLEETMPSPYGR
1.8	1846.902084	-0.011352	GTSRVDDKPSSPGDSSKK

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

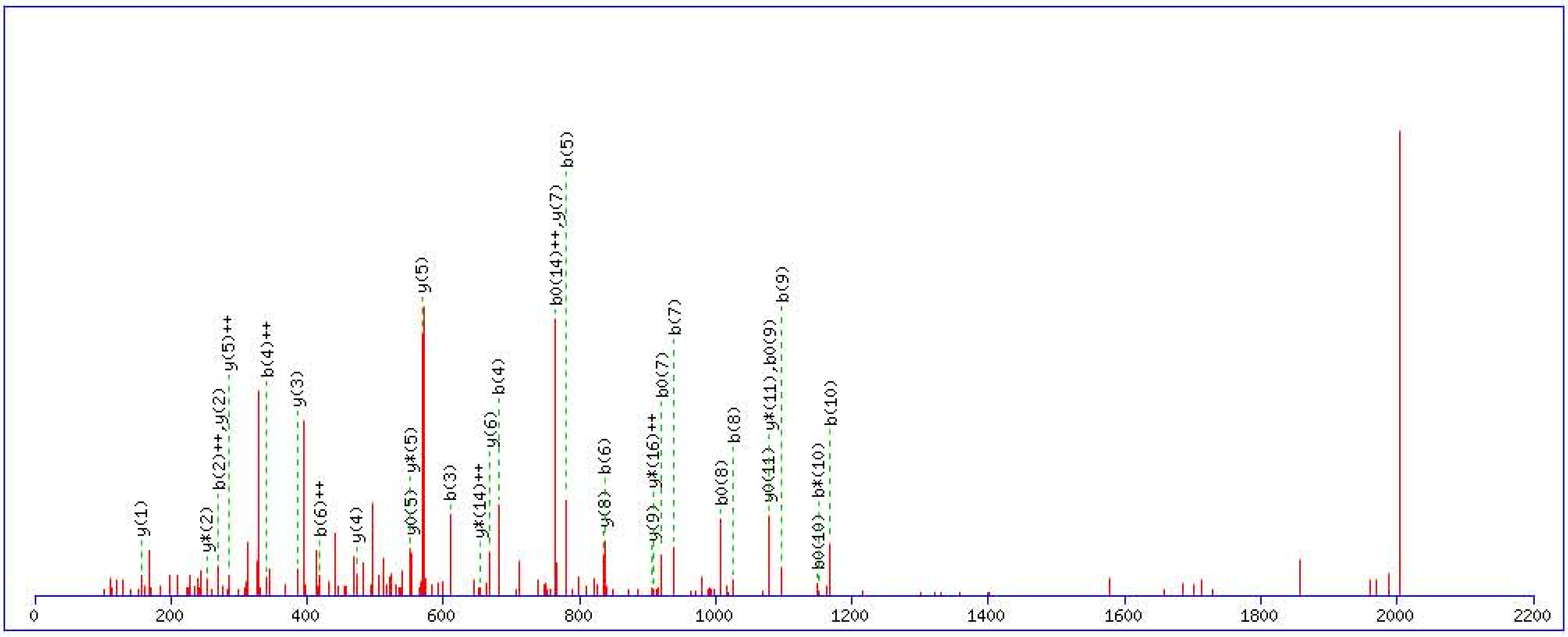
Mascot Search Results

Peptide View

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

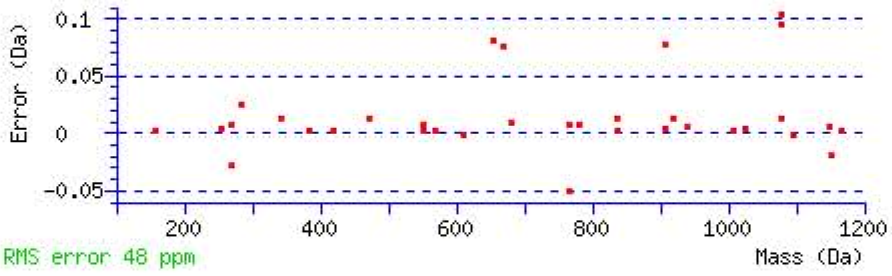
Match to Query 48226: 1930.973082 from(644.664970,3+) rtinseconds(1674) index(39887)
Title: Locus:1.1.1.3032.13 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

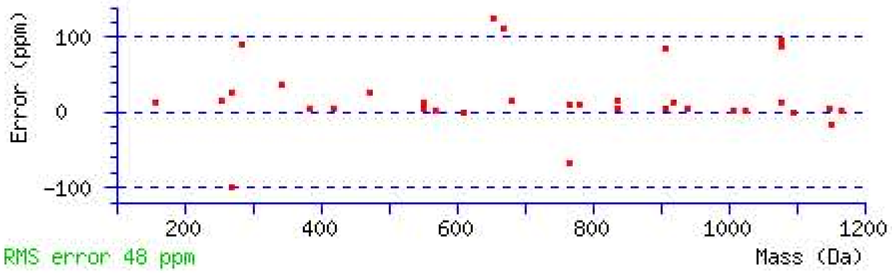
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1930.957108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.004
Matches : 34/172 fragment ions using 89 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	539.301016	**270.154146**	522.274467	261.640872			Q	1832.895960	916.951618	1815.869411	908.438344	1814.885395	907.946336	16
3	***610.338130***	305.672703	593.311581	297.159429			A	1393.670634	697.338955	1376.644085	688.825681	1375.660069	688.333673	15
4	***681.375244***	**341.191260**	664.348695	332.677986			A	1322.633520	661.820398	1305.606971	653.307124	1304.622955	652.815116	14
5	***780.443658***	390.725467	763.417109	382.212193			V	1251.596406	626.301841	1234.569857	617.788567	1233.585841	617.296559	13
6	***837.465122***	**419.236199**	820.438573	410.722925			G	1152.527992	576.767634	1135.501443	568.254360	1134.517427	567.762352	12
7	***938.512801***	469.760039	921.486252	461.246764	920.502236	460.754756	T	1095.506528	548.256902	1078.479979	539.743628	1077.495963	539.251620	11
8	***1025.544829***	513.276053	1008.518280	504.762778	1007.534264	504.270770	S	994.458849	497.733063	977.432300	489.219788	976.448284	488.727780	10
9	***1096.581943***	548.794610	1079.555394	540.281335	1078.571378	539.789327	A	***907.426821***	454.217049	890.400272	445.703774	889.416256	445.211766	9
10	***1167.619057***	584.313167	1150.592508	575.799892	1149.608492	575.307884	A	***836.389707***	418.698492	819.363158	410.185217	818.379142	409.693209	8
11	1264.671821	632.839549	1247.645272	624.326274	1246.661256	623.834266	P	***765.352593***	383.179935	748.326044	374.666660	747.342028	374.174652	7
12	1363.740235	682.373756	1346.713686	673.860481	1345.729670	673.368473	V	***668.299829***	334.653553	651.273280	326.140278	650.289264	325.648270	6
13	1460.792999	730.900138	1443.766450	722.386863	1442.782434	721.894855	P	***569.231415***	285.119346	552.204866	276.606071	551.220850	276.114063	5
14	1547.825027	774.416152	1530.798478	765.902877	1529.814462	765.410869	S	***472.178651***	236.592964	455.152102	228.079689	454.168086	227.587681	4
15	1662.851970	831.929623	1645.825421	823.416349	1644.841405	822.924341	D	***385.146623***	193.076949	368.120074	184.563675	367.136058	184.071667	3
16	1776.894897	888.951087	1759.868348	880.437812	1758.884332	879.945804	N	***270.119680***	135.563478	253.093131	127.050203			2
17							H	***156.076753***	78.542014					1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.5	1930.957108	0.015974	VQAAVGTSAAPVPSDNH

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

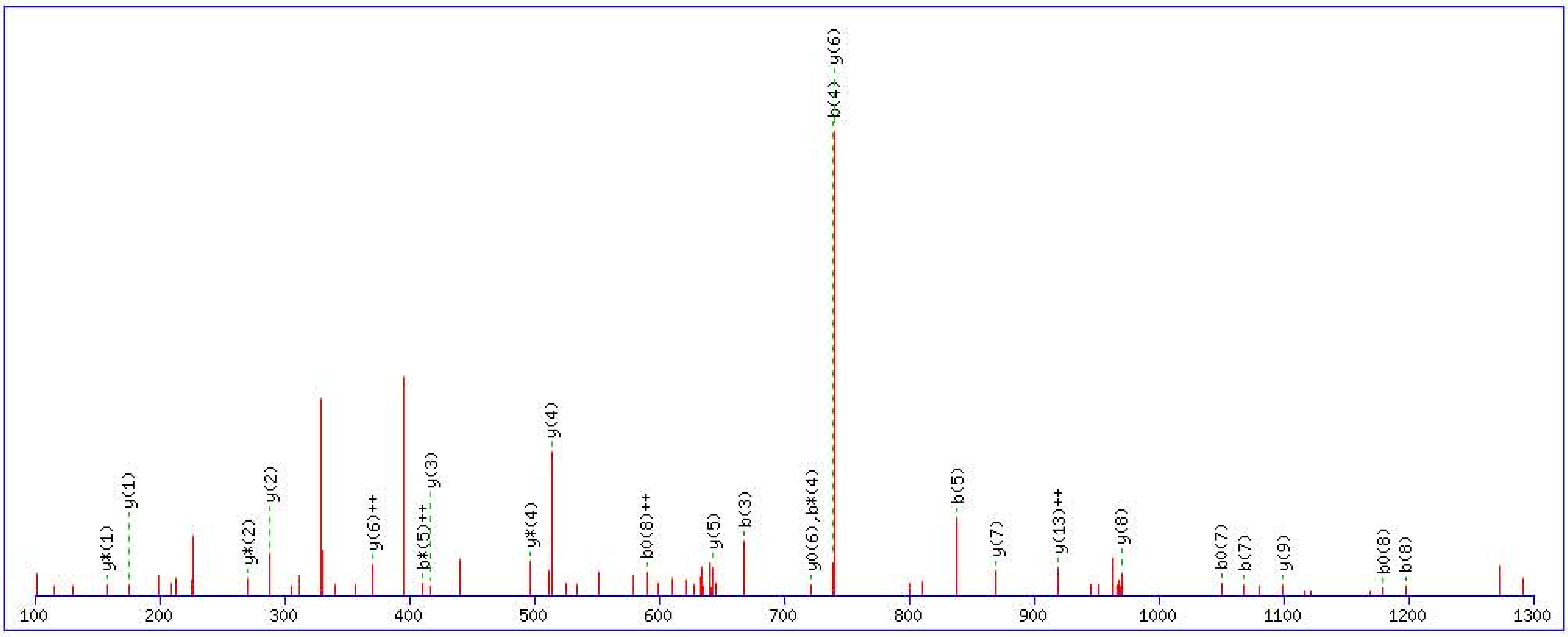
Mascot Search Results

Peptide View

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

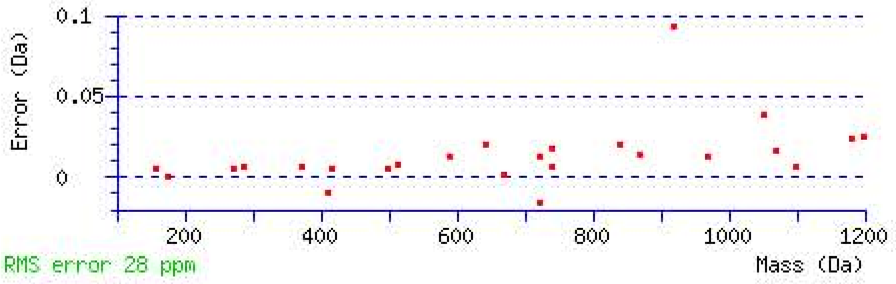
Match to Query 48393: 1935.986442 from(646.336090,3+) rtinseconds(1866) index(59736)
Title: Locus:1.1.1.3073.15 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

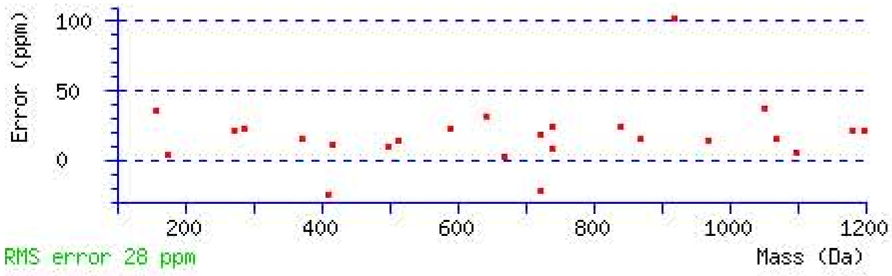
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1935.961151
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 6.3e-005
Matches : 25/146 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	100.075690	50.541483					V							14
2	229.118283	115.062780			211.107718	106.057497	E	1837.900042	919.453659	1820.873493	910.940385	1819.889477	910.448376	13
3	**668.343609**	334.675443	651.317060	326.162168	650.333044	325.670160	Q	1708.857449	854.932363	1691.830900	846.419088	1690.846884	845.927080	12
4	**739.380723**	370.194000	722.354174	361.680725	721.370158	361.188717	A	1269.632123	635.319700	1252.605574	626.806425	1251.621558	626.314417	11
5	**838.449137**	419.728207	821.422588	411.214932	820.438572	410.722924	V	1198.595009	599.801143	1181.568460	591.287868	1180.584444	590.795860	10
6	967.491730	484.249503	950.465181	475.736228	949.481165	475.244220	E	***1099.526595***	550.266936	1082.500046	541.753661	1081.516030	541.261653	9
7	**1068.539409**	534.773343	1051.512860	526.260068	1050.528844	525.768060	T	***970.484002***	485.745639	953.457453	477.232365	952.473437	476.740357	8
8	**1197.582002**	599.294639	1180.555453	590.781365	1179.571437	590.289356	E	***869.436323***	435.221800	852.409774	426.708525	851.425758	426.216517	7
9	1294.634766	647.821021	1277.608217	639.307747	1276.624201	638.815738	P	***740.393730***	370.700503	723.367181	362.187229	722.383165	361.695221	6
10	1423.677359	712.342318	1406.650810	703.829043	1405.666794	703.337035	E	***643.340966***	322.174121	626.314417	313.660847	625.330401	313.168839	5
11	1520.730123	760.868700	1503.703574	752.355425	1502.719558	751.863417	P	***514.298373***	257.652825	497.271824	249.139550	496.287808	248.647542	4
12	1649.772716	825.389996	1632.746167	816.876722	1631.762151	816.384714	E	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
13	1762.856780	881.932028	1745.830231	873.418754	1744.846215	872.926746	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 VEQAVETEPEPELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.7	1935.961151	0.025291	VEQAVETEPEPELR
1.9	1935.991028	-0.004586	TDLKTFMGKAQNQK
1.9	1935.991028	-0.004586	TDLKTFMGKAQNQK

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

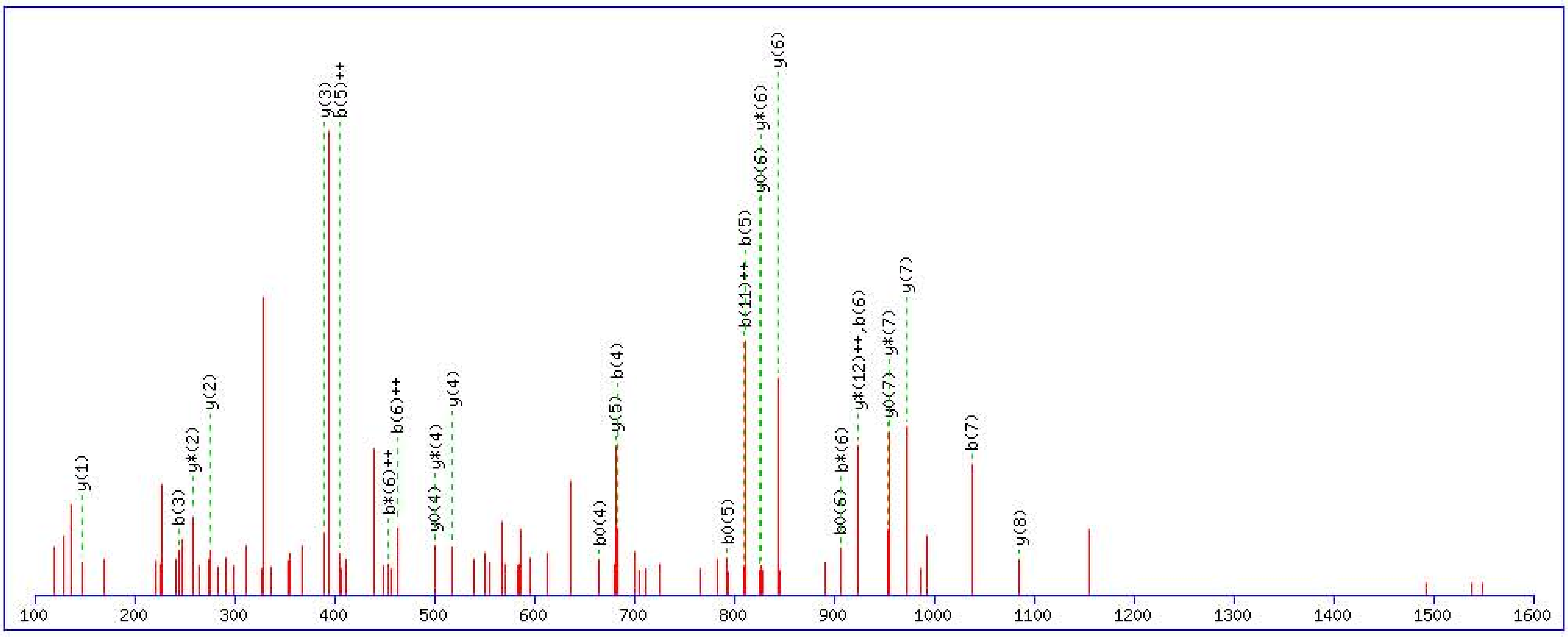
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

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

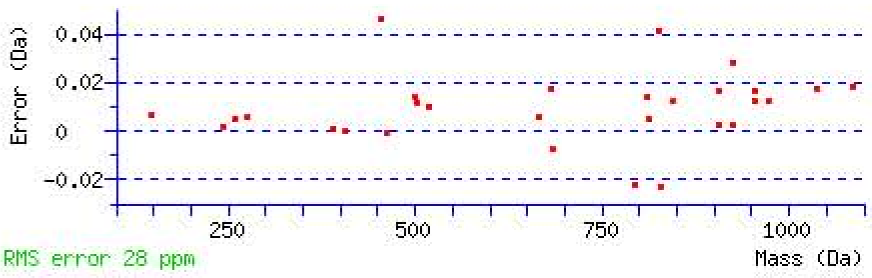
Match to Query 51006: 2008.037352 from(670.353060,3+) rtinseconds(2483) index(45458)
Title: Locus:1.1.1.3313.17 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

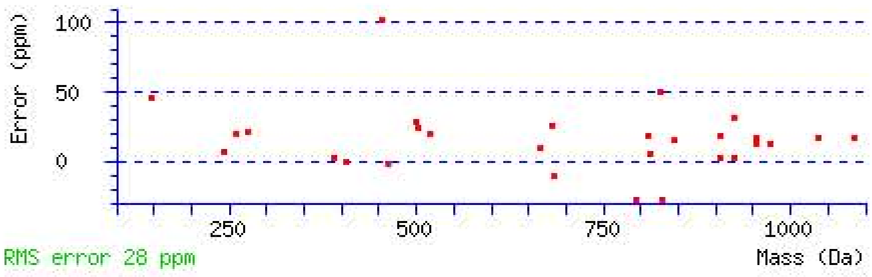
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2008.008789
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.00066
Matches : 29/146 fragment ions using 59 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							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
34.6	2008.008789	0.028563	SGVQQLIQYYQDQK
30.3	2008.008789	0.028563	SGVQQLIQYYQDQK
16.1	2008.008789	0.028563	SGVQQLIQYYQDQK
12.6	2008.008789	0.028563	SGVQQLIQYYQDQK
12.5	2008.008789	0.028563	SGVQQLIQYYQDQK
0.6	2008.063568	-0.026216	QQLEAQRAEAERLR

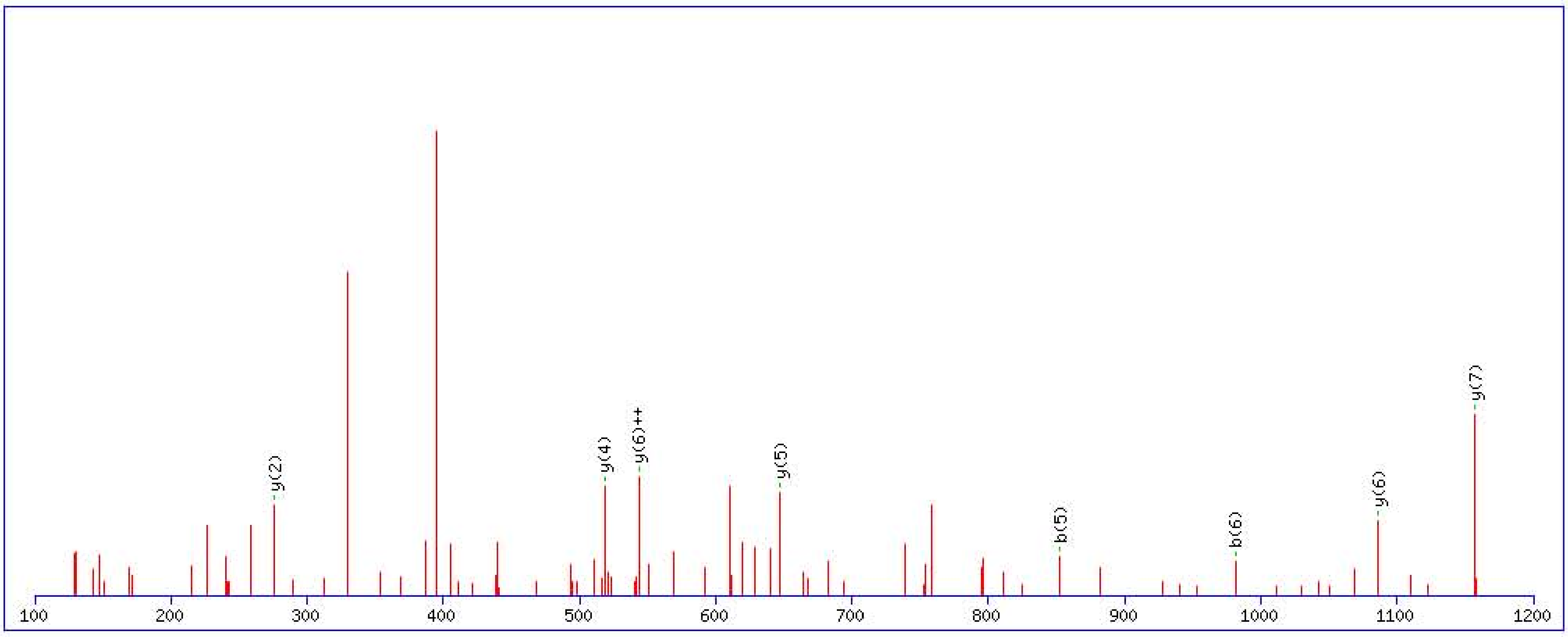
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

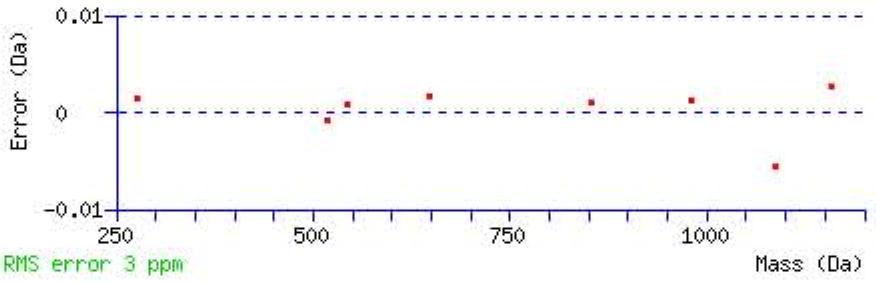
Match to Query 25458: 1255.648568 from(628.831560,2+) rtinseconds(1532) index(21246)
Title: Locus:1.1.1.2676.15 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

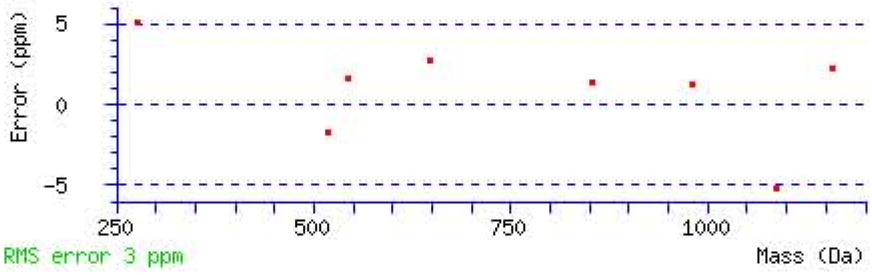
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1255.648193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.012
Matches : 8/72 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	100.075690	50.541483					V							8
2	171.112804	86.060040					A	*1157.587087*	579.297182	1140.560538	570.783907	1139.576522	570.291899	7
3	610.338130	305.672703	593.311581	297.159429			Q	*1086.549973*	543.778625	1069.523424	535.265350	1068.539408	534.773342	6
4	739.380723	370.194000	722.354174	361.680725	721.370158	361.188717	E	*647.324647*	324.165962	630.298098	315.652687	629.314082	315.160679	5
5	**852.464787**	426.736032	835.438238	418.222757	834.454222	417.730749	L	*518.282054*	259.644665	501.255505	251.131391	500.271489	250.639383	4
6	**981.507380**	491.257328	964.480831	482.744054	963.496815	482.252046	E	405.197990	203.102633	388.171441	194.589359	387.187425	194.097351	3
7	1110.549973	555.778625	1093.523424	547.265350	1092.539408	546.773342	E	*276.155397*	138.581336	259.128848	130.068062	258.144832	129.576054	2
8							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VAQELEEK
(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	1255.648193	0.000375	VAQELEEK
13.7	1255.659424	-0.010856	QAEKNVEK
8.2	1255.659439	-0.010871	GLQGEKGEK
7.9	1255.656067	-0.007499	ALPIQSFSHEK
7.7	1255.659439	-0.010871	STGAQPKEK
7.2	1255.645508	0.003060	TRMIEANIHR
7.0	1255.640793	0.007775	DTHKKLEEEK
6.0	1255.648193	0.000375	EQVEIAEK
5.7	1255.659439	-0.010871	LLIENGVSMHK
5.6	1255.648193	0.000375	QALEDLEK

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

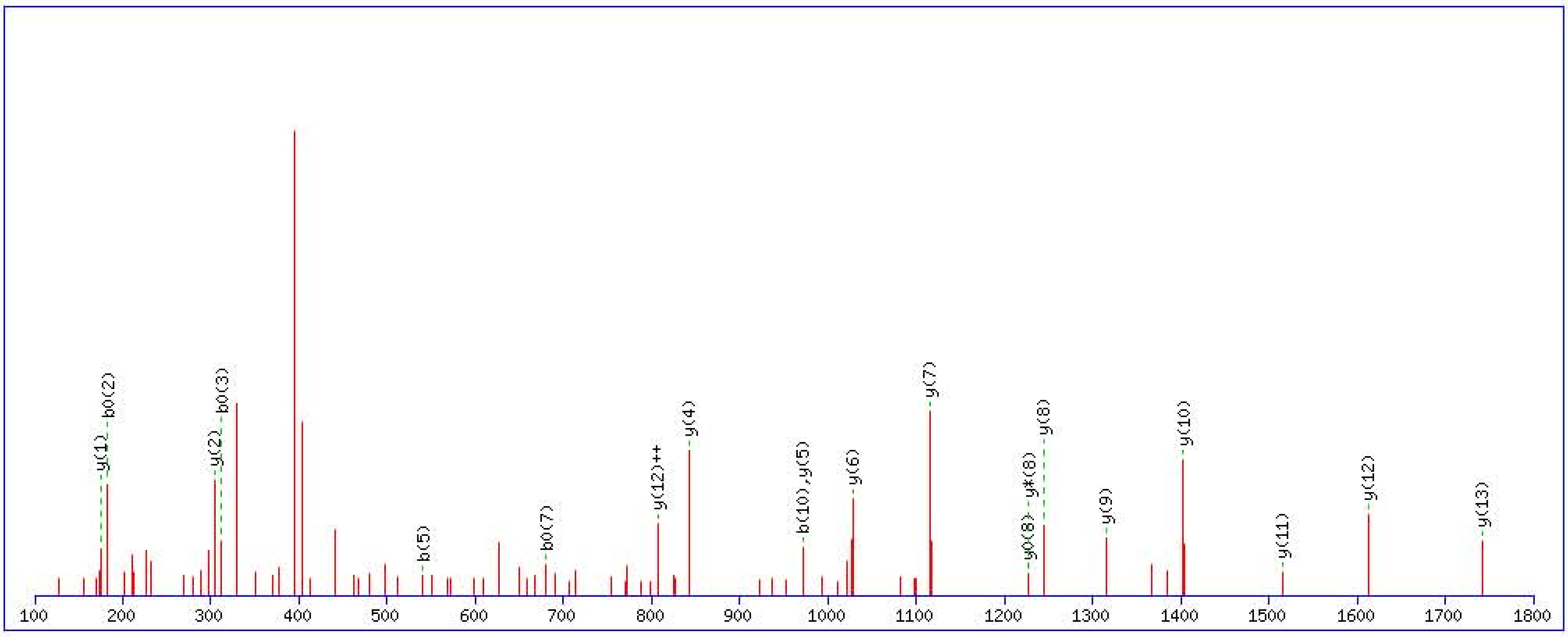
Mascot Search Results

Peptide View

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

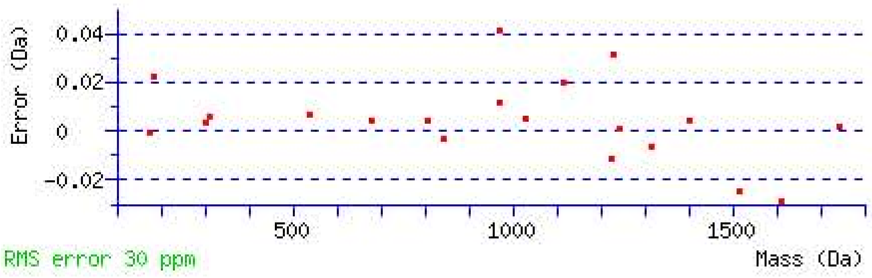
Match to Query 48495: 1940.961552 from(647.994460,3+) rtinseconds(1695) index(22419)
Title: Locus:1.1.1.2733.7 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

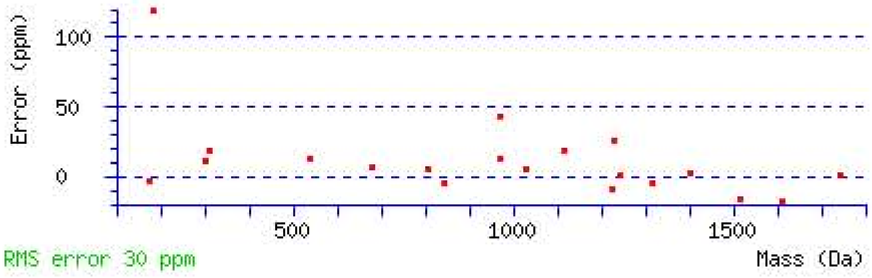
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 90 **Expect:** 2.8e-008
Matches : 20/142 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	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
89.6	1940.951324	0.010228	VTEPISAESGEQVER

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

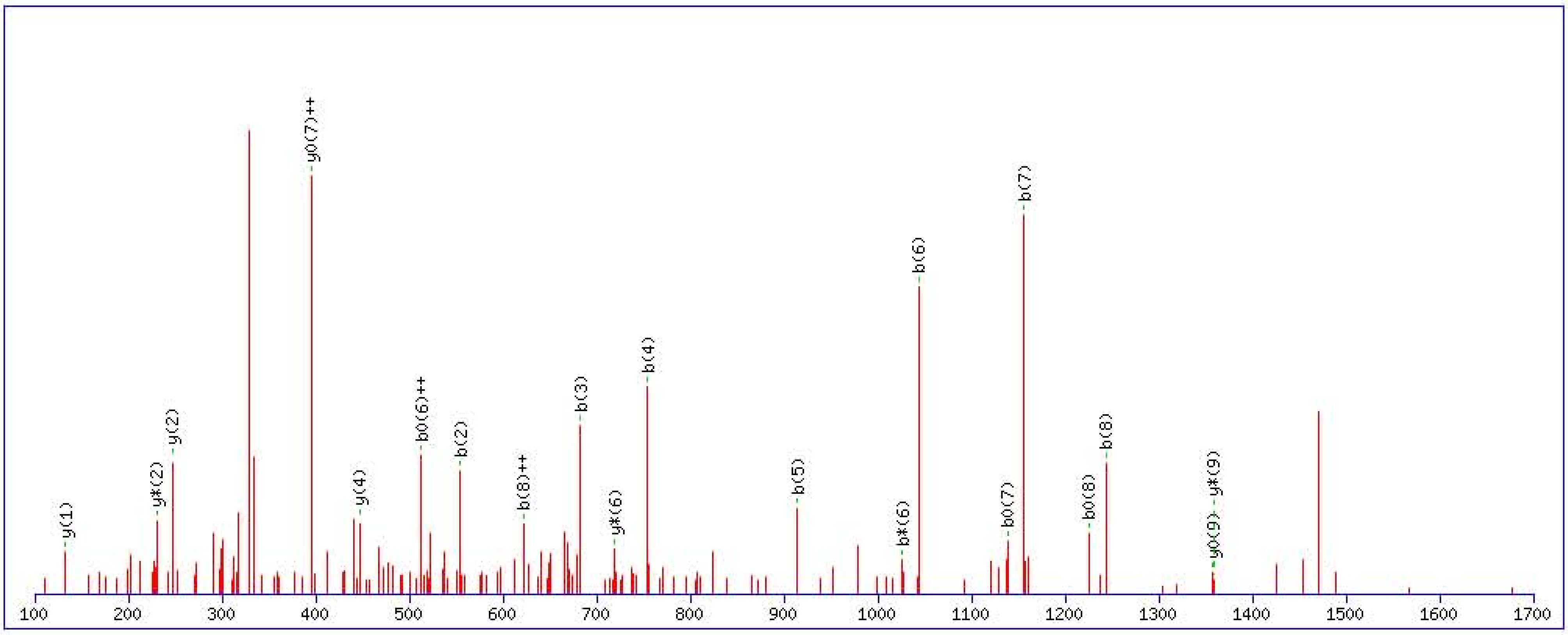
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

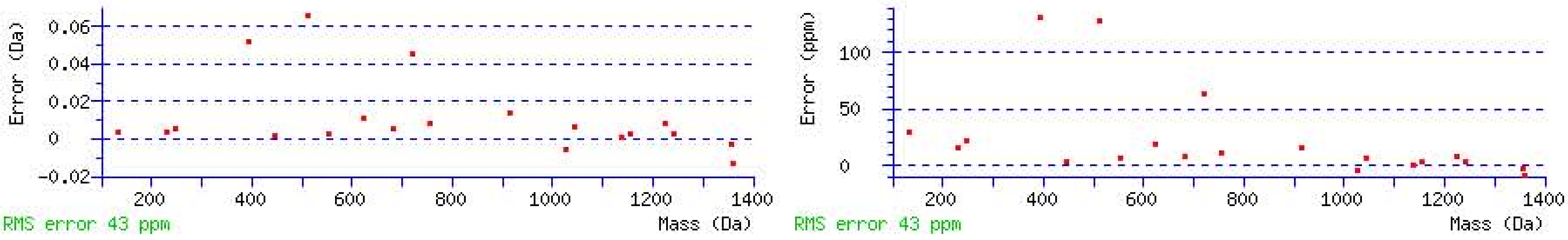
Match to Query 34553: 1488.640068 from(745.327310,2+) rtinseconds(1644) index(21995)
Title: Locus:1.1.1.2715.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1488.633682
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 61 **Expect:** 3.2e-006
Matches : 21/100 fragment ions using 28 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	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
61.1	1488.633682	0.006386	NQEACELSNN

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

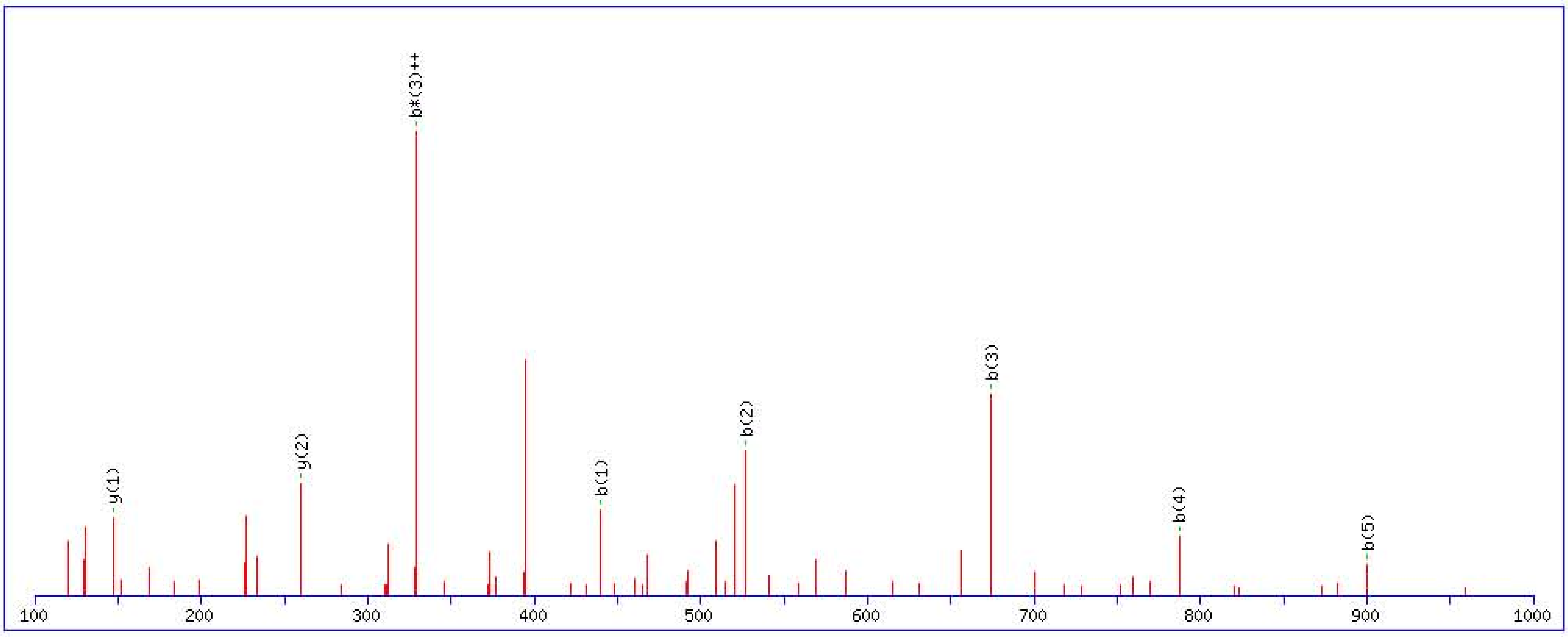
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSFLLK**
Found in **AGAP2_HUMAN**, Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=AGAP2 PE=1 SV=2

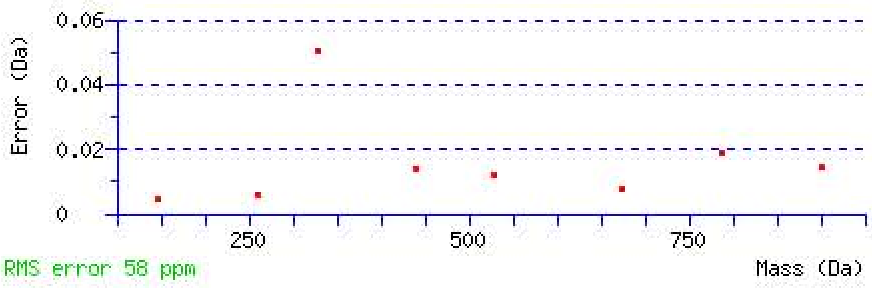
Match to Query 17419: 1045.613508 from(523.814030,2+) rtinseconds(2051) index(61072)
Title: Locus:1.1.1.3137.4 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

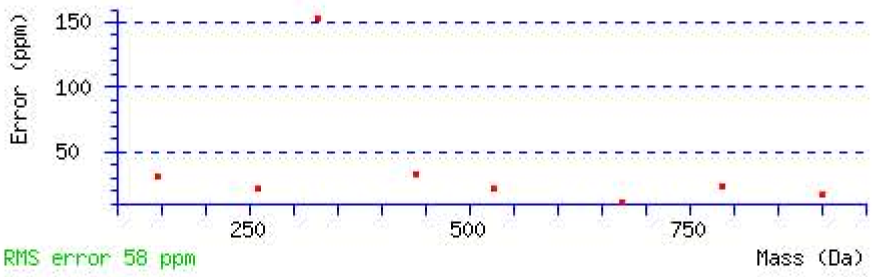
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1045.599411
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00032
Matches : 8/50 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	***440.232602***	220.619939	423.206053	212.106664			Q							6
2	***527.264630***	264.135953	510.238081	255.622679	509.254065	255.130671	S	607.381374	304.194325	590.354825	295.681051	589.370809	295.189043	5
3	***674.333044***	337.670160	657.306495	329.156885	656.322479	328.664877	F	520.349346	260.678311	503.322797	252.165037			4
4	***787.417108***	394.212192	770.390559	385.698917	769.406543	385.206909	L	373.280932	187.144104	356.254383	178.630830			3
5	***900.501172***	450.754224	883.474623	442.240950	882.490607	441.748942	L	**260.196868**	130.602072	243.170319	122.088798			2
6							K	**147.112804**	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	1045.599411	0.014097	QSFLLK
35.6	1045.599411	0.014097	SQFLIK
19.7	1045.601883	0.011625	EESISKLIK
19.7	1045.613113	0.000395	ESKKSNLLK
19.5	1045.599426	0.014082	VFLCPGLLK
19.3	1045.599411	0.014097	SQLFLK
16.6	1045.628387	-0.014879	FIRQEIIK
16.6	1045.620514	-0.007006	KETMALILK
16.6	1045.599411	0.014097	QVFAPMLLK
16.6	1045.599396	0.014112	YQALLK

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

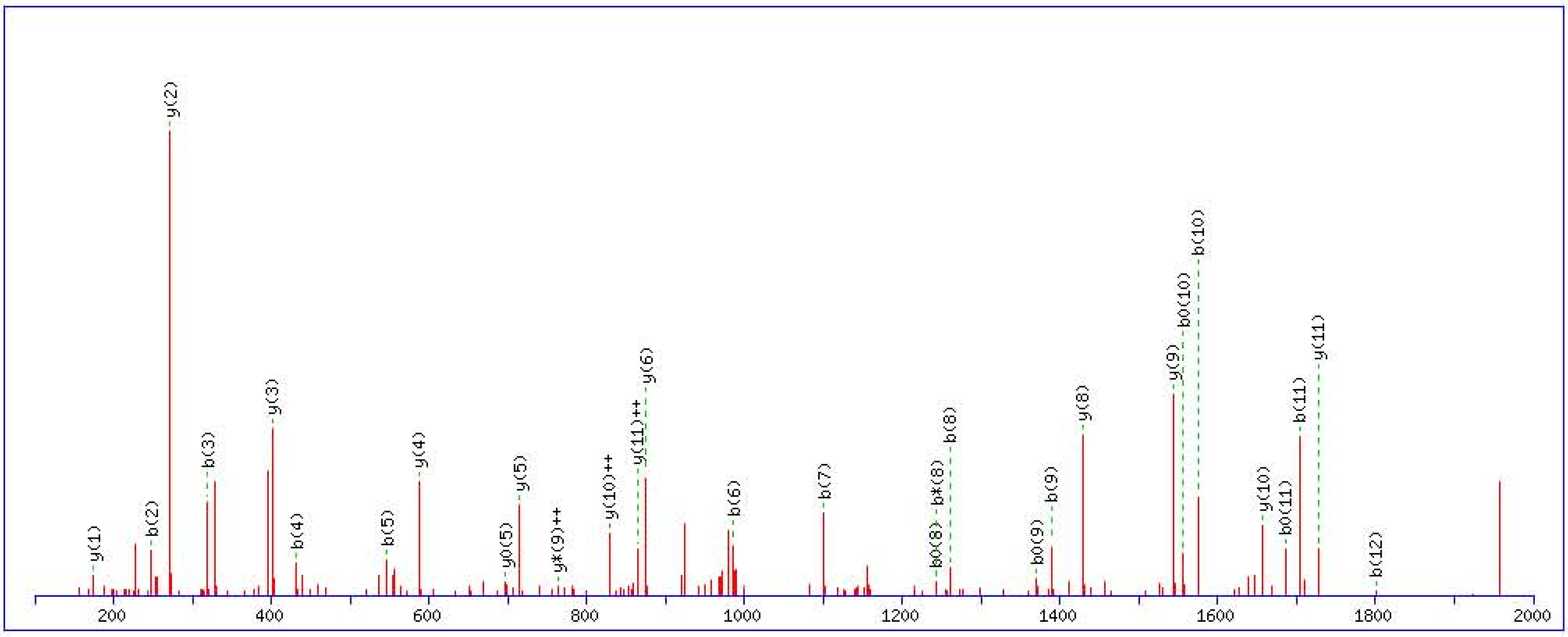
Mascot Search Results

Peptide View

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

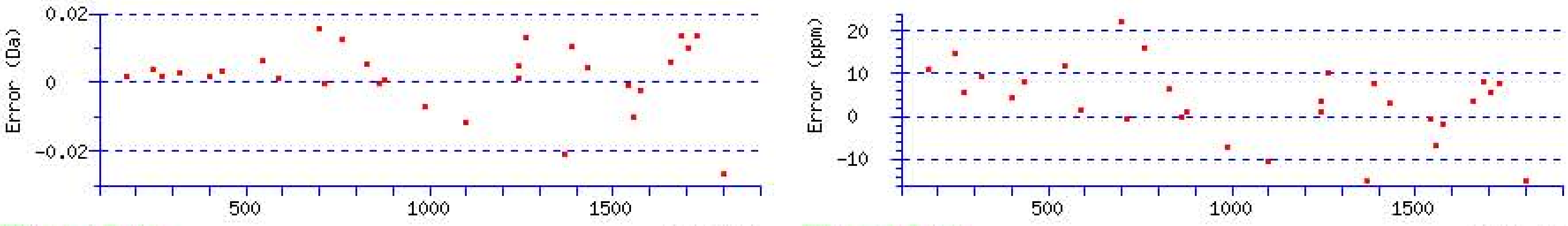
Match to Query 49336: 1973.875668 from(987.945110,2+) rtinseconds(1957) index(24401)
Title: Locus:1.1.1.2823.22 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1973.854614
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 74  Expect: 2.8e-007
Matches : 30/130 fragment ions using 51 most intense peaks   (help)
```

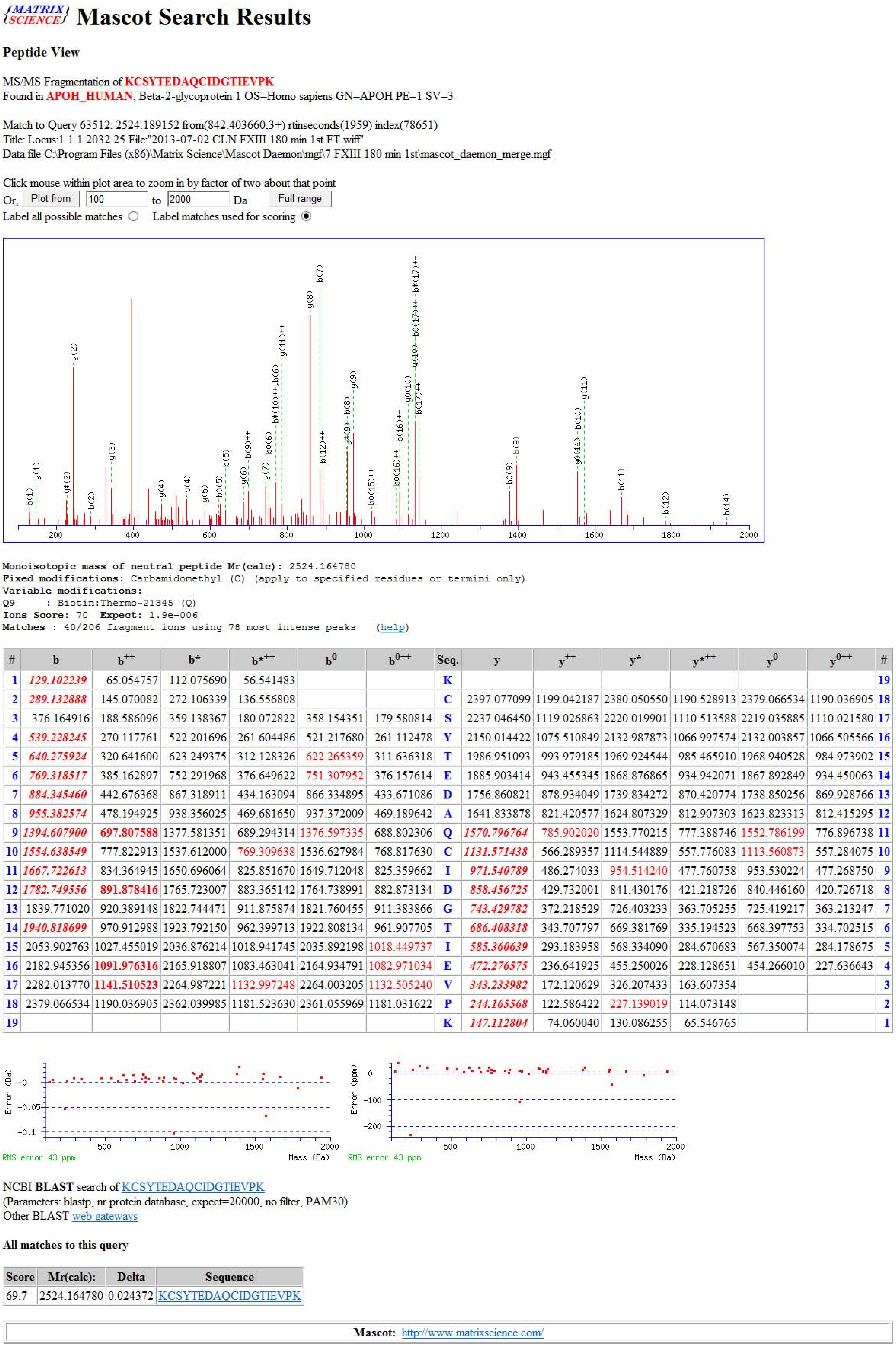
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							13
2	***248.069953***	124.538614			230.059388	115.533332	C	1887.829872	944.418574	1870.803323	935.905300	1869.819307	935.413292	12
3	***319.107067***	160.057171			301.096502	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
73.5	1973.854614	0.021054	SCALDQNCQWEPR
36.1	1973.854614	0.021054	SCALDQNCQWEPR
14.4	1973.853729	0.021939	DSPETGEEMGRAEGAWPR



{MATRIX SCIENCE} 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 63512: 2524.189152 from(842.403660,3+) rtinseconds(1959) index(78651)
Title: Locus:1.1.1.2032.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\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): 2524.164780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 70  Expect: 1.9e-006
Matches : 40/206 fragment ions using 78 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
69.7	2524.164780	0.024372	KCSYTEDAQCIDGTIEVPK

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

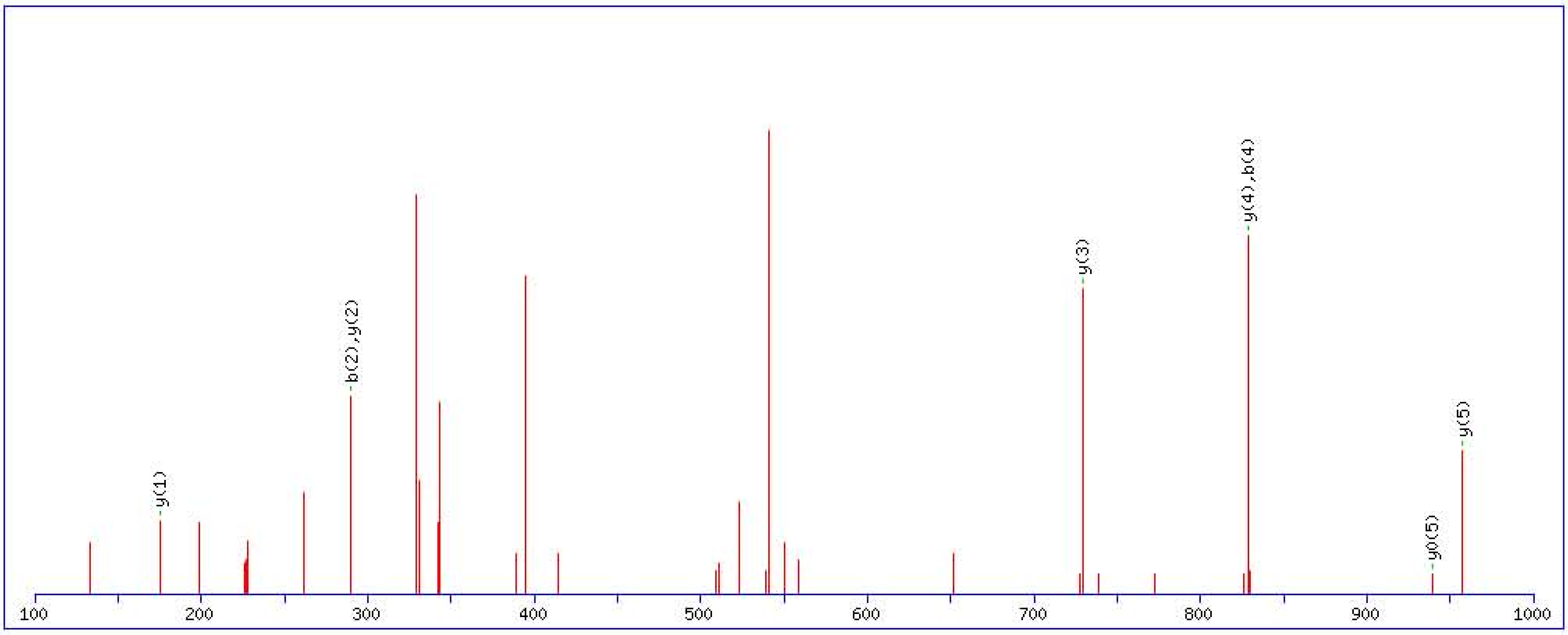
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

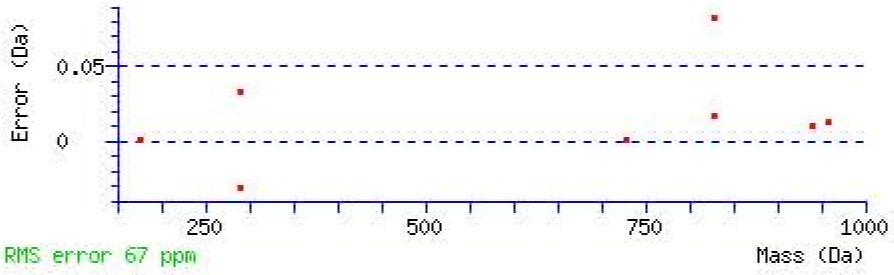
Match to Query 19907: 1116.514948 from(559.264750,2+) rtinseconds(1316) index(55989)
Title: Locus:1.1.1.2881.20 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

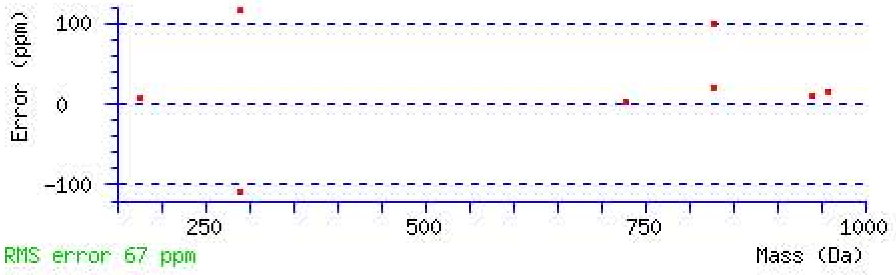
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1116.505600
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.013
Matches : 8/50 fragment ions using 16 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	161.037925	81.022600					C							6
2	**290.080518**	145.543897			272.069953	136.538615	E	***957.482228***	479.244752	940.455679	470.731478	939.471663	470.239470	5
3	389.148932	195.078104			371.138367	186.072822	V	***828.439635***	414.723456	811.413086	406.210181	810.429070	405.718173	4
4	**828.374258**	414.690767	811.347709	406.177493	810.363693	405.685485	Q	***729.371221***	365.189249	712.344672	356.675974	711.360656	356.183966	3
5	943.401201	472.204239	926.374652	463.690964	925.390636	463.198956	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
6							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of CEVQDR
(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	1116.505600	0.009348	CEVQDR
6.9	1116.527206	-0.012258	TSTSGTHRDR
5.5	1116.505600	0.009348	DICQDR
5.5	1116.502228	0.012720	SWDQDR
0.7	1116.504700	0.010248	ELQAEQEDR
0.3	1116.523346	-0.008398	ETQSADR
0.3	1116.524689	-0.009741	QHRQFMDR
0.2	1116.509644	0.005304	CFSVLGFCK

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

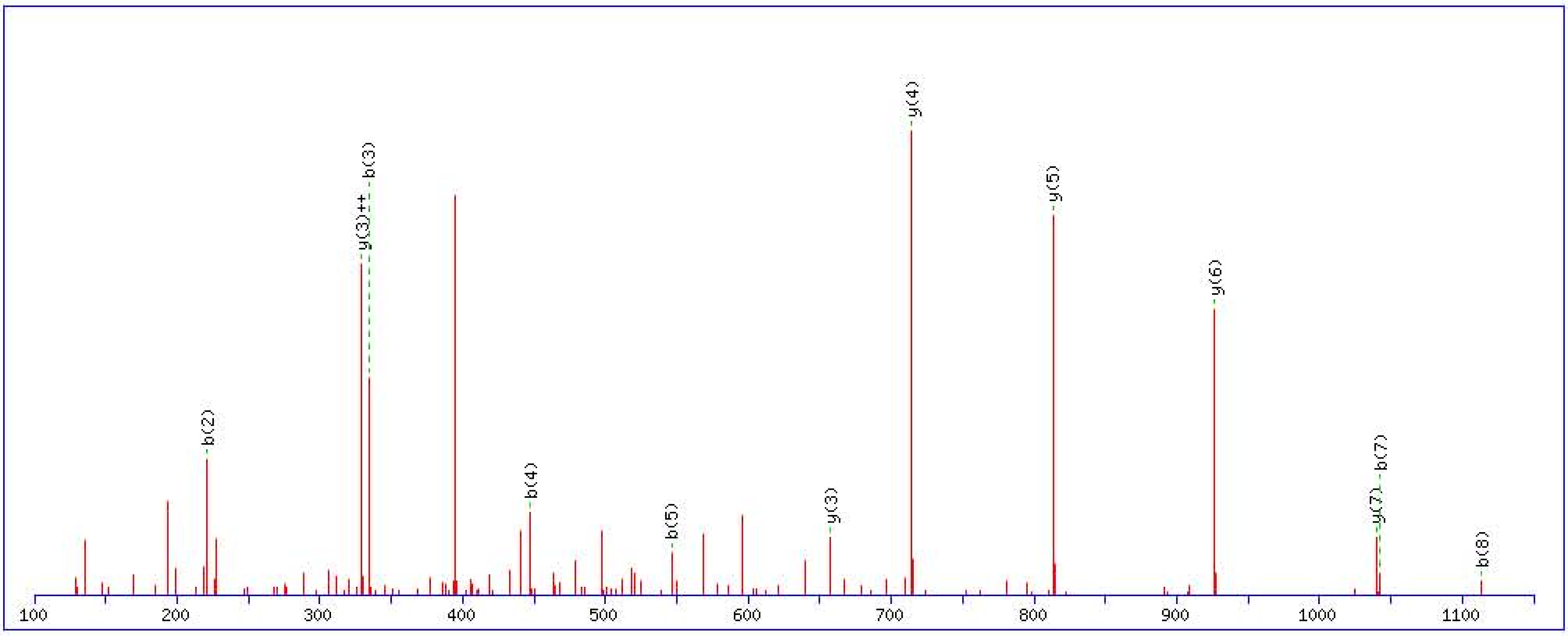
{MATRIX SCIENCE} Mascot Search Results

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

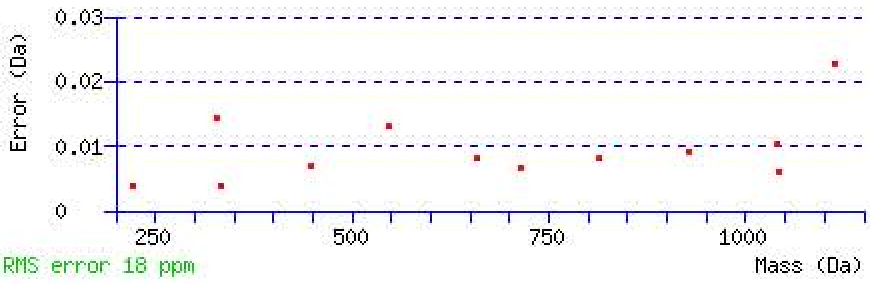
Match to Query 25502: 1258.723368 from(630.368960,2+) rtinseconds(2041) index(42506)
Title: Locus:1.1.1.3160.7 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

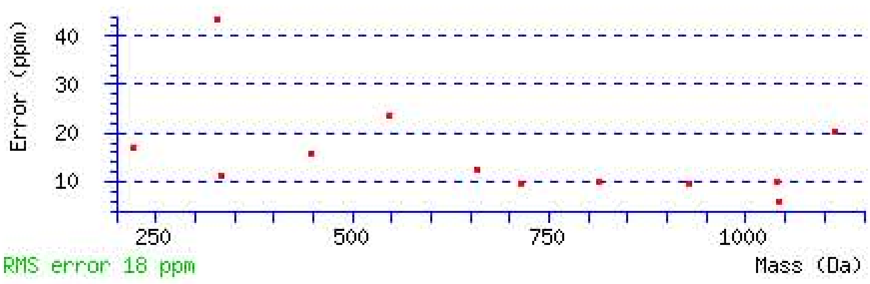
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1258.710754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.021
Matches : 12/52 fragment ions using 28 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
28.4	1258.710754	0.012614	GYILVGQAK
10.6	1258.721970	0.001398	GYILQAKR
8.3	1258.717941	0.005427	RILAKVQEMR
2.1	1258.739731	-0.016363	ALDFRTPLKAK

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

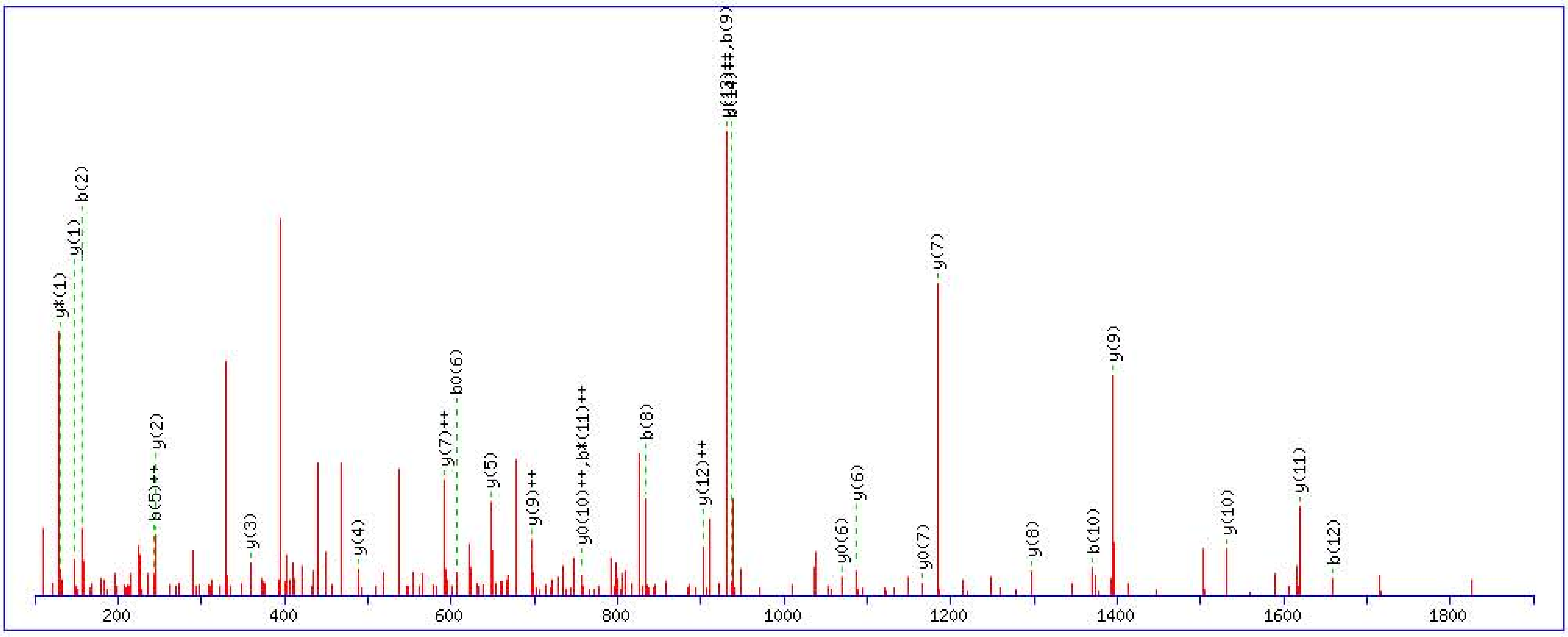
Mascot Search Results

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

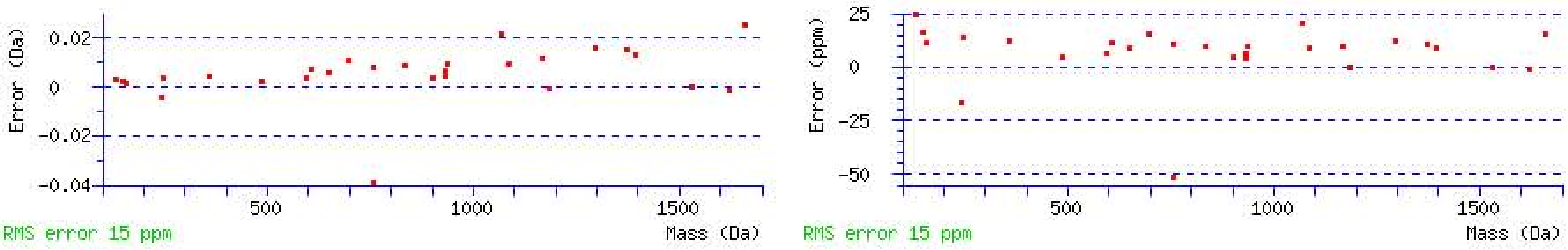
Match to Query 27978: 2017.045272 from(673.355700,3+) rtinseconds(2045) index(42527)
Title: Locus:1.1.1.3161.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 2017.027771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0017
Matches : 28/136 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							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



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
29.9	2017.027771	0.017501	GVGWSHPLPQCEIVK

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

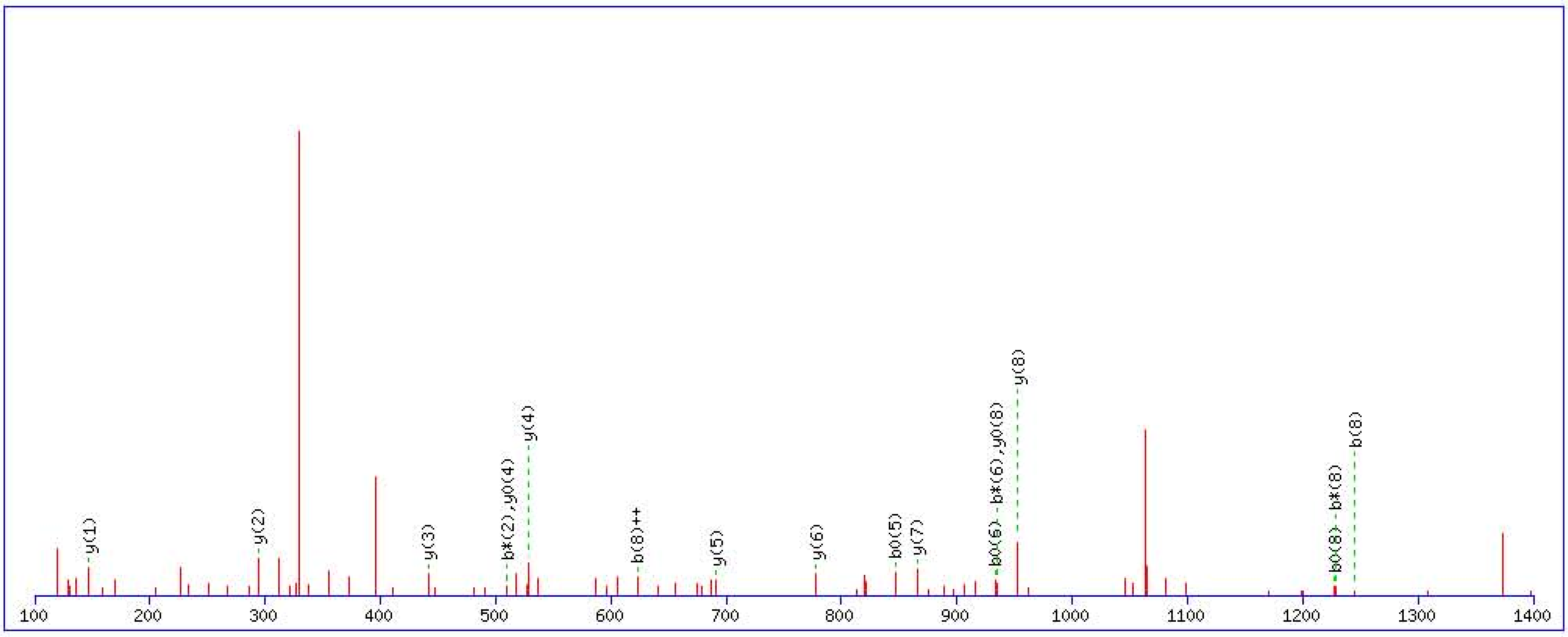
{MATRIX SCIENCE} Mascot Search Results

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

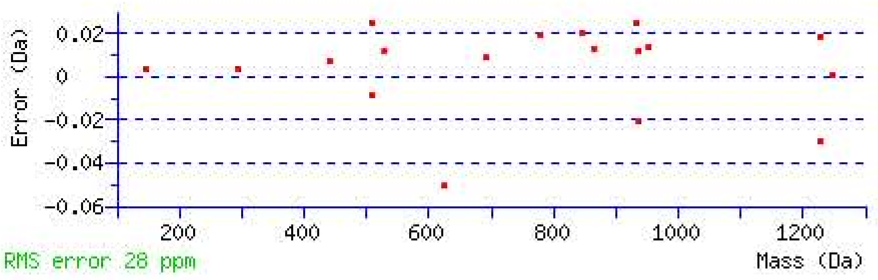
Match to Query 30342: 1390.679148 from(696.346850,2+) rtinseconds(2106) index(42938)
Title: Locus:1.1.1.3182.17 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

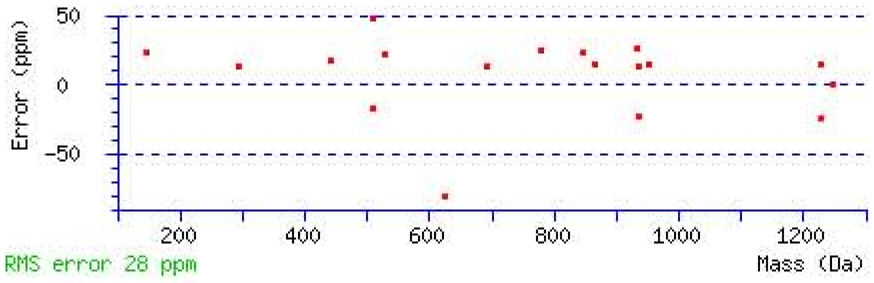
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1390.659119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 31 **Expect:** 0.0089
Matches : 18/88 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	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
31.2	1390.659119	0.020029	QSSSYSFFK
8.7	1390.691467	-0.012319	VTKEMNEFIHK
5.8	1390.676208	0.002940	AEKSSSTDQK
4.7	1390.676208	0.002940	LTENNSQPLMTK
2.4	1390.670135	0.009013	YRNQESKSSHR
2.3	1390.659088	0.020060	YFSKKEWEMK
1.6	1390.688766	-0.009618	YMHRNREITR
1.4	1390.673706	0.005442	TLNADLMMFAHK
0.5	1390.658447	0.020701	AAVKCCPEESLK
0.5	1390.664963	0.014185	EEGLEEGLLQMK

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

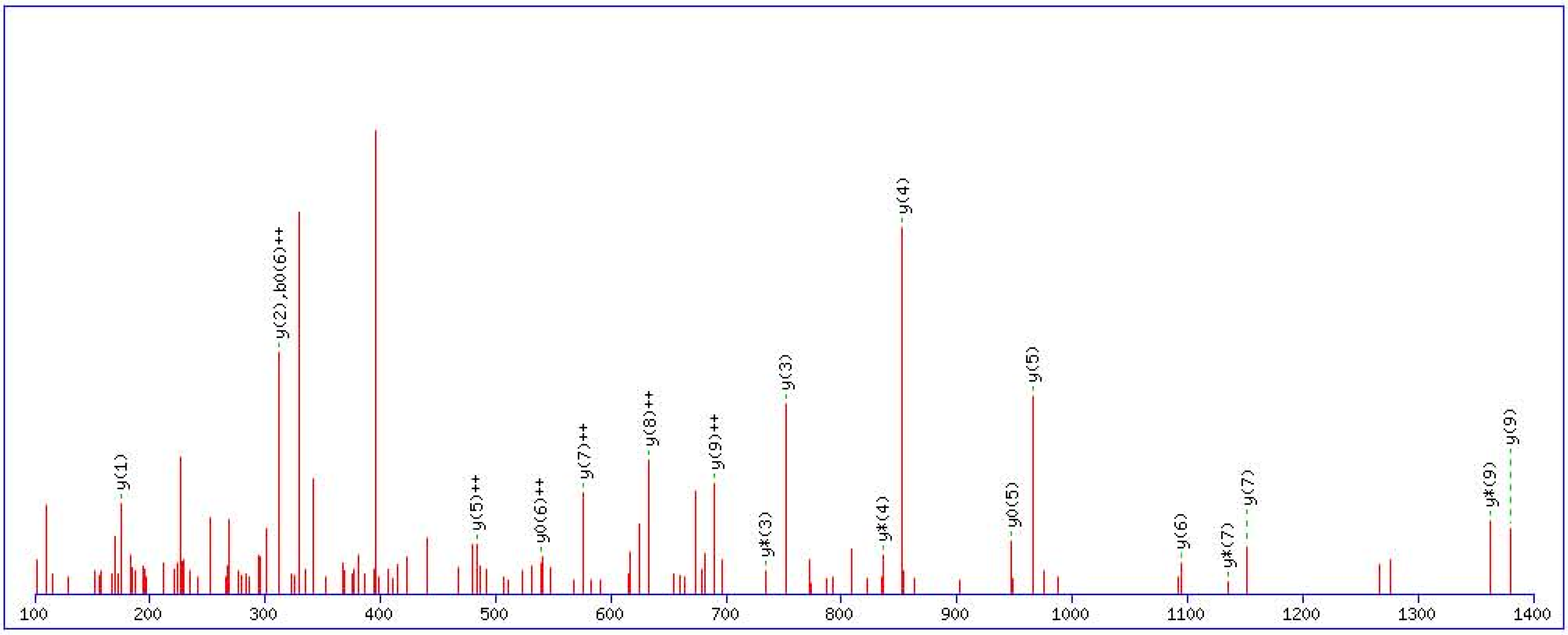
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

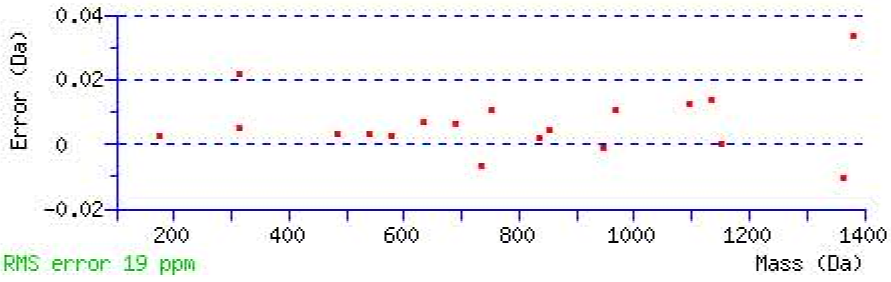
Match to Query 34685: 1491.764922 from(498.262250,3+) rtinseconds(1410) index(38060)
Title: Locus:1.1.1.2940.8 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

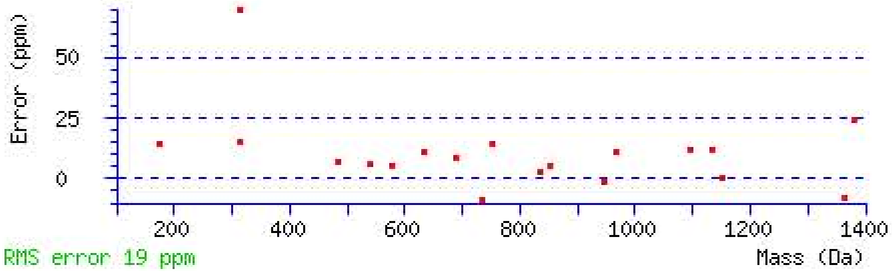


```
Monoisotopic mass of neutral peptide Mr(calc): 1491.761612
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00011
Matches : 19/92 fragment ions using 36 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							10
2	228.134267	114.570771	211.107718	106.057497			N	***1379.684844***	690.346060	1362.658295	681.832786	1361.674279	681.340778	9
3	342.177194	171.592235	325.150645	163.078960			N	1265.641917	633.324596	1248.615368	624.811322	1247.631352	624.319314	8
4	399.198658	200.102967	382.172109	191.589692			G	***1151.598990***	576.303133	1134.572441	567.789859	1133.588425	567.297850	7
5	528.241251	264.624264	511.214702	256.110989	510.230686	255.618981	E	***1094.577526***	547.792401	1077.550977	539.279127	1076.566961	538.787119	6
6	641.325315	321.166296	624.298766	312.653021	623.314750	312.161013	I	***965.534933***	483.271105	948.508384	474.757830	947.524368	474.265822	5
7	742.372994	371.690135	725.346445	363.176861	724.362429	362.684853	T	***852.450869***	426.729073	835.424320	418.215798	834.440304	417.723790	4
8	1181.598320	591.302798	1164.571771	582.789524	1163.587755	582.297516	Q	***751.403190***	376.205233	734.376641	367.691959			3
9	1318.657232	659.832254	1301.630683	651.318980	1300.646667	650.826972	H	***312.177864***	156.592570	295.151315	148.079295			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 19 ppm



RMS error 19 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.6	1491.761612	0.003310	LNNGEITQHR
0.5	1491.745667	0.019255	EQAVIPLTDSEYK
0.3	1491.756927	0.007995	IEEVIGTGSFGEVR

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

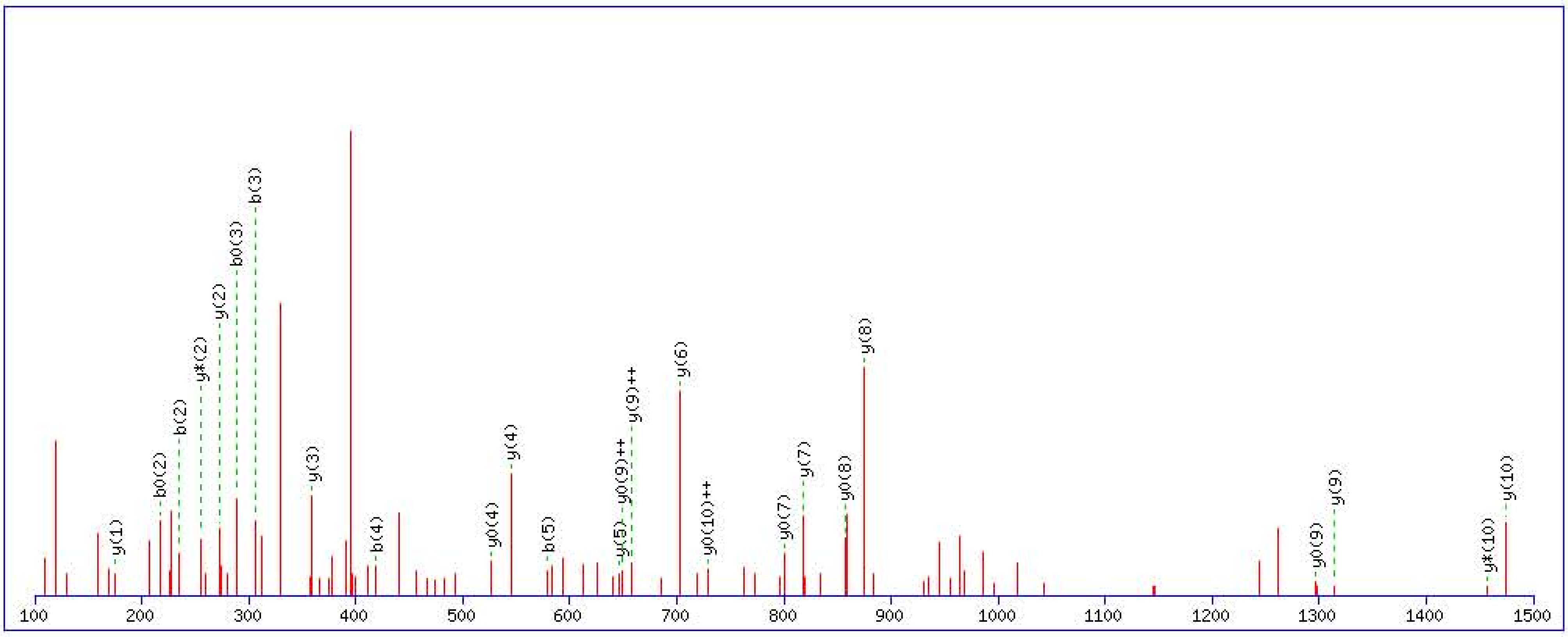
Mascot Search Results

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

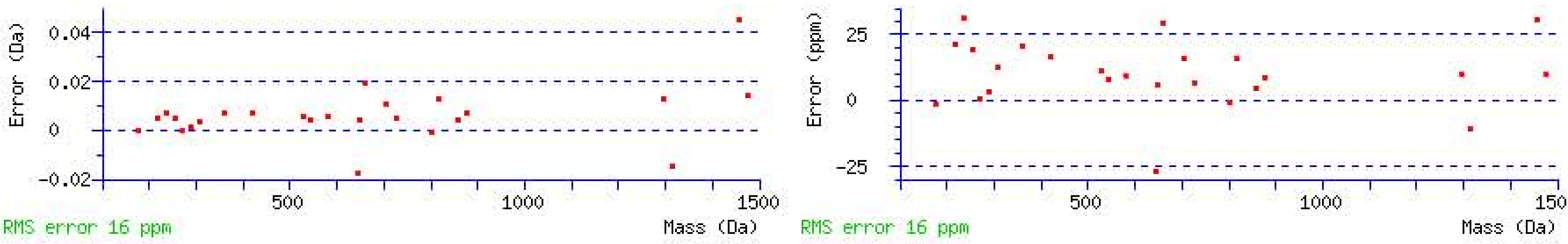
Match to Query 47341: 1891.896222 from(631.639350,3+) rtinseconds(2137) index(43135)
Title: Locus:1.1.1.3193.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1891.870941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0071
Matches : 25/140 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	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
33.9	1891.870941	0.025281	FSAICQGDGTWSPR

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

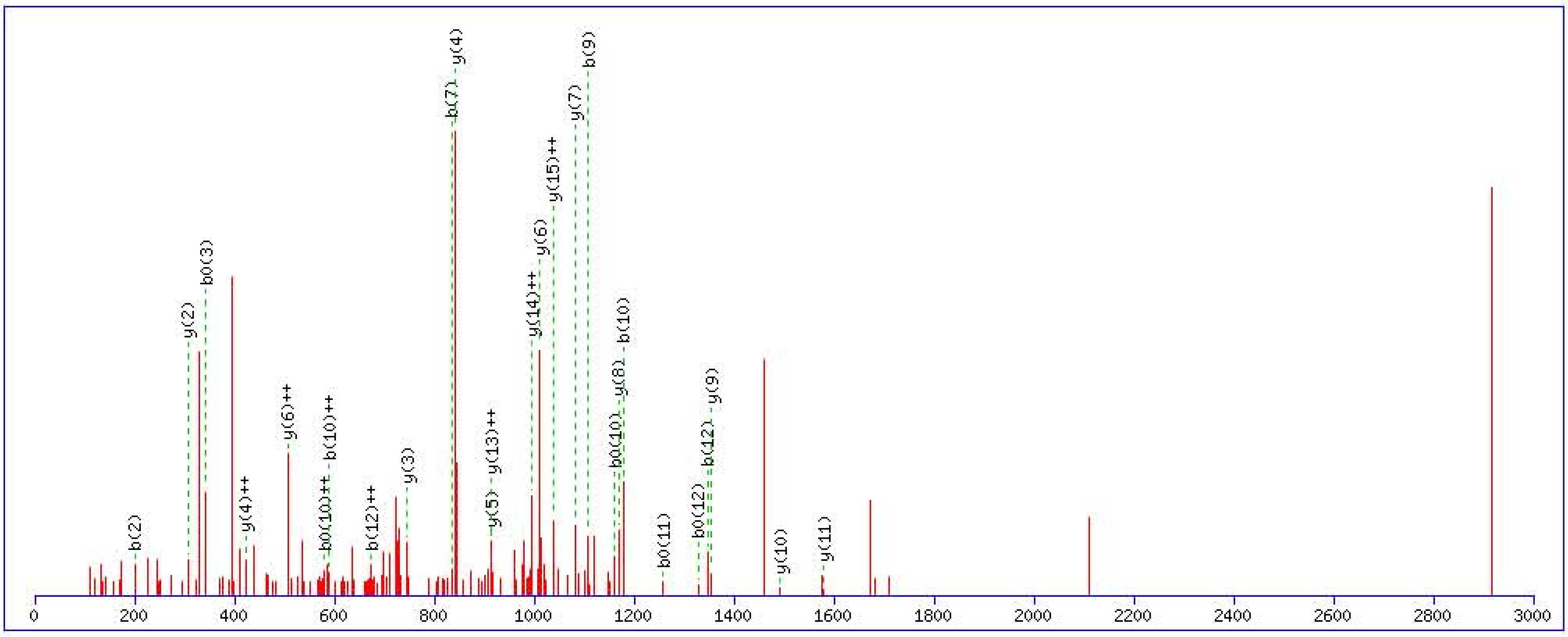
Mascot Search Results

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

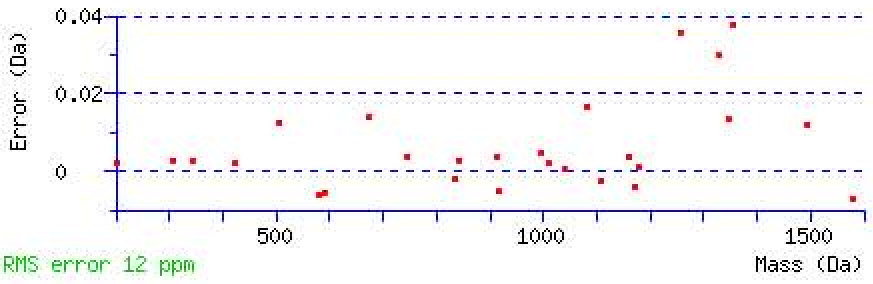
Match to Query 55133: 2189.009832 from(730.677220,3+) rtinseconds(1778) index(40624)
Title: Locus:1.1.1.3068.19 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

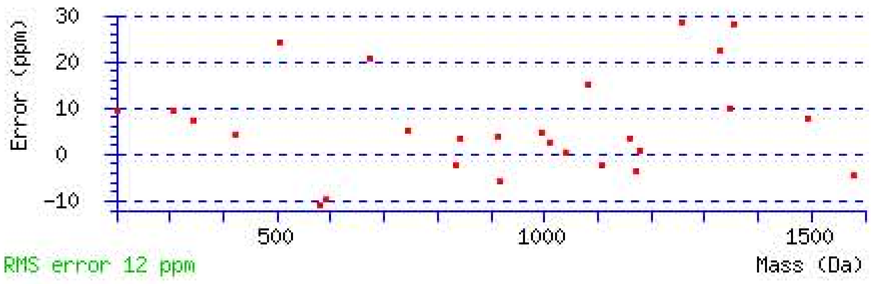


```
Monoisotopic mass of neutral peptide Mr(calc): 2188.985626
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0026
Matches : 27/138 fragment ions using 67 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							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



RMS error 12 ppm



RMS error 12 ppm

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
37.0	2188.985626	0.024206	LSCSYSHWSAPAPQCK

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

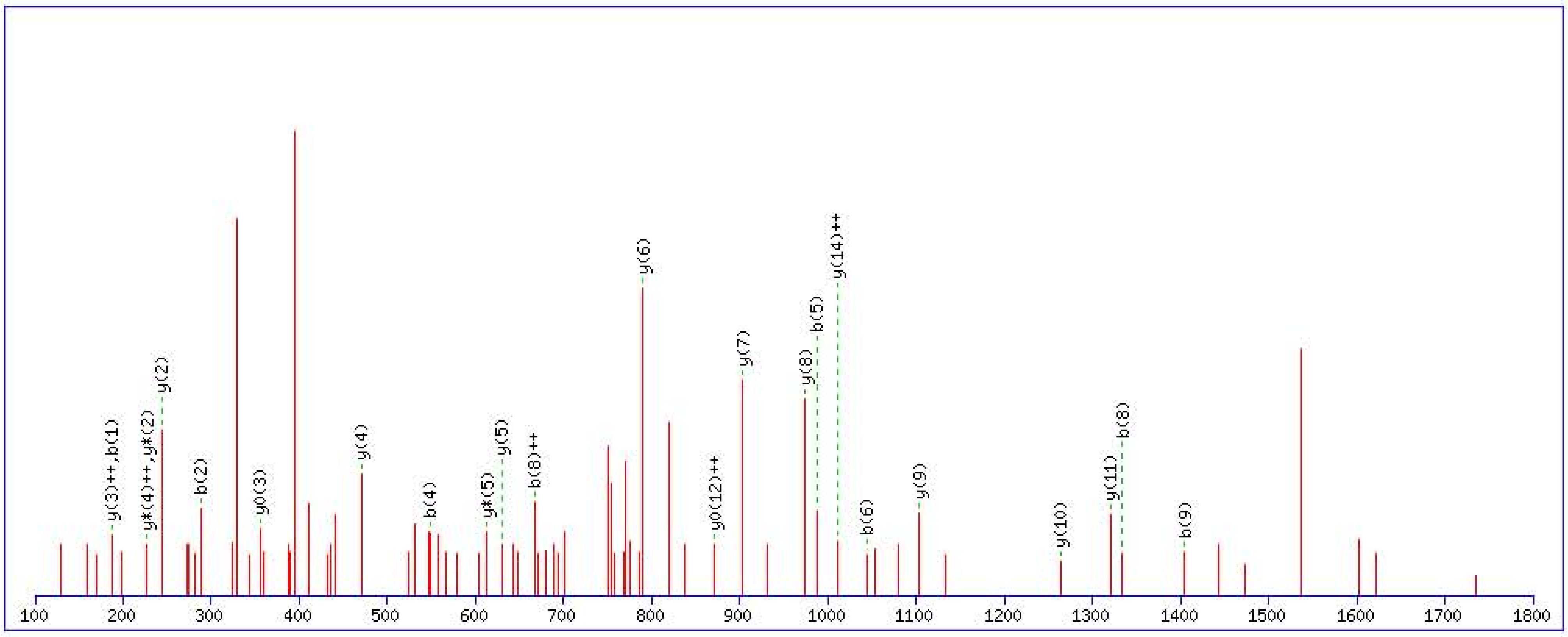
Mascot Search Results

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

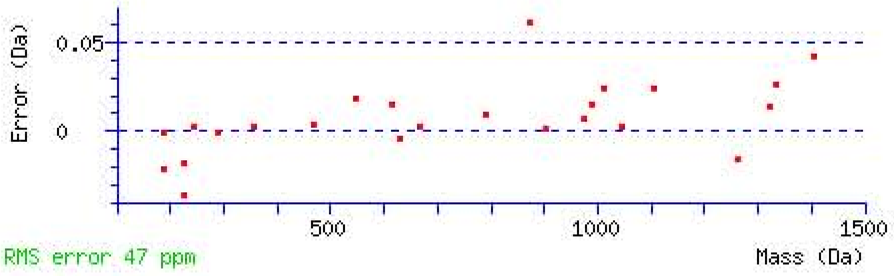
Match to Query 58197: 2306.029062 from(769.683630,3+) rtinseconds(2109) index(42961)
Title: Locus:1.1.1.3183.19 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

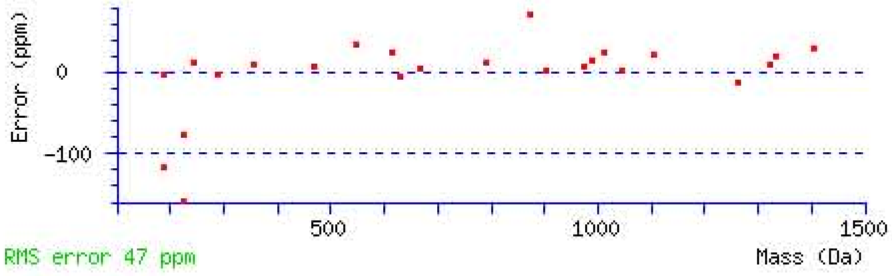
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2305.999237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.001
Matches : 24/166 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	***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





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
38.8	2305.999237	0.029825	WTPYQGCEALCCPEPK

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

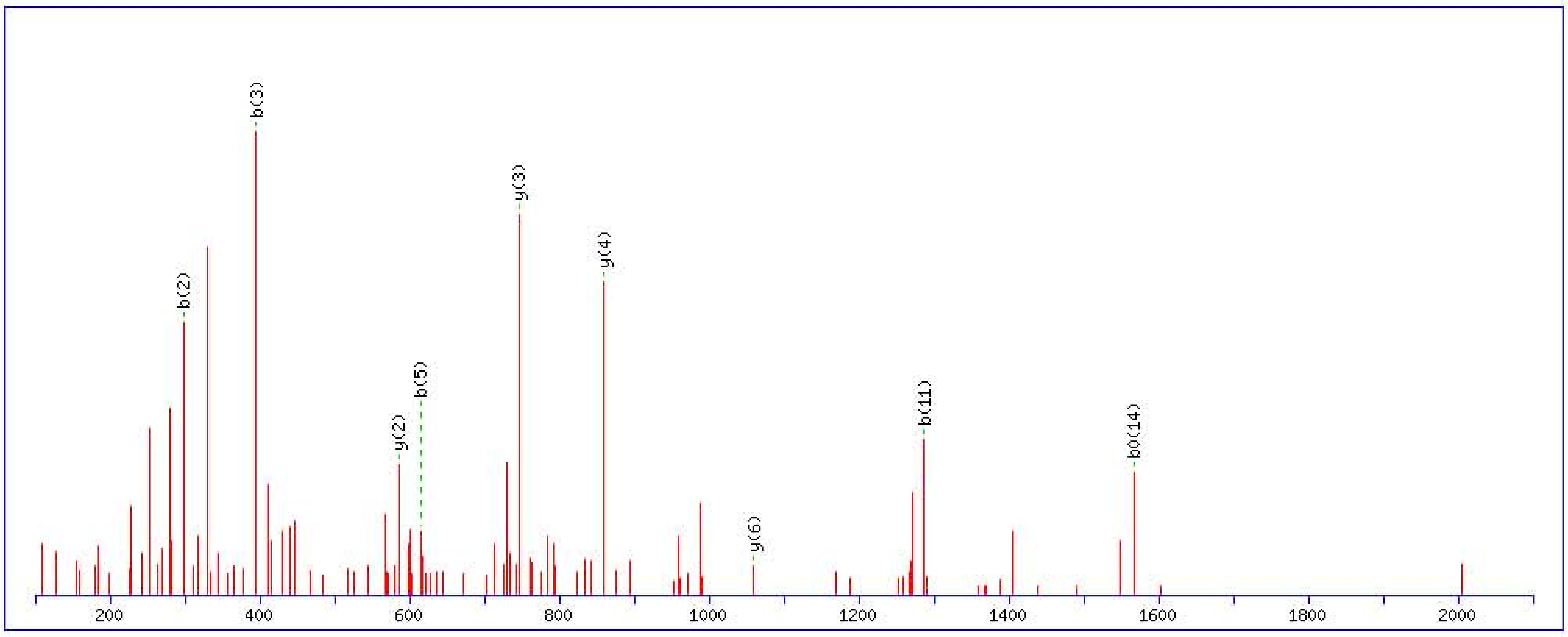
Mascot Search Results

Peptide View

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

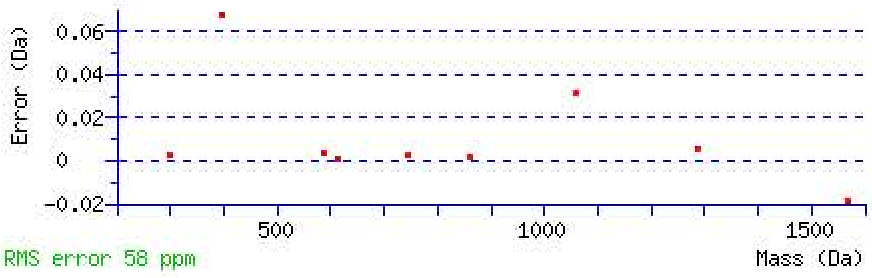
Match to Query 63761: 2542.221456 from(636.562640,4+) rtinseconds(1576) index(39350)
Title: Locus:1.1.1.2998.10 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

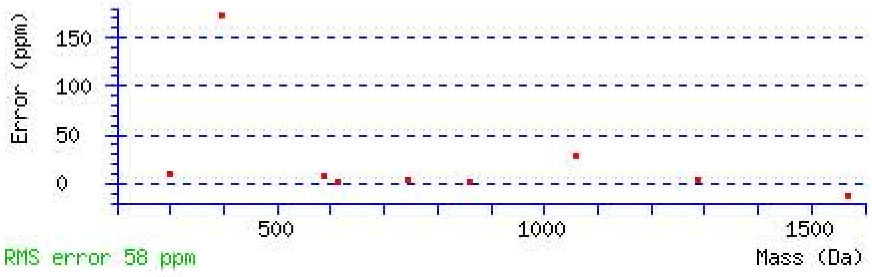
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2542.201859
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18 : Biotin:Thermo-21345 (Q)
Ions Score: 25 **Expect:** 0.066
Matches : 9/182 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	161.037925	81.022600					C							19
2	***298.096837***	149.552056					H	2383.178469	1192.092872	2366.151920	1183.579598	2365.167904	1183.087590	18
3	***395.149601***	198.078439					P	2246.119557	1123.563416	2229.093008	1115.050142	2228.108992	1114.558134	17
4	452.171065	226.589170					G	2149.066793	1075.037034	2132.040244	1066.523760	2131.056228	1066.031752	16
5	***615.234394***	308.120835					Y	2092.045329	1046.526302	2075.018780	1038.013028	2074.034764	1037.521020	15
6	743.329357	372.168317	726.302808	363.655042			K	1928.982000	964.994638	1911.955451	956.481364	1910.971435	955.989356	14
7	840.382121	420.694699	823.355572	412.181424			P	1800.887037	900.947157	1783.860488	892.433882	1782.876472	891.941874	13
8	941.429800	471.218538	924.403251	462.705264	923.419235	462.213256	T	1703.834273	852.420775	1686.807724	843.907500	1685.823708	843.415492	12
9	1042.477479	521.742378	1025.450930	513.229103	1024.466914	512.737095	T	1602.786594	801.896935	1585.760045	793.383661	1584.776029	792.891653	11
10	1157.504422	579.255849	1140.477873	570.742575	1139.493857	570.250567	D	1501.738915	751.373096	1484.712366	742.859821	1483.728350	742.367813	10
11	***1286.547015***	643.777146	1269.520466	635.263871	1268.536450	634.771863	E	1386.711972	693.859624	1369.685423	685.346350	1368.701407	684.854342	9
12	1383.599779	692.303528	1366.573230	683.790253	1365.589214	683.298245	P	1257.669379	629.338328	1240.642830	620.825053	1239.658814	620.333045	8
13	1484.647458	742.827367	1467.620909	734.314093	1466.636893	733.822085	T	1160.616615	580.811946	1143.590066	572.298671	1142.606050	571.806663	7
14	1585.695137	793.351207	1568.668588	784.837932	1567.684572	784.345924	T	***1059.568936***	530.288106	1042.542387	521.774832	1041.558371	521.282824	6
15	1684.763551	842.885414	1667.737002	834.372139	1666.752986	833.880131	V	958.521257	479.764267	941.494708	471.250992			5
16	1797.847615	899.427446	1780.821066	890.914171	1779.837050	890.422163	I	***859.452843***	430.230060	842.426294	421.716785			4
17	1957.878264	979.442770	1940.851715	970.929496	1939.867699	970.437488	C	***746.368779***	373.688028	729.342230	365.174753			3
18	2397.103590	1199.055433	2380.077041	1190.542158	2379.093025	1190.050151	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 CHPGYKPTTDEPTTVICQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.2	2542.201859	0.019597	CHPGYKPTTDEPTTVICQK

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

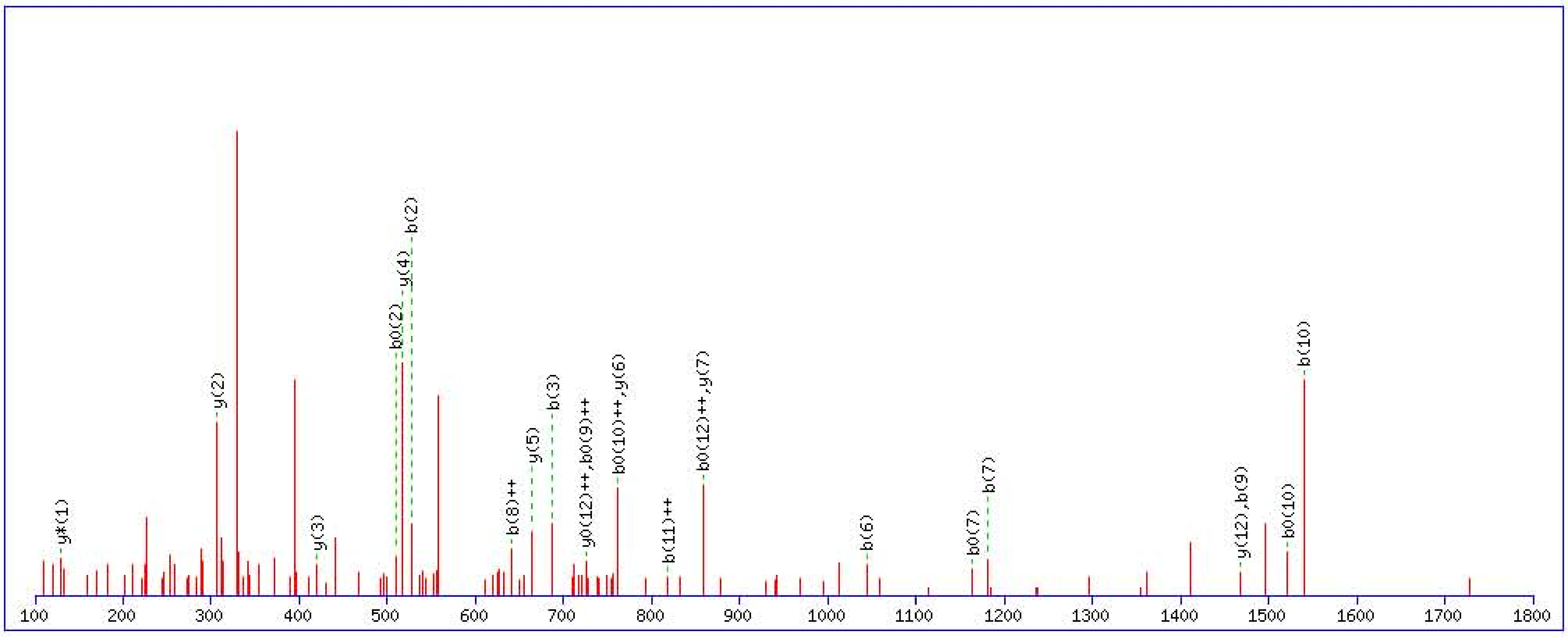
Mascot Search Results

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

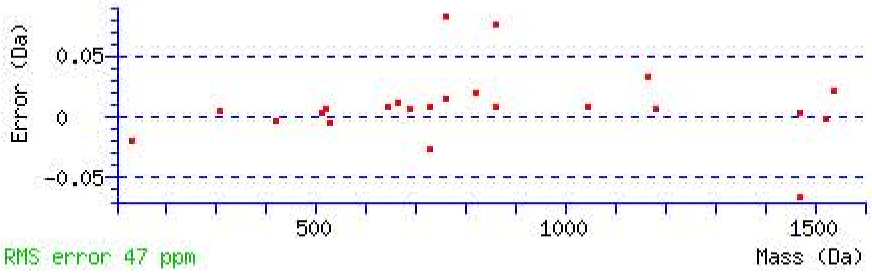
Match to Query 23658: 2396.137776 from(600.041720,4+) rtinseconds(2312) index(44346)
Title: Locus:1.1.1.3254.6 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

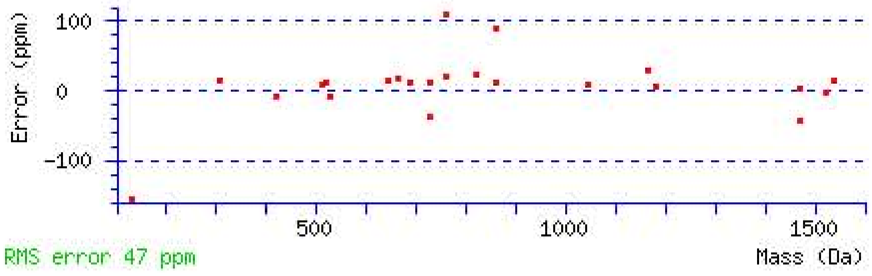
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2396.111572
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.018
Matches : 23/172 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	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
30.9	2396.111572	0.026204	SQCLEDHTWAPPFPICK

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

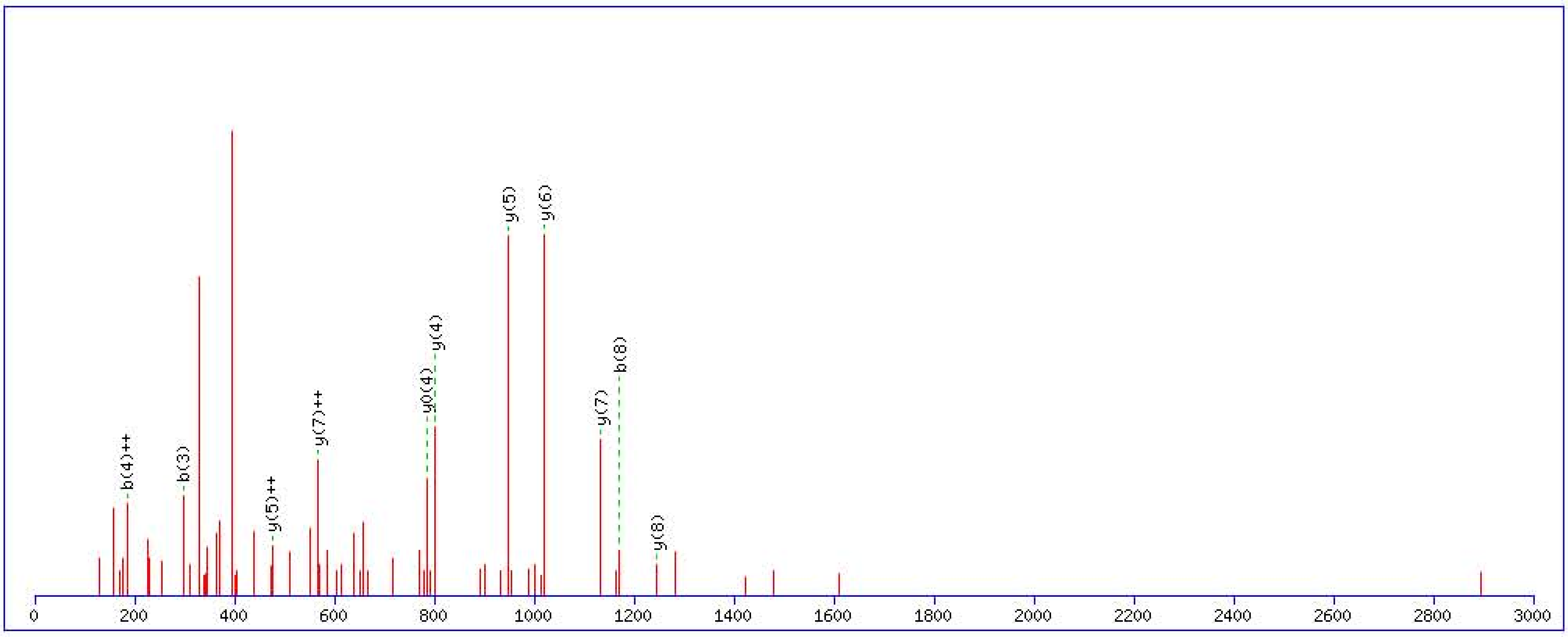
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

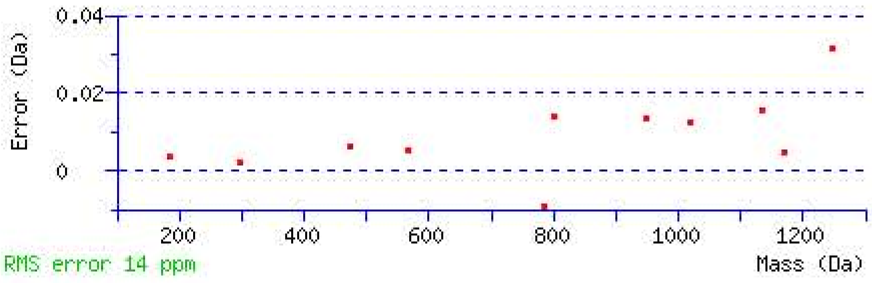
Match to Query 27307: 1316.727068 from(659.370810,2+) rtinseconds(2206) index(43668)
Title: Locus:1.1.1.3217.9 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

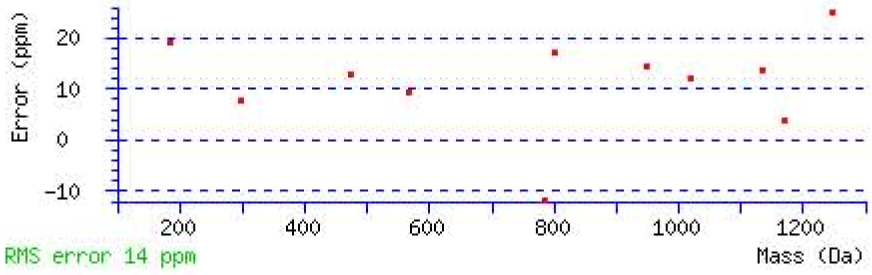
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1316.716217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.024
Matches : 12/72 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	72.044390	36.525833					A							9
2	**185.128454**	93.067865					L	***1246.686407***	623.846842	1229.659858	615.333567	1228.675842	614.841559	8
3	**298.212518**	149.609897					L	***1133.602343***	567.304810	1116.575794	558.791535	1115.591778	558.299527	7
4	369.249632	185.128454					A	***1020.518279***	510.762778	1003.491730	502.249503	1002.507714	501.757495	6
5	516.318046	258.662661					F	***949.481165***	475.244221	932.454616	466.730946	931.470600	466.238938	5
6	955.543372	478.275324	938.516823	469.762049			Q	***802.412751***	401.710014	785.386202	393.196739	784.402186	392.704731	4
7	1084.585965	542.796621	1067.559416	534.283346	1066.575400	533.791338	E	363.187425	182.097351	346.160876	173.584076	345.176860	173.092068	3
8	**1171.617993**	586.312635	1154.591444	577.799360	1153.607428	577.307352	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 ALLAFQESK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.2	1316.716217	0.010851	ALLAFQESK
7.5	1316.731308	-0.004240	KTFPISGARGGAR
7.4	1316.742050	-0.014982	AILCRKGKPMK
4.5	1316.731293	-0.004225	RVLAFISRNQN
3.3	1316.741165	-0.014097	ALSEKSLQRSAK
2.7	1316.733994	-0.006926	LALVINGDFLDK
2.7	1316.745224	-0.018156	SPLQLQTVIYR
2.4	1316.745193	-0.018125	LAALEEFRLQK
1.2	1316.729950	-0.002882	KTLSEVERDLK
0.5	1316.723434	0.003634	ILASMPSRTIGR

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

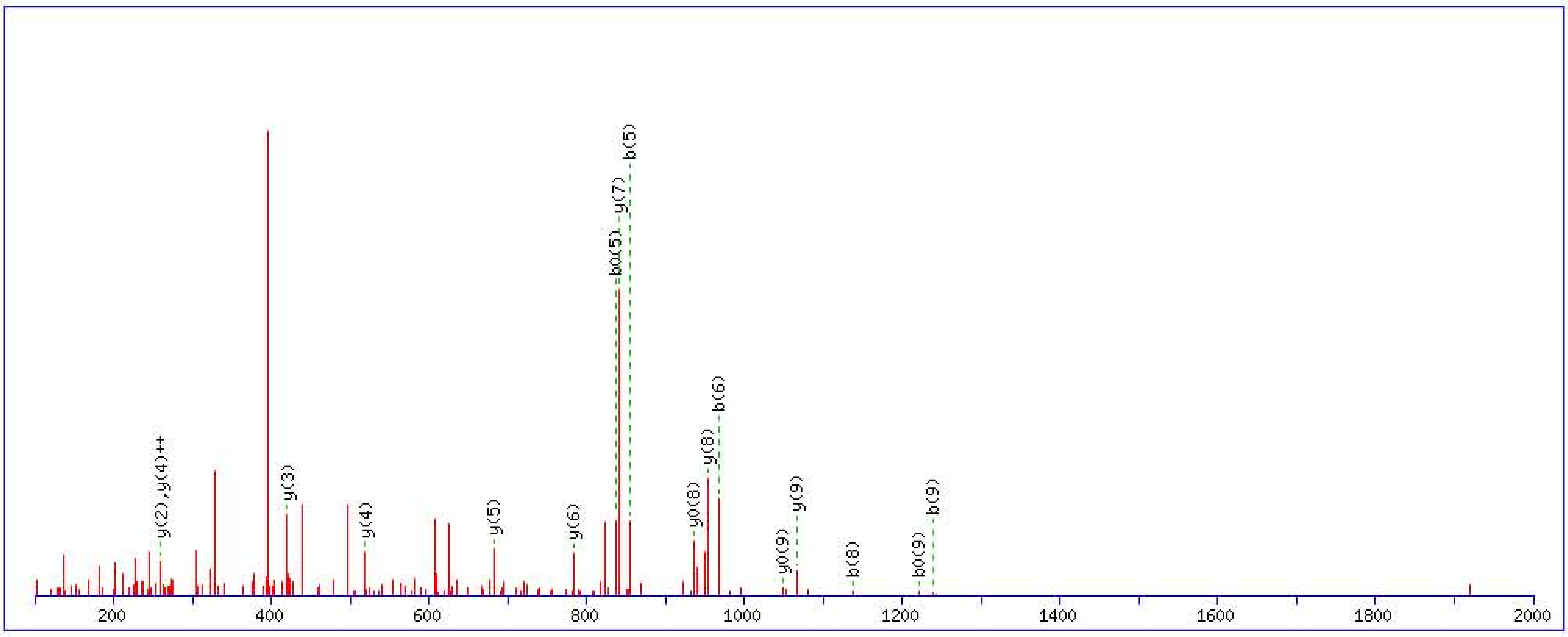
{MATRIX SCIENCE} Mascot Search Results

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

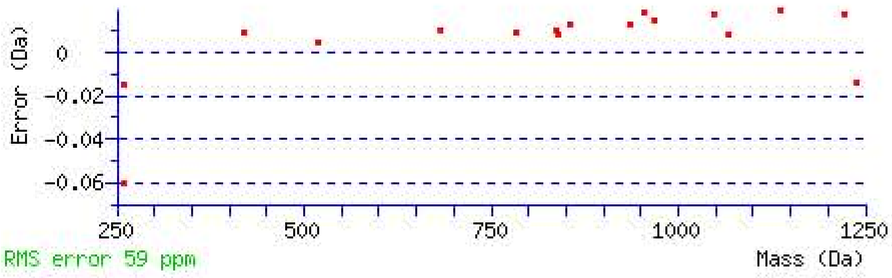
Match to Query 47955: 1919.017362 from(640.679730,3+) rtinseconds(2461) index(45278)
Title: Locus:1.1.1.3306.4 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

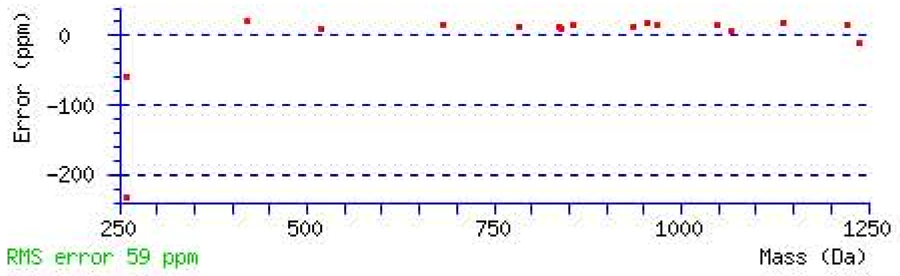
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1918.989639
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0055
Matches : 17/138 fragment ions using 34 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							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
36.4	1918.989639	0.027723	EVEGQILGTYVCIK

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

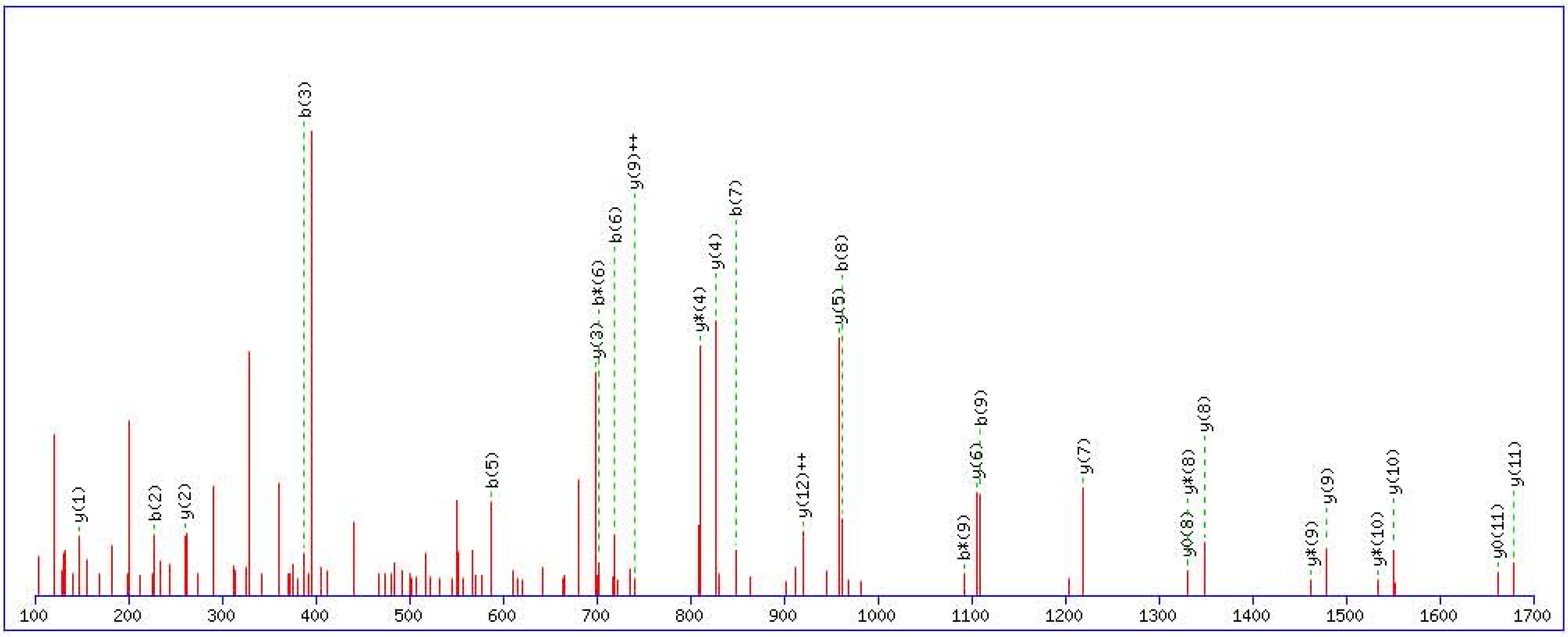
Mascot Search Results

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

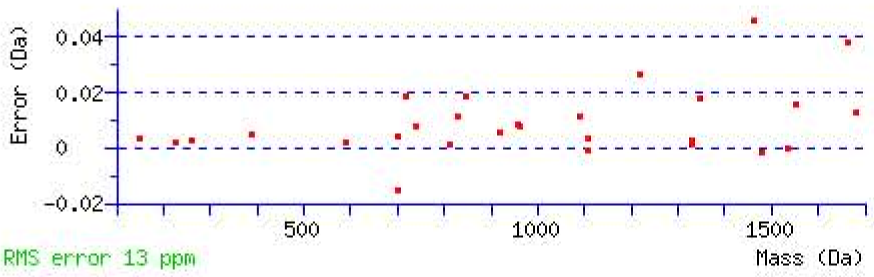
Match to Query 52450: 2065.973112 from(689.664980,3+) rtinseconds(3067) index(49782)
Title: Locus:1.1.1.3513.5 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

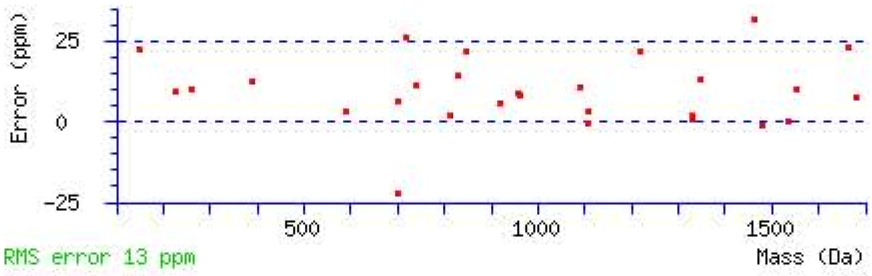
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2065.945709
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 1.5e-005
Matches : 28/136 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	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
60.1	2065.945709	0.027403	NLCEAMENFMQQLK
58.1	2065.945709	0.027403	NLCEAMENFMQQLK
17.3	2066.002350	-0.029238	AQLQMMENLISSSQETIK
7.9	2066.002350	-0.029238	AQLQMMENLISSSQETIK

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

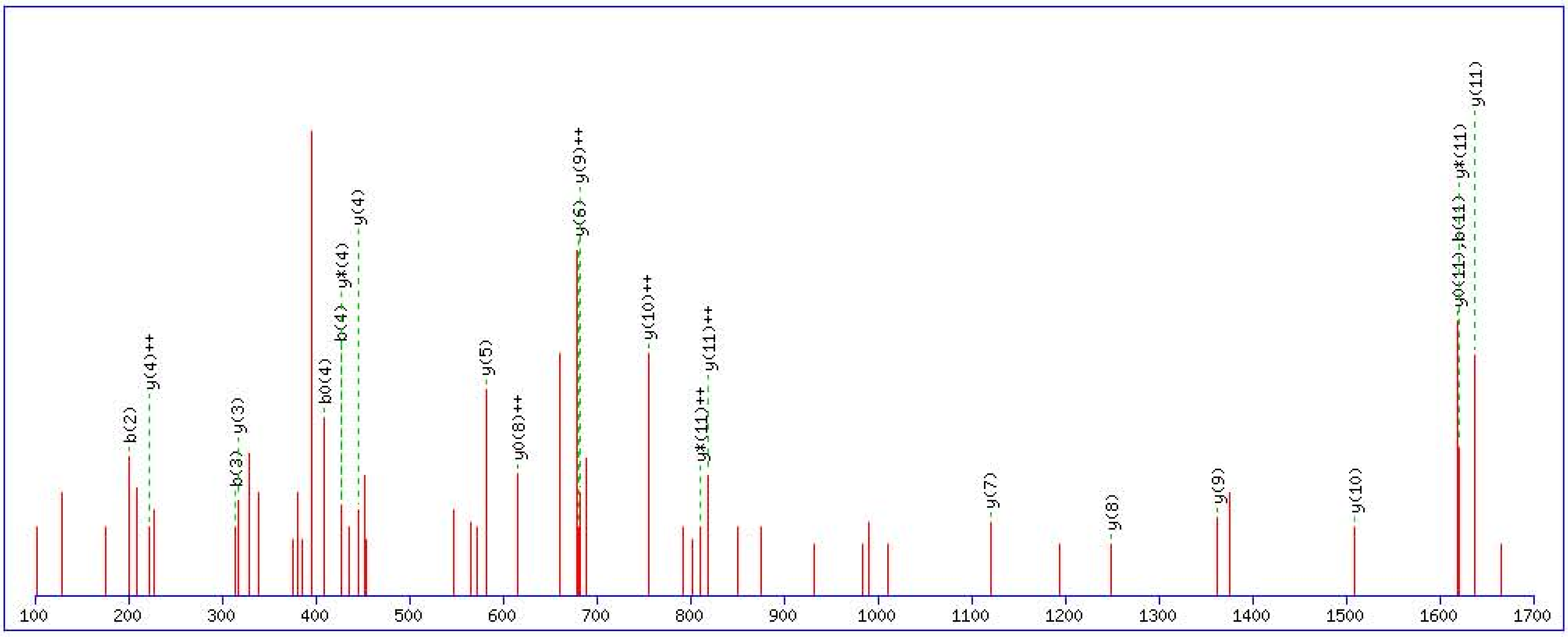
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EALIQFLEQVHQGIK**
Found in **CBPN_HUMAN**, Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1

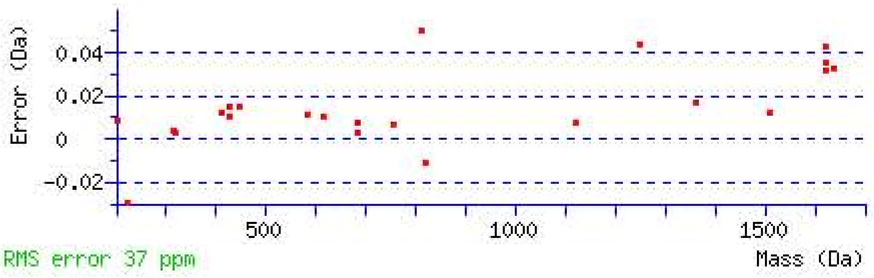
Match to Query 52419: 2063.154012 from(688.725280,3+) rtinseconds(2745) index(47364)
Title: Locus:1.1.1.3403.10 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

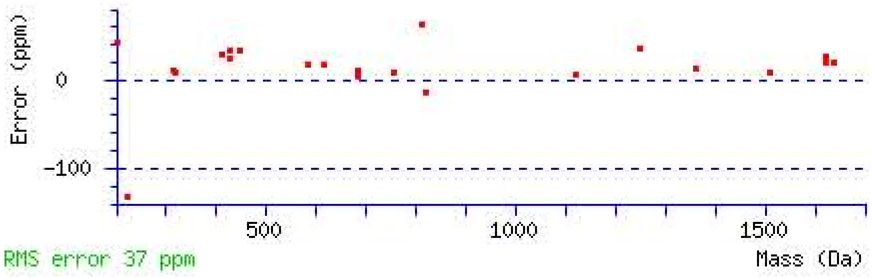
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2063.123749
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.0043
Matches : 23/146 fragment ions using 54 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							15
2	**201.086983**	101.047130			183.076418	92.041847	A	1935.088453	968.047865	1918.061904	959.534590	1917.077888	959.042582	14
3	**314.171047**	157.589161			296.160482	148.583879	L	1864.051339	932.529307	1847.024790	924.016033	1846.040774	923.524025	13
4	**427.255111**	214.131193			409.244546	205.125911	I	1750.967275	875.987276	1733.940726	867.474001	1732.956710	866.981993	12
5	555.313689	278.160483	538.287140	269.647208	537.303124	269.155200	Q	***1637.883211***	819.445244	1620.856662	810.931969	1619.872646	810.439961	11
6	702.382103	351.694690	685.355554	343.181415	684.371538	342.689407	F	***1509.824633***	755.415955	1492.798084	746.902680	1491.814068	746.410672	10
7	815.466167	408.236722	798.439618	399.723447	797.455602	399.231439	L	***1362.756219***	681.881748	1345.729670	673.368473	1344.745654	672.876465	9
8	944.508760	472.758018	927.482211	464.244744	926.498195	463.752736	E	***1249.672155***	625.339716	1232.645606	616.826441	1231.661590	616.334433	8
9	1383.734086	692.370681	1366.707537	683.857407	1365.723521	683.365399	Q	***1120.629562***	560.818419	1103.603013	552.305144			7
10	1482.802500	741.904888	1465.775951	733.391614	1464.791935	732.899606	V	***681.404236***	341.205756	664.377687	332.692481			6
11	**1619.861412**	810.434344	1602.834863	801.921070	1601.850847	801.429062	H	***582.335822***	291.671549	565.309273	283.158274			5
12	1747.919990	874.463633	1730.893441	865.950359	1729.909425	865.458351	Q	***445.276910***	223.142093	428.250361	214.628818			4
13	1804.941454	902.974365	1787.914905	894.461091	1786.930889	893.969083	G	***317.218332***	159.112804	300.191783	150.599529			3
14	1918.025518	959.516397	1900.998969	951.003123	1900.014953	950.511114	I	260.196868	130.602072	243.170319	122.088797			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.8	2063.123749	0.030263	EALIQFLEQVHQGIK
13.8	2063.123749	0.030263	EALIQFLEQVHQGIK
8.6	2063.123749	0.030263	EALIQFLEQVHQGIK

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

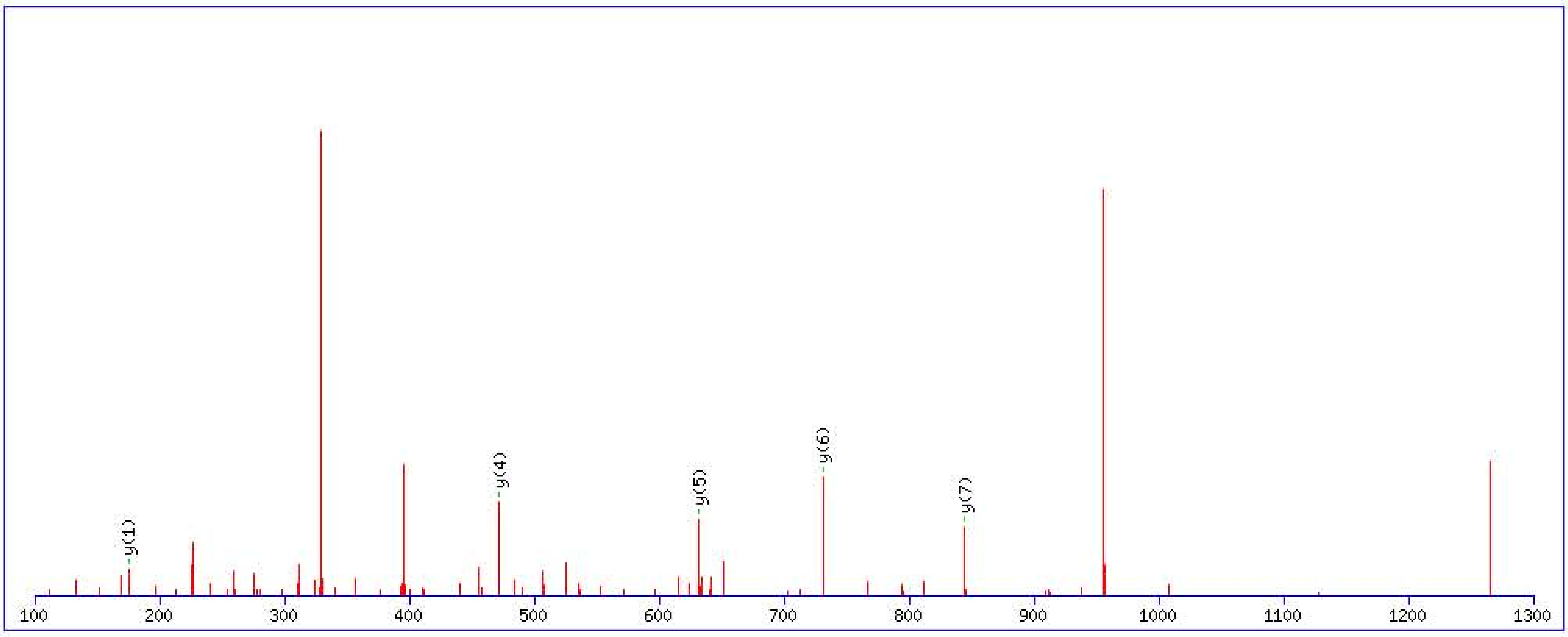
Mascot Search Results

Peptide View

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

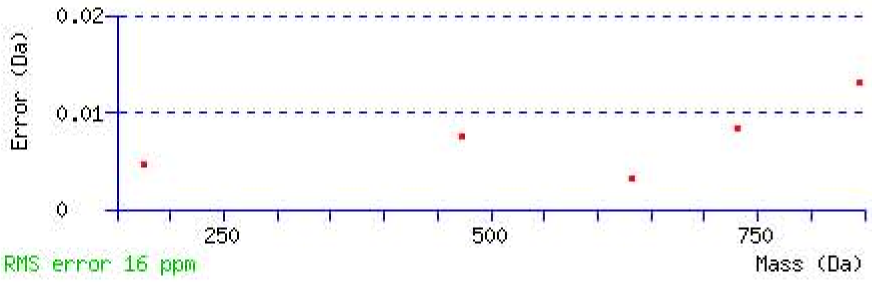
Match to Query 26453: 1282.699288 from(642.356920,2+) rtinseconds(1748) index(40424)
Title: Locus:1.1.1.3058.14 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

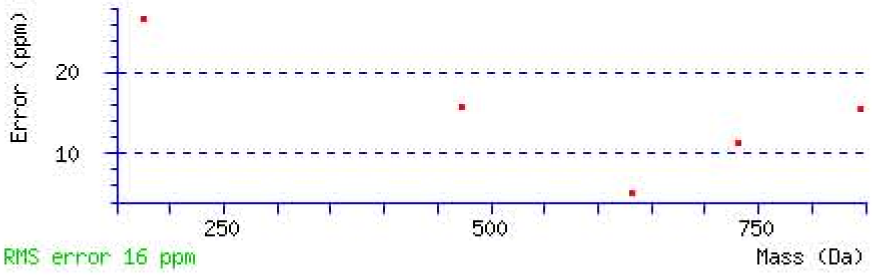
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1282.688995
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.033
Matches : 5/70 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	440.232602	220.619939	423.206053	212.106664			Q							8
2	553.316666	277.161971	536.290117	268.648697			L	***844.470936***	422.739106	827.444387	414.225831	826.460371	413.733823	7
3	652.385080	326.696178	635.358531	318.182904			V	***731.386872***	366.197074	714.360323	357.683799	713.376307	357.191791	6
4	812.415729	406.711503	795.389180	398.198228			C	***632.318458***	316.662867	615.291909	308.149592	614.307893	307.657584	5
5	909.468493	455.237885	892.441944	446.724610			P	***472.287809***	236.647542	455.261260	228.134268	454.277244	227.642260	4
6	1008.536907	504.772092	991.510358	496.258817			V	375.235045	188.121160	358.208496	179.607886	357.224480	179.115878	3
7	1109.584586	555.295931	1092.558037	546.782657	1091.574021	546.290648	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 QLVCPVTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.4	1282.688995	0.010293	QLVCPVTR
10.9	1282.717957	-0.018669	QLGLTERR
9.1	1282.688065	0.011223	EEAAGIARPLEK
8.6	1282.699341	-0.000053	LSAISLGQGQGPR
5.9	1282.693466	0.005822	FQIPWKHATR
5.8	1282.699326	-0.000038	IGRIIEGSPADR
5.8	1282.681549	0.017739	QLEERAAR
5.8	1282.685593	0.013695	QLEGLWAR
4.8	1282.710556	-0.011268	RLPGENVKTNR
3.3	1282.704041	-0.004753	AAALVRRGCGPR

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

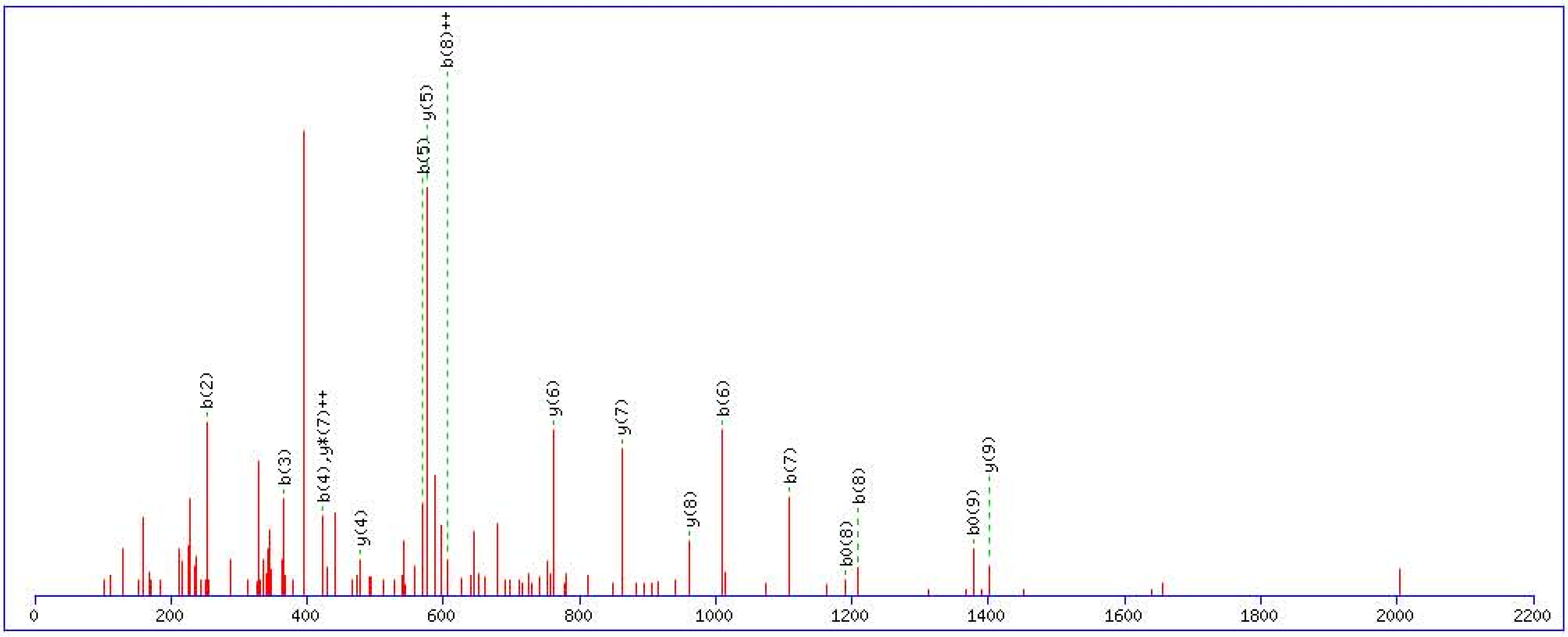
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

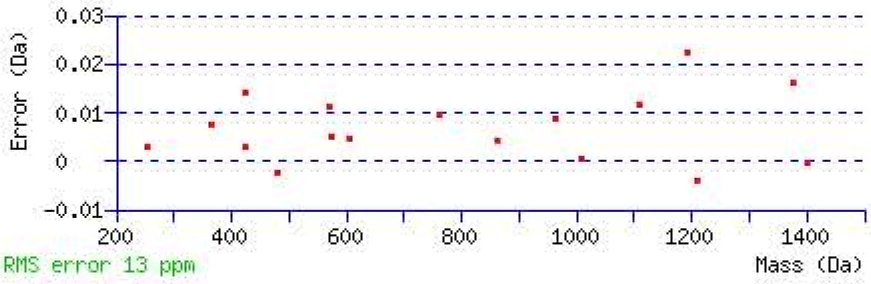
Match to Query 49236: 1968.967182 from(657.329670,3+) rtinseconds(2309) index(44325)
Title: Locus:1.1.1.3253.9 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

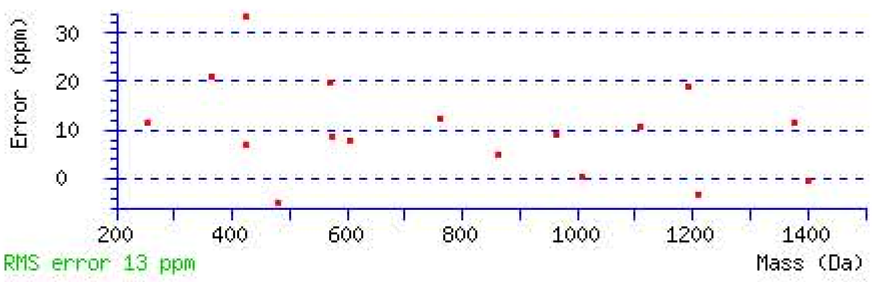
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1968.940399
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.021
Matches : 17/144 fragment ions using 40 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							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
27.1	1968.940399	0.026783	DHLGFQVTWPDESK
9.2	1968.949585	0.017597	EGQMESVEAAMSSKTLKK

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

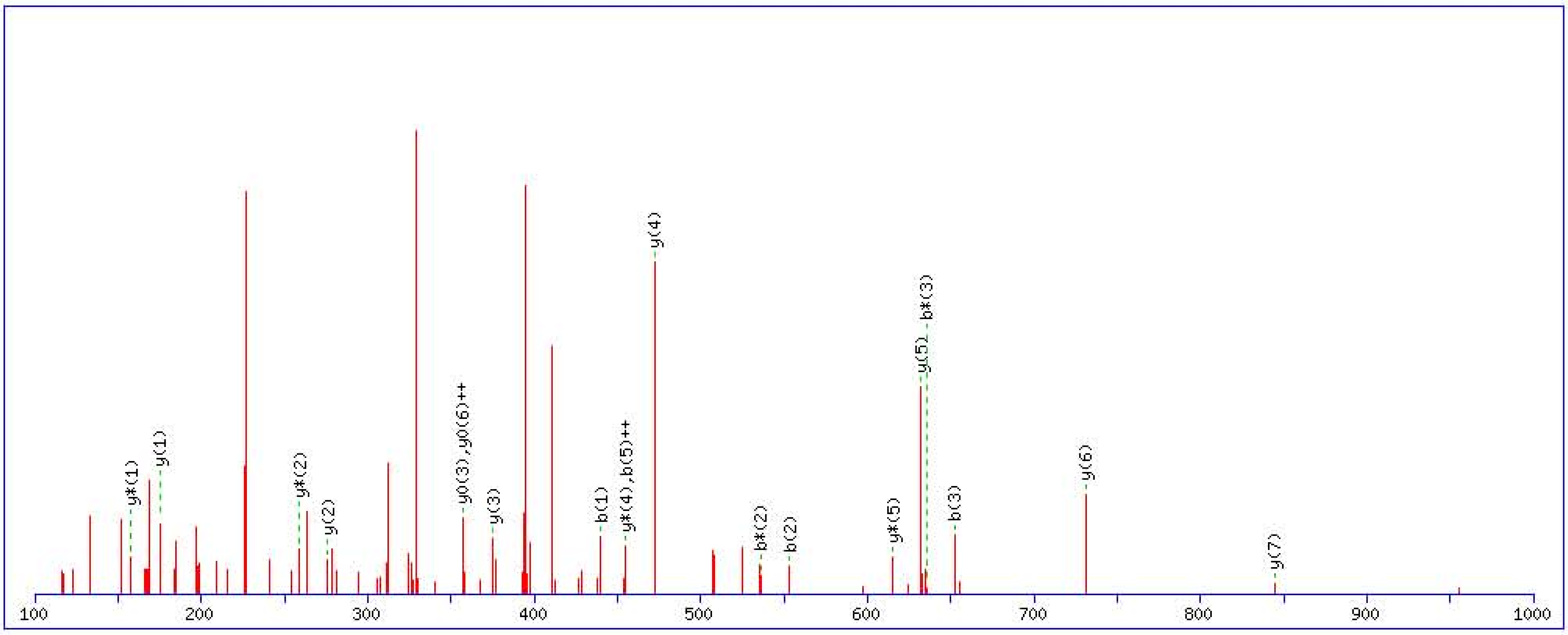
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

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

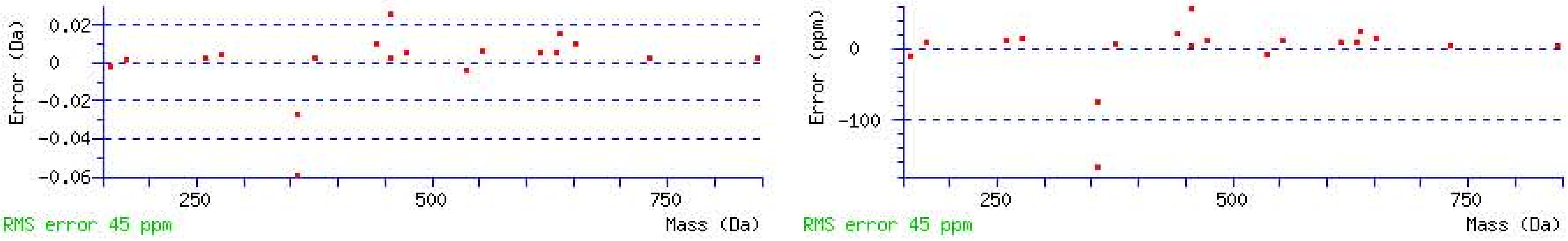
Match to Query 8155: 1282.694802 from(428.572210,3+) rtinseconds(1753) index(40450)
Title: Locus:1.1.1.3060.4 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1282.688995
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.003
Matches : 19/70 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	**440.232602**	220.619939	423.206053	212.106664			Q							8
2	**553.316666**	277.161971	536.290117	268.648697			L	***844.470936***	422.739106	827.444387	414.225831	826.460371	413.733823	7
3	**652.385080**	326.696178	635.358531	318.182904			V	***731.386872***	366.197074	714.360323	357.683799	713.376307	357.191791	6
4	812.415729	406.711503	795.389180	398.198228			C	***632.318458***	316.662867	615.291909	308.149592	614.307893	307.657584	5
5	909.468493	455.237885	892.441944	446.724610			P	***472.287809***	236.647542	455.261260	228.134268	454.277244	227.642260	4
6	1008.536907	504.772092	991.510358	496.258817			V	***375.235045***	188.121160	358.208496	179.607886	357.224480	179.115878	3
7	1109.584586	555.295931	1092.558037	546.782657	1091.574021	546.290648	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 QLVCPVTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.2	1282.688995	0.005807	QLVCPVTR
0.4	1282.677750	0.017052	VTKYCLICVK
0.3	1282.681595	0.013207	KNMGGLGGLVHGK

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

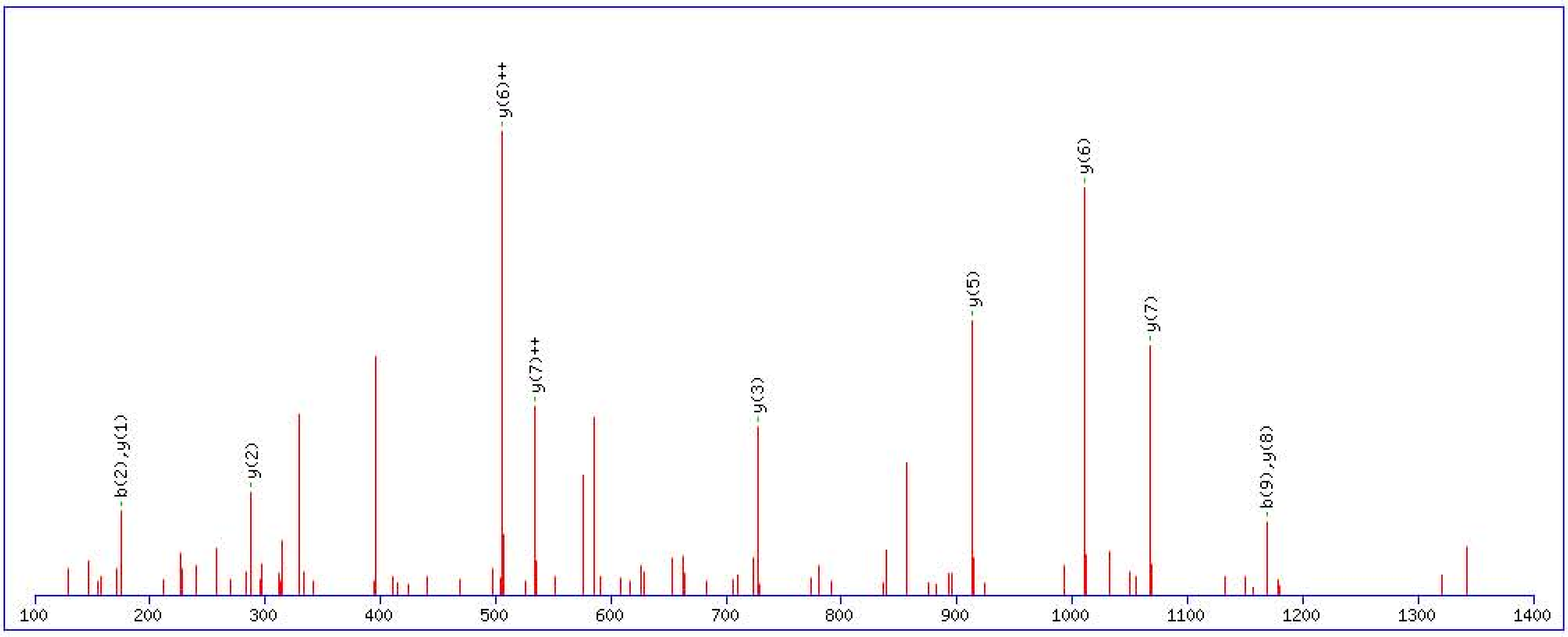
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

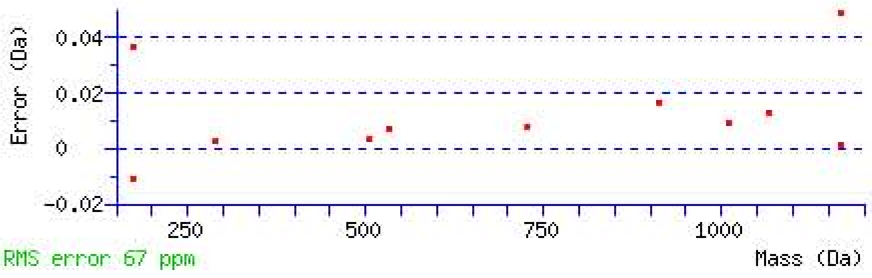
Match to Query 27906: 1341.689068 from(671.851810,2+) rtinseconds(1568) index(57761)
Title: Locus:1.1.1.2969.19 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

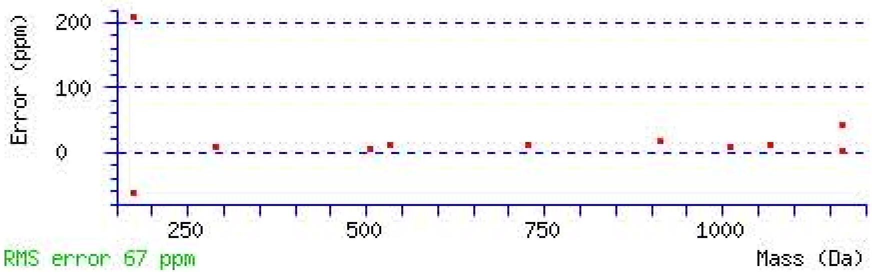
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1341.671082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 58 **Expect:** 4.1e-005
Matches : 11/88 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							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
57.9	1341.671082	0.017986	SSTGPGEQLR
12.4	1341.674911	0.014157	TSPERREPGTGR
10.8	1341.686142	0.002926	RTGAPAQADSRGR
10.7	1341.704117	-0.015049	VSVWENVPVGTR
5.2	1341.707443	-0.018375	QEKEIQTR
4.2	1341.697556	-0.008488	QASEWVRR
4.1	1341.693512	-0.004444	ASEQERRR
4.0	1341.694199	-0.005131	KGAFFSWSRTR
3.8	1341.696198	-0.007130	KQAEEIGEK
3.7	1341.688828	0.000240	DDAQLSGLPSALR

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

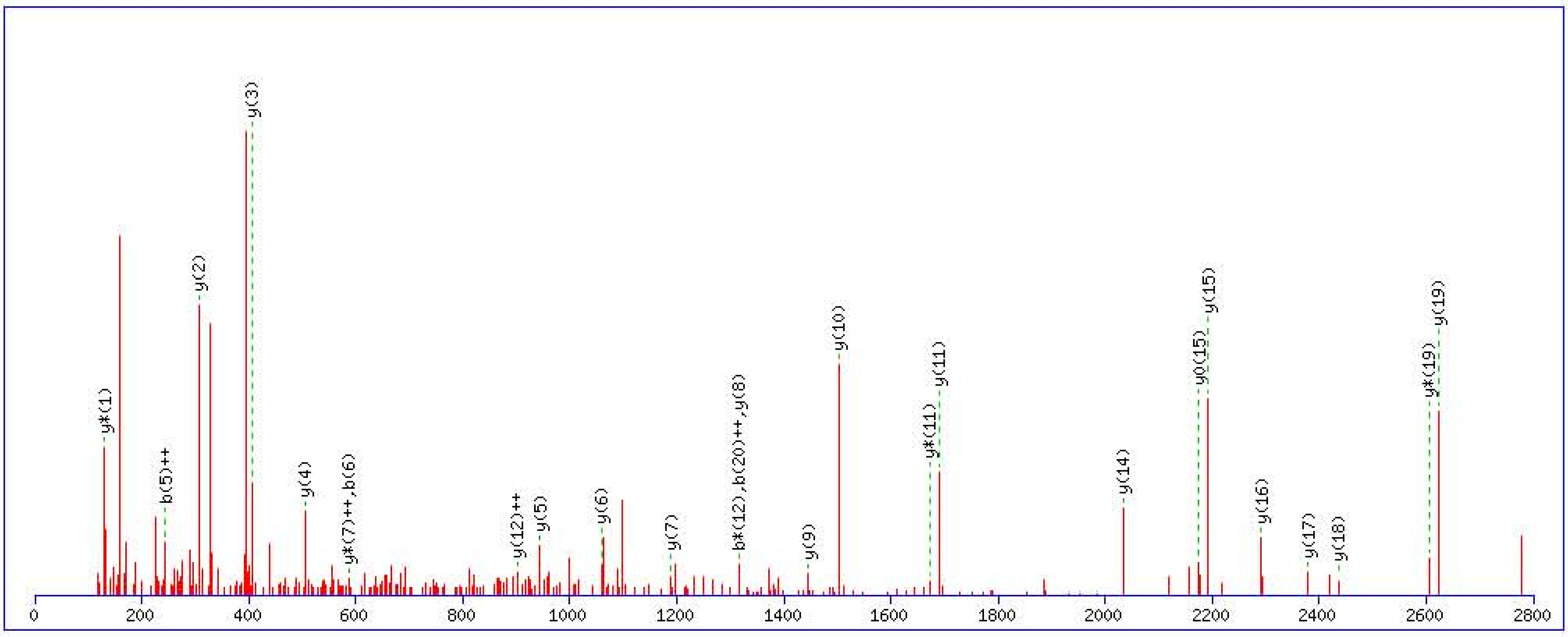
Mascot Search Results

Peptide View

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

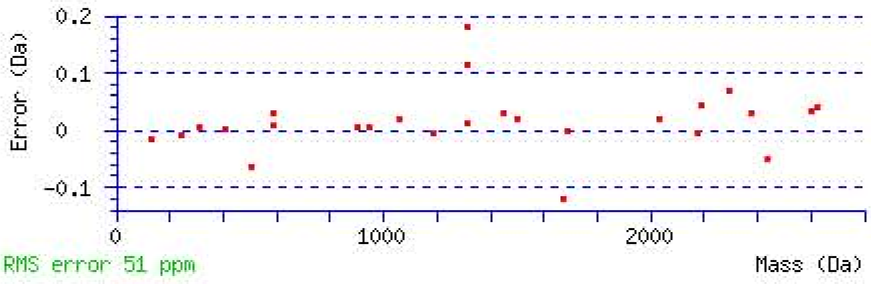
Match to Query 66750: 2777.263496 from(695.323150,4+) rtinseconds(2117) index(43008)
Title: Locus:1.1.1.3186.9 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

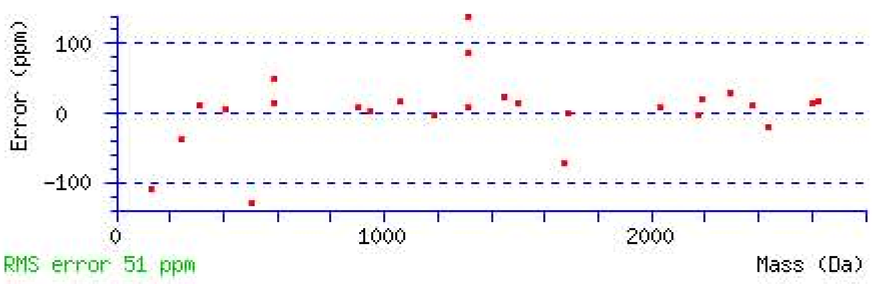


```
Monoisotopic mass of neutral peptide Mr(calc): 2777.224792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17     : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 1.6e-006
Matches : 26/204 fragment ions using 69 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							21
2	157.097154	79.052215					V	2721.210571	1361.108923	2704.184022	1352.595649	2703.200006	1352.103641	20
3	343.176467	172.091872					W	***2622.142157***	1311.574716	2605.115608	1303.061442	2604.131592	1302.569434	19
4	400.197931	200.602603					G	***2436.062844***	1218.535060	2419.036295	1210.021785	2418.052279	1209.529777	18
5	487.229959	**244.118617**			469.219394	235.113335	S	***2379.041380***	1190.024328	2362.014831	1181.511053	2361.030815	1181.019045	17
6	586.298373	293.652825			568.287808	284.647542	V	***2292.009352***	1146.508314	2274.982803	1137.995039	2273.998787	1137.503031	16
7	746.329022	373.668149			728.318457	364.662867	C	***2192.940938***	1096.974107	2175.914389	1088.460832	2174.930373	1087.968824	15
8	861.355965	431.181621			843.345400	422.176338	D	***2032.910289***	1016.958782	2015.883740	1008.445508	2014.899724	1007.953500	14
9	976.382908	488.695092			958.372343	479.689809	D	1917.883346	959.445311	1900.856797	950.932036	1899.872781	950.440028	13
10	1090.425835	545.716556	1073.399286	537.203281	1072.415270	536.711273	N	1802.856403	901.931840	1785.829854	893.418565	1784.845838	892.926557	12
11	1276.505148	638.756212	1259.478599	630.242938	1258.494583	629.750929	W	***1688.813476***	844.910376	1671.786927	836.397101	1670.802911	835.905093	11
12	1333.526612	667.266944	1316.500063	658.753670	1315.516047	658.261661	G	***1502.734163***	751.870719	1485.707614	743.357445	1484.723598	742.865437	10
13	1462.569205	731.788241	1445.542656	723.274966	1444.558640	722.782958	E	***1445.712699***	723.359987	1428.686150	714.846713	1427.702134	714.354705	9
14	1590.664168	795.835722	1573.637619	787.322448	1572.653603	786.830440	K	***1316.670106***	658.838691	1299.643557	650.325416	1298.659541	649.833408	8
15	1719.706761	860.357019	1702.680212	851.843744	1701.696196	851.351736	E	***1188.575143***	594.791209	1171.548594	586.277935	1170.564578	585.785927	7
16	1834.733704	917.870490	1817.707155	909.357216	1816.723139	908.865208	D	***1059.532550***	530.269913	1042.506001	521.756638	1041.521985	521.264630	6
17	2273.959030	1137.483153	2256.932481	1128.969878	2255.948465	1128.477870	Q	***944.505607***	472.756441	927.479058	464.243167			5
18	2373.027444	1187.017360	2356.000895	1178.504085	2355.016879	1178.012077	V	***505.280281***	253.143778	488.253732	244.630504			4
19	2472.095858	1236.551567	2455.069309	1228.038292	2454.085293	1227.546284	V	***406.211867***	203.609571	389.185318	195.096297			3
20	2632.126507	**1316.566891**	2615.099958	1308.053617	2614.115942	1307.561609	C	***307.143453***	154.075364	290.116904	145.562090			2
21							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 51 ppm



RMS error 51 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.9	2777.224792	0.038704	GVWGSVCDDNWGEKEDQVVCK

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

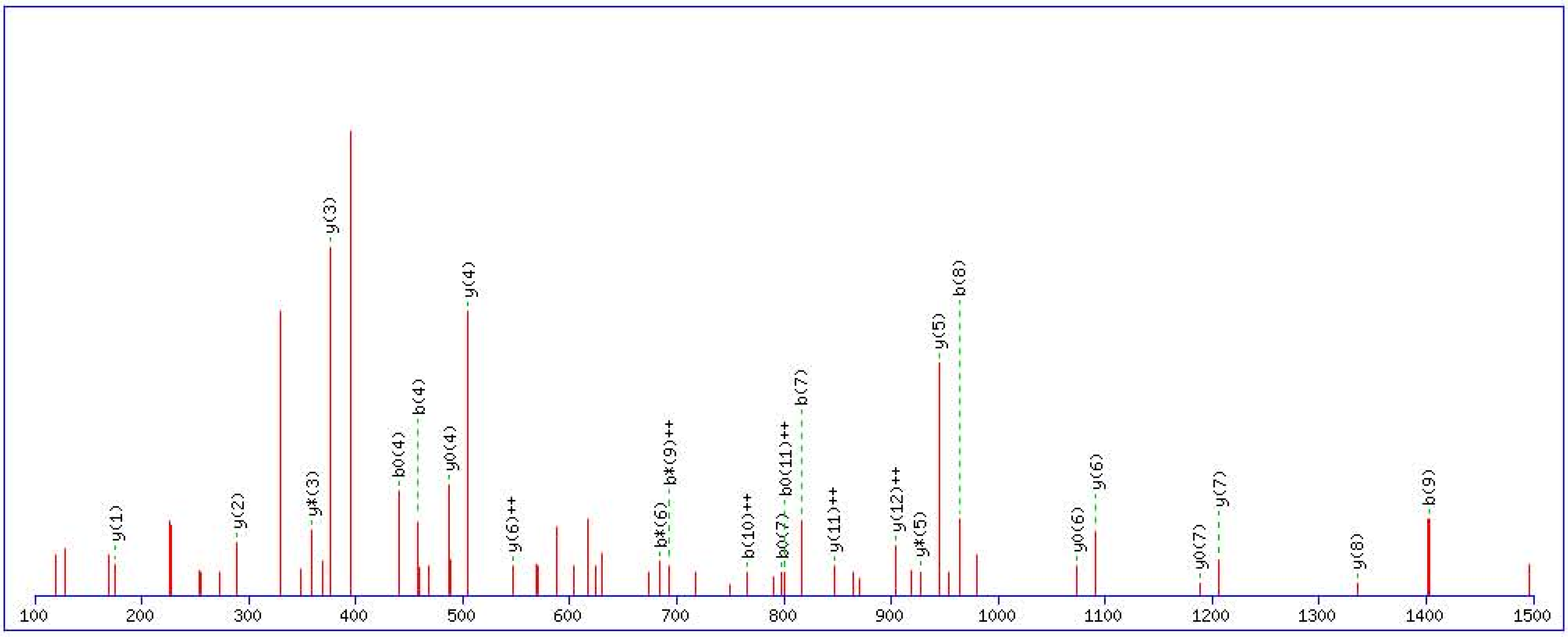
Mascot Search Results

Peptide View

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

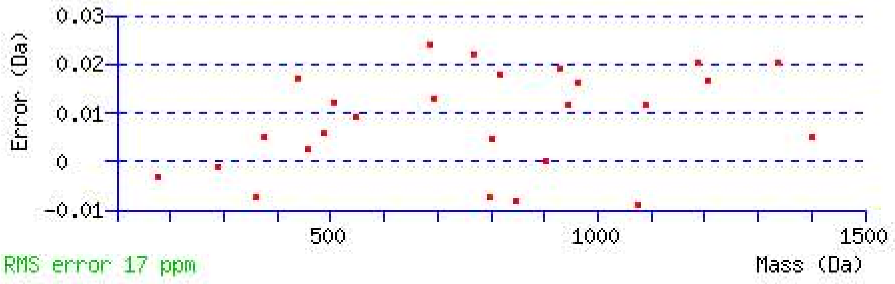
Match to Query 47572: 1905.873132 from(636.298320,3+) rtinseconds(1460) index(38453)
Title: Locus:1.1.1.2957.24 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

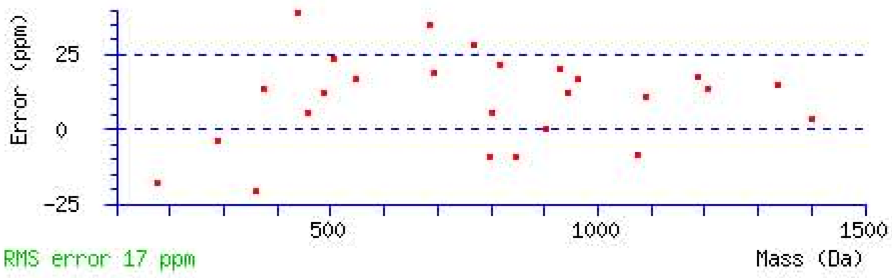
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1905.852676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0012
Matches : 26/134 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	100.075690	50.541483					V							13
2	215.102633	108.054954			197.092068	99.049672	D	1807.791552	904.399414	1790.765003	895.886140	1789.780987	895.394132	12
3	343.197596	172.102436	326.171047	163.589162	325.187031	163.097154	K	1692.764609	846.885943	1675.738060	838.372668	1674.754044	837.880660	11
4	**458.224539**	229.615908	441.197990	221.102633	440.213974	220.610625	D	1564.669646	782.838461	1547.643097	774.325187	1546.659081	773.833179	10
5	572.267466	286.637371	555.240917	278.124097	554.256901	277.632089	N	1449.642703	725.324990	1432.616154	716.811715	1431.632138	716.319707	9
6	701.310059	351.158668	684.283510	342.645393	683.299494	342.153385	E	***1335.599776***	668.303526	1318.573227	659.790252	1317.589211	659.298244	8
7	**816.337002**	408.672139	799.310453	400.158865	798.326437	399.666857	D	***1206.557183***	603.782230	1189.530634	595.268955	1188.546618	594.776947	7
8	**963.405416**	482.206346	946.378867	473.693072	945.394851	473.201064	F	***1091.530240***	546.268758	1074.503691	537.755484	1073.519675	537.263476	6
9	**1402.630742**	701.819009	1385.604193	693.305735	1384.620177	692.813727	Q	***944.461826***	472.734551	927.435277	464.221277	926.451261	463.729269	5
10	1531.673335	766.340306	1514.646786	757.827031	1513.662770	757.335023	E	***505.236500***	253.121888	488.209951	244.608614	487.225935	244.116606	4
11	1618.705363	809.856320	1601.678814	801.343045	1600.694798	800.851037	S	***376.193907***	188.600591	359.167358	180.087317	358.183342	179.595309	3
12	1732.748290	866.877783	1715.721741	858.364509	1714.737725	857.872501	N	***289.161879***	145.084577	272.135330	136.571303			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.4	1905.852676	0.020456	VDKDNEDFQESNR
9.8	1905.897095	-0.023963	LLYDEYMFYLVEHR
6.1	1905.892883	-0.019751	SHAAEPARDGVEASAEGPR

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

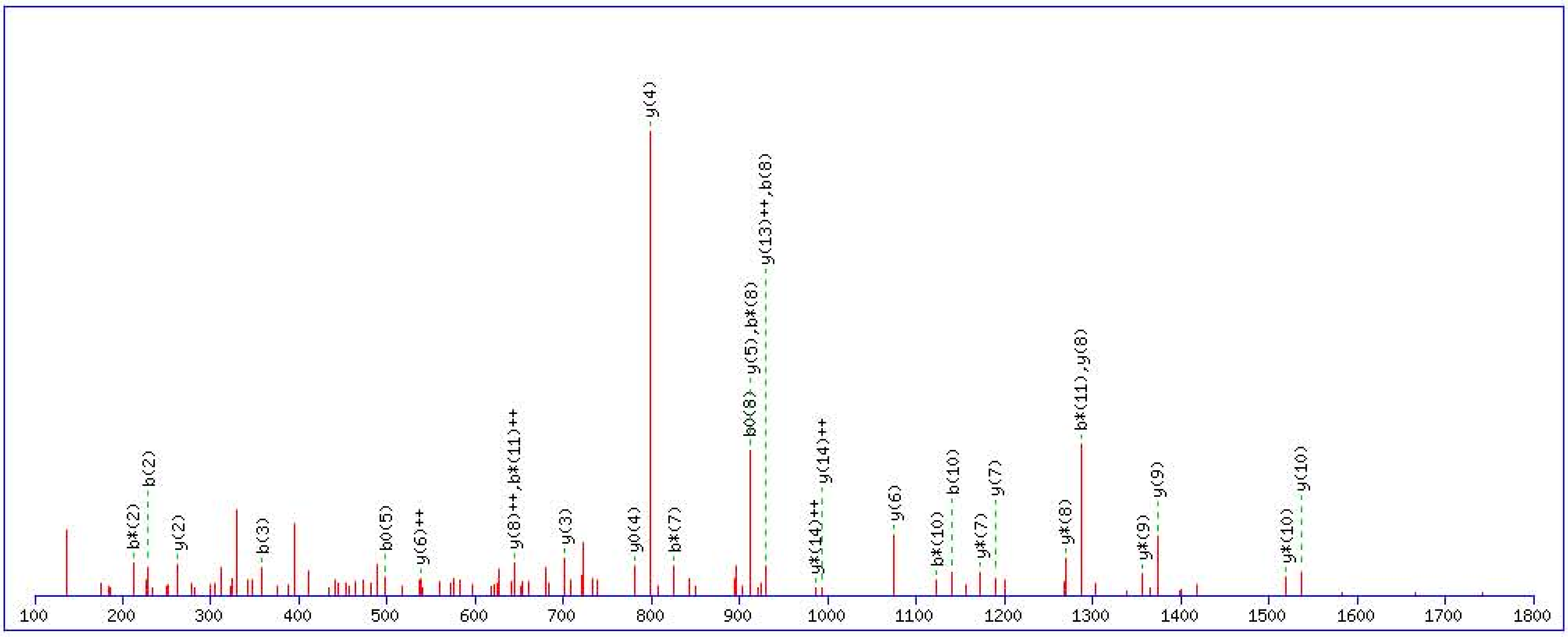
Mascot Search Results

Peptide View

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

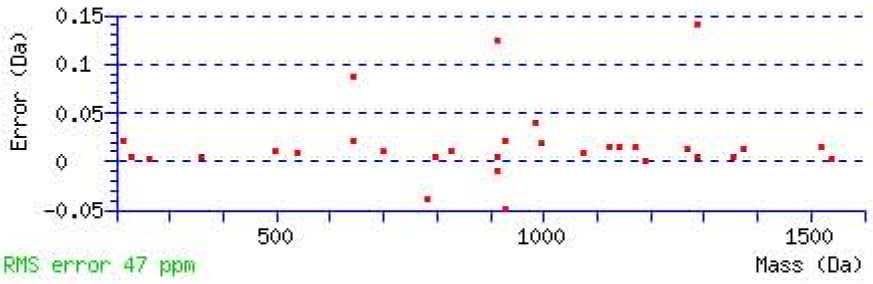
Match to Query 55742: 2214.005562 from(739.009130,3+) rtinseconds(1792) index(40721)
Title: Locus:1.1.1.3073.23 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

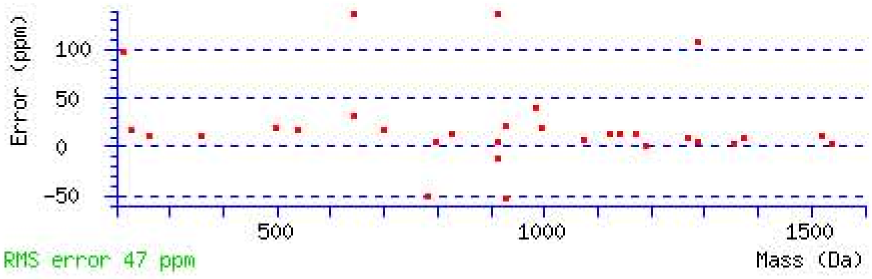
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2213.979980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 6e-005
Matches : 31/174 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	115.050203	58.028740	98.023654	49.515465			N							16
2	**229.093130**	115.050203	212.066581	106.536929			N	2100.944366	1050.975821	2083.917817	1042.462546	2082.933801	1041.970538	15
3	**358.135723**	179.571500	341.109174	171.058225	340.125158	170.566217	E	1986.901439	993.954358	1969.874890	985.441083	1968.890874	984.949075	14
4	415.157187	208.082232	398.130638	199.568957	397.146622	199.076949	G	1857.858846	929.433061	1840.832297	920.919787	1839.848281	920.427779	13
5	516.204866	258.606071	499.178317	250.092797	498.194301	249.600789	T	1800.837382	900.922329	1783.810833	892.409055	1782.826817	891.917047	12
6	679.268195	340.137736	662.241646	331.624461	661.257630	331.132453	Y	1699.789703	850.398490	1682.763154	841.885215	1681.779138	841.393207	11
7	842.331524	421.669400	825.304975	413.156126	824.320959	412.664118	Y	***1536.726374***	768.866825	1519.699825	760.353551	1518.715809	759.861543	10
8	**929.363552**	465.185414	912.337003	456.672140	911.352987	456.180132	S	***1373.663045***	687.335161	1356.636496	678.821886	1355.652480	678.329878	9
9	1026.416316	513.711796	1009.389767	505.198522	1008.405751	504.706514	P	***1286.631017***	643.819147	1269.604468	635.305872	1268.620452	634.813864	8
10	**1140.459243**	570.733260	1123.432694	562.219985	1122.448678	561.727977	N	***1189.578253***	595.292765	1172.551704	586.779490	1171.567688	586.287482	7
11	1303.522572	652.264924	1286.496023	643.751650	1285.512007	643.259642	Y	***1075.535326***	538.271301	1058.508777	529.758027	1057.524761	529.266019	6
12	1417.565499	709.286388	1400.538950	700.773113	1399.554934	700.281105	N	***912.471997***	456.739637	895.445448	448.226362	894.461432	447.734354	5
13	1514.618263	757.812770	1497.591714	749.299495	1496.607698	748.807487	P	***798.429070***	399.718173	781.402521	391.204899	780.418505	390.712891	4
14	1953.843589	977.425433	1936.817040	968.912158	1935.833024	968.420150	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
15	2040.875617	1020.941447	2023.849068	1012.428172	2022.865052	1011.936164	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of NNEGTYYSPNYNPQSR
(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	2213.979980	0.025582	NNEGTYYSPNYNPQSR

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

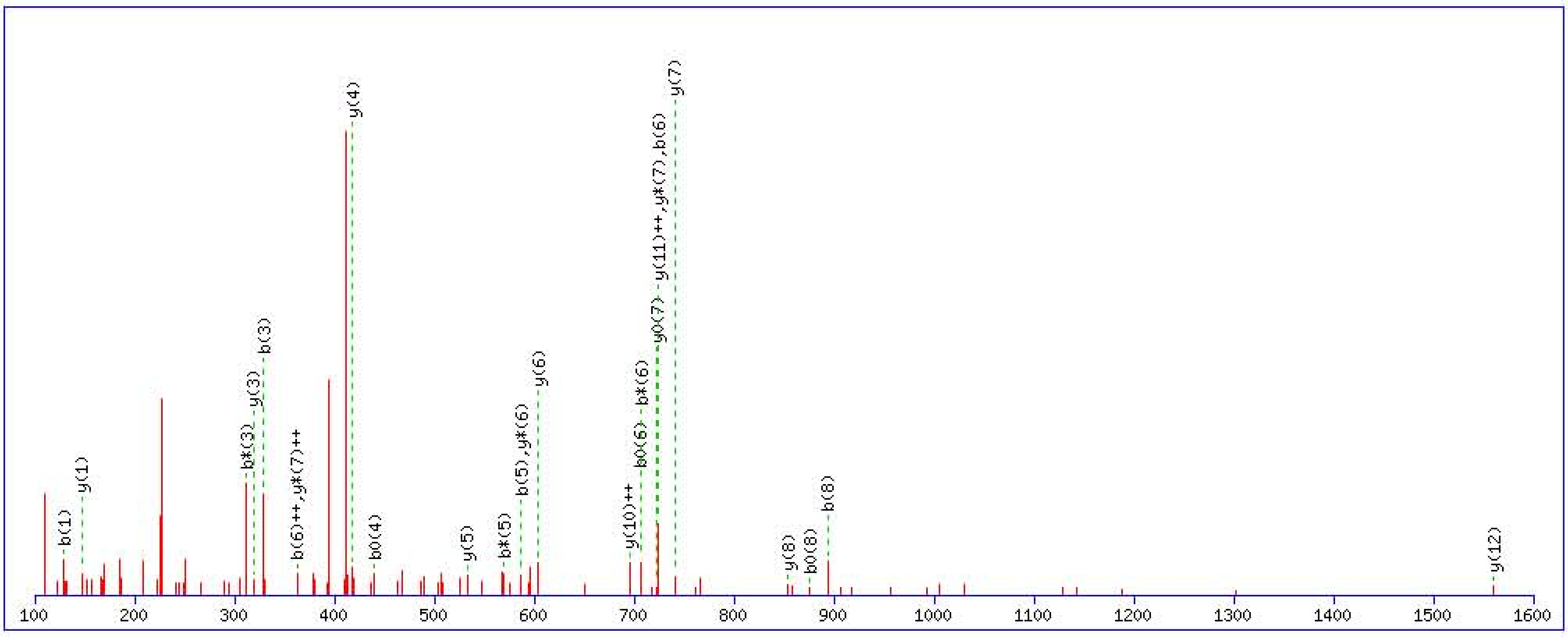
Mascot Search Results

Peptide View

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

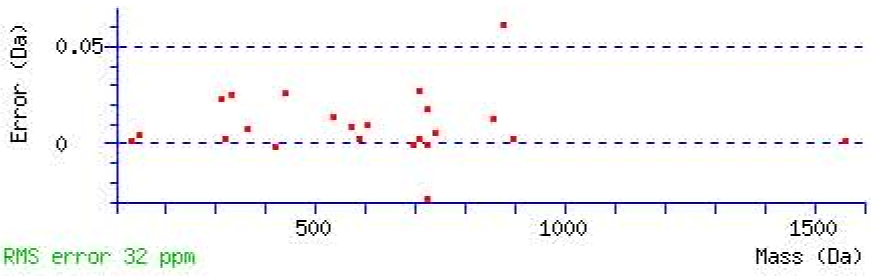
Match to Query 64021: 2566.338520 from(514.274980,5+) rtinseconds(1915) index(41557)
Title: Locus:1.1.1.3116.12 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

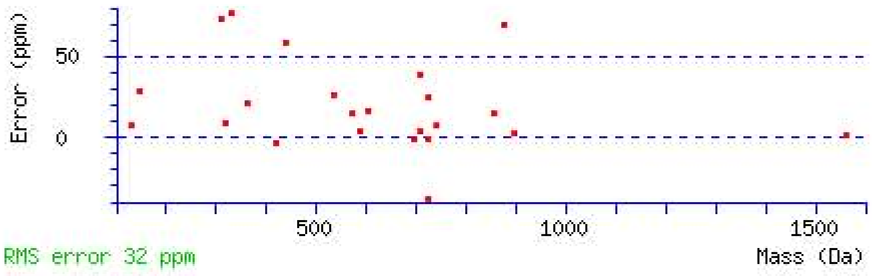
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2566.321335
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.063
Matches : 26/234 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	***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
26.2	2566.321335	0.017185	KAEEEHLGILGPQLHADVGDK

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

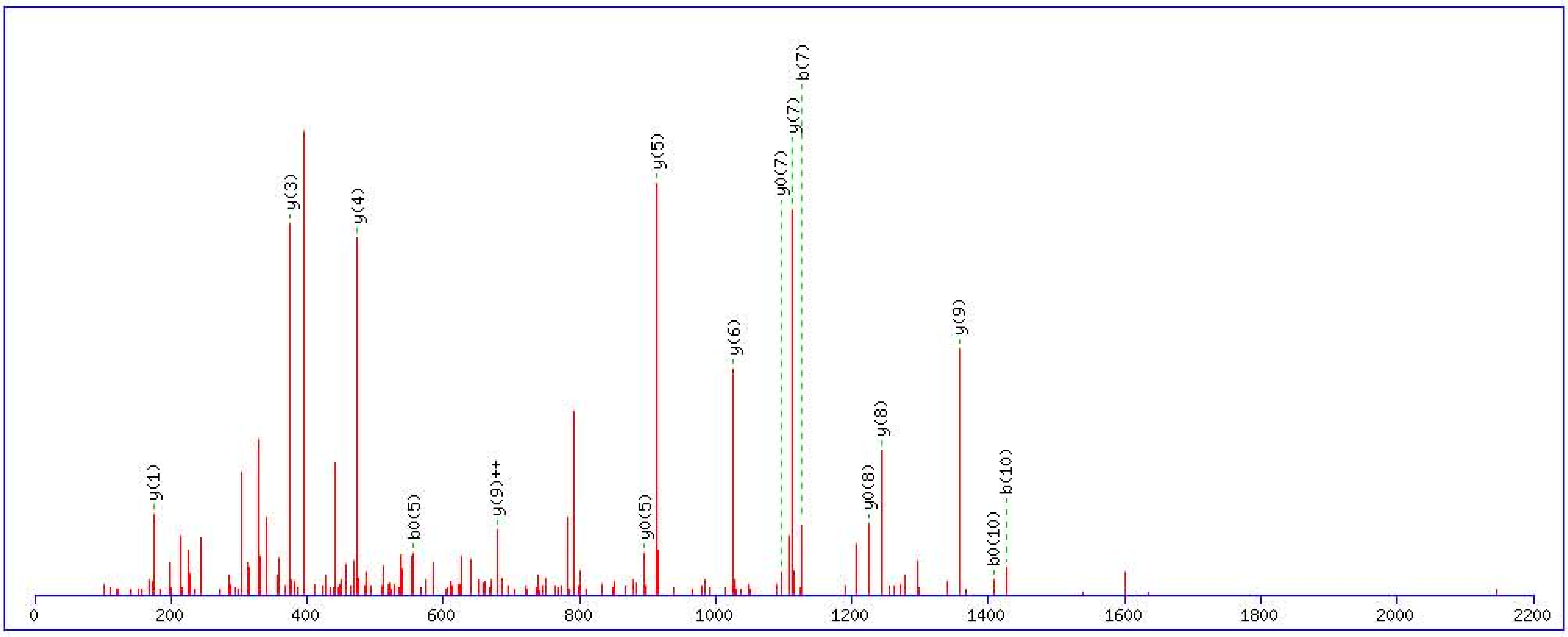
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

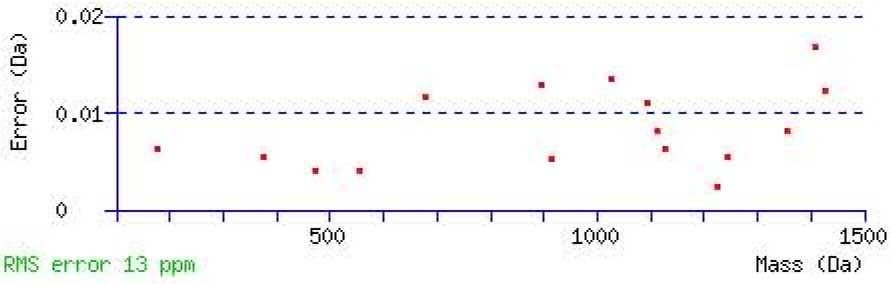
Match to Query 38727: 1598.810388 from(800.412470,2+) rtinseconds(1934) index(6126)
Title: Locus:1.1.1.2927.13 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

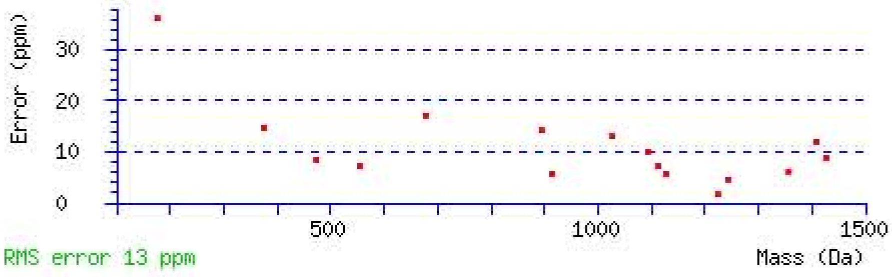
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from [0] to [2200] Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1598.797379
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 8e-005
Matches : 16/106 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							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
50.0	1598.797379	0.013009	ELDESLQVAER
5.9	1598.827271	-0.016883	LQGQLCDVSIR
5.7	1598.790024	0.020364	VTAEGDSHTEVVISR
3.4	1598.787506	0.022882	APQASGPSTPGYR
3.2	1598.823883	-0.013495	TPTEKVEKMFPHR
3.0	1598.797379	0.013009	LEESDVLQEAR
0.9	1598.789993	0.020395	AGATSGELPVVEAENR
0.9	1598.787506	0.022882	AGGSWDLAVQER
0.9	1598.797409	0.012979	EDVDDLVSQLR
0.7	1598.817352	-0.006964	DRAALCQLWR

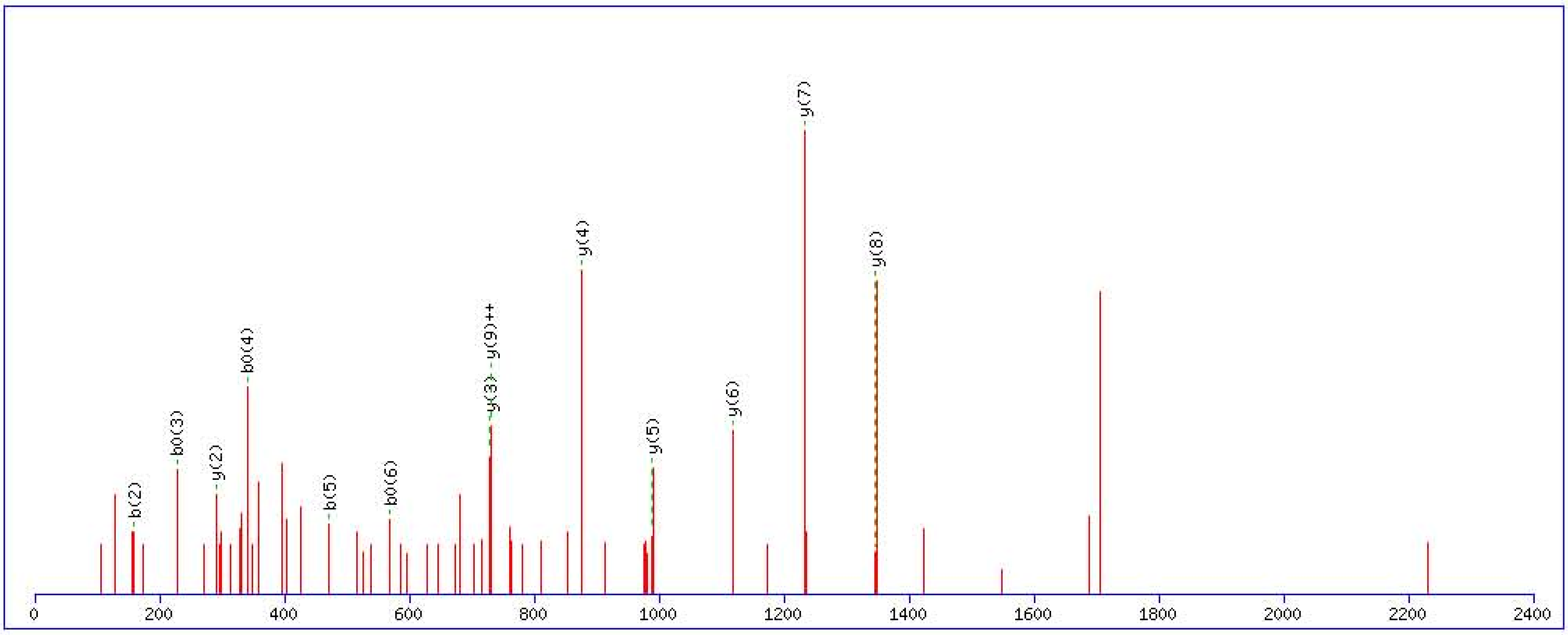
Mascot Search Results

Peptide View

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

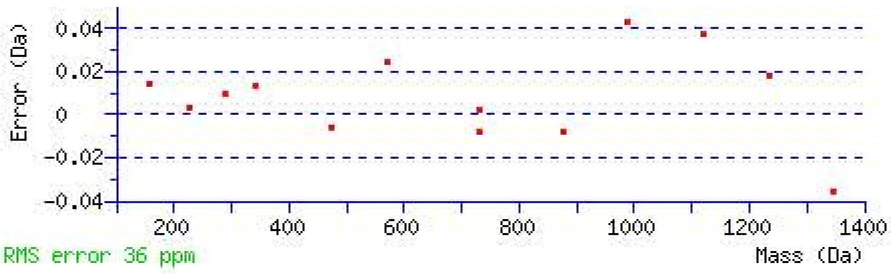
Match to Query 42610: 1703.875348 from(852.944950,2+) rtinseconds(2826) index(30250)
Title: Locus:1.1.1.3125.15 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

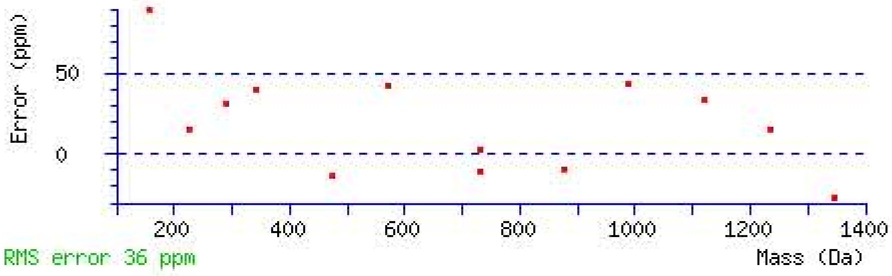
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 33 **Expect:** 0.015
Matches : 13/110 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							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





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
32.8	1703.855240	0.020108	ASSIIDELFQDR

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

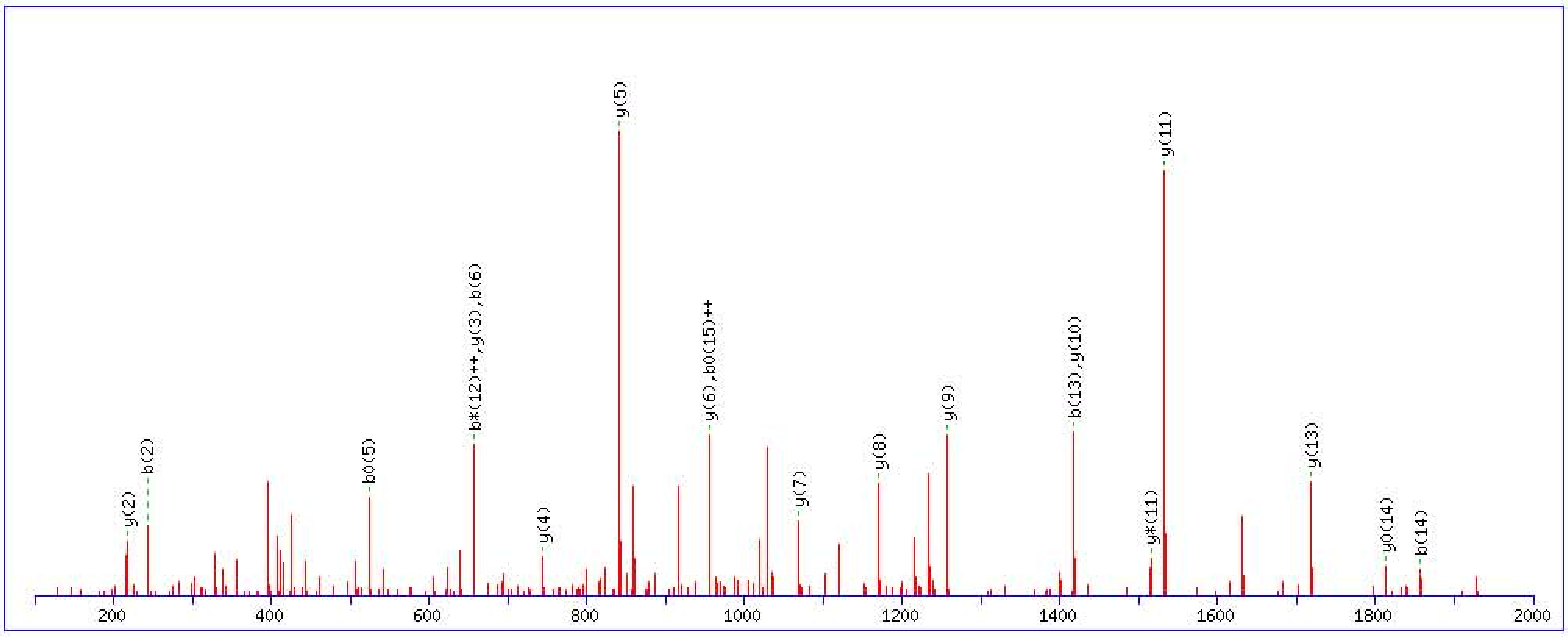
Mascot Search Results

Peptide View

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

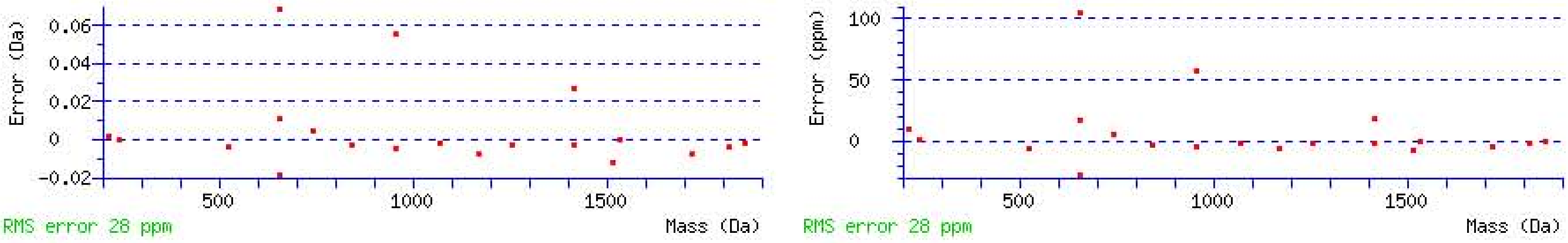
Match to Query 52570: 2073.005588 from(1037.510070,2+) rtinseconds(1778) index(23078)
Title: Locus:1.1.1.2761.25 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 2072.987061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 104 **Expect:** 5.4e-010
Matches : 20/156 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	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
103.8	2072.987061	0.018527	EILSVDCSTNNPSQAK
4.6	2073.023865	-0.018277	QAENAISANERFISAPNNK
0.2	2072.994492	0.011096	ELVKSGVLGADGVCMTFMK

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

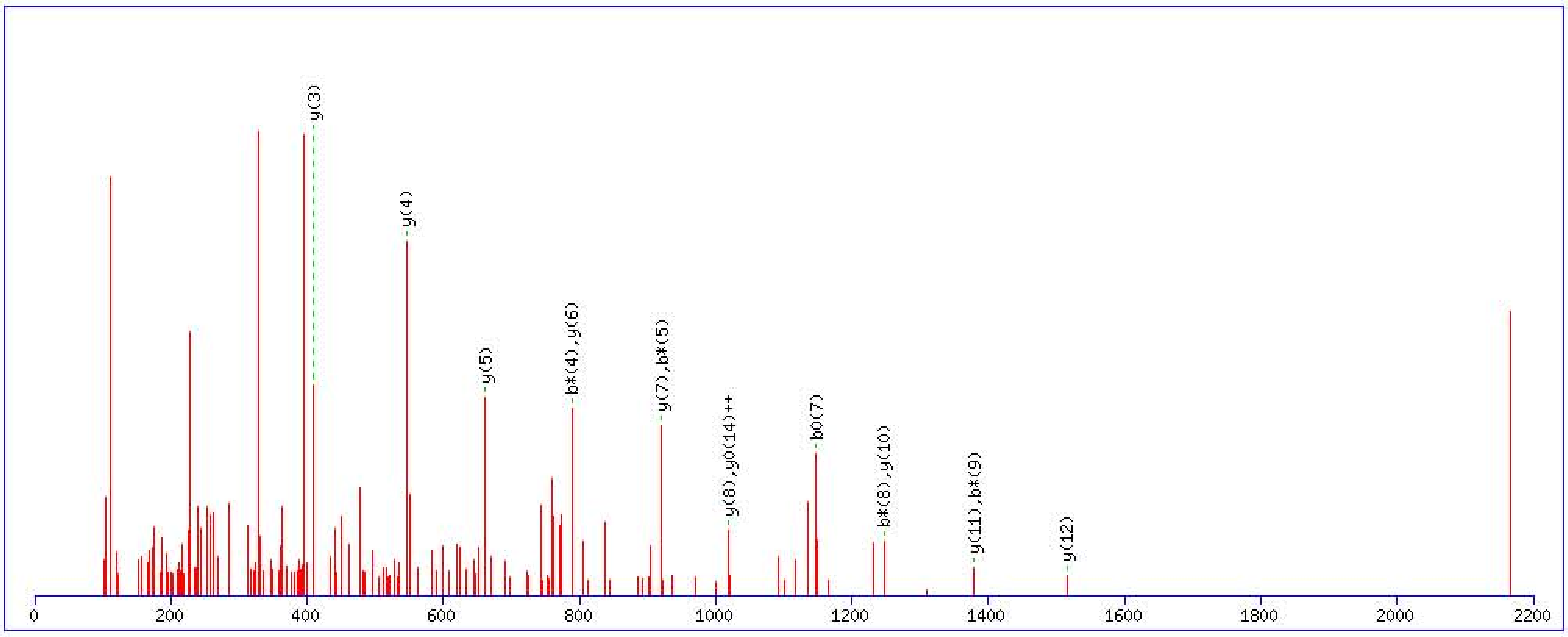
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

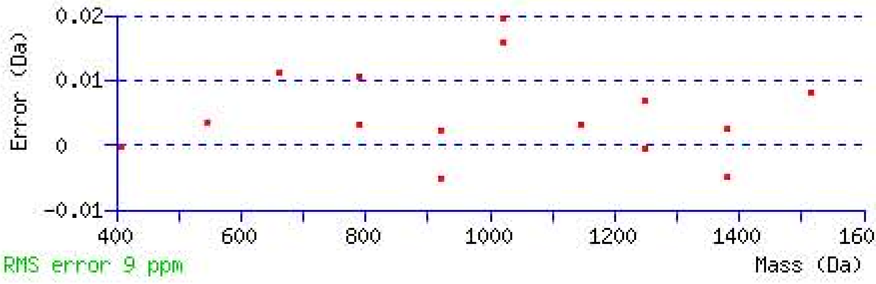
Match to Query 54969: 2183.015816 from(546.761230,4+) rtinseconds(1975) index(24500)
Title: Locus:1.1.1.2830.7 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

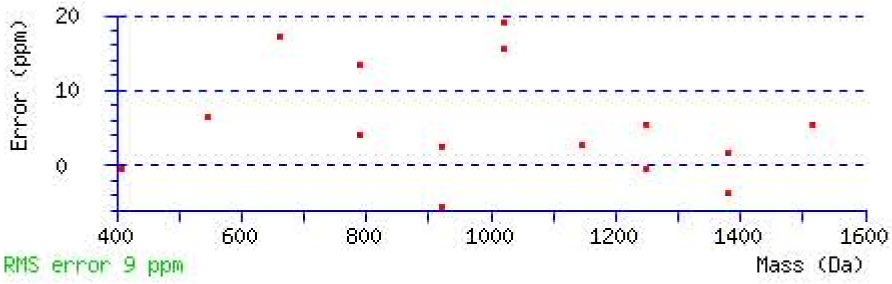
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
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: 63  Expect: 8.1e-006
Matches : 15/162 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	129.065854	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
62.6	2183.007446	0.008370	QQTHMLDVMQDHFSR
62.6	2183.007446	0.008370	QQTHMLDVMQDHFSR
3.9	2183.007446	0.008370	QQTHMLDVMQDHFSR

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

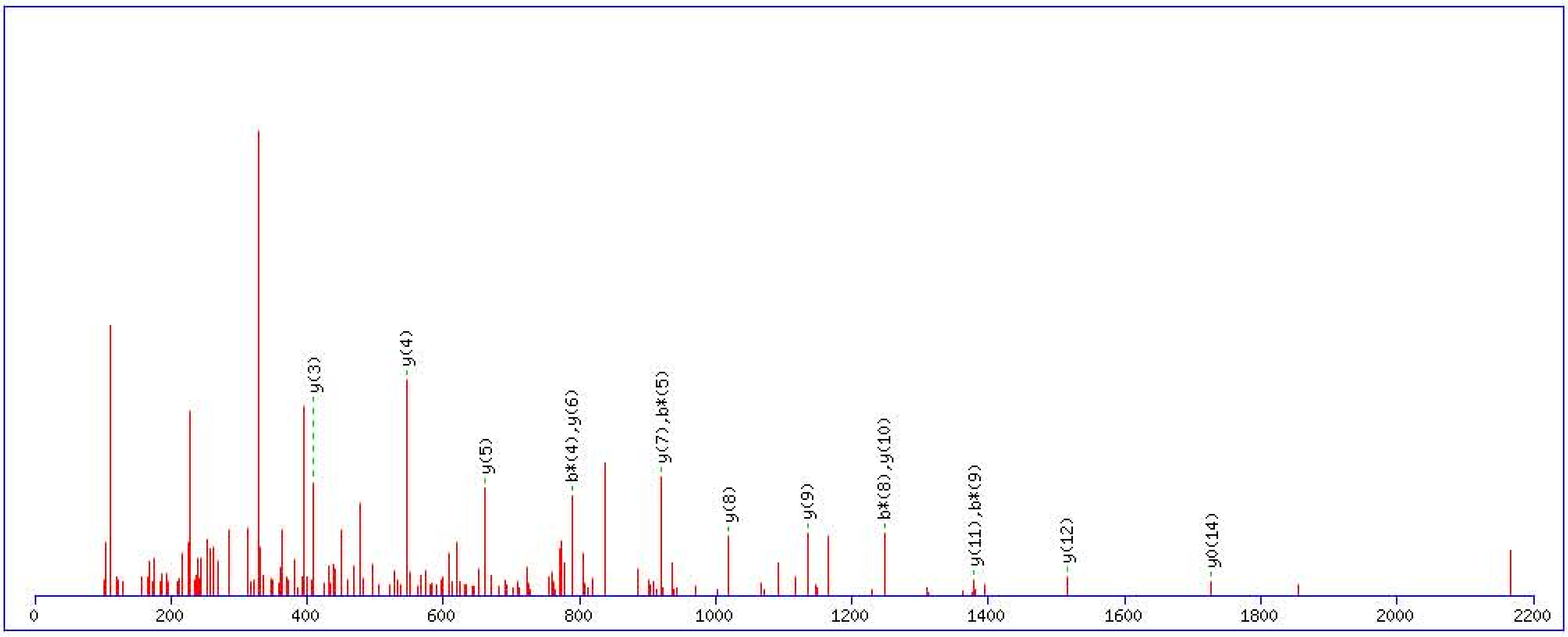
Mascot Search Results

Peptide View

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

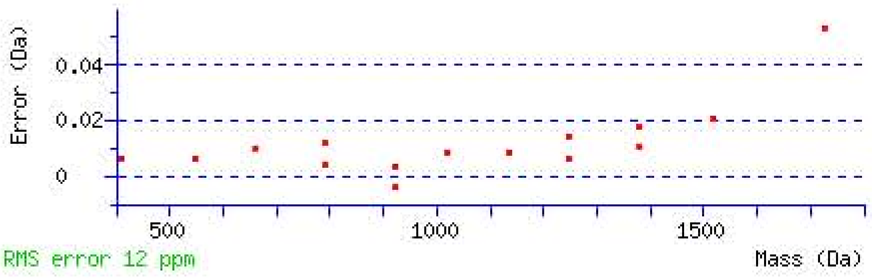
Match to Query 54975: 2183.026576 from(546.763920,4+) rtinseconds(1996) index(6498)
Title: Locus:1.1.1.2949.11 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

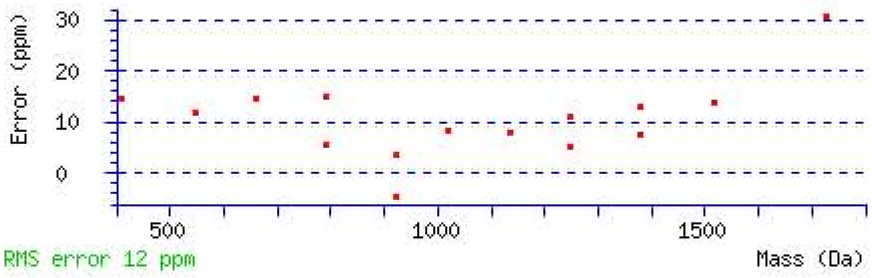
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2183.007446
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 74 **Expect:** 6.5e-007
Matches : 15/162 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	440.232602	220.619939	423.206053	212.106664			Q							15
2	568.291180	284.649228	551.264631	276.135954			Q	1744.789387	872.898332	1727.762838	864.385057	1726.778822	863.893049	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
74.0	2183.007446	0.019130	QQTHMLDVMQDHFSR
70.2	2183.007446	0.019130	QQTHMLDVMQDHFSR

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

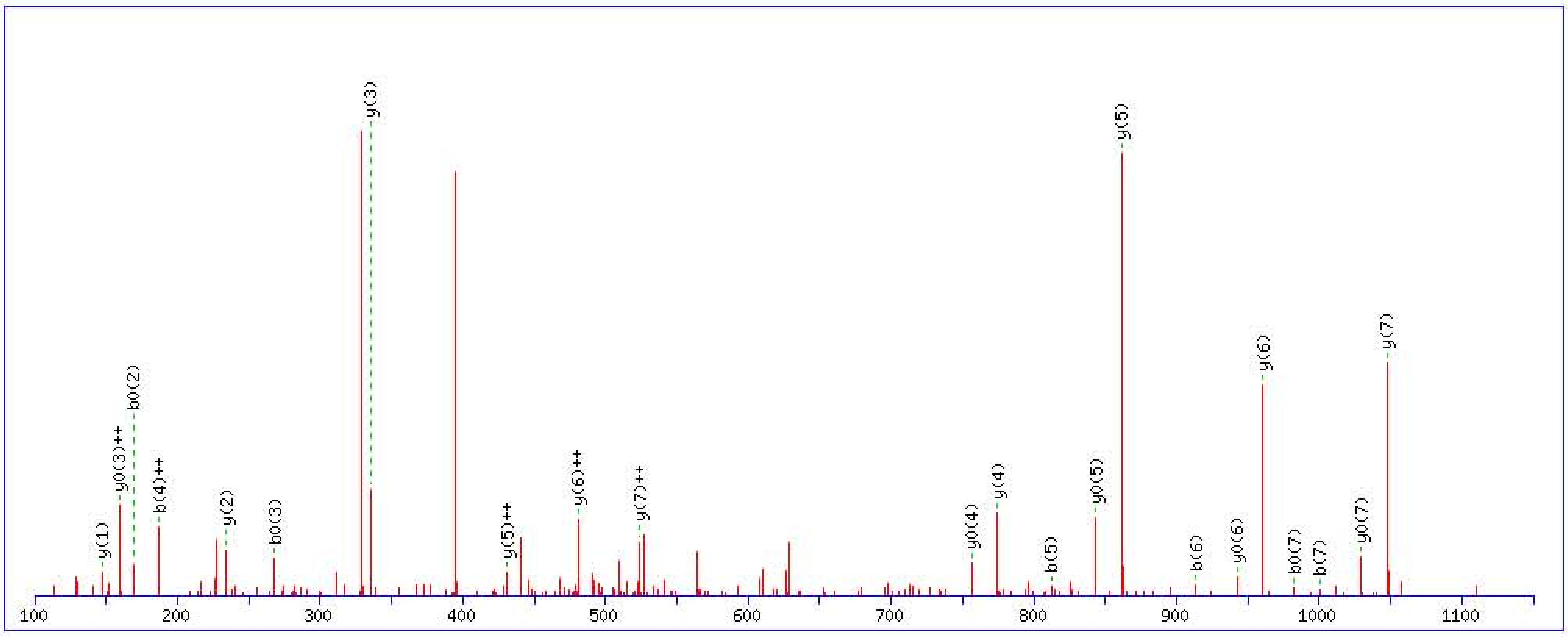
{MATRIX SCIENCE} **Mascot Search Results**

Peptide View

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

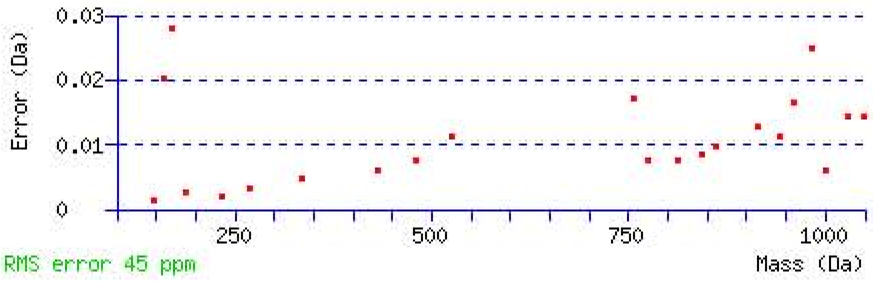
Match to Query 21707: 1145.626548 from(573.820550,2+) rtinseconds(1411) index(56607)
Title: Locus:1.1.1.2914.22 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

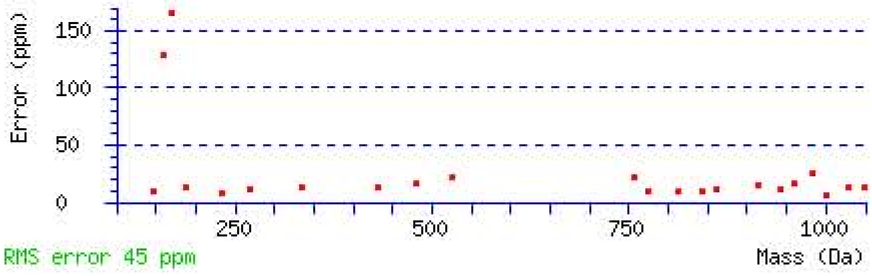
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1145.611450
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0051
Matches : 23/72 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	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
34.9	1145.611450	0.015098	VSVSQTSK
9.8	1145.629196	-0.002648	GEVLGLSSSLGK
5.5	1145.629181	-0.002633	VAKEVVEASSK
4.5	1145.611420	0.015128	KSIMVQSPEK
4.0	1145.619278	0.007270	WELQRSLSK
2.7	1145.629166	-0.002618	TALQEEIKSK
2.0	1145.623337	0.003211	WVDGGKPLFK
1.6	1145.622650	0.003898	VSMDLRANLK
1.5	1145.640411	-0.013863	EIKERVGTSK
1.4	1145.634537	-0.007989	WWKTLREK

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

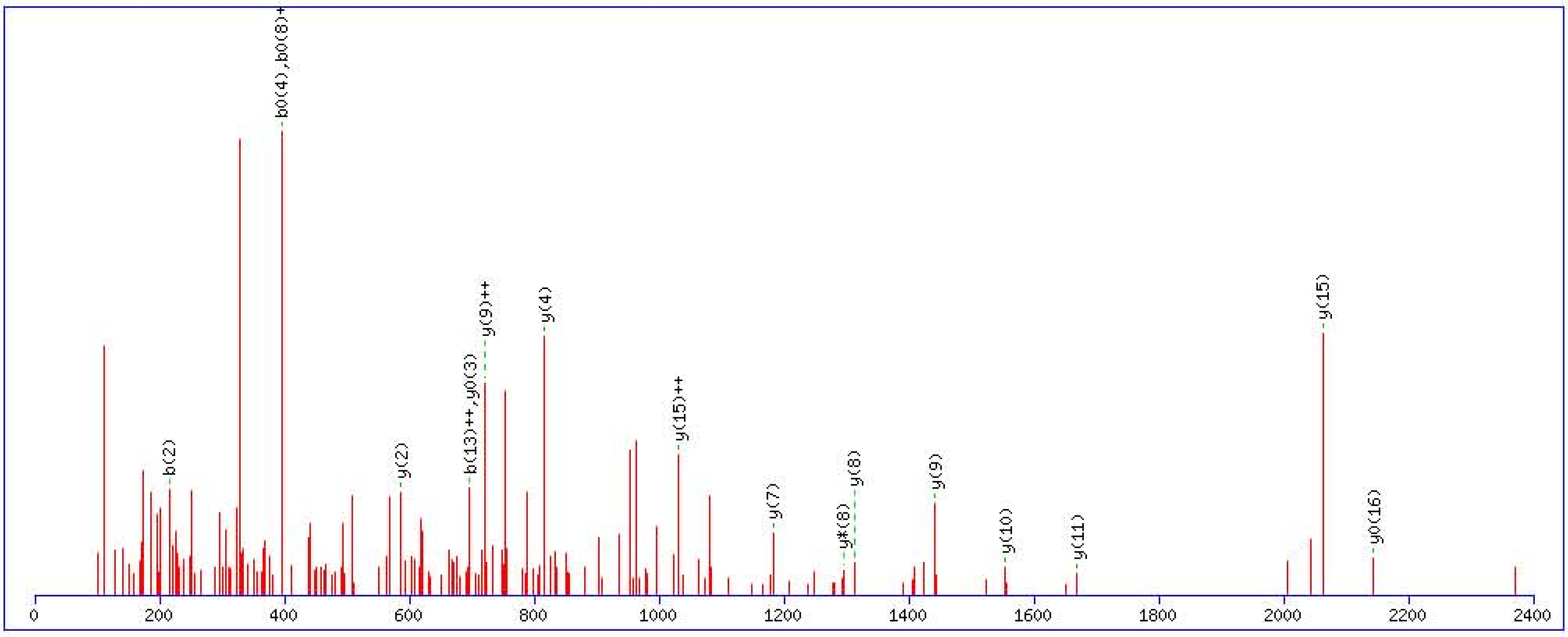
Mascot Search Results

Peptide View

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

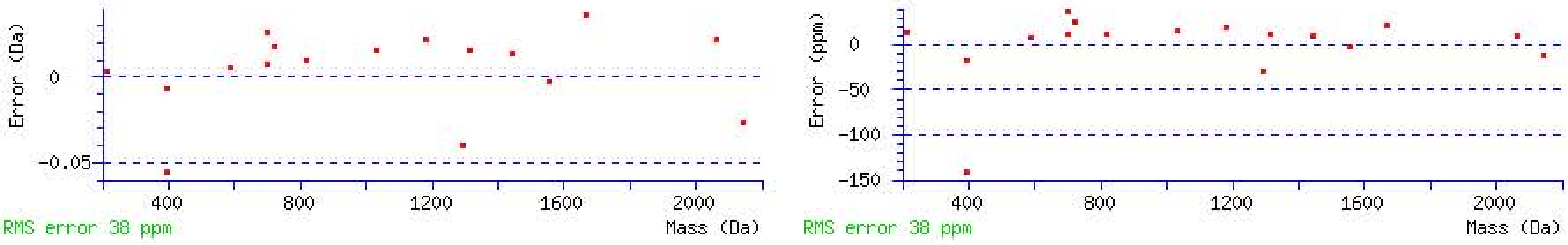
Match to Query 62121: 2474.241216 from(619.567580,4+) rtinseconds(1604) index(58042)
Title: Locus:1.1.1.2982.9 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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: 49  Expect: 0.0004
Matches : 17/194 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	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
48.6	2474.211121	0.030095	ITVVAGEHNIEETEHTEQK

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

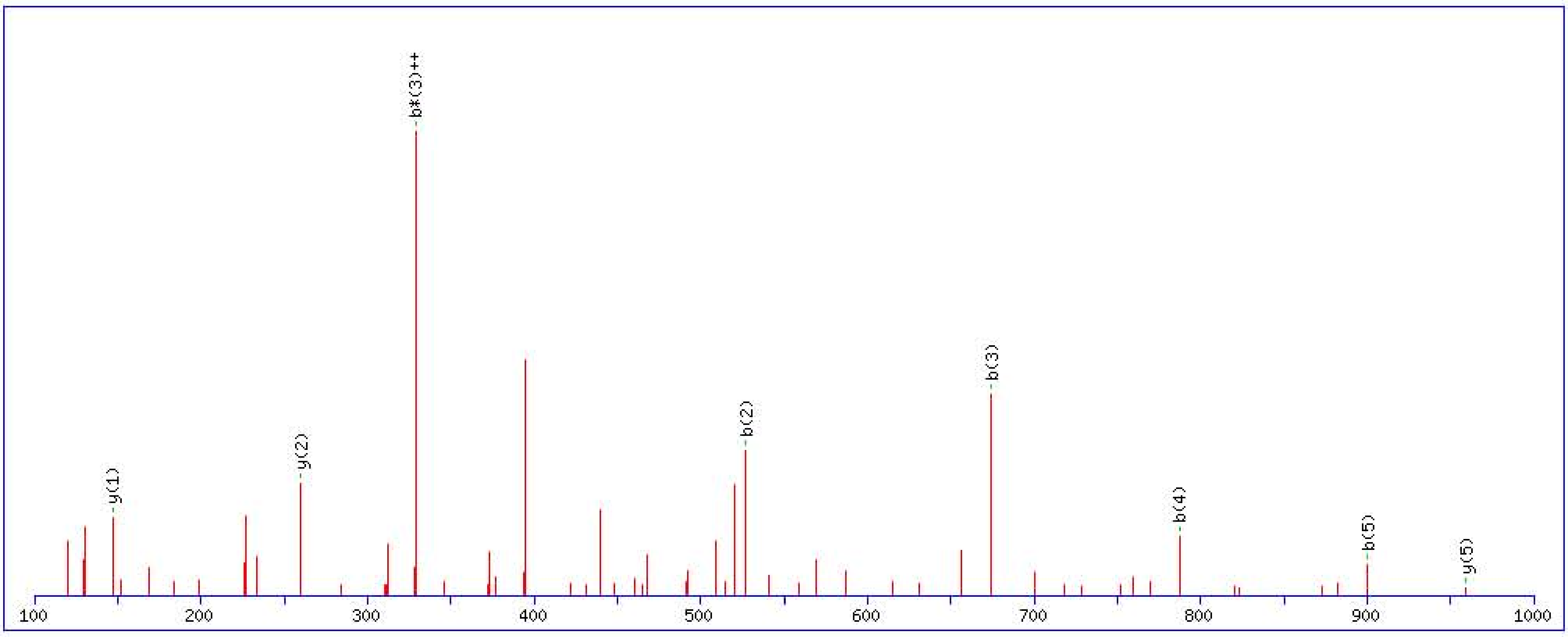
Mascot Search Results

Peptide View

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

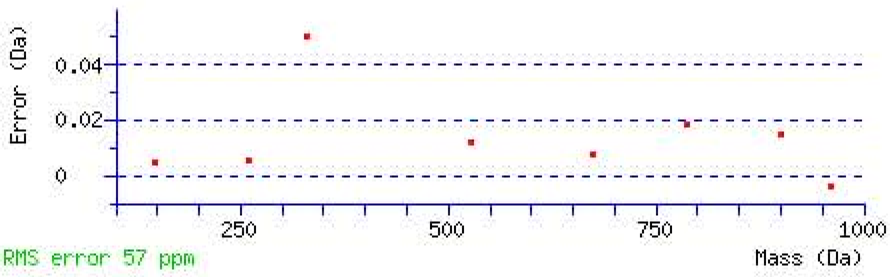
Match to Query 17419: 1045.613508 from(523.814030,2+) rtinseconds(2051) index(61072)
Title: Locus:1.1.1.3137.4 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

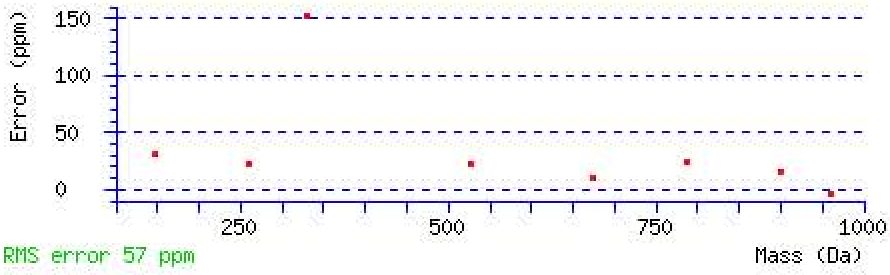
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1045.599411
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0028
Matches : 8/48 fragment ions using 9 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					6
2	***527.264630***	264.135953	510.238081	255.622679	509.254065	255.130671	Q	***959.574672***	480.290974	942.548123	471.777700	5
3	***674.333044***	337.670160	657.306495	329.156885	656.322479	328.664877	F	520.349346	260.678311	503.322797	252.165037	4
4	***787.417108***	394.212192	770.390559	385.698917	769.406543	385.206909	L	373.280932	187.144104	356.254383	178.630830	3
5	***900.501172***	450.754224	883.474623	442.240950	882.490607	441.748942	I	***260.196868***	130.602072	243.170319	122.088798	2
6							K	***147.112804***	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	1045.599411	0.014097	QSFLLK
35.6	1045.599411	0.014097	SQFLIK
19.7	1045.601883	0.011625	EESISKLIK
19.7	1045.613113	0.000395	ESKKSNLLK
19.5	1045.599426	0.014082	VFLCPGLLK
19.3	1045.599411	0.014097	SQLFLK
16.6	1045.628387	-0.014879	FIRQEIIK
16.6	1045.620514	-0.007006	KETMALILK
16.6	1045.599411	0.014097	QVFAPMLLK
16.6	1045.599396	0.014112	YQALLK

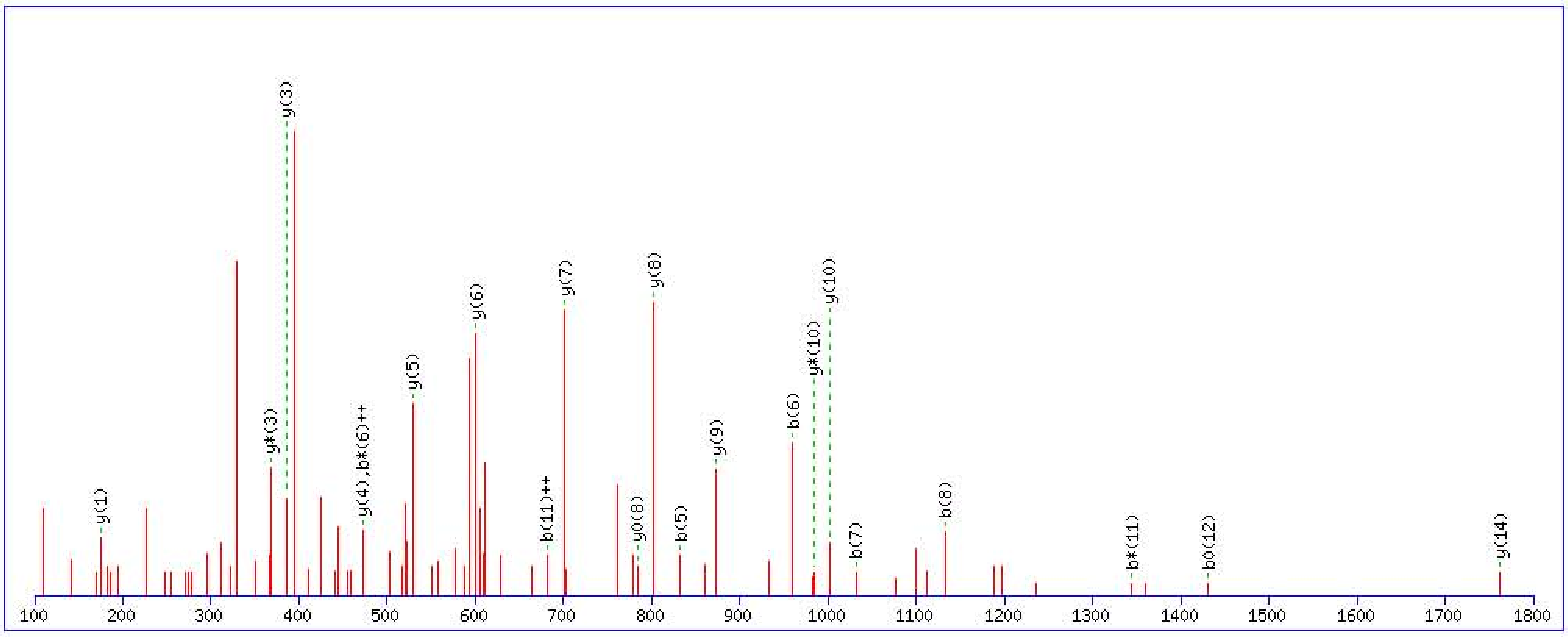
Mascot Search Results

Peptide View

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

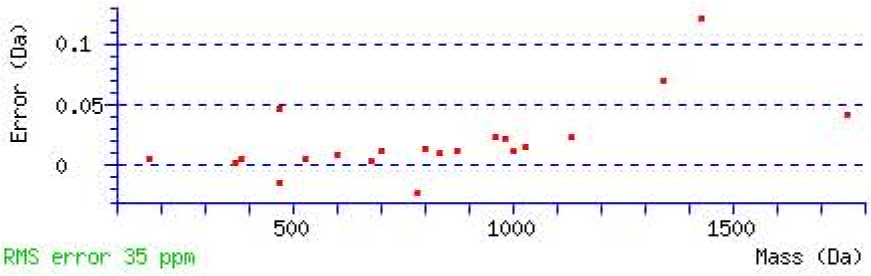
Match to Query 46075: 1831.960512 from(611.660780,3+) rtinseconds(1407) index(56579)
Title: Locus:1.1.1.2913.19 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

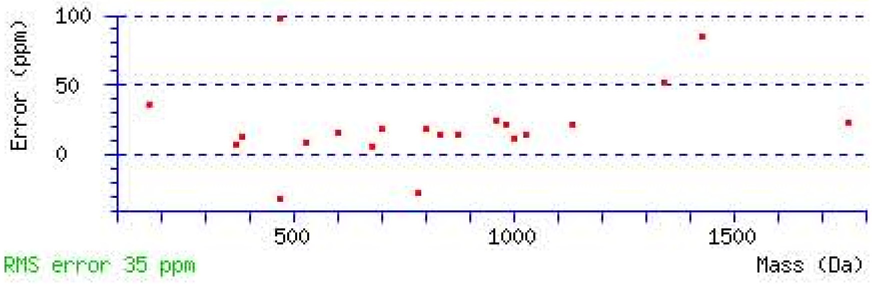
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1831.936295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00061
Matches : 21/150 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	72.044390	36.525833					A							15
2	169.097154	85.052215					P	***1761.906466***	881.456871	1744.879917	872.943597	1743.895901	872.451588	14
3	256.129182	128.568229			238.118617	119.562947	S	1664.853702	832.930489	1647.827153	824.417215	1646.843137	823.925206	13
4	393.188094	197.097685			375.177529	188.092402	H	1577.821674	789.414475	1560.795125	780.901200	1559.811109	780.409192	12
5	**832.413420**	416.710348	815.386871	408.197073	814.402855	407.705065	Q	1440.762762	720.885019	1423.736213	712.371744	1422.752197	711.879736	11
6	**960.471998**	480.739637	943.445449	472.226362	942.461433	471.734354	Q	***1001.537436***	501.272356	984.510887	492.759081	983.526871	492.267073	10
7	**1031.509112**	516.258194	1014.482563	507.744919	1013.498547	507.252911	A	***873.478858***	437.243067	856.452309	428.729792	855.468293	428.237784	9
8	**1132.556791**	566.782034	1115.530242	558.268759	1114.546226	557.776751	T	***802.441744***	401.724510	785.415195	393.211235	784.431179	392.719227	8
9	1233.604470	617.305873	1216.577921	608.792599	1215.593905	608.300591	T	***701.394065***	351.200671	684.367516	342.687396	683.383500	342.195388	7
10	1304.641584	652.824430	1287.615035	644.311156	1286.631019	643.819147	A	***600.346386***	300.676831	583.319837	292.163556	582.335821	291.671548	6
11	1361.663048	681.335162	1344.636499	672.821888	1343.652483	672.329879	G	***529.309272***	265.158274	512.282723	256.644999	511.298707	256.152991	5
12	1448.695076	724.851176	1431.668527	716.337902	1430.684511	715.845893	S	***472.287808***	236.647542	455.261259	228.134267	454.277243	227.642259	4
13	1545.747840	773.377558	1528.721291	764.864284	1527.737275	764.372276	P	***385.255780***	193.131528	368.229231	184.618253			3
14	1658.831904	829.919590	1641.805355	821.406316	1640.821339	820.914307	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 APSHQQATTAGSPLR
(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	1831.936295	0.024217	APSHQQATTAGSPLR
35.4	1831.936295	0.024217	APSHQQATTAGSPLR

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

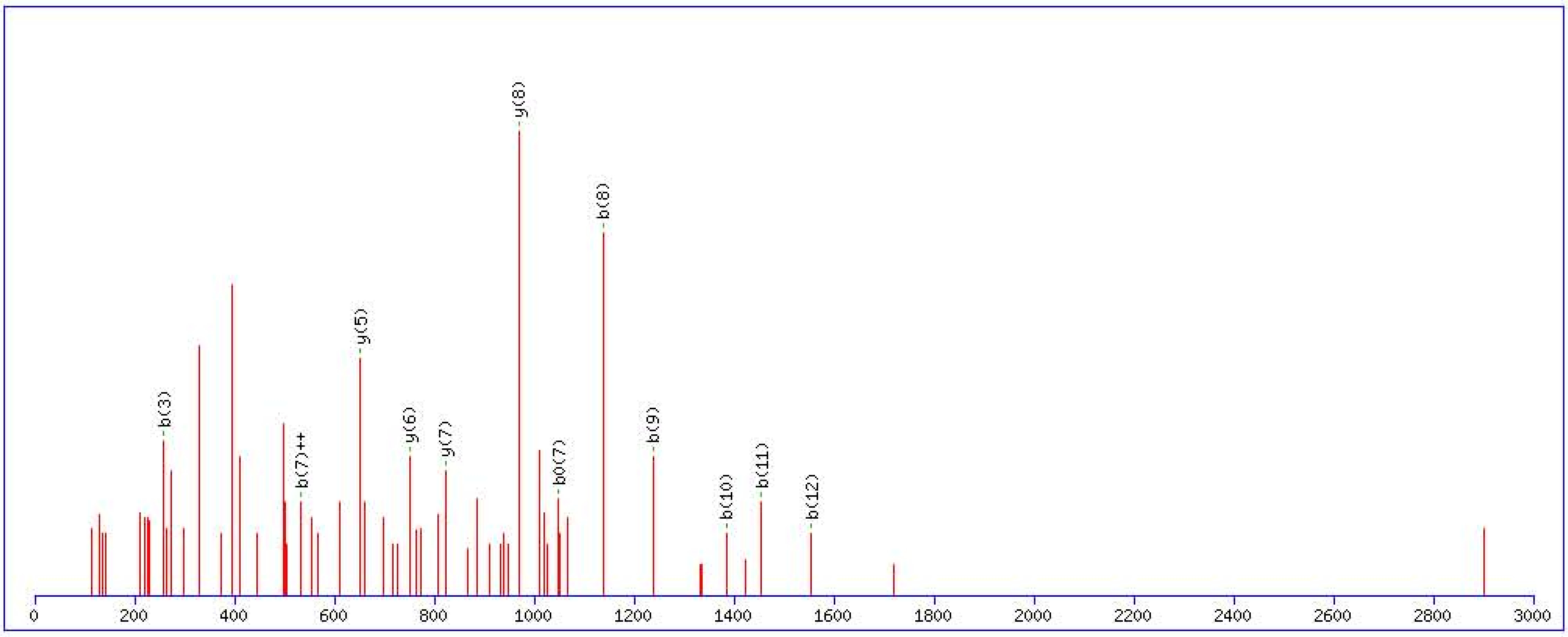
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

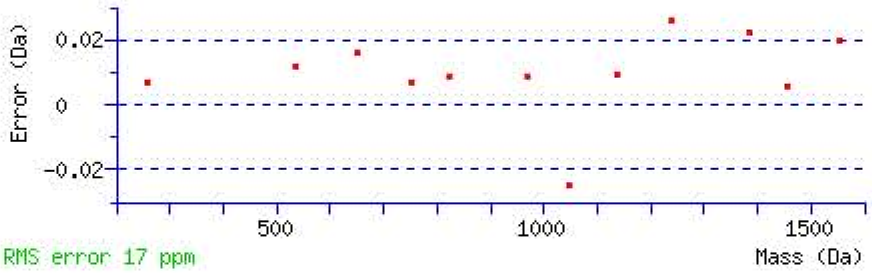
Match to Query 55490: 2205.101652 from(736.041160,3+) rtinseconds(2727) index(83683)
Title: Locus:1.1.1.2299.11 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

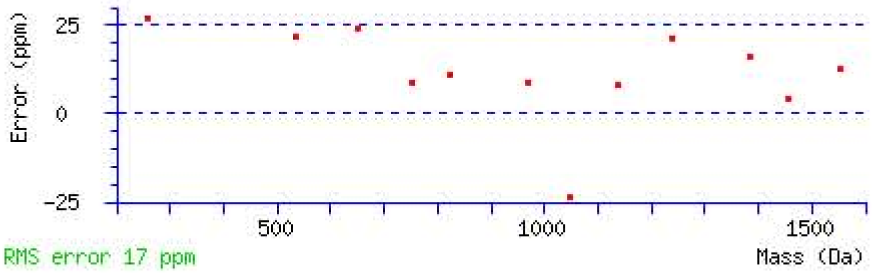
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2205.077591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.009
Matches : 12/174 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							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	628.293682	314.650479	611.267133	306.137205	610.283117	305.645197	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	1578.798477	789.902877	1561.771928	781.389602	1560.787912	780.897594	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
34.9	2205.077591	0.024061	AADIEQQAVFAVFDENK
34.9	2205.077591	0.024061	AADIEQQAVFAVFDENK

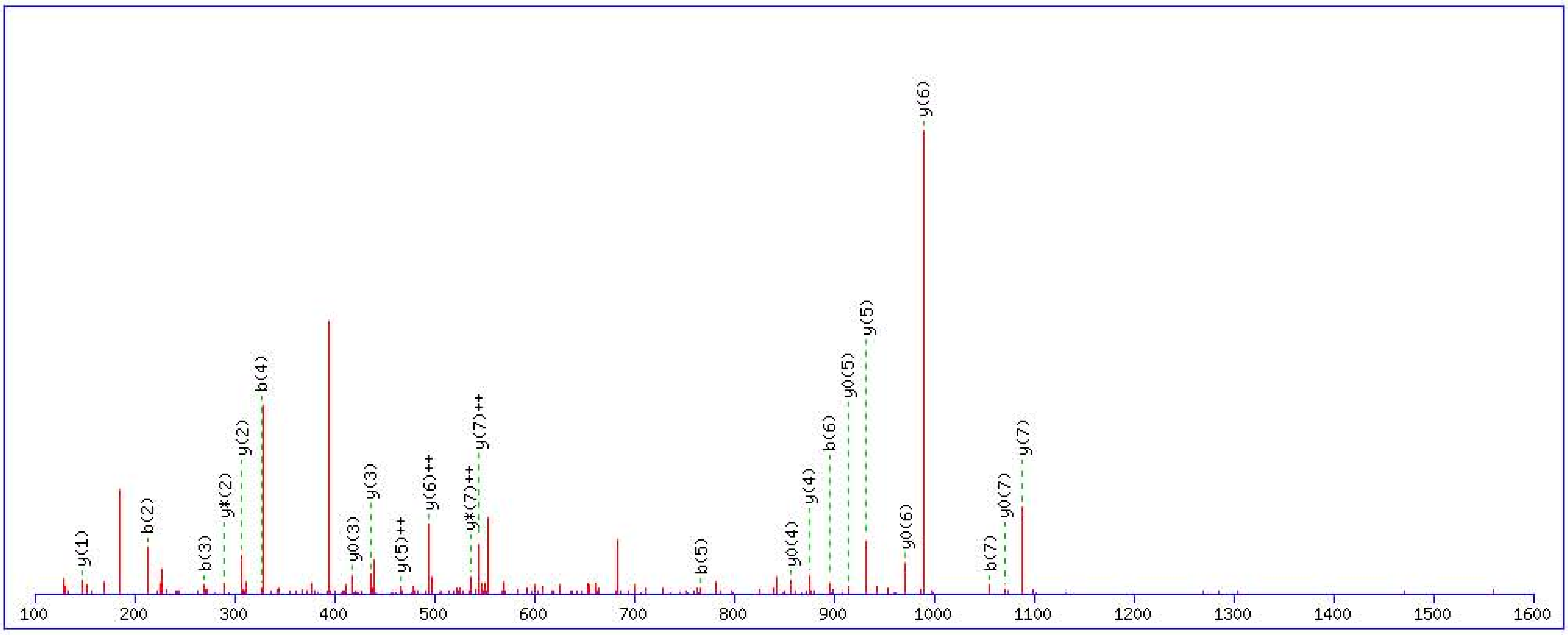
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

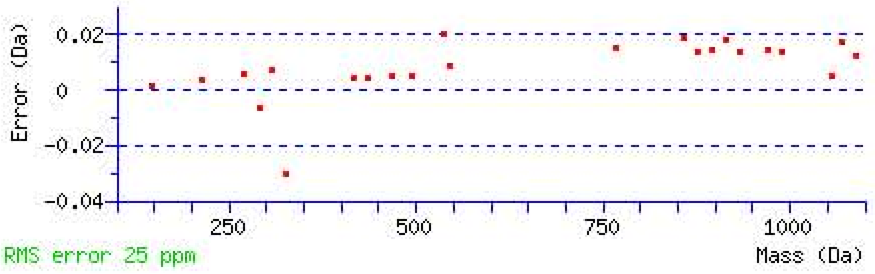
Match to Query 23708: 1200.614928 from(601.314740,2+) rtinseconds(1413) index(56631)
Title: Locus:1.1.1.2915.21 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

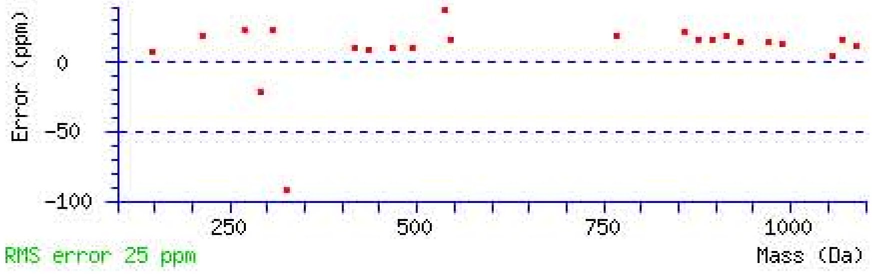
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1200.599503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.0029
Matches : 23/62 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					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
33.0	1200.599503	0.015425	IVGGQECK
5.6	1200.628479	-0.013551	IVQISGNSMPR
3.4	1200.621048	-0.006120	IRQKEEENR
2.1	1200.598587	0.016341	ILADLEEENR
1.3	1200.599503	0.015425	LIQGDGCK
0.4	1200.609863	0.005065	QTVEADVNGLR

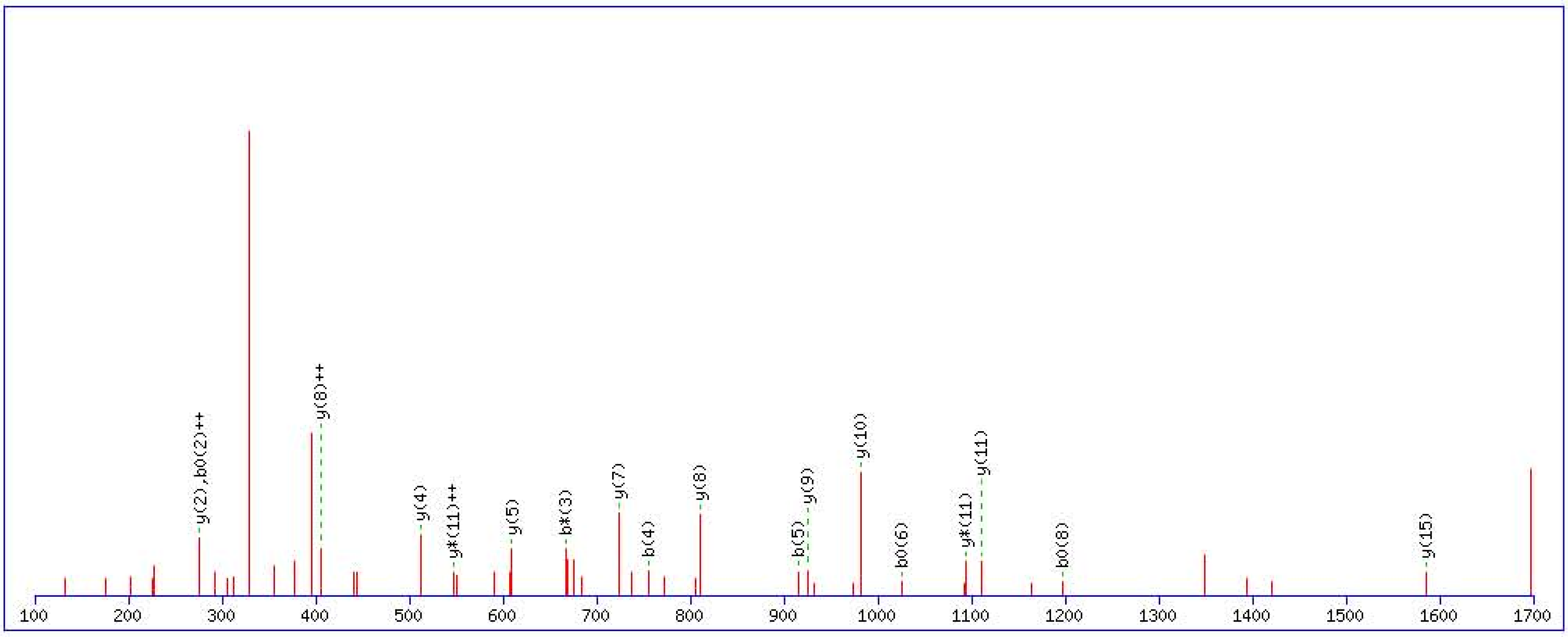
Mascot Search Results

Peptide View

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

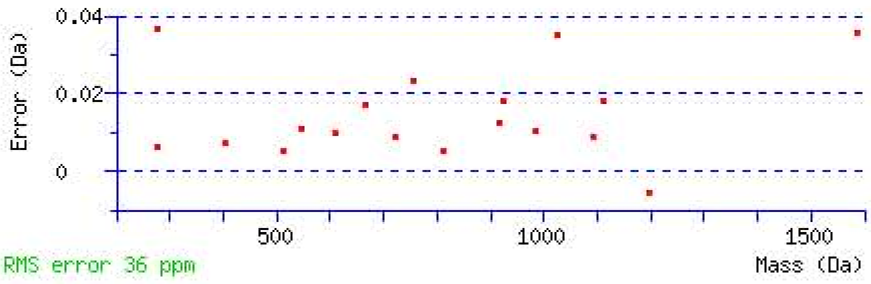
Match to Query 51371: 2023.911732 from(675.644520,3+) rtinseconds(1313) index(55970)
Title: Locus:1.1.1.2880.26 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

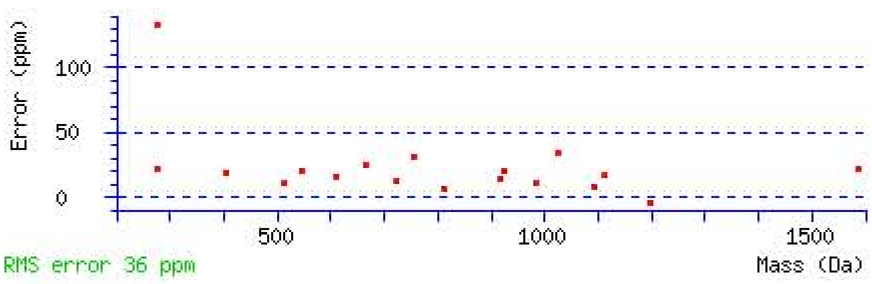
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 56  Expect: 5.9e-006
Matches : 18/176 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							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
56.4	2023.884033	0.027699	QEDACQGDSGGPHVTR
24.8	2023.884033	0.027699	QEDACQGDSGGPHVTR
0.6	2023.930908	-0.019176	WDAWNELKGTSKEDAMK

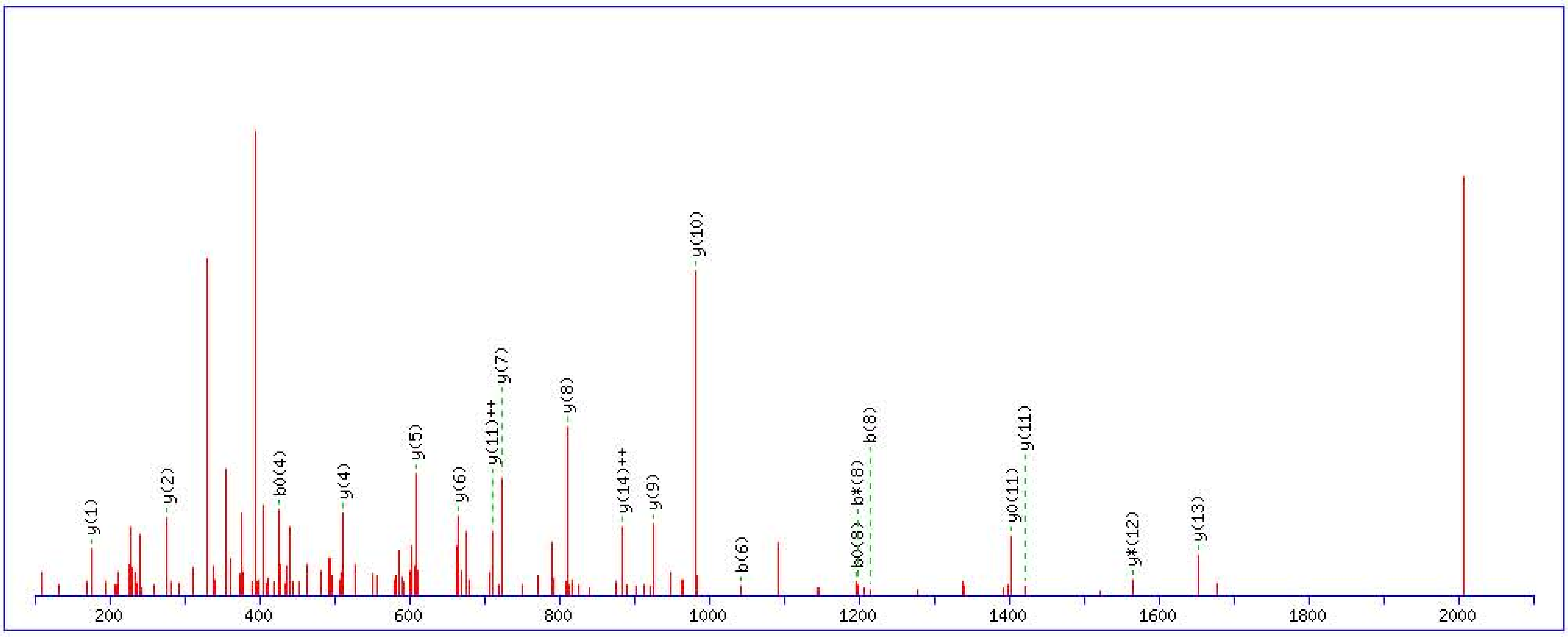
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

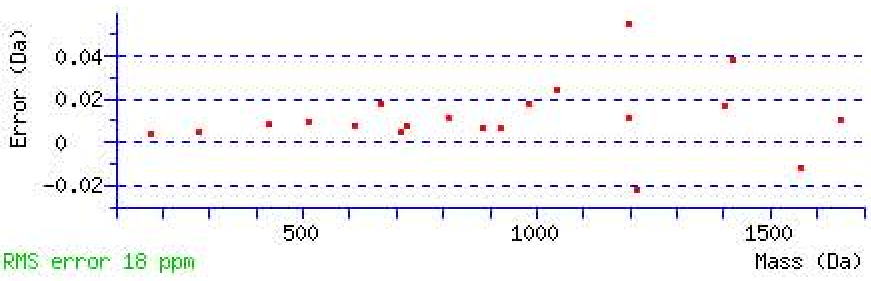
Match to Query 51373: 2023.912212 from(675.644680,3+) rtinseconds(1327) index(56070)
Title: Locus:1.1.1.2885.11 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

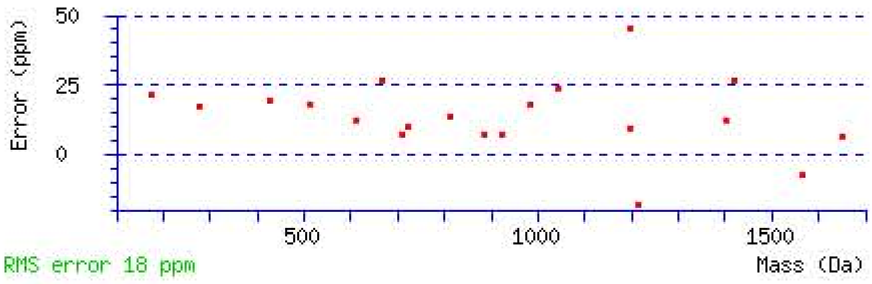
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2023.884033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 76  Expect: 8.7e-008
Matches : 20/176 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	129.065854	65.036565	112.039305	56.523291			Q							16
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	E	1896.832709	948.919993	1879.806160	940.406718	1878.822144	939.914710	15
3	373.135390	187.071333	356.108841	178.558059	355.124825	178.066051	D	1767.790116	884.398696	1750.763567	875.885422	1749.779551	875.393414	14
4	444.172504	222.589890	427.145955	214.076616	426.161939	213.584608	A	***1652.763173***	826.885225	1635.736624	818.371950	1634.752608	817.879942	13
5	604.203153	302.605215	587.176604	294.091940	586.192588	293.599932	C	1581.726059	791.366668	1564.699510	782.853393	1563.715494	782.361385	12
6	**1043.428479**	522.217878	1026.401930	513.704603	1025.417914	513.212595	Q	***1421.695410***	711.351343	1404.668861	702.838069	1403.684845	702.346061	11
7	1100.449943	550.728610	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	599.236799	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	671.263545	G	***723.389649***	362.198463	706.363100	353.685188	705.379084	353.193180	7
11	1416.551842	708.779559	1399.525293	700.266285	1398.541277	699.774277	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	748.300659	P	***609.346721***	305.176999	592.320172	296.663724	591.336156	296.171716	5
13	1650.663518	825.835397	1633.636969	817.322123	1632.652953	816.830115	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	866.364322	V	375.235045	188.121161	358.208496	179.607886	357.224480	179.115878	3
15	1850.779611	925.893444	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
75.8	2023.884033	0.028179	QEDACQGDSGGPHVTR
45.2	2023.884033	0.028179	QEDACQGDSGGPHVTR
0.5	2023.930908	-0.018696	WDAWNELKGTSKEDAMK

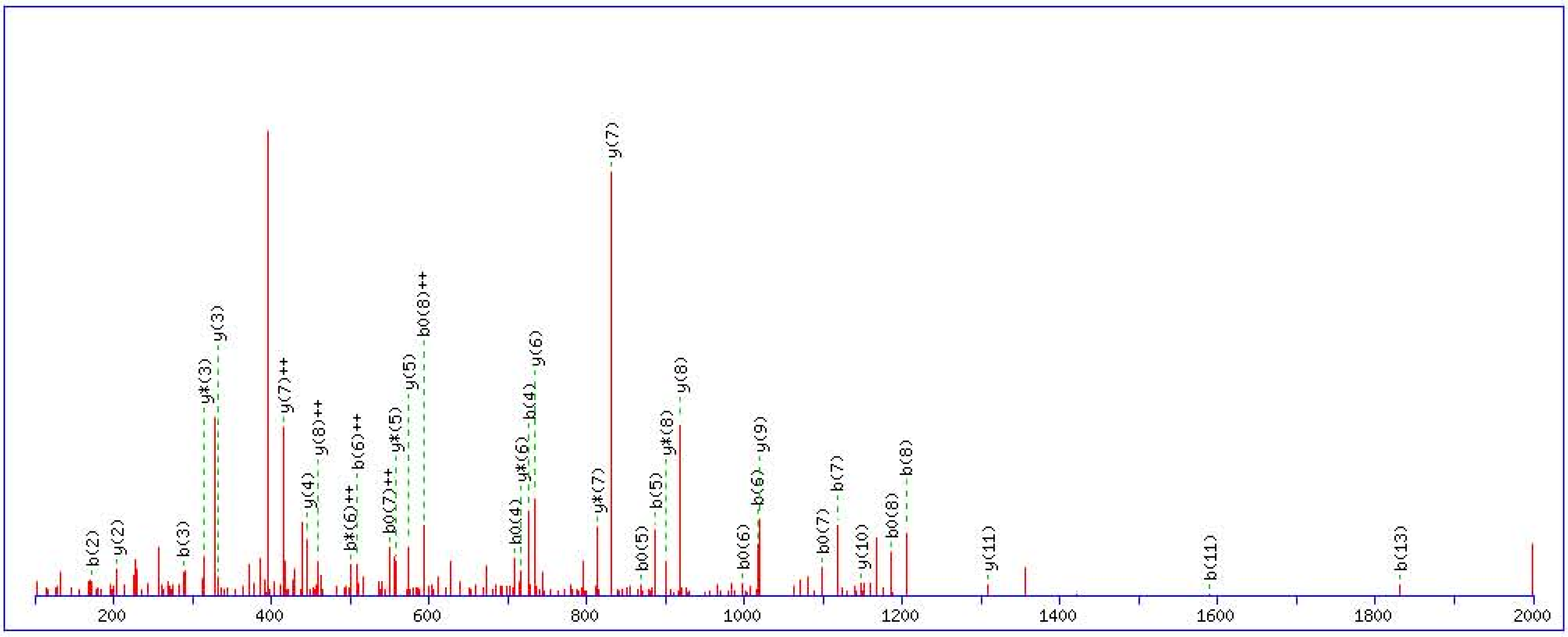
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

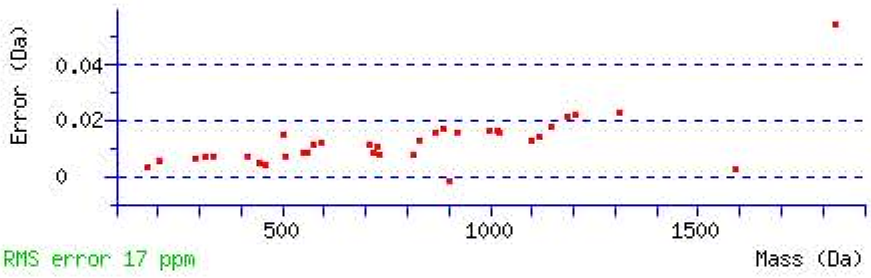
Match to Query 51616: 2033.854272 from(678.958700,3+) rtinseconds(1342) index(56128)
Title: Locus:1.1.1.2890.14 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

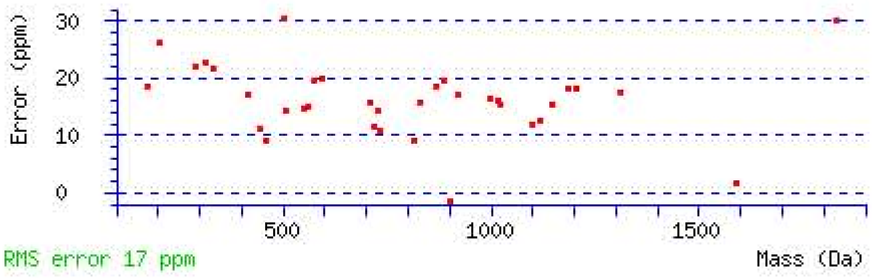
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2033.824127
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 5.5e-005
Matches : 35/148 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	116.034219	58.520748			98.023654	49.515465	D							15
2	***173.055683***	87.031479			155.045118	78.026197	G	1919.804446	960.405861	1902.777897	951.892587	1901.793881	951.400579	14
3	***288.082626***	144.544951			270.072061	135.539669	D	1862.782982	931.895129	1845.756433	923.381855	1844.772417	922.889847	13
4	***727.307952***	364.157614	710.281403	355.644340	709.297387	355.152332	Q	1747.756039	874.381658	1730.729490	865.868383	1729.745474	865.376375	12
5	***887.338601***	444.172939	870.312052	435.659664	869.328036	435.167656	C	***1308.530713***	654.768995	1291.504164	646.255720	1290.520148	645.763712	11
6	***1016.381194***	508.694235	999.354645	500.180961	998.370629	499.688953	E	***1148.500064***	574.753670	1131.473515	566.240396	1130.489499	565.748388	10
7	***1117.428873***	559.218075	1100.402324	550.704800	1099.418308	550.212792	T	***1019.457471***	510.232374	1002.430922	501.719099	1001.446906	501.227091	9
8	***1204.460901***	602.734089	1187.434352	594.220814	1186.450336	593.728806	S	***918.409792***	459.708534	901.383243	451.195260	900.399227	450.703252	8
9	1301.513665	651.260471	1284.487116	642.747196	1283.503100	642.255188	P	***831.377764***	416.192520	814.351215	407.679246			7
10	1461.544314	731.275795	1444.517765	722.762521	1443.533749	722.270513	C	***734.325000***	367.666138	717.298451	359.152864			6
11	***1589.602892***	795.305084	1572.576343	786.791810	1571.592327	786.299802	Q	***574.294351***	287.650814	557.267802	279.137539			5
12	1703.645819	852.326548	1686.619270	843.813273	1685.635254	843.321265	N	***446.235773***	223.621524	429.209224	215.108250			4
13	***1831.704397***	916.355837	1814.677848	907.842562	1813.693832	907.350554	Q	***332.192846***	166.600061	315.166297	158.086787			3
14	1888.725861	944.866569	1871.699312	936.353294	1870.715296	935.861286	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 DGDQCETSPCQNQGK
(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	2033.824127	0.030145	DGDQCETSPCQNQGK

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

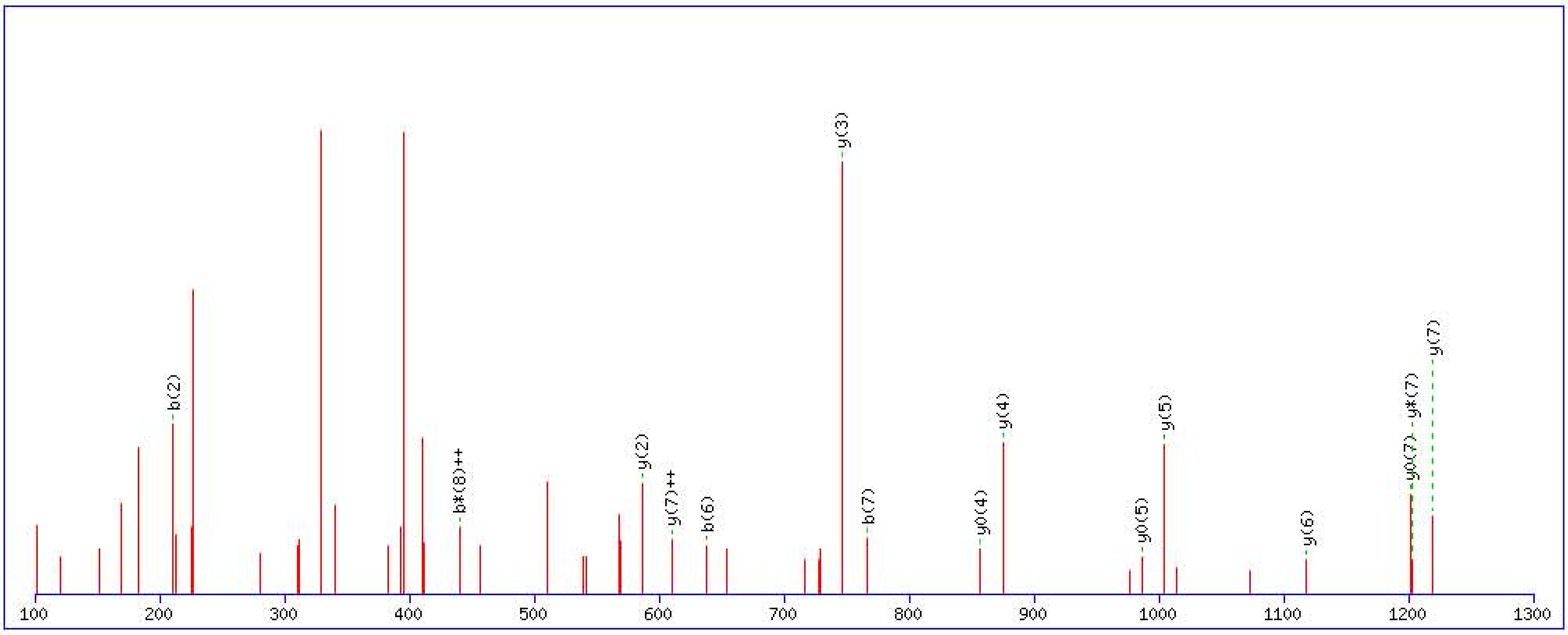
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPLVTNEECQK**
Found in **FA11_HUMAN**, Coagulation factor XI OS=Homo sapiens GN=F11 PE=1 SV=1

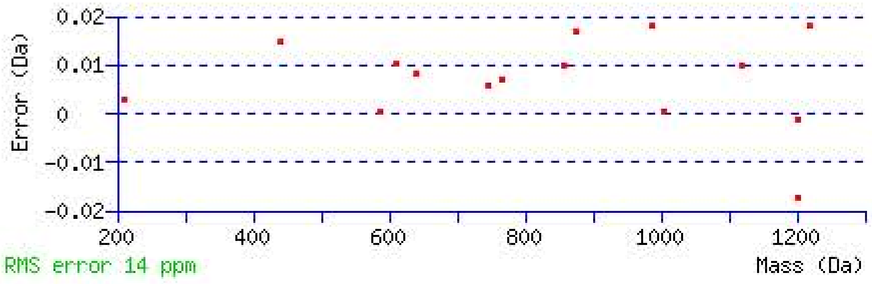
Match to Query 40962: 1640.836782 from(547.952870,3+) rtinseconds(1861) index(77829)
Title: Locus:1.1.1.1999.12 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

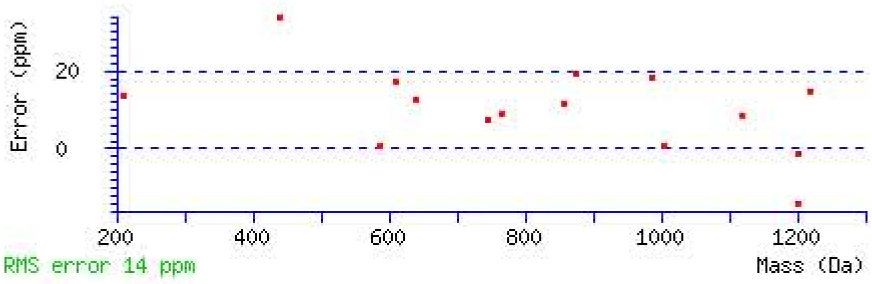
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1640.826584
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 31 **Expect:** 0.019
Matches : 15/96 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	114.091340	57.549308					I							11
2	**211.144104**	106.075690					P	1528.749813	764.878545	1511.723264	756.365270	1510.739248	755.873262	10
3	324.228168	162.617722					L	1431.697049	716.352163	1414.670500	707.838888	1413.686484	707.346880	9
4	423.296582	212.151929					V	1318.612985	659.810131	1301.586436	651.296856	1300.602420	650.804848	8
5	524.344261	262.675769			506.333696	253.670486	T	***1219.544571***	610.275924	1202.518022	601.762649	1201.534006	601.270641	7
6	**638.387188**	319.697232	621.360639	311.183958	620.376623	310.691950	N	***1118.496892***	559.752084	1101.470343	551.238810	1100.486327	550.746802	6
7	**767.429781**	384.218529	750.403232	375.705254	749.419216	375.213246	E	***1004.453965***	502.730621	987.427416	494.217346	986.443400	493.725338	5
8	896.472374	448.739825	879.445825	440.226551	878.461809	439.734543	E	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
9	1056.503023	528.755150	1039.476474	520.241875	1038.492458	519.749867	C	***746.368779***	373.688028	729.342230	365.174753			3
10	1495.728349	748.367813	1478.701800	739.854538	1477.717784	739.362530	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 IPLVTNEECQK
(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	1640.826584	0.010198	IPLVTNEECQK

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

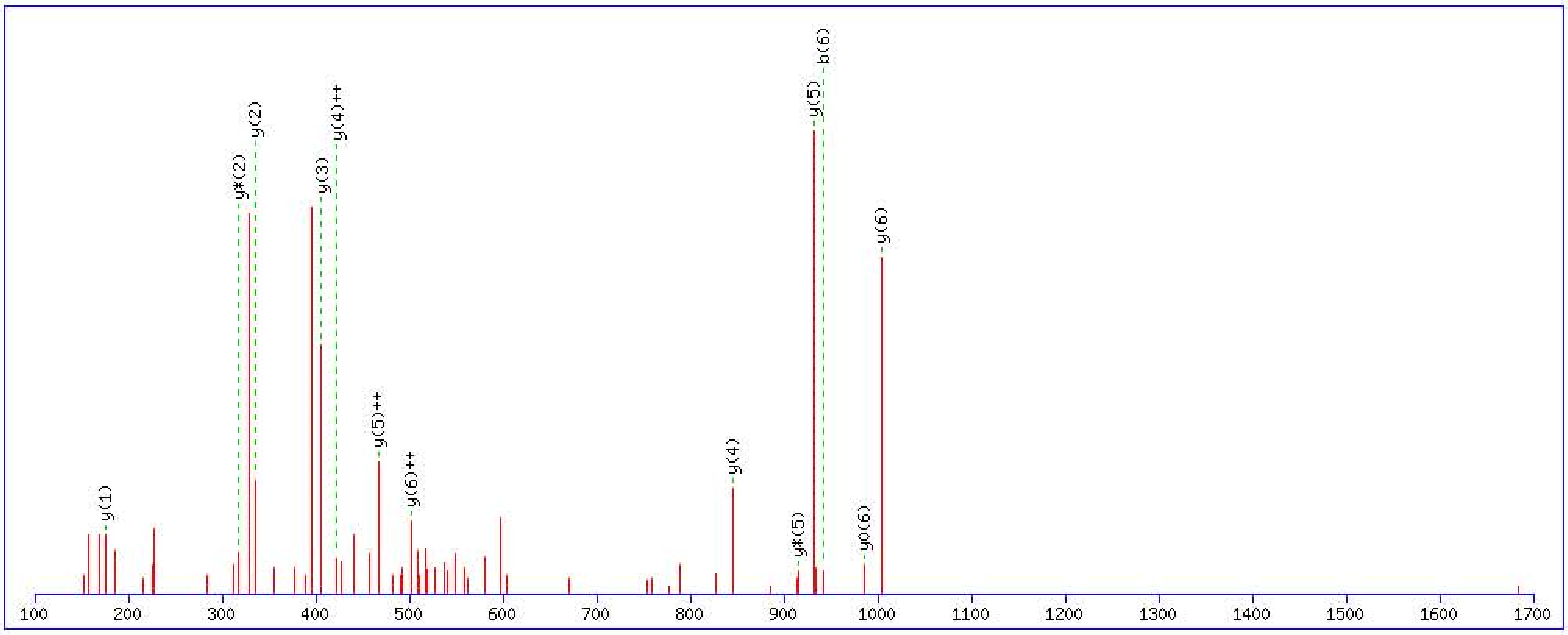
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

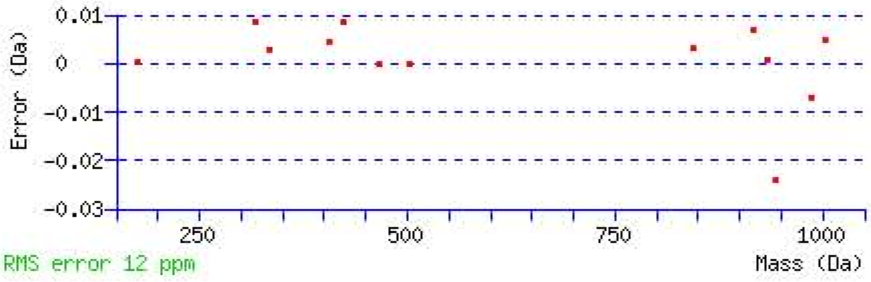
Match to Query 19886: 1115.558848 from(558.786700,2+) rtinseconds(1337) index(19767)
Title: Locus:1.1.1.2608.20 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

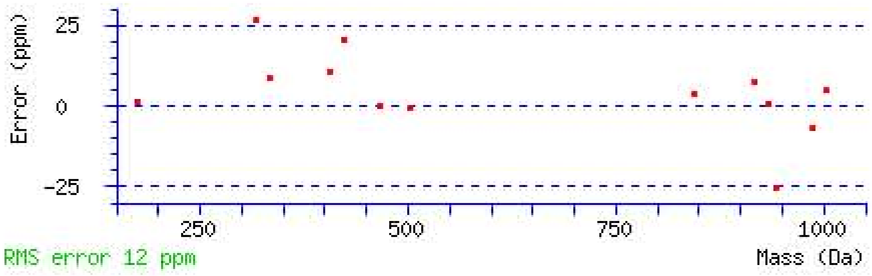
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1115.557953
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.021
Matches : 13/54 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	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
26.4	1115.557953	0.000895	LASQACR
8.1	1115.543350	0.015498	SFCYISALR
3.9	1115.557083	0.001765	IQEAAVQSDR
3.7	1115.550552	0.008296	LAAGSRCPER
0.7	1115.546722	0.012126	LAQDACK

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

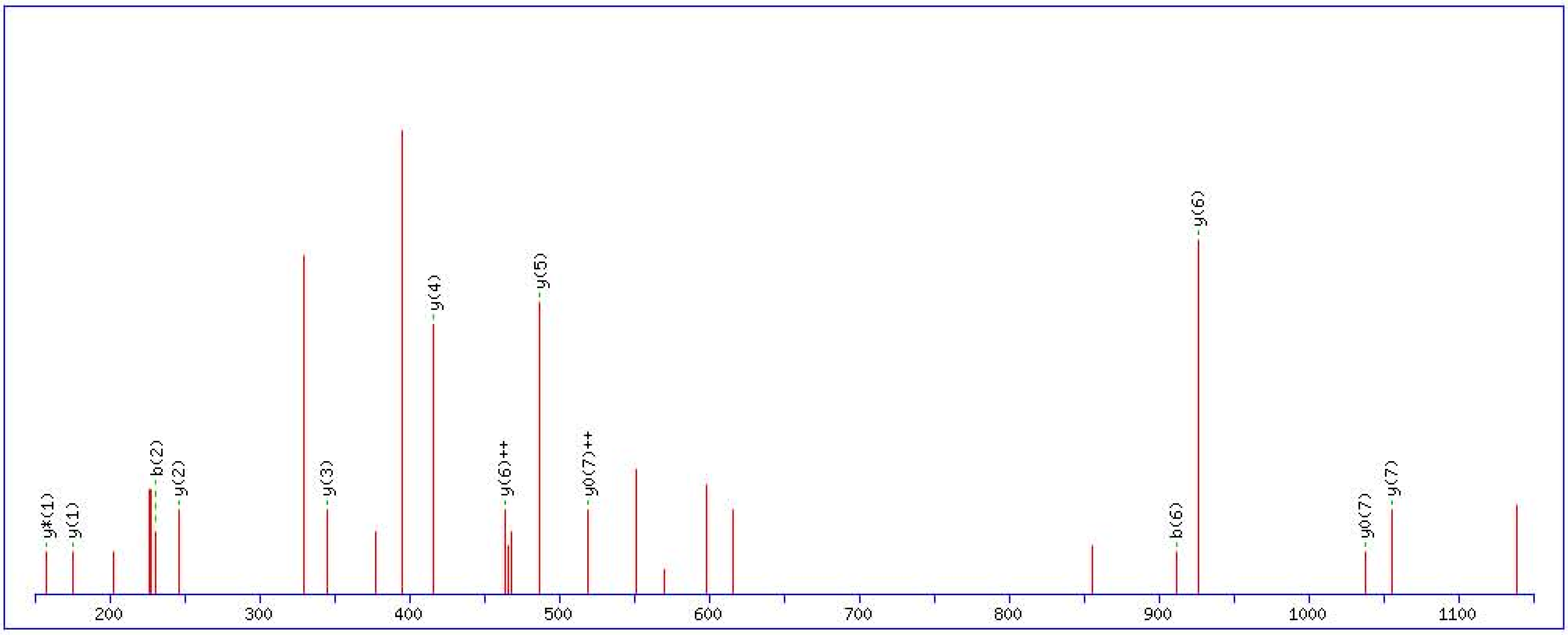
Mascot Search Results

Peptide View

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

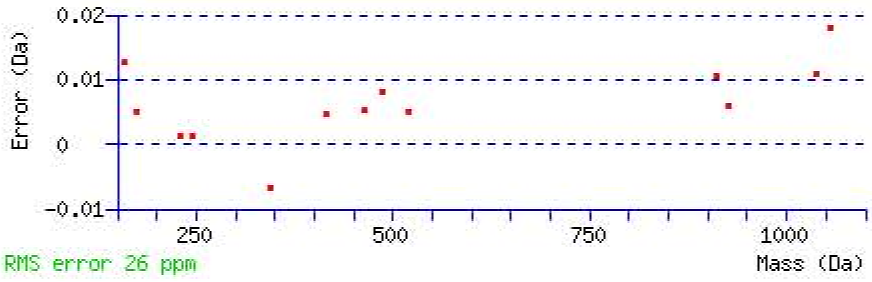
Match to Query 22045: 1155.611268 from(578.812910,2+) rtinseconds(1380) index(2442)
Title: Locus:1.1.1.2734.23 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

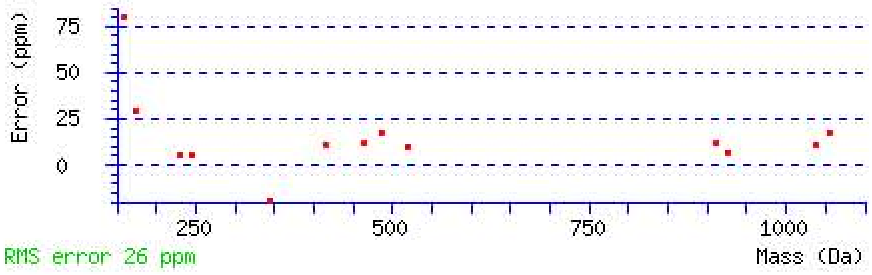
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1155.607010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00029
Matches : 13/68 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	**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





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
44.8	1155.607010	0.004258	TEQAAVAR
6.7	1155.607025	0.004243	VQDSAVAR
3.4	1155.626114	-0.014846	APGGHLHLQAR
1.8	1155.599594	0.011674	TKESKHEAAR
1.4	1155.607040	0.004228	TPACVPVSIGR

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

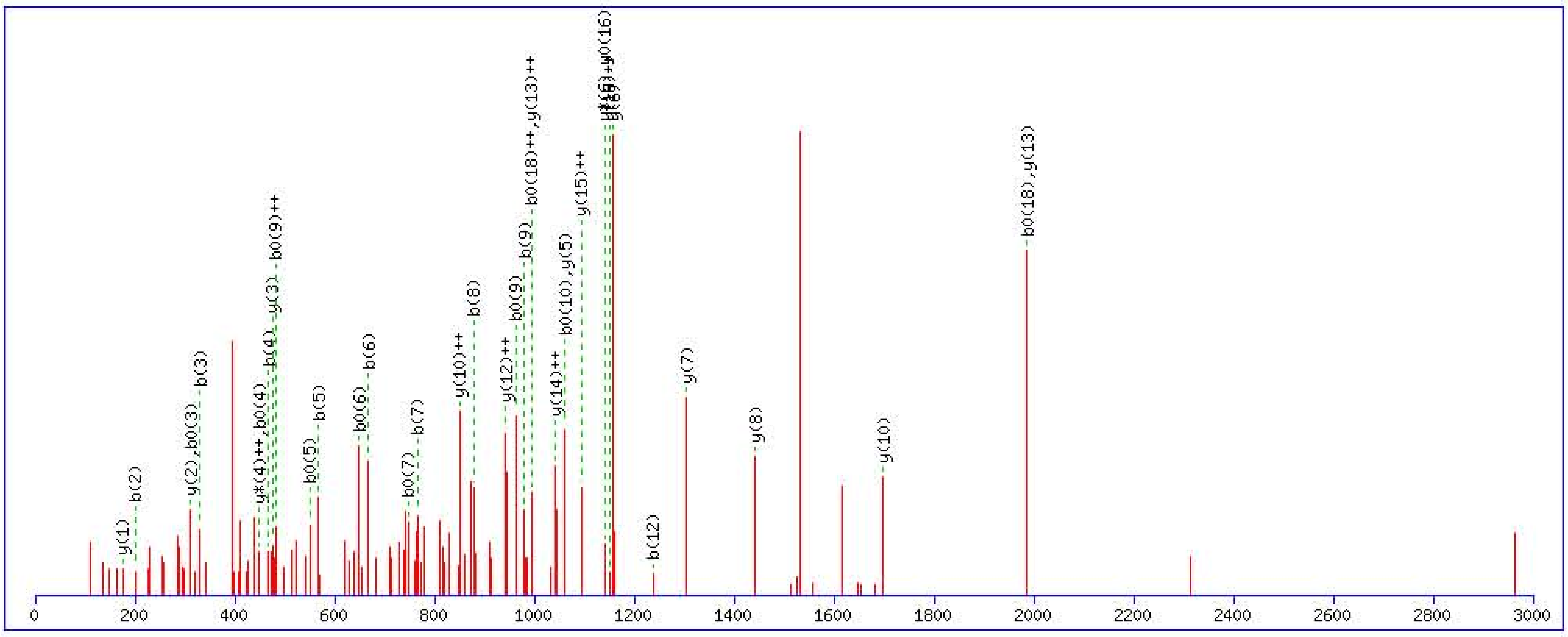
MATRIX SCIENCE Mascot Search Results

Peptide View

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

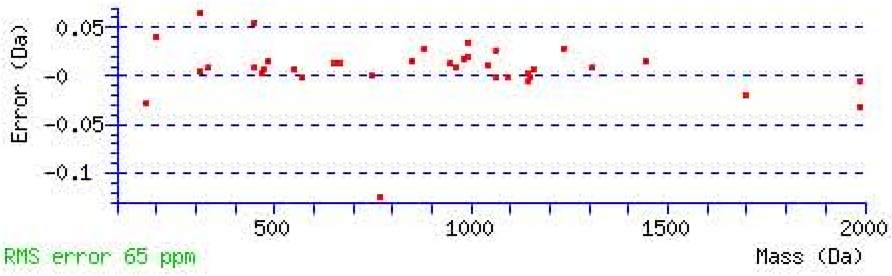
Match to Query 70982: 3064.506336 from(767.133860,4+) rtinseconds(2122) index(79660)
Title: Locus:1.1.1.2089.21 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

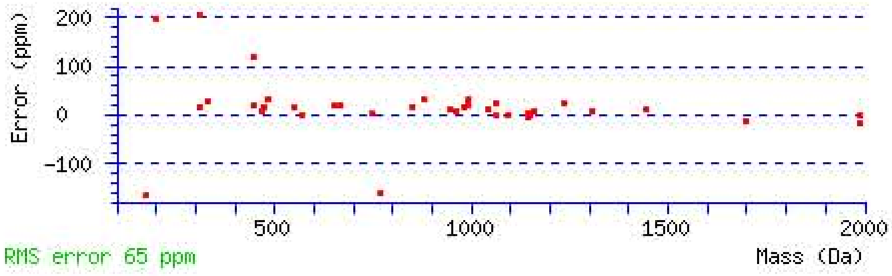
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3064.468796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00035
Matches : 37/204 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	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
48.8	3064.468796	0.037540	AEEHTVVLTVTGEPCHFPFQYHR

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

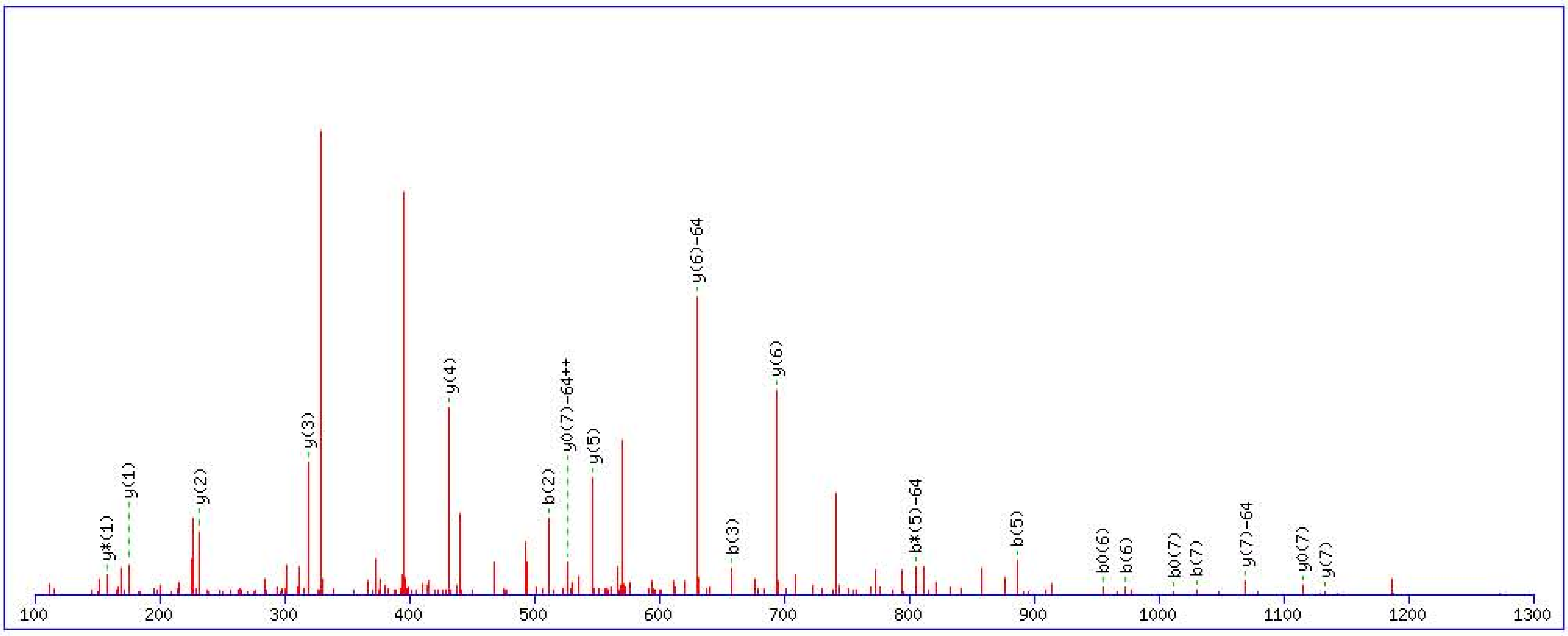
{MATRIX SCIENCE} Mascot Search Results

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

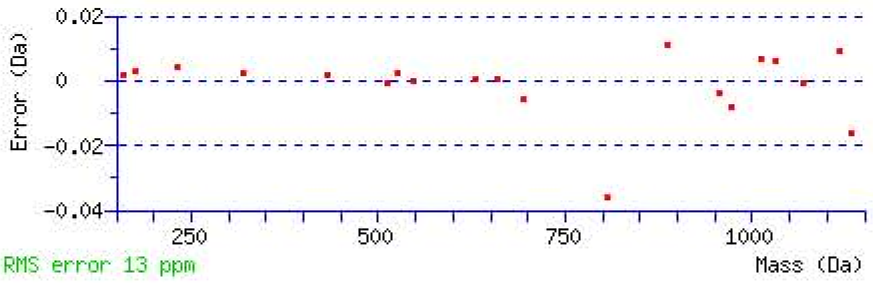
Match to Query 23774: 1203.576108 from(602.795330,2+) rtinseconds(1448) index(20610)
Title: Locus:1.1.1.2647.7 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

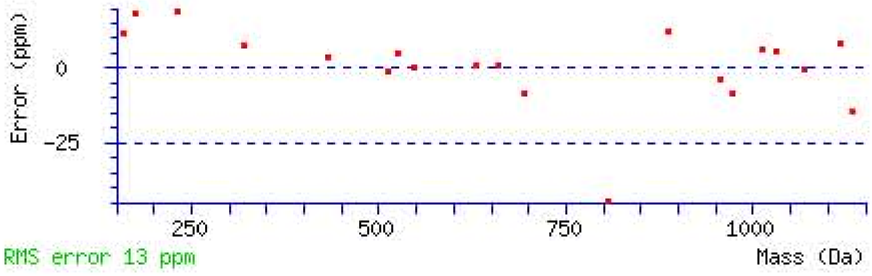
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 45  Expect: 0.00052
Matches : 20/112 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							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
44.5	1203.574005	0.002103	AQMDLSGR
9.0	1203.577820	-0.001712	EAQQRQAAMR
8.4	1203.588394	-0.012286	LFGQETPEQR
3.3	1203.588394	-0.012286	ADAAVWTLSDR
2.9	1203.584351	-0.008243	SGSPISSEERR
0.6	1203.581848	-0.005740	ALCSAAQAAWR
0.1	1203.573090	0.003018	ETAAAAEEKER

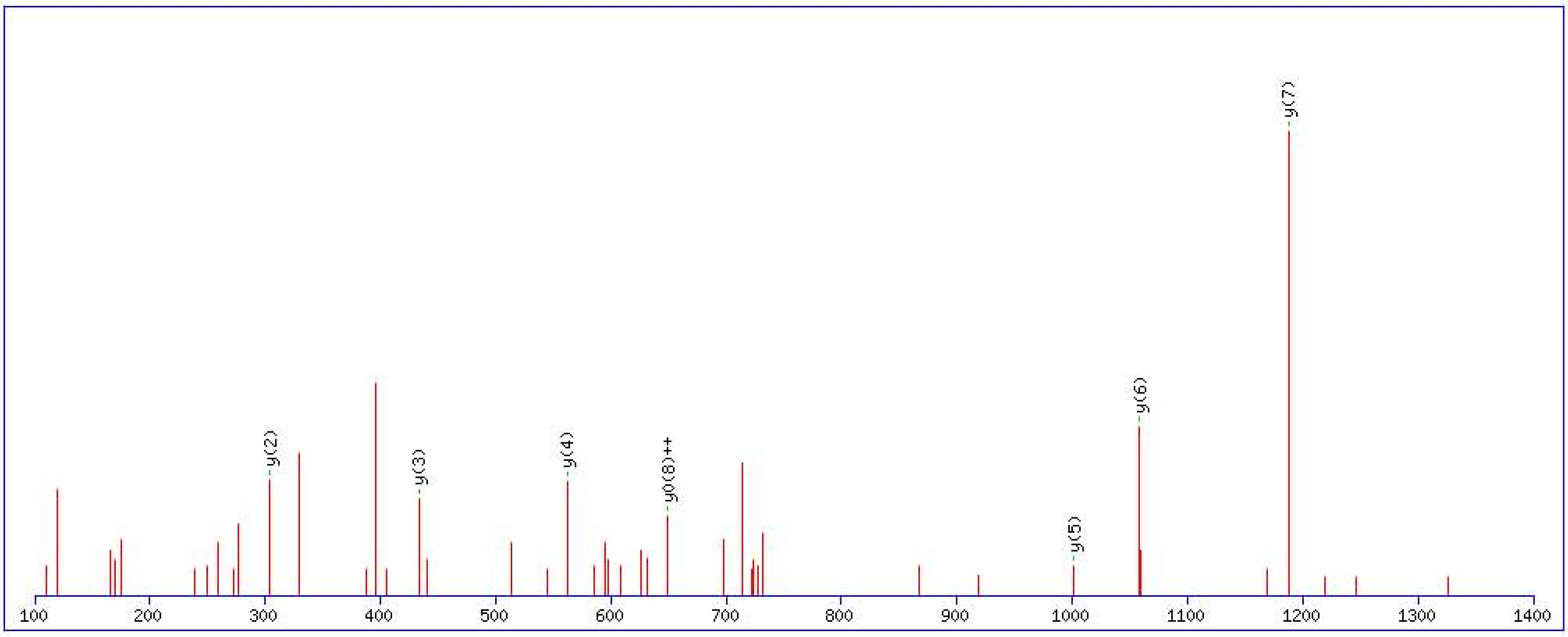
{MATRIX SCIENCE} Mascot Search Results

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

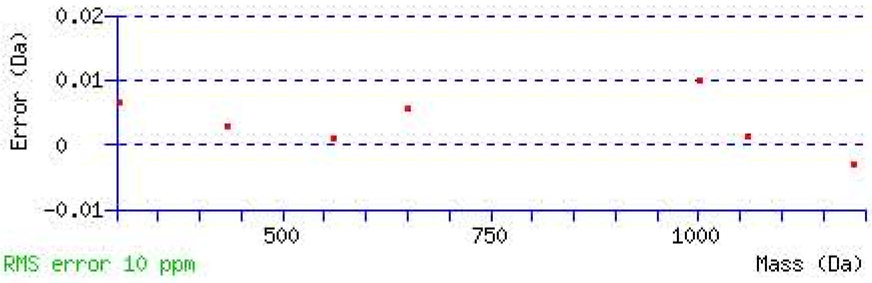
Match to Query 33728: 1461.661348 from(731.837950,2+) rtinseconds(1470) index(20778)
Title: Locus:1.1.1.2654.24 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

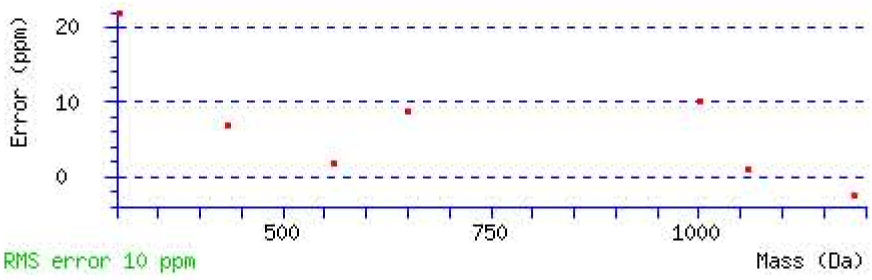
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1461.655807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.0019
Matches : 7/88 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							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
36.4	1461.655807	0.005541	FQEGQEEER
7.5	1461.640564	0.020784	NSGTQSDGEEK
2.8	1461.676956	-0.015608	MSGQVGDLSPSQEK
0.9	1461.640564	0.020784	VMTDVAGNPEEER
0.5	1461.655807	0.005541	FQEGQEEER
0.2	1461.648392	0.012956	HREELSDYEER

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

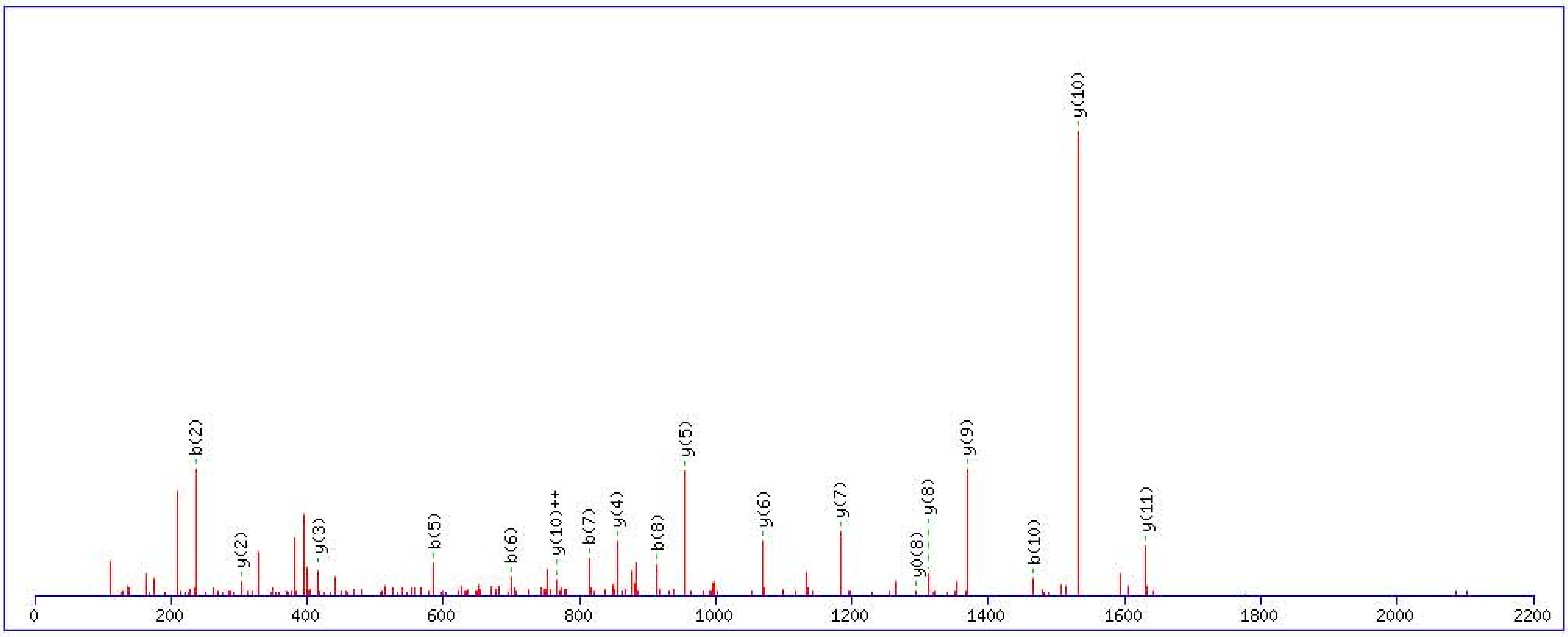
{MATRIX SCIENCE} Mascot Search Results

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

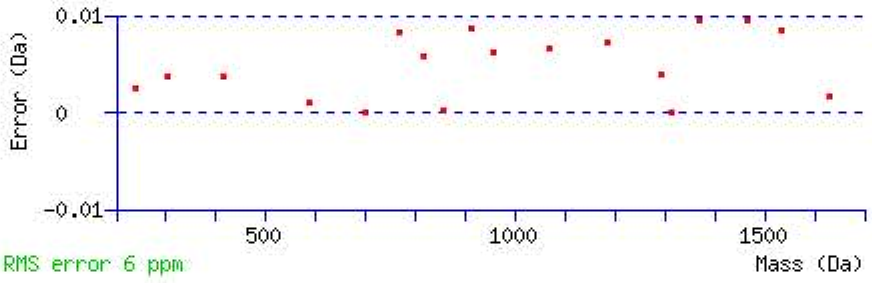
Match to Query 44364: 1766.931928 from(884.473240,2+) rtinseconds(1922) index(24133)
Title: Locus:1.1.1.2811.21 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

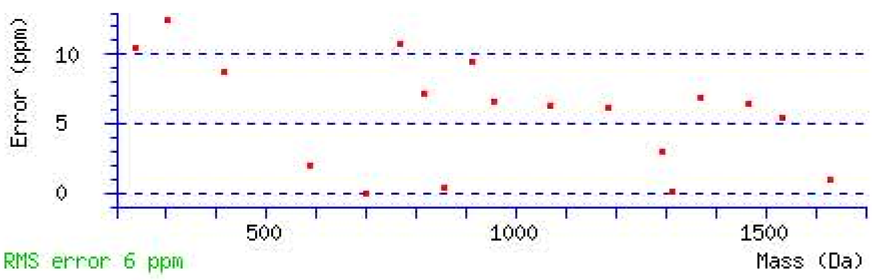
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1766.913773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 1.2e-006
Matches : 18/98 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	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



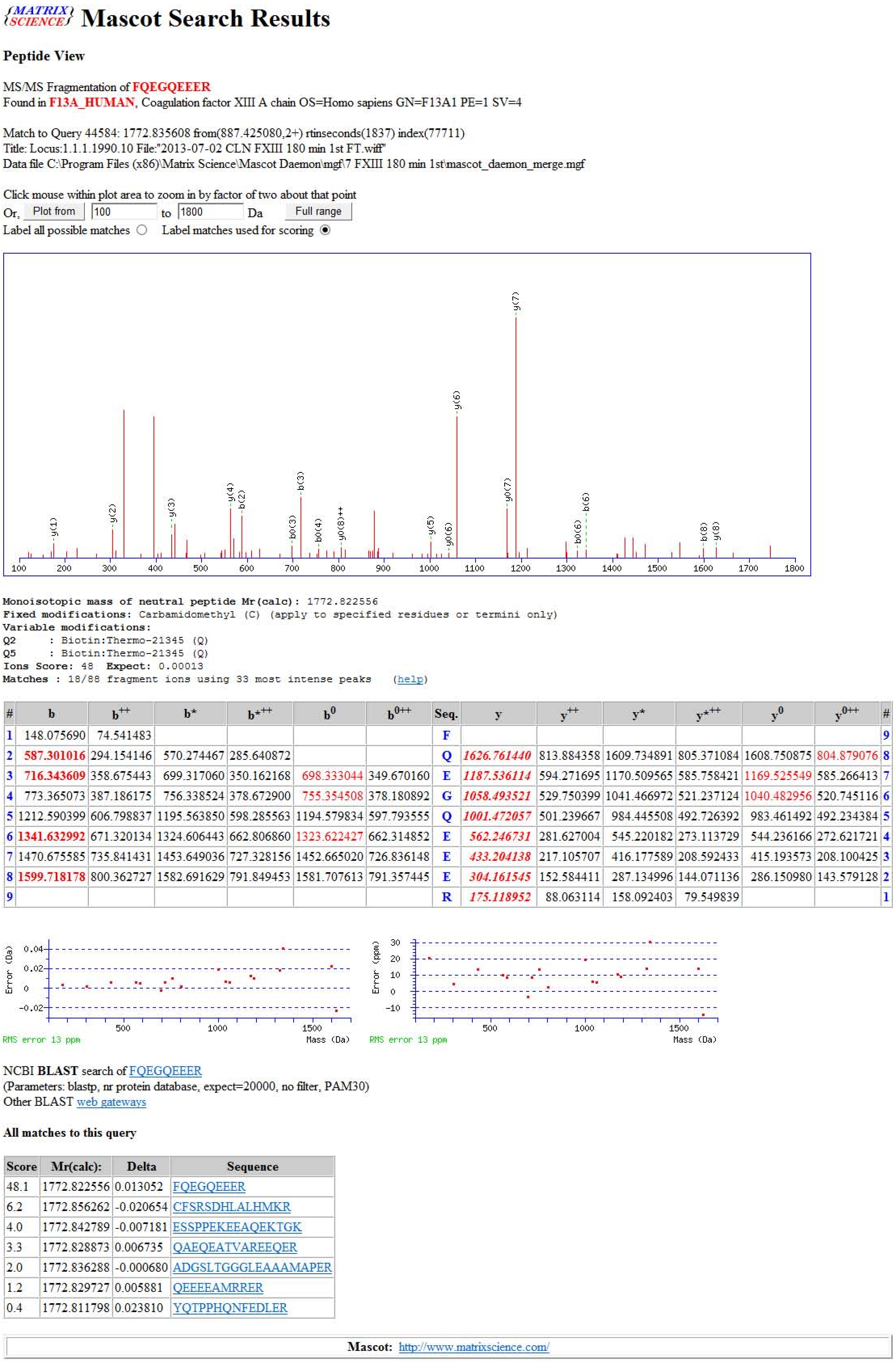


NCBI **BLAST** search of HVYGELDVQIQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.2	1766.913773	0.018155	HVYGELDVQIQR
46.2	1766.913773	0.018155	HVYGELDVQIQR
0.9	1766.934906	-0.002978	QITSPVSGINGDIR

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



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 44584: 1772.835608 from(887.425080,2+) rtinseconds(1837) index(77711)
Title: Locus:1.1.1.1990.10 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\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): 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: 48 **Expect:** 0.00013
Matches : 18/88 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	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
48.1	1772.822556	0.013052	FQEGQEEER
6.2	1772.856262	-0.020654	CFSRSDHLALHMKR
4.0	1772.842789	-0.007181	ESSPPEKEEAQEKTGK
3.3	1772.828873	0.006735	QAEQEATVAREEQER
2.0	1772.836288	-0.000680	ADGSLTGGGLEAAAMAPER
1.2	1772.829727	0.005881	QEEEEAMRRER
0.4	1772.811798	0.023810	YQTPPHQNFEDLER

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

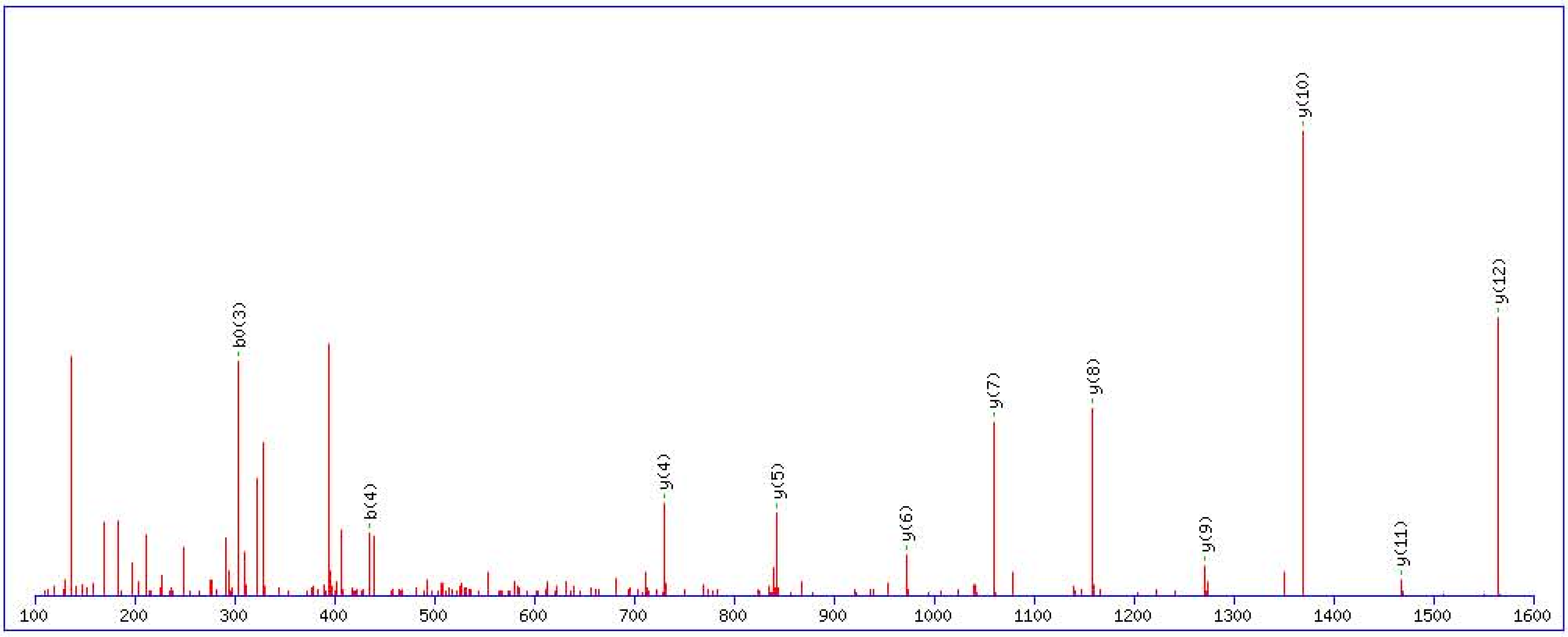
Mascot Search Results

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

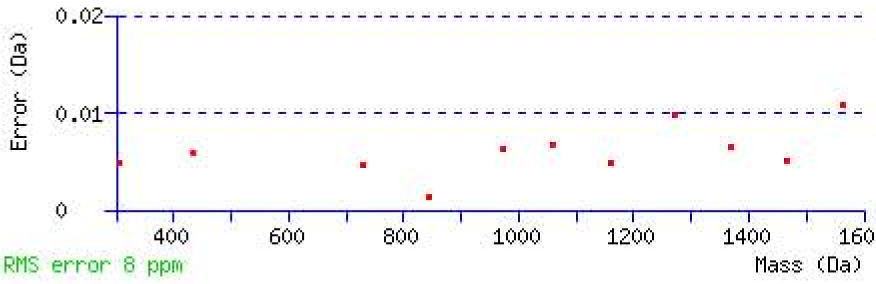
Match to Query 49905: 1998.104922 from(667.042250,3+) rtinseconds(2738) index(29715)
Title: Locus:1.1.1.3094.8 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

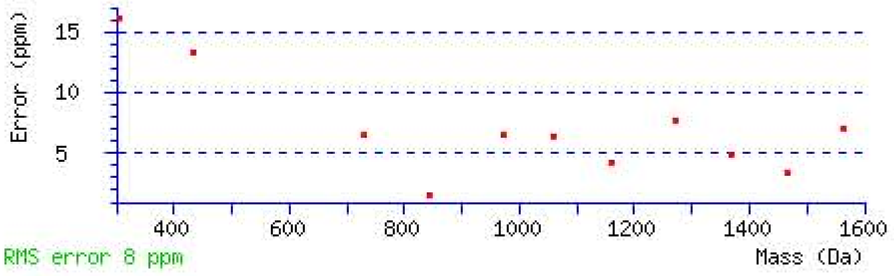
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 63  Expect: 3e-006
Matches : 11/150 fragment ions using 15 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
62.6	1998.085983	0.018939	GTYIPVPIVSELQSGK
3.7	1998.099731	0.005191	GDEVVVELVENGKKVTVGK

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

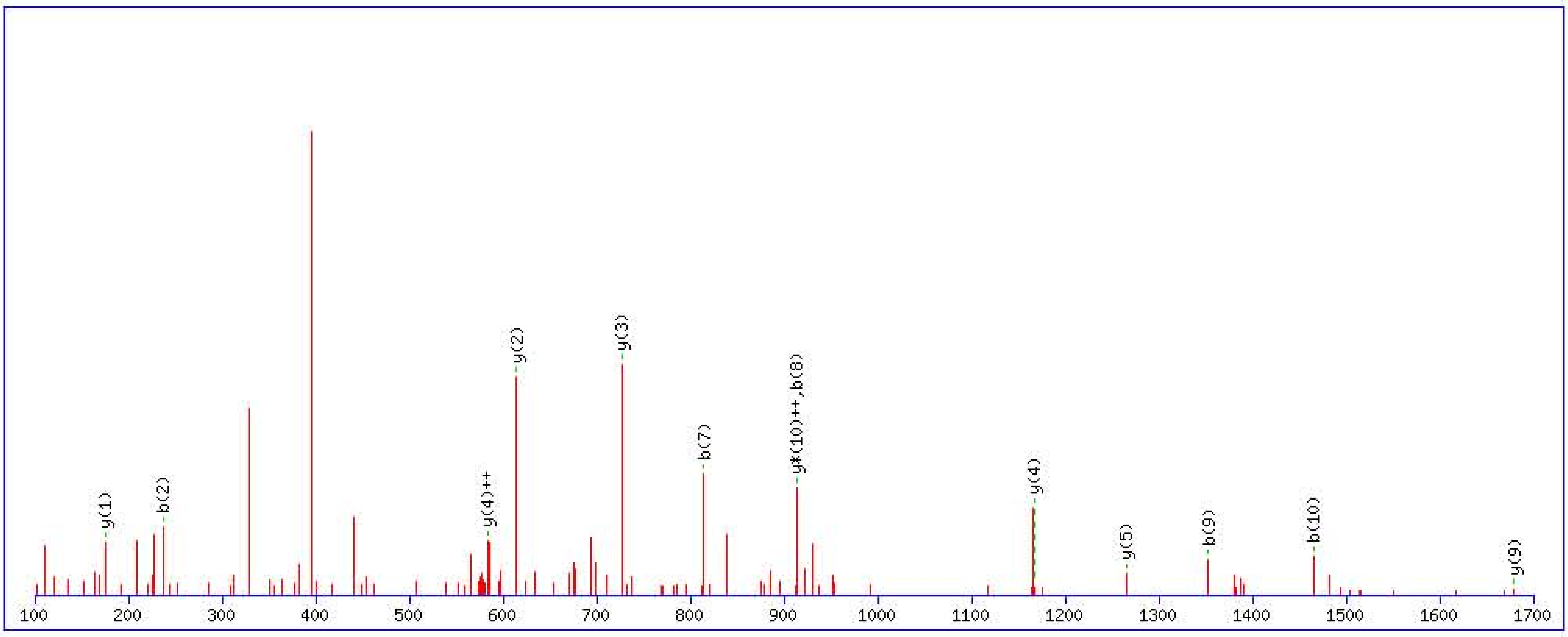
{MATRIX SCIENCE} Mascot Search Results

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

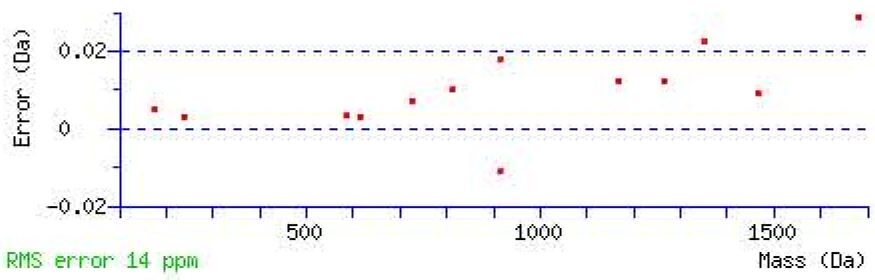
Match to Query 52658: 2078.101212 from(693.707680,3+) rtinseconds(2164) index(7569)
Title: Locus:1.1.1.3007.19 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

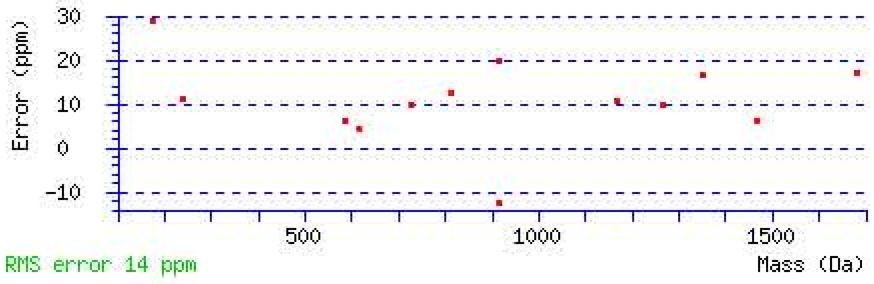
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2078.080521
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0018
Matches : 13/98 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	138.066188	69.536732					H							12
2	***237.134602***	119.070939					V	1942.028889	971.518082	1925.002340	963.004808	1924.018324	962.512800	11
3	400.197931	200.602603					Y	1842.960475	921.983875	1825.933926	913.470601	1824.949910	912.978593	10
4	457.219395	229.113335					G	***1679.897146***	840.452211	1662.870597	831.938937	1661.886581	831.446929	9
5	586.261988	293.634632			568.251423	284.629349	E	1622.875682	811.941479	1605.849133	803.428204	1604.865117	802.936196	8
6	699.346052	350.176664			681.335487	341.171382	L	1493.833089	747.420183	1476.806540	738.906908	1475.822524	738.414900	7
7	***814.372995***	407.690136			796.362430	398.684853	D	1380.749025	690.878150	1363.722476	682.364876	1362.738460	681.872868	6
8	***913.441409***	457.224342			895.430844	448.219060	V	***1265.722082***	633.364679	1248.695533	624.851405			5
9	***1352.666735***	676.837006	1335.640186	668.323731	1334.656170	667.831723	Q	***1166.653668***	583.830472	1149.627119	575.317198			4
10	***1465.750799***	733.379037	1448.724250	724.865763	1447.740234	724.373755	I	***727.428342***	364.217809	710.401793	355.704534			3
11	1904.976125	952.991700	1887.949576	944.478426	1886.965560	943.986418	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 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
41.2	2078.080521	0.020691	HVYGELDVQIQR
16.2	2078.116699	-0.015487	RPRGDVESRLDALQR
12.5	2078.130615	-0.029403	VEAEGQLQQLREVLR
11.9	2078.124084	-0.022872	SPQESRRLSIQR
11.9	2078.090881	0.010331	WIAQDLSSLAGLLDQHGVR
6.8	2078.128098	-0.026886	QLLRWKEAEQR
4.8	2078.089493	0.011719	EIKQDISSLRYELLEDK
2.4	2078.101608	-0.000396	LSEAAALAGLQEQR
1.3	2078.112839	-0.011627	AAALRATQEELQR
1.3	2078.080505	0.020707	AVWEAEQLGGLQR

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

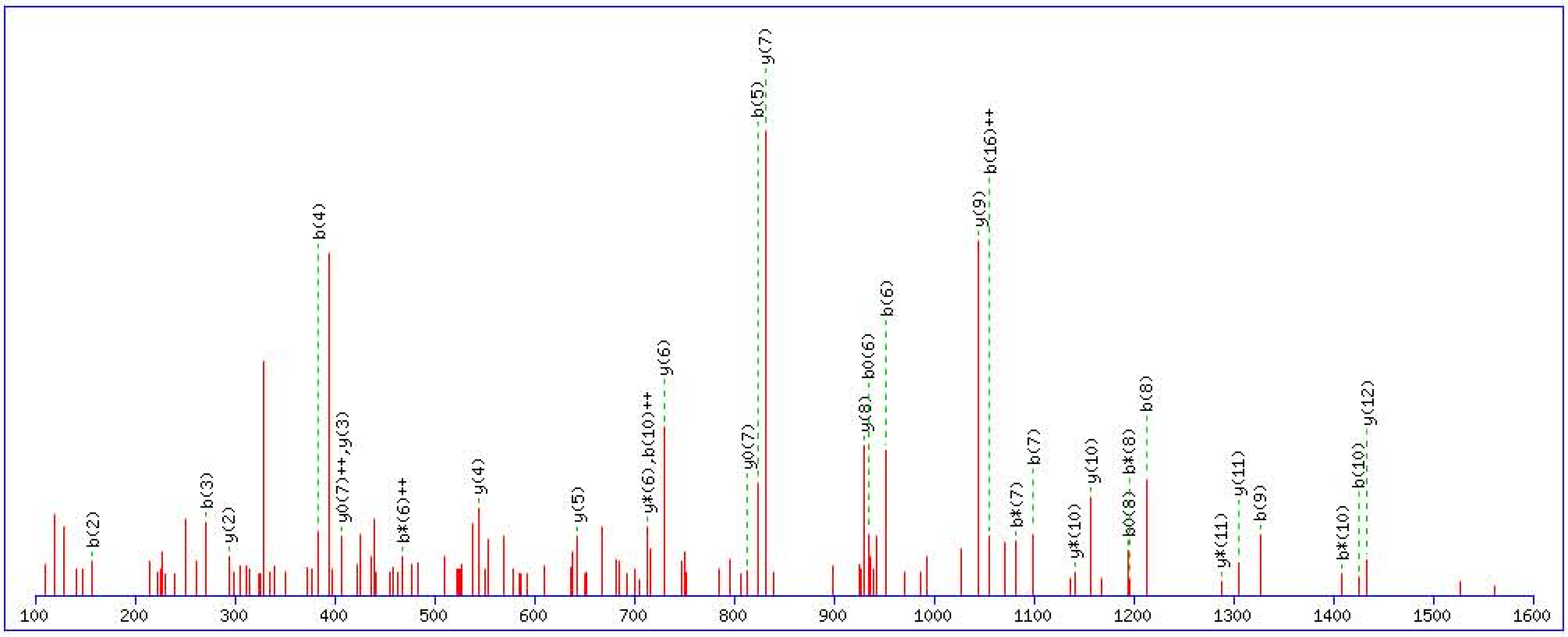
Mascot Search Results

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

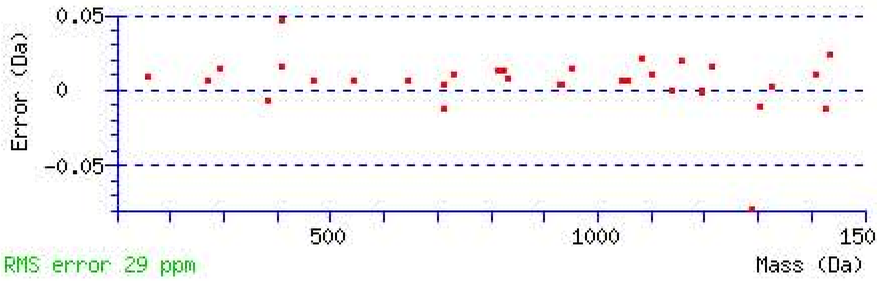
Match to Query 56754: 2255.236692 from(752.752840,3+) rtinseconds(2970) index(31335)
Title: Locus:1.1.1.3174.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

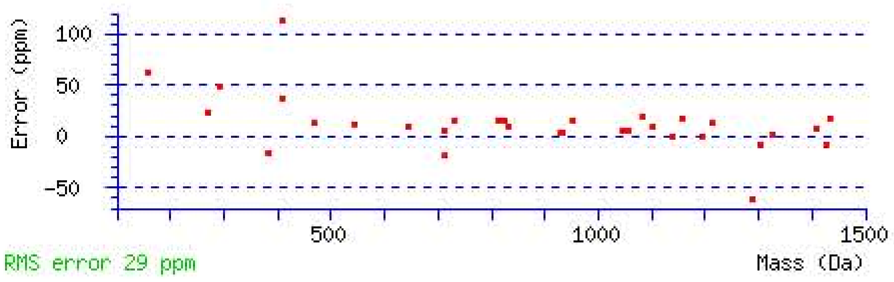
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2255.213654
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 2.3e-006
Matches : 33/168 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	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
68.5	2255.213654	0.023038	GVNLQEFLNVTSVHLFK

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

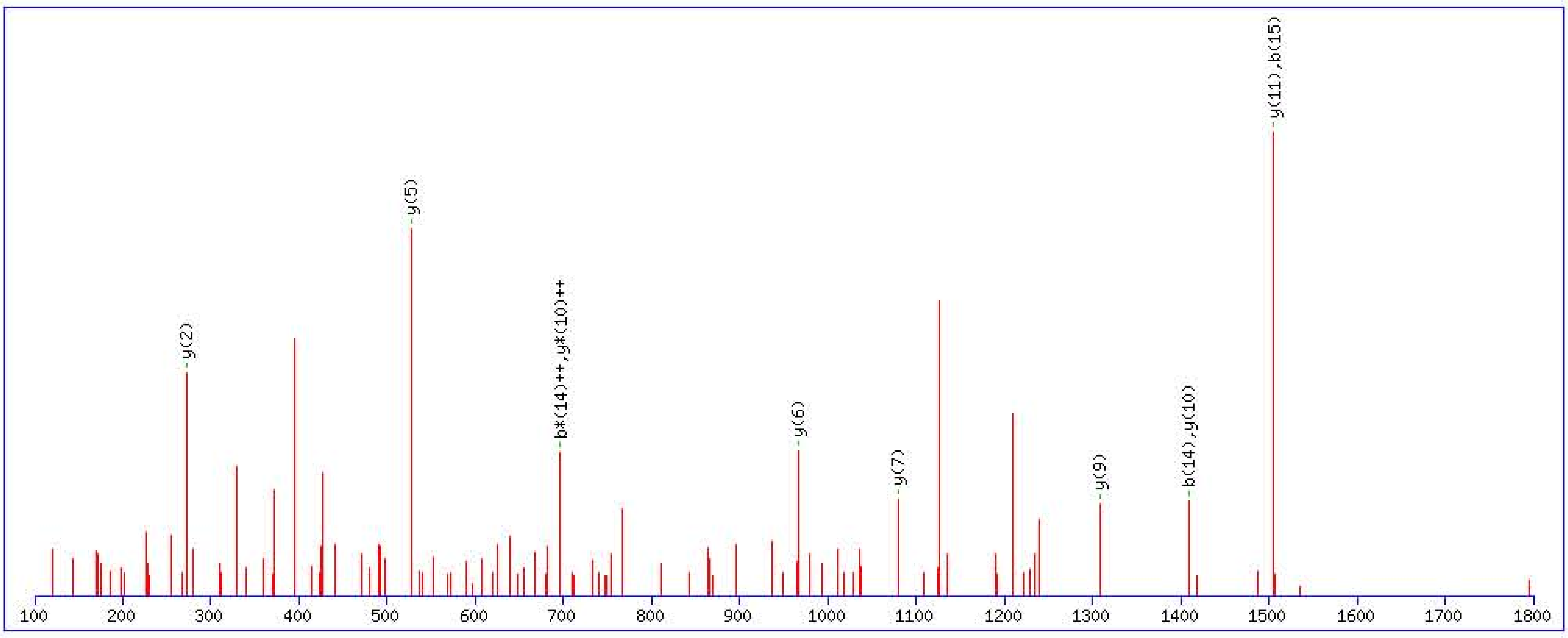
Mascot Search Results

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

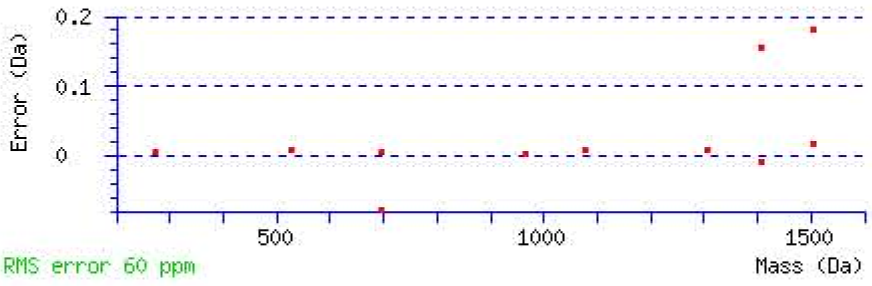
Match to Query 69217: 2912.491936 from(729.130260,4+) rtinseconds(2511) index(9842)
Title: Locus:1.1.1.3128.16 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

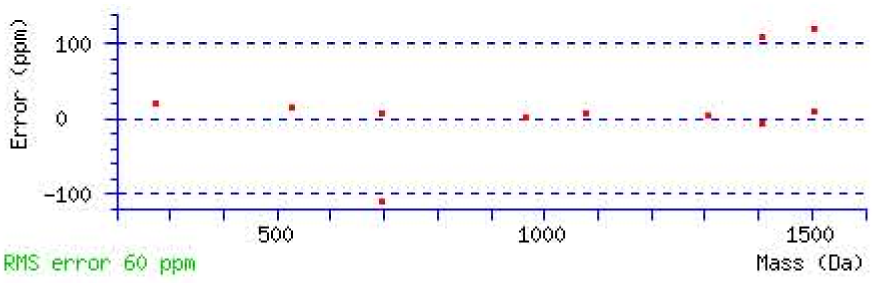
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 32 **Expect:** 0.02
Matches : 11/254 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							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
31.6	2912.470200	0.021736	AVPPNNSNAAEDDLPTVELQGVVPR

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

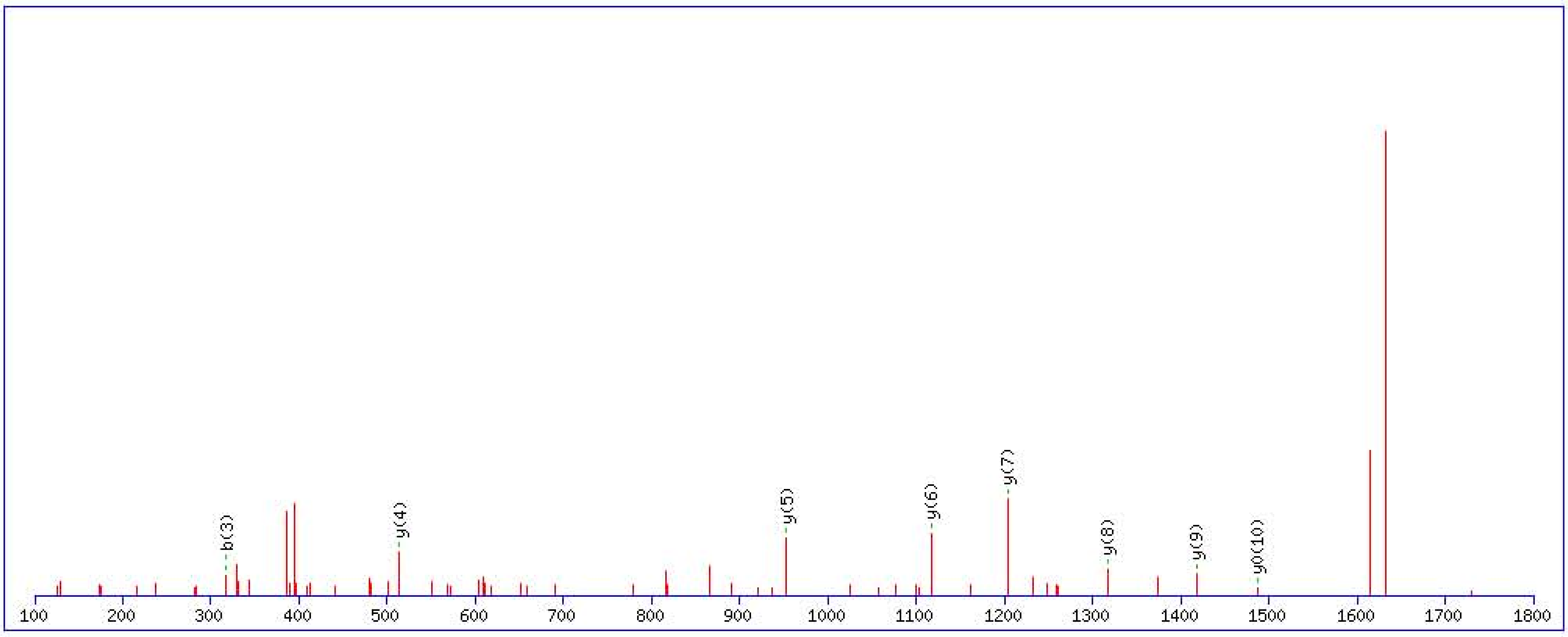
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSTLSYQEPLR**
Found in **F13B_HUMAN**, Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3

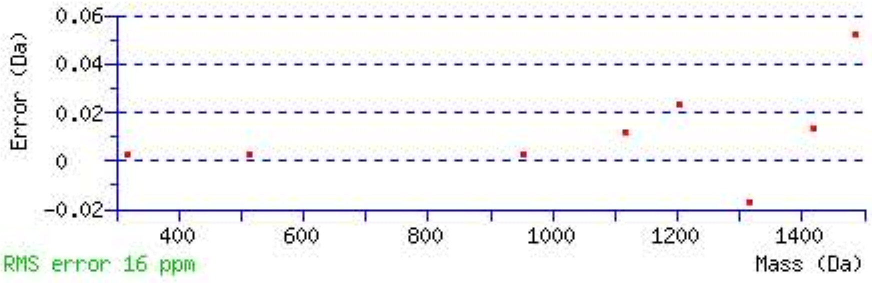
Match to Query 40619: 1631.848688 from(816.931620,2+) rtinseconds(1929) index(78398)
Title: Locus:1.1.1.2022.22 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

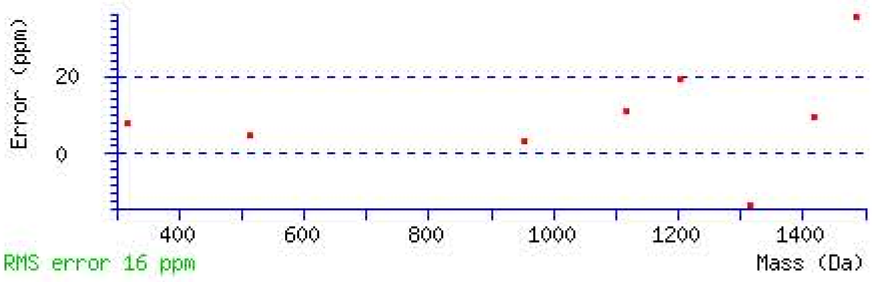
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1631.834106
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.0013
Matches : 8/112 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	129.065854	65.036565	112.039305	56.523291			**Q**							11
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	**S**	1504.782827	752.895052	1487.756278	744.381777	1486.772262	743.889769	10
3	317.145561	159.076418	300.119012	150.563144	299.134996	150.071136	**T**	***1417.750799***	709.379038	1400.724250	700.865763	1399.740234	700.373755	9
4	430.229625	215.618450	413.203076	207.105176	412.219060	206.613168	**L**	***1316.703120***	658.855198	1299.676571	650.341924	1298.692555	649.849916	8
5	517.261653	259.134465	500.235104	250.621190	499.251088	250.129182	**S**	***1203.619056***	602.313166	1186.592507	593.799892	1185.608491	593.307884	7
6	680.324982	340.666129	663.298433	332.152855	662.314417	331.660847	**Y**	***1116.587028***	558.797152	1099.560479	550.283878	1098.576463	549.791870	6
7	1119.550308	560.278792	1102.523759	551.765518	1101.539743	551.273510	**Q**	***953.523699***	477.265488	936.497150	468.752213	935.513134	468.260205	5
8	1248.592901	624.800089	1231.566352	616.286814	1230.582336	615.794806	**E**	***514.298373***	257.652825	497.271824	249.139550	496.287808	248.647542	4
9	1345.645665	673.326471	1328.619116	664.813196	1327.635100	664.321188	**P**	385.255780	193.131528	368.229231	184.618253			3
10	1458.729729	729.868503	1441.703180	721.355228	1440.719164	720.863220	**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 QSTLSYQEPLR
(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	1631.834106	0.014582	QSTLSYQEPLR
2.8	1631.866440	-0.017752	ITEEERRMASVLAK
0.6	1631.826691	0.021997	EADAVSYKISREHK
0.5	1631.832733	0.015955	EELLLLEMEQLEK
0.5	1631.855194	-0.006506	ELLEKENIMKQNK

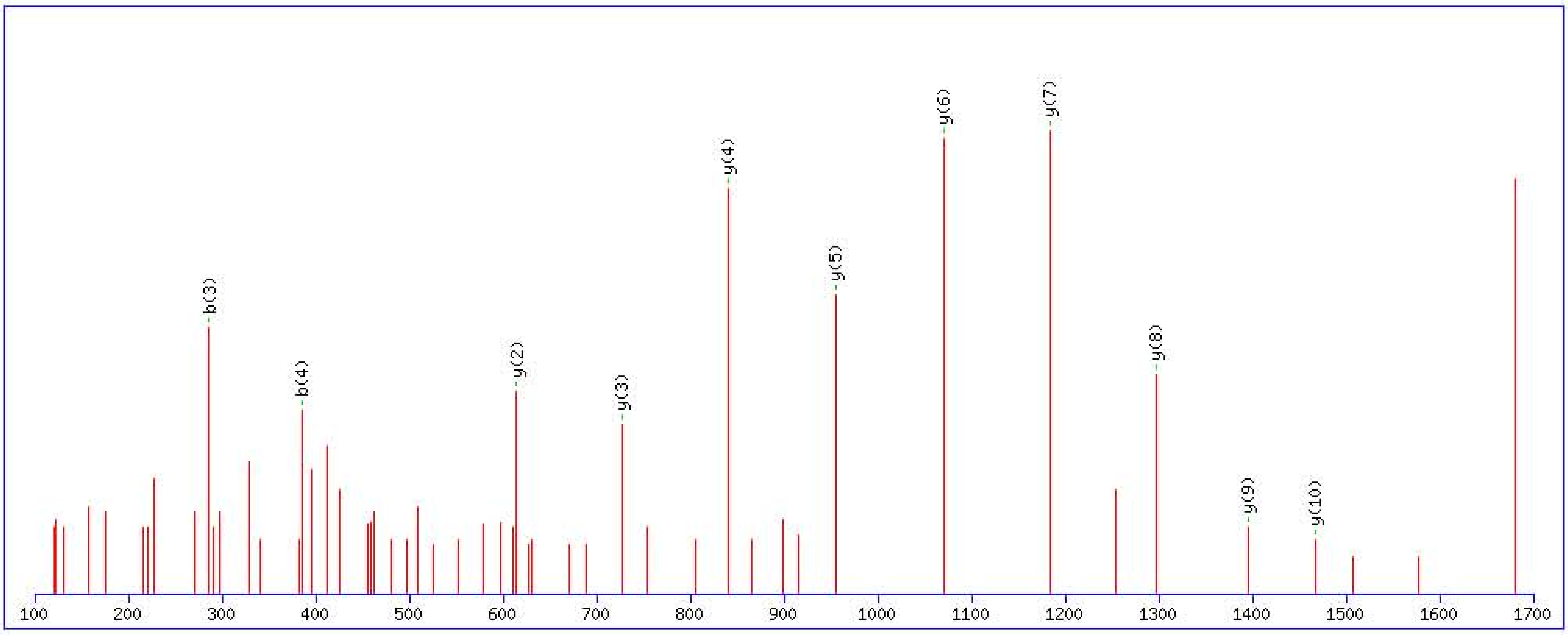
{MATRIX SCIENCE} Mascot Search Results

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

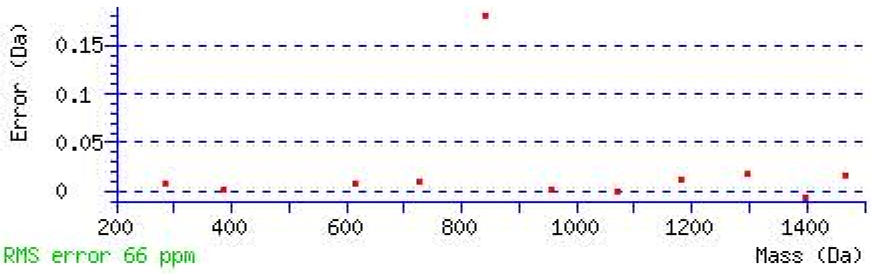
Match to Query 41986: 1679.983188 from(840.998870,2+) rtinseconds(3099) index(32066)
Title: Locus:1.1.1.3218.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

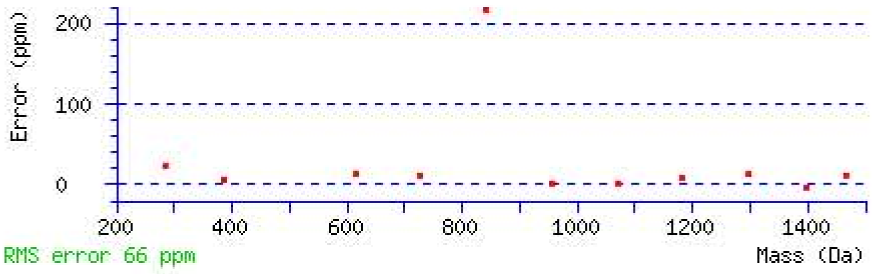
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1679.964401
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 75  Expect: 2.3e-007
Matches : 11/104 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	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
74.8	1679.964401	0.018787	TIAVLLDDILQR

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

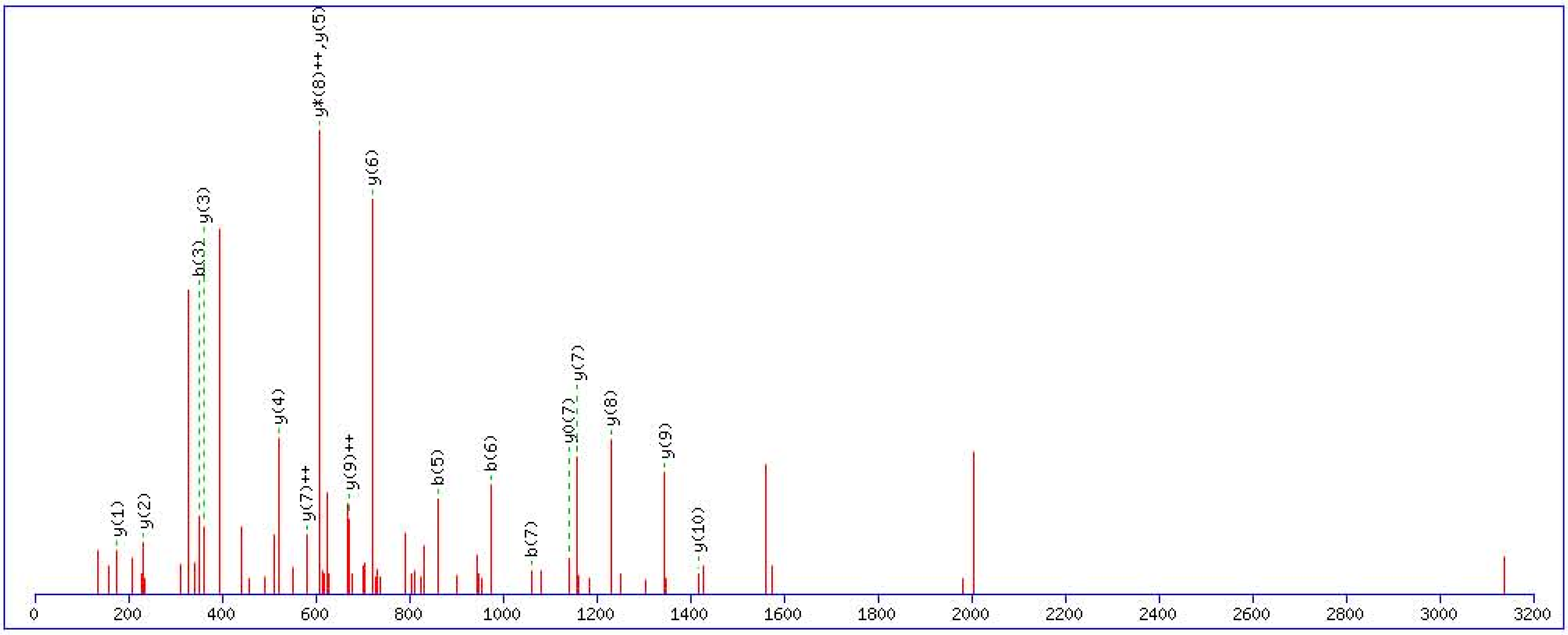
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YADAQLSCQGR**
Found in **COL11_HUMAN**, Collectin-11 OS=Homo sapiens GN=COLEC11 PE=1 SV=1

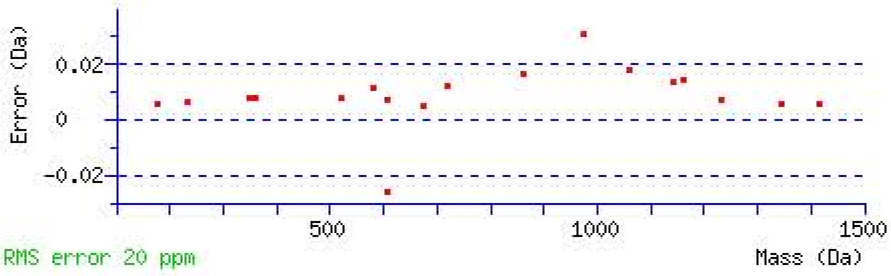
Match to Query 37571: 1578.749588 from(790.382070,2+) rtinseconds(1619) index(58129)
Title: Locus:1.1.1.2987.16 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

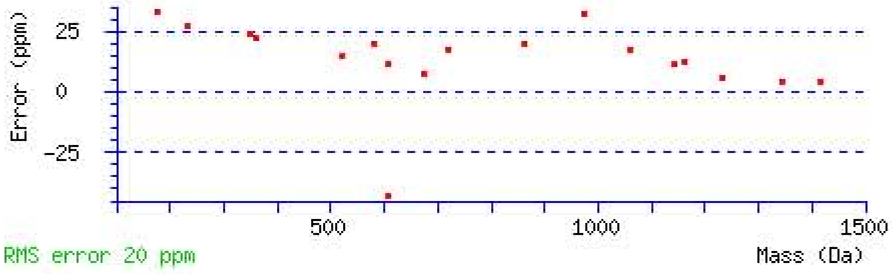


```
Monoisotopic mass of neutral peptide Mr(calc): 1578.728271
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 1.8e-005
Matches : 18/100 fragment ions using 38 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							11
2	235.107719	118.057498					A	***1416.672232***	708.839754	1399.645683	700.326480	1398.661667	699.834472	10
3	**350.134662**	175.570969			332.124097	166.565687	D	***1345.635118***	673.321197	1328.608569	664.807923	1327.624553	664.315915	9
4	421.171776	211.089526			403.161211	202.084243	A	***1230.608175***	615.807726	1213.581626	607.294451	1212.597610	606.802443	8
5	**860.397102**	430.702189	843.370553	422.188915	842.386537	421.696907	Q	***1159.571061***	580.289169	1142.544512	571.775894	1141.560496	571.283886	7
6	**973.481166**	487.244221	956.454617	478.730947	955.470601	478.238939	L	***720.345735***	360.676506	703.319186	352.163231	702.335170	351.671223	6
7	**1060.513194**	530.760235	1043.486645	522.246961	1042.502629	521.754953	S	***607.261671***	304.134474	590.235122	295.621199	589.251106	295.129191	5
8	1220.543843	610.775560	1203.517294	602.262285	1202.533278	601.770277	C	***520.229643***	260.618460	503.203094	252.105185			4
9	1348.602421	674.804849	1331.575872	666.291574	1330.591856	665.799566	Q	***360.198994***	180.603135	343.172445	172.089860			3
10	1405.623885	703.315581	1388.597336	694.802306	1387.613320	694.310298	G	***232.140416***	116.573846	215.113867	108.060571			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 20 ppm



RMS error 20 ppm

NCBI **BLAST** search of YADAQLSCQGR
(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	1578.728271	0.021317	YADAQLSCQGR
22.4	1578.728271	0.021317	YADAQLSCQGR
8.9	1578.754776	-0.005188	FSWMGRQAGGR

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

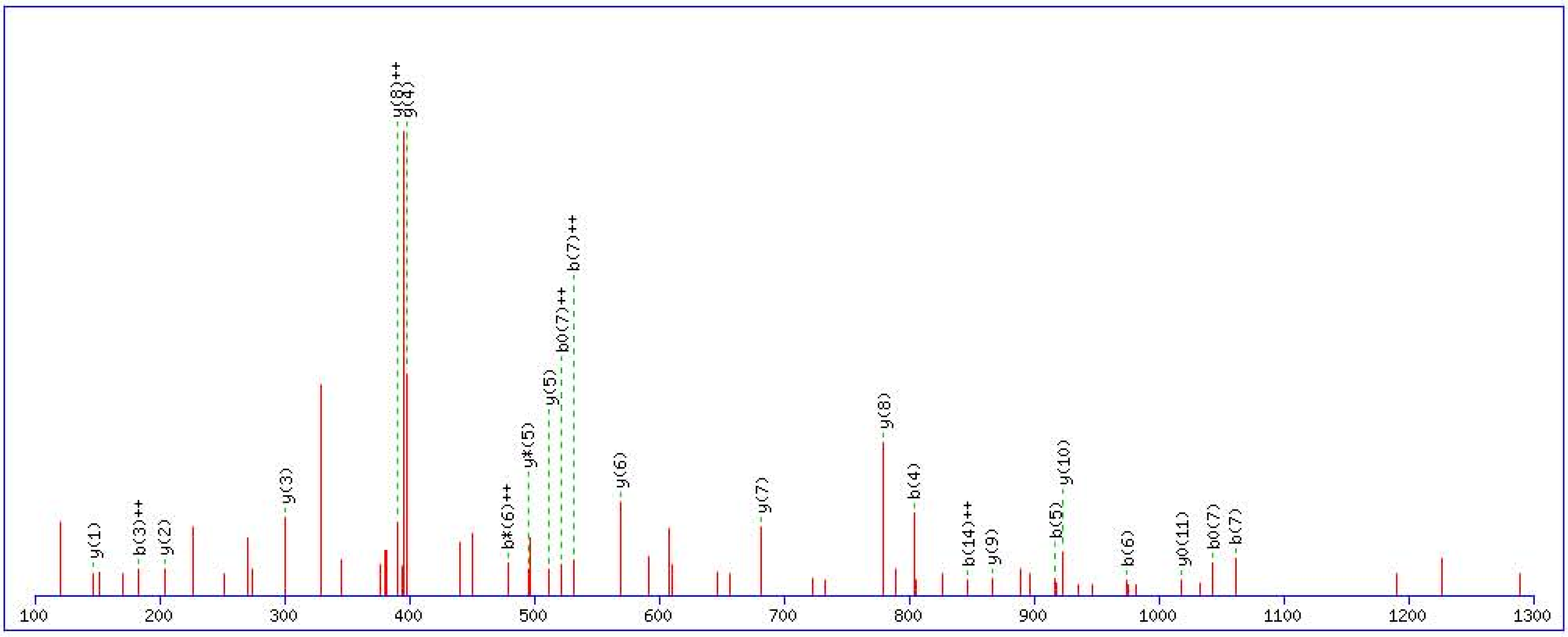
Mascot Search Results

Peptide View

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

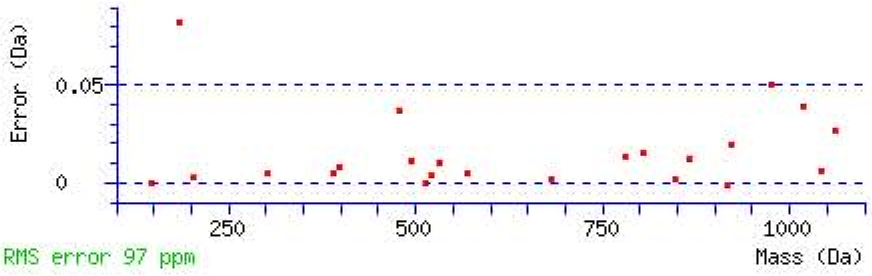
Match to Query 24456: 1838.934132 from(613.985320,3+) rtinseconds(2082) index(42783)
Title: Locus:1.1.1.3174.9 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

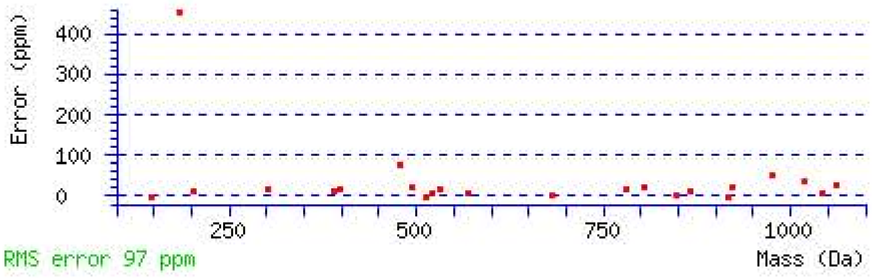


```
Monoisotopic mass of neutral peptide Mr(calc): 1838.917160
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.0013
Matches : 23/134 fragment ions using 56 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483					F							15
2	308.106339	154.556807					C	1692.856010	846.931643	1675.829461	838.418369	1674.845445	837.926360	14
3	365.127803	**183.067539**					G	1532.825361	766.916318	1515.798812	758.403044	1514.814796	757.911036	13
4	**804.353129**	402.680203	787.326580	394.166928			Q	1475.803897	738.405587	1458.777348	729.892312	1457.793332	729.400304	12
5	**917.437193**	459.222235	900.410644	450.708960			L	1036.578571	518.792924	1019.552022	510.279649	1018.568006	509.787641	11
6	**974.458657**	487.732967	957.432108	479.219692			G	***923.494507***	462.250892	906.467958	453.737617	905.483942	453.245609	10
7	**1061.490685**	**531.248981**	1044.464136	522.735706	1043.480120	522.243698	S	***866.473043***	433.740160	849.446494	425.226885	848.462478	424.734877	9
8	1158.543449	579.775363	1141.516900	571.262088	1140.532884	570.770080	P	***779.441015***	390.224145	762.414466	381.710871			8
9	1271.627513	636.317395	1254.600964	627.804120	1253.616948	627.312112	L	***682.388251***	341.697763	665.361702	333.184489			7
10	1328.648977	664.828127	1311.622428	656.314852	1310.638412	655.822844	G	***569.304187***	285.155732	552.277638	276.642457			6
11	1442.691904	721.849590	1425.665355	713.336316	1424.681339	712.844308	N	***512.282723***	256.645000	495.256174	248.131725			5
12	1539.744668	770.375972	1522.718119	761.862698	1521.734103	761.370690	P	***398.239796***	199.623536	381.213247	191.110261			4
13	1636.797432	818.902354	1619.770883	810.389080	1618.786867	809.897072	P	***301.187032***	151.097154	284.160483	142.583879			3
14	1693.818896	**847.413086**	1676.792347	838.899812	1675.808331	838.407804	G	***204.134268***	102.570772	187.107719	94.057497			2
15							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 97 ppm



RMS error 97 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.1	1838.917160	0.016972	FCGQLGSPLGNPPGK

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

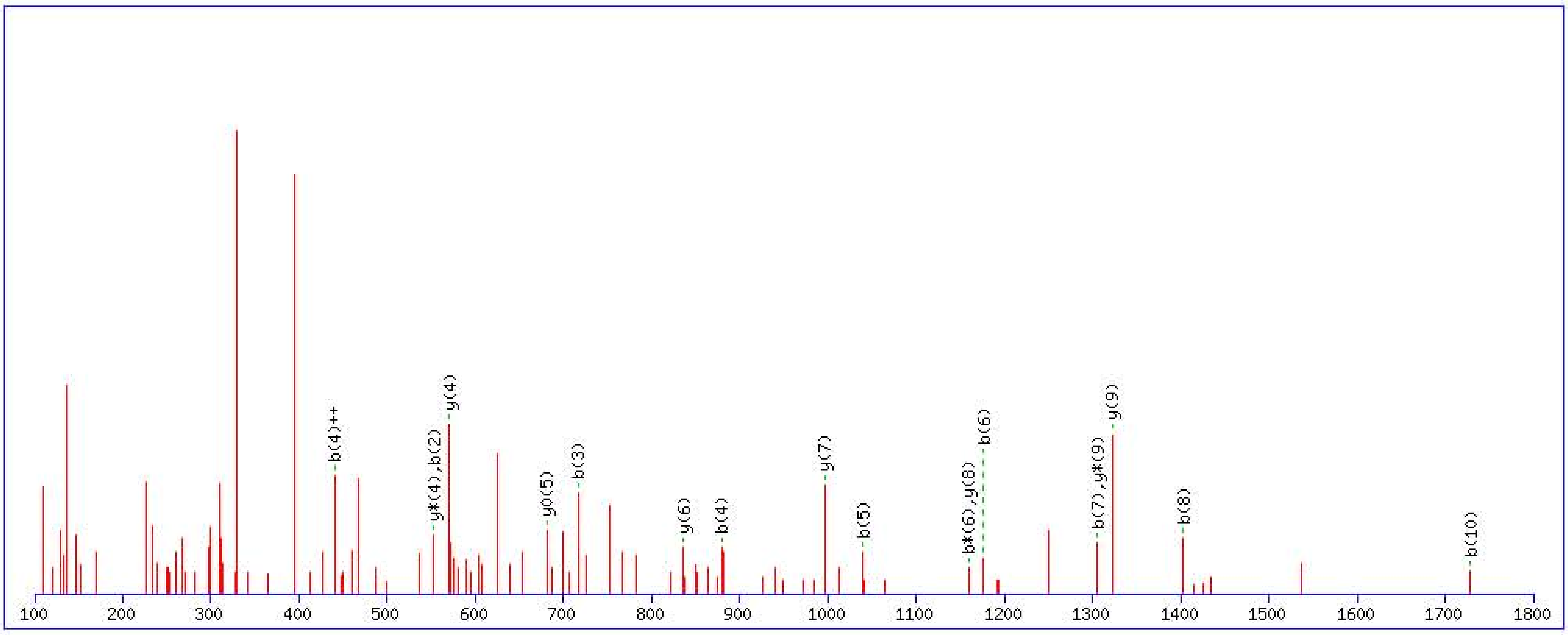
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

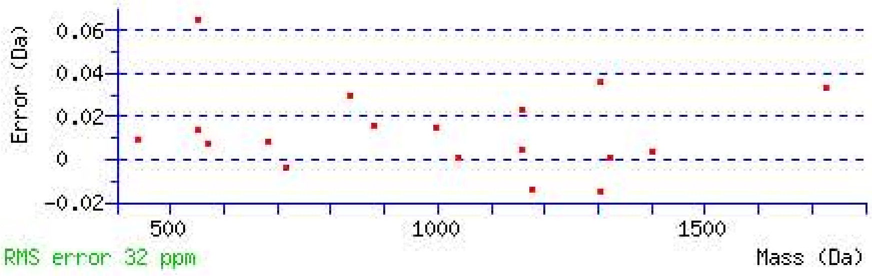
Match to Query 47052: 1873.869132 from(625.630320,3+) rtinseconds(1682) index(39942)
Title: Locus:1.1.1.3035.7 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

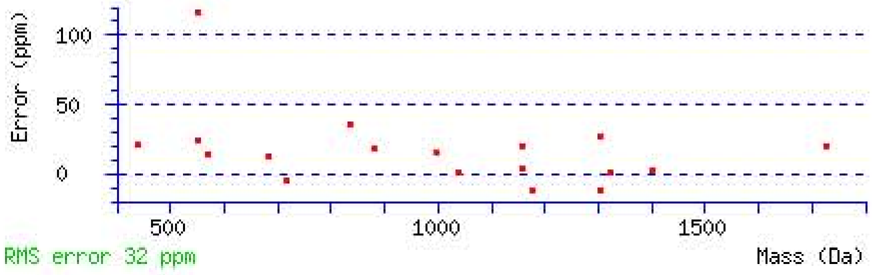
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1873.853119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.00071
Matches : 18/98 fragment ions using 30 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	***553.316666***	277.161971	536.290117	268.648697			Q	1761.776364	881.391820	1744.749815	872.878546	1743.765799	872.386538	10
3	***716.379995***	358.693636	699.353446	350.180361			Y	**1322.551038**	661.779157	1305.524489	653.265883	1304.540473	652.773875	9
4	***879.443324***	440.225300	862.416775	431.712026			Y	**1159.487709**	580.247493	1142.461160	571.734218	1141.477144	571.242210	8
5	***1039.473973***	520.240625	1022.447424	511.727350			C	**996.424380**	498.715828	979.397831	490.202554	978.413815	489.710546	7
6	***1176.532885***	588.770081	1159.506336	580.256806			H	**836.393731**	418.700504	819.367182	410.187229	818.383166	409.695221	6
7	***1305.575478***	653.291377	1288.548929	644.778103	1287.564913	644.286094	E	699.334819	350.171048	682.308270	341.657773	681.324254	341.165765	5
8	***1402.628242***	701.817759	1385.601693	693.304485	1384.617677	692.812477	P	**570.292226**	285.649751	553.265677	277.136477			4
9	1565.691571	783.349424	1548.665022	774.836149	1547.681006	774.344141	Y	473.239462	237.123369	456.212913	228.610095			3
10	***1728.754900***	864.881088	1711.728351	856.367814	1710.744335	855.875806	Y	310.176133	155.591705	293.149584	147.078430			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.0	1873.853119	0.016013	IQYYCHEPYYK
3.4	1873.862854	0.006278	NTHSAELPPPDQPSPCK

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

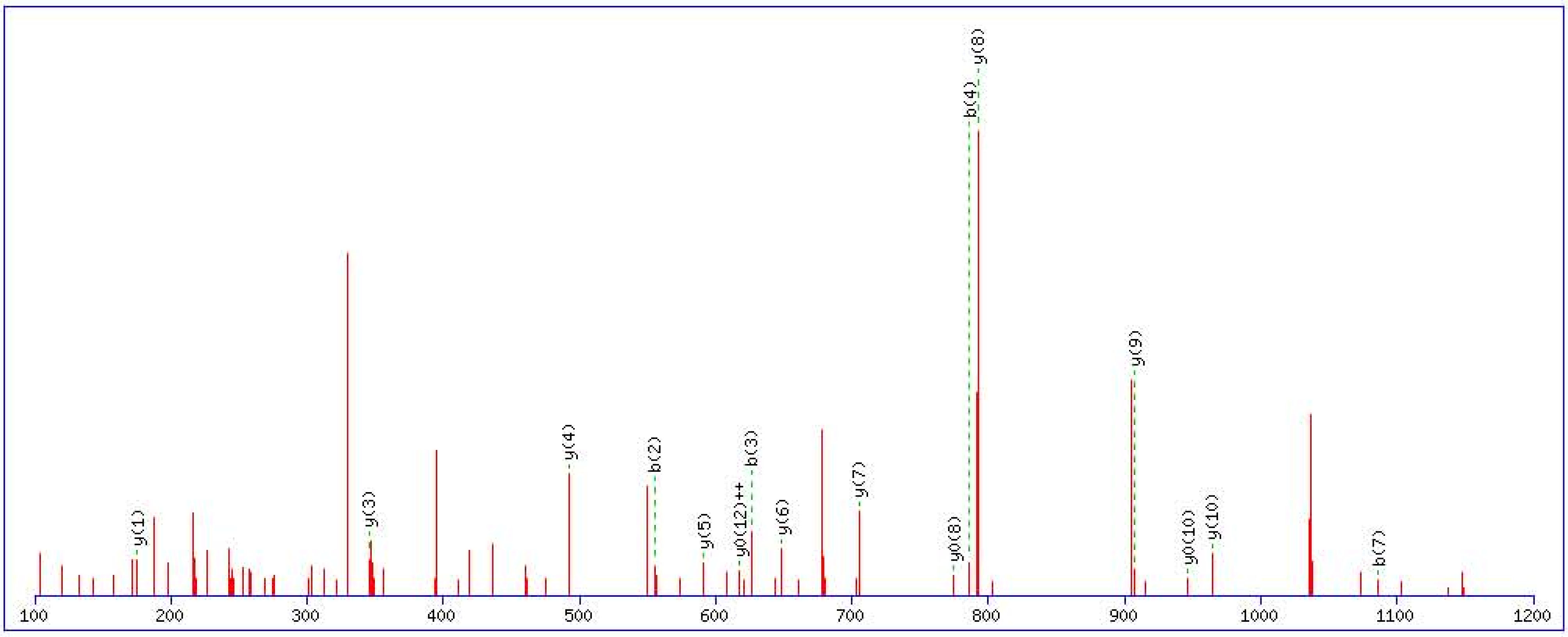
Mascot Search Results

Peptide View

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

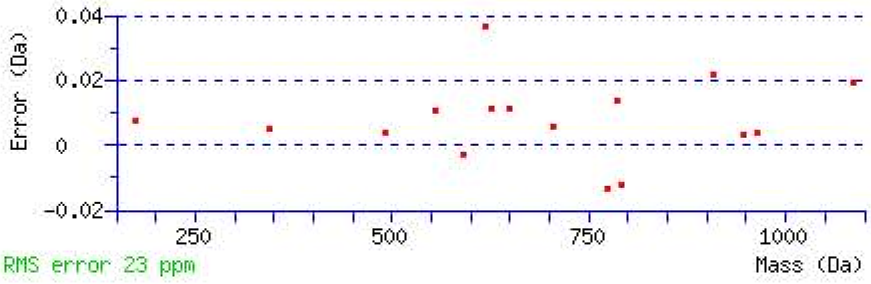
Match to Query 47104: 1876.873302 from(626.631710,3+) rtinseconds(1947) index(41833)
Title: Locus:1.1.1.3127.13 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

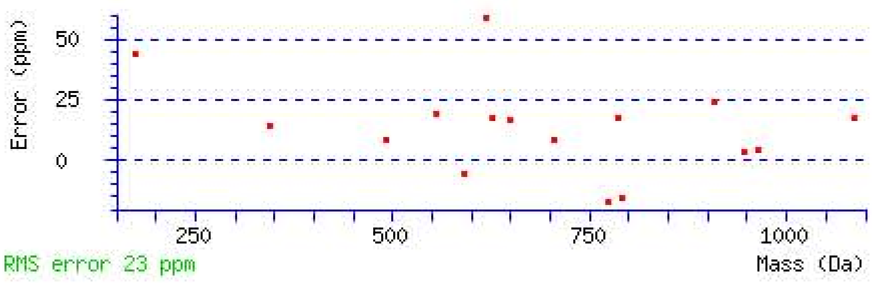
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1876.856033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0072
Matches : 16/152 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	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
32.5	1876.856033	0.017269	QDACQGDSGGVFAVR
26.1	1876.856033	0.017269	QDACQGDSGGVFAVR

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

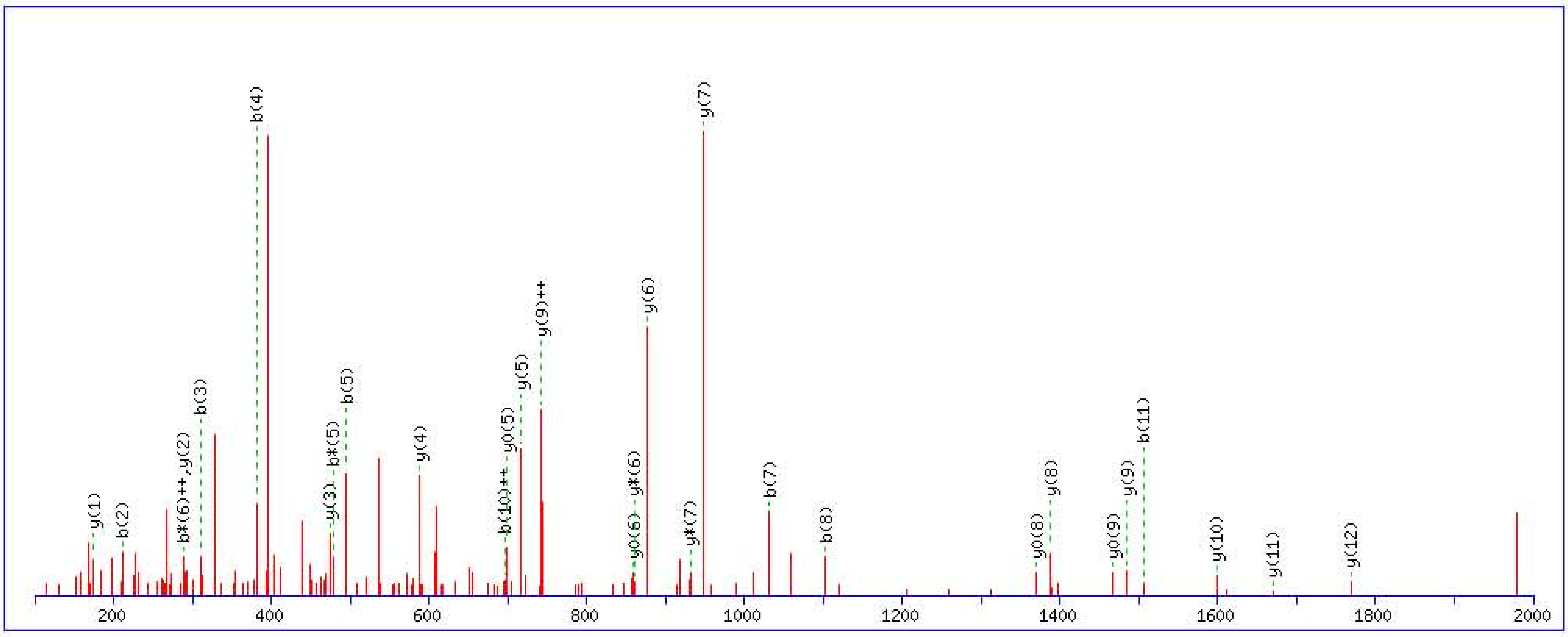
Mascot Search Results

Peptide View

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

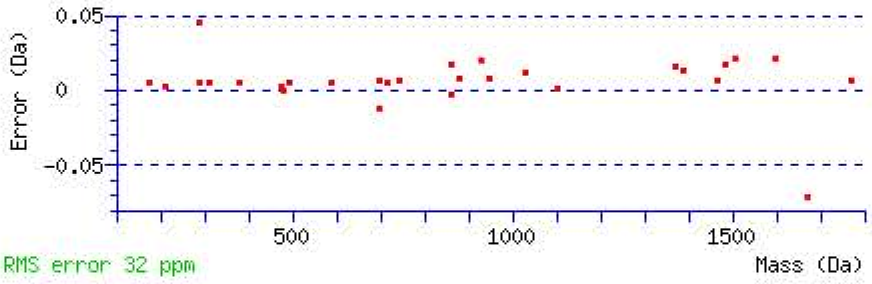
Match to Query 49420: 1978.013472 from(660.345100,3+) rtinseconds(2243) index(43939)
Title: Locus:1.1.1.3230.8 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

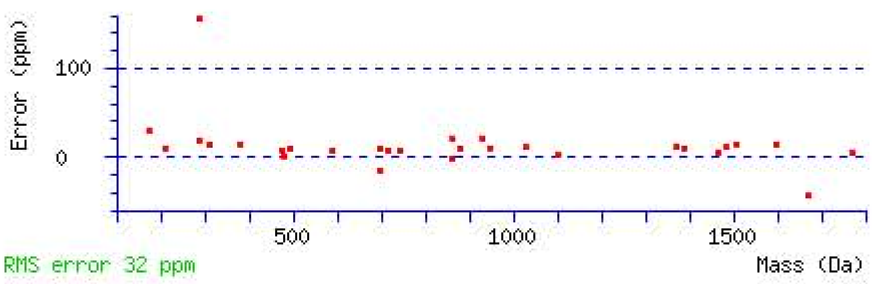
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1977.991684
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 67  Expect: 5.1e-006
Matches : 29/122 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	**211.144104**	106.075690					P	1865.914921	933.461099	1848.888372	924.947824	1847.904356	924.455816	13
3	**310.212518**	155.609897					V	***1768.862157***	884.934717	1751.835608	876.421442	1750.851592	875.929434	12
4	**381.249632**	191.128454					A	***1669.793743***	835.400510	1652.767194	826.887235	1651.783178	826.395227	11
5	**495.292559**	248.149917	478.266010	239.636643			N	***1598.756629***	799.881953	1581.730080	791.368678	1580.746064	790.876670	10
6	592.345323	296.676300	575.318774	288.163025			P	***1484.713702***	742.860489	1467.687153	734.347215	1466.703137	733.855207	9
7	**1031.570649**	516.288963	1014.544100	507.775688			Q	***1387.660938***	694.334107	1370.634389	685.820833	1369.650373	685.328825	8
8	**1102.607763**	551.807520	1085.581214	543.294245			A	***948.435612***	474.721444	931.409063	466.208170	930.425047	465.716162	7
9	1262.638412	631.822844	1245.611863	623.309570			C	***877.398498***	439.202887	860.371949	430.689613	859.387933	430.197605	6
10	1391.681005	696.344141	1374.654456	687.830866	1373.670440	687.338858	E	***717.367849***	359.187563	700.341300	350.674288	699.357284	350.182280	5
11	**1505.723932**	753.365604	1488.697383	744.852330	1487.713367	744.360322	N	***588.325256***	294.666266	571.298707	286.152991			4
12	1691.803245	846.405261	1674.776696	837.891986	1673.792680	837.399978	W	***474.282329***	237.644802	457.255780	229.131528			3
13	1804.887309	902.947293	1787.860760	894.434018	1786.876744	893.942010	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 LPVANPQACENWLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.0	1977.991684	0.021788	LPVANPQACENWLR

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

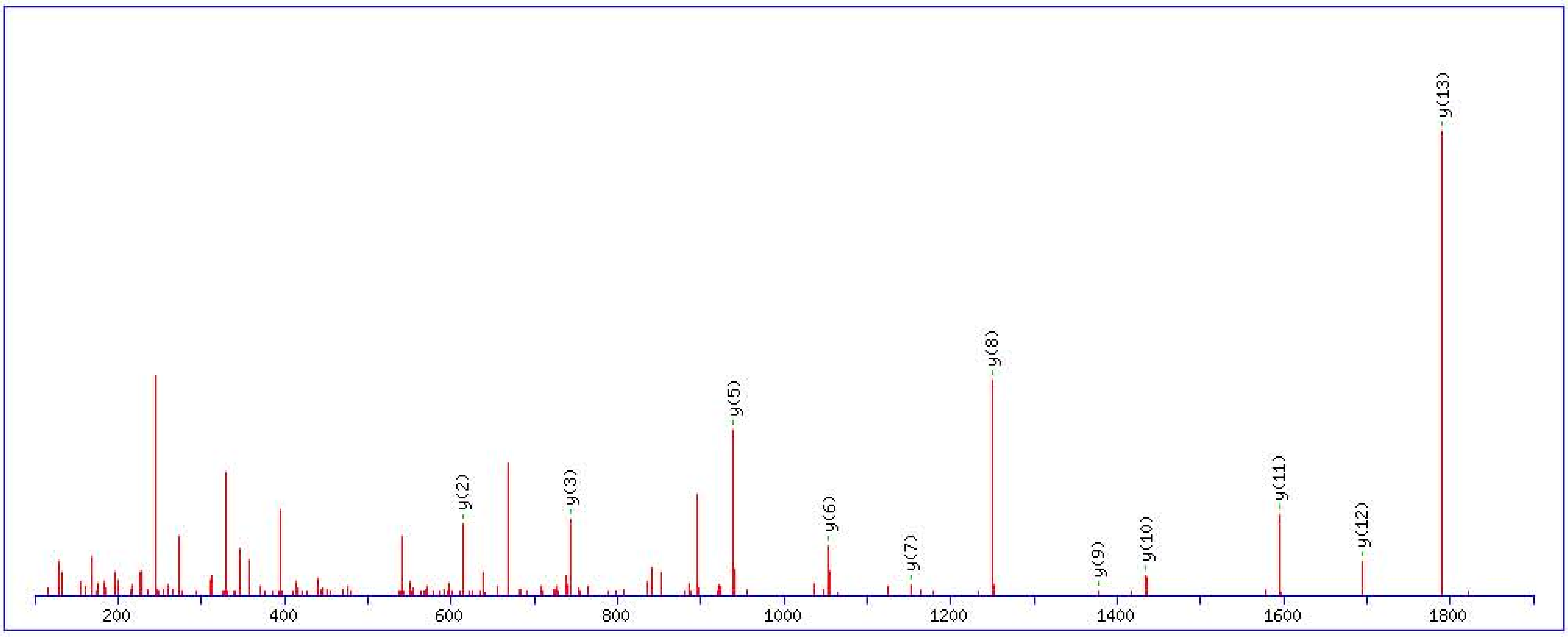
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

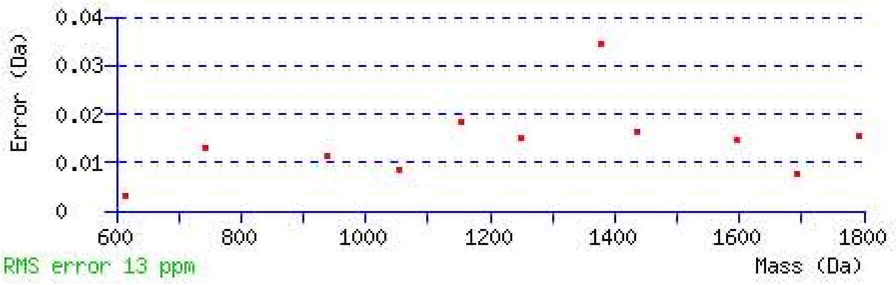
Match to Query 52417: 2063.077272 from(688.699700,3+) rtinseconds(1772) index(59157)
Title: Locus:1.1.1.3040.19 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

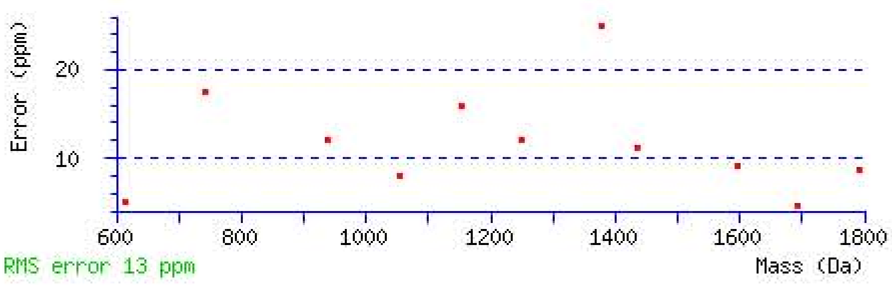
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2063.047852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 82  Expect: 3.2e-008
Matches : 11/128 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	161.037925	81.022600					C							15
2	274.121989	137.564632					L	1904.024472	952.515874	1886.997923	944.002600	1886.013907	943.510592	14
3	371.174753	186.091014					P	***1790.940408***	895.973842	1773.913859	887.460568	1772.929843	886.968560	13
4	470.243167	235.625221					V	***1693.887644***	847.447460	1676.861095	838.934186	1675.877079	838.442178	12
5	630.273816	315.640546					C	***1594.819230***	797.913253	1577.792681	789.399979	1576.808665	788.907971	11
6	687.295280	344.151278					G	***1434.788581***	717.897929	1417.762032	709.384654	1416.778016	708.892646	10
7	815.390243	408.198760	798.363694	399.685485			K	***1377.767117***	689.387197	1360.740568	680.873922	1359.756552	680.381914	9
8	912.443007	456.725142	895.416458	448.211867			P	***1249.672154***	625.339715	1232.645605	616.826441	1231.661589	616.334433	8
9	1011.511421	506.259349	994.484872	497.746074			V	***1152.619390***	576.813333	1135.592841	568.300059	1134.608825	567.808051	7
10	1125.554348	563.280812	1108.527799	554.767538			N	***1053.550976***	527.279126	1036.524427	518.765852	1035.540411	518.273844	6
11	1222.607112	611.807194	1205.580563	603.293920			P	***939.508049***	470.257663	922.481500	461.744388	921.497484	461.252380	5
12	1321.675526	661.341401	1304.648977	652.828127			V	842.455285	421.731281	825.428736	413.218006	824.444720	412.725998	4
13	1450.718119	725.862698	1433.691570	717.349423	1432.707554	716.857415	E	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
14	1889.943445	945.475361	1872.916896	936.962086	1871.932880	936.470078	Q	***614.344278***	307.675777	597.317729	299.162503			2
15							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.4	2063.047852	0.029420	CLPVCGKPVNPVEQR
2.3	2063.050781	0.026491	AKVNSEAPAANAVKAGGTDHR
0.5	2063.046982	0.030290	LVGCAIIHVNGDSPEEVVR

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

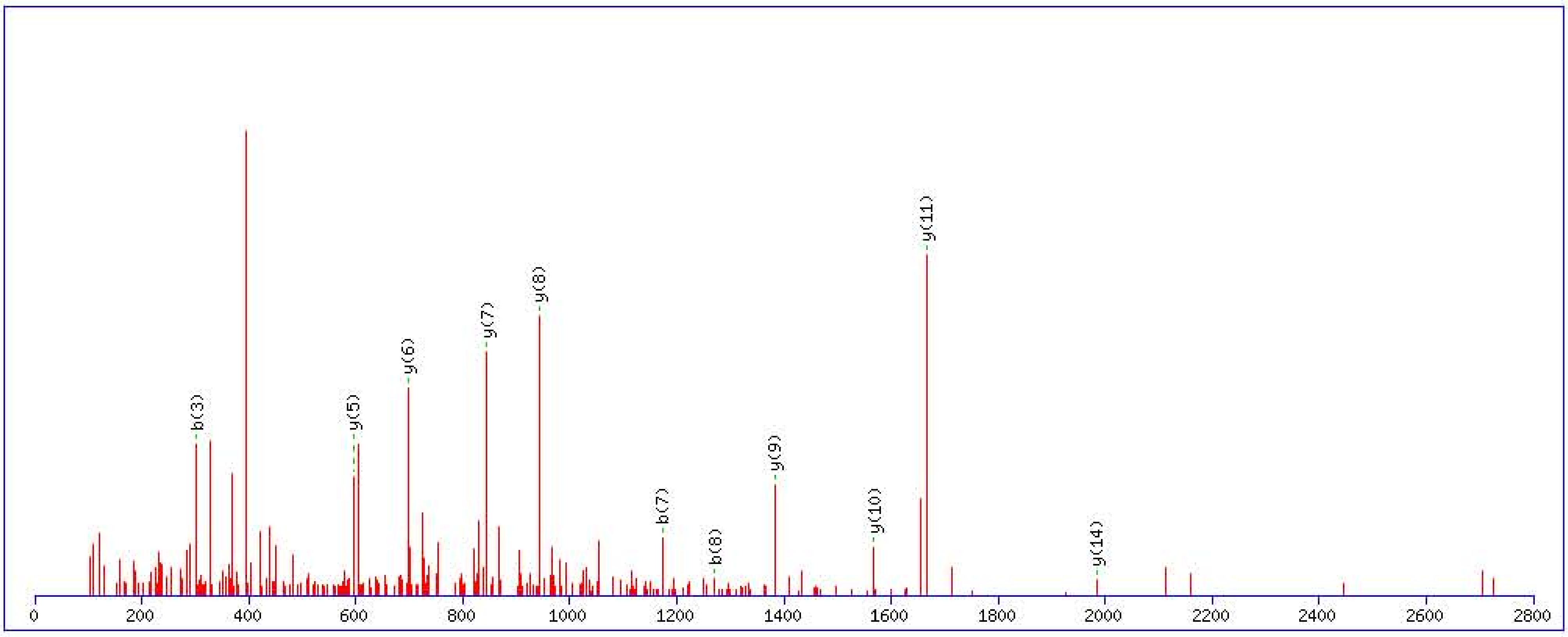
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

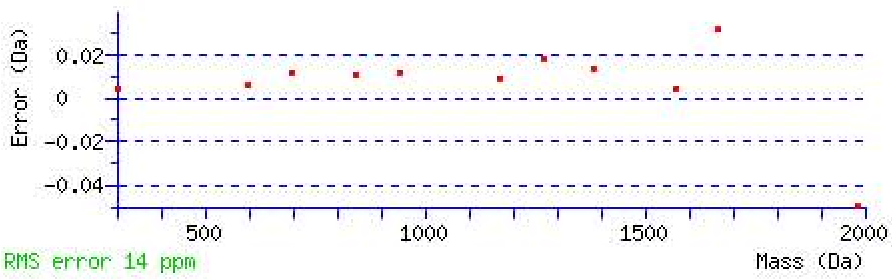
Match to Query 53409: 2114.065962 from(705.695930,3+) rtinseconds(2625) index(46465)
Title: Locus:1.1.1.3362.8 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

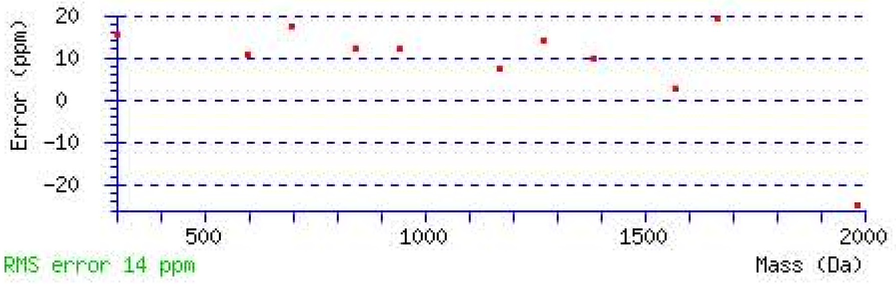
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2114.034256
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00041
Matches : 11/136 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	132.047761	66.527518					M							15
2	189.069225	95.038250					G	***1984.001034***	992.504155	1966.974485	983.990881	1965.990469	983.498873	14
3	**303.112152**	152.059714	286.085603	143.546439			N	1926.979570	963.993423	1909.953021	955.480149	1908.969005	954.988141	13
4	450.180566	225.593921	433.154017	217.080646			F	1812.936643	906.971960	1795.910094	898.458685	1794.926078	897.966677	12
5	547.233330	274.120303	530.206781	265.607029			P	***1665.868229***	833.437753	1648.841680	824.924478	1647.857664	824.432470	11
6	733.312643	367.159960	716.286094	358.646685			W	***1568.815465***	784.911371	1551.788916	776.398096	1550.804900	775.906088	10
7	**1172.537969**	586.772623	1155.511420	578.259348			Q	***1382.736152***	691.871714	1365.709603	683.358440	1364.725587	682.866432	9
8	**1271.606383**	636.306830	1254.579834	627.793555			V	***943.510826***	472.259051	926.484277	463.745777	925.500261	463.253769	8
9	1418.674797	709.841037	1401.648248	701.327762			F	***844.442412***	422.724844	827.415863	414.211570	826.431847	413.719562	7
10	1519.722476	760.364876	1502.695927	751.851602	1501.711911	751.359594	T	***697.373998***	349.190637	680.347449	340.677363	679.363433	340.185355	6
11	1633.765403	817.386340	1616.738854	808.873065	1615.754838	808.381057	N	***596.326319***	298.666798	579.299770	290.153523			5
12	1746.849467	873.928372	1729.822918	865.415097	1728.838902	864.923089	I	482.283392	241.645334	465.256843	233.132059			4
13	1883.908379	942.457828	1866.881830	933.944553	1865.897814	933.452545	H	369.199328	185.103302	352.172779	176.590028			3
14	1940.929843	970.968559	1923.903294	962.455285	1922.919278	961.963277	G	232.140416	116.573846	215.113867	108.060572			2
15							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of MGNFPWQVFTNIHGR
(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	2114.034256	0.031706	MGNFPWQVFTNIHGR

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

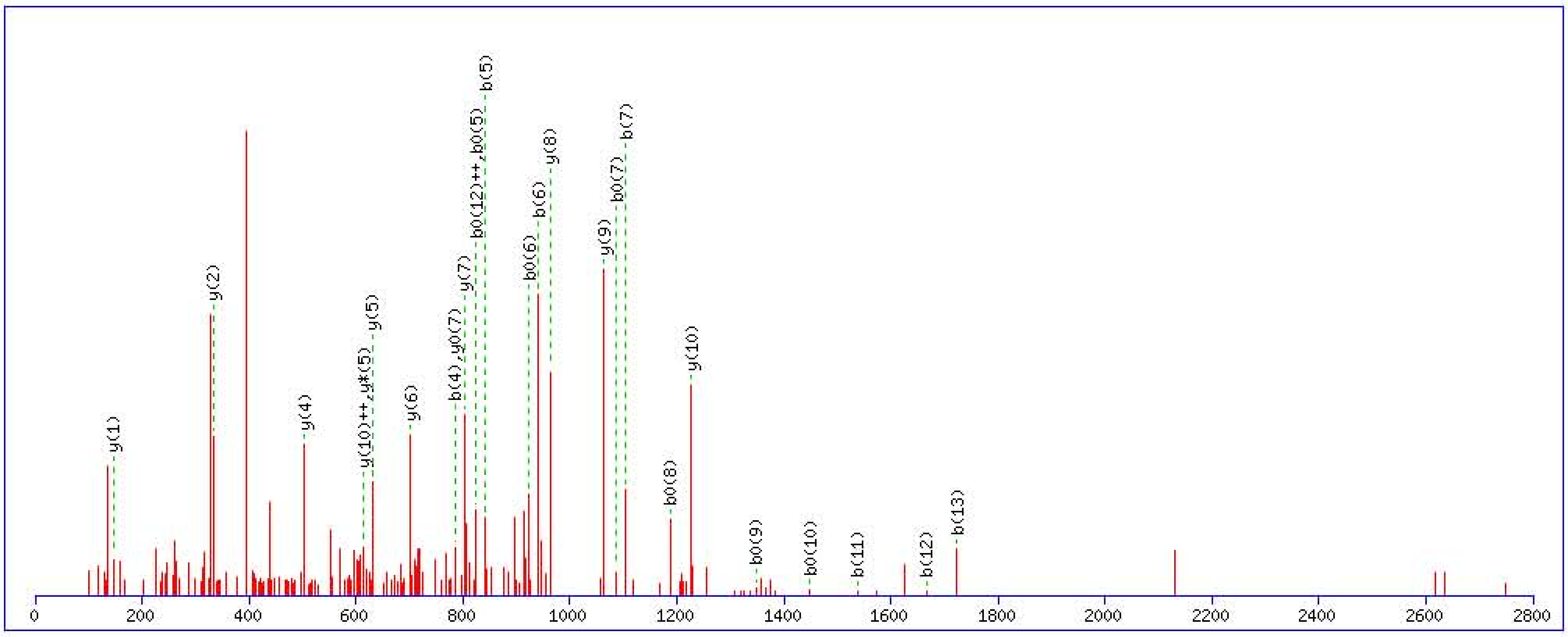
Mascot Search Results

Peptide View

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

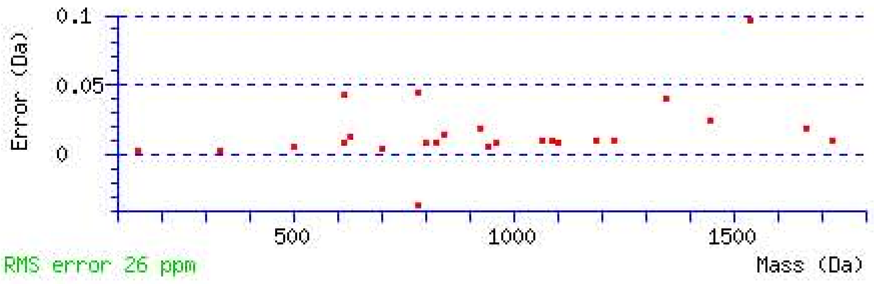
Match to Query 54565: 2167.035102 from(723.352310,3+) rtinseconds(2160) index(43334)
Title: Locus:1.1.1.3201.16 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

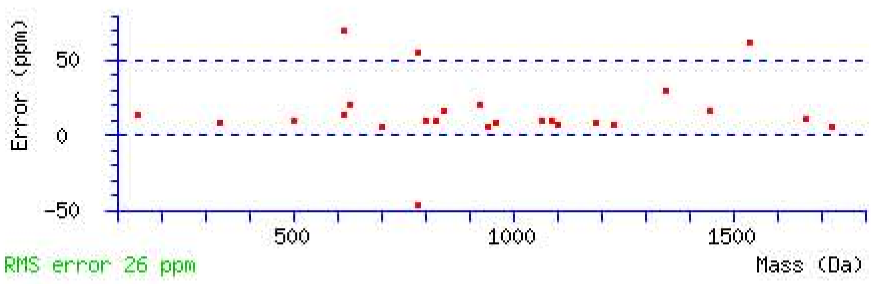
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2167.007813
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 46 **Expect:** 0.00047
Matches : 26/162 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	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
46.3	2167.007813	0.027289	ESEQGVYTCTAQGIWK

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

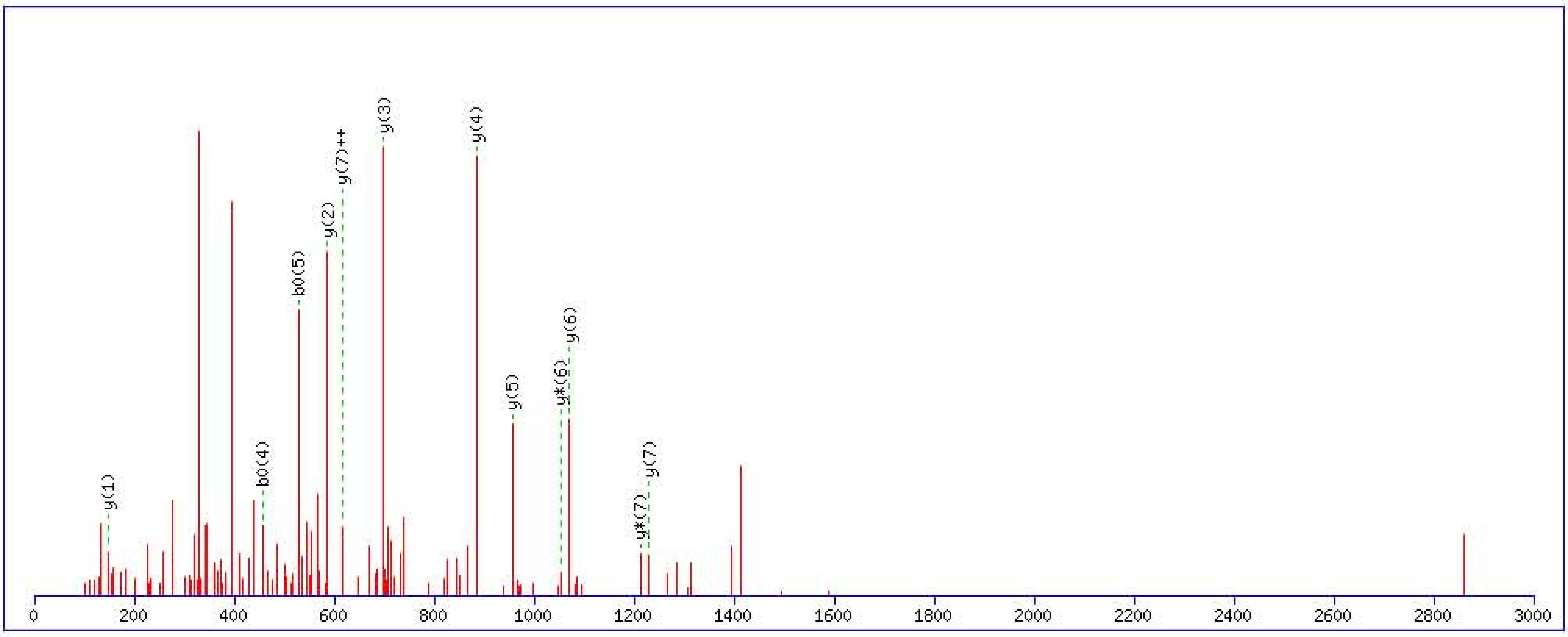
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EACNAWLQK**
Found in **C1RL_HUMAN**, Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2

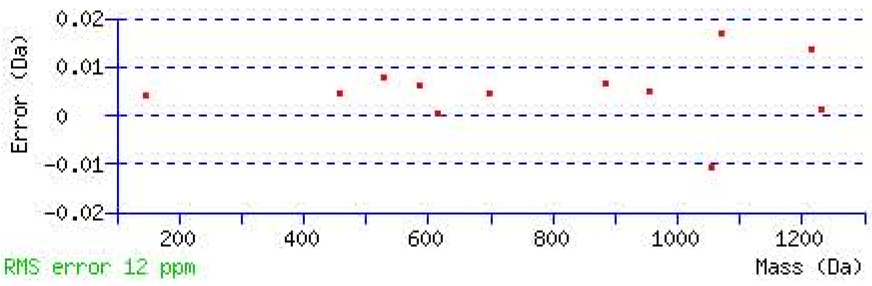
Match to Query 32628: 1429.694368 from(715.854460,2+) rtinseconds(1941) index(78499)
Title: Locus:1.1.1.2026.23 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

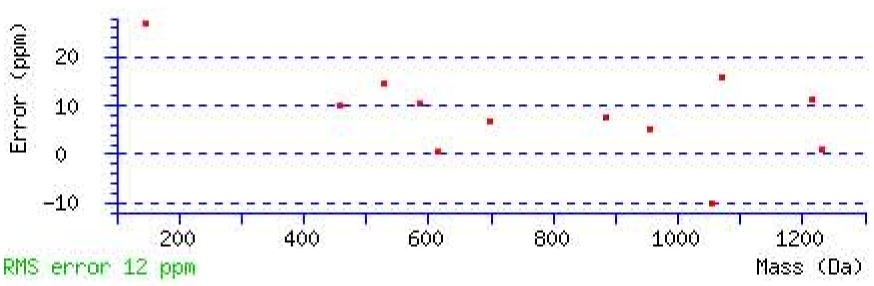
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1429.684601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0038
Matches : 12/74 fragment ions using 25 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	201.086983	101.047130			183.076418	92.041847	A	1301.649311	651.328293	1284.622762	642.815019	8
3	361.117632	181.062454			343.107067	172.057172	C	***1230.612197***	615.809736	1213.585648	607.296462	7
4	475.160559	238.083918	458.134010	229.570643	457.149994	229.078635	N	***1070.581548***	535.794412	1053.554999	527.281138	6
5	546.197673	273.602475	529.171124	265.089200	528.187108	264.597192	A	***956.538621***	478.772948	939.512072	470.259674	5
6	732.276986	366.642131	715.250437	358.128857	714.266421	357.636849	W	***885.501507***	443.254392	868.474958	434.741117	4
7	845.361050	423.184163	828.334501	414.670889	827.350485	414.178881	L	***699.422194***	350.214735	682.395645	341.701461	3
8	1284.586376	642.796826	1267.559827	634.283552	1266.575811	633.791543	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 EACNAWLQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.4	1429.684601	0.009767	EACNAWLQK
10.1	1429.680588	0.013780	MRIHCLENVDK
7.2	1429.679886	0.014482	MDDKELIEYFK
6.8	1429.687103	0.007265	QSEADNNTLK
5.4	1429.687988	0.006380	CNTPAMGLQK
5.1	1429.702362	-0.007994	LSNWESQQK
5.1	1429.705719	-0.011351	EANALAMQQK
4.7	1429.705734	-0.011366	MGAQGAQESIK
4.3	1429.690918	0.003450	AGDGERARAEAAEK
4.1	1429.705719	-0.011351	EANALAMQQK

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

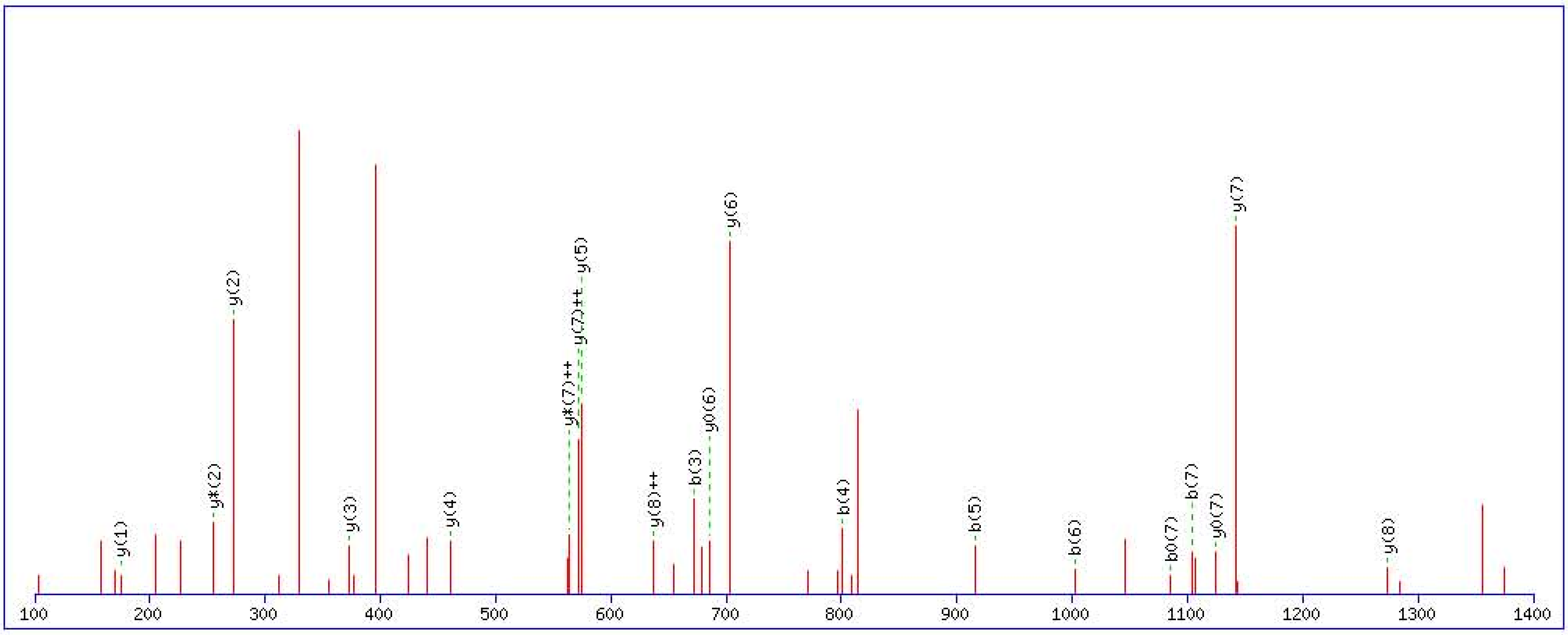
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMQENSTPR**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

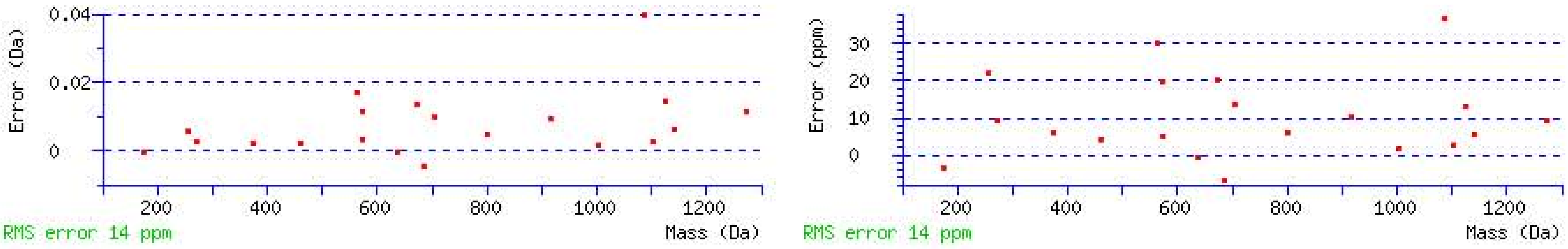
Match to Query 29703: 1373.655888 from(687.835220,2+) rtinseconds(1365) index(37778)
Title: Locus:1.1.1.2924.26 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1373.643143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00016
Matches : 20/88 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	102.054955	51.531116			84.044390	42.525833	T							9
2	233.095440	117.051358			215.084875	108.046076	M	***1273.602754***	637.305015	1256.576205	628.791741	1255.592189	628.299733	8
3	**672.320766**	336.664021	655.294217	328.150747	654.310201	327.658739	Q	***1142.562269***	571.784773	1125.535720	563.271498	1124.551704	562.779490	7
4	**801.363359**	401.185318	784.336810	392.672043	783.352794	392.180035	E	***703.336943***	352.172110	686.310394	343.658835	685.326378	343.166827	6
5	**915.406286**	458.206781	898.379737	449.693507	897.395721	449.201499	N	***574.294350***	287.650813	557.267801	279.137539	556.283785	278.645531	5
6	**1002.438314**	501.722795	985.411765	493.209521	984.427749	492.717513	S	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	4
7	**1103.485993**	552.246635	1086.459444	543.733360	1085.475428	543.241352	T	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
8	1200.538757	600.773017	1183.512208	592.259742	1182.528192	591.767734	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 TMQENSTPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.0	1373.643143	0.012745	TMQENSTPR
5.7	1373.635742	0.020146	DRGMPSDSPEKR

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

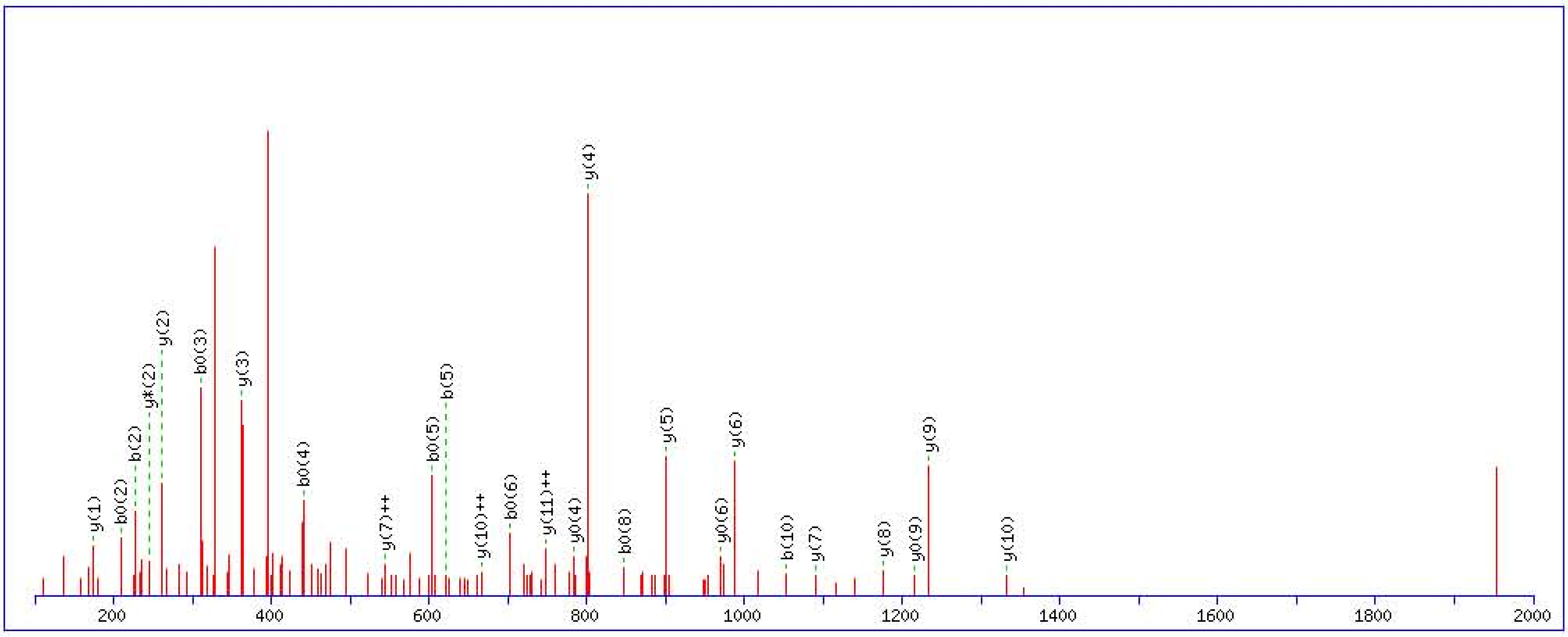
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPTMYVGSTSVQTSR**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

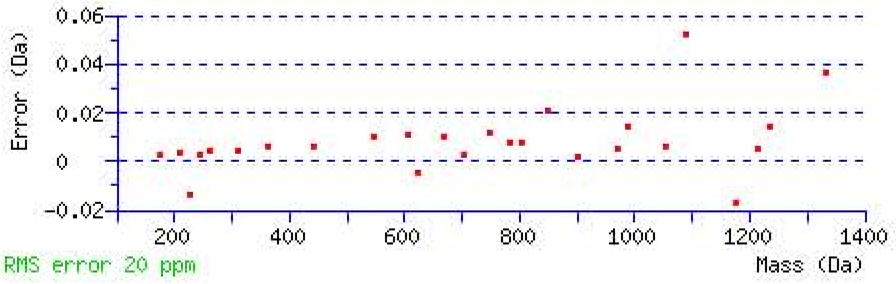
Match to Query 48766: 1952.953002 from(651.991610,3+) rtinseconds(1872) index(41195)
Title: Locus:1.1.1.3101.25 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

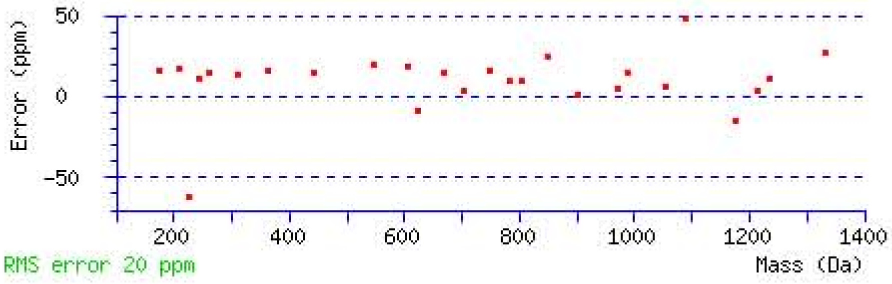
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1952.933594
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 9.3e-006
Matches : 26/144 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	130.049869	65.528572			112.039304	56.523290	E							15
2	**227.102633**	114.054954			209.092068	105.049672	P	1824.898269	912.952773	1807.871720	904.439498	1806.887704	903.947490	14
3	328.150312	164.578794			310.139747	155.573512	T	1727.845505	864.426391	1710.818956	855.913116	1709.834940	855.421108	13
4	459.190797	230.099036			441.180232	221.093754	M	1626.797826	813.902551	1609.771277	805.389277	1608.787261	804.897269	12
5	**622.254126**	311.630701			604.243561	302.625419	Y	1495.757341	748.382309	1478.730792	739.869034	1477.746776	739.377026	11
6	721.322540	361.164908			703.311975	352.159626	V	***1332.694012***	666.850644	1315.667463	658.337370	1314.683447	657.845362	10
7	778.344004	389.675640			760.333439	380.670358	G	***1233.625598***	617.316437	1216.599049	608.803163	1215.615033	608.311155	9
8	865.376032	433.191654			847.365467	424.186372	S	***1176.604134***	588.805705	1159.577585	580.292431	1158.593569	579.800423	8
9	966.423711	483.715494			948.413146	474.710211	T	***1089.572106***	545.289691	1072.545557	536.776417	1071.561541	536.284409	7
10	**1053.455739**	527.231508			1035.445174	518.226225	S	***988.524427***	494.765852	971.497878	486.252577	970.513862	485.760569	6
11	1152.524153	576.765715			1134.513588	567.760432	V	***901.492399***	451.249838	884.465850	442.736563	883.481834	442.244555	5
12	1591.749479	796.378378	1574.722930	787.865103	1573.738914	787.373095	Q	***802.423985***	401.715631	785.397436	393.202356	784.413420	392.710348	4
13	1692.797158	846.902217	1675.770609	838.388943	1674.786593	837.896935	T	***363.198659***	182.102968	346.172110	173.589693	345.188094	173.097685	3
14	1779.829186	890.418231	1762.802637	881.904957	1761.818621	881.412949	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 EPTMYVGSTSVQTSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.2	1952.933594	0.019408	EPTMYVGSTSVQTSR
2.5	1952.944794	0.008208	MNQVTSKYANQSAGK

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

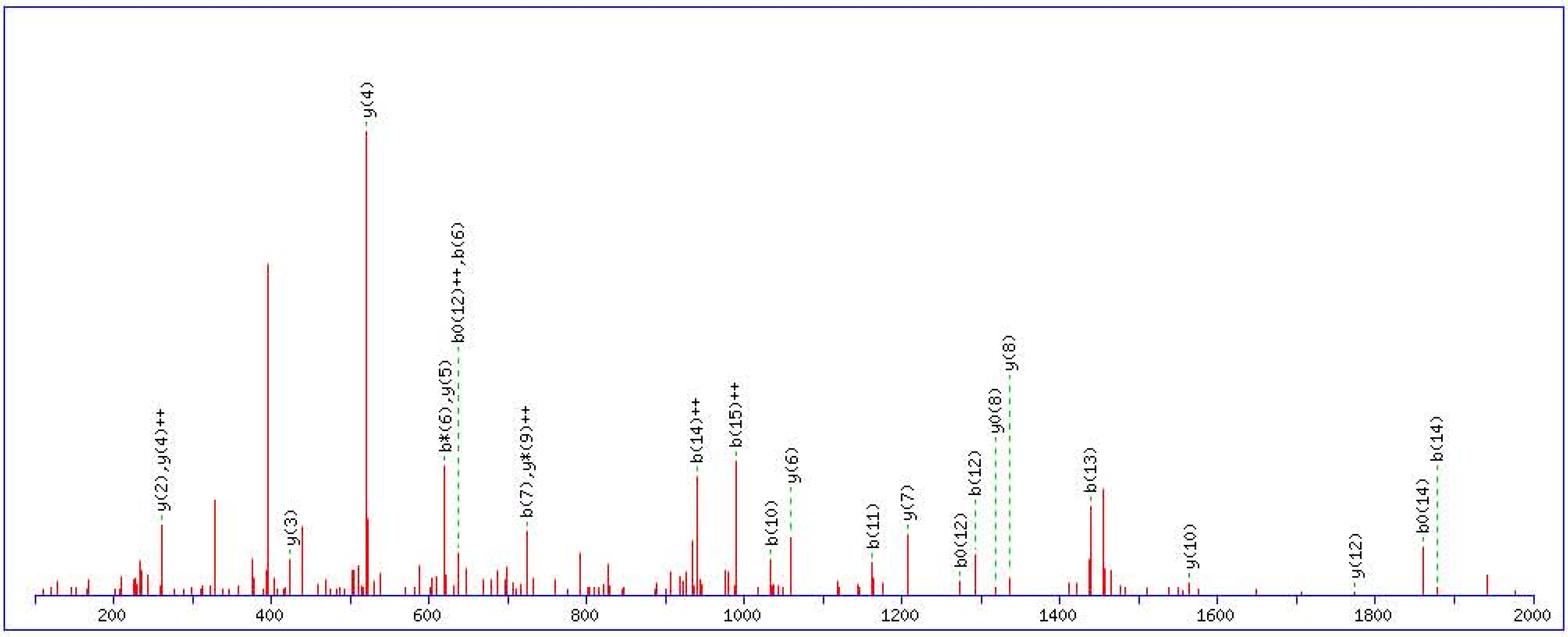
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSNNPHSPIVEEFQVPYNK**
Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

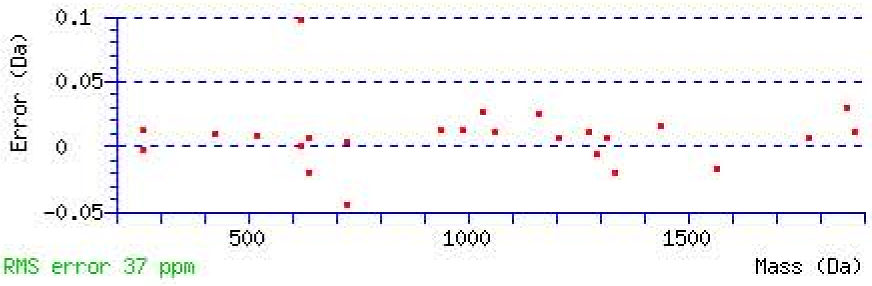
Match to Query 63004: 2496.246582 from(833.089470,3+) rtinseconds(2094) index(42857)
Title: Locus:1.1.1.3178.14 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

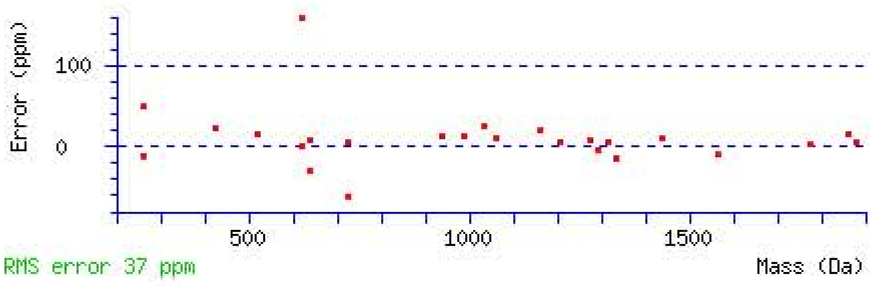


```
Monoisotopic mass of neutral peptide Mr(calc): 2496.210724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14    : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 5.7e-005
Matches : 25/198 fragment ions using 37 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							19
2	175.071332	88.039304			157.060767	79.034021	S	2410.185992	1205.596634	2393.159443	1197.083359	2392.175427	1196.591351	18
3	289.114259	145.060768	272.087710	136.547493	271.103694	136.055485	N	2323.153964	1162.080620	2306.127415	1153.567345	2305.143399	1153.075337	17
4	403.157186	202.082231	386.130637	193.568957	385.146621	193.076949	N	2209.111037	1105.059156	2192.084488	1096.545882	2191.100472	1096.053874	16
5	500.209950	250.608613	483.183401	242.095339	482.199385	241.603331	P	2095.068110	1048.037693	2078.041561	1039.524418	2077.057545	1039.032410	15
6	**637.268862**	319.138069	620.242313	310.624795	619.258297	310.132787	H	1998.015346	999.511311	1980.988797	990.998037	1980.004781	990.506028	14
7	**724.300890**	362.654083	707.274341	354.140808	706.290325	353.648800	S	1860.956434	930.981855	1843.929885	922.468581	1842.945869	921.976572	13
8	821.353654	411.180465	804.327105	402.667191	803.343089	402.175183	P	***1773.924406***	887.465841	1756.897857	878.952567	1755.913841	878.460559	12
9	934.437718	467.722497	917.411169	459.209223	916.427153	458.717215	I	1676.871642	838.939459	1659.845093	830.426185	1658.861077	829.934177	11
10	**1033.506132**	517.256704	1016.479583	508.743429	1015.495567	508.251421	V	***1563.787578***	782.397427	1546.761029	773.884153	1545.777013	773.392145	10
11	**1162.548725**	581.778000	1145.522176	573.264726	1144.538160	572.772718	E	1464.719164	732.863220	1447.692615	724.349946	1446.708599	723.857938	9
12	**1291.591318**	646.299297	1274.564769	637.786023	1273.580753	637.294015	E	***1335.676571***	668.341924	1318.650022	659.828649	1317.666006	659.336641	8
13	**1438.659732**	719.833504	1421.633183	711.320230	1420.649167	710.828222	F	***1206.633978***	603.820627	1189.607429	595.307353			7
14	**1877.885058**	**939.446167**	1860.858509	930.932893	1859.874493	930.440885	Q	***1059.565564***	530.286420	1042.539015	521.773146			6
15	1976.953472	**988.980374**	1959.926923	980.467100	1958.942907	979.975092	V	***620.340238***	310.673757	603.313689	302.160483			5
16	2074.006236	1037.506756	2056.979687	1028.993481	2055.995671	1028.501473	P	***521.271824***	261.139550	504.245275	252.626275			4
17	2237.069565	1119.038420	2220.043016	1110.525146	2219.059000	1110.033138	Y	***424.219060***	212.613168	407.192511	204.099894			3
18	2351.112492	1176.059884	2334.085943	1167.546609	2333.101927	1167.054601	N	***261.155731***	131.081503	244.129182	122.568229			2
19							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 37 ppm



RMS error 37 ppm

NCBI **BLAST** search of SSNNPHSPIVEEFQVPYNK
(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	2496.210724	0.035858	SSNNPHSPIVEEFQVPYNK
0.1	2496.236603	0.009979	RPVFSHCQVPETQKTDTR

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

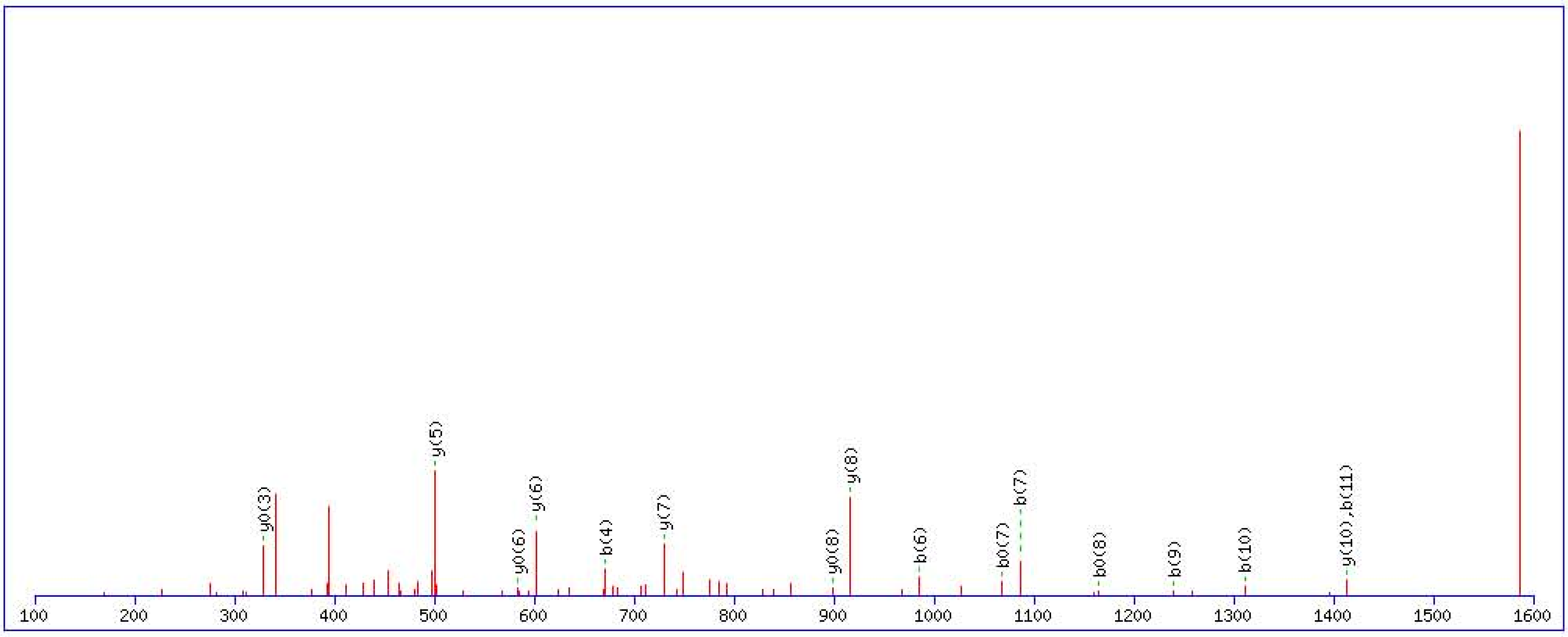
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSGQWQTPGATR**
Found in **CO2_HUMAN**, Complement C2 OS=Homo sapiens GN=C2 PE=1 SV=2

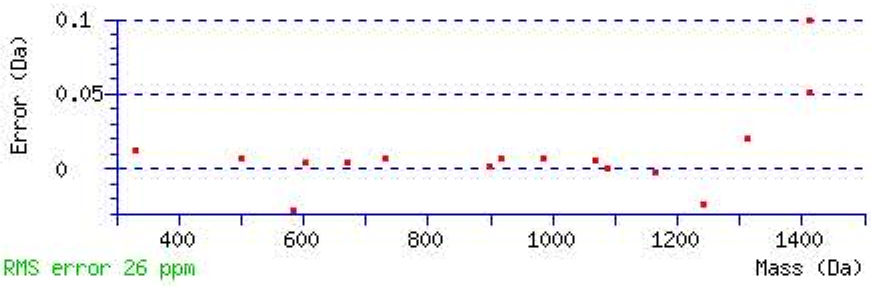
Match to Query 38021: 1585.779268 from(793.896910,2+) rtinseconds(1723) index(77058)
Title: Locus:1.1.1.1951.8 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

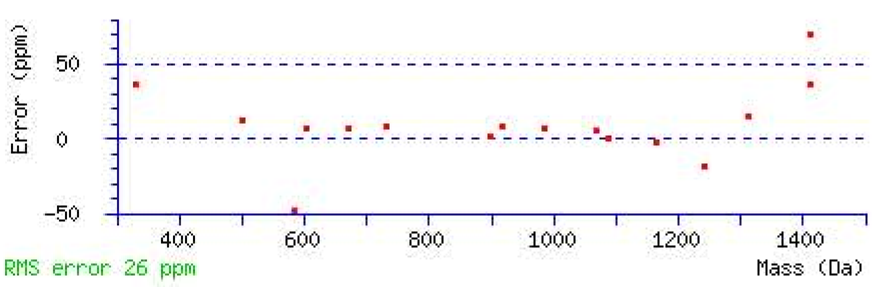
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1585.767120
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.00099
Matches : 16/124 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							12
2	175.071332	88.039304			157.060767	79.034021	S	1499.742361	750.374818	1482.715812	741.861544	1481.731796	741.369536	11
3	232.092796	116.550036			214.082231	107.544753	G	***1412.710333***	706.858805	1395.683784	698.345530	1394.699768	697.853522	10
4	***671.318122***	336.162699	654.291573	327.649425	653.307557	327.157417	Q	1355.688869	678.348072	1338.662320	669.834798	1337.678304	669.342790	9
5	857.397435	429.202356	840.370886	420.689081	839.386870	420.197073	W	***916.463543***	458.735410	899.436994	450.222135	898.452978	449.730127	8
6	***985.456013***	493.231645	968.429464	484.718370	967.445448	484.226362	Q	***730.384230***	365.695753	713.357681	357.182478	712.373665	356.690470	7
7	***1086.503692***	543.755484	1069.477143	535.242210	1068.493127	534.750202	T	***602.325652***	301.666464	585.299103	293.153189	584.315087	292.661181	6
8	1183.556456	592.281866	1166.529907	583.768592	1165.545891	583.276584	P	***501.277973***	251.142624	484.251424	242.629350	483.267408	242.137342	5
9	***1240.577920***	620.792598	1223.551371	612.279324	1222.567355	611.787315	G	404.225209	202.616242	387.198660	194.102968	386.214644	193.610960	4
10	***1311.615034***	656.311155	1294.588485	647.797881	1293.604469	647.305872	A	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	3
11	***1412.662713***	706.834994	1395.636164	698.321720	1394.652148	697.829712	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 SSGQWQTPGATR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.5	1585.767120	0.012148	SSGQWQTPGATR
20.4	1585.767120	0.012148	SSGQWQTPGATR
6.1	1585.769592	0.009676	ETDHKSLSSSPDKR
5.4	1585.767075	0.012193	AWENLGEQMGKAPR
2.5	1585.765717	0.013551	DLEEALPALEEAMR
1.6	1585.796082	-0.016814	AGGSWDLAVQERAAR
0.7	1585.769653	0.009615	GDVGTAGSVGGTGEPGLR

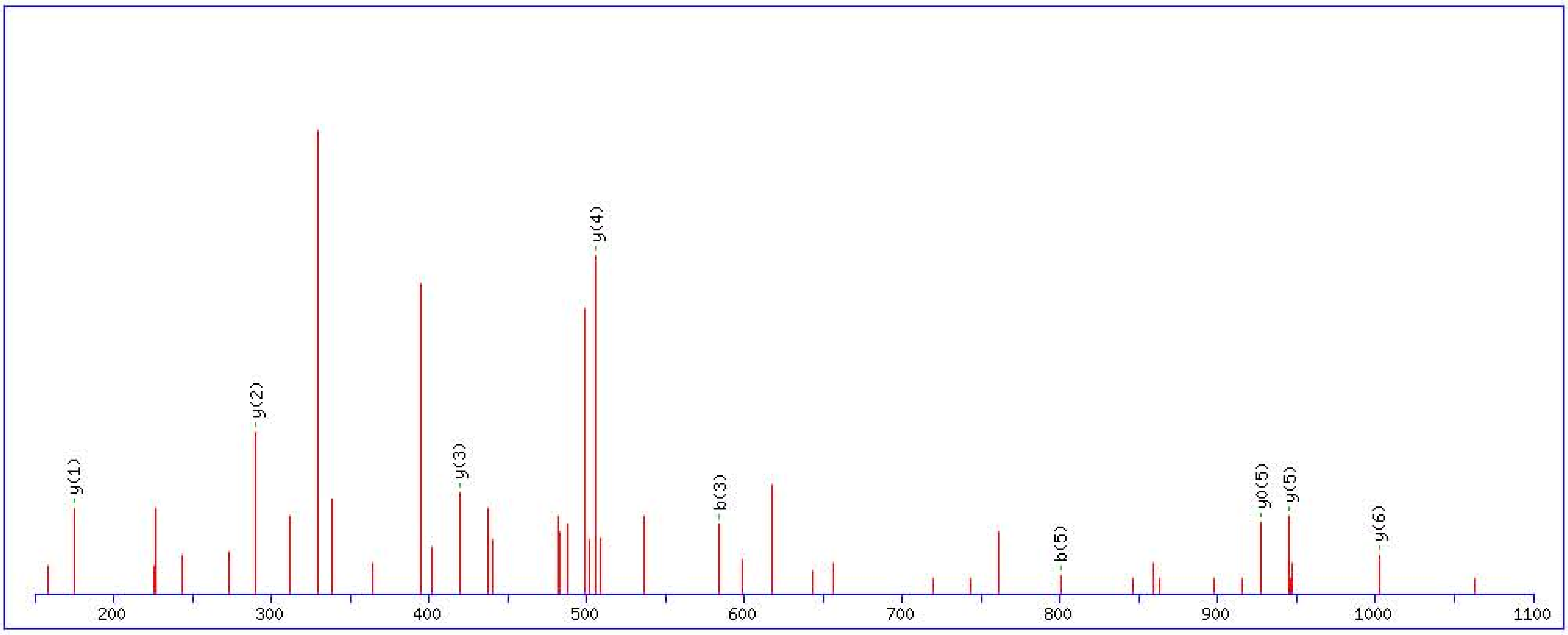
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGQSEDR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

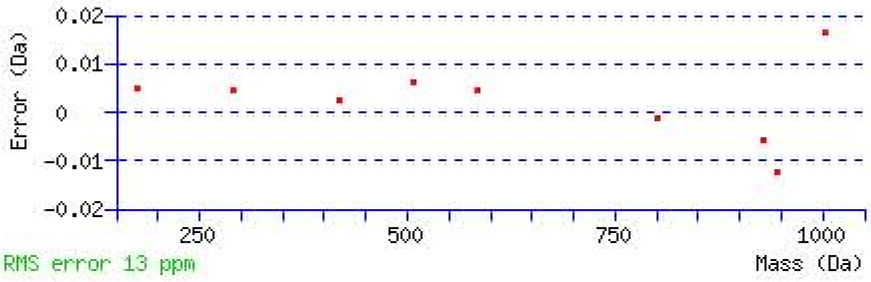
Match to Query 18672: 1088.498388 from(545.256470,2+) rtinseconds(1127) index(36296)
Title: Locus:1.1.1.2841.14 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

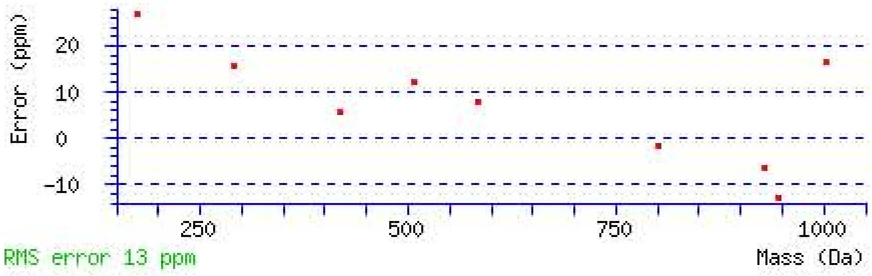
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1088.492050
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0024
Matches : 9/66 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	88.039304	44.523290			70.028739	35.518008	S							7
2	145.060768	73.034022			127.050203	64.028740	G	***1002.467306***	501.737291	985.440757	493.224017	984.456741	492.732009	6
3	**584.286094**	292.646685	567.259545	284.133411	566.275529	283.641403	Q	***945.445842***	473.226559	928.419293	464.713285	927.435277	464.221277	5
4	671.318122	336.162699	654.291573	327.649425	653.307557	327.157417	S	***506.220516***	253.613896	489.193967	245.100621	488.209951	244.608613	4
5	**800.360715**	400.683996	783.334166	392.170721	782.350150	391.678713	E	***419.188488***	210.097882	402.161939	201.584608	401.177923	201.092600	3
6	915.387658	458.197467	898.361109	449.684192	897.377093	449.192185	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
7							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SGQSEDR
(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	1088.492050	0.006338	SGQSEDR
9.7	1088.509811	-0.011423	GAEAGSVVDER
4.7	1088.509811	-0.011423	DAAPLTSSGDR
3.8	1088.492065	0.006323	LSDPAVCGDR
2.5	1088.499908	-0.001520	KNWGGQEDR
1.6	1088.510681	-0.012293	ATMQGDR

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

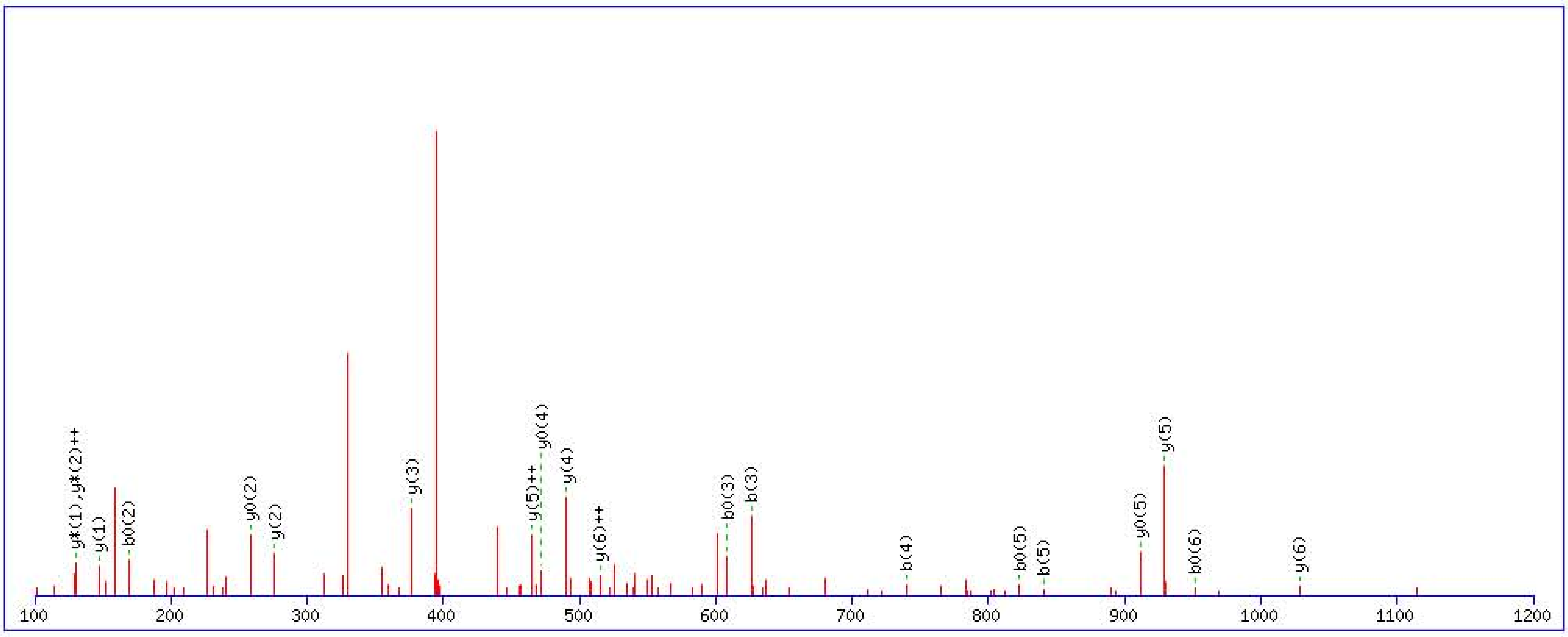
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVQLTEK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

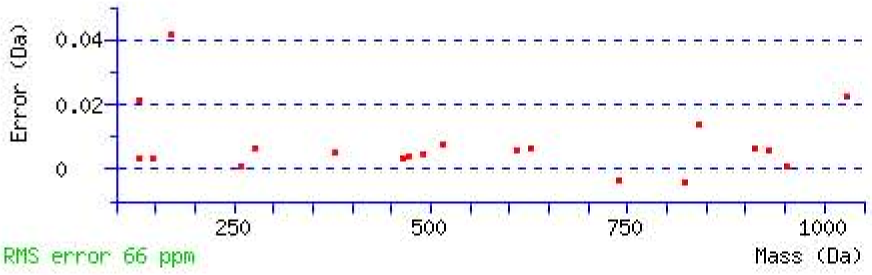
Match to Query 19864: 1114.614168 from(558.314360,2+) rtinseconds(1527) index(38977)
Title: Locus:1.1.1.2981.13 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

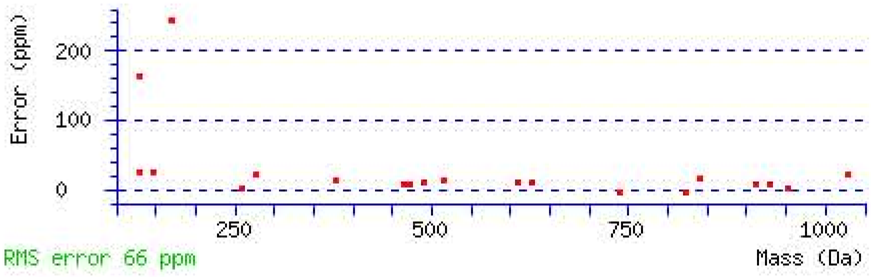
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1114.605621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.024
Matches : 20/66 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	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
30.0	1114.605621	0.008547	SVQLTEK
13.8	1114.613480	0.000688	SVFAKHGLEK
11.8	1114.623367	-0.009199	SIQDAELLVK
6.1	1114.623383	-0.009215	QVTEAVVIEK
5.9	1114.609451	0.004717	SVARLSPETR
5.2	1114.623337	-0.009169	EKNLILEEK
5.2	1114.623352	-0.009184	ILDAIKEADK
5.0	1114.624695	-0.010527	EKHHNILPK
4.9	1114.623367	-0.009199	ASVGLEVLAEK
3.6	1114.623352	-0.009184	LVEALAAATEK

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

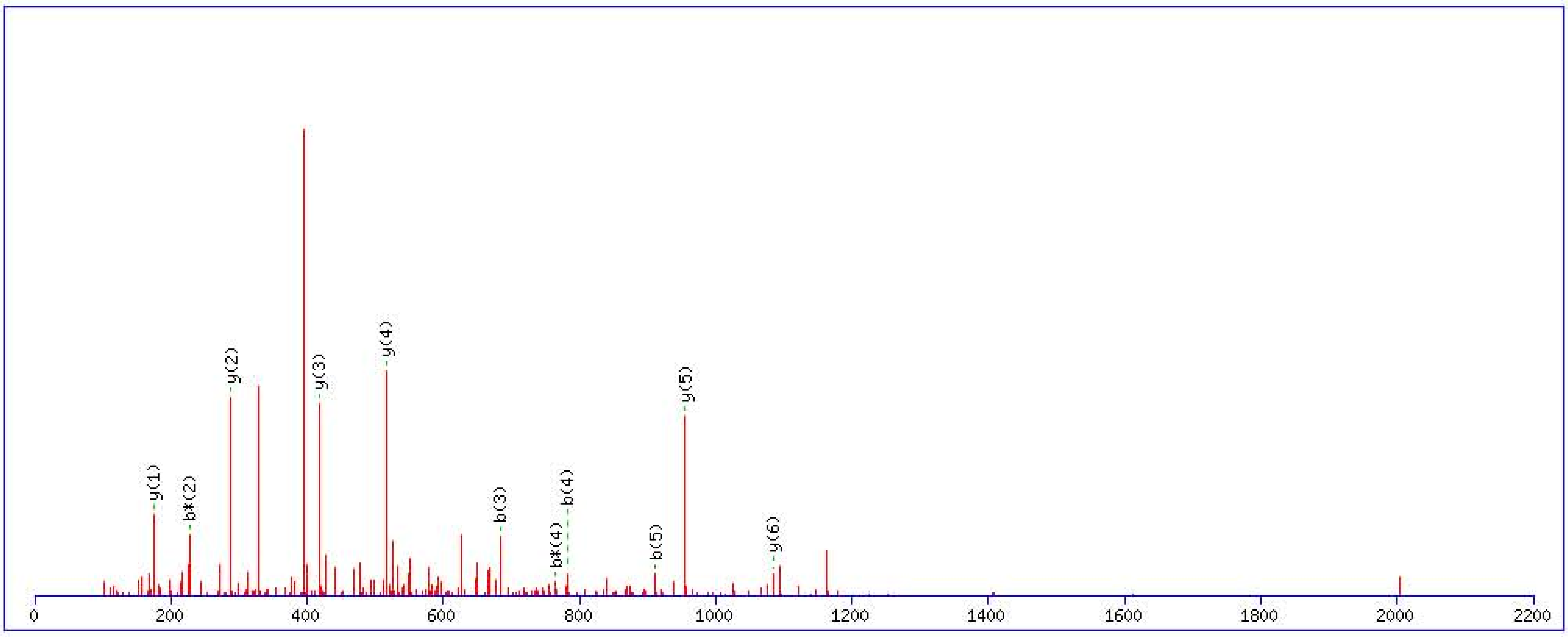
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NEQVEIR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

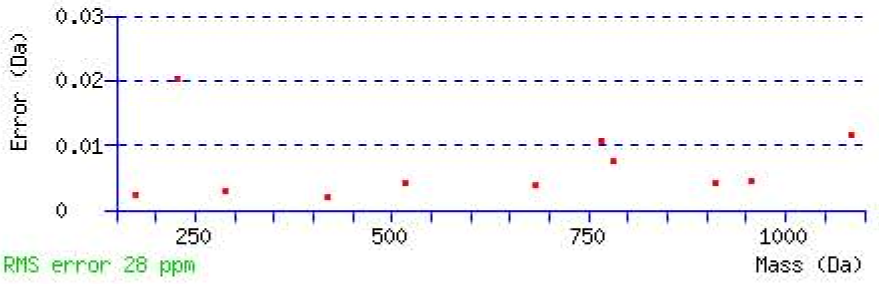
Match to Query 23651: 1197.625528 from(599.820040,2+) rtinseconds(1623) index(39605)
Title: Locus:1.1.1.3014.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

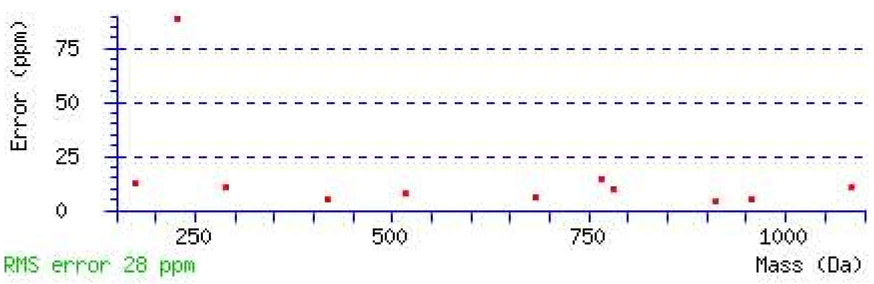
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 35  Expect: 0.0065
Matches : 11/66 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	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
35.0	1197.617569	0.007959	NEQVEIR
14.8	1197.636215	-0.010687	GVSQMPLR
12.2	1197.617569	0.007959	QEVNELR
10.7	1197.617569	0.007959	NQEDLLR
8.3	1197.617569	0.007959	LQDNELR
6.9	1197.628815	-0.003287	QLSMQVHALR
6.4	1197.640045	-0.014517	QCQLQRPLR
6.3	1197.621399	0.004129	EKHSTQAKNR
4.4	1197.617584	0.007944	QDLDQLR
4.1	1197.640030	-0.014502	NKVMEHRLR

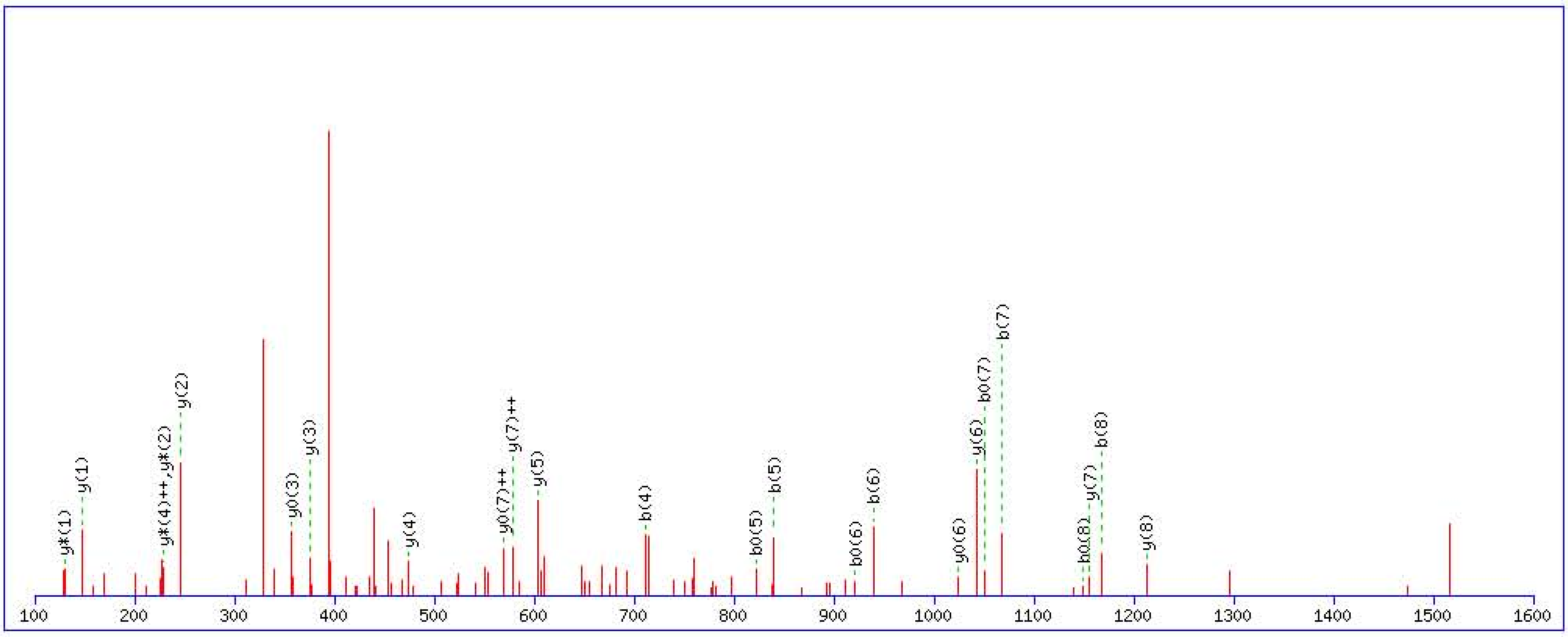
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGLQEVEVK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

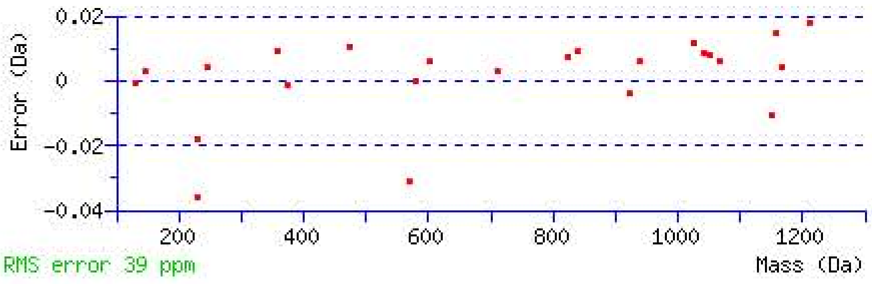
Match to Query 27220: 1312.718308 from(657.366430,2+) rtinseconds(1800) index(40784)
Title: Locus:1.1.1.3076.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

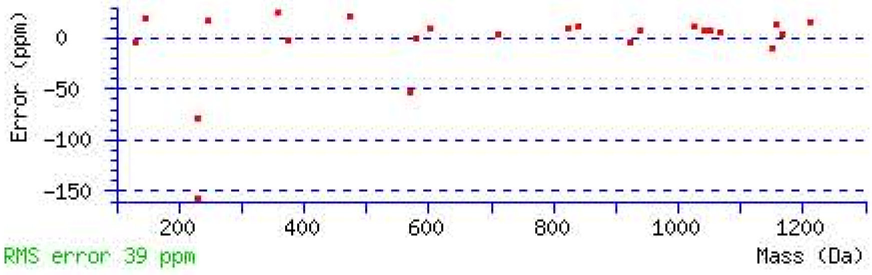
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 48  Expect: 0.00029
Matches : 24/86 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	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
47.6	1312.706070	0.012238	TGLQEVEVK
9.3	1312.713913	0.004395	KVFEKYTTAAR
8.4	1312.699524	0.018784	TIMHLMINNVK
6.8	1312.728546	-0.010238	QGSRGTAVVK
6.5	1312.721130	-0.002822	QVEVLTNQRAR
5.7	1312.735077	-0.016769	TSQGGAGVSPLLVK
5.2	1312.732346	-0.014038	EARQRVQSLAR
4.2	1312.728516	-0.010208	KPQRGMPKVEK
3.7	1312.702682	0.015626	IQYSLGKYDVK
3.1	1312.735046	-0.016738	DLKLDNVLLDR

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

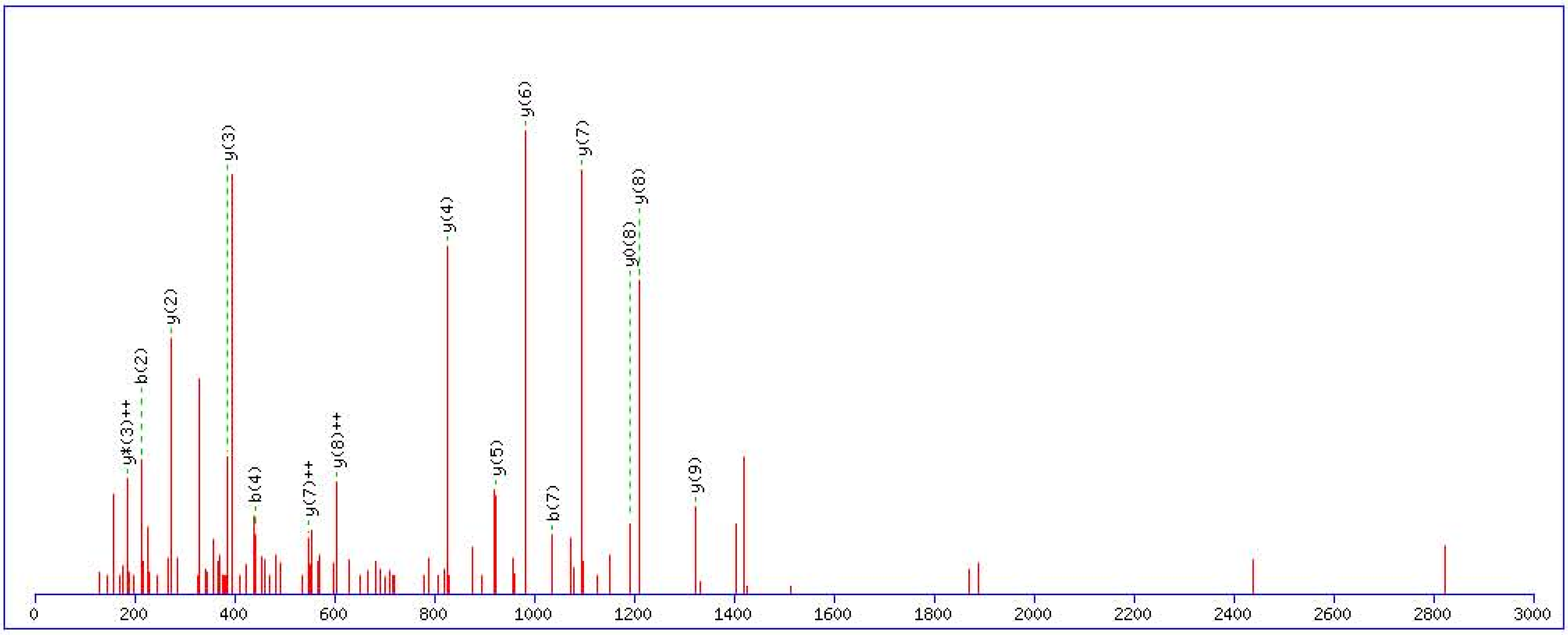
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLLDGVQNPR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

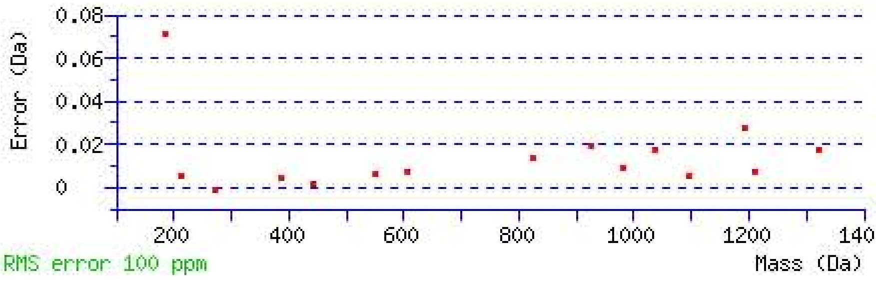
Match to Query 32070: 1420.804348 from(711.409450,2+) rtinseconds(1974) index(42065)
Title: Locus:1.1.1.3136.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

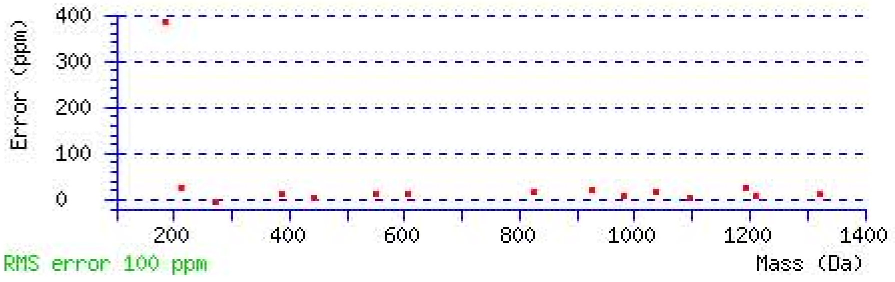
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1420.786057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 9.7e-005
Matches : 15/78 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							10
2	**213.159754**	107.083515					L	***1322.724918***	661.866097	1305.698369	653.352823	1304.714353	652.860814	9
3	326.243818	163.625547					L	***1209.640854***	605.324065	1192.614305	596.810791	1191.630289	596.318783	8
4	**441.270761**	221.139018			423.260196	212.133736	D	***1096.556790***	548.782033	1079.530241	540.268758	1078.546225	539.776750	7
5	498.292225	249.649750			480.281660	240.644468	G	***981.529847***	491.268562	964.503298	482.755287			6
6	597.360639	299.183958			579.350074	290.178675	V	***924.508383***	462.757830	907.481834	454.244555			5
7	**1036.585965**	518.796621	1019.559416	510.283346	1018.575400	509.791338	Q	***825.439969***	413.223623	808.413420	404.710348			4
8	1150.628892	575.818084	1133.602343	567.304810	1132.618327	566.812801	N	***386.214643***	193.610959	369.188094	185.097685			3
9	1247.681656	624.344466	1230.655107	615.831192	1229.671091	615.339183	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 VLLDGVQNPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	1420.786057	0.018291	VLLDGVQNPR
0.2	1420.786041	0.018307	DPLSPAVRQK

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

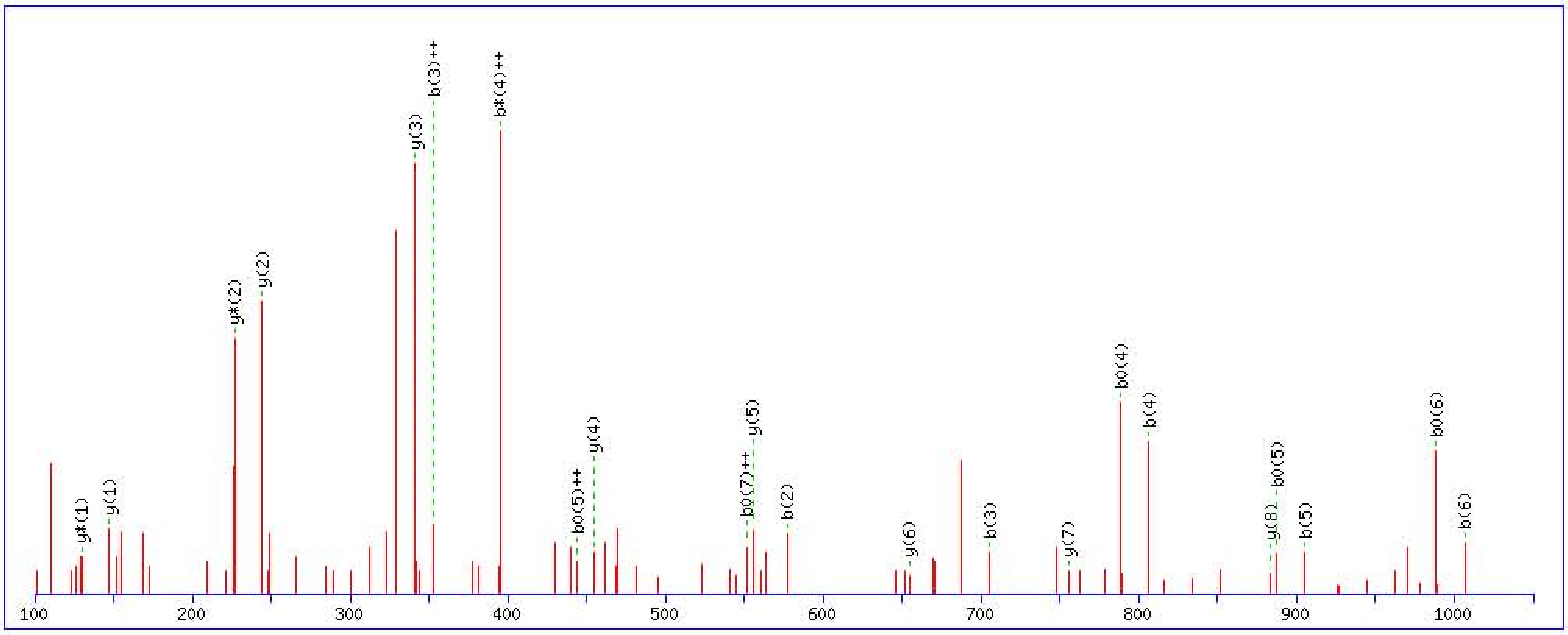
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQQTVTIPPK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

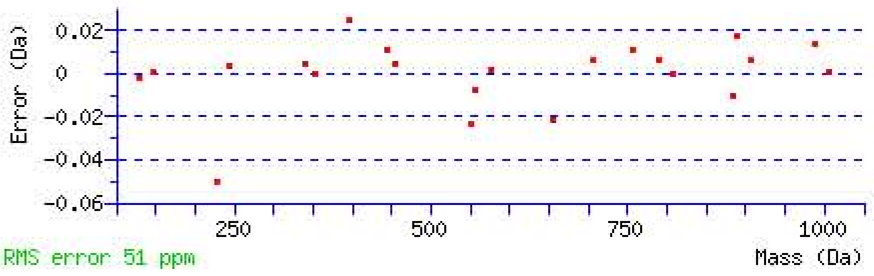
Match to Query 33668: 1458.808572 from(487.276800,3+) rtinseconds(1524) index(38949)
Title: Locus:1.1.1.2980.10 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

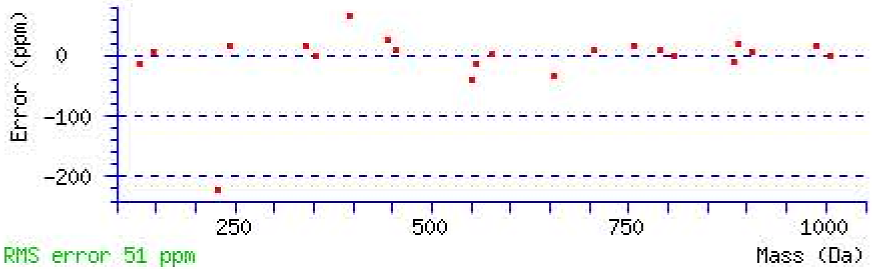
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1458.801712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.0069
Matches : 22/92 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	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
32.4	1458.801712	0.006860	HQQTVTIPPK
25.1	1458.801712	0.006860	HQQTVTIPPK
8.8	1458.819473	-0.010901	GNVGIGGSAVPPPPIK
0.1	1458.805542	0.003030	VPTRSLRTSTWR

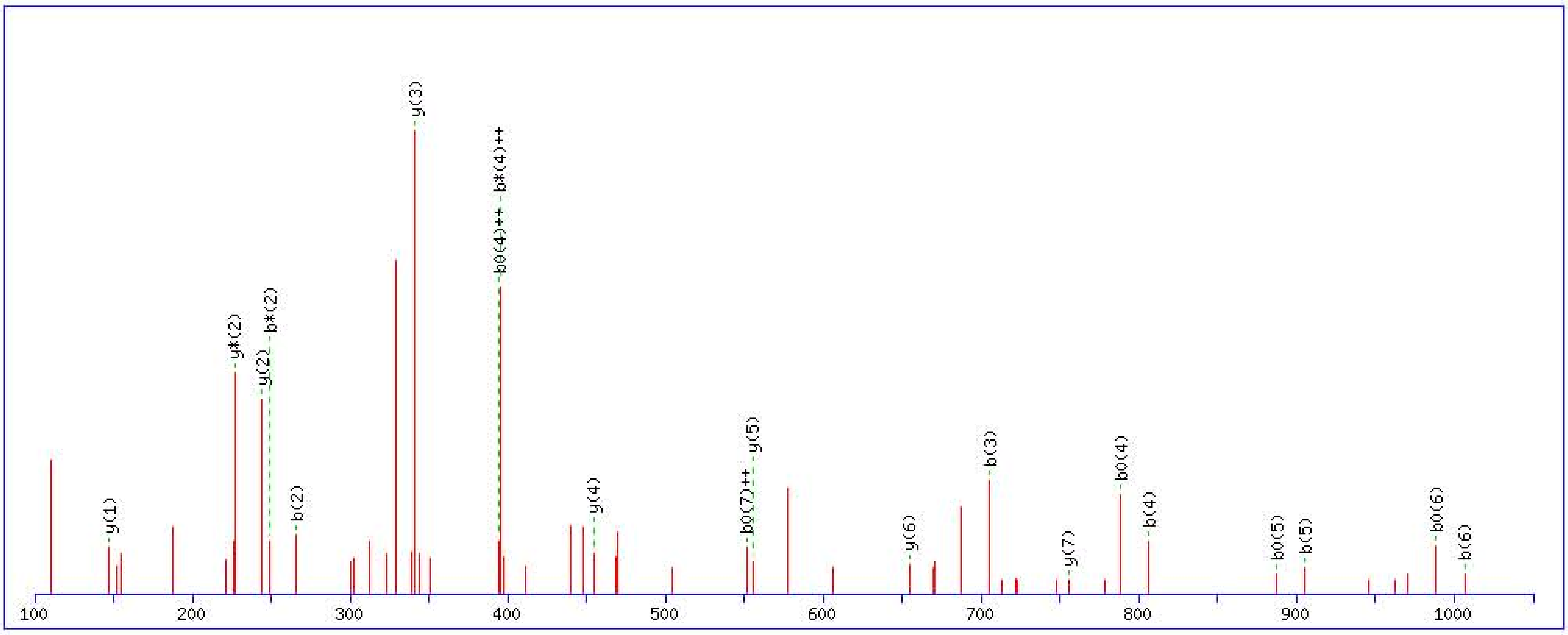
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQQTVTIPPK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

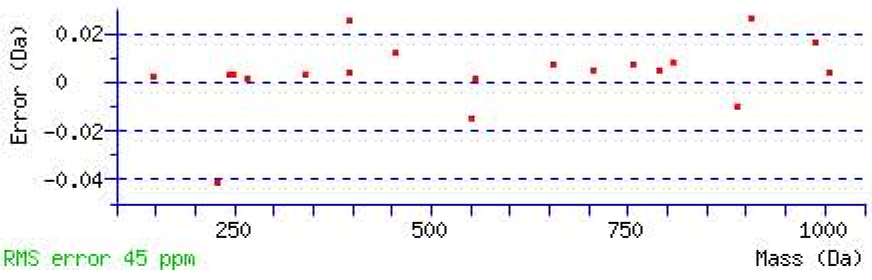
Match to Query 33673: 1458.809472 from(487.277100,3+) rtinseconds(1536) index(39036)
Title: Locus:1.1.1.2984.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

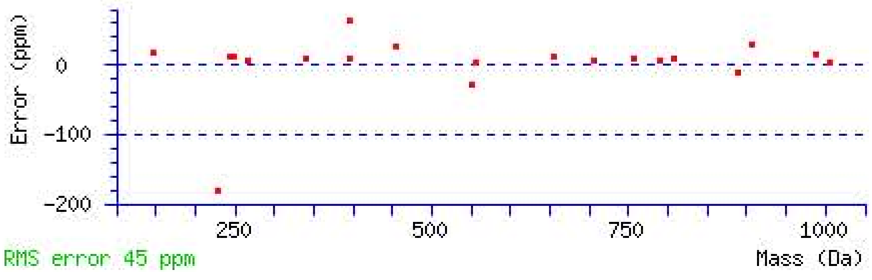


```
Monoisotopic mass of neutral peptide Mr(calc): 1458.801712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0048
Matches : 20/92 fragment ions using 41 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	138.066188	69.536732					H							10
2	**266.124766**	133.566021	249.098217	125.052746			Q	1322.750072	661.878674	1305.723523	653.365400	1304.739507	652.873392	9
3	**705.350092**	353.178684	688.323543	344.665410			Q	1194.691494	597.849385	1177.664945	589.336111	1176.680929	588.844102	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



RMS error 45 ppm



RMS error 45 ppm

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
33.3	1458.801712	0.007760	HQQTVTIPPK
33.3	1458.801712	0.007760	HQQTVTIPPK
8.6	1458.819473	-0.010001	GNVGIGGSAVPPPPIK

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

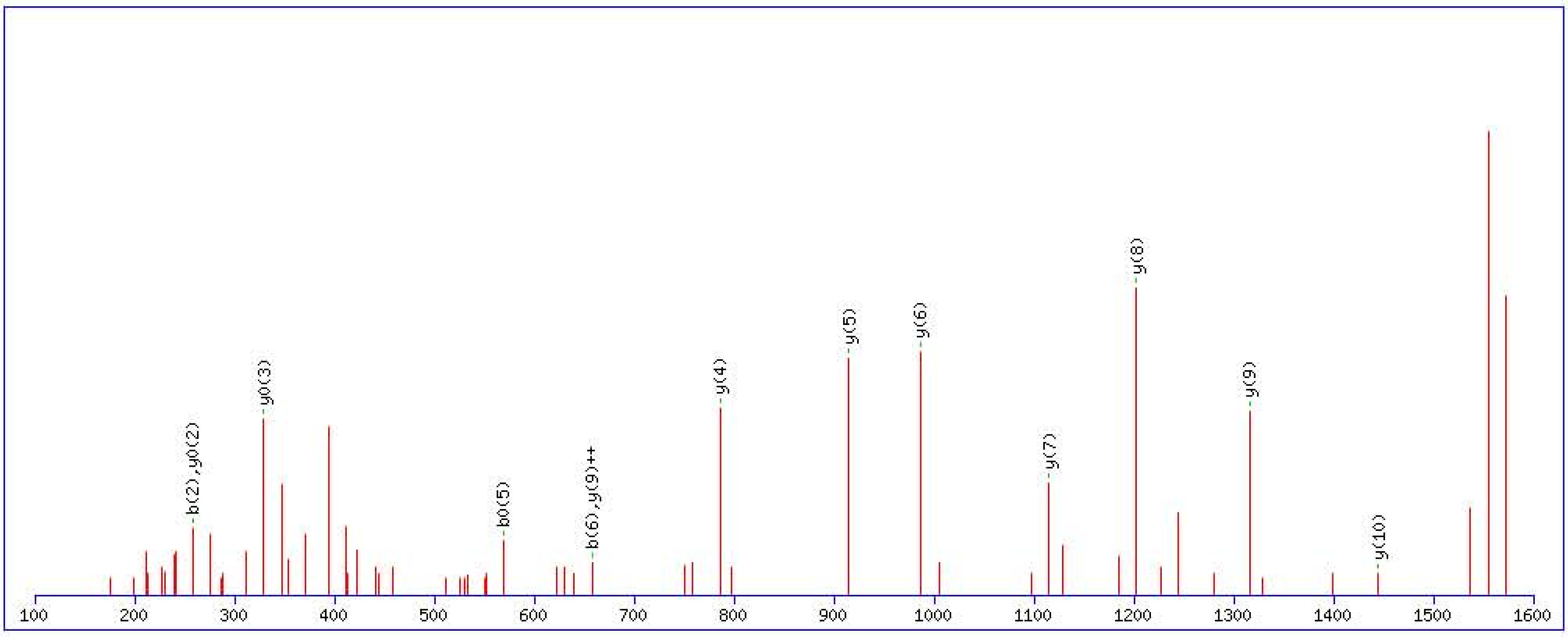
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QELSEAEQATR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

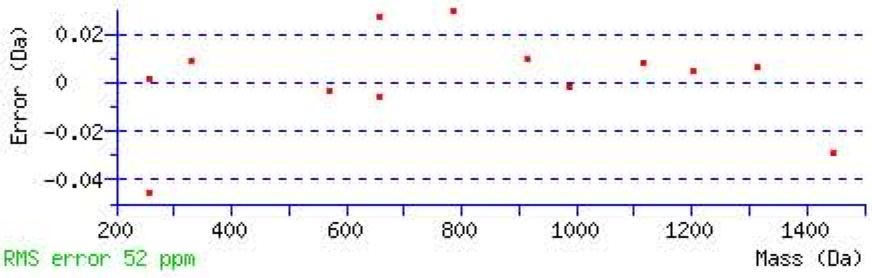
Match to Query 37144: 1571.777308 from(786.895930,2+) rtinseconds(1539) index(39065)
Title: Locus:1.1.1.2985.15 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

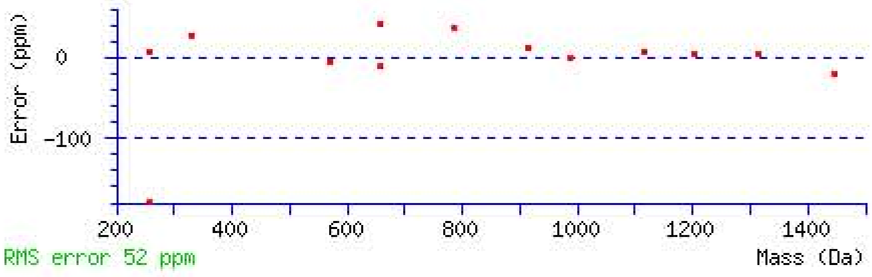
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1571.761322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 2.4e-005
Matches : 13/116 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	129.065854	65.036565	112.039305	56.523291			Q							11
2	**258.108447**	129.557862	241.081898	121.044587	240.097882	120.552579	E	***1444.710056***	722.858666	1427.683507	714.345392	1426.699491	713.853384	10
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	L	***1315.667463***	658.337370	1298.640914	649.824095	1297.656898	649.332087	9
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	S	***1202.583399***	601.795337	1185.556850	593.282063	1184.572834	592.790055	8
5	587.267132	294.137204	570.240583	285.623930	569.256567	285.131922	E	***1115.551371***	558.279324	1098.524822	549.766049	1097.540806	549.274041	7
6	**658.304246**	329.655761	641.277697	321.142487	640.293681	320.650479	A	***986.508778***	493.758027	969.482229	485.244753	968.498213	484.752745	6
7	787.346839	394.177058	770.320290	385.663783	769.336274	385.171775	E	***915.471664***	458.239470	898.445115	449.726196	897.461099	449.234188	5
8	1226.572165	613.789721	1209.545616	605.276446	1208.561600	604.784438	Q	***786.429071***	393.718174	769.402522	385.204899	768.418506	384.712891	4
9	1297.609279	649.308278	1280.582730	640.795003	1279.598714	640.302995	A	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	3
10	1398.656958	699.832117	1381.630409	691.318843	1380.646393	690.826835	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
11							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QELSEAEQATR
(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	1571.761322	0.015986	QELSEAEQATR
15.8	1571.753952	0.023356	KQGGSPDEPDSKATR
9.5	1571.765366	0.011942	QELAVFCSPEPPAK
8.7	1571.790298	-0.012990	QEAQAELQKRDEK
7.8	1571.797699	-0.020391	KELNIEPTDLMNR
6.9	1571.791199	-0.013891	MQSLRPEQTR
6.4	1571.797760	-0.020452	MASVAVDPQPSVVTR
5.9	1571.761322	0.015986	QELSEAEQATR
5.7	1571.757965	0.019343	QEDDLANINQWVK
5.3	1571.761337	0.015971	EKADGTEQVER

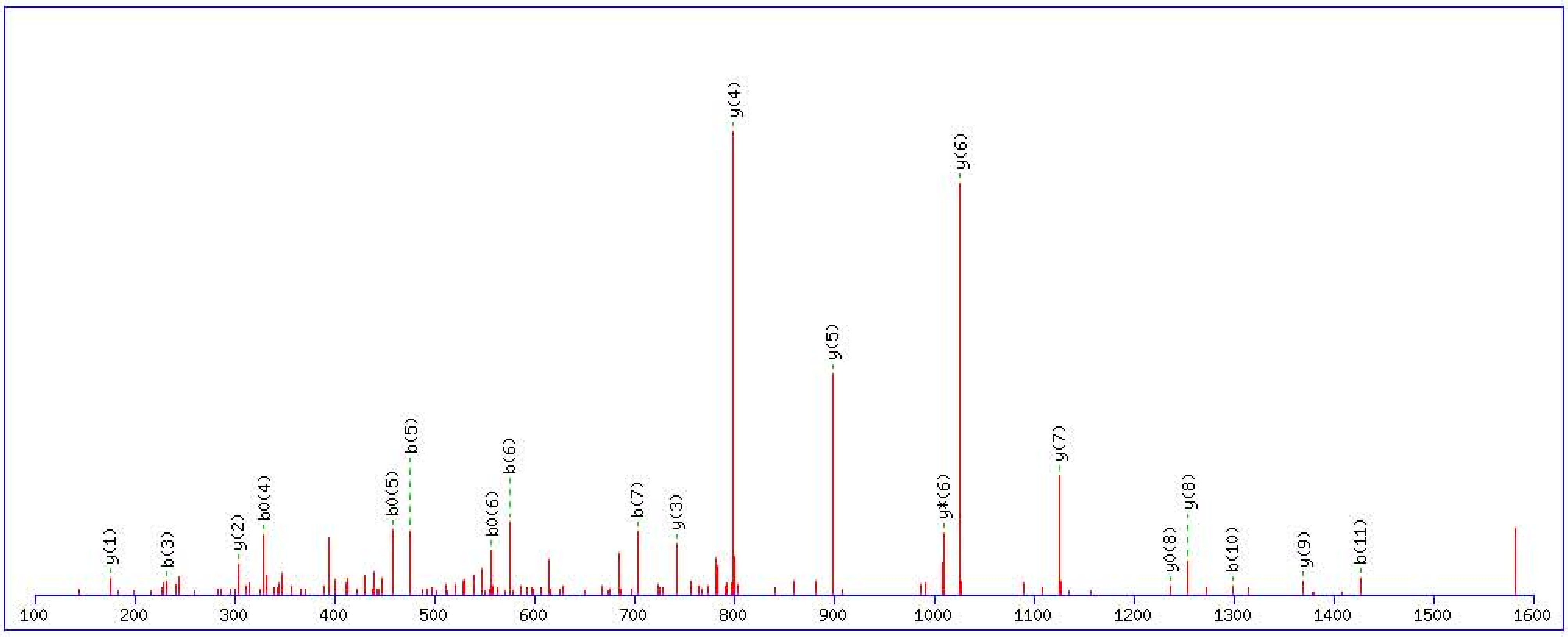
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

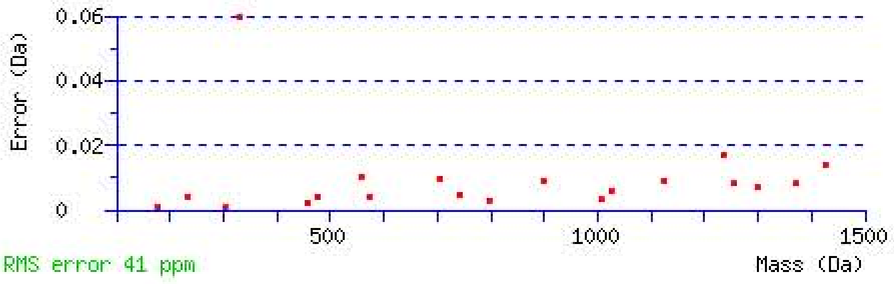
Match to Query 38760: 1599.788328 from(800.901440,2+) rtinseconds(1539) index(39066)
Title: Locus:1.1.1.2985.16 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

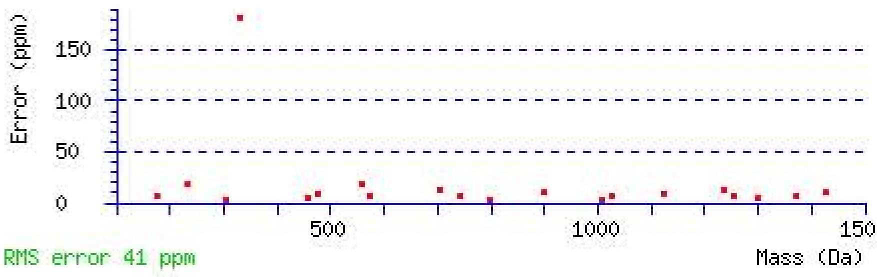
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1599.767517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 75  Expect: 6.6e-007
Matches : 20/106 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	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





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
74.8	1599.767517	0.020811	SGSDEVQVGQQR
59.6	1599.767517	0.020811	SGSDEVQVGQQR
32.5	1599.767517	0.020811	SGSDEVQVGQQR
11.4	1599.767471	0.020857	AMNAANLNIPPSDTR
10.1	1599.796677	-0.008349	DINDNPPIFPMTVK
8.3	1599.767502	0.020826	LHMLSSVDLNGQDR
4.8	1599.792648	-0.004320	SSAEVTPDLQSR
3.3	1599.793976	-0.005648	QRSSGIWENGR
3.3	1599.810394	-0.022066	SAAQPSTSPAEVQSLK
2.4	1599.779388	0.008940	RFPDFSYITQNGR

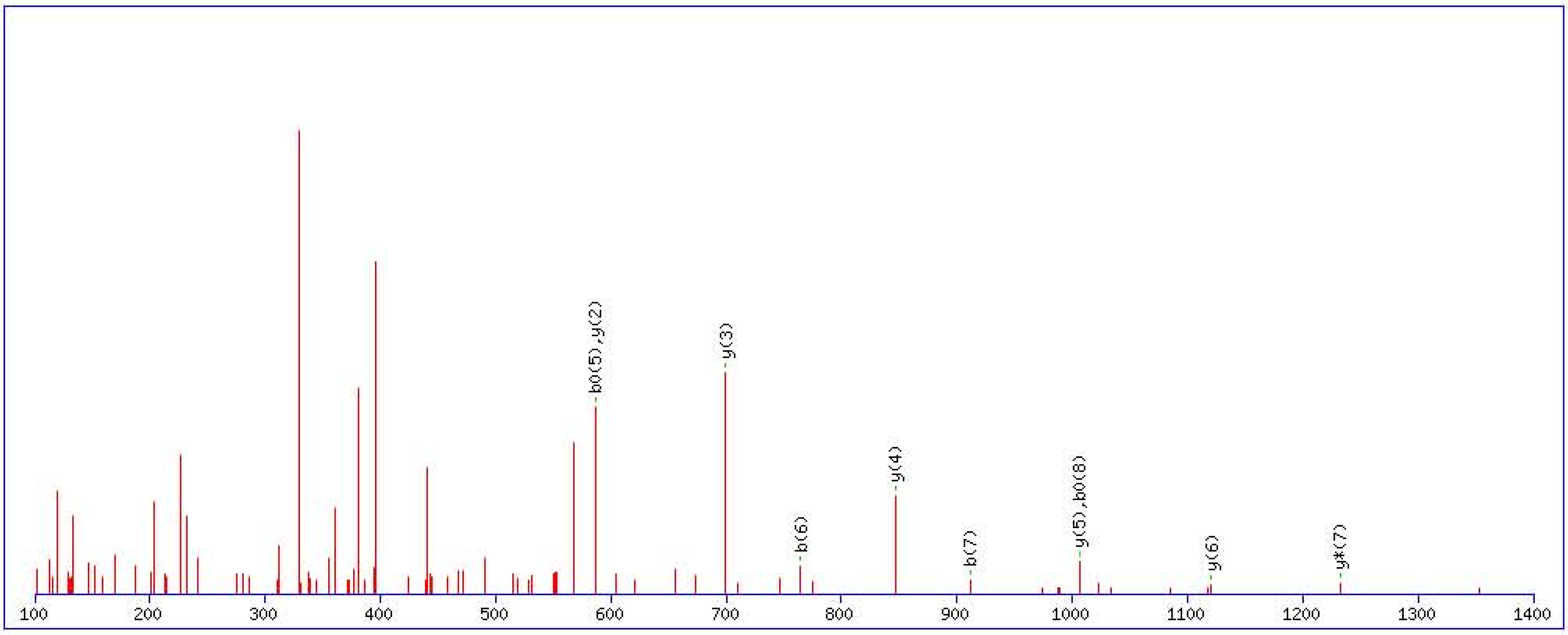
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CAEENCFIQK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

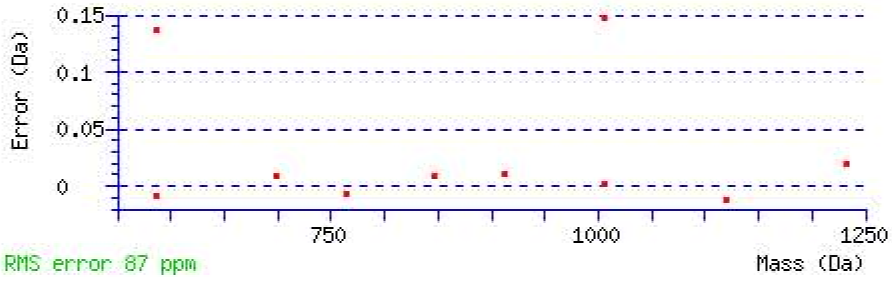
Match to Query 39073: 1608.719472 from(537.247100,3+) rtinseconds(1776) index(40615)
Title: Locus:1.1.1.3068.10 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

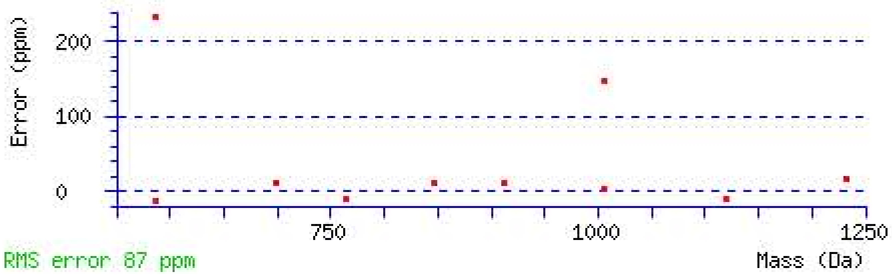
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1608.709839
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.025
Matches : 10/84 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	161.037925	81.022600					C							10
2	232.075039	116.541158					A	1449.686484	725.346880	1432.659935	716.833606	1431.675919	716.341598	9
3	361.117632	181.062454			343.107067	172.057172	E	1378.649370	689.828323	1361.622821	681.315049	1360.638805	680.823041	8
4	490.160225	245.583751			472.149660	236.578468	E	1249.606777	625.307027	1232.580228	616.793752	1231.596212	616.301744	7
5	604.203152	302.605214	587.176603	294.091940	586.192587	293.599932	N	***1120.564184***	560.785730	1103.537635	552.272456			6
6	**764.233801**	382.620539	747.207252	374.107264	746.223236	373.615256	C	***1006.521257***	503.764267	989.494708	495.250992			5
7	**911.302215**	456.154746	894.275666	447.641471	893.291650	447.149463	F	***846.490608***	423.748942	829.464059	415.235668			4
8	1024.386279	512.696777	1007.359730	504.183503	1006.375714	503.691495	I	***699.422194***	350.214735	682.395645	341.701461			3
9	1463.611605	732.309441	1446.585056	723.796166	1445.601040	723.304158	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 CAEENCFIQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.1	1608.709839	0.009633	CAEENCFIQK

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

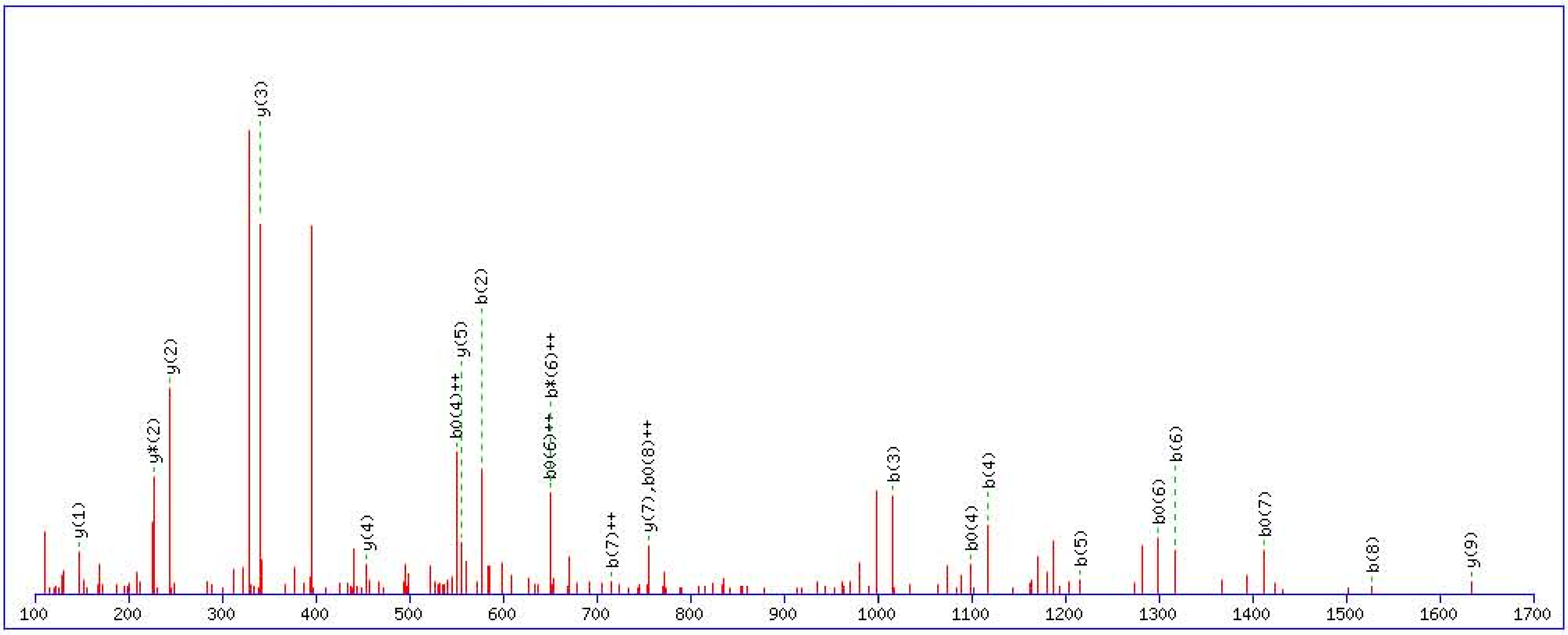
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQQTVTIPPK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

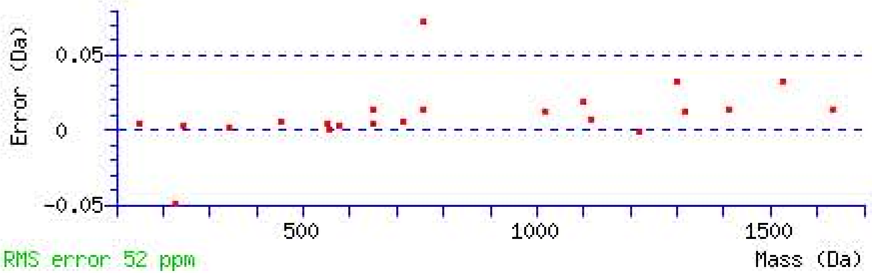
Match to Query 44506: 1769.983092 from(591.001640,3+) rtinseconds(1924) index(41637)
Title: Locus:1.1.1.3119.17 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

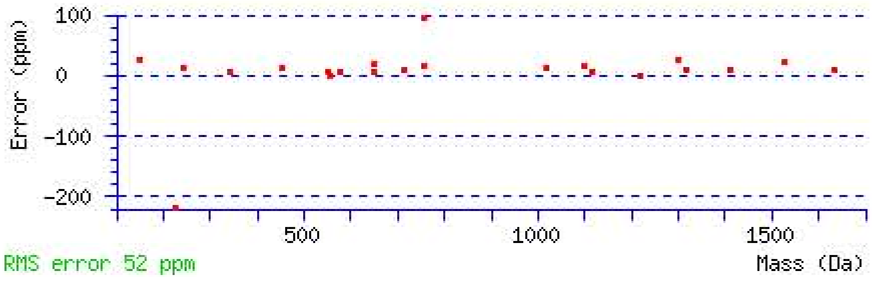
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 32  Expect: 0.01
Matches : 22/92 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	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
31.6	1769.968460	0.014632	HQQTVTIPPK
10.5	1769.961029	0.022063	WMLSRDRASTLPLPK

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

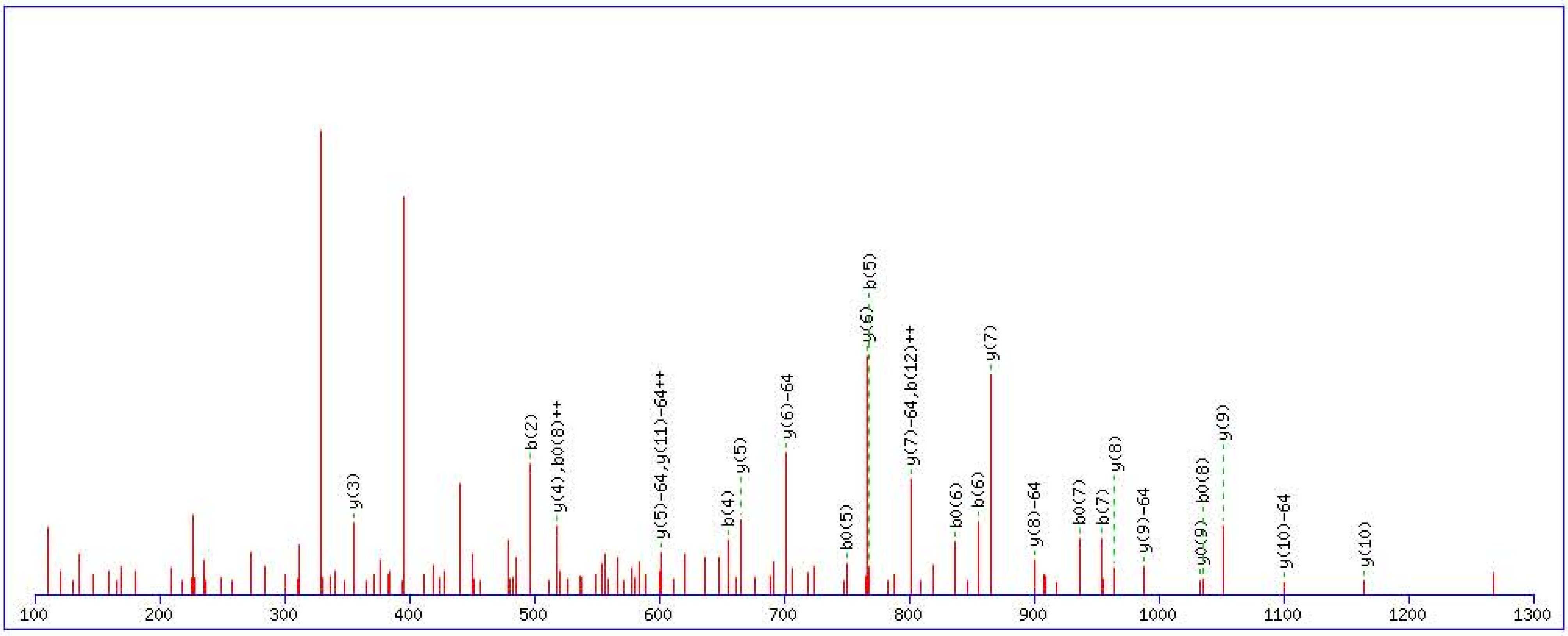
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQGTLSVVTMYHAK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

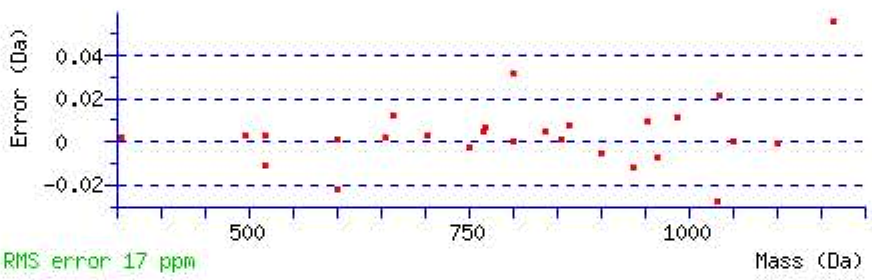
Match to Query 45802: 1817.930922 from(606.984250,3+) rtinseconds(1794) index(40733)
Title: Locus:1.1.1.3074.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

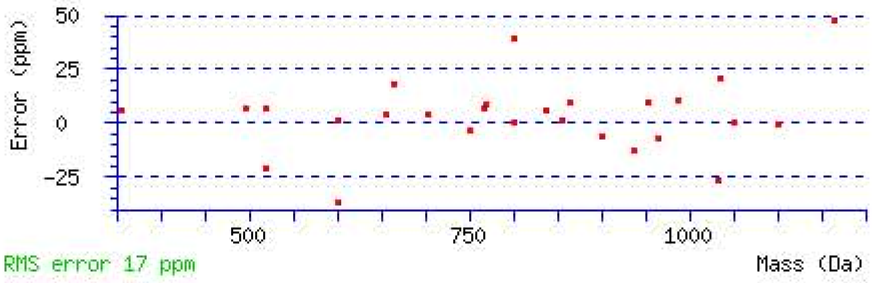
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 41  Expect: 0.0022
Matches : 27/214 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							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
41.1	1817.916824	0.014098	GQGTLSVVTMYHAK

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

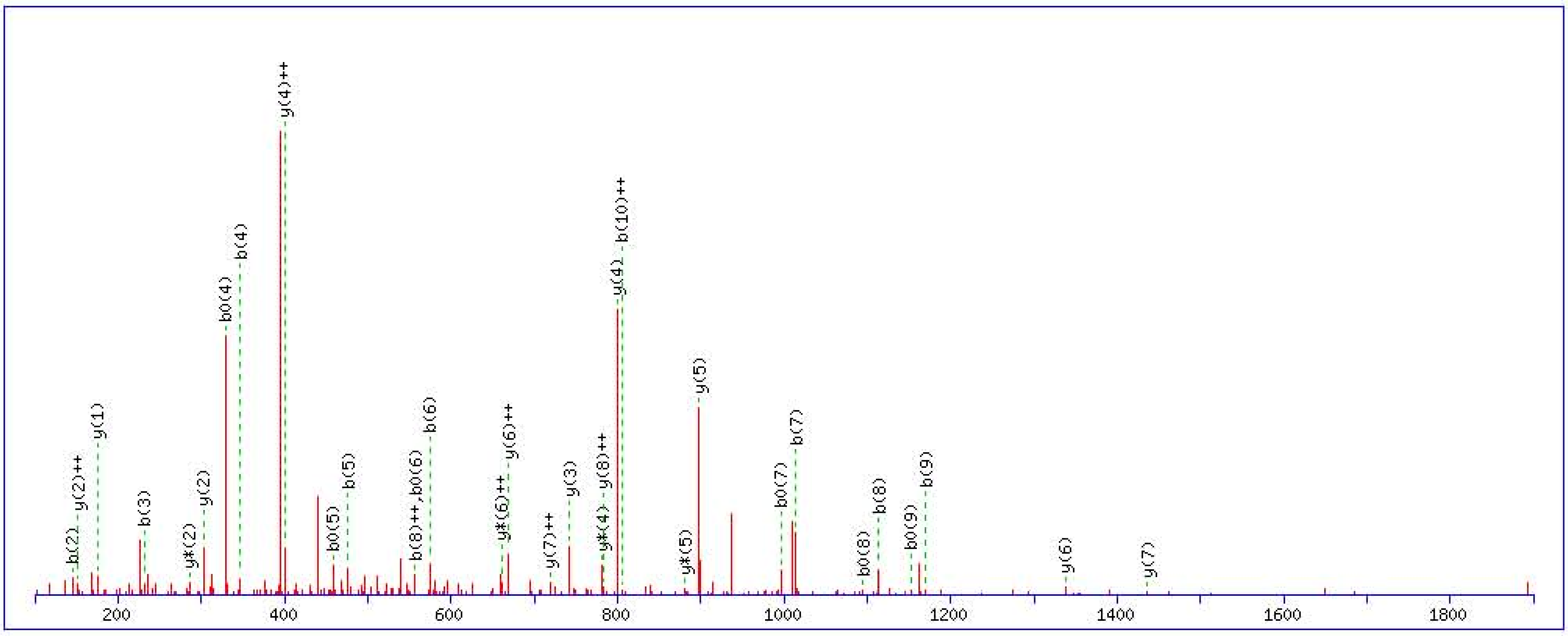
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

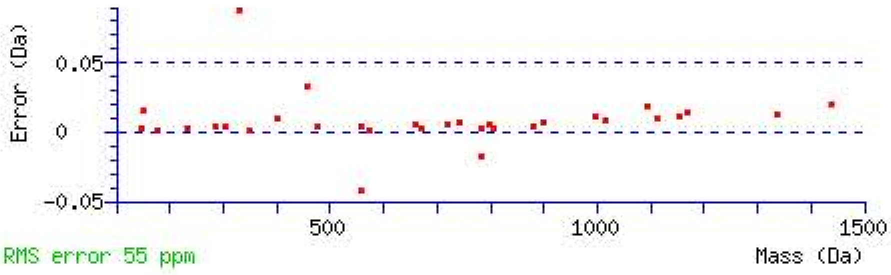
Match to Query 47805: 1910.953272 from(637.991700,3+) rtinseconds(1872) index(41194)
Title: Locus:1.1.1.3101.24 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

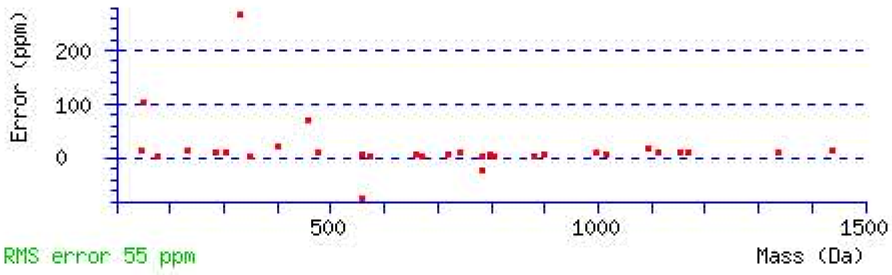
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 26  Expect: 0.057
Matches : 32/106 fragment ions using 81 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
29.5	1910.938263	0.015009	YVTSAPMPEPQAPGR
26.4	1910.934265	0.019007	SGSDEVQVGQQR
20.8	1910.934265	0.019007	SGSDEVQVGQQR

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

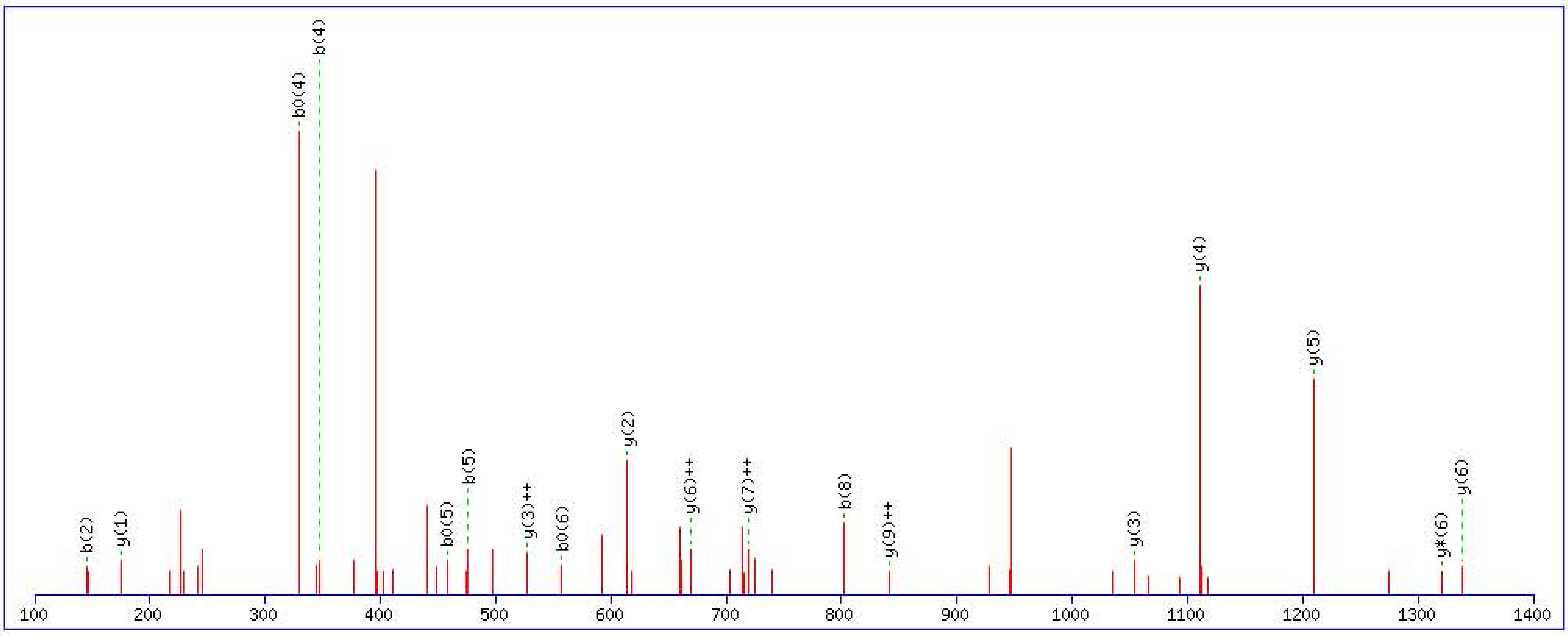
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

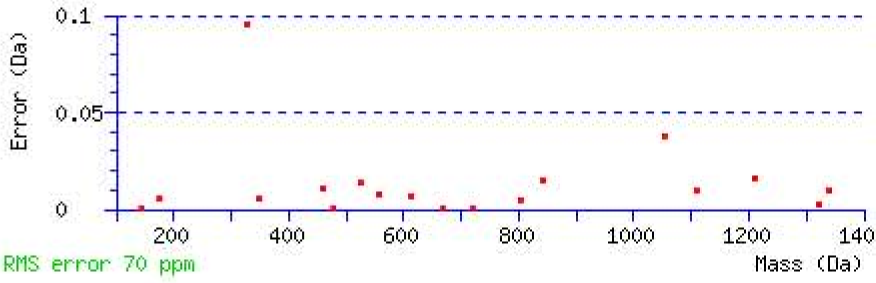
Match to Query 47806: 1910.955072 from(637.992300,3+) rtinseconds(1924) index(41639)
Title: Locus:1.1.1.3119.19 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

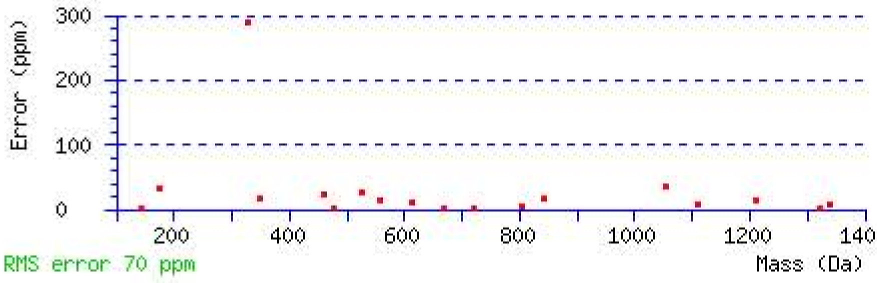
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 28  Expect: 0.01
Matches : 18/106 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	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
27.8	1910.934265	0.020807	SGSDEVQVGQQR
7.3	1910.934265	0.020807	SGSDEVQVGQQR
6.3	1910.958542	-0.003470	TDDYGRDLSSVQTLLTK
3.8	1910.934265	0.020807	SGSDEVQVGQQR
0.5	1910.934891	0.020181	KLSVEEFFMDLHNFR
0.1	1910.960709	-0.005637	VGAPAWREAAQAMAR

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

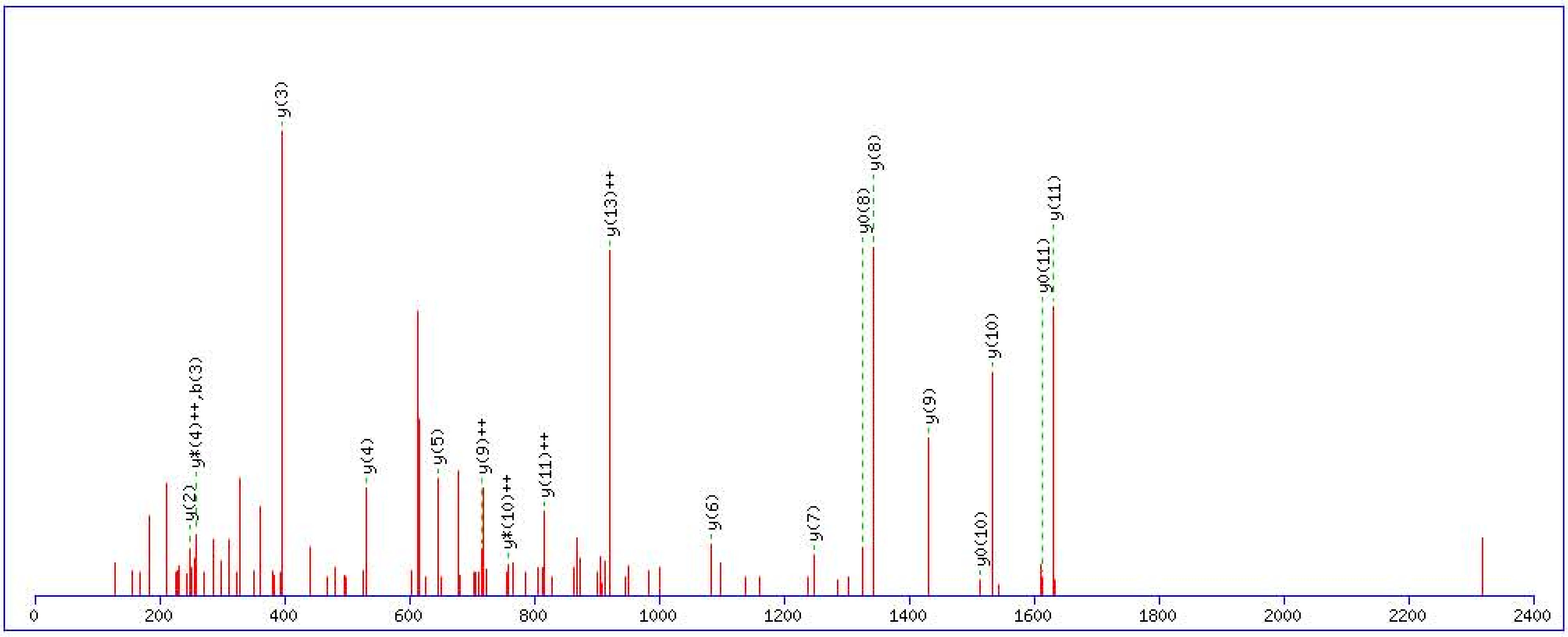
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGIPIVTSPYQIHFTK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

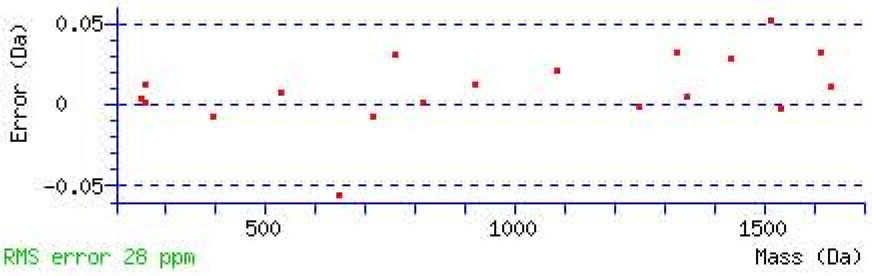
Match to Query 53079: 2098.158672 from(700.393500,3+) rtinseconds(2289) index(44200)
Title: Locus:1.1.1.3246.13 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

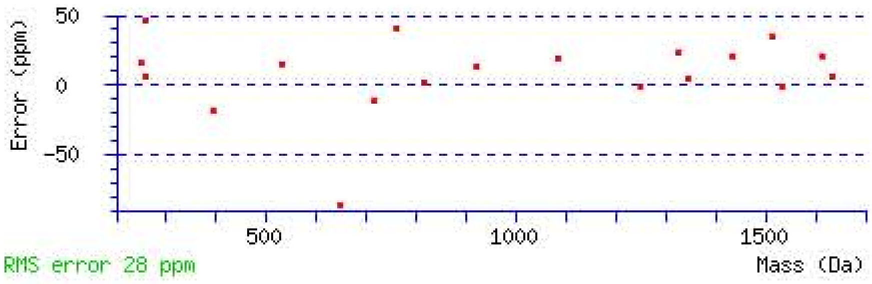
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2098.128525
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0025
Matches : 19/158 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							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
37.8	2098.128525	0.030147	SGIPIVTSPYQIHFTK

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

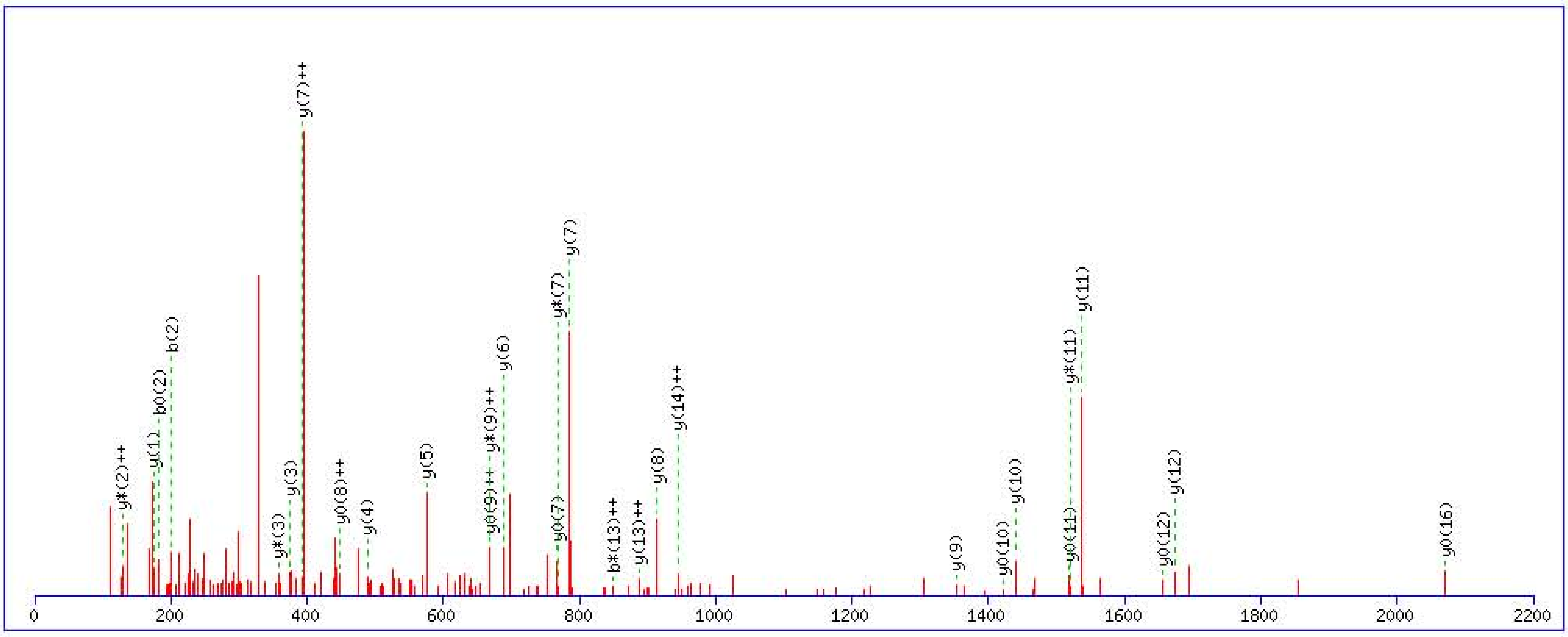
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSINTHPSQKPLSITVR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

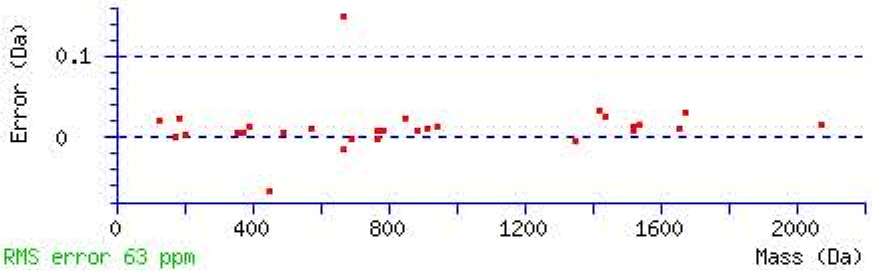
Match to Query 55408: 2201.253856 from(551.320740,4+) rtinseconds(1865) index(41134)
Title: Locus:1.1.1.3099.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

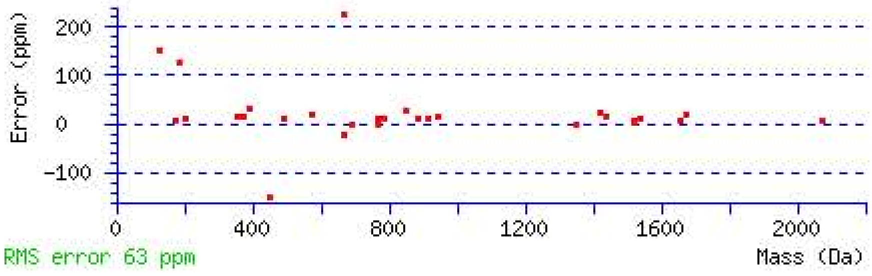
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2201.235428
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.014
Matches : 29/180 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	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
26.5	2201.235428	0.018428	LSINTHPSQKPLSITVR

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

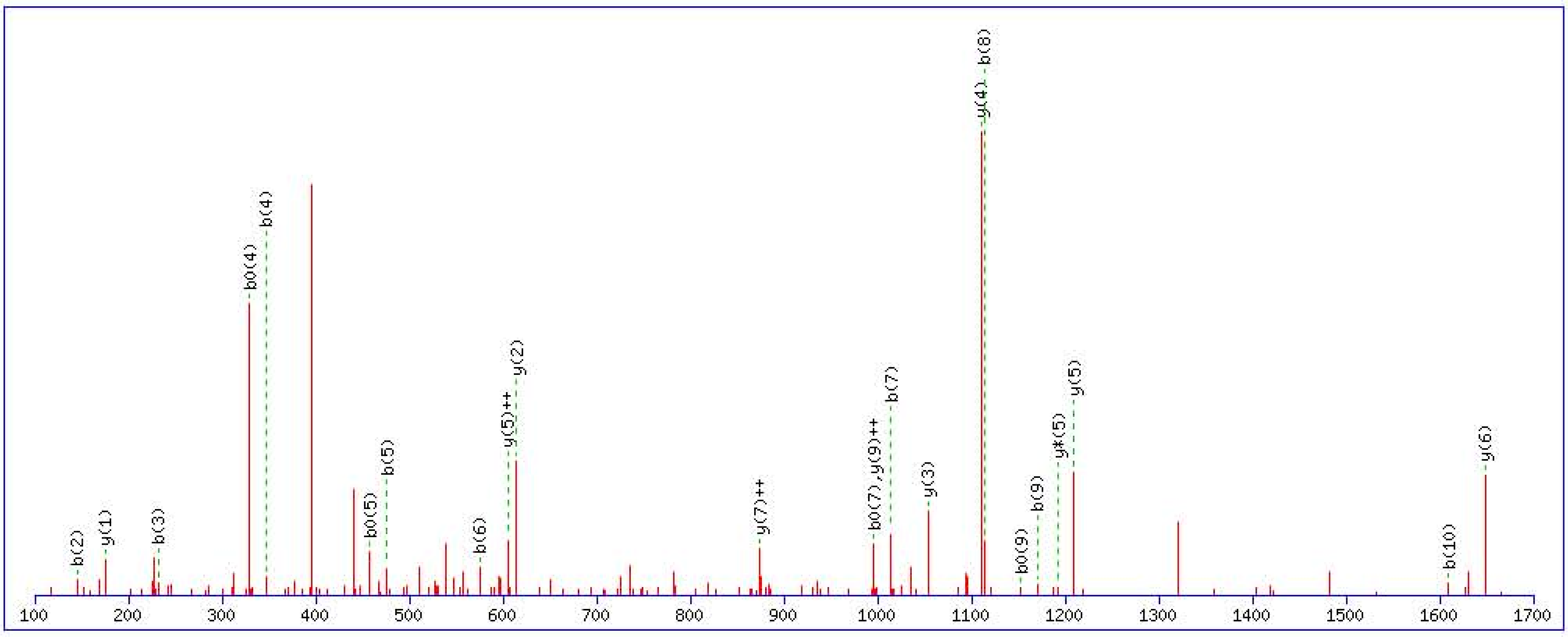
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGSDEVQVGQQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

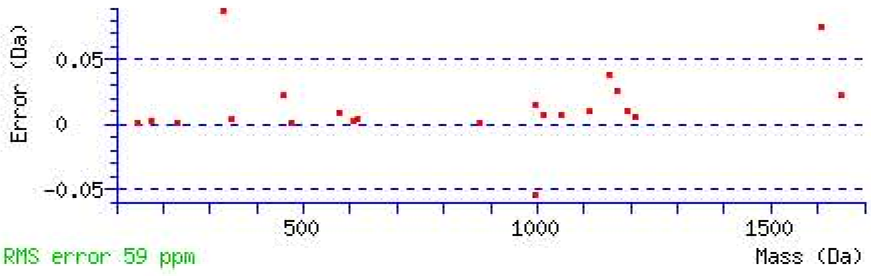
Match to Query 56036: 2222.133702 from(741.718510,3+) rtinseconds(2109) index(42959)
Title: Locus:1.1.1.3183.17 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

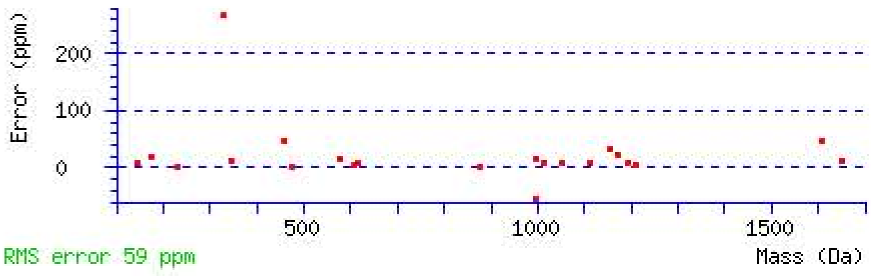


```
Monoisotopic mass of neutral peptide Mr(calc): 2222.101013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Q10     : Biotin:Thermo-21345 (Q)
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0038
Matches : 23/106 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	88.039304	44.523290			70.028739	35.518008	S							12
2	*145.060768*	73.034022			127.050203	64.028740	G	2136.076250	1068.541763	2119.049701	1060.028488	2118.065685	1059.536480	11
3	*232.092796*	116.550036			214.082231	107.544753	S	2079.054786	1040.031031	2062.028237	1031.517756	2061.044221	1031.025748	10
4	*347.119739*	174.063507			329.109174	165.058225	D	1992.022758	996.515017	1974.996209	988.001743	1974.012193	987.509735	9
5	*476.162332*	238.584804			458.151767	229.579522	E	1876.995815	939.001546	1859.969266	930.488271	1858.985250	929.996263	8
6	*575.230746*	288.119011			557.220181	279.113729	V	1747.953222	874.480249	1730.926673	865.966975			7
7	*1014.456072*	507.731674	997.429523	499.218400	996.445507	498.726392	Q	**1648.884808**	824.946042	1631.858259	816.432768			6
8	*1113.524486*	557.265881	1096.497937	548.752607	1095.513921	548.260599	V	**1209.659482**	605.333379	1192.632933	596.820105			5
9	*1170.545950*	585.776613	1153.519401	577.263339	1152.535385	576.771330	G	**1110.591068**	555.799172	1093.564519	547.285898			4
10	*1609.771276*	805.389276	1592.744727	796.876002	1591.760711	796.383994	Q	**1053.569604**	527.288440	1036.543055	518.775166			3
11	2048.996602	1025.001939	2031.970053	1016.488665	2030.986037	1015.996657	Q	**614.344278**	307.675777	597.317729	299.162503			2
12							R	**175.118952**	88.063114	158.092403	79.549839			1



RMS error 59 ppm



RMS error 59 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
31.5	2222.101013	0.032689	SGSDEVQVGQQR
5.4	2222.116058	0.017644	GILSQMGRHSQSRSHSK
4.3	2222.125290	0.008412	TDDYGRDLSSVQTLLTK
3.0	2222.130417	0.003285	YHEALSRTHNSRLPLADSR
1.6	2222.129944	0.003758	EQQRQEELEKQR
1.6	2222.129944	0.003758	EQQRQEELEKQR
1.6	2222.129944	0.003758	EQQRQEELEKQR
1.0	2222.152618	-0.018916	LIPHMHSIIQYMLQR

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

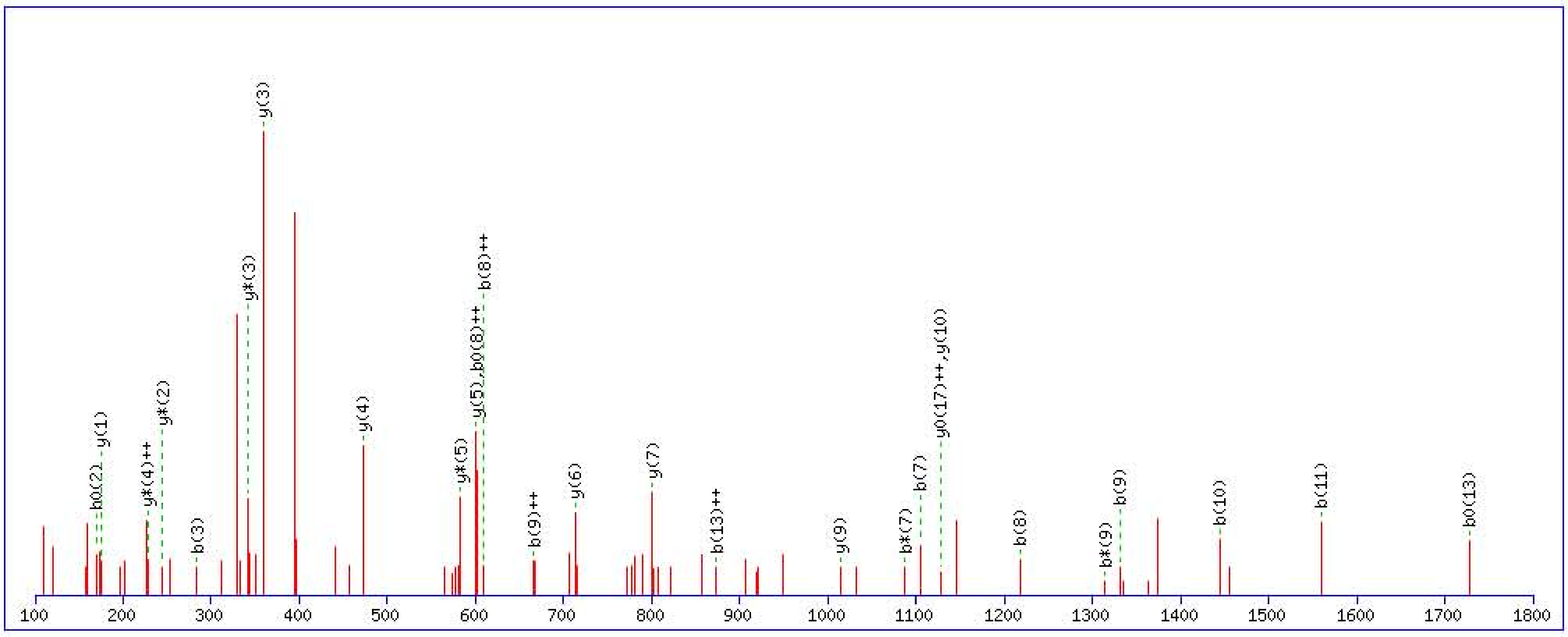
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAPDHQELNLDVSLQLPSR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

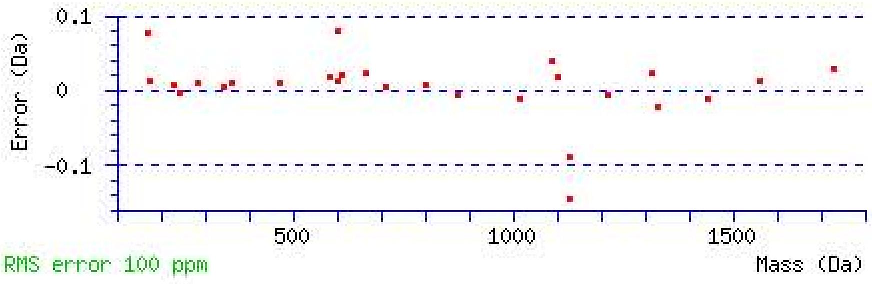
Match to Query 61557: 2457.263656 from(615.323190,4+) rtinseconds(2503) index(45627)
Title: Locus:1.1.1.3320.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

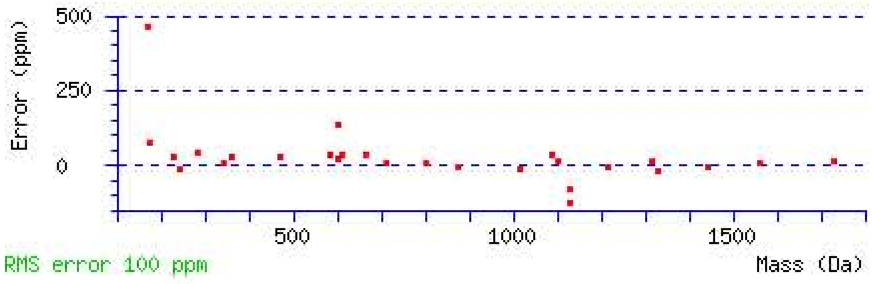


```
Monoisotopic mass of neutral peptide Mr(calc): 2457.232193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.007
Matches : 27/204 fragment ions using 66 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 100 ppm



RMS error 100 ppm

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
27.5	2457.232193	0.031463	DAPDHQELNLDVSLQLPSR
4.6	2457.243423	0.020233	TGLSDAFMILNPSPDVPESRRR

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

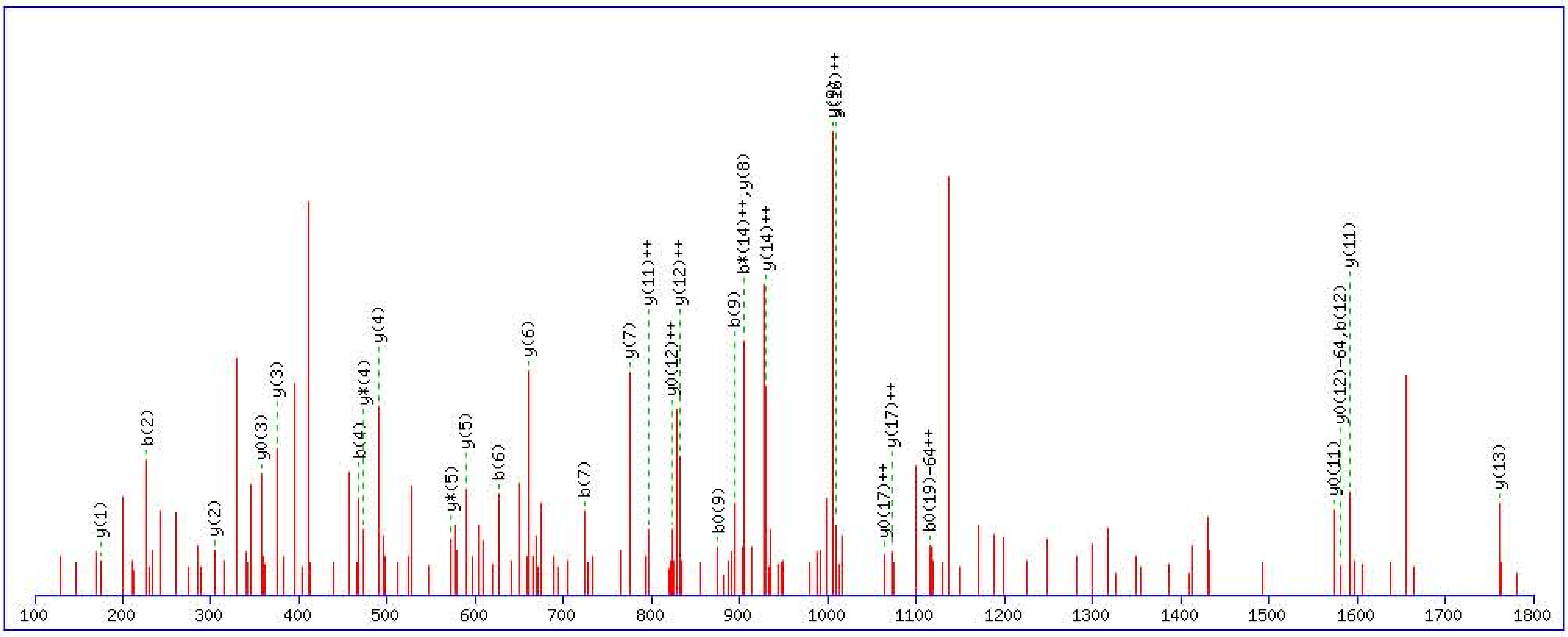
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLQGTPVAQMTEDAVDAER**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

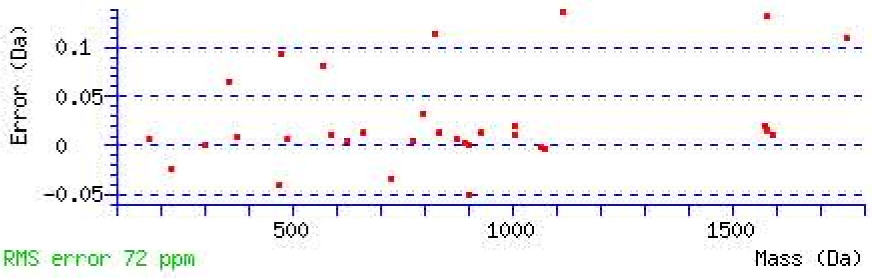
Match to Query 62440: 2483.271102 from(828.764310,3+) rtinseconds(2516) index(45738)
Title: Locus:1.1.1.3324.22 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

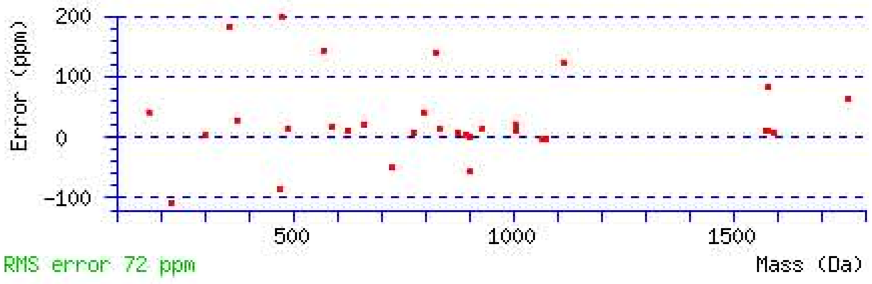
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2483.239990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
M11     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 37  Expect: 0.0062
Matches : 32/324 fragment ions using 81 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	2371.163212	1186.085244	2354.136663	1177.571969	2353.152647	1177.079961	19
3	340.259468	170.633372					L	2258.079148	1129.543212	2241.052599	1121.029938	2240.068583	1120.537930	18
4	**468.318046**	234.662661	451.291497	226.149386			Q	2144.995084	1073.001180	2127.968535	1064.487905	2126.984519	1063.995898	17
5	525.339510	263.173393	508.312961	254.660119			G	2016.936506	1008.971891	1999.909957	1000.458617	1998.925941	999.966609	16
6	**626.387189**	313.697233	609.360640	305.183958	608.376624	304.691950	T	1959.915042	980.461159	1942.888493	971.947885	1941.904477	971.455877	15
7	**723.439953**	362.223615	706.413404	353.710340	705.429388	353.218332	P	1858.867363	929.937320	1841.840814	921.424045	1840.856798	920.932037	14
8	822.508367	411.757822	805.481818	403.244547	804.497802	402.752539	V	***1761.814599***	881.410938	1744.788050	872.897663	1743.804034	872.405655	13
9	**893.545481**	447.276379	876.518932	438.763104	875.534916	438.271096	A	1662.746185	831.876731	1645.719636	823.363456	1644.735620	822.871448	12
10	1332.770807	666.889042	1315.744258	658.375767	1314.760242	657.883759	Q	***1591.709071***	796.358174	1574.682522	787.844899	1573.698506	787.352891	11
11	1479.806207	740.406742	1462.779658	731.893467	1461.795642	731.401459	M	1152.483745	576.745511	1135.457196	568.232236	1134.473180	567.740228	10
12	**1580.853886**	790.930581	1563.827337	782.417307	1562.843321	781.925299	T	***1005.448345***	503.227811	988.421796	494.714536	987.437780	494.222528	9
13	1709.896479	855.451878	1692.869930	846.938603	1691.885914	846.446595	E	***904.400666***	452.703971	887.374117	444.190697	886.390101	443.698689	8
14	1824.923422	912.965349	1807.896873	904.452075	1806.912857	903.960067	D	***775.358073***	388.182675	758.331524	379.669400	757.347508	379.177392	7
15	1895.960536	948.483906	1878.933987	939.970632	1877.949971	939.478624	A	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.663921	6
16	1995.028950	998.018113	1978.002401	989.504839	1977.018385	989.012831	V	***589.294016***	295.150646	572.267467	286.637372	571.283451	286.145364	5
17	2110.055893	1055.531585	2093.029344	1047.018310	2092.045328	1046.526302	D	***490.225602***	245.616439	473.199053	237.103165	472.215037	236.611157	4
18	2181.093007	1091.050142	2164.066458	1082.536867	2163.082442	1082.044859	A	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
19	2310.135600	1155.571438	2293.109051	1147.058164	2292.125035	1146.566156	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
36.5	2483.239990	0.031112	ILLQGTPVAQMTEDAVDAER
11.0	2483.239990	0.031112	ILLQGTPVAQMTEDAVDAER

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

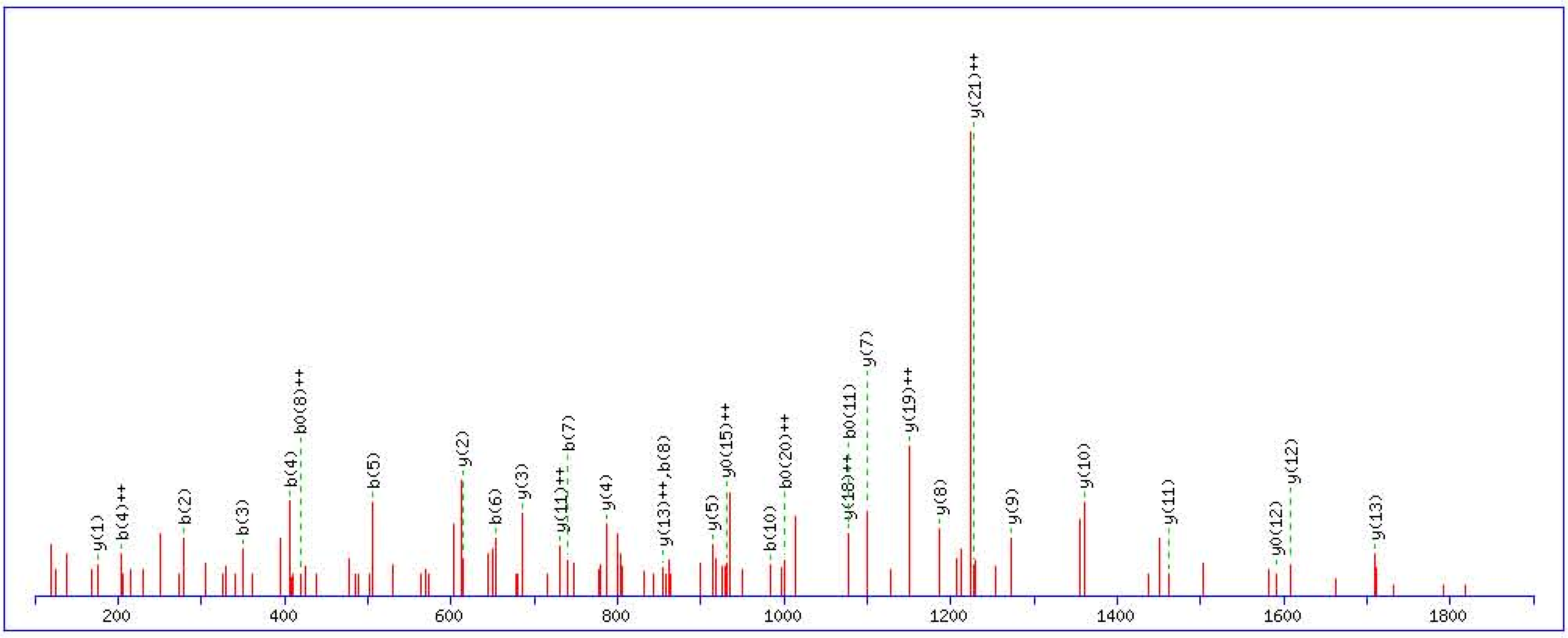
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DYAGVFSDAGLTFTSSSGQQTAQR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

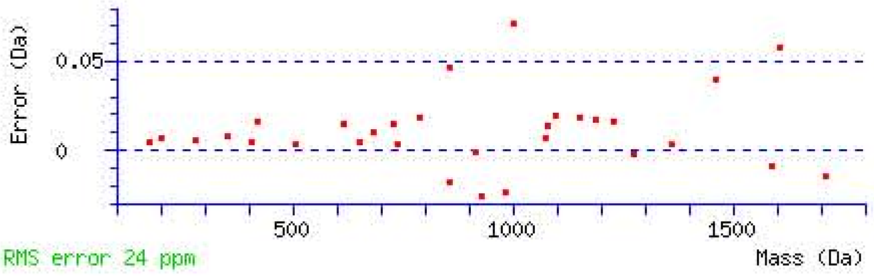
Match to Query 67198: 2804.345052 from(935.788960,3+) rtinseconds(2684) index(46851)
Title: Locus:1.1.1.3382.22 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

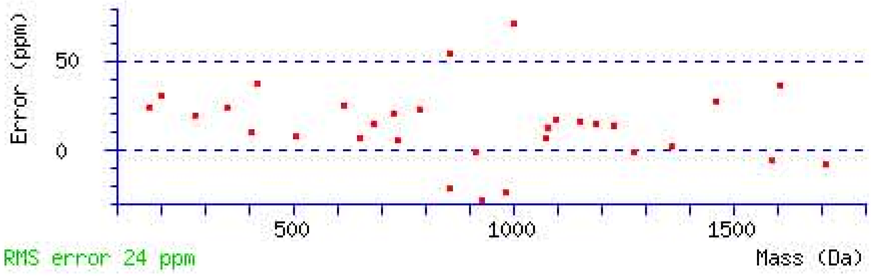


```
Monoisotopic mass of neutral peptide Mr(calc): 2804.307587
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q23     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1.6e-005
Matches : 31/234 fragment ions using 75 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							24
2	***279.097548***	140.052412			261.086983	131.047130	Y	2690.287895	1345.647585	2673.261346	1337.134311	2672.277330	1336.642303	23
3	***350.134662***	175.570969			332.124097	166.565687	A	2527.224566	1264.115921	2510.198017	1255.602646	2509.214001	1255.110638	22
4	***407.156126***	204.081701			389.145561	195.076418	G	2456.187452	1228.597364	2439.160903	1220.084089	2438.176887	1219.592081	21
5	***506.224540***	253.615908			488.213975	244.610626	V	2399.165988	1200.086632	2382.139439	1191.573357	2381.155423	1191.081349	20
6	***653.292954***	327.150115			635.282389	318.144833	F	2300.097574	1150.552425	2283.071025	1142.039150	2282.087009	1141.547142	19
7	***740.324982***	370.666129			722.314417	361.660846	S	2153.029160	1077.018218	2136.002611	1068.504943	2135.018595	1068.012935	18
8	***855.351925***	428.179600			837.341360	419.174318	D	2065.997132	1033.502204	2048.970583	1024.988929	2047.986567	1024.496921	17
9	926.389039	463.698157			908.378474	454.692875	A	1950.970189	975.988733	1933.943640	967.475458	1932.959624	966.983450	16
10	***983.410503***	492.208890			965.399938	483.203607	G	1879.933075	940.470176	1862.906526	931.956901	1861.922510	931.464893	15
11	1096.494567	548.750922			1078.484002	539.745639	L	1822.911611	911.959444	1805.885062	903.446169	1804.901046	902.954161	14
12	1197.542246	599.274761			1179.531681	590.269478	T	***1709.827547***	855.417412	1692.800998	846.904137	1691.816982	846.412129	13
13	1344.610660	672.808968			1326.600095	663.803686	F	***1608.779868***	804.893572	1591.753319	796.380298	1590.769303	795.888290	12
14	1445.658339	723.332808			1427.647774	714.327525	T	***1461.711454***	731.359365	1444.684905	722.846091	1443.700889	722.354083	11
15	1532.690367	766.848822			1514.679802	757.843539	S	***1360.663775***	680.835526	1343.637226	672.322251	1342.653210	671.830243	10
16	1619.722395	810.364836			1601.711830	801.359553	S	***1273.631747***	637.319512	1256.605198	628.806237	1255.621182	628.314229	9
17	1706.754423	853.880850			1688.743858	844.875567	S	***1186.599719***	593.803498	1169.573170	585.290223	1168.589154	584.798215	8
18	1763.775887	882.391582			1745.765322	873.386299	G	***1099.567691***	550.287484	1082.541142	541.774209	1081.557126	541.282201	7
19	1891.834465	946.420871	1874.807916	937.907596	1873.823900	937.415588	Q	1042.546227	521.776752	1025.519678	513.263477	1024.535662	512.771469	6
20	2019.893043	1010.450160	2002.866494	1001.936885	2001.882478	1001.444877	Q	***914.487649***	457.747463	897.461100	449.234188	896.477084	448.742180	5
21	2120.940722	1060.973999	2103.914173	1052.460724	2102.930157	1051.968716	T	***786.429071***	393.718174	769.402522	385.204899	768.418506	384.712891	4
22	2191.977836	1096.492556	2174.951287	1087.979281	2173.967271	1087.487273	A	***685.381392***	343.194334	668.354843	334.681060			3
23	2631.203162	1316.105219	2614.176613	1307.591945	2613.192597	1307.099937	Q	***614.344278***	307.675777	597.317729	299.162503			2
24							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 24 ppm



RMS error 24 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.5	2804.307587	0.037465	DYAGVFSDAGLTFTSSSGQQTAQR
38.4	2804.307587	0.037465	DYAGVFSDAGLTFTSSSGQQTAQR
38.3	2804.307587	0.037465	DYAGVFSDAGLTFTSSSGQQTAQR

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

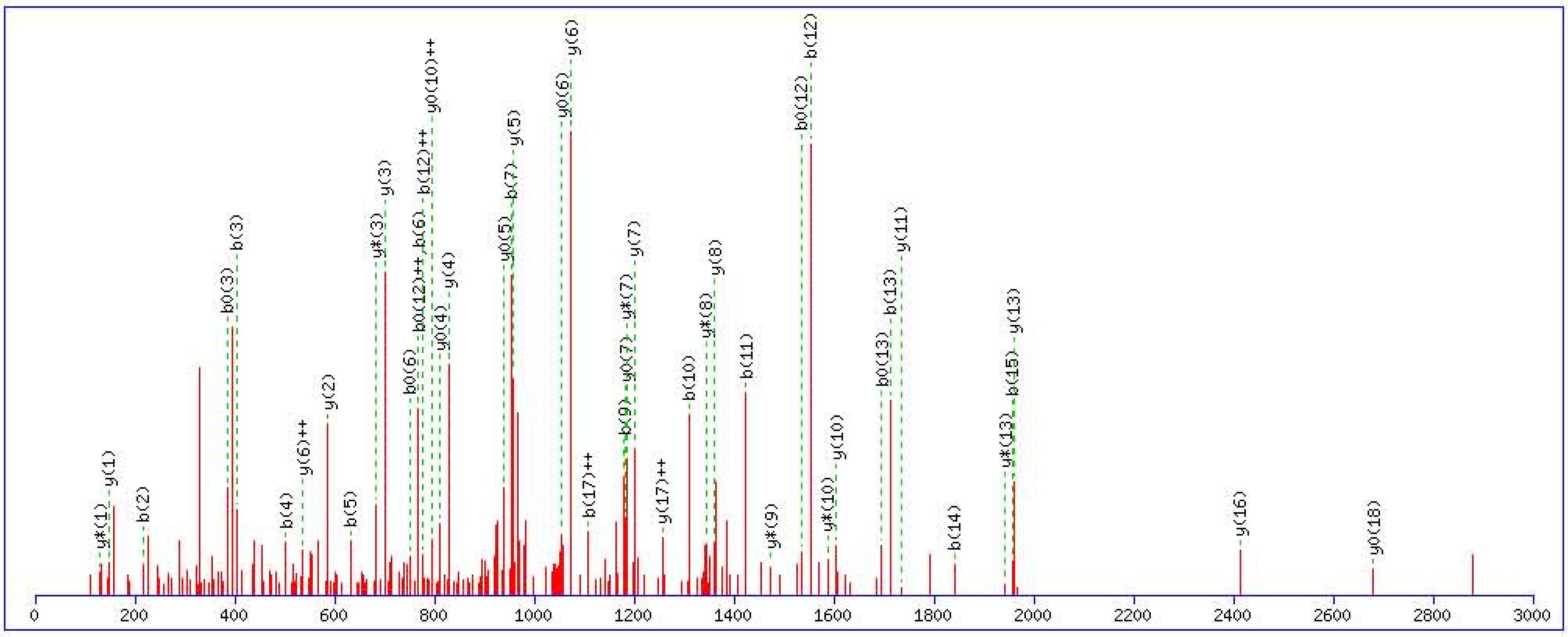
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTWVEHWPEEDECQDEENQK**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

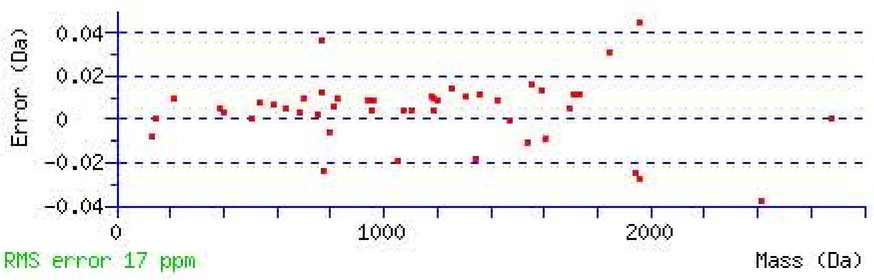
Match to Query 69262: 2913.228612 from(972.083480,3+) rtinseconds(2115) index(42999)
Title: Locus:1.1.1.3185.17 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

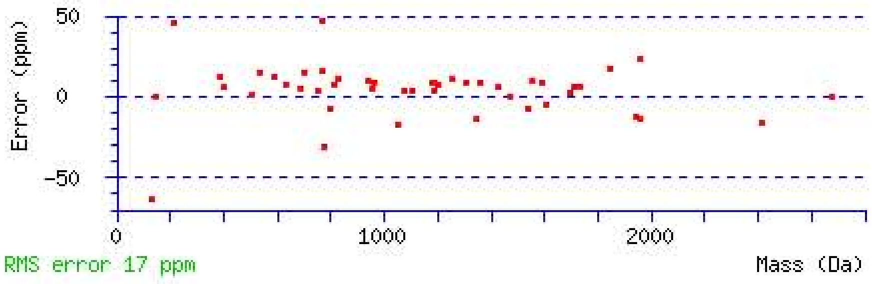
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2913.185776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19    : Biotin:Thermo-21345 (Q)
Ions Score: 81  Expect: 2e-008
Matches : 47/196 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	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
80.9	2913.185776	0.042836	DTWVEHWPEEDECQDEENQK
34.9	2913.185776	0.042836	DTWVEHWPEEDECQDEENQK

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

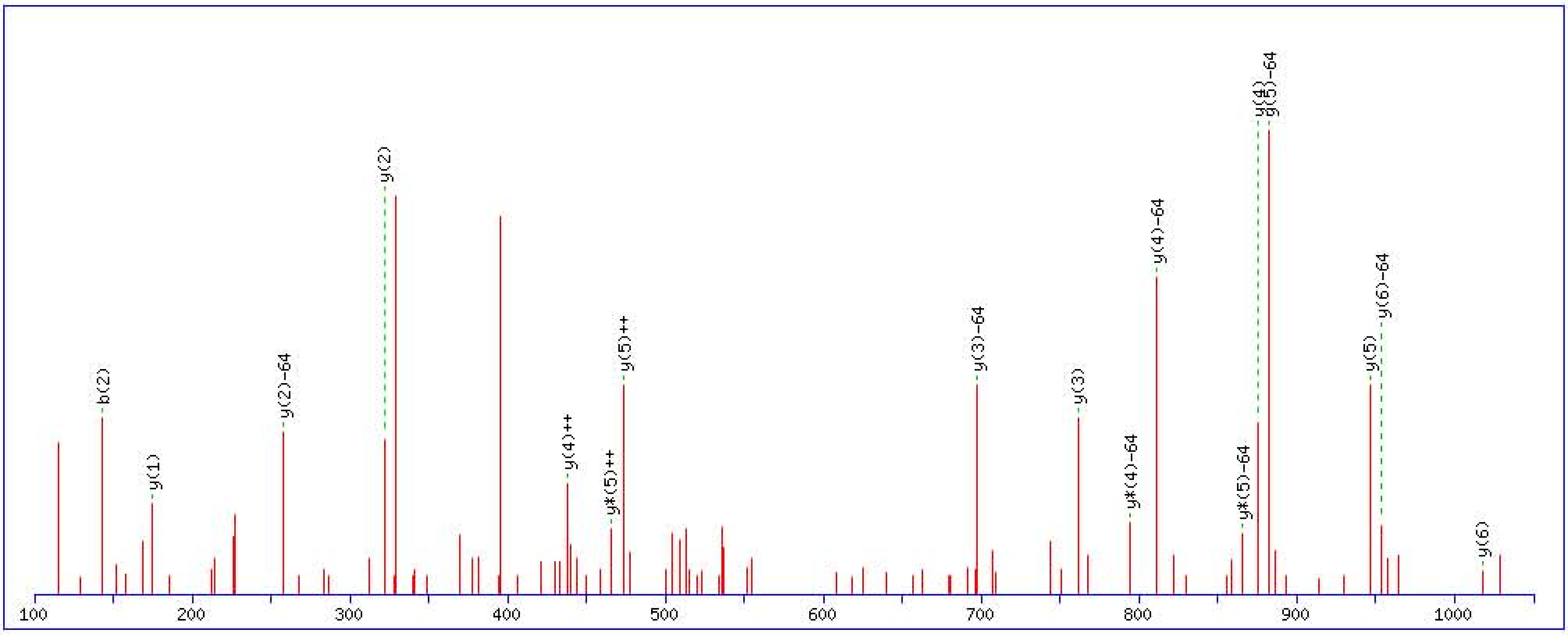
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAANQMR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

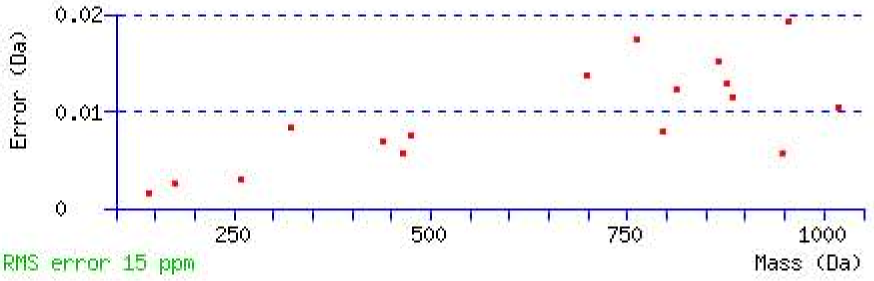
Match to Query 18669: 1087.538228 from(544.776390,2+) rtinseconds(1115) index(54655)
Title: Locus:1.1.1.2811.17 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

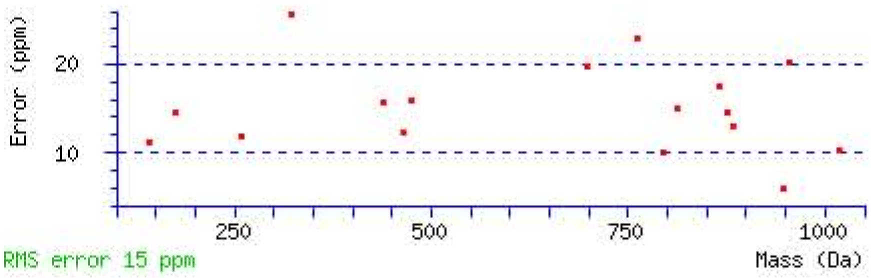
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1087.526642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
M6     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 34  Expect: 0.0081
Matches : 17/66 fragment ions using 29 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					7
2	143.081504	72.044390			A	***1017.496833***	509.252055	1000.470284	500.738780	6
3	214.118618	107.562947			A	***946.459719***	473.733498	929.433170	465.220223	5
4	328.161545	164.584410	311.134996	156.071136	N	***875.422605***	438.214941	858.396056	429.701666	4
5	767.386871	384.197074	750.360322	375.683799	Q	***761.379678***	381.193477	744.353129	372.680203	3
6	914.422271	457.714774	897.395722	449.201499	M	***322.154352***	161.580814	305.127803	153.067540	2
7					R	***175.118952***	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.1	1087.526642	0.011586	AAANQMR

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

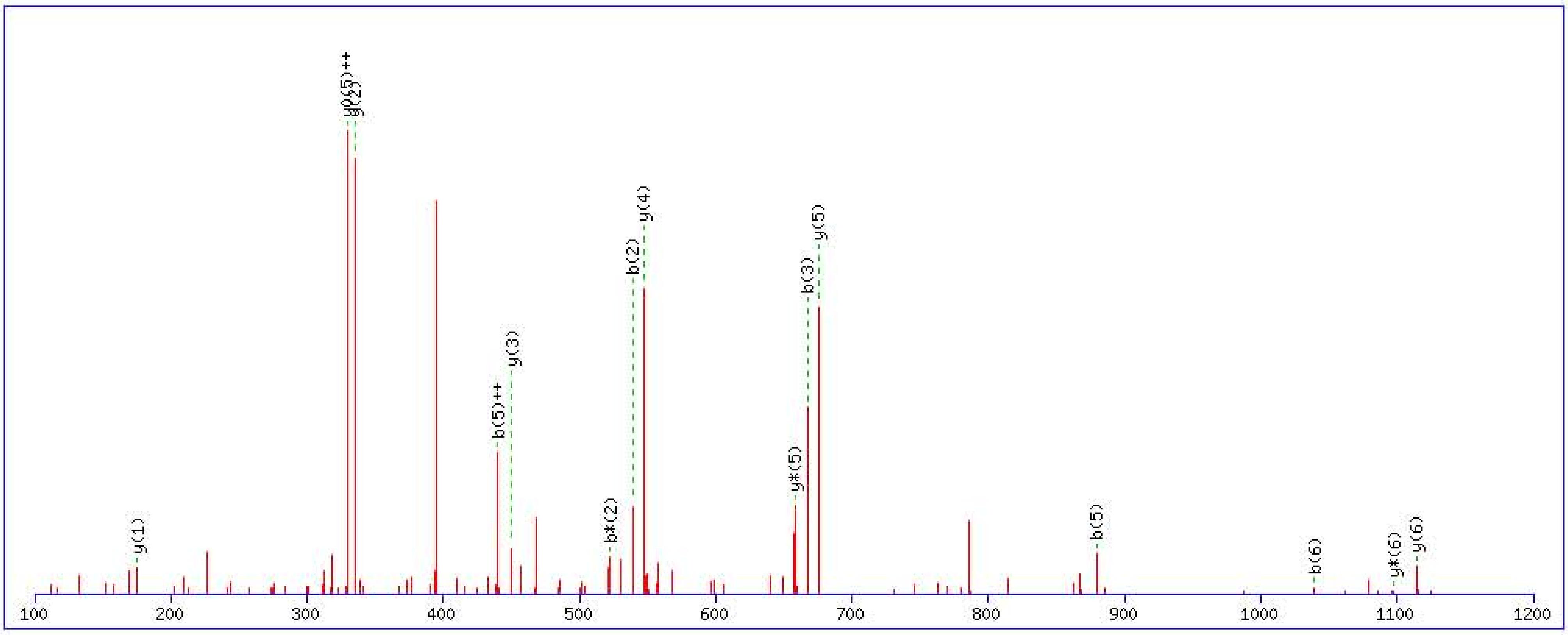
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQQPDCR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

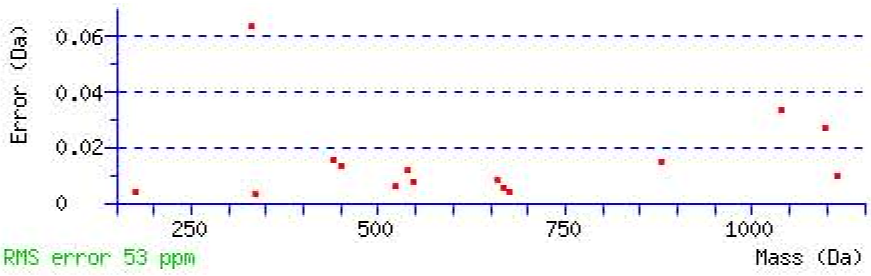
Match to Query 24040: 1212.589348 from(607.301950,2+) rtinseconds(1279) index(55722)
Title: Locus:1.1.1.2868.23 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

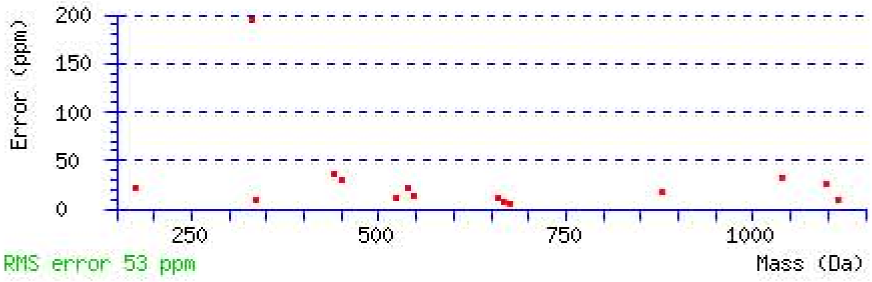
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 30  Expect: 0.0081
Matches : 15/58 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
30.3	1212.574356	0.014992	VQQPDCR
13.9	1212.574356	0.014992	VQQPDCR
7.8	1212.592102	-0.002754	VQEDQQR
7.1	1212.596115	-0.006767	YFVEAGAMAVR
4.7	1212.592758	-0.003410	IYYVDHFTR

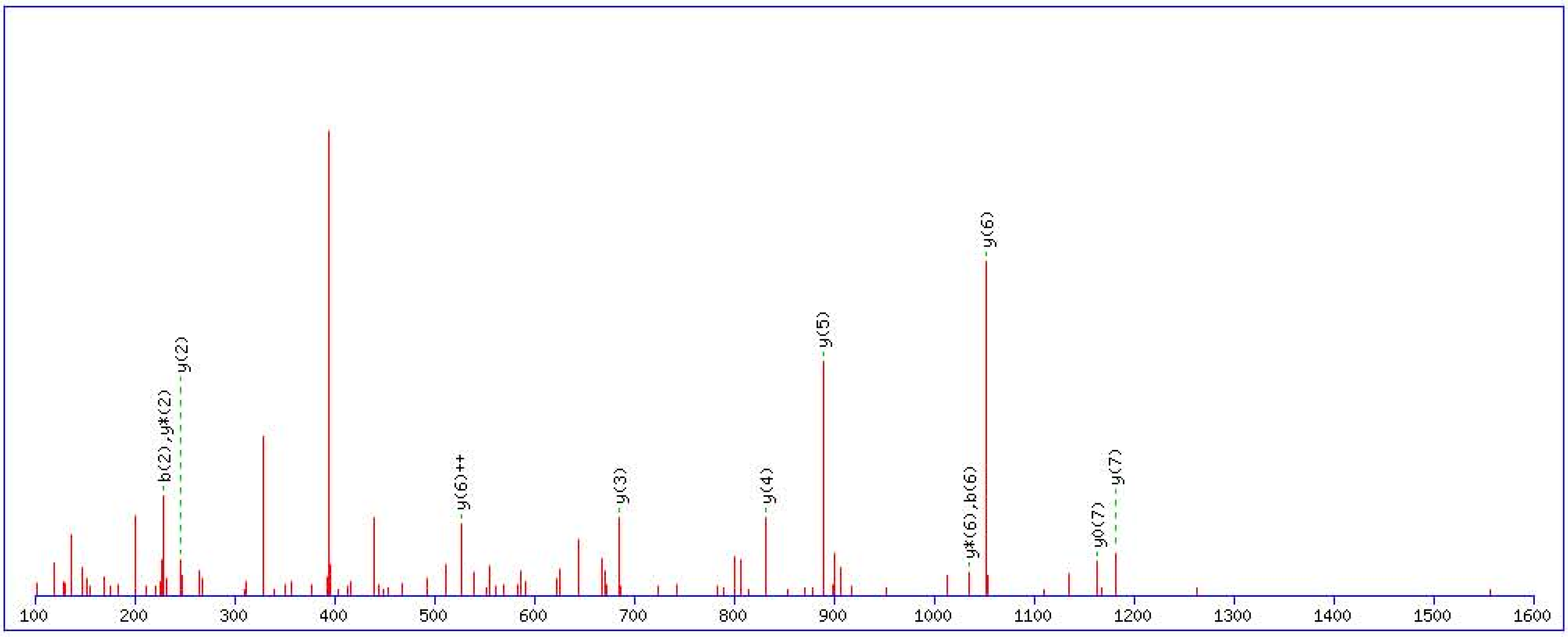
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEYGFQVK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

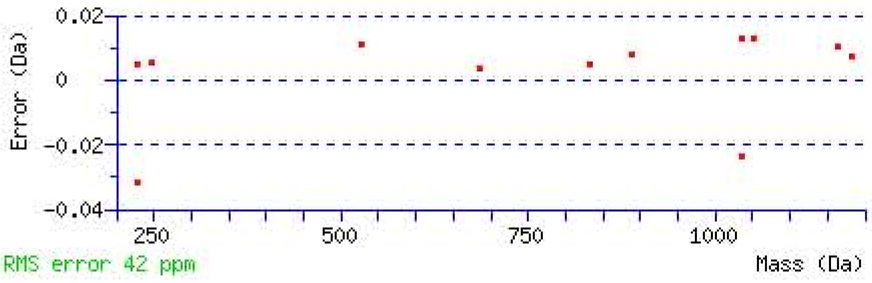
Match to Query 26222: 1279.675648 from(640.845100,2+) rtinseconds(1967) index(42006)
Title: Locus:1.1.1.3134.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

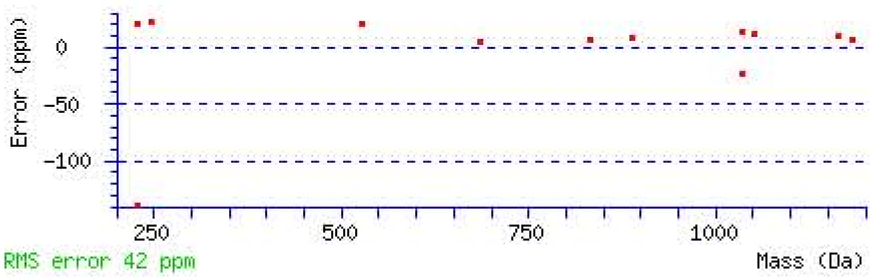
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1279.663483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.0073
Matches : 12/60 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							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
28.5	1279.663483	0.012165	VEYGFQVK
5.3	1279.687958	-0.012310	LIKSMESVMVK
4.1	1279.684601	-0.008953	TKPLMTEFSVK
3.3	1279.681229	-0.005581	EVTVKEWYVK
2.5	1279.684601	-0.008953	MSASAVFILDVK
2.2	1279.663483	0.012165	QFVGYLDK
0.4	1279.677216	-0.001568	VFKTEDTQGKK

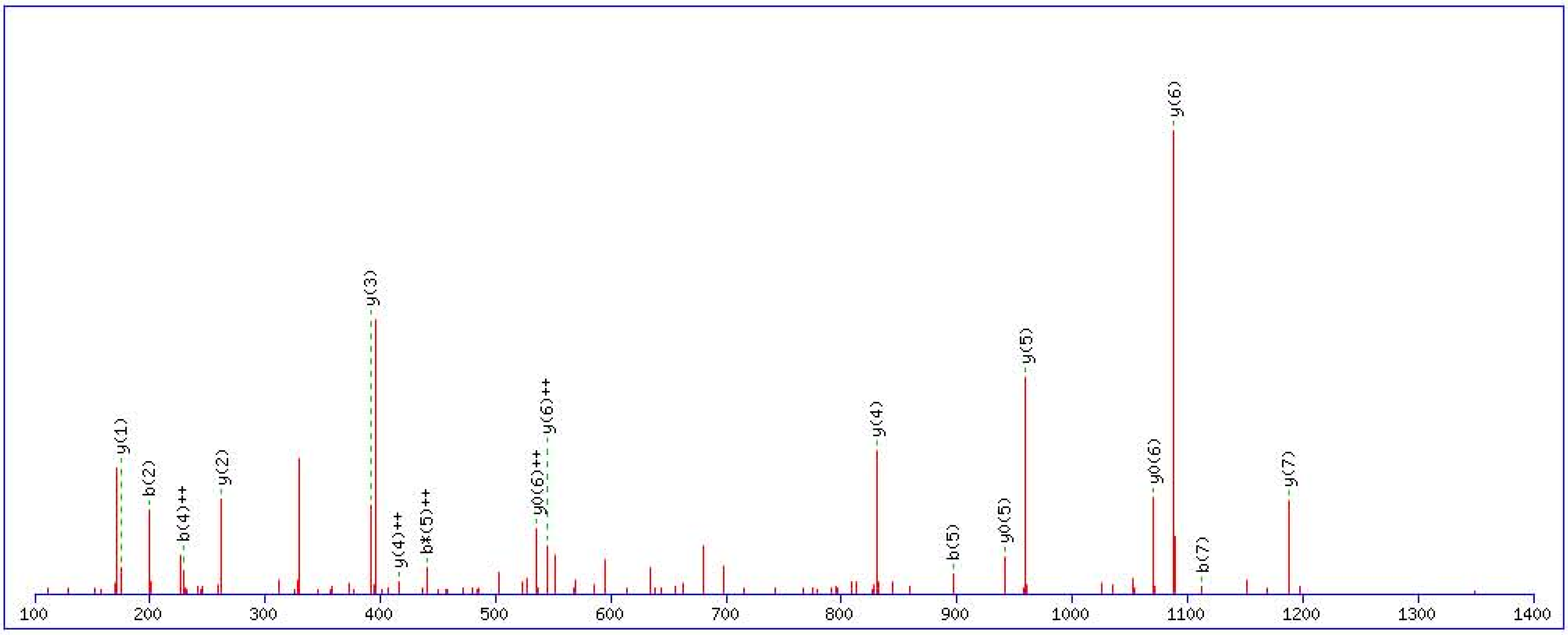
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVEEQESR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

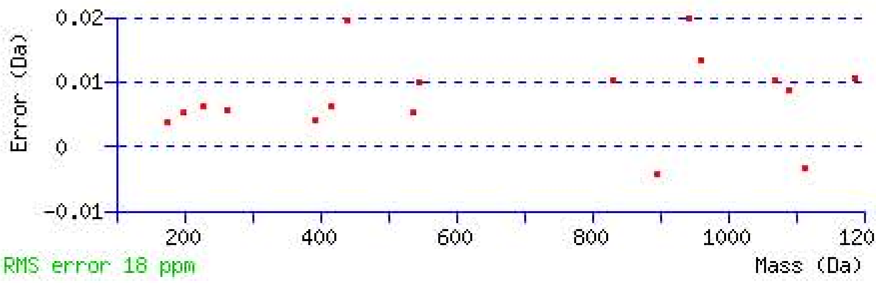
Match to Query 26583: 1285.650468 from(643.832510,2+) rtinseconds(1364) index(56276)
Title: Locus:1.1.1.2898.7 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

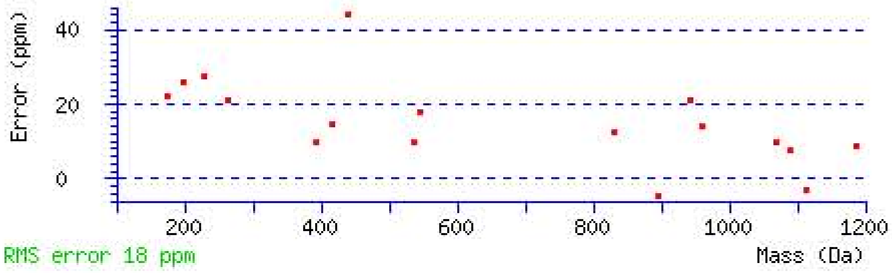
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1285.633621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.00064
Matches : 17/70 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	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
39.8	1285.633621	0.016847	VVEEQESR
5.4	1285.662598	-0.012130	TPERLSLEGER
3.3	1285.637451	0.013017	TAPASGSAPRESR
2.3	1285.660126	-0.009658	QSNGIFPGR
1.2	1285.644867	0.005601	DTLHSAMAVVSR

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

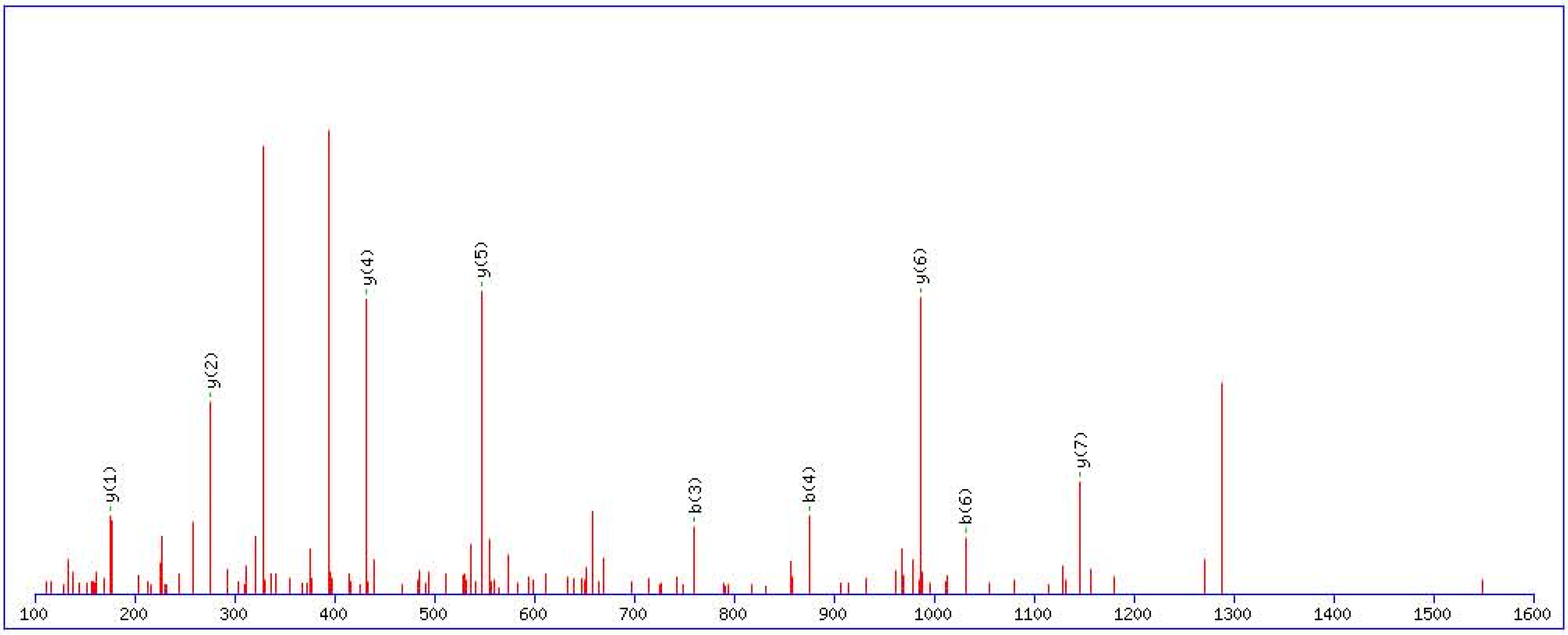
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CCQDGVTR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

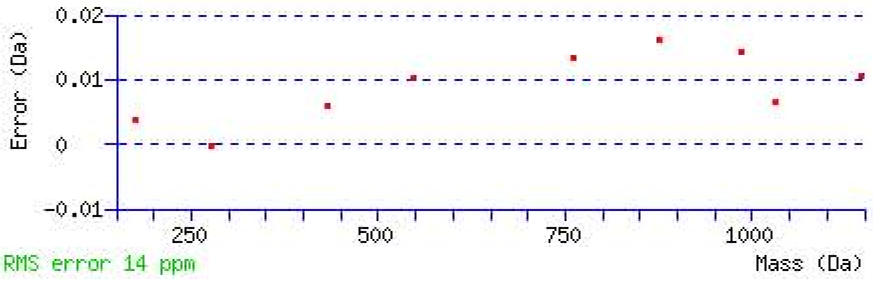
Match to Query 27051: 1305.577488 from(653.796020,2+) rtinseconds(1370) index(56305)
Title: Locus:1.1.1.2900.13 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

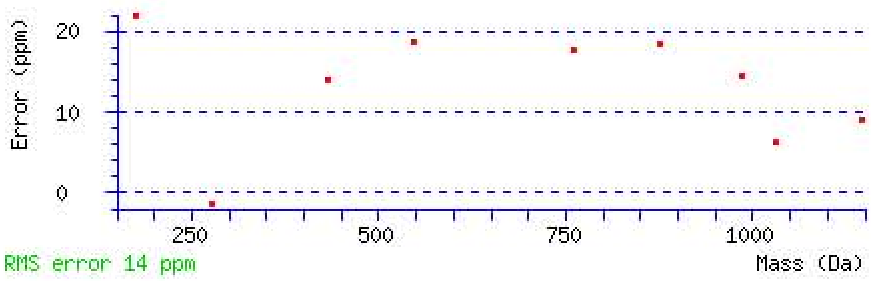
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1305.562820
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 0.00011
Matches : 9/72 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

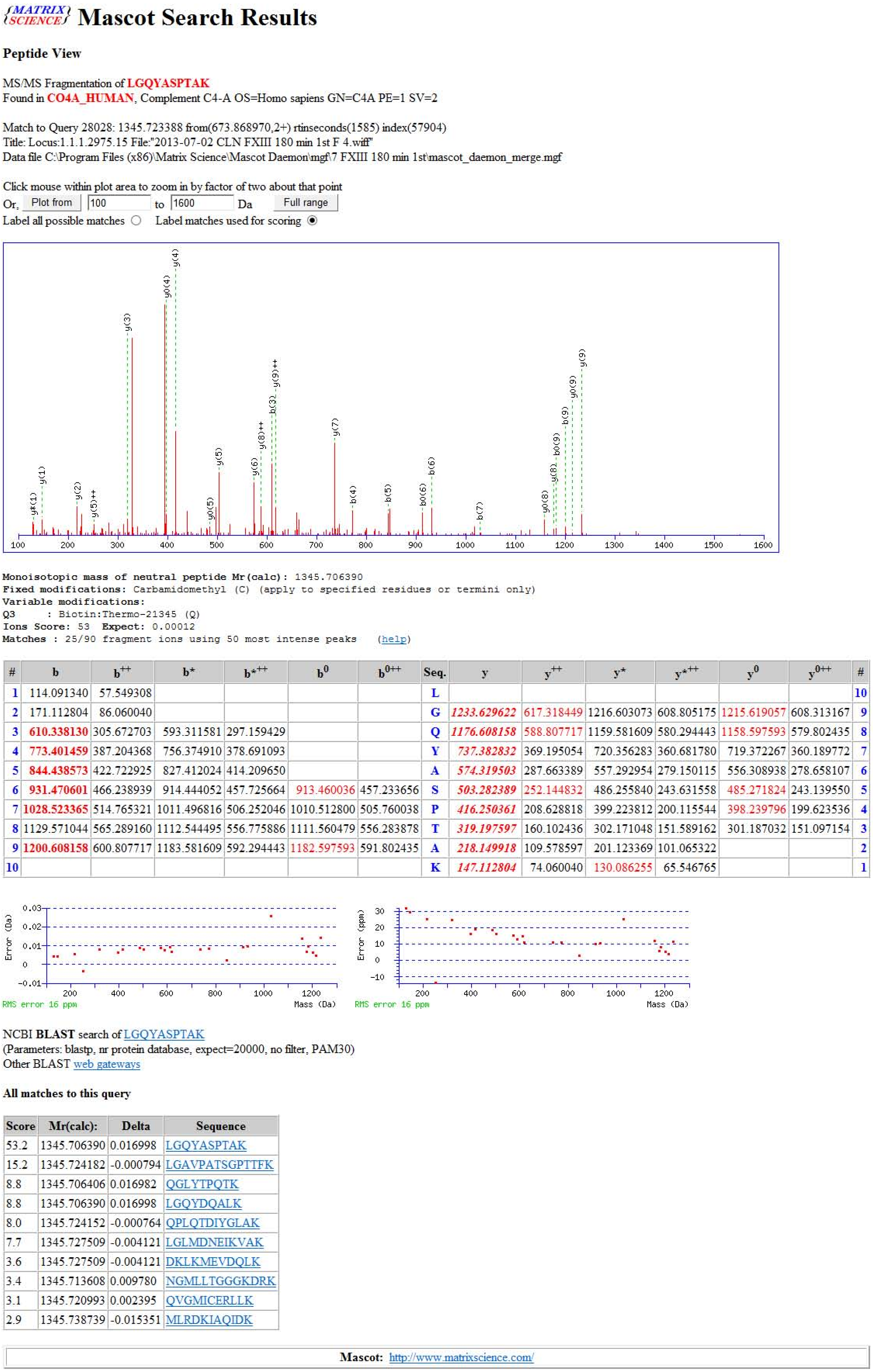




NCBI **BLAST** search of CCQDGVTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.3	1305.562820	0.014668	CCQDGVTR
19.5	1305.588409	-0.010921	CRSSTPADAWR
6.1	1305.577194	0.000294	CDAGWLADGSVR
5.0	1305.562805	0.014683	CCTSPSQR



{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 28028: 1345.723388 from(673.868970,2+) rtinseconds(1585) index(57904)
Title: Locus:1.1.1.2975.15 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\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): 1345.706390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 0.00012
Matches : 25/90 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	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
53.2	1345.706390	0.016998	LGQYASPTAK
15.2	1345.724182	-0.000794	LGAVPATSGPTTFK
8.8	1345.706406	0.016982	QGLYTPQTK
8.8	1345.706390	0.016998	LGQYDQALK
8.0	1345.724152	-0.000764	QPLQTDIYGLAK
7.7	1345.727509	-0.004121	LGLMDNEIKVAK
3.6	1345.727509	-0.004121	DKLKMEVDQLK
3.4	1345.713608	0.009780	NGMLLTGGGKDRK
3.1	1345.720993	0.002395	QVGMICERLLK
2.9	1345.738739	-0.015351	MLRDKIAQIDK

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

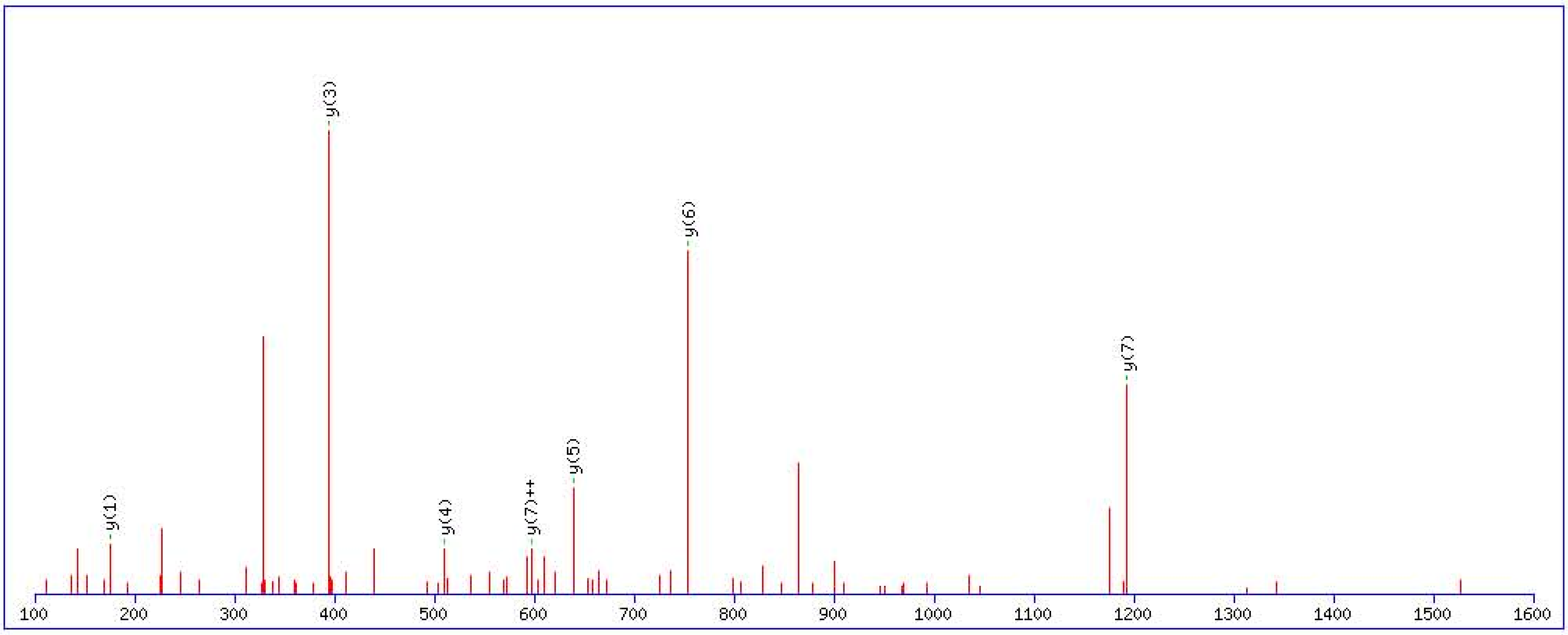
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLQDEDGYR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

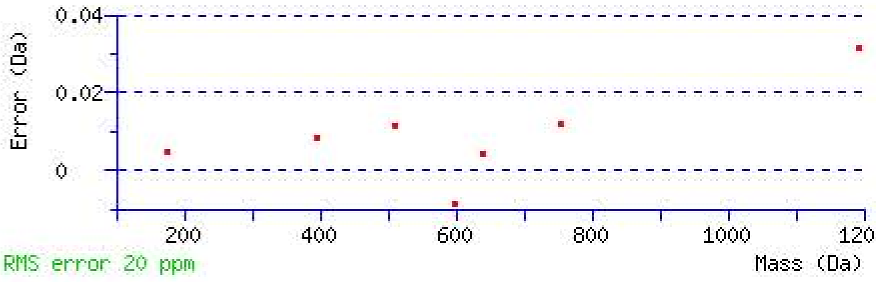
Match to Query 29262: 1362.640488 from(682.327520,2+) rtinseconds(1716) index(58728)
Title: Locus:1.1.1.3021.6 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

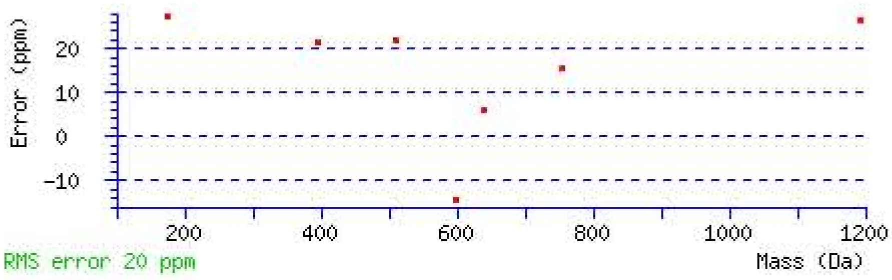
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1362.623795
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.0003
Matches : 7/80 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
40.1	1362.623795	0.016693	GLQDEDGYR
2.4	1362.623795	0.016693	TGFLEIDEHMR
0.2	1362.652756	-0.012268	GLAADERAEFER

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

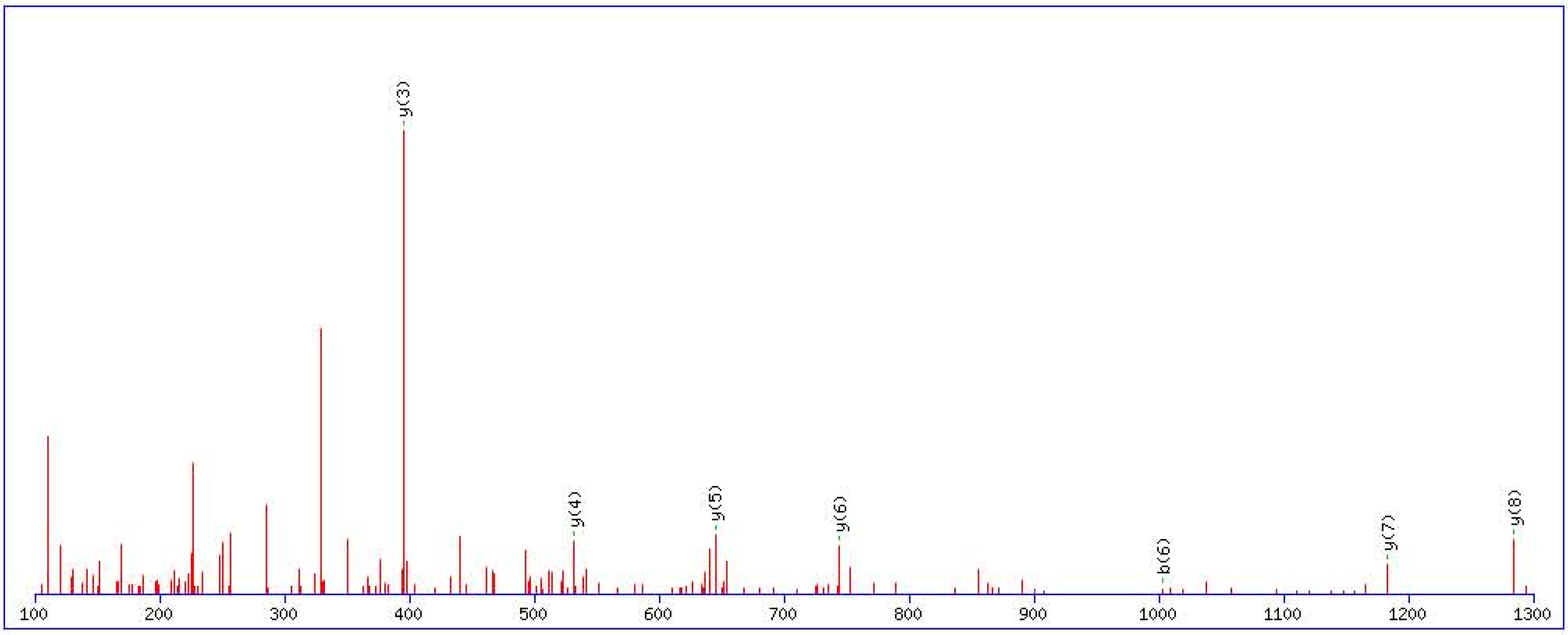
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITQVLHFTK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

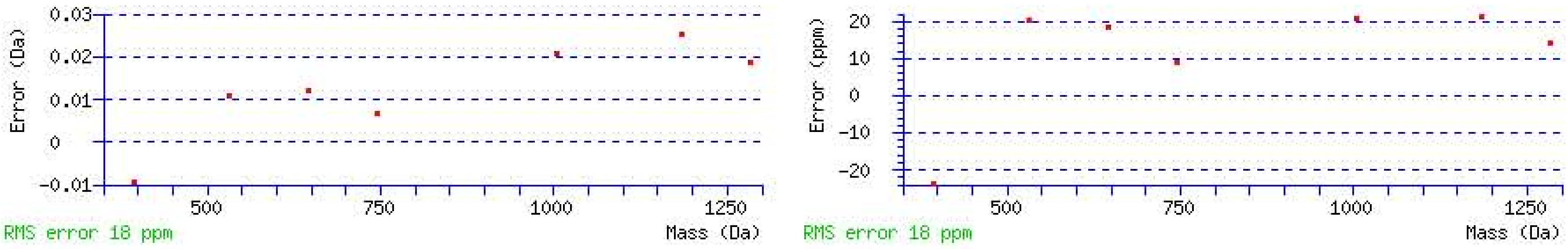
Match to Query 30668: 1396.804962 from(466.608930,3+) rtinseconds(1929) index(60253)
Title: Locus:1.1.1.3095.4 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1396.790085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.00032
Matches : 7/88 fragment ions using 12 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	114.091340	57.549308					I							9
2	215.139019	108.073147			197.128454	99.067865	T	***1284.713292***	642.860284	1267.686743	634.347010	1266.702727	633.855002	8
3	654.364345	327.685811	637.337796	319.172536	636.353780	318.680528	Q	***1183.665613***	592.336445	1166.639064	583.823170	1165.655048	583.331162	7
4	753.432759	377.220018	736.406210	368.706743	735.422194	368.214735	V	***744.440287***	372.723782	727.413738	364.210507	726.429722	363.718499	6
5	866.516823	433.762050	849.490274	425.248775	848.506258	424.756767	L	***645.371873***	323.189575	628.345324	314.676300	627.361308	314.184292	5
6	**1003.575735**	502.291506	986.549186	493.778231	985.565170	493.286223	H	***532.287809***	266.647543	515.261260	258.134268	514.277244	257.642260	4
7	1150.644149	575.825713	1133.617600	567.312438	1132.633584	566.820430	F	***395.228897***	198.118086	378.202348	189.604812	377.218332	189.112804	3
8	1251.691828	626.349552	1234.665279	617.836278	1233.681263	617.344270	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
9							K	147.112804	74.060040	130.086255	65.546765			1



NCBI **BLAST** search of ITQVLHFTK
(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	1396.790085	0.014877	ITQVLHFTK
0.1	1396.792557	0.012405	LLGELQEQIVQK

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

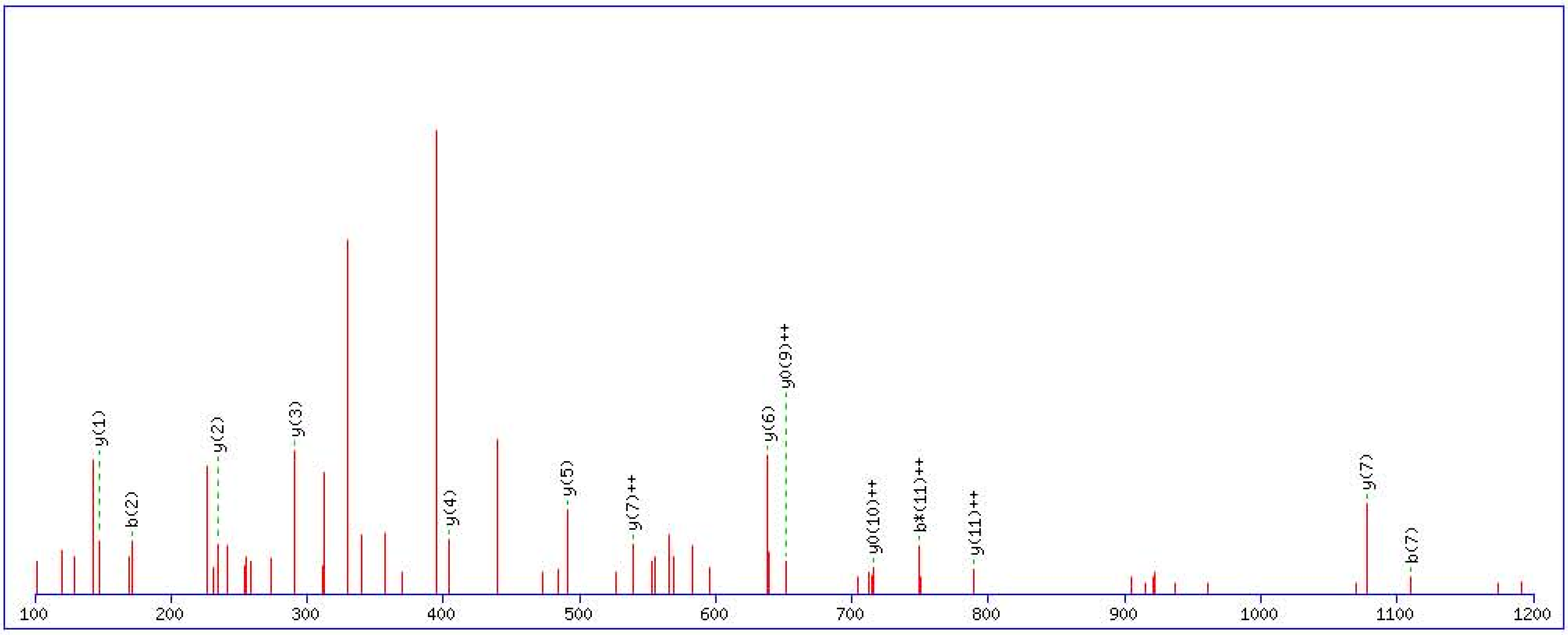
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLEEELQFSLGSK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

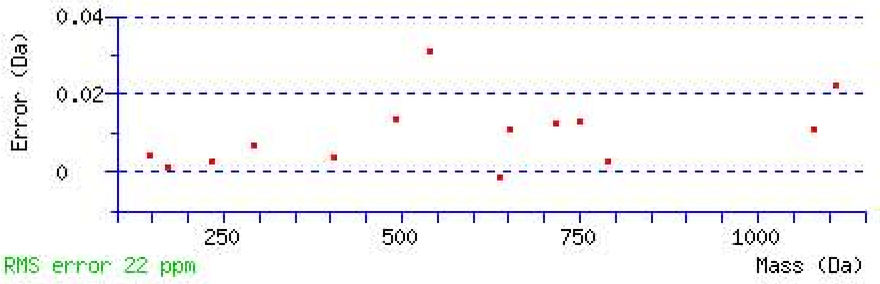
Match to Query 43800: 1746.906942 from(583.309590,3+) rtinseconds(2518) index(82303)
Title: Locus:1.1.1.2227.11 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

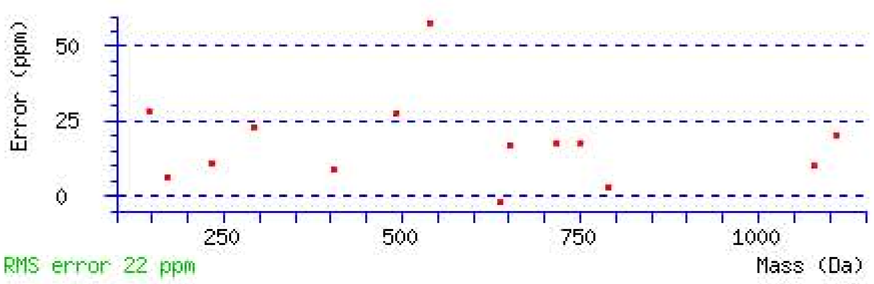
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1746.886200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.02
Matches : 14/126 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	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
31.4	1746.886200	0.020742	GLEEELQFSLGSK

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

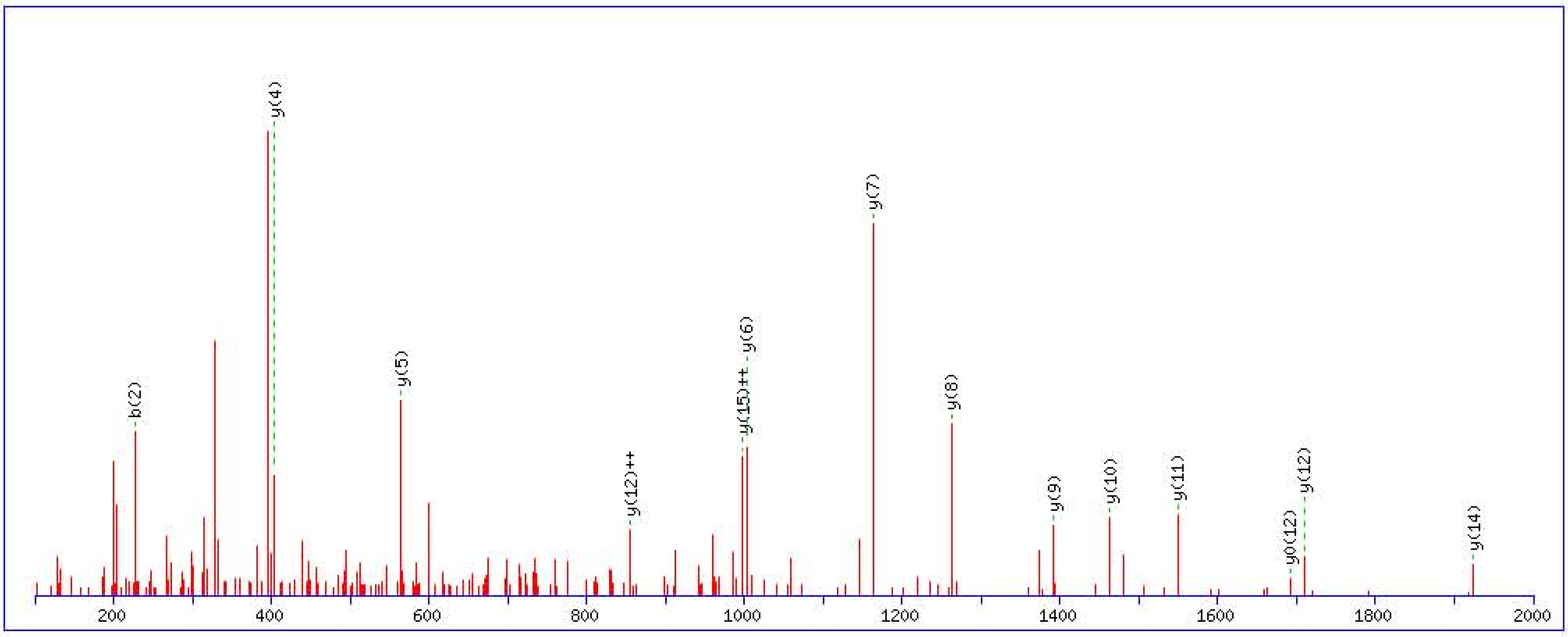
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLATLCSAEVCQCAEGK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

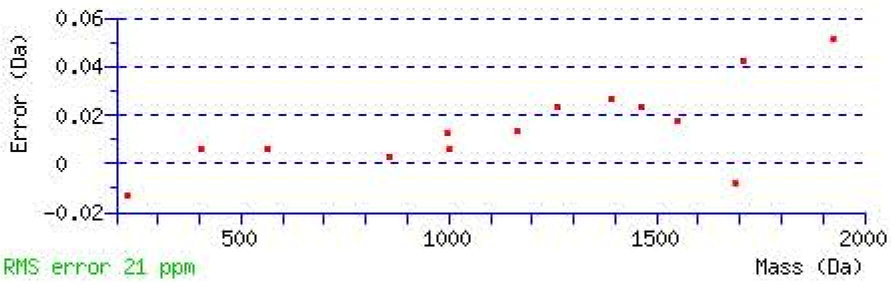
Match to Query 55978: 2220.063222 from(741.028350,3+) rtinseconds(2096) index(79511)
Title: Locus:1.1.1.2080.16 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

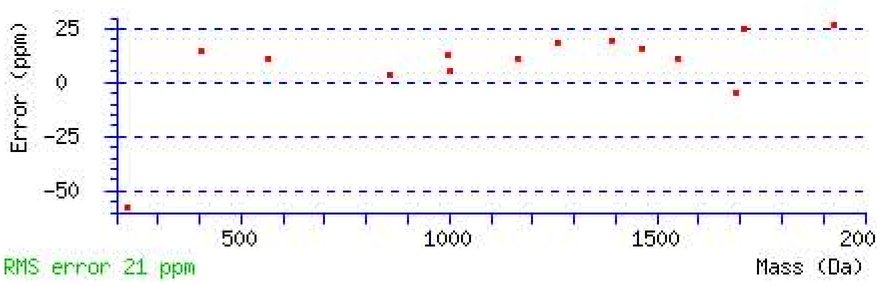
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2220.041092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 75  Expect: 1.1e-007
Matches : 14/160 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					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
75.0	2220.041092	0.022130	LLATLCSAEVCQCAEGK
0.7	2220.048080	0.015142	EPQEGAELPEATGTTSHR

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

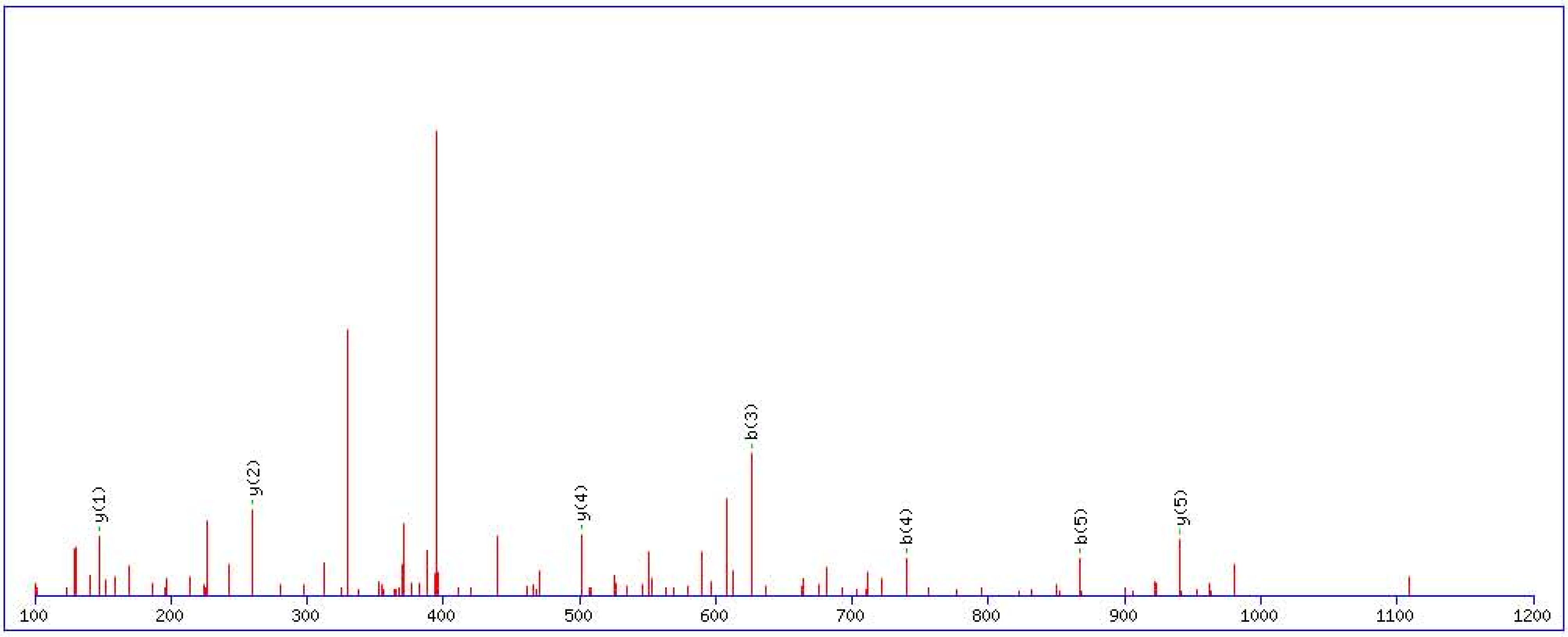
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEQIQLK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

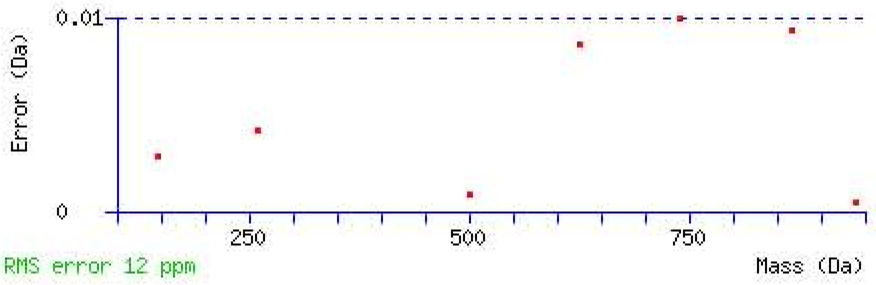
Match to Query 20254: 1125.629968 from(563.822260,2+) rtinseconds(1733) index(40301)
Title: Locus:1.1.1.3053.8 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

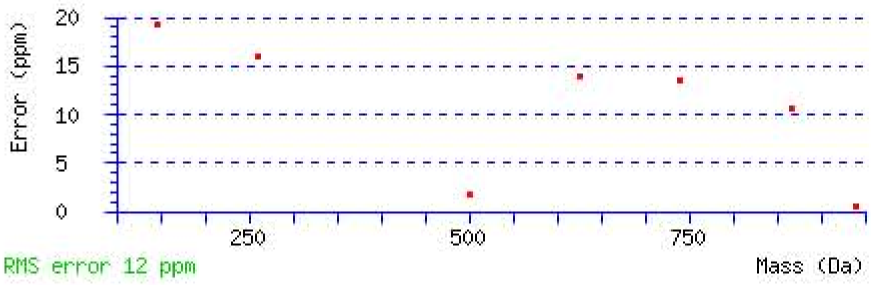
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 28  Expect: 0.033
Matches : 7/56 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**							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
28.0	1125.621597	0.008371	GEQIQLK
12.4	1125.632828	-0.002860	KLCLSHLQK
12.3	1125.621597	0.008371	EQVAQLK
12.2	1125.632813	-0.002845	EQAARLK
9.7	1125.636856	-0.006888	WAAQVIK
7.6	1125.629486	0.000482	RVDGWPVGLK
7.1	1125.621597	0.008371	GEQIQLK
7.1	1125.633499	-0.003531	VSHFLPWIK
6.3	1125.639359	-0.009391	LTNTTAPPALK
6.2	1125.618240	0.011728	GTNVFKGYLK

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

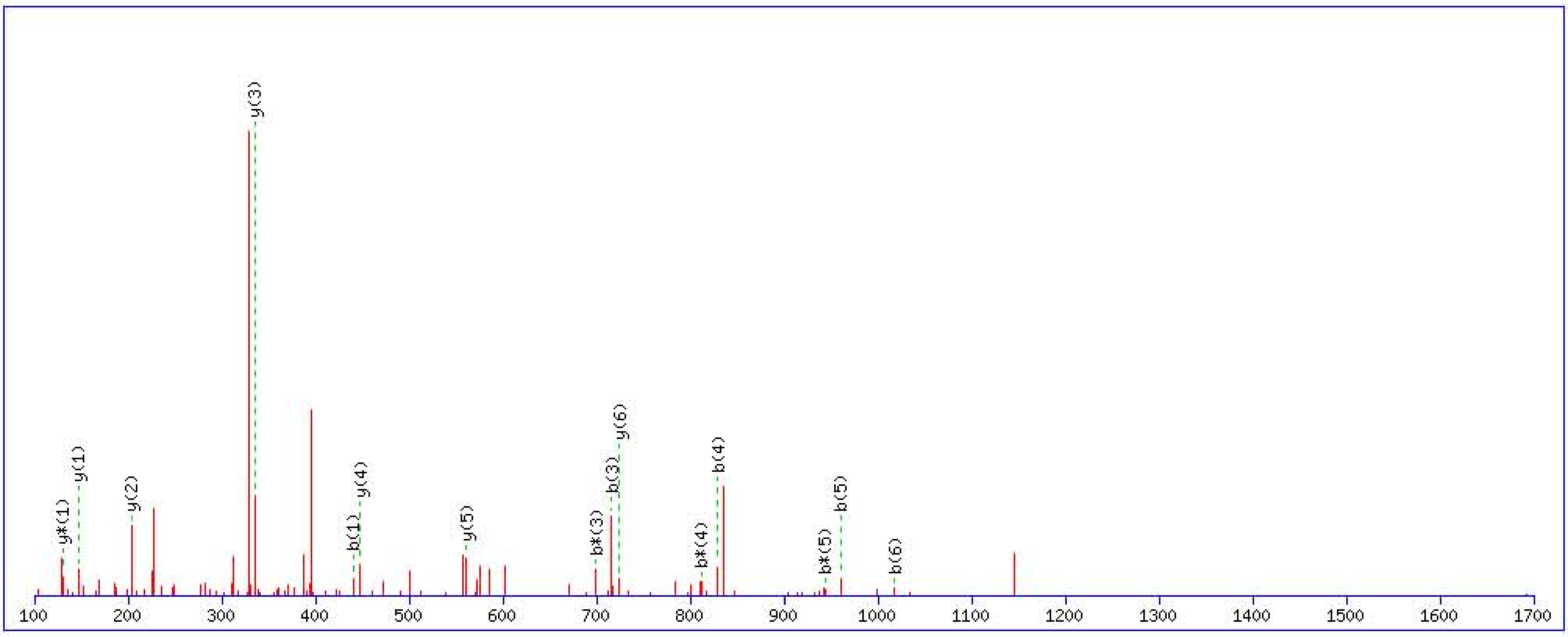
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYLIMGK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

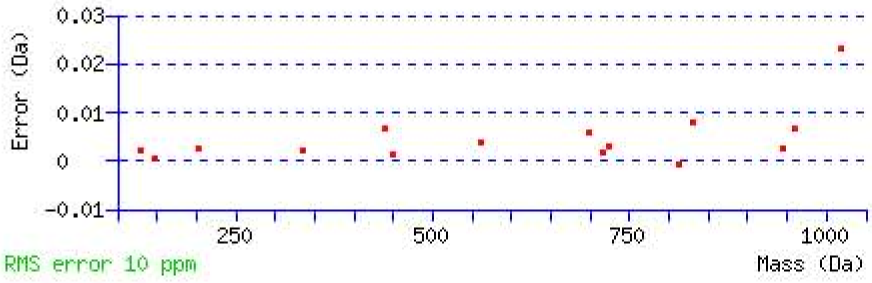
Match to Query 22316: 1162.636188 from(582.325370,2+) rtinseconds(2079) index(42769)
Title: Locus:1.1.1.3173.6 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

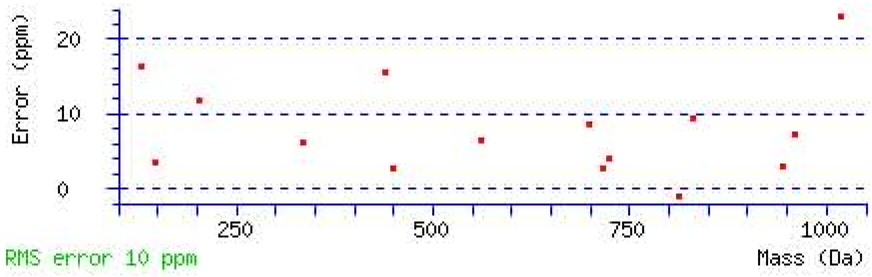
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1162.624237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.015
Matches : 15/48 fragment ions using 30 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	**440.232602**	220.619939	423.206053	212.106664	Q					7
2	603.295931	302.151604	586.269382	293.638329	Y	***724.406210***	362.706743	707.379661	354.193469	6
3	**716.379995**	358.693636	699.353446	350.180361	L	***561.342881***	281.175079	544.316332	272.661804	5
4	**829.464059**	415.235668	812.437510	406.722393	I	***448.258817***	224.633046	431.232268	216.119772	4
5	**960.504544**	480.755910	943.477995	472.242636	M	***335.174753***	168.091014	318.148204	159.577740	3
6	**1017.526008**	509.266642	1000.499459	500.753368	G	***204.134268***	102.570772	187.107719	94.057497	2
7					K	***147.112804***	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of QYLIMGK
(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	1162.624237	0.011951	QYLIMGK
13.1	1162.641998	-0.005810	QYLTSLK
10.2	1162.626724	0.009464	ESILKADMLK
8.3	1162.626740	0.009448	EVLKMDTSIK
5.0	1162.623383	0.012805	ELFGLDTLQK
4.0	1162.624069	0.012119	VGRCRSLSTK
3.2	1162.639313	-0.003125	QRHLNGK
2.9	1162.635956	0.000232	WGGFLGRRSK
2.6	1162.649216	-0.013028	RVKTQMSLGK
1.5	1162.620697	0.015491	QLSGQRFTAR

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

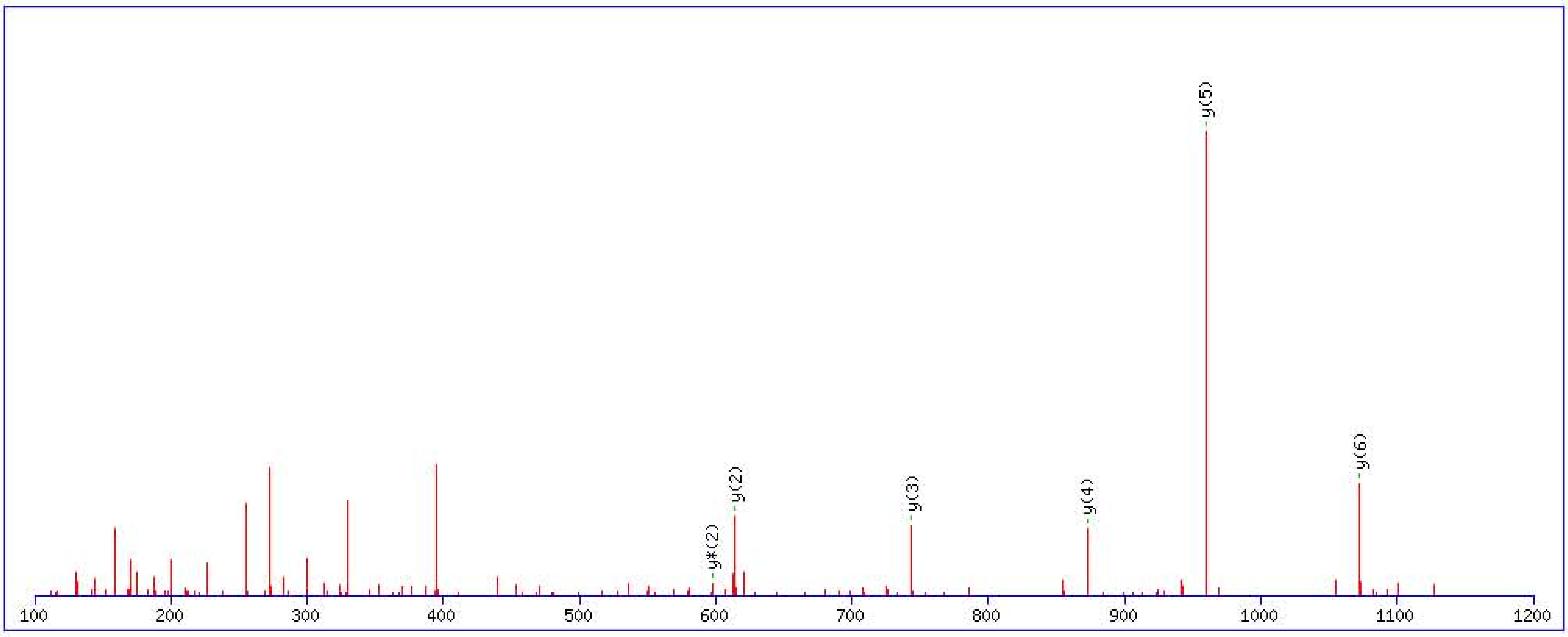
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLSEEQR**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

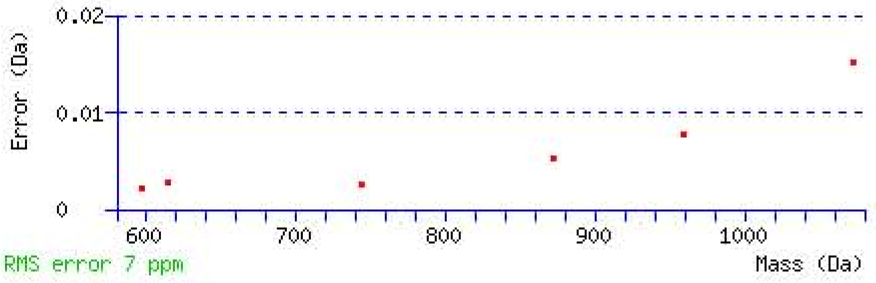
Match to Query 25488: 1257.628988 from(629.821770,2+) rtinseconds(1802) index(40800)
Title: Locus:1.1.1.3077.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

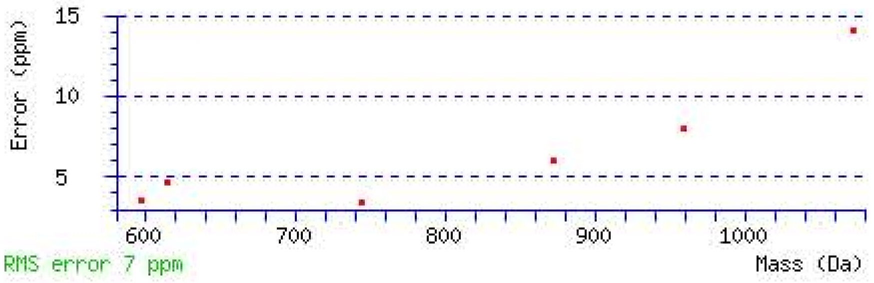
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1257.617569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.022
Matches : 6/54 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	187.086589	94.046932					**W**							7
2	300.170653	150.588965					**L**	***1072.545556***	536.776416	1055.519007	528.263142	1054.534991	527.771134	6
3	387.202681	194.104979			369.192116	185.099696	**S**	***959.461492***	480.234384	942.434943	471.721109	941.450927	471.229101	5
4	516.245274	258.626275			498.234709	249.620993	**E**	***872.429464***	436.718370	855.402915	428.205095	854.418899	427.713087	4
5	645.287867	323.147572			627.277302	314.142289	**E**	***743.386871***	372.197073	726.360322	363.683799	725.376306	363.191791	3
6	1084.513193	542.760235	1067.486644	534.246960	1066.502628	533.754952	**Q**	***614.344278***	307.675777	597.317729	299.162502			2
7							**R**	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of WLSEEQR
(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	1257.617569	0.011419	WLSEEQR
13.5	1257.621414	0.007574	ASSNRSWTPPR
6.7	1257.620071	0.008917	EGLEEGDQILR
3.2	1257.617599	0.011389	QADVFPDR
2.7	1257.631287	-0.002299	ADAEEALKQQR
2.6	1257.621445	0.007543	GFRGETGPQGPR
2.0	1257.638687	-0.009699	EGEMALLSKHK
1.7	1257.617584	0.011404	SVMEAPFPAPGR
1.3	1257.617569	0.011419	WEALPAMPTAR
0.8	1257.613541	0.015447	APGPATASAAAAMR

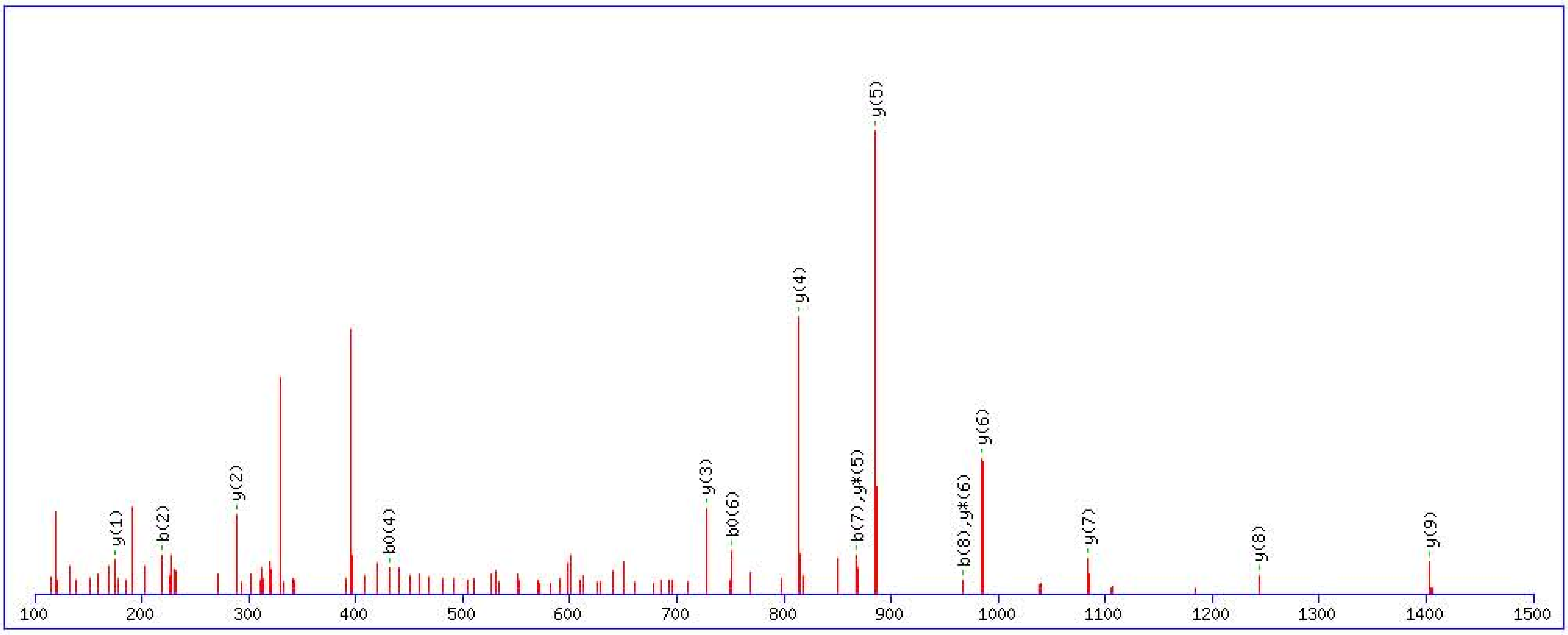
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFTECCVVASQLR**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

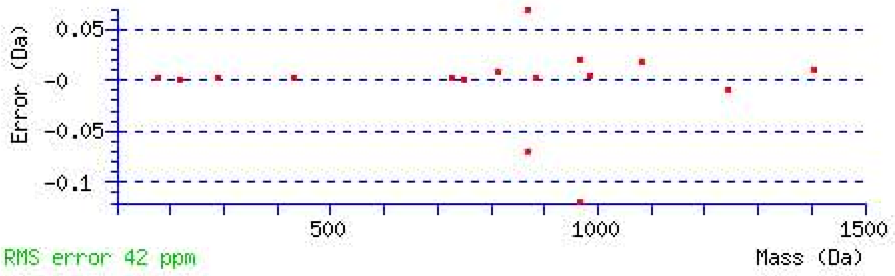
Match to Query 46488: 1850.895702 from(617.972510,3+) rtinseconds(2151) index(25760)
Title: Locus:1.1.1.2891.13 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

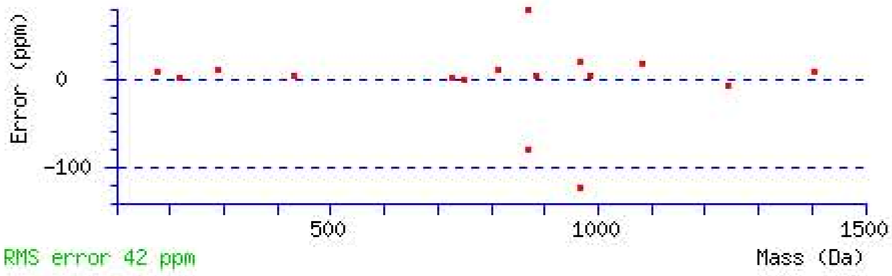
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1850.884140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.002
Matches : 16/114 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	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
40.6	1850.884140	0.011562	AFTECCVVASQLR

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

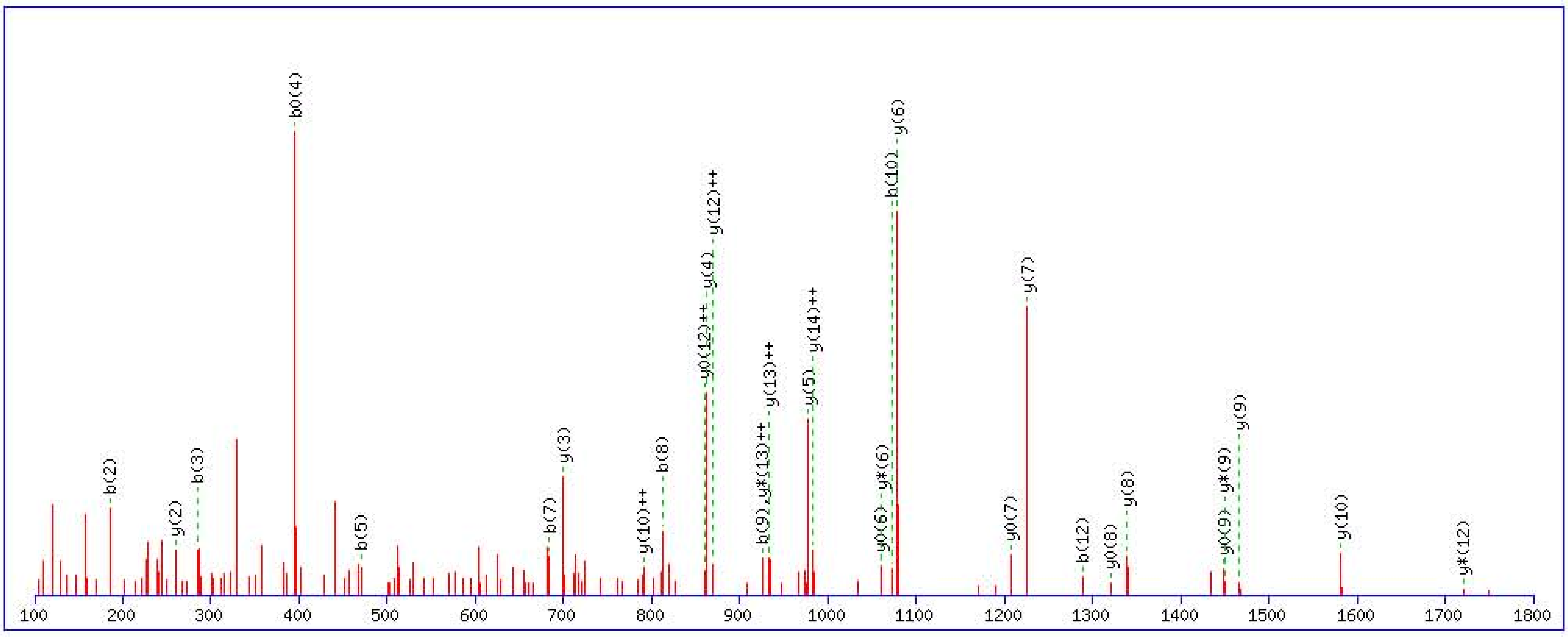
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALVEGVDQLFTDYQIK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

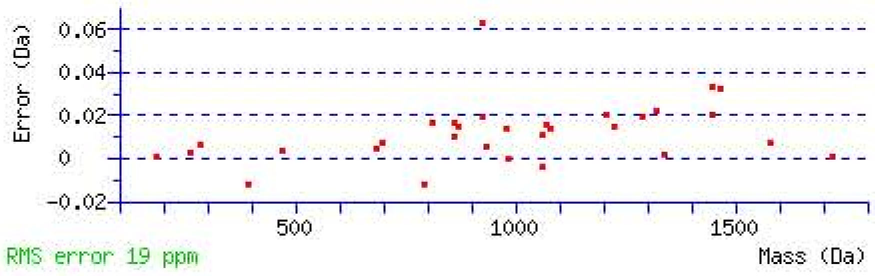
Match to Query 54105: 2149.144902 from(717.388910,3+) rtinseconds(2812) index(47857)
Title: Locus:1.1.1.3426.5 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

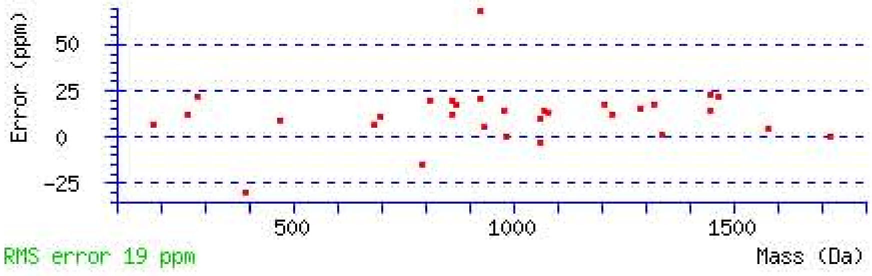
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2149.112930
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.00029
Matches : 31/152 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	72.044390	36.525833					A							16
2	***185.128454***	93.067865					L	2079.083093	1040.045184	2062.056544	1031.531910	2061.072528	1031.039902	15
3	***284.196868***	142.602072					V	1965.999029	983.503153	1948.972480	974.989878	1947.988464	974.497870	14
4	413.239461	207.123369			395.228896	198.118086	E	1866.930615	933.968946	1849.904066	925.455671	1848.920050	924.963663	13
5	***470.260925***	235.634100			452.250360	226.628818	G	1737.888022	869.447649	1720.861473	860.934375	1719.877457	860.442367	12
6	569.329339	285.168308			551.318774	276.163025	V	1680.866558	840.936917	1663.840009	832.423643	1662.855993	831.931635	11
7	***684.356282***	342.681779			666.345717	333.676496	D	***1581.798144***	791.402710	1564.771595	782.889436	1563.787579	782.397428	10
8	***812.414860***	406.711068	795.388311	398.197793	794.404295	397.705785	Q	***1466.771201***	733.889239	1449.744652	725.375964	1448.760636	724.883956	9
9	***925.498924***	463.253100	908.472375	454.739825	907.488359	454.247818	L	***1338.712623***	669.859950	1321.686074	661.346675	1320.702058	660.854667	8
10	***1072.567338***	536.787307	1055.540789	528.274033	1054.556773	527.782025	F	***1225.628559***	613.317918	1208.602010	604.804643	1207.617994	604.312635	7
11	1173.615017	587.311147	1156.588468	578.797872	1155.604452	578.305864	T	***1078.560145***	539.783711	1061.533596	531.270436	1060.549580	530.778428	6
12	***1288.641960***	644.824618	1271.615411	636.311344	1270.631395	635.819336	D	***977.512466***	489.259871	960.485917	480.746597	959.501901	480.254589	5
13	1451.705289	726.356283	1434.678740	717.843008	1433.694724	717.351000	Y	***862.485523***	431.746400	845.458974	423.233125			4
14	1890.930615	945.968946	1873.904066	937.455671	1872.920050	936.963663	Q	***699.422194***	350.214735	682.395645	341.701461			3
15	2004.014679	1002.510978	1986.988130	993.997703	1986.004114	993.505695	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 ALVEGVDQLFTDYQIK
(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	2149.112930	0.031972	ALVEGVDQLFTDYQIK
3.2	2149.112930	0.031972	ALVEGVDQLFTDYQIK
3.0	2149.116257	0.028645	QDEQLAMKLLTYELK
2.7	2149.116257	0.028645	QDEQLAMKLLTYELK

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

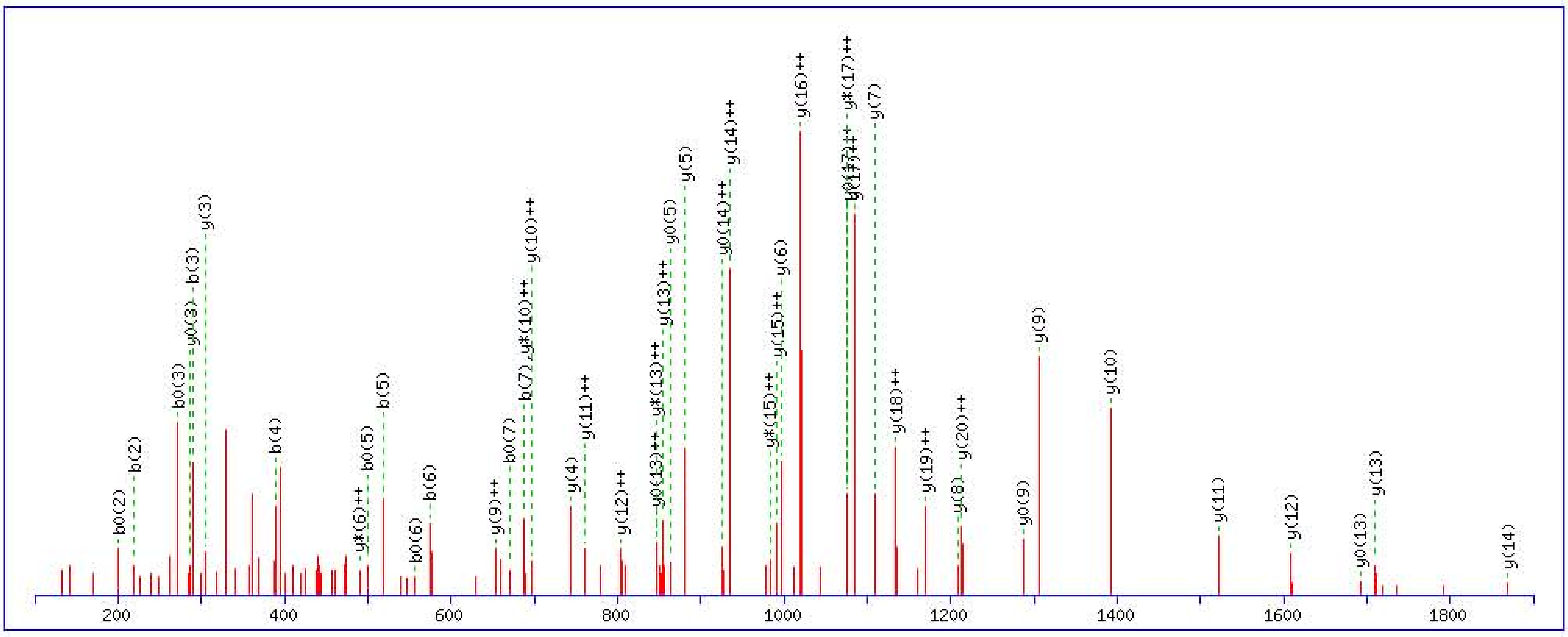
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MSAVEGICTSESPVIDHQGTK**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

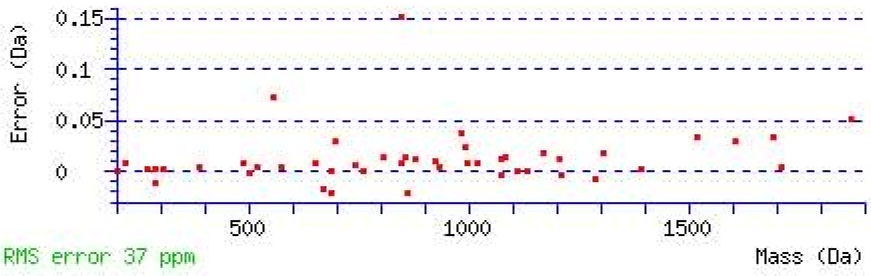
Match to Query 63908: 2556.238212 from(853.086680,3+) rtinseconds(1936) index(41744)
Title: Locus:1.1.1.3123.24 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

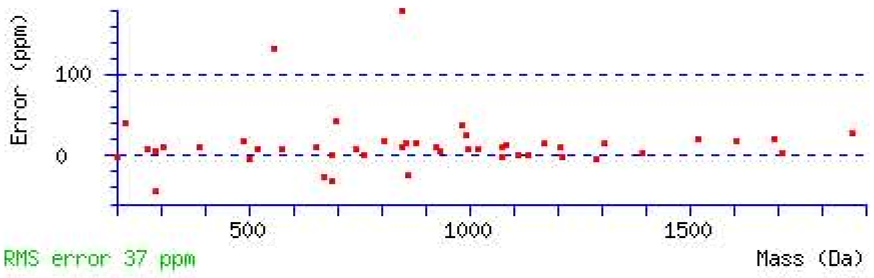
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 78  Expect: 4e-007
Matches : 47/202 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	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
78.0	2556.202240	0.035972	MSAVEGICTSESPVIDHQGTK

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

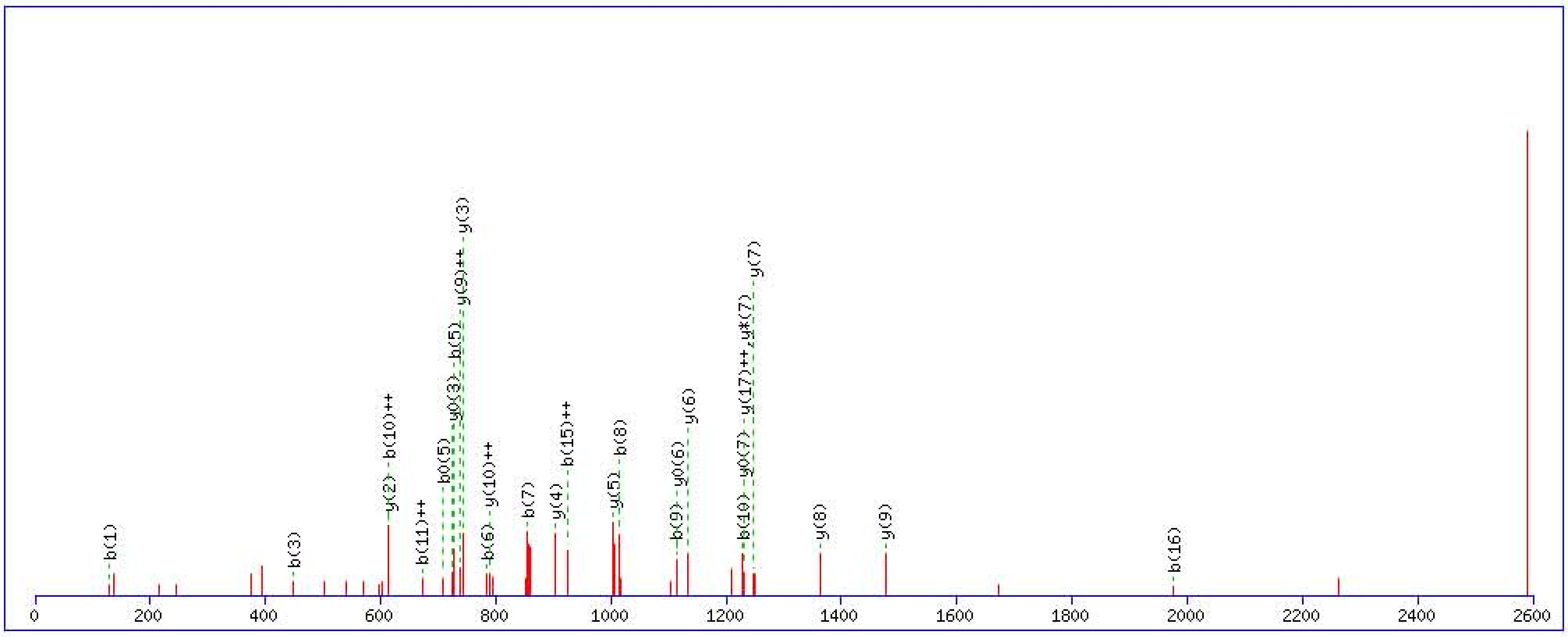
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KCCYDGACVNNDETCEQR**
Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

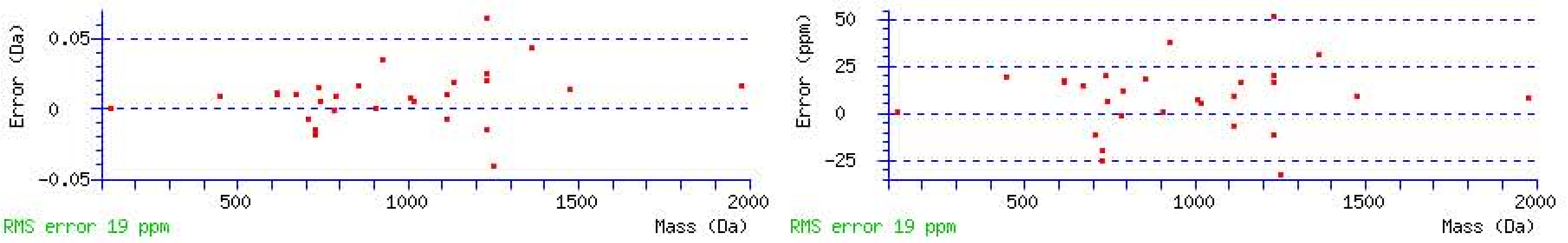
Match to Query 64336: 2589.046032 from(864.022620,3+) rtinseconds(1422) index(38149)
Title: Locus:1.1.1.2944.26 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 2589.017487
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Biotin:Thermo-21345 (Q)
Ions Score: 59 **Expect:** 1.1e-006
Matches : 28/192 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	***129.102239***	65.054757	112.075690	56.541483			K							18
2	289.132888	145.070082	272.106339	136.556808			C	2461.929800	1231.468538	2444.903251	1222.955263	2443.919235	1222.463255	17
3	***449.163537***	225.085407	432.136988	216.572132			C	2301.899151	1151.453213	2284.872602	1142.939939	2283.888586	1142.447931	16
4	612.226866	306.617071	595.200317	298.103797			Y	2141.868502	1071.437889	2124.841953	1062.924614	2123.857937	1062.432606	15
5	***727.253809***	364.130543	710.227260	355.617268	709.243244	355.125260	D	1978.805173	989.906225	1961.778624	981.392950	1960.794608	980.900942	14
6	***784.275273***	392.641275	767.248724	384.128000	766.264708	383.635992	G	1863.778230	932.392753	1846.751681	923.879479	1845.767665	923.387471	13
7	***855.312387***	428.159832	838.285838	419.646557	837.301822	419.154549	A	1806.756766	903.882021	1789.730217	895.368747	1788.746201	894.876739	12
8	***1015.343036***	508.175156	998.316487	499.661882	997.332471	499.169874	C	1735.719652	868.363464	1718.693103	859.850190	1717.709087	859.358182	11
9	***1114.411450***	557.709363	1097.384901	549.196089	1096.400885	548.704081	V	1575.689003	788.348140	1558.662454	779.834865	1557.678438	779.342857	10
10	***1228.454377***	**614.730827**	1211.427828	606.217552	1210.443812	605.725544	N	***1476.620589***	738.813933	1459.594040	730.300658	1458.610024	729.808650	9
11	1342.497304	**671.752290**	1325.470755	663.239016	1324.486739	662.747008	N	***1362.577662***	681.792469	1345.551113	673.279195	1344.567097	672.787187	8
12	1457.524247	729.265762	1440.497698	720.752487	1439.513682	720.260479	D	***1248.534735***	624.771006	1231.508186	616.257731	1230.524170	615.765723	7
13	1586.566840	793.787058	1569.540291	785.273784	1568.556275	784.781776	E	***1133.507792***	567.257534	1116.481243	558.744260	1115.497227	558.252252	6
14	1687.614519	844.310898	1670.587970	835.797623	1669.603954	835.305615	T	***1004.465199***	502.736238	987.438650	494.222963	986.454634	493.730955	5
15	1847.645168	**924.326222**	1830.618619	915.812948	1829.634603	915.320940	C	***903.417520***	452.212398	886.390971	443.699124	885.406955	443.207116	4
16	***1976.687761***	988.847519	1959.661212	980.334244	1958.677196	979.842236	E	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
17	2415.913087	1208.460182	2398.886538	1199.946907	2397.902522	1199.454899	Q	***614.344278***	307.675777	597.317729	299.162503			2
18							R	175.118952	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of KCCYDGACVNNDETCEQR
(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	2589.017487	0.028545	KCCYDGACVNNDETCEQR

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

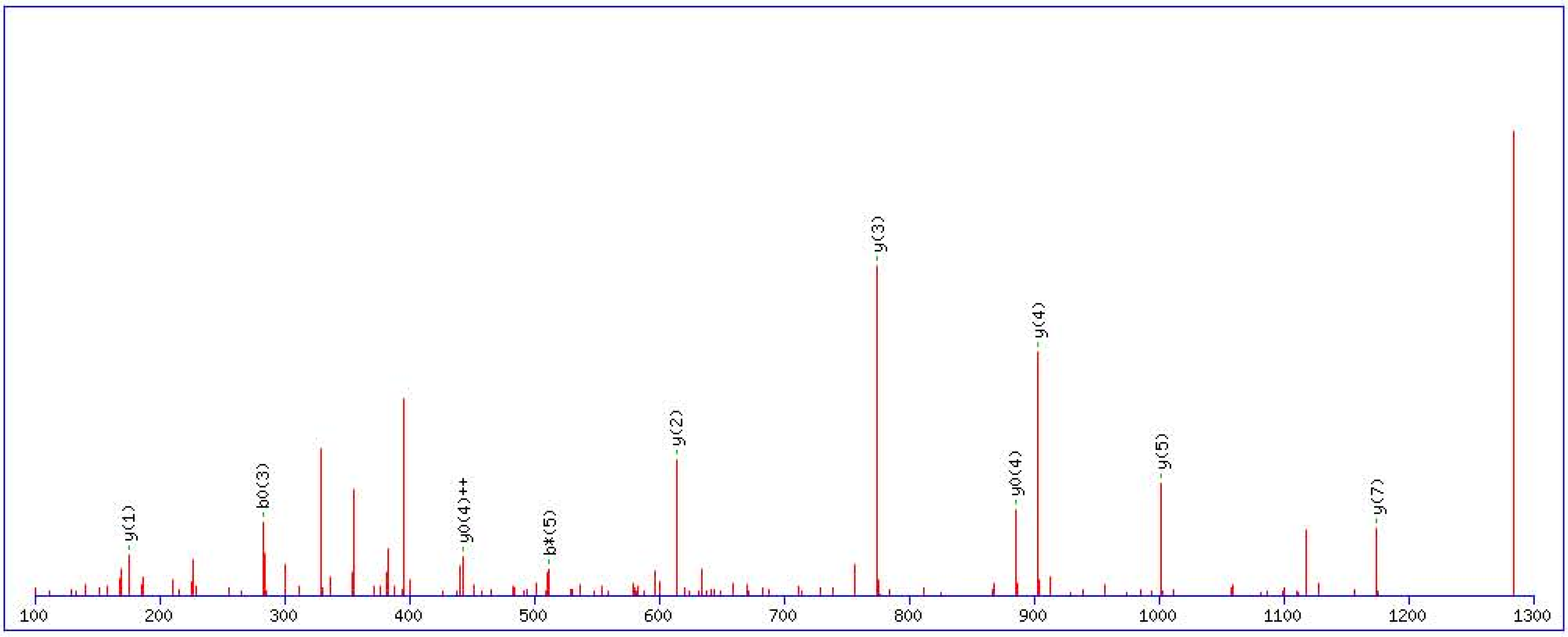
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGDVECQR**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

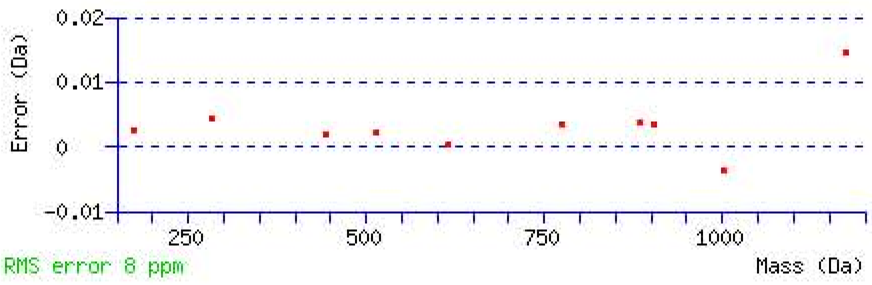
Match to Query 26972: 1301.587528 from(651.801040,2+) rtinseconds(1330) index(19715)
Title: Locus:1.1.1.2606.11 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

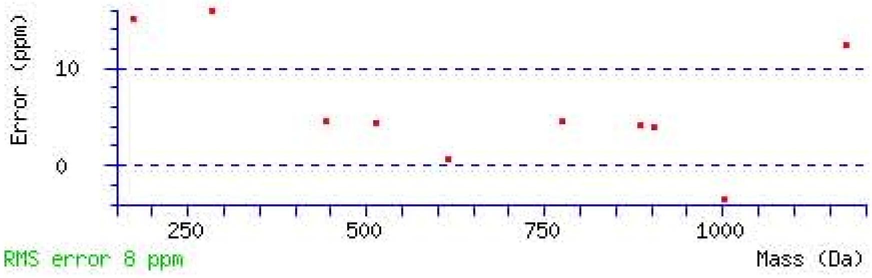
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 48  Expect: 7.8e-005
Matches : 10/74 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
48.2	1301.585648	0.001880	QGDVECQR
7.8	1301.584747	0.002781	QESPSQENIDR
7.3	1301.584763	0.002765	KATEDAEGGDGPR
6.1	1301.604721	-0.017193	QSSTYHRHMR
5.2	1301.584747	0.002781	ESENLASGDQPR
3.1	1301.585617	0.001911	ADNNMQGNK
1.1	1301.604263	-0.016735	CPAAMTVMHLR
0.5	1301.604263	-0.016735	CPAAMTVMHLR

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

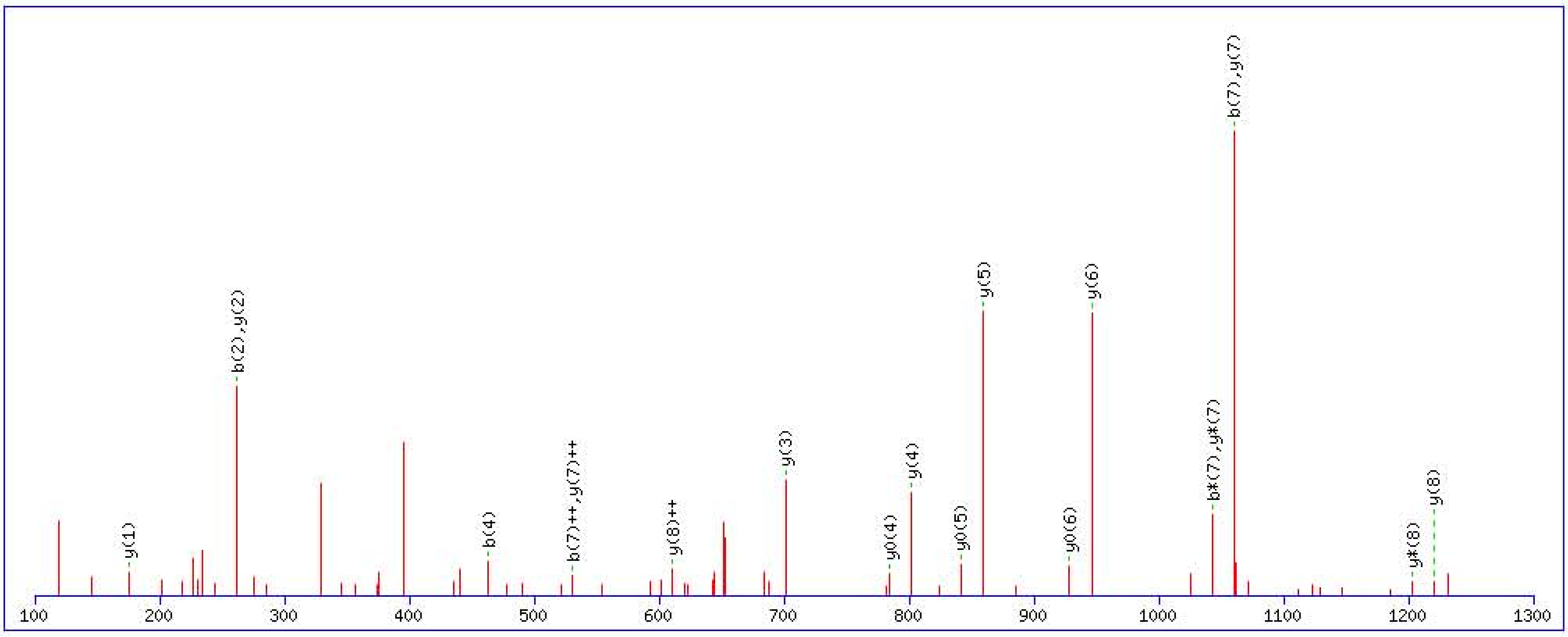
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TCNSGTQSR**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

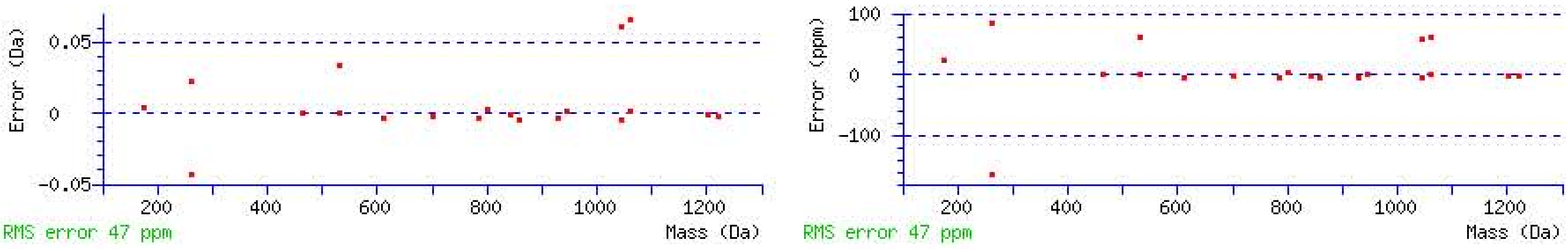
Match to Query 27363: 1320.593288 from(661.303920,2+) rtinseconds(1062) index(18207)
Title: Locus:1.1.1.2512.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1320.591461
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 2.3e-006
Matches : 20/90 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	102.054955	51.531116			84.044390	42.525833	T							9
2	**262.085604**	131.546440			244.075039	122.541158	C	***1220.551053***	610.779165	1203.524504	602.265890	1202.540488	601.773882	8
3	376.128531	188.567904	359.101982	180.054629	358.117966	179.562621	N	***1060.520404***	530.763840	1043.493855	522.250566	1042.509839	521.758558	7
4	**463.160559**	232.083917	446.134010	223.570643	445.149994	223.078635	S	***946.477477***	473.742377	929.450928	465.229102	928.466912	464.737094	6
5	520.182023	260.594650	503.155474	252.081375	502.171458	251.589367	G	***859.445449***	430.226363	842.418900	421.713088	841.434884	421.221080	5
6	621.229702	311.118489	604.203153	302.605215	603.219137	302.113207	T	***802.423985***	401.715631	785.397436	393.202356	784.413420	392.710348	4
7	**1060.455028**	530.731152	1043.428479	522.217878	1042.444463	521.725870	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
8	1147.487056	574.247166	1130.460507	565.733892	1129.476491	565.241884	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 TCNSGTQSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.0	1320.591461	0.001827	TCNSGTQSR
14.0	1320.599289	-0.006001	NELPMHHNSSR
5.8	1320.584045	0.009243	SQGCSREASPSR
5.4	1320.609192	-0.015904	MTSERAPSPSSR
5.3	1320.597946	-0.004658	LMNTNDLEESR
5.2	1320.605804	-0.012516	TSAHYEENKSR
3.6	1320.588074	0.005214	MNSAAGFSHLDR

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

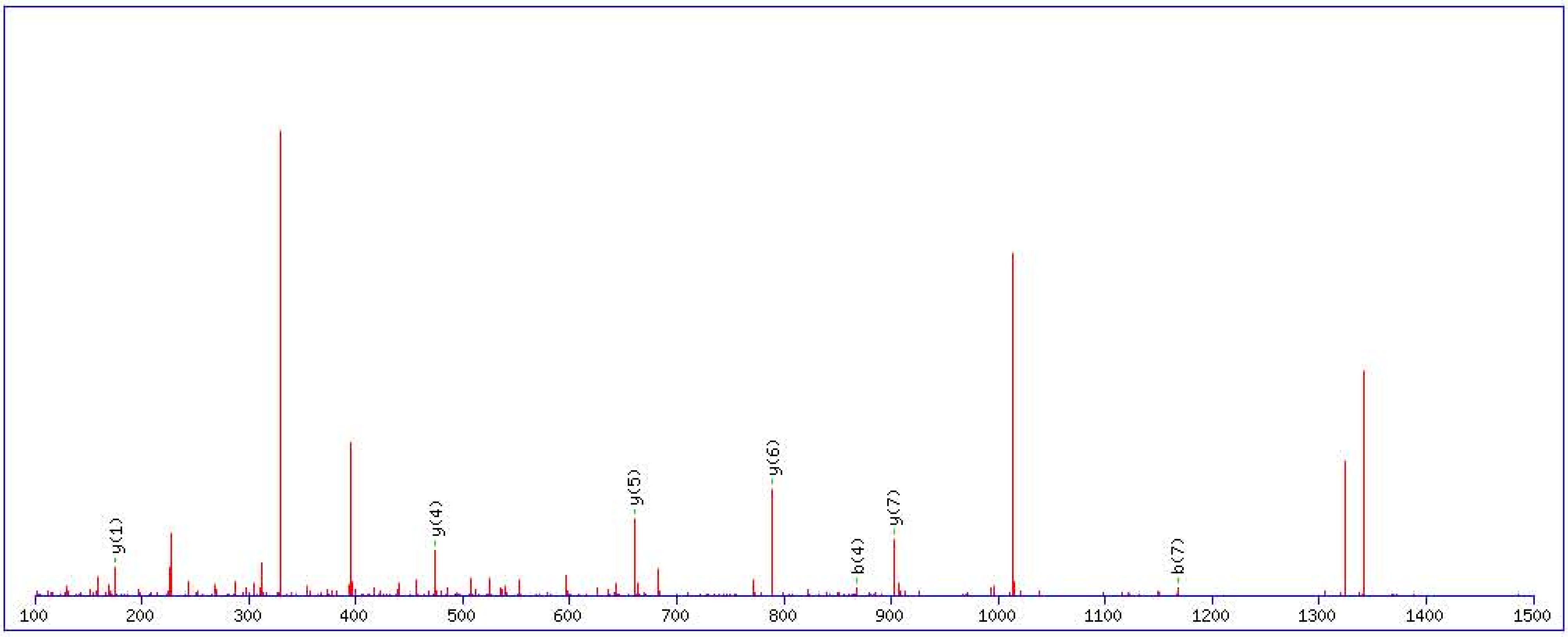
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLEWGLER**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

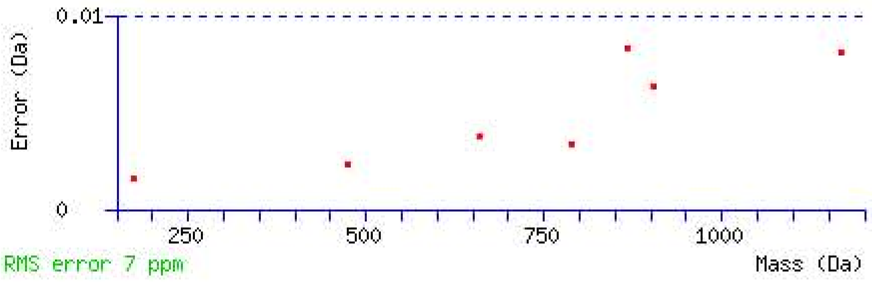
Match to Query 27869: 1340.698748 from(671.356650,2+) rtinseconds(2205) index(26192)
Title: Locus:1.1.1.2910.7 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

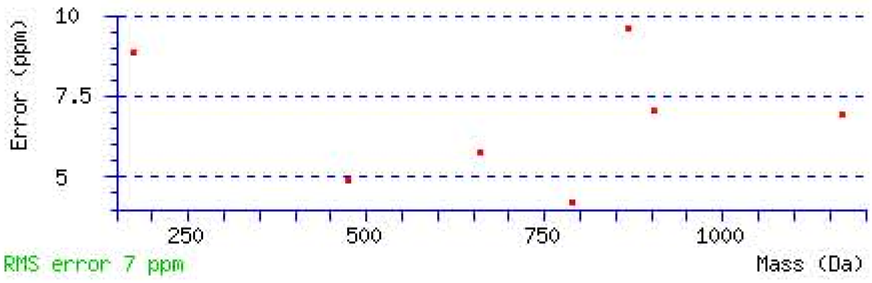
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1340.691071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.026
Matches : 7/78 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	440.232602	220.619939	423.206053	212.106664			Q							8
2	553.316666	277.161971	536.290117	268.648697			L	***902.473043***	451.740160	885.446494	443.226885	884.462478	442.734877	7
3	682.359259	341.683268	665.332710	333.169993	664.348694	332.677985	E	***789.388979***	395.198128	772.362430	386.684853	771.378414	386.192845	6
4	**868.438572**	434.722924	851.412023	426.209650	850.428007	425.717642	W	***660.346386***	330.676831	643.319837	322.163556	642.335821	321.671548	5
5	925.460036	463.233656	908.433487	454.720382	907.449471	454.228374	G	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
6	1038.544100	519.775688	1021.517551	511.262414	1020.533535	510.770406	L	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
7	**1167.586693**	584.296985	1150.560144	575.783710	1149.576128	575.291702	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.6	1340.691071	0.007677	QLEWGLER
22.9	1340.712204	-0.013456	QLDSLLGER
11.2	1340.687042	0.011706	QINDSANLR
7.3	1340.687057	0.011691	GSSPKQSPSR
7.1	1340.713531	-0.014783	SAYIRQHR
6.6	1340.691071	0.007677	QWLEDALR
6.2	1340.687042	0.011706	ALGSAAADAQR
6.2	1340.716019	-0.017271	EAKAQALQAQQR
6.0	1340.706146	-0.007398	IFNRNSGLHQR
6.0	1340.683655	0.015093	IYYLSQERNR

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

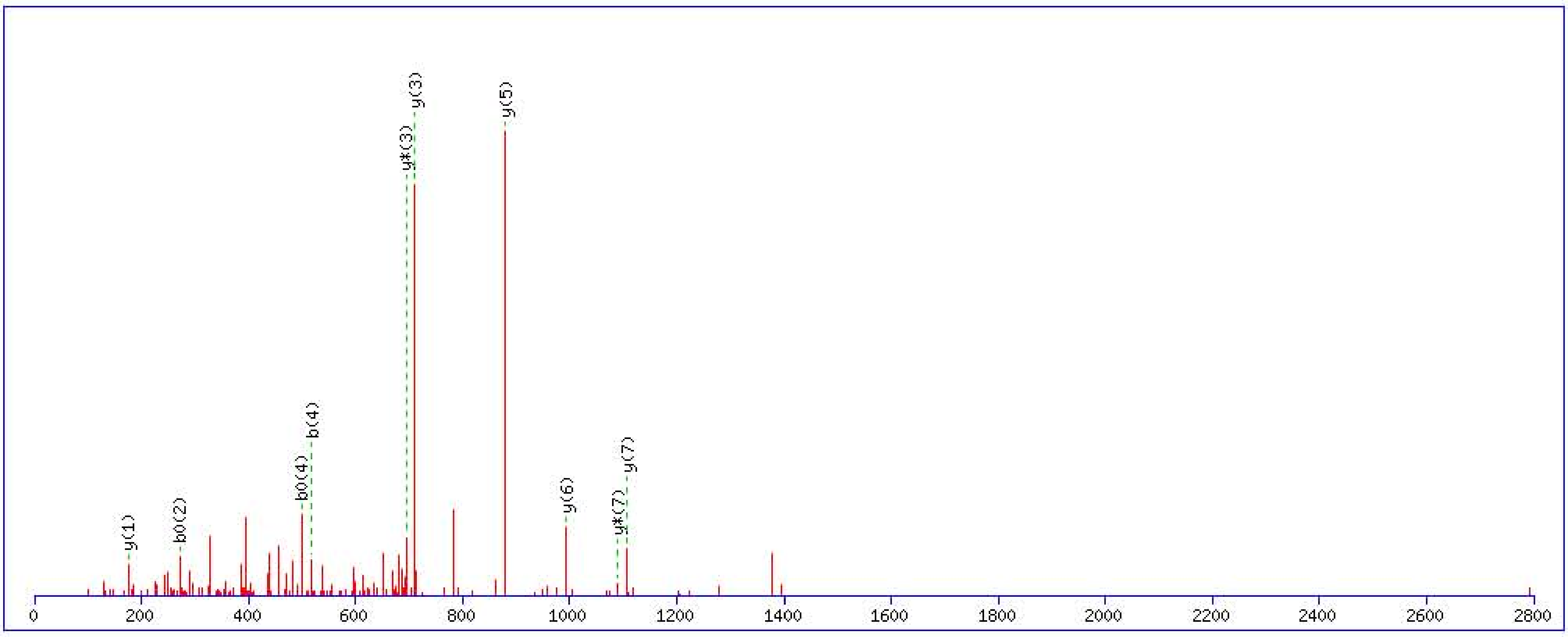
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ECNNPAPQR**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

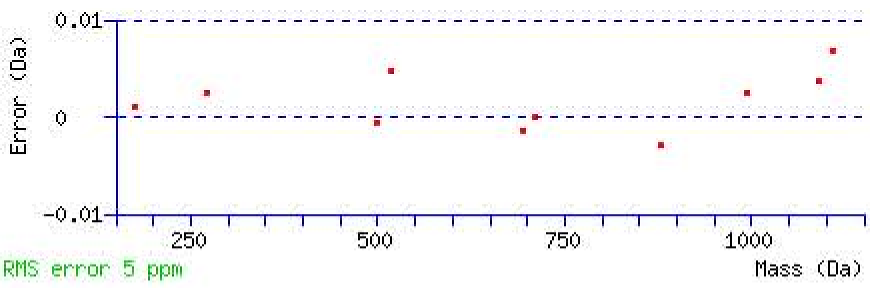
Match to Query 30627: 1395.643128 from(698.828840,2+) rtinseconds(1271) index(19364)
Title: Locus:1.1.1.2585.16 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

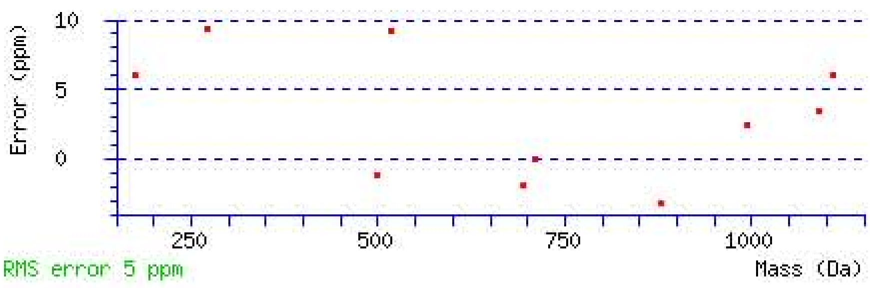
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1395.638718
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.00065
Matches : 10/76 fragment ions using 13 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	290.080518	145.543897			272.069953	136.538615	C	1267.603423	634.305350	1250.576874	625.792075	8
3	404.123445	202.565361	387.096896	194.052086	386.112880	193.560078	N	***1107.572774***	554.290025	1090.546225	545.776751	7
4	**518.166372**	259.586824	501.139823	251.073550	500.155807	250.581542	N	***993.529847***	497.268562	976.503298	488.755287	6
5	615.219136	308.113206	598.192587	299.599932	597.208571	299.107924	P	***879.486920***	440.247098	862.460371	431.733824	5
6	686.256250	343.631763	669.229701	335.118489	668.245685	334.626481	A	782.434156	391.720716	765.407607	383.207442	4
7	783.309014	392.158145	766.282465	383.644871	765.298449	383.152863	P	***711.397042***	356.202159	694.370493	347.688885	3
8	1222.534340	611.770808	1205.507791	603.257534	1204.523775	602.765526	Q	614.344278	307.675777	597.317729	299.162503	2
9							R	***175.118952***	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.4	1395.638718	0.004410	ECNNPAPQR
5.2	1395.663849	-0.020721	KMMEEAKFNPR
4.9	1395.656494	-0.013366	SSPDNSPVHGMLR
4.0	1395.645264	-0.002136	LNKDFTCDVER
2.7	1395.629974	0.013154	NKSMSQAETEGAK
2.4	1395.631332	0.011796	HLQENTQSHMR
1.8	1395.663849	-0.020721	KMMEEAKFNPR
0.5	1395.638733	0.004395	DIVNMLMHHDR

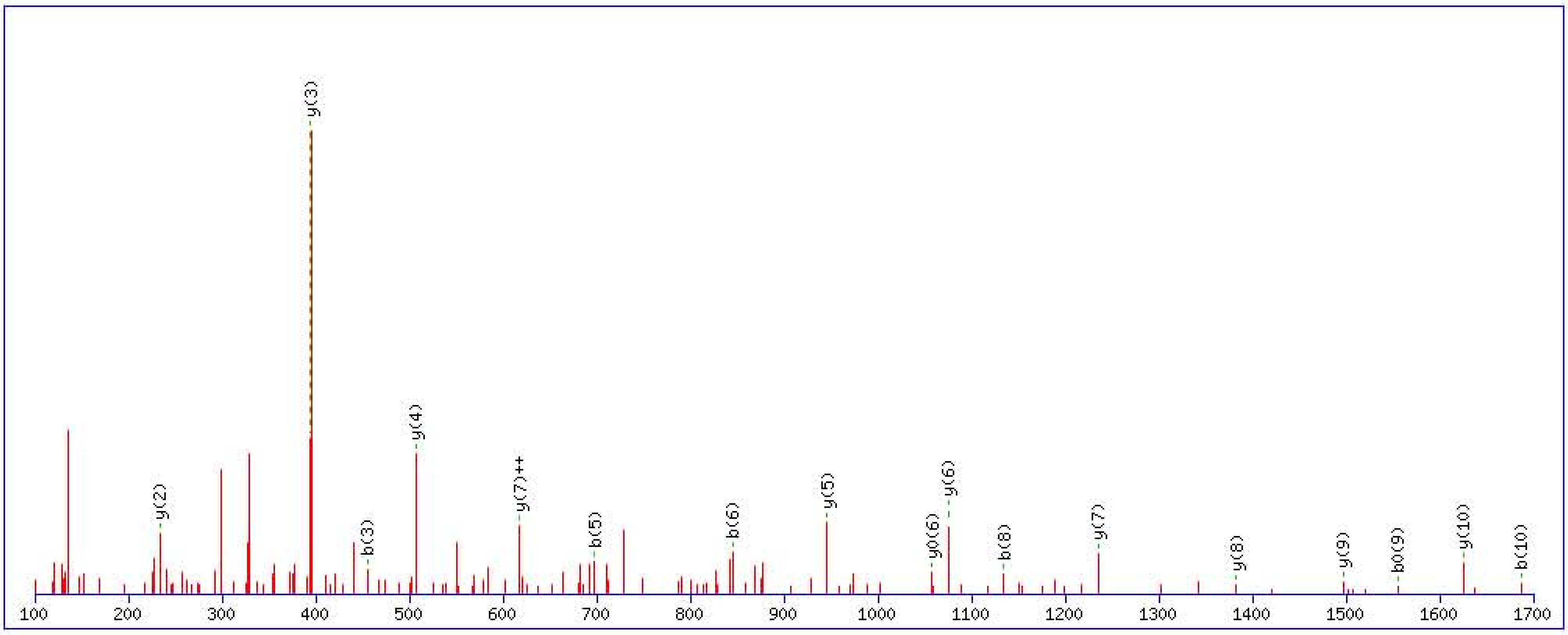
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YYQENFCEQICSK**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

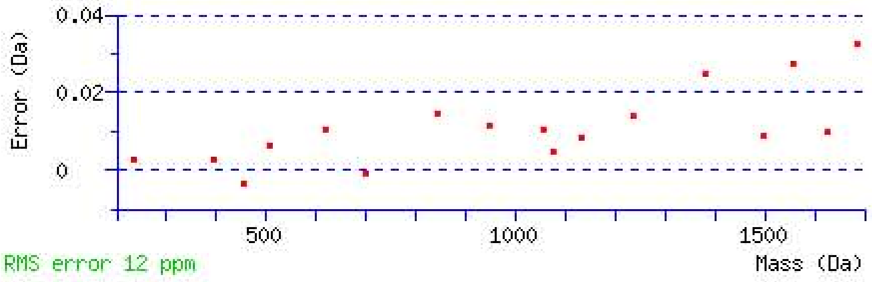
Match to Query 52672: 2078.905422 from(693.975750,3+) rtinseconds(2027) index(24876)
Title: Locus:1.1.1.2848.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

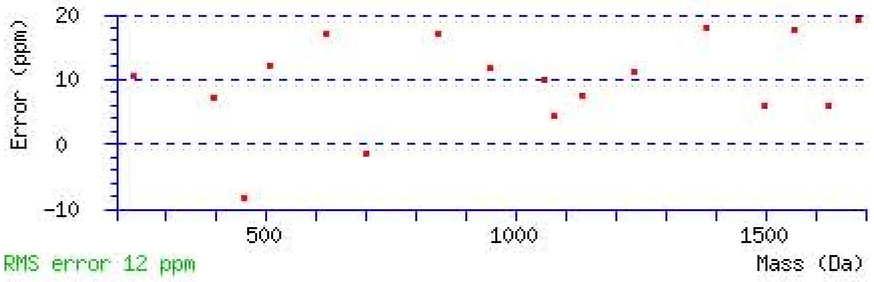
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2078.889984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00016
Matches : 17/132 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	164.070605	82.538940					Y							13
2	327.133934	164.070605					Y	1916.833954	958.920615	1899.807405	950.407341	1898.823389	949.915333	12
3	**455.192512**	228.099894	438.165963	219.586620			Q	1753.770625	877.388951	1736.744076	868.875676	1735.760060	868.383668	11
4	584.235105	292.621191	567.208556	284.107916	566.224540	283.615908	E	***1625.712047***	813.359662	1608.685498	804.846387	1607.701482	804.354379	10
5	**698.278032**	349.642654	681.251483	341.129380	680.267467	340.637372	N	***1496.669454***	748.838365	1479.642905	740.325091	1478.658889	739.833083	9
6	**845.346446**	423.176861	828.319897	414.663587	827.335881	414.171579	F	***1382.626527***	691.816902	1365.599978	683.303627	1364.615962	682.811619	8
7	1005.377095	503.192186	988.350546	494.678911	987.366530	494.186903	C	***1235.558113***	618.282695	1218.531564	609.769420	1217.547548	609.277412	7
8	**1134.419688**	567.713482	1117.393139	559.200208	1116.409123	558.708200	E	***1075.527464***	538.267370	1058.500915	529.754096	1057.516899	529.262088	6
9	1573.645014	787.326145	1556.618465	778.812871	1555.634449	778.320863	Q	***946.484871***	473.746074	929.458322	465.232799	928.474306	464.740791	5
10	**1686.729078**	843.868177	1669.702529	835.354903	1668.718513	834.862895	I	***507.259545***	254.133411	490.232996	245.620136	489.248980	245.128128	4
11	1846.759727	923.883502	1829.733178	915.370227	1828.749162	914.878219	C	***394.175481***	197.591379	377.148932	189.078104	376.164916	188.586096	3
12	1933.791755	967.399516	1916.765206	958.886241	1915.781190	958.394233	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 YYQENFCEQICSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	2078.889984	0.015438	YYQENFCEQICSK

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

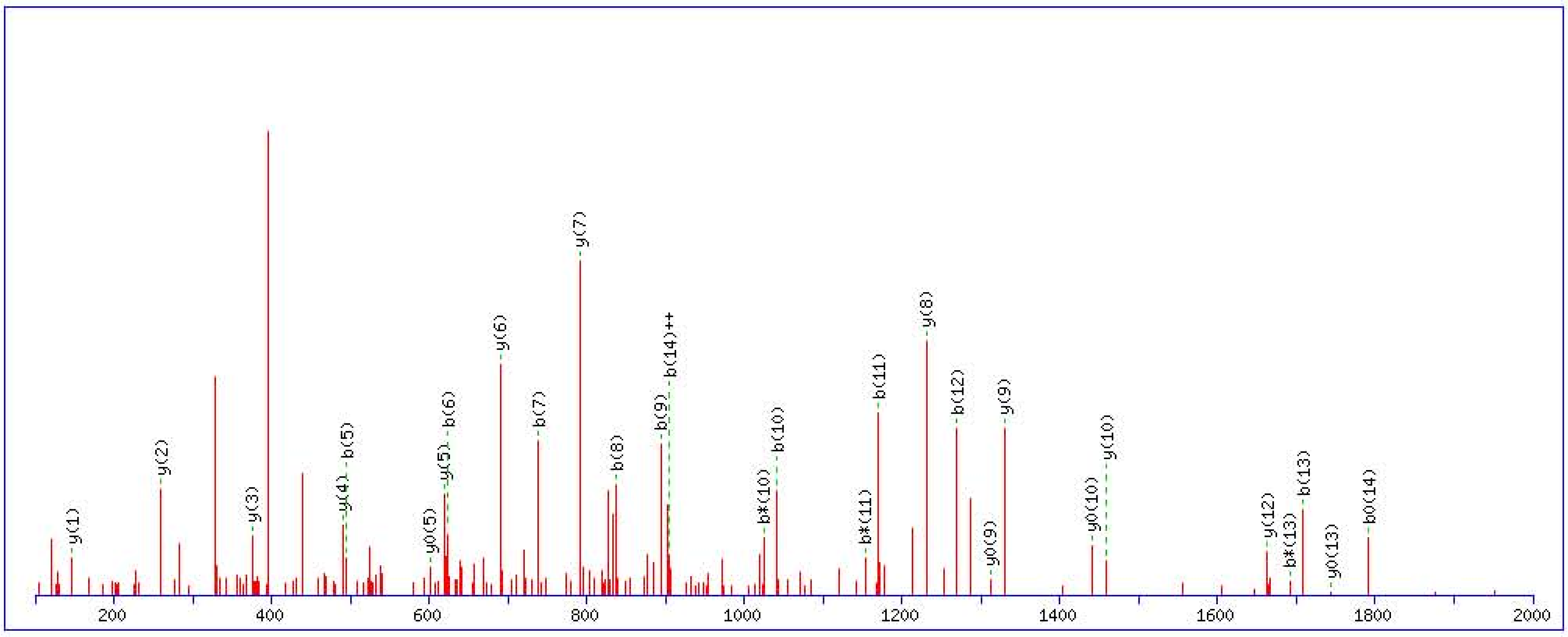
{MATRIX SCIENCE} # Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPANLENVGFEVQTAEDDLK**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

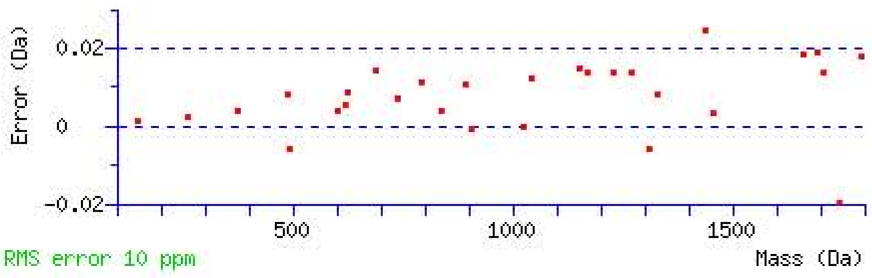
Match to Query 63051: 2498.268222 from(833.763350,3+) rtinseconds(2630) index(28875)
Title: Locus:1.1.1.3057.7 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

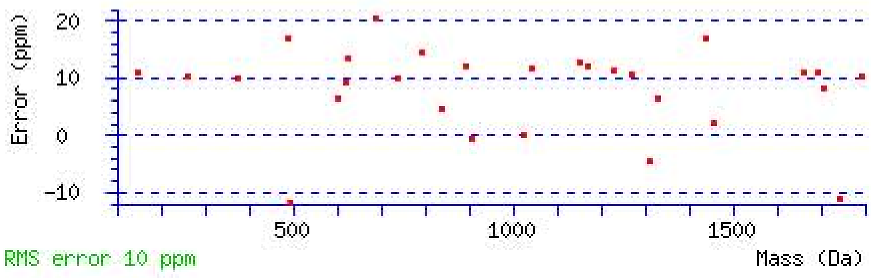
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2498.236282
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 3.6e-006
Matches : 29/208 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	100.075690	50.541483					V							20
2	197.128454	99.067865					P	2400.175154	1200.591215	2383.148605	1192.077940	2382.164589	1191.585932	19
3	268.165568	134.586422					A	2303.122390	1152.064833	2286.095841	1143.551558	2285.111825	1143.059550	18
4	382.208495	191.607885	365.181946	183.094611			N	2232.085276	1116.546276	2215.058727	1108.033001	2214.074711	1107.540993	17
5	***495.292559***	248.149917	478.266010	239.636643			L	2118.042349	1059.524812	2101.015800	1051.011538	2100.031784	1050.519530	16
6	***624.335152***	312.671214	607.308603	304.157940	606.324587	303.665932	E	2004.958285	1002.982781	1987.931736	994.469506	1986.947720	993.977498	15
7	***738.378079***	369.692678	721.351530	361.179403	720.367514	360.687395	N	1875.915692	938.461484	1858.889143	929.948210	1857.905127	929.456202	14
8	***837.446493***	419.226885	820.419944	410.713610	819.435928	410.221602	V	1761.872765	881.440021	1744.846216	872.926746	1743.862200	872.434738	13
9	***894.467957***	447.737617	877.441408	439.224342	876.457392	438.732334	G	***1662.804351***	831.905814	1645.777802	823.392539	1644.793786	822.900531	12
10	***1041.536371***	521.271824	1024.509822	512.758549	1023.525806	512.266541	F	1605.782887	803.395082	1588.756338	794.881807	1587.772322	794.389799	11
11	***1170.578964***	585.793120	1153.552415	577.279846	1152.568399	576.787838	E	***1458.714473***	729.860875	1441.687924	721.347600	1440.703908	720.855592	10
12	***1269.647378***	635.327327	1252.620829	626.814053	1251.636813	626.322045	V	***1329.671880***	665.339578	1312.645331	656.826304	1311.661315	656.334296	9
13	***1708.872704***	854.939990	1691.846155	846.426716	1690.862139	845.934708	Q	***1230.603466***	615.805371	1213.576917	607.292097	1212.592901	606.800089	8
14	1809.920383	905.463830	1792.893834	896.950555	1791.909818	896.458547	T	***791.378140***	396.192708	774.351591	387.679434	773.367575	387.187426	7
15	1880.957497	940.982387	1863.930948	932.469112	1862.946932	931.977104	A	***690.330461***	345.668869	673.303912	337.155594	672.319896	336.663586	6
16	2010.000090	1005.503683	1992.973541	996.990409	1991.989525	996.498401	E	***619.293347***	310.150312	602.266798	301.637037	601.282782	301.145029	5
17	2125.027033	1063.017154	2108.000484	1054.503880	2107.016468	1054.011872	D	***490.250754***	245.629015	473.224205	237.115740	472.240189	236.623732	4
18	2240.053976	1120.530626	2223.027427	1112.017351	2222.043411	1111.525343	D	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
19	2353.138040	1177.072658	2336.111491	1168.559383	2335.127475	1168.067375	L	***260.196868***	130.602072	243.170319	122.088798			2
20							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.1	2498.236282	0.031940	VPANLENVGFEVQTAEDDLK

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

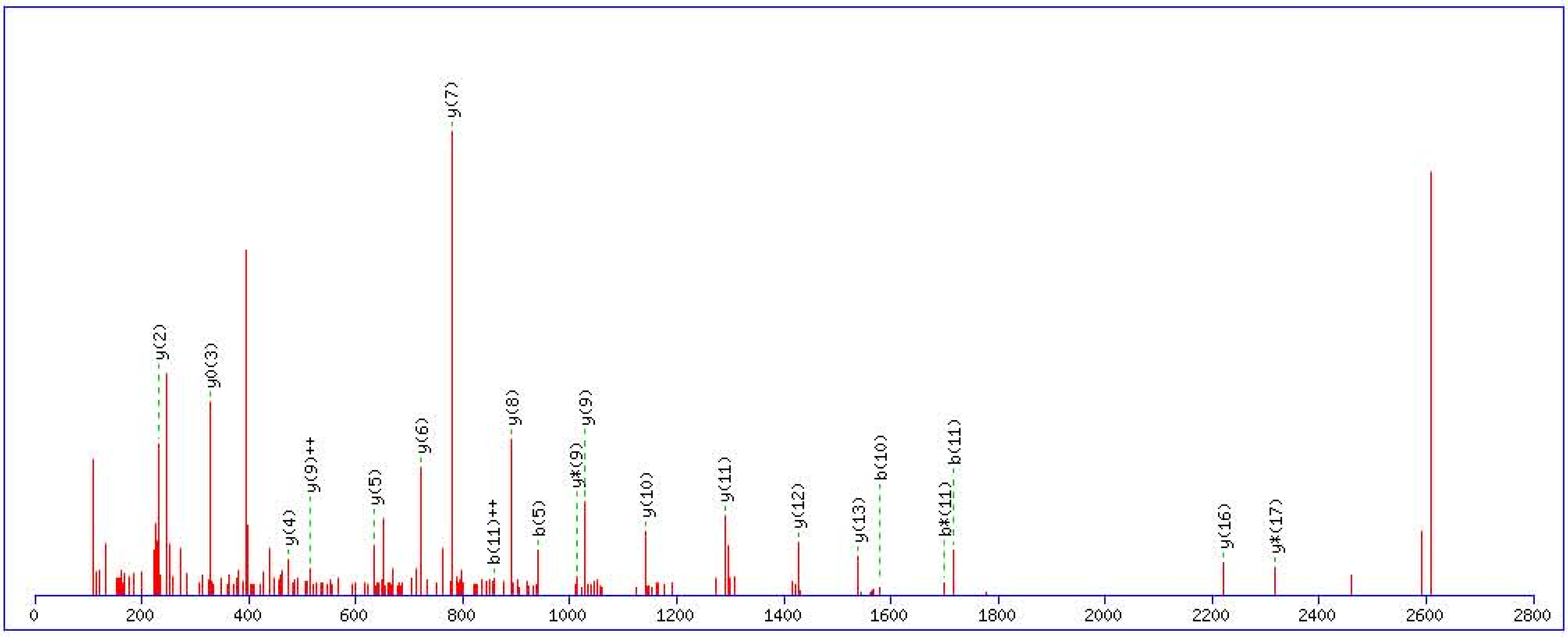
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CLNNQQLHFLHIGSCQDGR**
Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

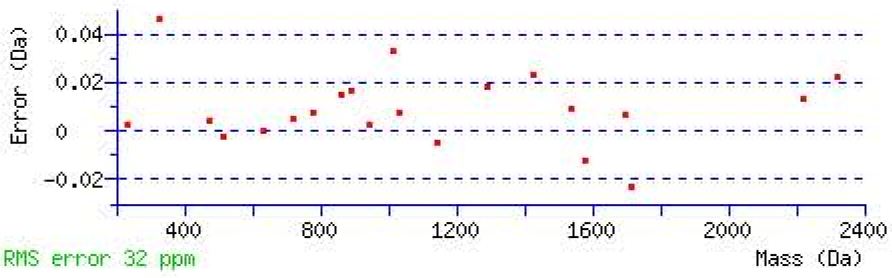
Match to Query 64623: 2607.238016 from(652.816780,4+) rtinseconds(1981) index(24548)
Title: Locus:1.1.1.2832.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

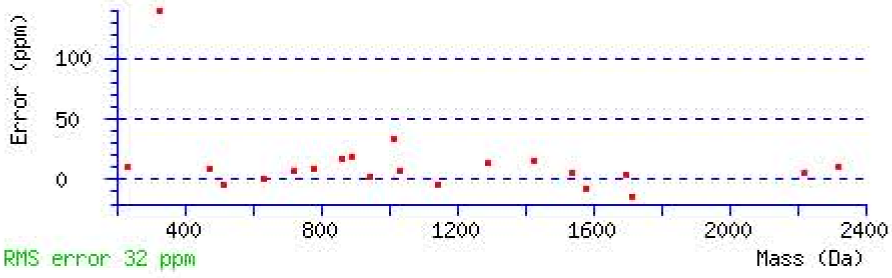
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2607.225708
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 76 **Expect:** 9.7e-008
Matches : 21/182 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	161.037925	81.022600					C							19
2	274.121989	137.564632					L	2448.202330	1224.604803	2431.175781	1216.091528	2430.191765	1215.599520	18
3	388.164916	194.586096	371.138367	186.072822			N	2335.118266	1168.062771	2318.091717	1159.549496	2317.107701	1159.057488	17
4	502.207843	251.607560	485.181294	243.094285			N	***2221.075339***	1111.041307	2204.048790	1102.528033	2203.064774	1102.036025	16
5	**941.433169**	471.220223	924.406620	462.706948			Q	2107.032412	1054.019844	2090.005863	1045.506569	2089.021847	1045.014561	15
6	1069.491747	535.249512	1052.465198	526.736237			Q	1667.807086	834.407181	1650.780537	825.893906	1649.796521	825.401898	14
7	1182.575811	591.791543	1165.549262	583.278269			L	***1539.748508***	770.377892	1522.721959	761.864617	1521.737943	761.372609	13
8	1319.634723	660.320999	1302.608174	651.807725			H	***1426.664444***	713.835860	1409.637895	705.322585	1408.653879	704.830577	12
9	1466.703137	733.855207	1449.676588	725.341932			F	***1289.605532***	645.306404	1272.578983	636.793129	1271.594967	636.301121	11
10	**1579.787201**	790.397238	1562.760652	781.883964			L	***1142.537118***	571.772197	1125.510569	563.258922	1124.526553	562.766914	10
11	**1716.846113**	858.926694	1699.819564	850.413420			H	***1029.453054***	515.230165	1012.426505	506.716890	1011.442489	506.224882	9
12	1829.930177	915.468726	1812.903628	906.955452			I	***892.394142***	446.700709	875.367593	438.187434	874.383577	437.695426	8
13	1886.951641	943.979458	1869.925092	935.466184			G	***779.310078***	390.158677	762.283529	381.645402	761.299513	381.153394	7
14	1973.983669	987.495472	1956.957120	978.982198	1955.973104	978.490190	S	***722.288614***	361.647945	705.262065	353.134671	704.278049	352.642663	6
15	2134.014318	1067.510797	2116.987769	1058.997522	2116.003753	1058.505514	C	***635.256586***	318.131931	618.230037	309.618656	617.246021	309.126648	5
16	2262.072896	1131.540086	2245.046347	1123.026811	2244.062331	1122.534803	Q	***475.225937***	238.116606	458.199388	229.603332	457.215372	229.111324	4
17	2377.099839	1189.053557	2360.073290	1180.540283	2359.089274	1180.048275	D	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	3
18	2434.121303	1217.564289	2417.094754	1209.051015	2416.110738	1208.559007	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 CLNNQQLHFLHIGSCQDGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.5	2607.225708	0.012308	CLNNQQLHFLHIGSCQDGR
73.1	2607.225708	0.012308	CLNNQQLHFLHIGSCQDGR
0.8	2607.235611	0.002405	AQTTVTCMENGWSPTPRCIRVK

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

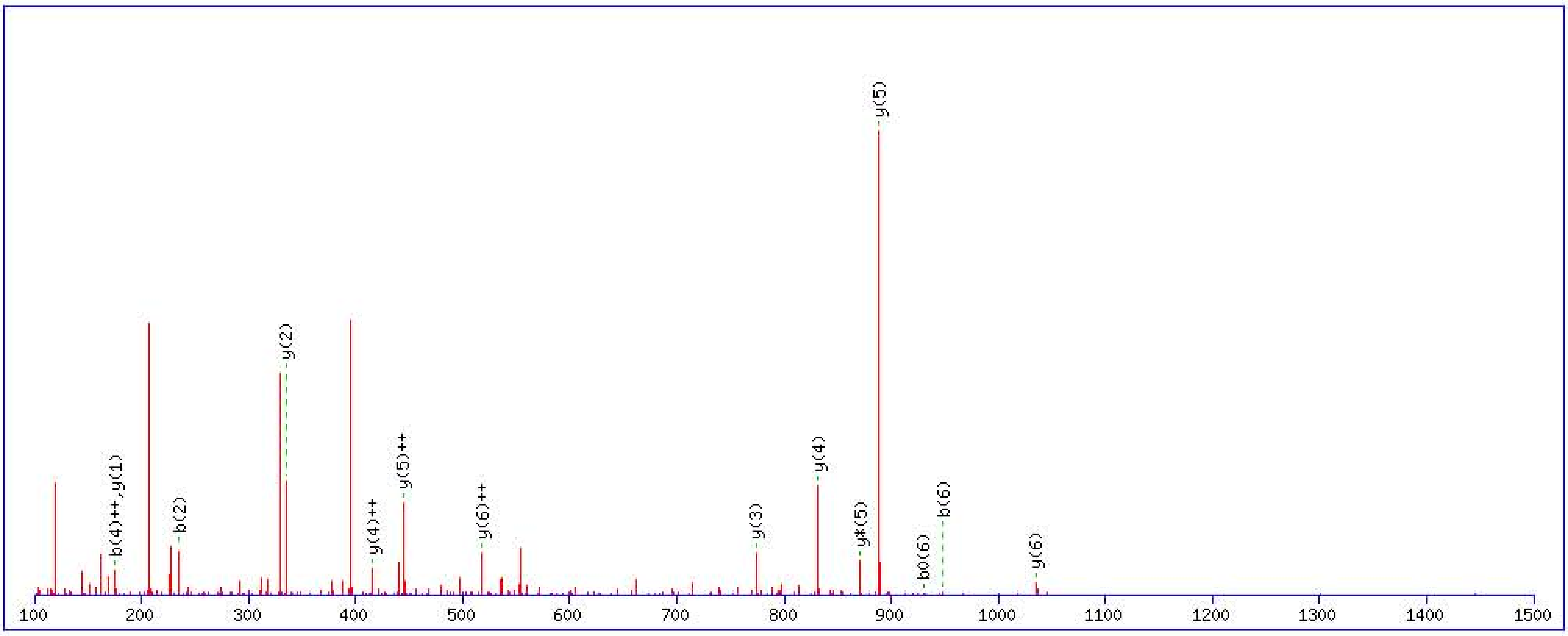
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFGGQCR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

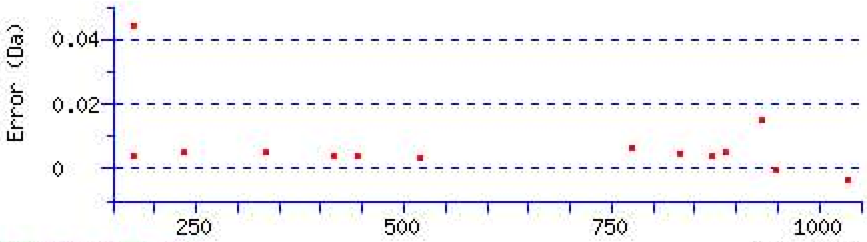
Match to Query 20167: 1121.515008 from(561.764780,2+) rtinseconds(1514) index(3415)
Title: Locus:1.1.1.2781.12 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

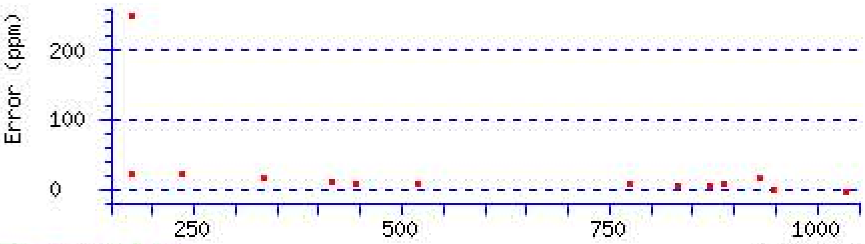


```
Monoisotopic mass of neutral peptide Mr(calc): 1121.511032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.0059
Matches : 14/52 fragment ions using 30 most intense peaks   (help)
```

#	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



RMS error 67 ppm



RMS error 67 ppm

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
27.9	1121.511032	0.003976	SFGGQCR
4.0	1121.500259	0.014749	HPGFHQEDR
1.5	1121.502274	0.012734	MSVEEQIDR

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

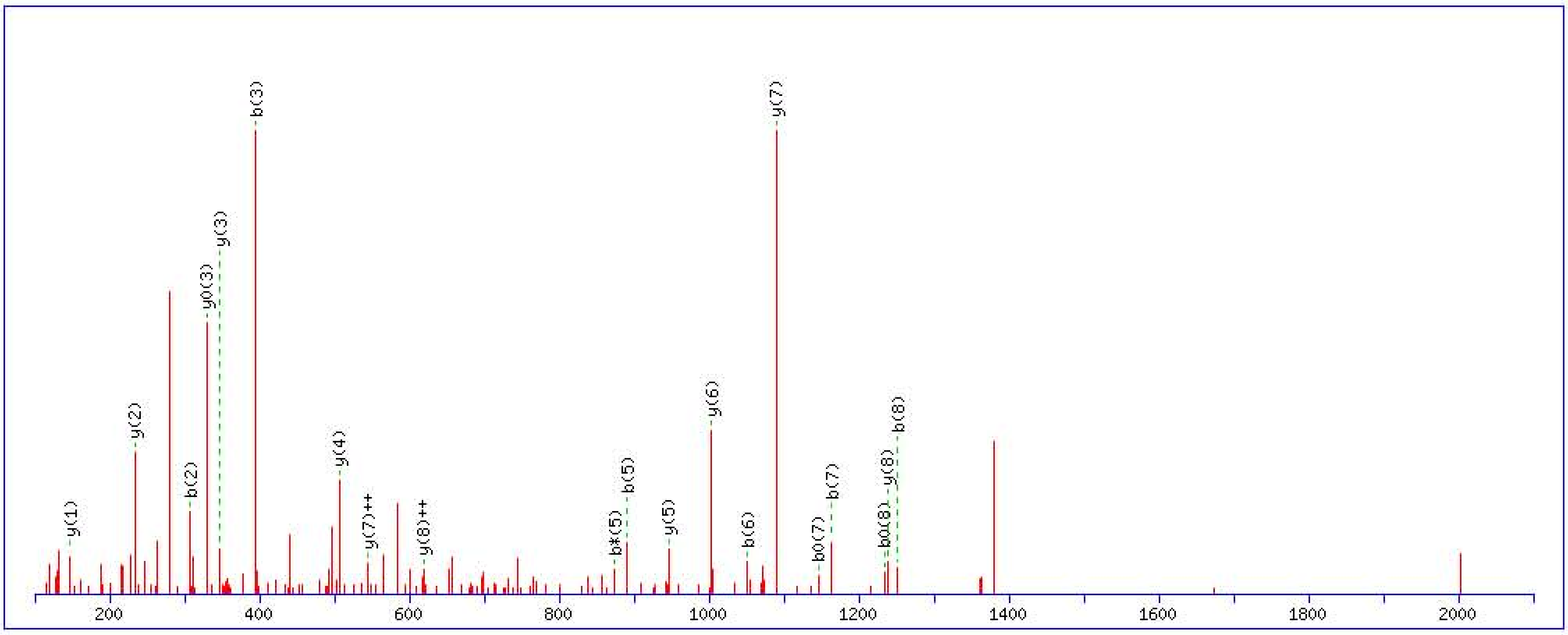
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **CFSGQCISK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

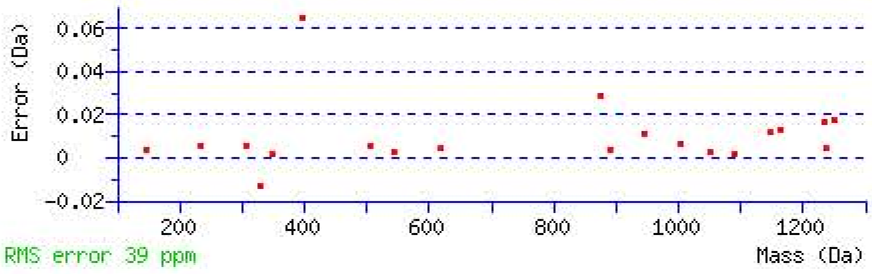
Match to Query 30650: 1396.635748 from(699.325150,2+) rtinseconds(1644) index(4189)
Title: Locus:1.1.1.2826.11 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

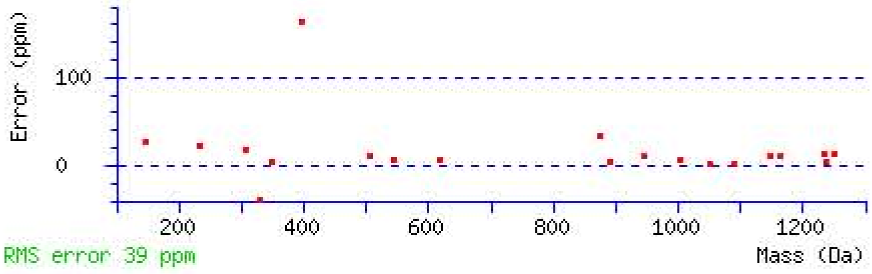
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 50 **Expect:** 8.6e-005
Matches : 20/82 fragment ions using 39 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
50.1	1396.630157	0.005591	CFSGQCISK
15.9	1396.629272	0.006476	QLSQAEATDFCK
2.5	1396.629257	0.006491	CPSSYNILDNSK
2.2	1396.629257	0.006491	FDNLMNQKEDK

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

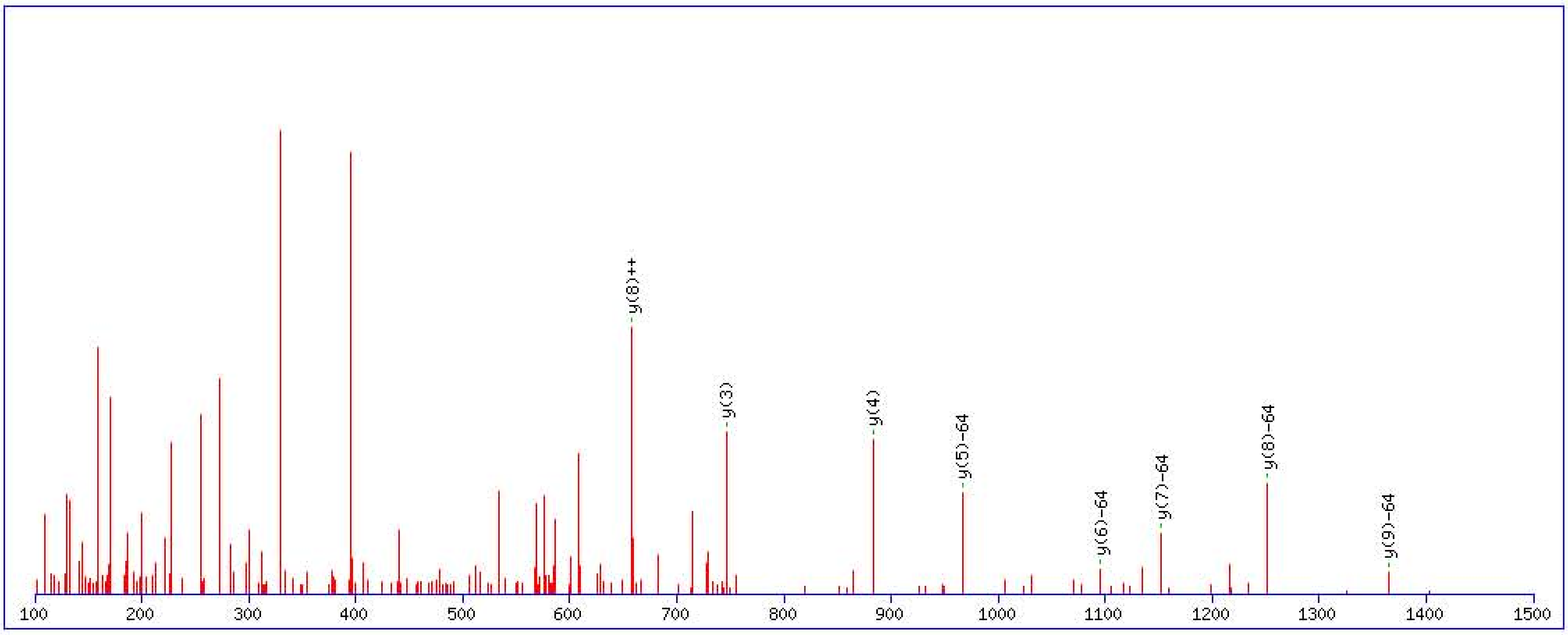
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLVGEMHCQK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

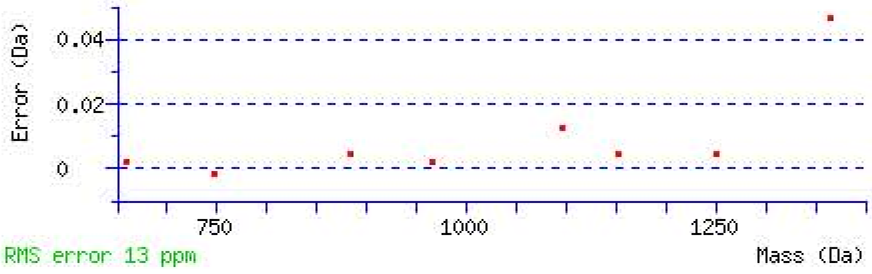
Match to Query 39330: 1613.759232 from(538.927020,3+) rtinseconds(1652) index(4224)
Title: Locus:1.1.1.2829.8 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

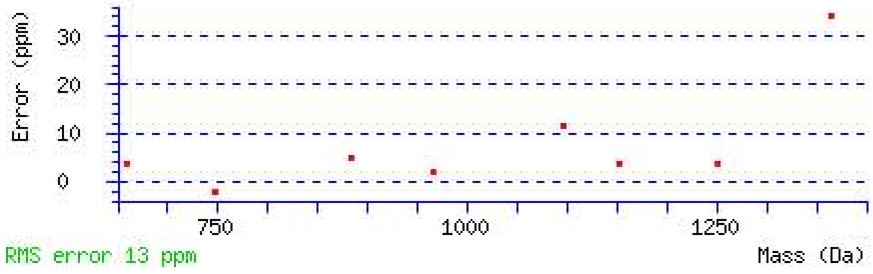
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1613.751663
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.003
Matches : 8/120 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	187.086589	94.046932					W							10
2	300.170653	150.588965					L	*1364.681341*	682.844309	1347.654792	674.331034	1346.670776	673.839026	9
3	399.239067	200.123172					V	*1251.597277*	626.302277	1234.570728	617.789002	1233.586712	617.296994	8
4	456.260531	228.633904					G	*1152.528863*	576.768070	1135.502314	568.254795	1134.518298	567.762787	7
5	585.303124	293.155200			567.292559	284.149918	E	*1095.507399*	548.257338	1078.480850	539.744063	1077.496834	539.252055	6
6	668.340239	334.673758			650.329674	325.668475	M	*966.464806*	483.736041	949.438257	475.222766			5
7	805.399151	403.203214			787.388586	394.197931	H	*883.427691*	442.217484	866.401142	433.704209			4
8	965.429800	483.218538			947.419235	474.213255	C	*746.368779*	373.688028	729.342230	365.174753			3
9	1404.655126	702.831201	1387.628577	694.317927	1386.644561	693.825919	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 WLVGEMHCQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.0	1613.751663	0.007569	WLVGEMHCQK

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

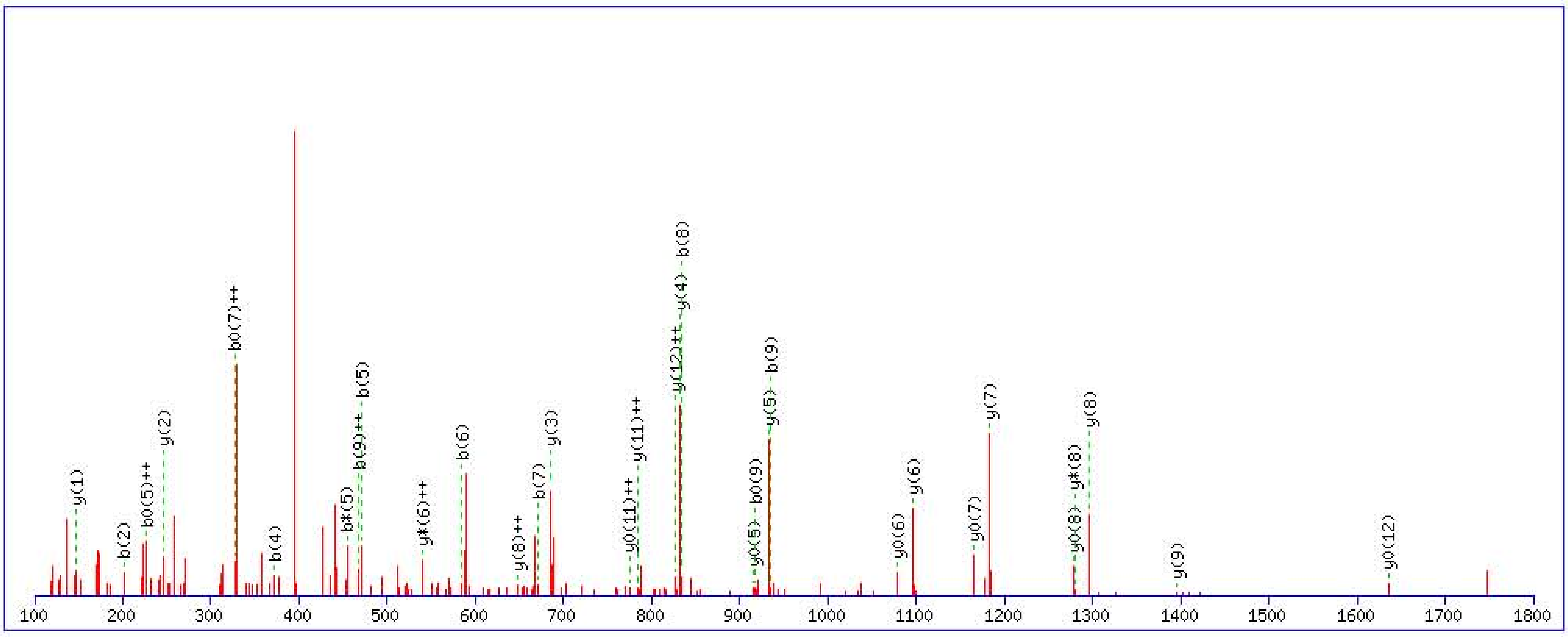
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSGNVLSYTFQVK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

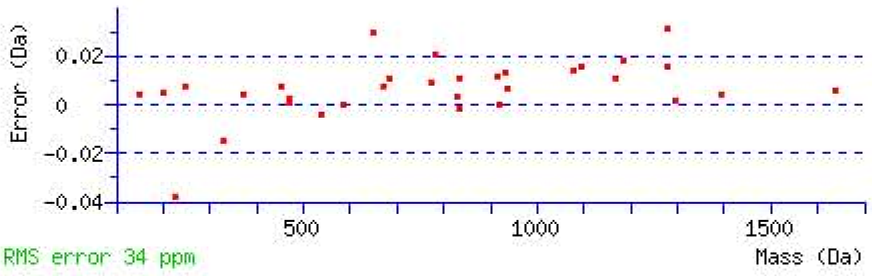
Match to Query 44316: 1765.961682 from(589.661170,3+) rtinseconds(2461) index(9479)
Title: Locus:1.1.1.3111.6 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

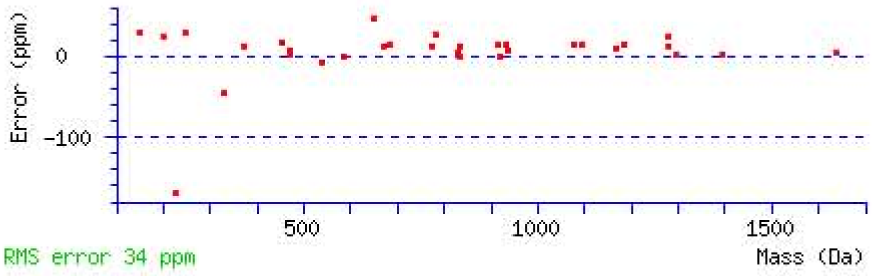
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 29  Expect: 0.006
Matches : 32/128 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	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
28.9	1765.943680	0.018002	LSGNVLSYTFQVK
5.2	1765.950882	0.010800	VTGNVSKKTNYLVMGR

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

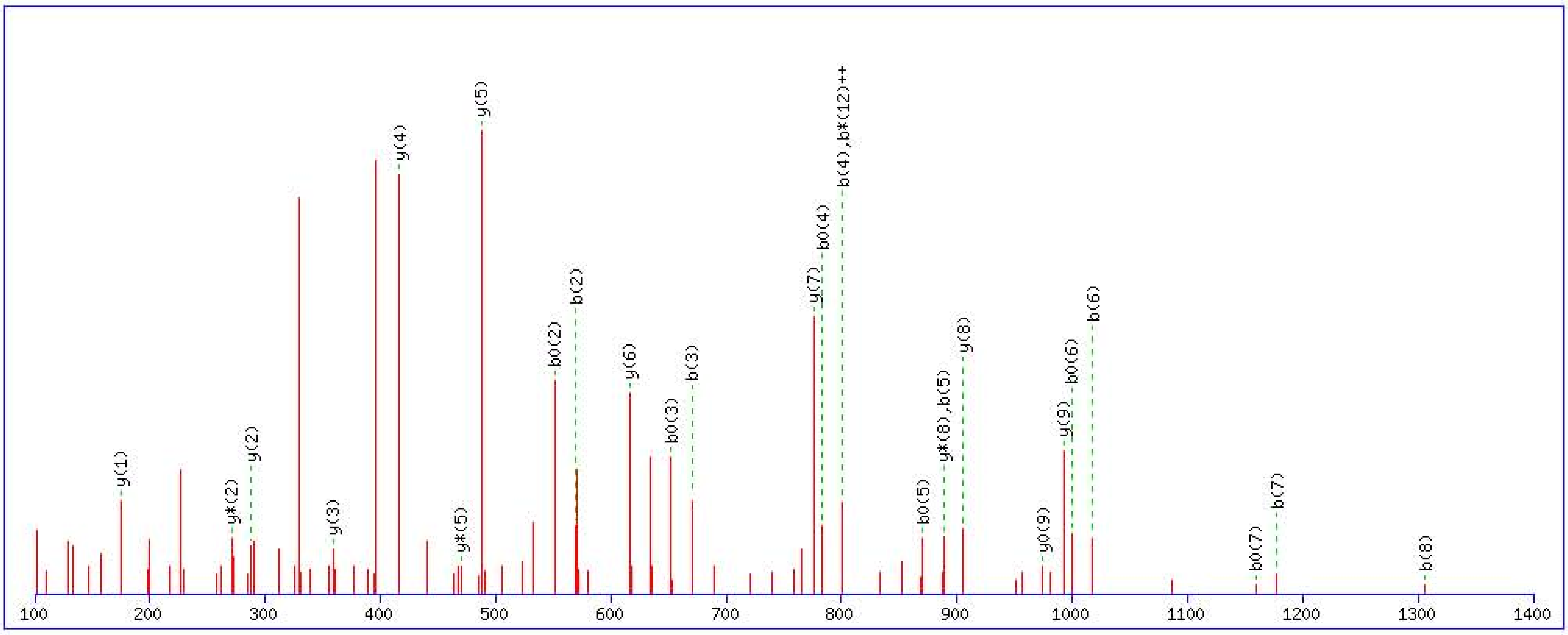
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQTMSECEAGALR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

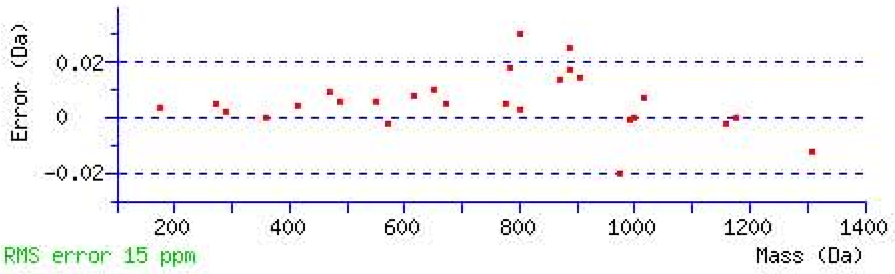
Match to Query 45076: 1791.804882 from(598.275570,3+) rtinseconds(1743) index(4840)
Title: Locus:1.1.1.2861.10 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

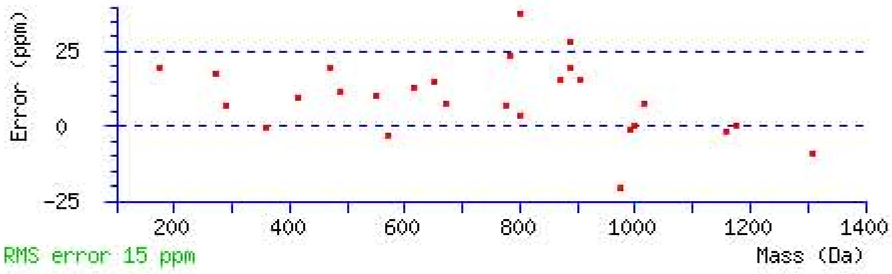
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1791.795349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 2.1e-005
Matches : 27/132 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							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





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
56.7	1791.795349	0.009533	EQTMSECEAGALR

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

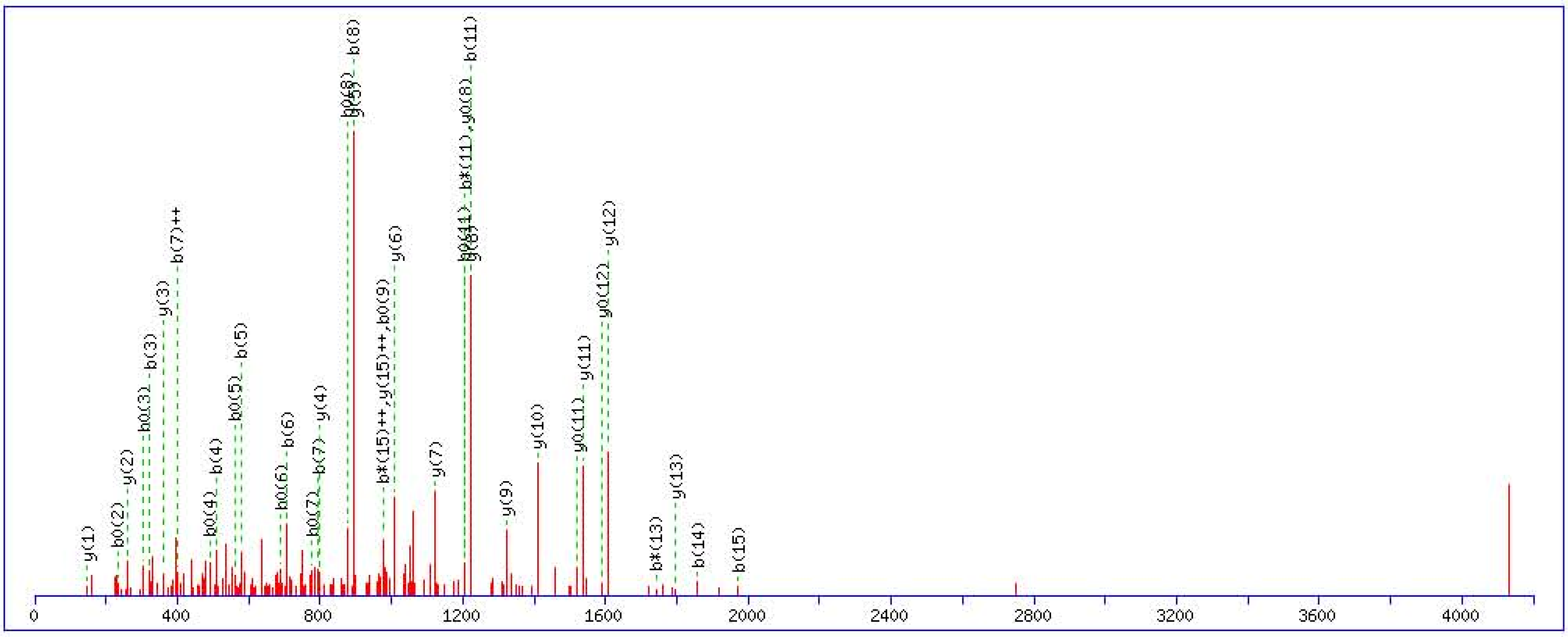
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSAWAESVTNLPQVIK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

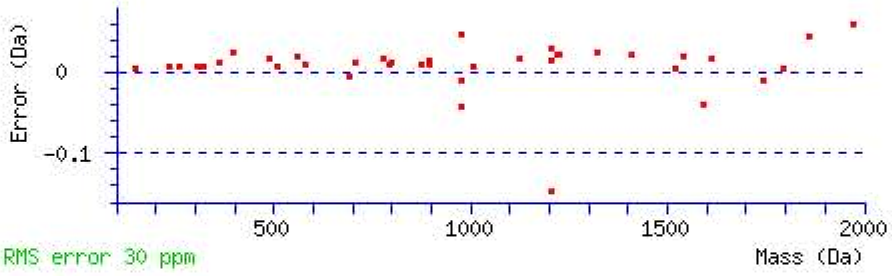
Match to Query 53443: 2116.132128 from(1059.073340,2+) rtinseconds(2572) index(10181)
Title: Locus:1.1.1.3149.26 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

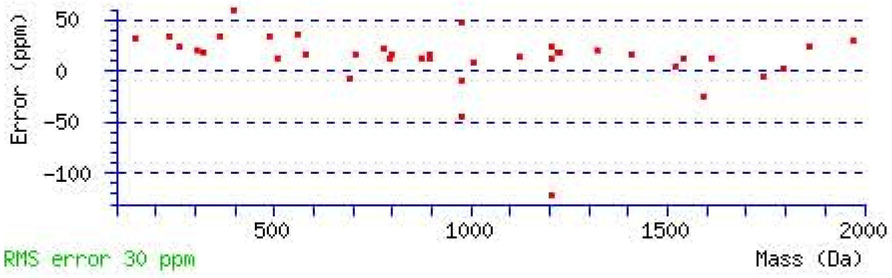
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2116.102676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 1e-006
Matches : 39/146 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	164.070605	82.538940					Y							16
2	251.102633	126.054954			233.092068	117.049672	S	1954.046646	977.526961	1937.020097	969.013687	1936.036081	968.521679	15
3	**322.139747**	161.573512			304.129182	152.568229	A	1867.014618	934.010947	1849.988069	925.497673	1849.004053	925.005665	14
4	**508.219060**	254.613168			490.208495	245.607886	W	***1795.977504***	898.492390	1778.950955	889.979116	1777.966939	889.487108	13
5	**579.256174**	290.131725			561.245609	281.126443	A	***1609.898191***	805.452734	1592.871642	796.939459	1591.887626	796.447451	12
6	**708.298767**	354.653022			690.288202	345.647739	E	***1538.861077***	769.934177	1521.834528	761.420902	1520.850512	760.928894	11
7	**795.330795**	398.169036			777.320230	389.163753	S	***1409.818484***	705.412880	1392.791935	696.899606	1391.807919	696.407598	10
8	**894.399209**	447.703243			876.388644	438.697960	V	***1322.786456***	661.896866	1305.759907	653.383592	1304.775891	652.891584	9
9	995.446888	498.227082			977.436323	489.221800	T	***1223.718042***	612.362659	1206.691493	603.849385	1205.707477	603.357377	8
10	1109.489815	555.248546	1092.463266	546.735271	1091.479250	546.243263	N	***1122.670363***	561.838820	1105.643814	553.325545			7
11	**1222.573879**	611.790578	1205.547330	603.277303	1204.563314	602.785295	L	***1008.627436***	504.817356	991.600887	496.304082			6
12	1319.626643	660.316960	1302.600094	651.803685	1301.616078	651.311677	P	***895.543372***	448.275324	878.516823	439.762050			5
13	1758.851969	879.929623	1741.825420	871.416348	1740.841404	870.924340	Q	***798.490608***	399.748942	781.464059	391.235668			4
14	**1857.920383**	929.463830	1840.893834	920.950555	1839.909818	920.458547	V	***359.265282***	180.136279	342.238733	171.623004			3
15	**1971.004447**	986.005862	1953.977898	977.492587	1952.993882	977.000579	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 YSAWAESVTNLPQVIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.0	2116.102676	0.029452	YSAWAESVTNLPQVIK
0.2	2116.145798	-0.013670	AGCPMLALEVLSKMPKVIK

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

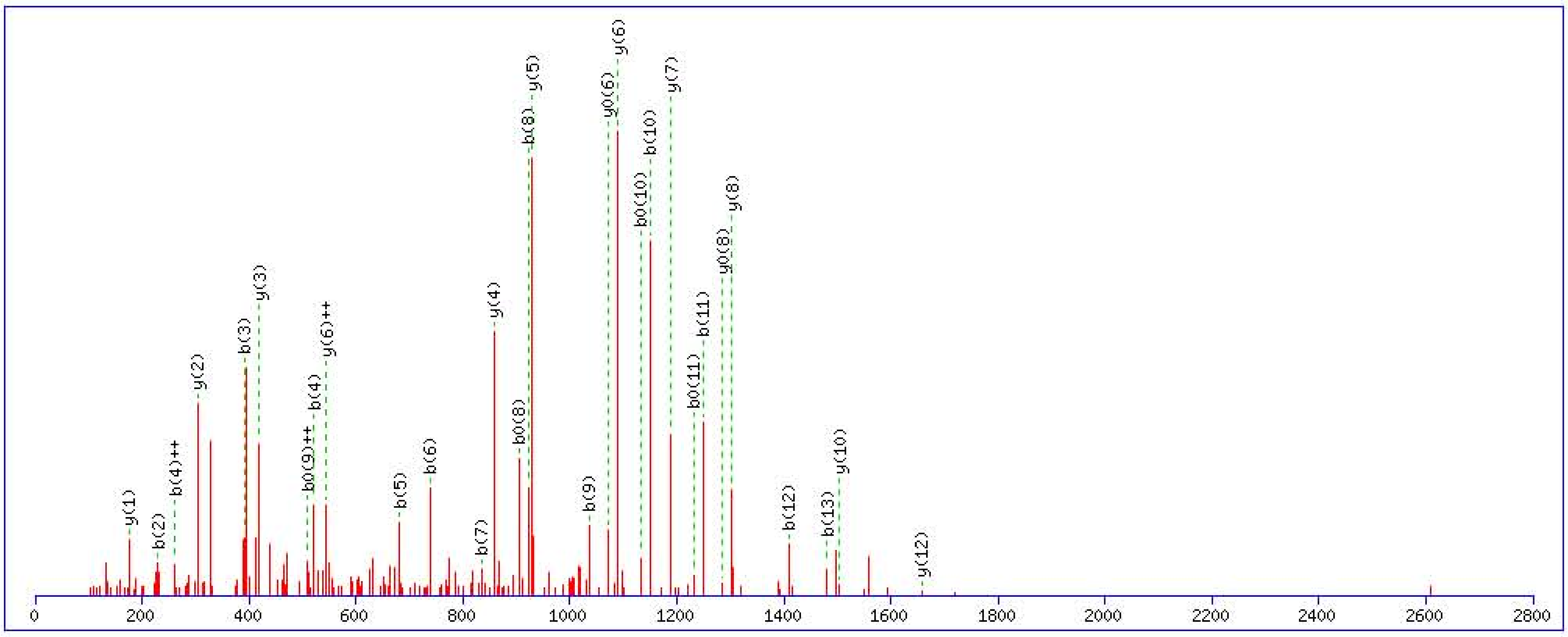
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPYECGPSLDVCAQDER**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

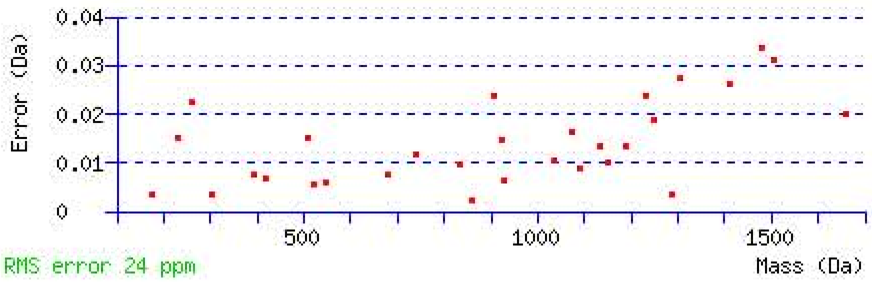
Match to Query 58913: 2337.018612 from(780.013480,3+) rtinseconds(2095) index(7095)
Title: Locus:1.1.1.2983.14 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

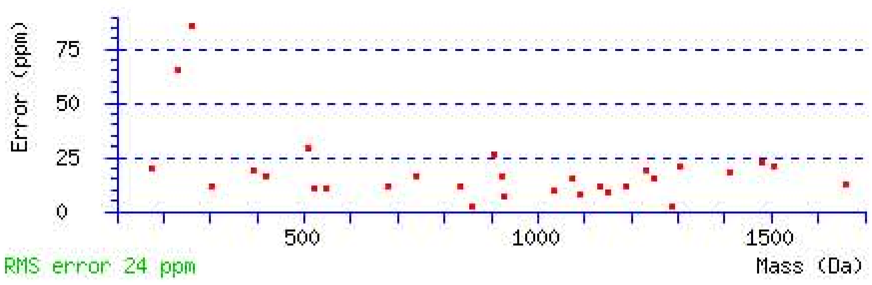
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2336.989792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 1.7e-006
Matches : 30/158 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	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
64.4	2336.989792	0.028820	MPYECGPSLDVCAQDER

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

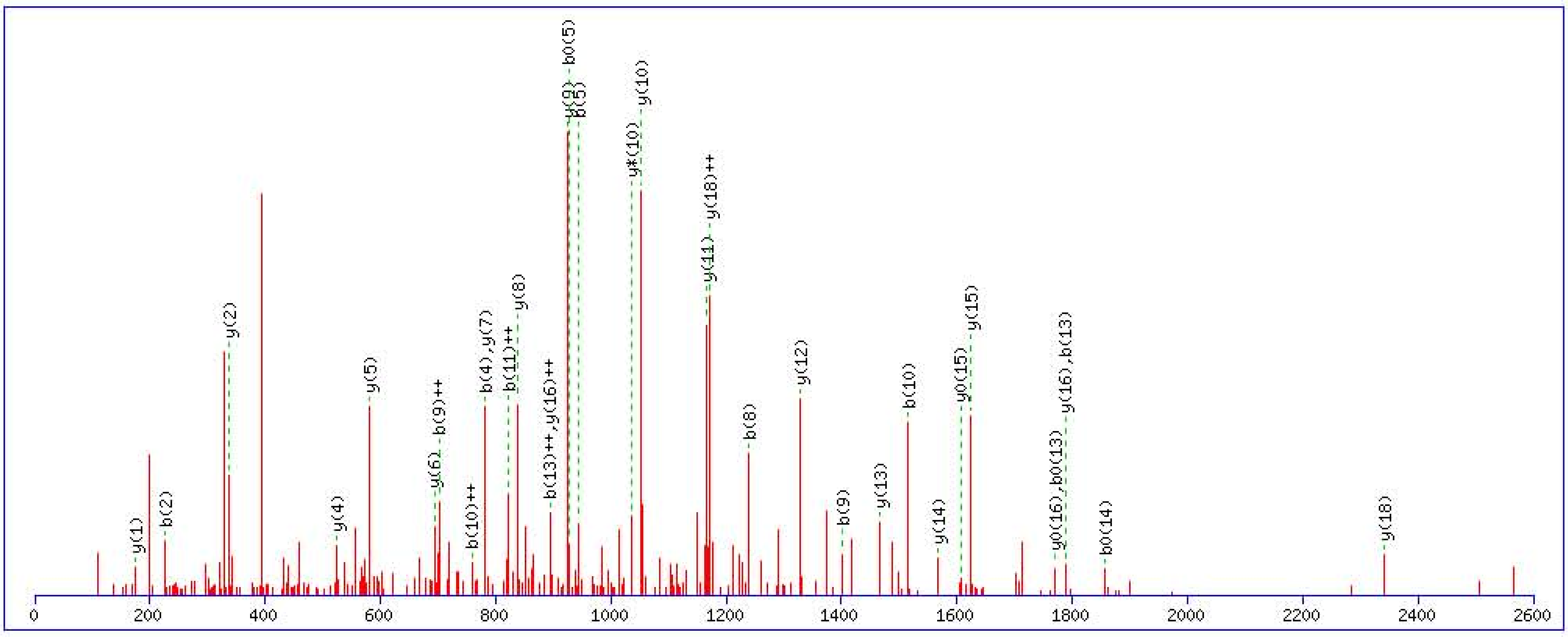
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIDQYGTHYLQSGSLGGEYR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

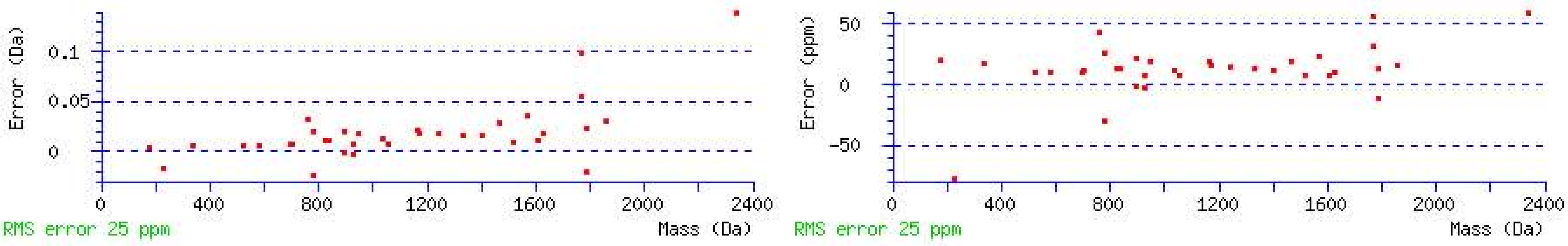
Match to Query 64030: 2567.282172 from(856.768000,3+) rtinseconds(2104) index(7146)
Title: Locus:1.1.1.2986.16 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 2567.247849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 100  Expect: 3e-009
Matches : 35/214 fragment ions using 59 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							20
2	**227.175404**	114.091340					I	2455.171074	1228.089175	2438.144525	1219.575900	2437.160509	1219.083892	19
3	342.202347	171.604811			324.191782	162.599529	D	***2342.087010***	1171.547143	2325.060461	1163.033868	2324.076445	1162.541860	18
4	**781.427673**	391.217475	764.401124	382.704200	763.417108	382.212192	Q	2227.060067	1114.033671	2210.033518	1105.520397	2209.049502	1105.028389	17
5	**944.491002**	472.749139	927.464453	464.235864	926.480437	463.743856	Y	***1787.834741***	894.421009	1770.808192	885.907734	1769.824176	885.415726	16
6	1001.512466	501.259871	984.485917	492.746597	983.501901	492.254589	G	***1624.771412***	812.889344	1607.744863	804.376070	1606.760847	803.884062	15
7	1102.560145	551.783710	1085.533596	543.270436	1084.549580	542.778428	T	***1567.749948***	784.378612	1550.723399	775.865338	1549.739383	775.373330	14
8	**1239.619057**	620.313166	1222.592508	611.799892	1221.608492	611.307884	H	***1466.702269***	733.854773	1449.675720	725.341498	1448.691704	724.849490	13
9	**1402.682386**	**701.844831**	1385.655837	693.331557	1384.671821	692.839548	Y	***1329.643357***	665.325317	1312.616808	656.812042	1311.632792	656.320034	12
10	**1515.766450**	**758.386863**	1498.739901	749.873588	1497.755885	749.381580	L	***1166.580028***	583.793652	1149.553479	575.280378	1148.569463	574.788370	11
11	1643.825028	**822.416152**	1626.798479	813.902878	1625.814463	813.410869	Q	***1053.495964***	527.251620	1036.469415	518.738346	1035.485399	518.246338	10
12	1730.857056	865.932166	1713.830507	857.418892	1712.846491	856.926884	S	***925.437386***	463.222331	908.410837	454.709057	907.426821	454.217049	9
13	**1787.878520**	**894.442898**	1770.851971	885.929624	1769.867955	885.437615	G	***838.405358***	419.706317	821.378809	411.193043	820.394793	410.701035	8
14	1874.910548	937.958912	1857.883999	929.445638	1856.899983	928.953630	S	***781.383894***	391.195585	764.357345	382.682311	763.373329	382.190303	7
15	1987.994612	994.500944	1970.968063	985.987670	1969.984047	985.495661	L	***694.351866***	347.679571	677.325317	339.166297	676.341301	338.674289	6
16	2045.016076	1023.011676	2027.989527	1014.498402	2027.005511	1014.006393	G	***581.267802***	291.137539	564.241253	282.624265	563.257237	282.132257	5
17	2102.037540	1051.522408	2085.010991	1043.009133	2084.026975	1042.517125	G	***524.246338***	262.626807	507.219789	254.113533	506.235773	253.621525	4
18	2231.080133	1116.043704	2214.053584	1107.530430	2213.069568	1107.038422	E	467.224874	234.116075	450.198325	225.602801	449.214309	225.110793	3
19	2394.143462	1197.575369	2377.116913	1189.062094	2376.132897	1188.570086	Y	***338.182281***	169.594778	321.155732	161.081504			2
20							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
99.9	2567.247849	0.034323	LIDQYGTHYLQSGSLGGEYR
17.4	2567.247849	0.034323	LIDQYGTHYLQSGSLGGEYR

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

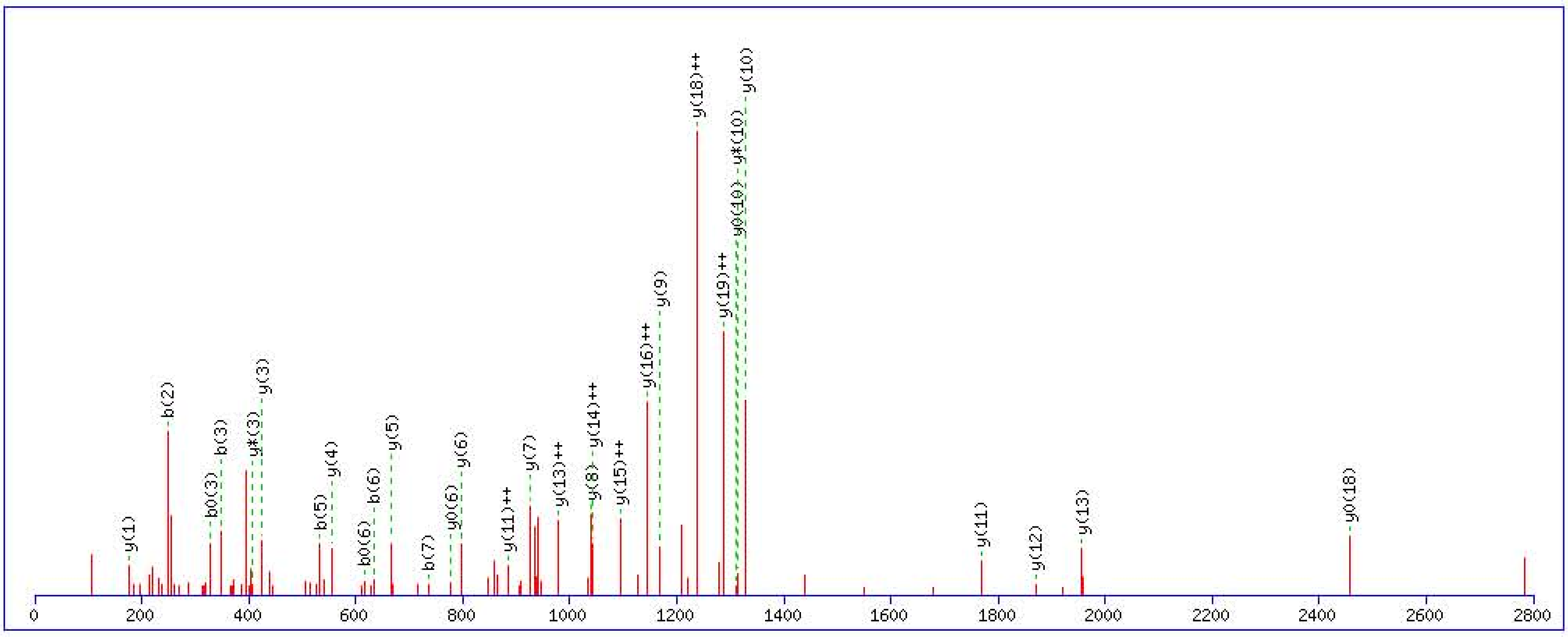
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SCVGETTESTQCEDEELEHLR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

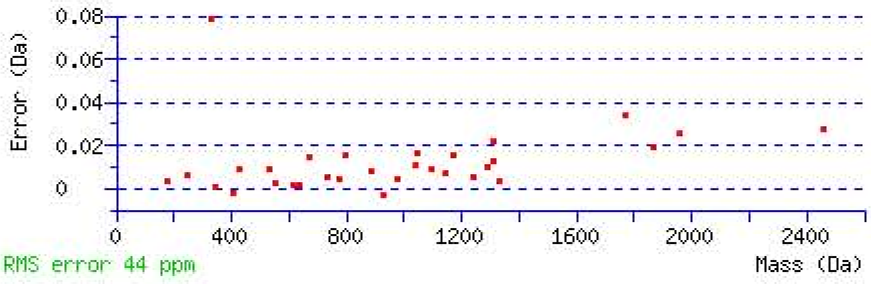
Match to Query 67441: 2819.232072 from(940.751300,3+) rtinseconds(1888) index(5741)
Title: Locus:1.1.1.2911.26 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

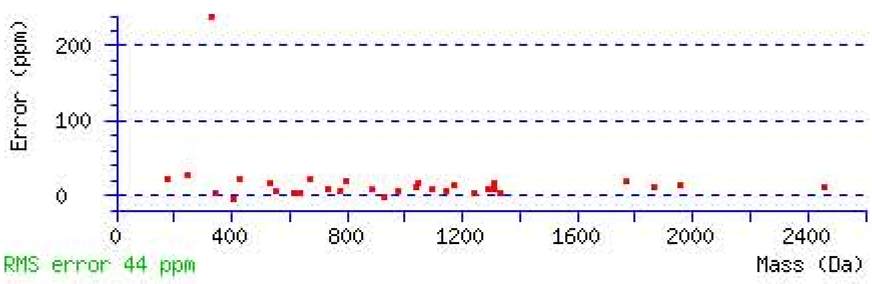
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2819.204803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 81  Expect: 4.5e-008
Matches : 31/214 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	88.039304	44.523290			70.028739	35.518008	S							21
2	**248.069953**	124.538614			230.059388	115.533332	C	2733.180060	1367.093668	2716.153511	1358.580393	2715.169495	1358.088385	20
3	**347.138367**	174.072822			329.127802	165.067539	V	2573.149411	1287.078343	2556.122862	1278.565069	2555.138846	1278.073061	19
4	404.159831	202.583553			386.149266	193.578271	G	2474.080997	1237.544136	2457.054448	1229.030862	2456.070432	1228.538854	18
5	**533.202424**	267.104850			515.191859	258.099568	E	2417.059533	1209.033404	2400.032984	1200.520130	2399.048968	1200.028122	17
6	**634.250103**	317.628690			616.239538	308.623407	T	2288.016940	1144.512108	2270.990391	1135.998833	2270.006375	1135.506825	16
7	**735.297782**	368.152529			717.287217	359.147247	T	2186.969261	1093.988268	2169.942712	1085.474994	2168.958696	1084.982986	15
8	864.340375	432.673826			846.329810	423.668543	E	2085.921582	1043.464429	2068.895033	1034.951154	2067.911017	1034.459146	14
9	951.372403	476.189840			933.361838	467.184557	S	***1956.878989***	978.943133	1939.852440	970.429858	1938.868424	969.937850	13
10	1052.420082	526.713679			1034.409517	517.708397	T	***1869.846961***	935.427119	1852.820412	926.913844	1851.836396	926.421836	12
11	1491.645408	746.326342	1474.618859	737.813068	1473.634843	737.321060	Q	***1768.799282***	884.903279	1751.772733	876.390005	1750.788717	875.897997	11
12	1651.676057	826.341667	1634.649508	817.828392	1633.665492	817.336384	C	***1329.573956***	665.290616	1312.547407	656.777342	1311.563391	656.285334	10
13	1780.718650	890.862963	1763.692101	882.349689	1762.708085	881.857681	E	***1169.543307***	585.275292	1152.516758	576.762017	1151.532742	576.270009	9
14	1895.745593	948.376435	1878.719044	939.863160	1877.735028	939.371152	D	***1040.500714***	520.753995	1023.474165	512.240721	1022.490149	511.748713	8
15	2024.788186	1012.897731	2007.761637	1004.384457	2006.777621	1003.892449	E	***925.473771***	463.240524	908.447222	454.727249	907.463206	454.235241	7
16	2153.830779	1077.419027	2136.804230	1068.905753	2135.820214	1068.413745	E	***796.431178***	398.719227	779.404629	390.205953	778.420613	389.713945	6
17	2266.914843	1133.961059	2249.888294	1125.447785	2248.904278	1124.955777	L	***667.388585***	334.197931	650.362036	325.684656	649.378020	325.192648	5
18	2395.957436	1198.482356	2378.930887	1189.969081	2377.946871	1189.477074	E	***554.304521***	277.655899	537.277972	269.142624	536.293956	268.650616	4
19	2533.016348	1267.011812	2515.989799	1258.498537	2515.005783	1258.006529	H	***425.261928***	213.134602	408.235379	204.621328			3
20	2646.100412	1323.553844	2629.073863	1315.040569	2628.089847	1314.548562	L	288.203016	144.605146	271.176467	136.091872			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.6	2819.204803	0.027269	SCVGETTESTQCEDEELEHLR

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

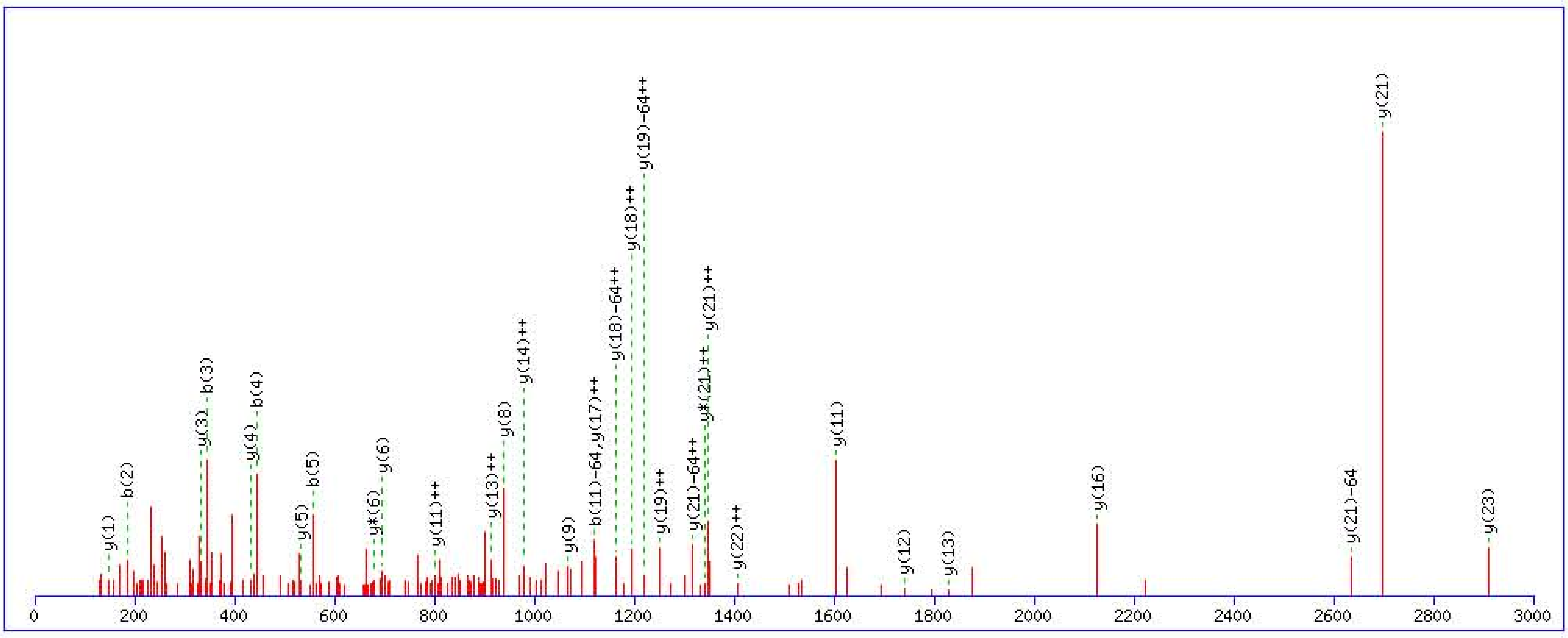
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IACVLPVLMDGIQSHPQKPFYTVGEK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

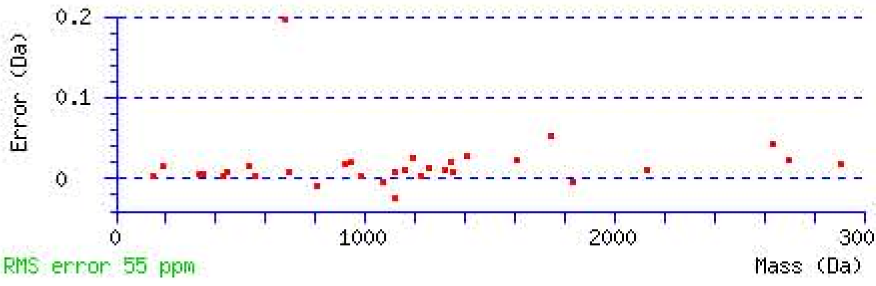
Match to Query 74276: 3253.709816 from(814.434730,4+) rtinseconds(2371) index(8988)
Title: Locus:1.1.1.3079.19 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

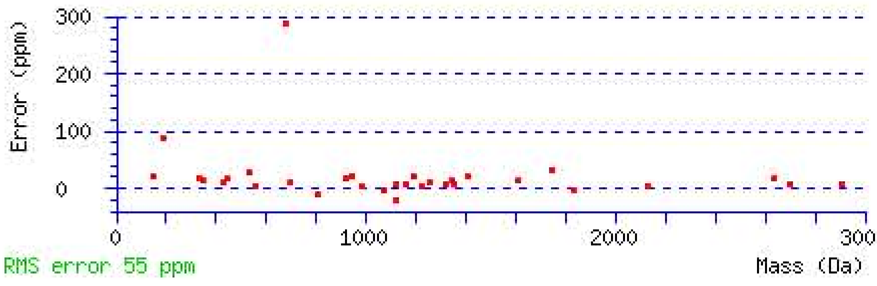
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3253.670181
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q17    : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0005
Matches : 32/396 fragment ions using 103 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	3141.593386	1571.300331	3124.566837	1562.787056	3123.582821	1562.295048	25
3	**345.159103**	173.083190					C	3070.556272	1535.781774	3053.529723	1527.268499	3052.545707	1526.776491	24
4	**444.227517**	222.617397					V	***2910.525623***	1455.766449	2893.499074	1447.253175	2892.515058	1446.761167	23
5	**557.311581**	279.159429					L	2811.457209	1406.232242	2794.430660	1397.718968	2793.446644	1397.226960	22
6	654.364345	327.685811					P	***2698.373145***	1349.690210	2681.346596	1341.176936	2680.362580	1340.684928	21
7	753.432759	377.220018					V	2601.320381	1301.163828	2584.293832	1292.650554	2583.309816	1292.158546	20
8	866.516823	433.762050					L	2502.251967	1251.629621	2485.225418	1243.116347	2484.241402	1242.624339	19
9	1013.552223	507.279750					M	2389.167903	1195.087589	2372.141354	1186.574315	2371.157338	1186.082307	18
10	1128.579166	564.793221			1110.568601	555.787939	D	2242.132503	1121.569889	2225.105954	1113.056615	2224.121938	1112.564607	17
11	1185.600630	593.303953			1167.590065	584.298670	G	***2127.105560***	1064.056418	2110.079011	1055.543143	2109.094995	1055.051135	16
12	1298.684694	649.845985			1280.674129	640.840702	I	2070.084096	1035.545686	2053.057547	1027.032411	2052.073531	1026.540403	15
13	1426.743272	713.875274	1409.716723	705.362000	1408.732707	704.869991	Q	1957.000032	979.003654	1939.973483	970.490380	1938.989467	969.998372	14
14	1513.775300	757.391288	1496.748751	748.878014	1495.764735	748.386006	S	***1828.941454***	914.974365	1811.914905	906.461091	1810.930889	905.969083	13
15	1650.834212	825.920744	1633.807663	817.407470	1632.823647	816.915461	H	***1741.909426***	871.458351	1724.882877	862.945077	1723.898861	862.453068	12
16	1747.886976	874.447126	1730.860427	865.933852	1729.876411	865.441844	P	***1604.850514***	802.928895	1587.823965	794.415621	1586.839949	793.923612	11
17	2187.112302	1094.059789	2170.085753	1085.546514	2169.101737	1085.054506	Q	1507.797750	754.402513	1490.771201	745.889239	1489.787185	745.397230	10
18	2315.207265	1158.107270	2298.180716	1149.593996	2297.196700	1149.101988	K	***1068.572424***	534.789850	1051.545875	526.276575	1050.561859	525.784567	9
19	2412.260029	1206.633652	2395.233480	1198.120378	2394.249464	1197.628370	P	***940.477461***	470.742368	923.450912	462.229094	922.466896	461.737086	8
20	2559.328443	1280.167859	2542.301894	1271.654585	2541.317878	1271.162577	F	843.424697	422.215986	826.398148	413.702712	825.414132	413.210704	7
21	2722.391772	1361.699524	2705.365223	1353.186249	2704.381207	1352.694241	Y	***696.356283***	348.681779	679.329734	340.168505	678.345718	339.676497	6
22	2823.439451	1412.223363	2806.412902	1403.710089	2805.428886	1403.218081	T	***533.292954***	267.150115	516.266405	258.636840	515.282389	258.144832	5
23	2922.507865	1461.757570	2905.481316	1453.244296	2904.497300	1452.752288	V	***432.245275***	216.626275	415.218726	208.113001	414.234710	207.620993	4
24	2979.529329	1490.268302	2962.502780	1481.755028	2961.518764	1481.263020	G	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	3
25	3108.571922	1554.789599	3091.545373	1546.276324	3090.561357	1545.784316	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
37.0	3253.670181	0.039635	IACVLPVLMDGIQSHPQKPFYTVGEK
19.4	3253.670181	0.039635	IACVLPVLMDGIQSHPQKPFYTVGEK
1.8	3253.750809	-0.040993	LGHTVKNIIISQMNSFLCFFLFAVLIGR

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

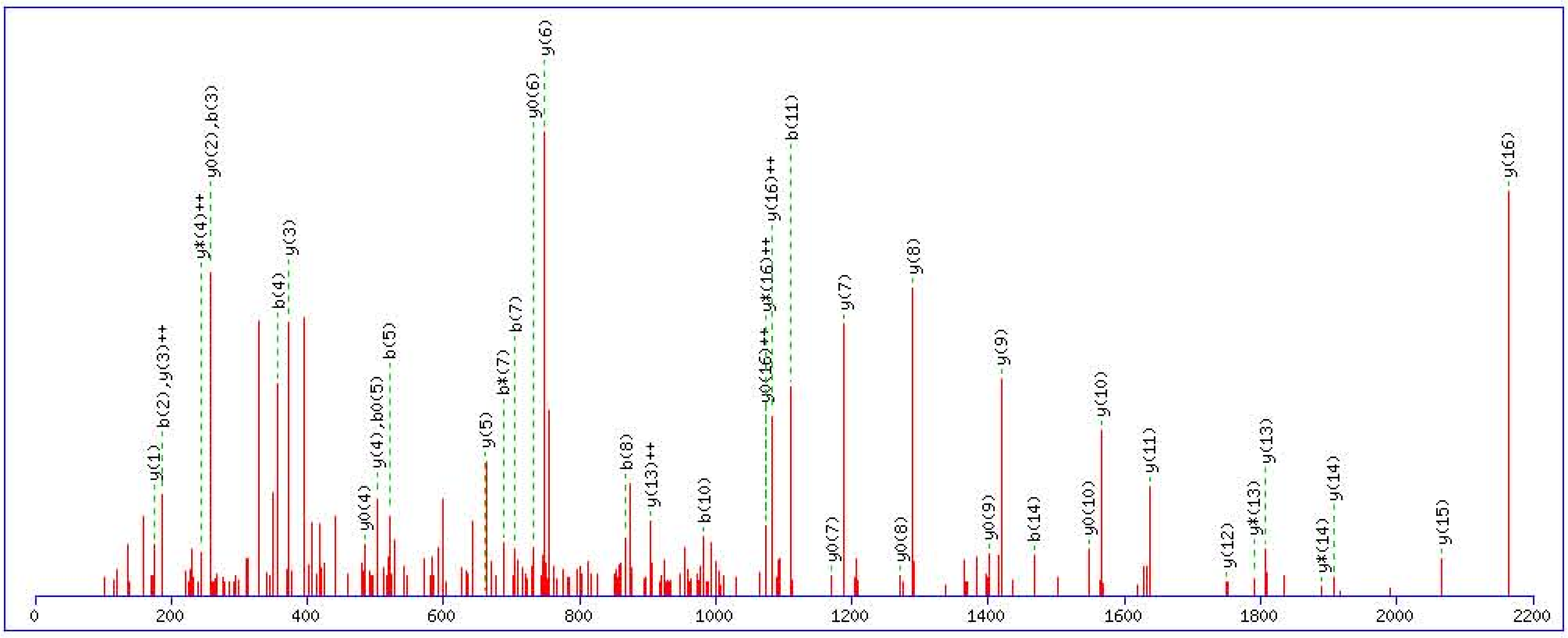
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVAVYGQYGGQPCVGNAFETQSCEPTR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

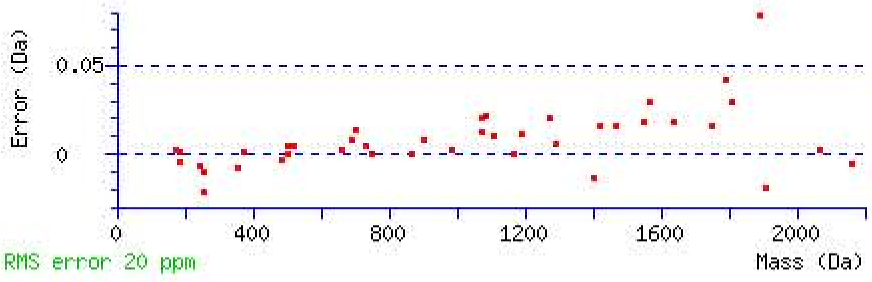
Match to Query 74865: 3272.504376 from(819.133370,4+) rtinseconds(2147) index(7423)
Title: Locus:1.1.1.3001.23 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

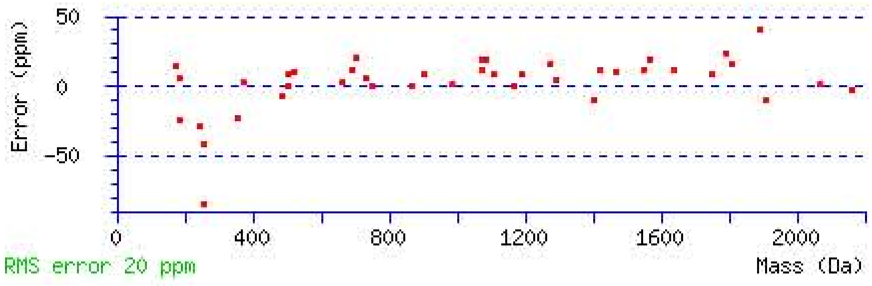
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3272.468933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21 : Biotin:Thermo-21345 (Q)
Ions Score: 86 **Expect:** 2.8e-008
Matches : 41/298 fragment ions using 78 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
86.4	3272.468933	0.035443	SVAVYGQYGGQPCVGNAFETQSCEPTR
7.8	3272.468933	0.035443	SVAVYGQYGGQPCVGNAFETQSCEPTR

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

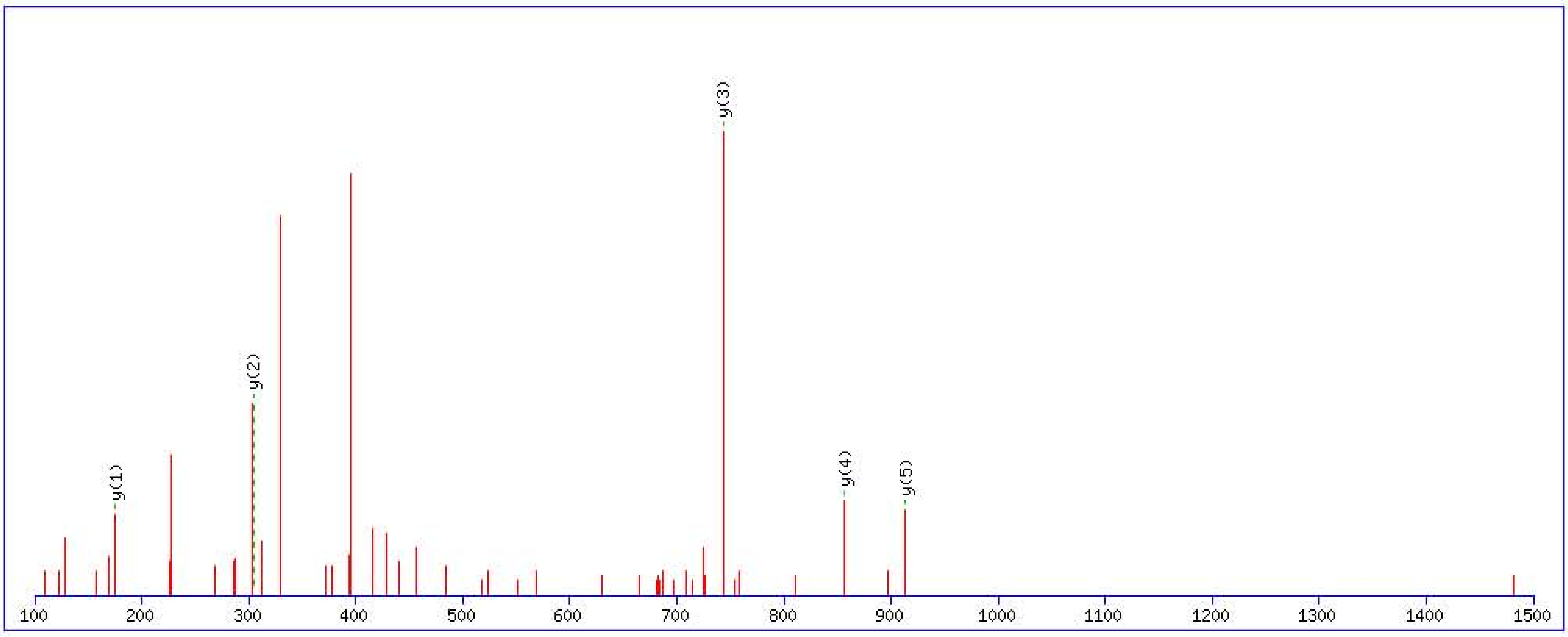
{MATRIX SCIENCE} Mascot Search Results

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

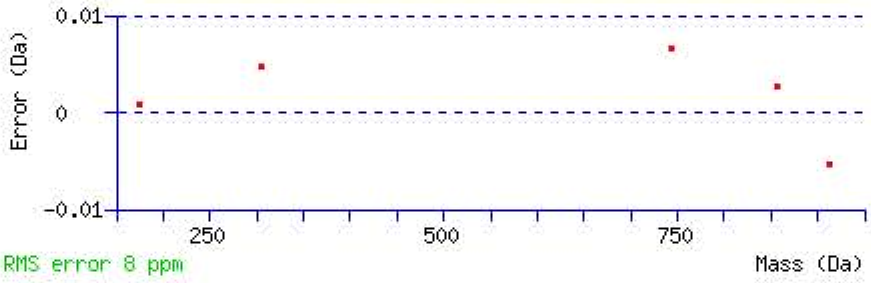
Match to Query 15344: 983.531128 from(492.772840,2+) rtinseconds(1413) index(56623)
Title: Locus:1.1.1.2915.13 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

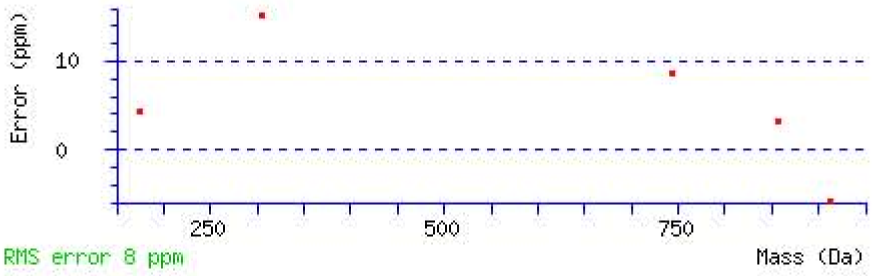
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 983.522217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.008
Matches : 5/44 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	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
33.8	983.522217	0.008911	AGIQER
20.3	983.522217	0.008911	QIQER
20.3	983.522217	0.008911	QLQER
19.7	983.522217	0.008911	AGLEQR
9.4	983.522217	0.008911	IQQER
9.4	983.522217	0.008911	LQQER
8.8	983.522202	0.008926	KLMENPPR
8.8	983.522217	0.008911	QLEQR
8.8	983.530090	0.001038	QLLNHFGR
6.4	983.522217	0.008911	QQLER

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

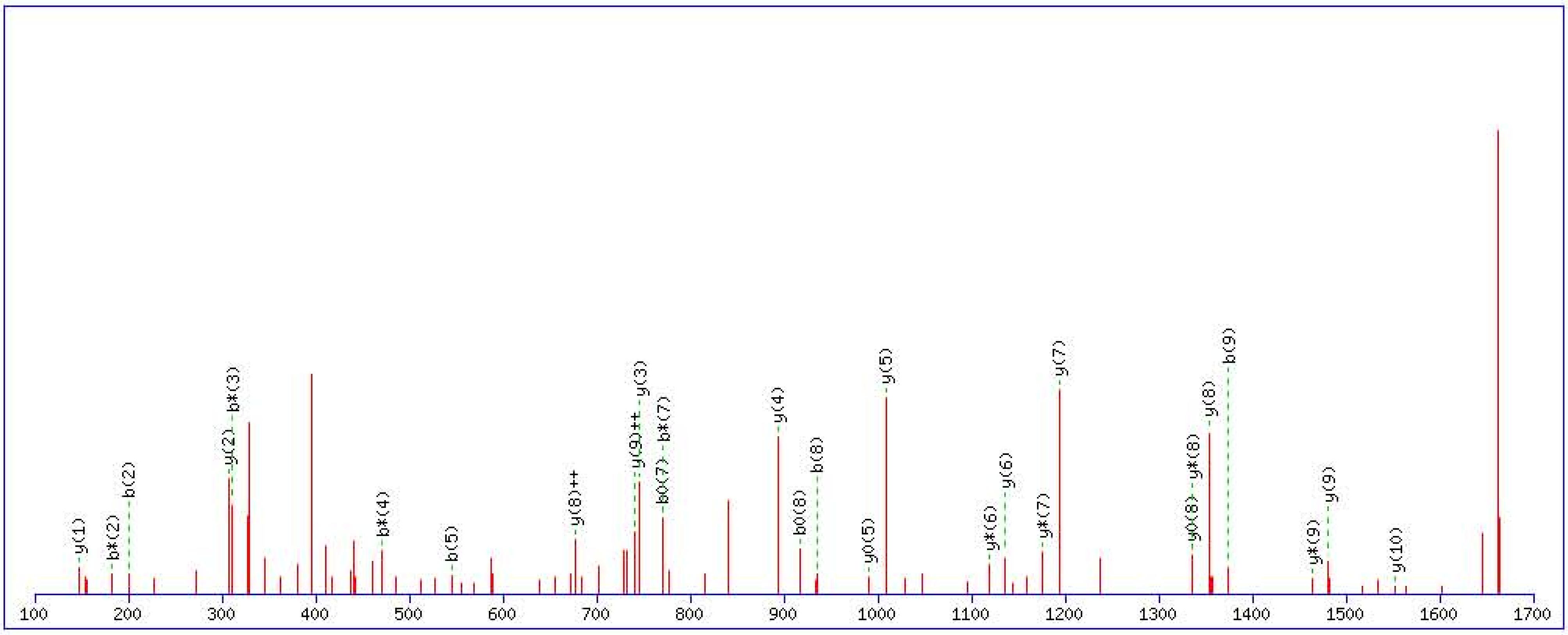
Mascot Search Results

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

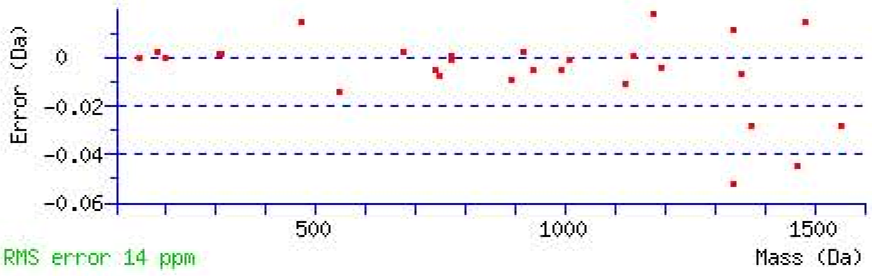
Match to Query 41959: 1679.726908 from(840.870730,2+) rtinseconds(1504) index(21018)
Title: Locus:1.1.1.2666.20 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

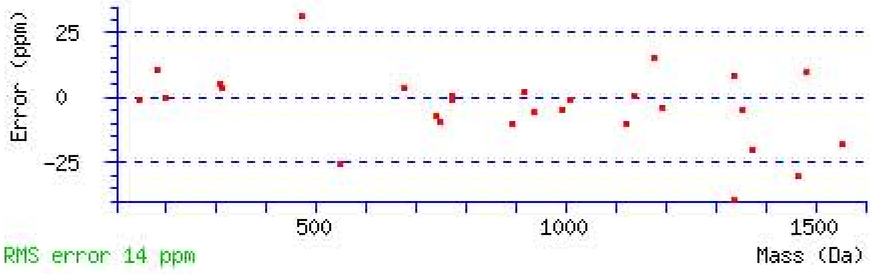
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 70  Expect: 4.8e-007
Matches : 28/100 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	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
69.8	1679.721832	0.005076	QAQCGQDFQCK
29.6	1679.721832	0.005076	QAQCGQDFQCK
4.2	1679.721832	0.005076	QAQCGQDFQCK

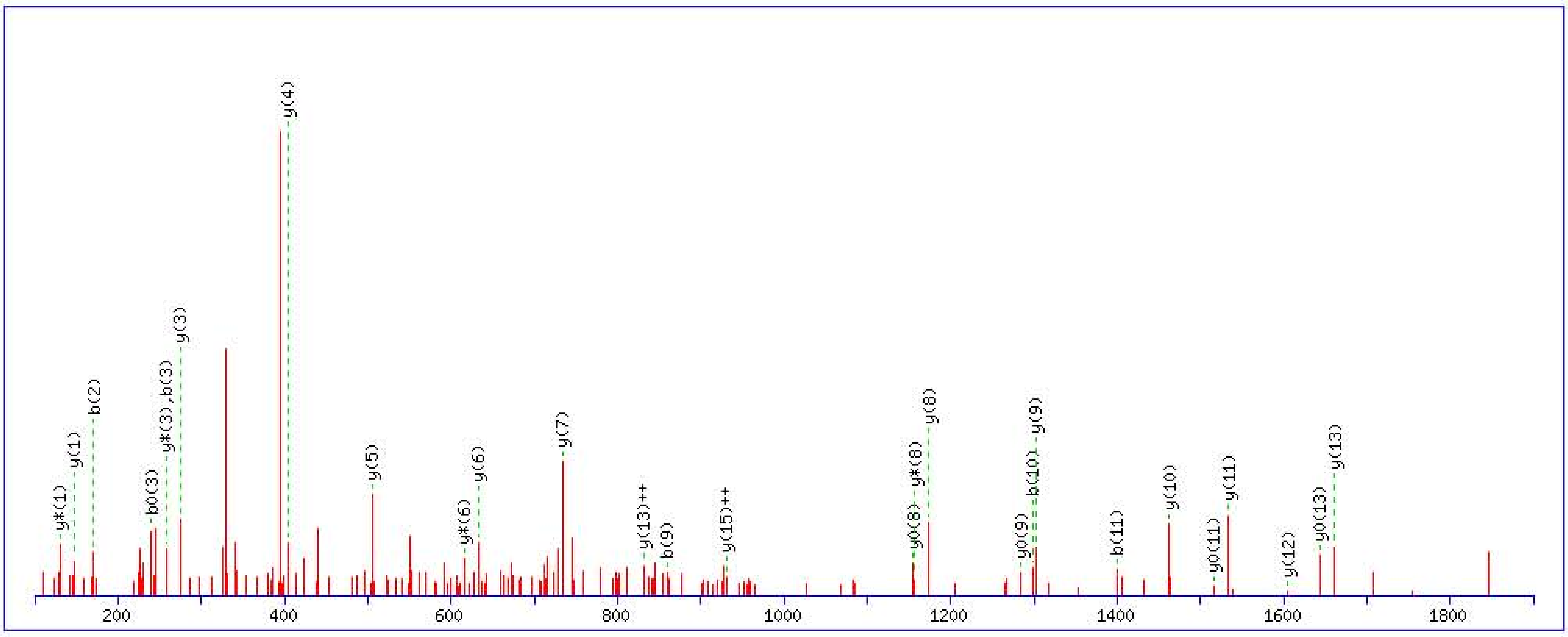
Mascot Search Results

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

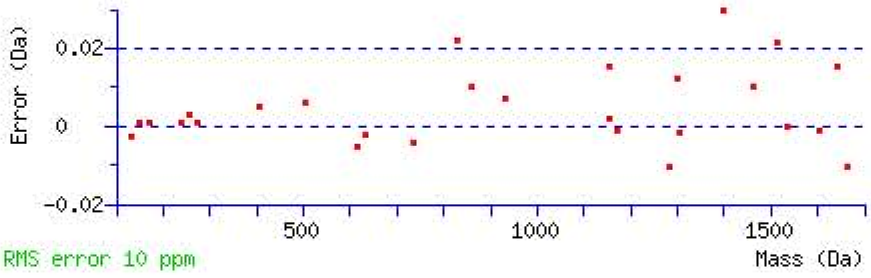
Match to Query 51558: 2030.984832 from(678.002220,3+) rtinseconds(1689) index(22368)
Title: Locus:1.1.1.2731.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

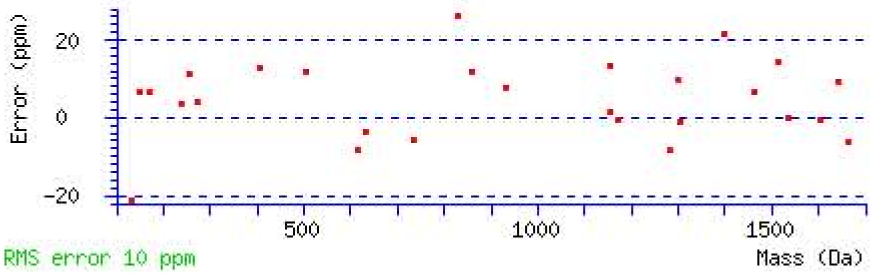
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2030.976501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 6e-005
Matches : 28/164 fragment ions using 64 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
56.1	2030.976501	0.008331	LGSLGAACEQTQTEGAK
33.8	2030.976501	0.008331	LGSLGAACEQTQTEGAK

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

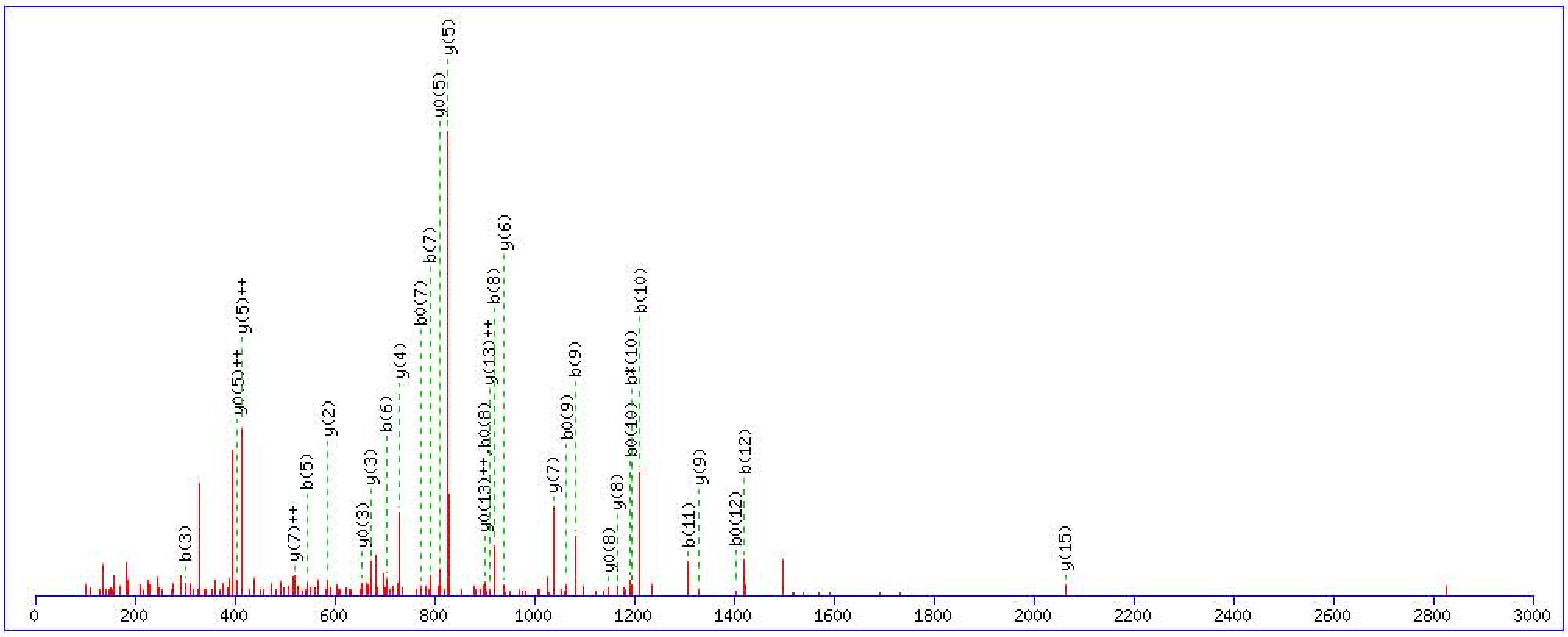
{MATRIX SCIENCE} Mascot Search Results

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

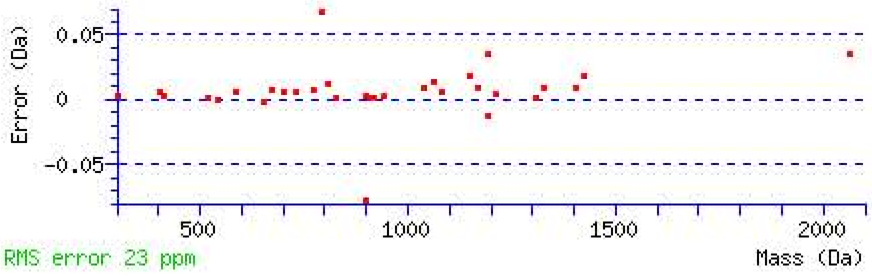
Match to Query 56552: 2247.035082 from(750.018970,3+) rtinseconds(1884) index(23844)
Title: Locus:1.1.1.2798.19 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

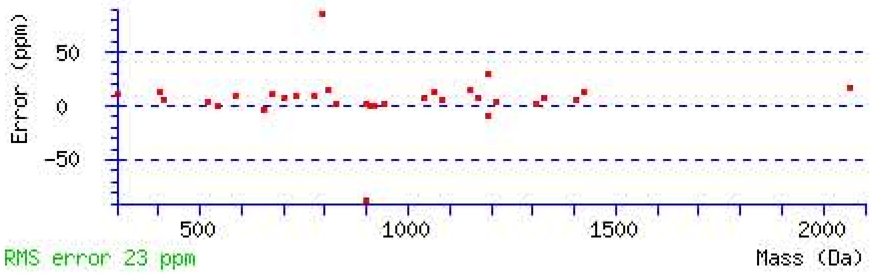
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2247.018753
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00013
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	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
42.2	2247.018753	0.016329	AIDEDCSQYEPIPGSQK
0.7	2247.063034	-0.027952	VTDANDNPPVFSQDVYR

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

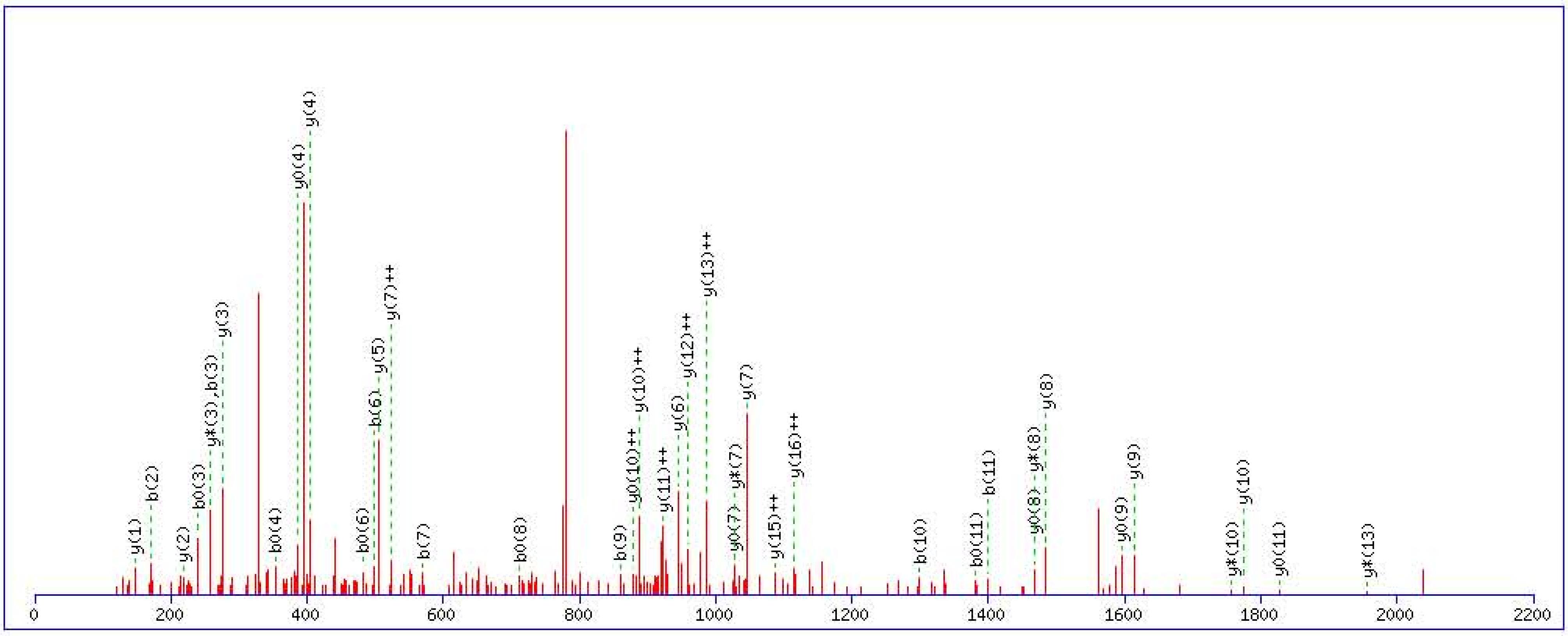
Mascot Search Results

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

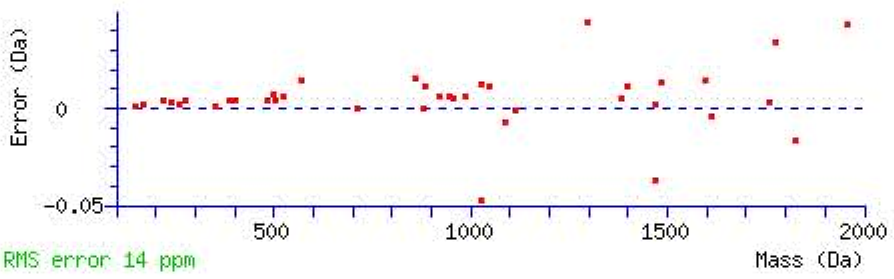
Match to Query 58969: 2342.175522 from(781.732450,3+) rtinseconds(1999) index(42217)
Title: Locus:1.1.1.3145.14 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

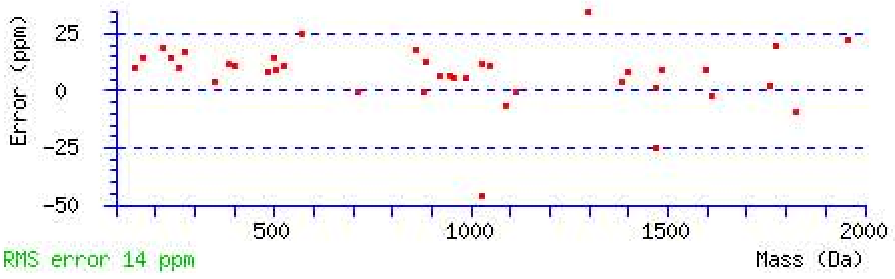
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2342.143250
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.0006
Matches : 40/164 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	114.091340	57.549308					L							17
2	**171.112804**	86.060040					G	2230.066475	1115.536875	2213.039926	1107.023601	2212.055910	1106.531593	16
3	**258.144832**	129.576054			240.134267	120.570772	S	2173.045011	1087.026143	2156.018462	1078.512869	2155.034446	1078.020861	15
4	371.228896	186.118086			353.218331	177.112804	L	2086.012983	1043.510129	2068.986434	1034.996855	2068.002418	1034.504847	14
5	428.250360	214.628818			410.239795	205.623536	G	1972.928919	986.968098	1955.902370	978.454823	1954.918354	977.962815	13
6	**499.287474**	250.147375			481.276909	241.142093	A	1915.907455	958.457366	1898.880906	949.944091	1897.896890	949.452083	12
7	**570.324588**	285.665932			552.314023	276.660650	A	1844.870341	922.938809	1827.843792	914.425534	1826.859776	913.933526	11
8	730.355237	365.681257			712.344672	356.675974	C	***1773.833227***	887.420252	1756.806678	878.906977	1755.822662	878.414969	10
9	**859.397830**	430.202553			841.387265	421.197271	E	***1613.802578***	807.404927	1596.776029	798.891653	1595.792013	798.399645	9
10	**1298.623156**	649.815216	1281.596607	641.301942	1280.612591	640.809934	Q	***1484.759985***	742.883631	1467.733436	734.370356	1466.749420	733.878348	8
11	**1399.670835**	700.339056	1382.644286	691.825781	1381.660270	691.333773	T	***1045.534659***	523.270968	1028.508110	514.757693	1027.524094	514.265685	7
12	1838.896161	919.951719	1821.869612	911.438444	1820.885596	910.946436	Q	***944.486980***	472.747128	927.460431	464.233854	926.476415	463.741846	6
13	1939.943840	970.475558	1922.917291	961.962284	1921.933275	961.470276	T	***505.261654***	253.134465	488.235105	244.621191	487.251089	244.129183	5
14	2068.986433	1034.996854	2051.959884	1026.483580	2050.975868	1025.991572	E	***404.213975***	202.610626	387.187426	194.097351	386.203410	193.605343	4
15	2126.007897	1063.507586	2108.981348	1054.994312	2107.997332	1054.502304	G	***275.171382***	138.089329	258.144833	129.576055			3
16	2197.045011	1099.026144	2180.018462	1090.512869	2179.034446	1090.020861	A	***218.149918***	109.578597	201.123369	101.065323			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
47.1	2342.143250	0.032272	LGSLGAACEQTQTEGAK

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

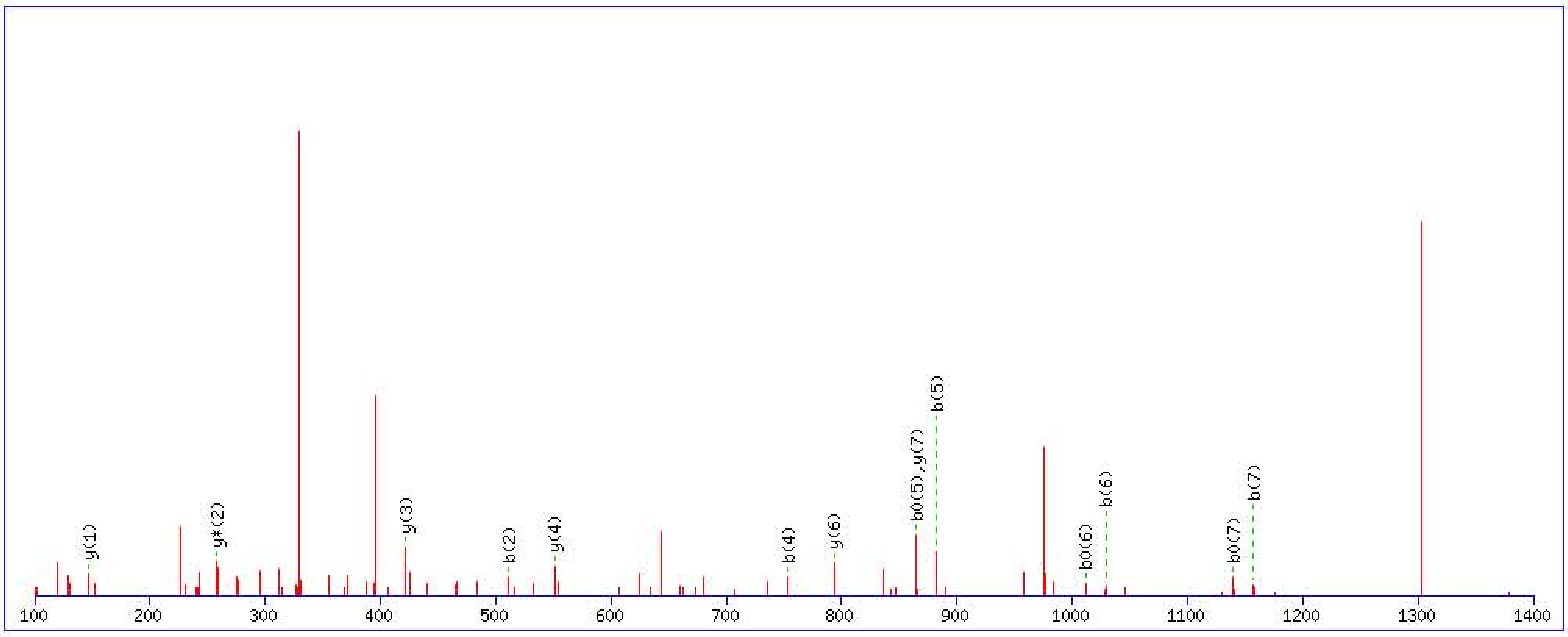
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QALEEFQK**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

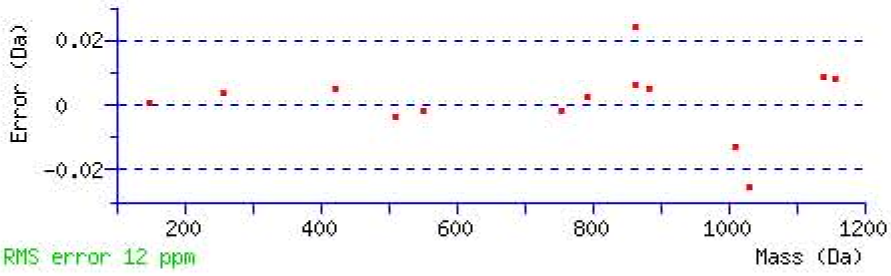
Match to Query 26994: 1302.670348 from(652.342450,2+) rtinseconds(1857) index(23620)
Title: Locus:1.1.1.2789.10 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

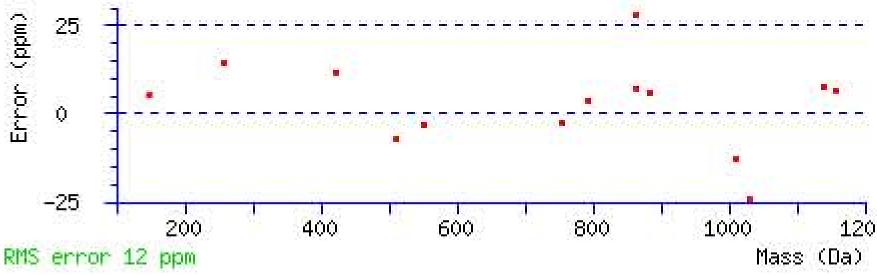
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1302.664185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.017
Matches : 14/72 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	440.232602	220.619939	423.206053	212.106664			Q							8
2	***511.269716***	256.138496	494.243167	247.625221			A	***864.446160***	432.726718	847.419611	424.213443	846.435595	423.721435	7
3	624.353780	312.680528	607.327231	304.167254			L	***793.409046***	397.208161	776.382497	388.694887	775.398481	388.202879	6
4	***753.396373***	377.201825	736.369824	368.688550	735.385808	368.196542	E	680.324982	340.666129	663.298433	332.152854	662.314417	331.660846	5
5	***882.438966***	441.723121	865.412417	433.209847	864.428401	432.717839	E	***551.282389***	276.144833	534.255840	267.631558	533.271824	267.139550	4
6	***1029.507380***	515.257328	1012.480831	506.744054	1011.496815	506.252046	F	***422.239796***	211.623536	405.213247	203.110261			3
7	***1157.565958***	579.286617	1140.539409	570.773343	1139.555393	570.281334	Q	275.171382	138.089329	258.144833	129.576054			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QALEEFQK
(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	1302.664185	0.006163	QALEEFQK
19.4	1302.689133	-0.018785	KEAQKSQAASQK
13.9	1302.667542	0.002806	KEALMQEK
13.1	1302.666641	0.003707	EKEAELKEAEK
8.4	1302.660156	0.010192	QQELCADLKAK
8.1	1302.660141	0.010207	EAEGKLAAQMQK
7.4	1302.668045	0.002303	QPAGPASATPPGPR
7.3	1302.677917	-0.007569	SSATIQNETPKK
6.8	1302.671387	-0.001039	EAQKQLAQMTR
6.5	1302.656815	0.013533	AQATAQDPVFQK

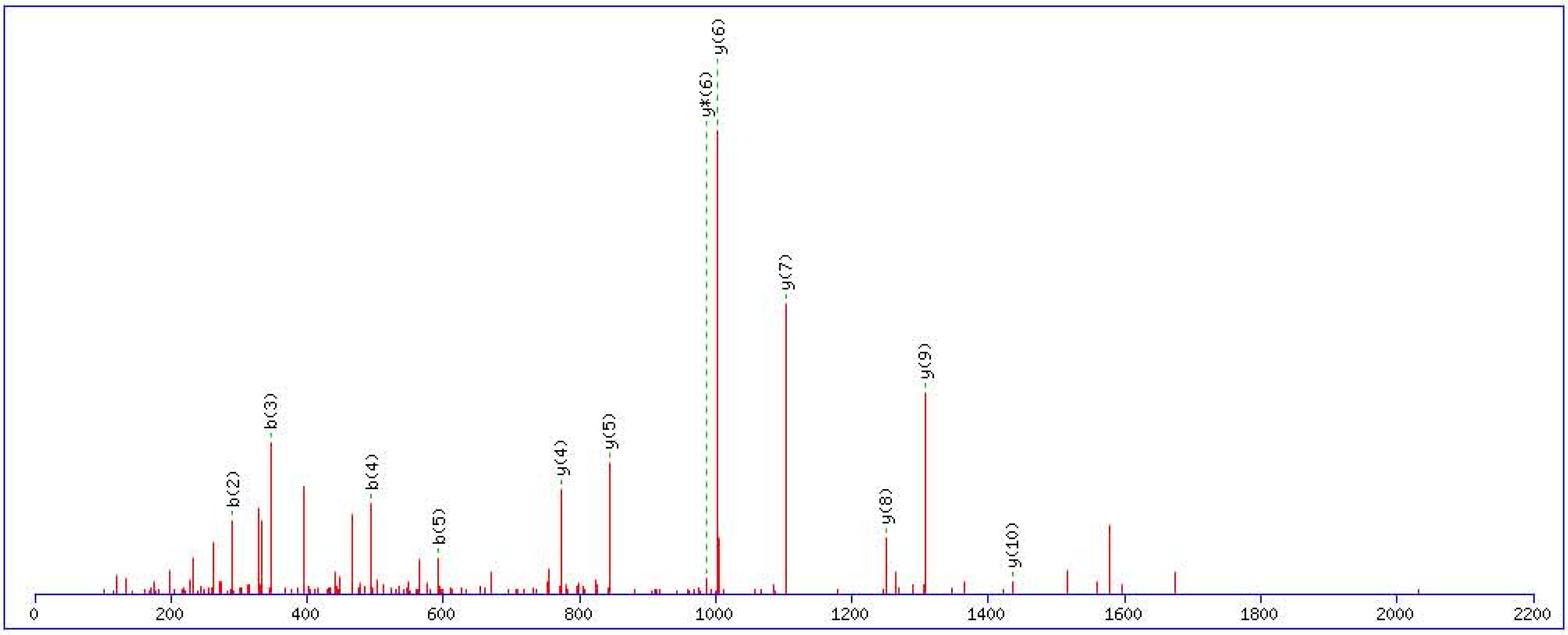
{MATRIX SCIENCE} Mascot Search Results

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

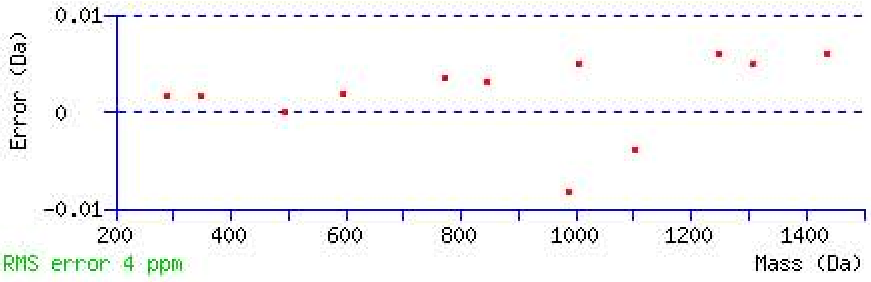
Match to Query 38411: 1594.713028 from(798.363790,2+) rtinseconds(1751) index(22868)
Title: Locus:1.1.1.2752.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

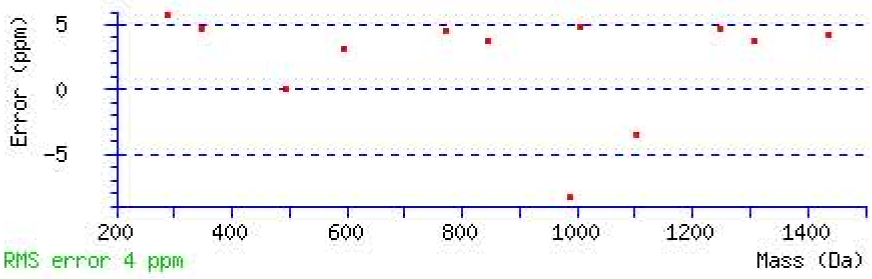
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1594.705460
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 61 **Expect:** 6.1e-006
Matches : 12/100 fragment ions using 15 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
60.7	1594.705460	0.007568	CEGFVCAQTGR

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

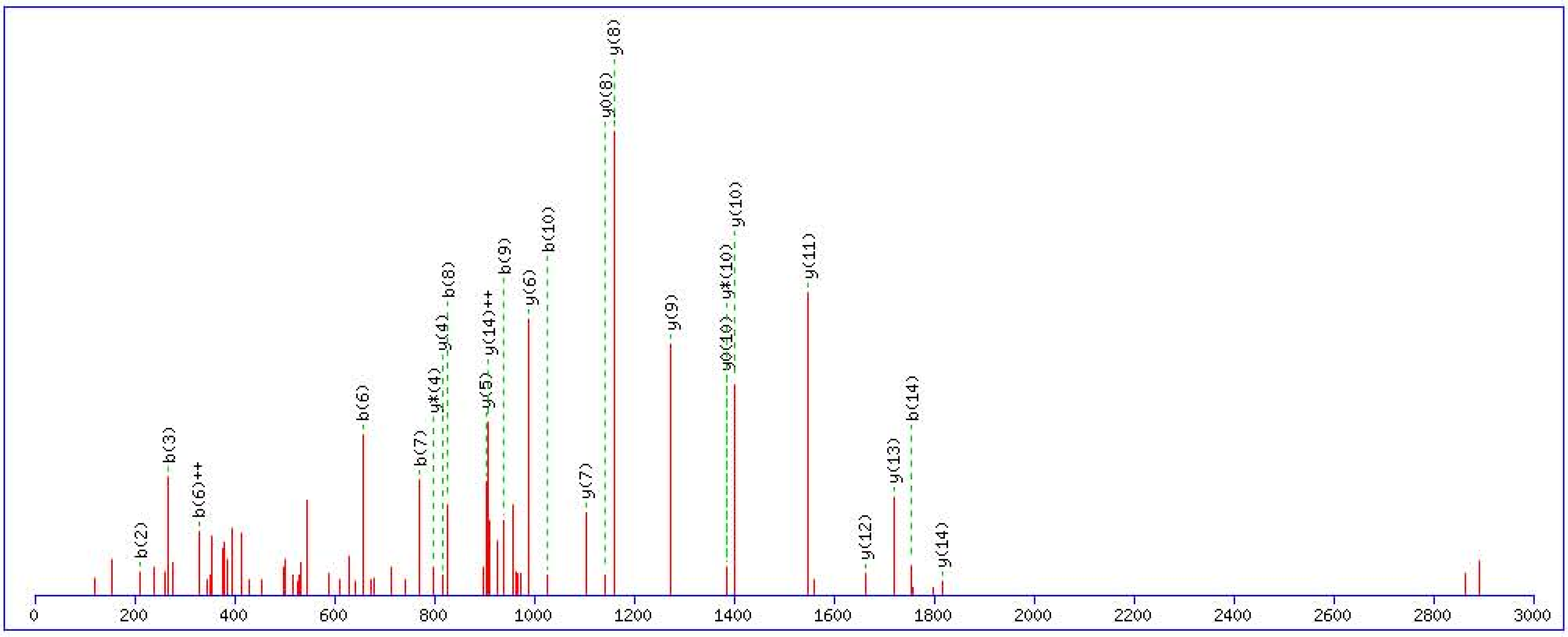
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPGIFELGISSQSDR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

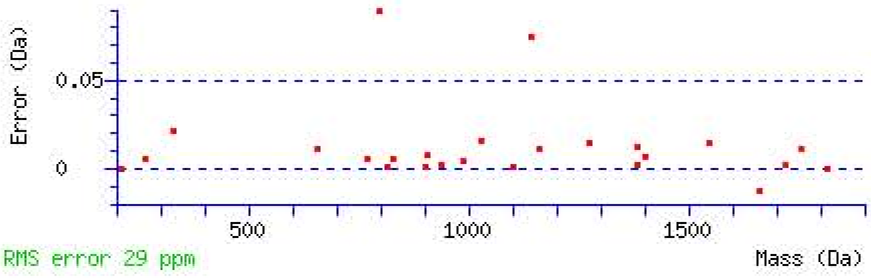
Match to Query 48204: 1929.027908 from(965.521230,2+) rtinseconds(2656) index(29030)
Title: Locus:1.1.1.3066.21 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

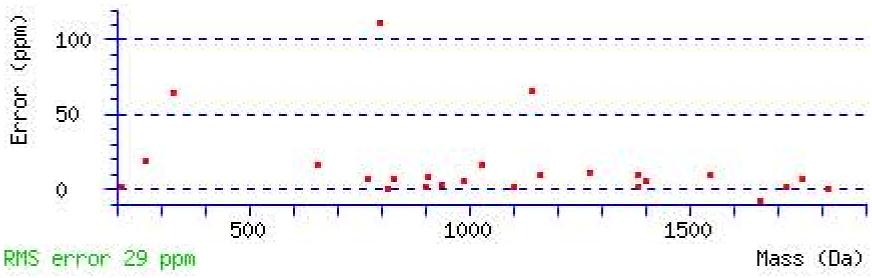
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1929.002975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 68 **Expect:** 2.1e-006
Matches : 25/134 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					I							15
2	**211.144104**	106.075690					P	***1816.926196***	908.966736	1799.899647	900.453462	1798.915631	899.961454	14
3	**268.165568**	134.586422					G	***1719.873432***	860.440354	1702.846883	851.927080	1701.862867	851.435072	13
4	381.249632	191.128454					I	***1662.851968***	831.929622	1645.825419	823.416348	1644.841403	822.924340	12
5	528.318046	264.662661					F	***1549.767904***	775.387590	1532.741355	766.874316	1531.757339	766.382308	11
6	**657.360639**	329.183958			639.350074	320.178675	E	***1402.699490***	701.853383	1385.672941	693.340109	1384.688925	692.848101	10
7	**770.444703**	385.725990			752.434138	376.720707	L	***1273.656897***	637.332087	1256.630348	628.818812	1255.646332	628.326804	9
8	**827.466167**	414.236722			809.455602	405.231439	G	***1160.572833***	580.790055	1143.546284	572.276780	1142.562268	571.784772	8
9	**940.550231**	470.778754			922.539666	461.773471	I	***1103.551369***	552.279323	1086.524820	543.766048	1085.540804	543.274040	7
10	**1027.582259**	514.294768			1009.571694	505.289485	S	***990.467305***	495.737291	973.440756	487.224016	972.456740	486.732008	6
11	1114.614287	557.810782			1096.603722	548.805499	S	***903.435277***	452.221277	886.408728	443.708002	885.424712	443.215994	5
12	1553.839613	777.423445	1536.813064	768.910170	1535.829048	768.418162	Q	***816.403249***	408.705263	799.376700	400.191988	798.392684	399.699980	4
13	1640.871641	820.939459	1623.845092	812.426184	1622.861076	811.934176	S	377.177923	189.092600	360.151374	180.579325	359.167358	180.087317	3
14	**1755.898584**	878.452930	1738.872035	869.939656	1737.888019	869.447648	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 IPGIFELGISSQSDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.5	1929.002975	0.024933	IPGIFELGISSQSDR
7.4	1929.018219	0.009689	LPEFLVQLYSYMRVR
6.9	1929.020721	0.007187	RELEELSVGSDGVLIWK
4.8	1929.041840	-0.013932	ADEVLAEVTVSAQASAKIK
0.6	1929.047211	-0.019303	QAHSKYGQFLLVPSNLK

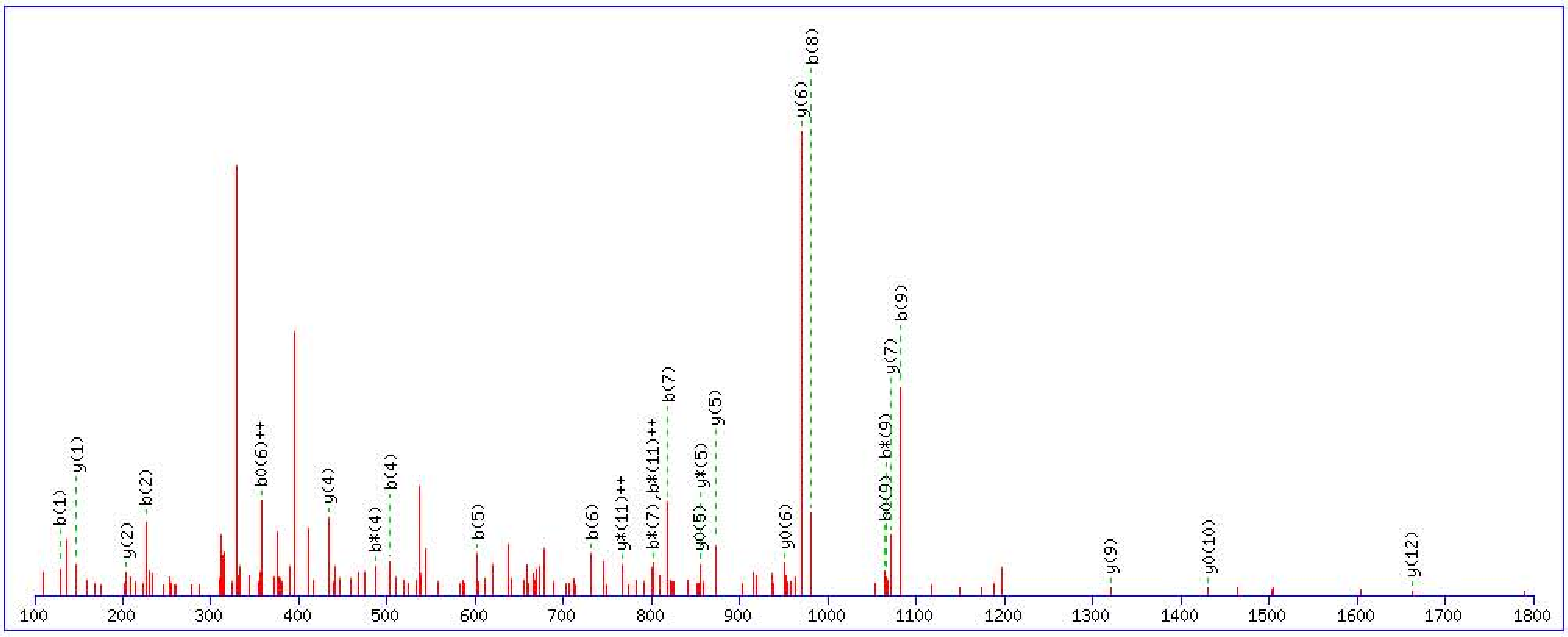
{MATRIX SCIENCE} Mascot Search Results

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

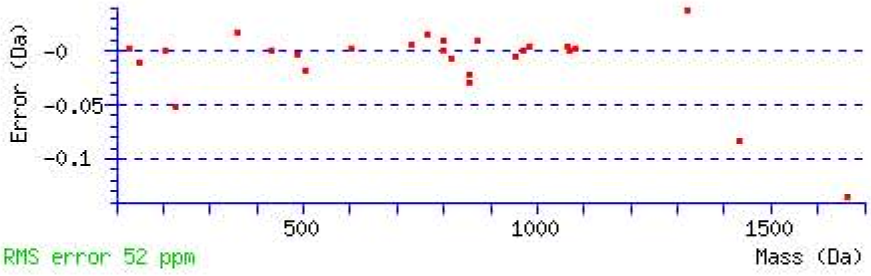
Match to Query 52076: 2050.024932 from(684.348920,3+) rtinseconds(1615) index(21797)
Title: Locus:1.1.1.2705.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

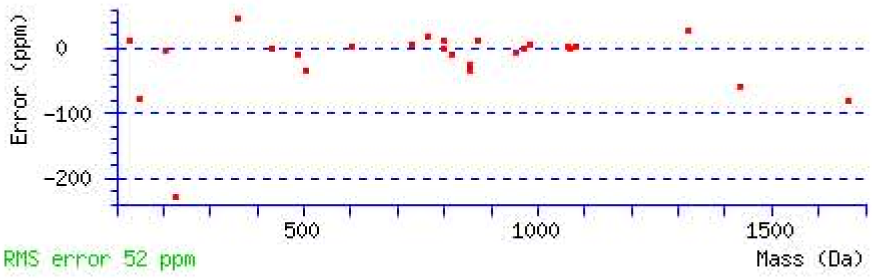
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2050.019348
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 0.00026
Matches : 27/152 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	***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	1618.793392	809.900334	1601.766843	801.387060	1600.782827	800.895052	Q	***872.465851***	436.736564	855.439302	428.223289	854.455286	427.731281	5
12	1719.841071	860.424174	1702.814522	851.910899	1701.830506	851.418891	T	***433.240525***	217.123900	416.213976	208.610626	415.229960	208.118618	4
13	1847.899649	924.453463	1830.873100	915.940188	1829.889084	915.448180	Q	332.192846	166.600061	315.166297	158.086786			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
50.0	2050.019348	0.005584	KPYNVESYTPQTQGK
42.3	2050.019348	0.005584	KPYNVESYTPQTQGK

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

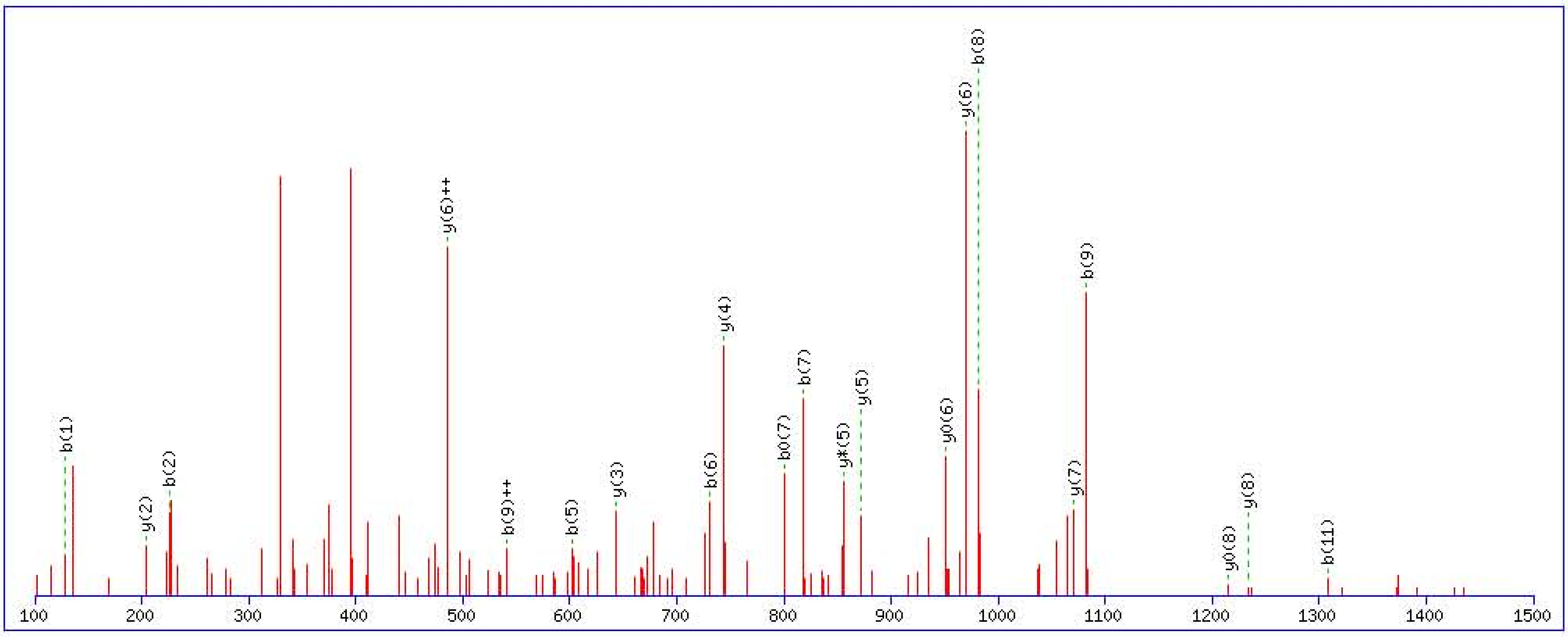
Mascot Search Results

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

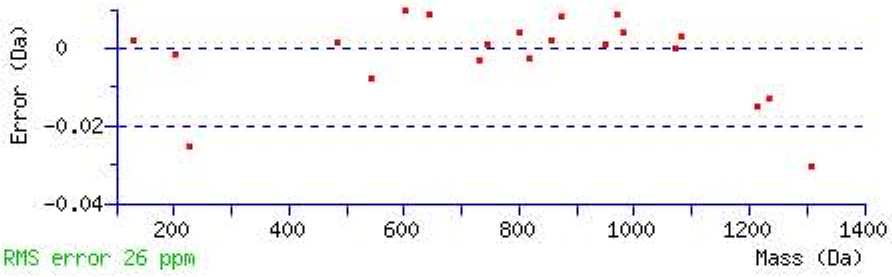
Match to Query 52077: 2050.025262 from(684.349030,3+) rtinseconds(1586) index(21647)
Title: Locus:1.1.1.2695.10 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

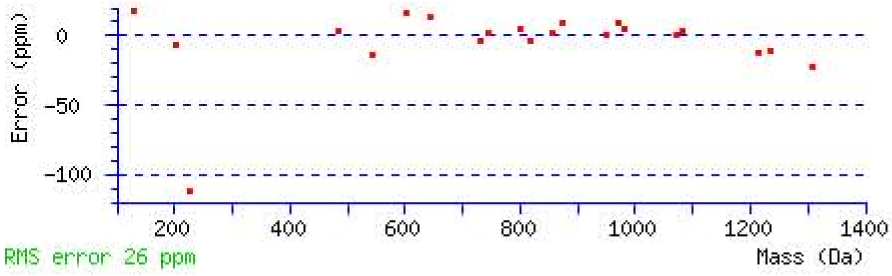
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 45  Expect: 9e-005
Matches : 21/152 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							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
45.2	2050.019348	0.005914	KPYNVESYTPQTQGK
27.0	2050.019348	0.005914	KPYNVESYTPQTQGK
2.0	2050.025192	0.000070	LKISNDGLQMEKDESSLK
0.8	2050.026566	-0.001304	LFVGMLNKQQSEDDVRR

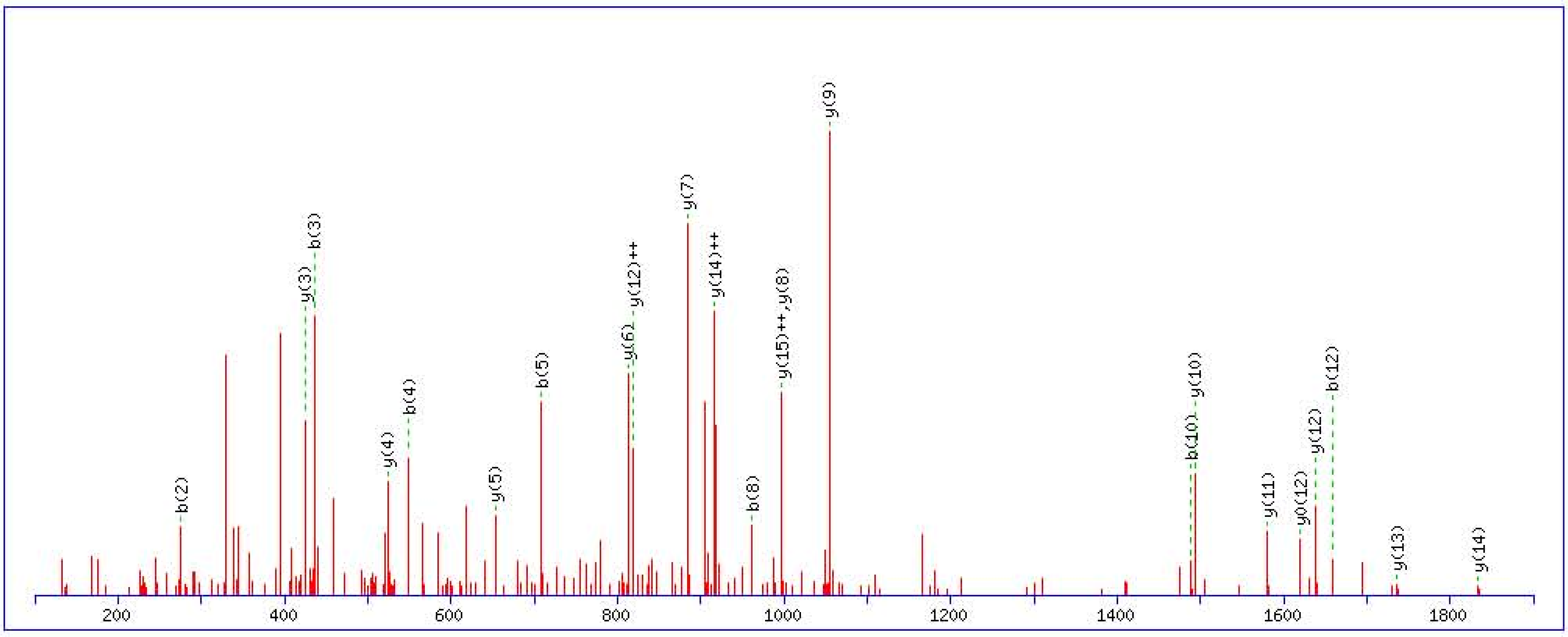
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CDCICPVGSQGLACEVSYR**
Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

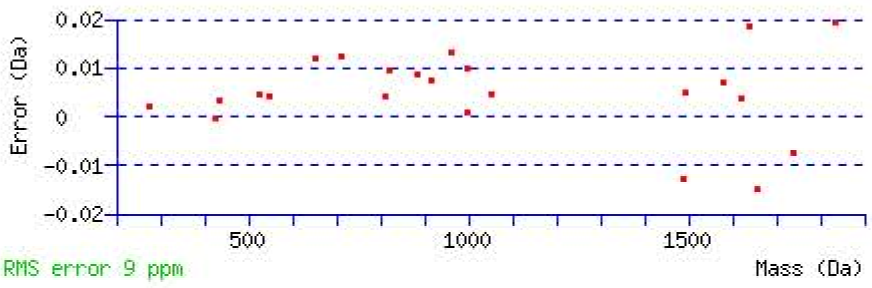
Match to Query 63740: 2541.121152 from(848.047660,3+) rtinseconds(2141) index(25672)
Title: Locus:1.1.1.2887.25 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

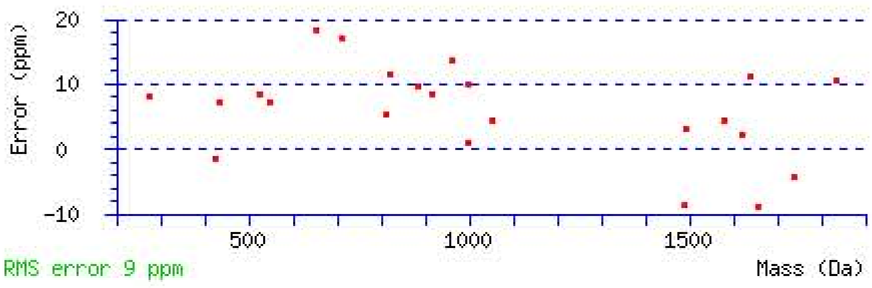
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2541.094299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 78 **Expect:** 1e-007
Matches : 23/192 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	161.037925	81.022600					C							19
2	**276.064868**	138.536072			258.054303	129.530790	D	2382.070908	1191.539092	2365.044359	1183.025817	2364.060343	1182.533809	18
3	**436.095517**	218.551397			418.084952	209.546114	C	2267.043965	1134.025620	2250.017416	1125.512346	2249.033400	1125.020338	17
4	**549.179581**	275.093429			531.169016	266.088146	I	2107.013316	1054.010296	2089.986767	1045.497021	2089.002751	1045.005013	16
5	**709.210230**	355.108753			691.199665	346.103471	C	1993.929252	997.468264	1976.902703	988.954990	1975.918687	988.462982	15
6	806.262994	403.635135			788.252429	394.629853	P	***1833.898603***	917.452940	1816.872054	908.939665	1815.888038	908.447657	14
7	905.331408	453.169342			887.320843	444.164060	V	***1736.845839***	868.926558	1719.819290	860.413283	1718.835274	859.921275	13
8	**962.352872**	481.680074			944.342307	472.674792	G	***1637.777425***	819.392351	1620.750876	810.879076	1619.766860	810.387068	12
9	1049.384900	525.196088			1031.374335	516.190806	S	***1580.755961***	790.881619	1563.729412	782.368344	1562.745396	781.876336	11
10	**1488.610226**	744.808751	1471.583677	736.295477	1470.599661	735.803469	Q	***1493.723933***	747.365605	1476.697384	738.852330	1475.713368	738.360322	10
11	1545.631690	773.319483	1528.605141	764.806209	1527.621125	764.314201	G	***1054.498607***	527.752941	1037.472058	519.239667	1036.488042	518.747659	9
12	**1658.715754**	829.861515	1641.689205	821.348241	1640.705189	820.856233	L	***997.477143***	499.242209	980.450594	490.728935	979.466578	490.236927	8
13	1729.752868	865.380072	1712.726319	856.866798	1711.742303	856.374790	A	***884.393079***	442.700178	867.366530	434.186903	866.382514	433.694895	7
14	1889.783517	945.395397	1872.756968	936.882122	1871.772952	936.390114	C	***813.355965***	407.181621	796.329416	398.668346	795.345400	398.176338	6
15	2018.826110	1009.916693	2001.799561	1001.403419	2000.815545	1000.911411	E	***653.325316***	327.166296	636.298767	318.653021	635.314751	318.161013	5
16	2117.894524	1059.450900	2100.867975	1050.937625	2099.883959	1050.445617	V	***524.282723***	262.645000	507.256174	254.131725	506.272158	253.639717	4
17	2204.926552	1102.966914	2187.900003	1094.453639	2186.915987	1093.961631	S	***425.214309***	213.110793	408.187760	204.597518	407.203744	204.105510	3
18	2367.989881	1184.498578	2350.963332	1175.985304	2349.979316	1175.493296	Y	338.182281	169.594778	321.155732	161.081504			2
19							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.9	2541.094299	0.026853	CDCICPVGSQGLACEVSYR

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

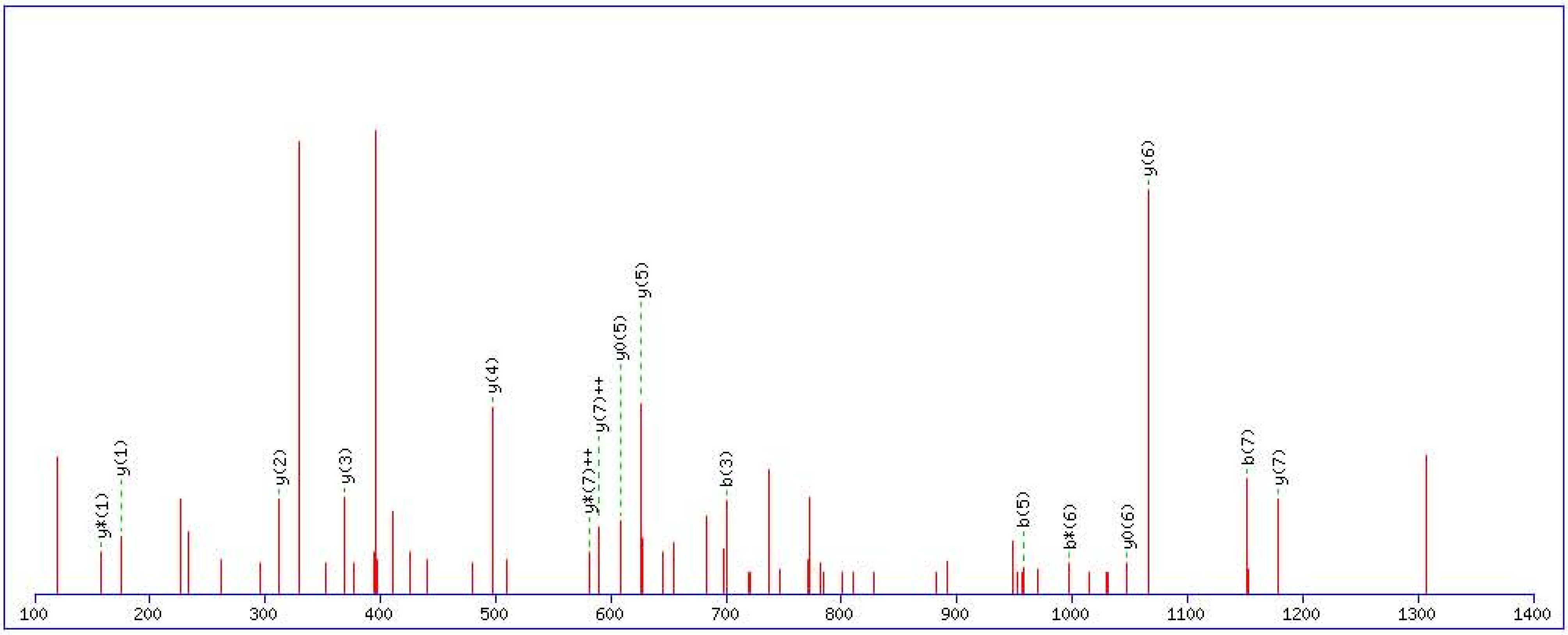
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLQEQGHR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

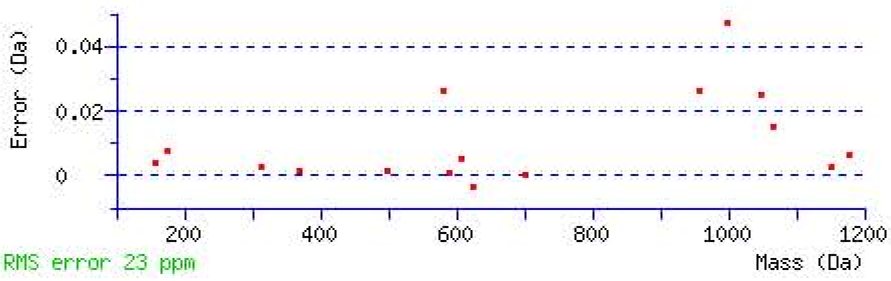
Match to Query 27481: 1324.684808 from(663.349680,2+) rtinseconds(1497) index(38756)
Title: Locus:1.1.1.2970.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

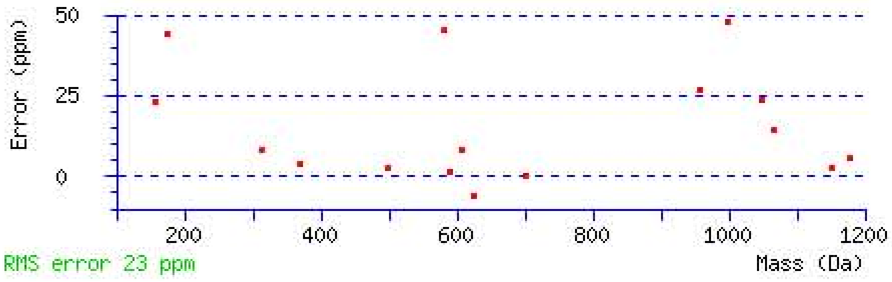
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1324.671021
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0027
Matches : 16/66 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	148.075690	74.541483					F							8
2	261.159754	131.083515					L	***1178.609889***	589.808583	1161.583340	581.295308	1160.599324	580.803300	7
3	**700.385080**	350.696178	683.358531	342.182904			Q	***1065.525825***	533.266551	1048.499276	524.753276	1047.515260	524.261268	6
4	829.427673	415.217475	812.401124	406.704200	811.417108	406.212192	E	***626.300499***	313.653888	609.273950	305.140613	608.289934	304.648605	5
5	**957.486251**	479.246764	940.459702	470.733489	939.475686	470.241481	Q	***497.257906***	249.132591	480.231357	240.619317			4
6	1014.507715	507.757496	997.481166	499.244221	996.497150	498.752213	G	***369.199328***	185.103302	352.172779	176.590028			3
7	**1151.566627**	576.286952	1134.540078	567.773677	1133.556062	567.281669	H	***312.177864***	156.592570	295.151315	148.079296			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FLQEQGHR
(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	1324.671021	0.013787	FLQEQGHR
13.9	1324.671021	0.013787	FLQEQGHR
8.1	1324.669647	0.015161	MKEIAEAYLGGK
5.2	1324.692795	-0.007987	YLDFSLFKHR
4.4	1324.696182	-0.011374	FFGGLCLDIKR
2.5	1324.682236	0.002572	QWRANPSR

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

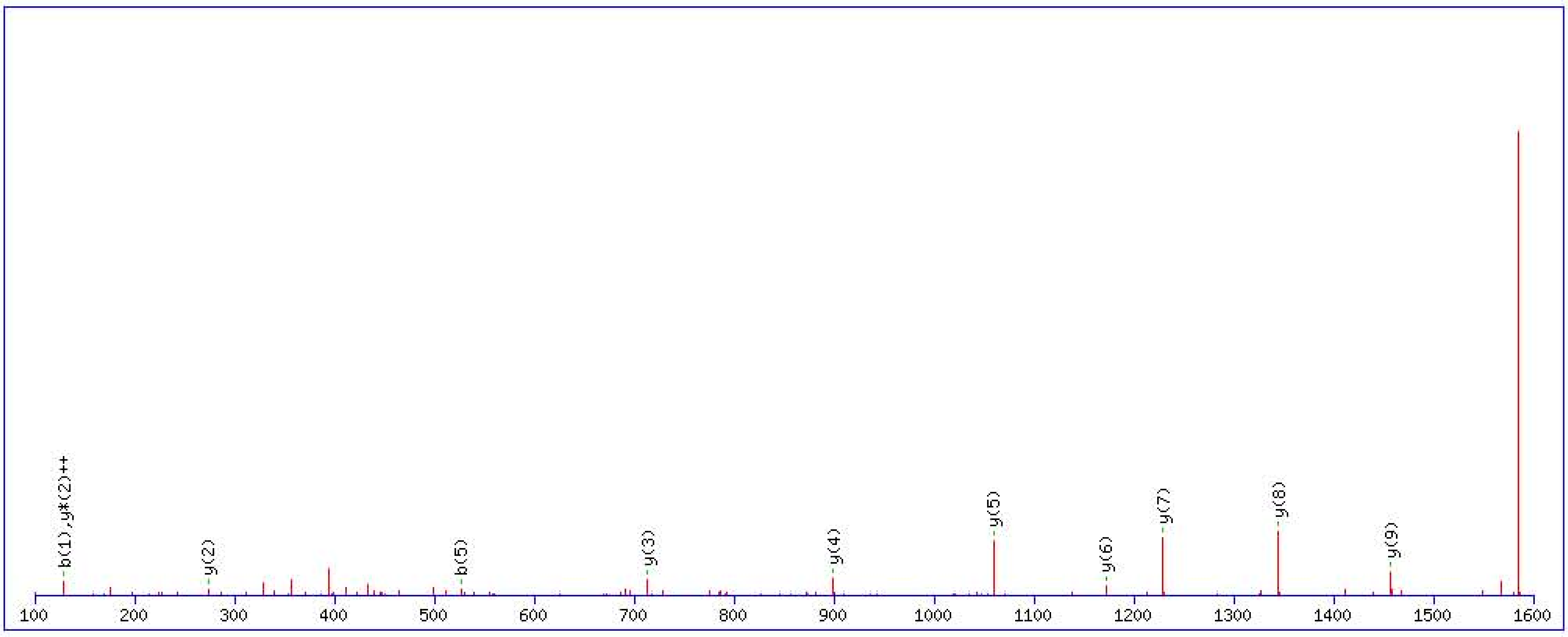
{MATRIX} {SCIENCE} Mascot Search Results

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

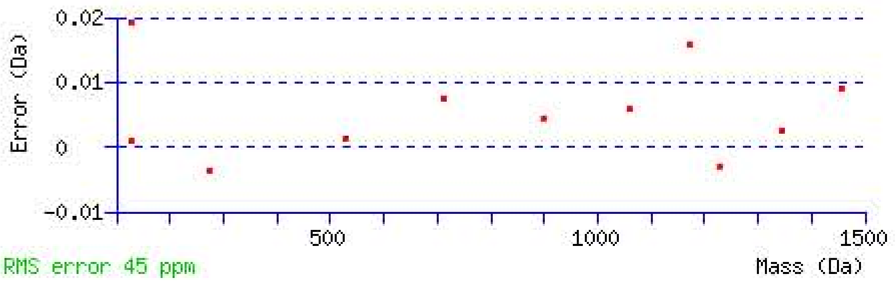
Match to Query 37982: 1584.840248 from(793.427400,2+) rtinseconds(2024) index(24858)
Title: Locus:1.1.1.2847.13 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

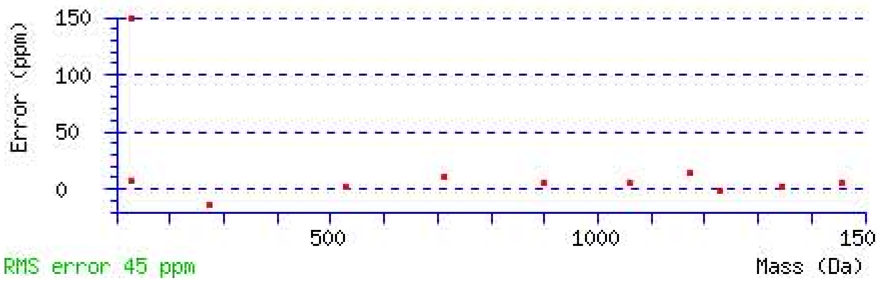
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1584.826874
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 9.2e-006
Matches : 11/90 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							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
64.8	1584.826874	0.013374	KLDGICWQVR
25.1	1584.858353	-0.018105	QLDGLAGLKGEGSRGK
8.7	1584.822830	0.017418	QLDQKCKQAR
8.7	1584.822830	0.017418	QLDQKCKQAR
8.1	1584.858337	-0.018089	LKSNDGEERLAVVR
5.8	1584.841278	-0.001030	QLAWVGDGVWVSIR
5.1	1584.819458	0.020790	QITRSWQEAR
3.3	1584.830704	0.009544	GAIRKACNAHGGVFK
2.1	1584.851822	-0.011574	SLTMARRGPAPVSSR
1.7	1584.848465	-0.008217	VKELGHSTQQFRR

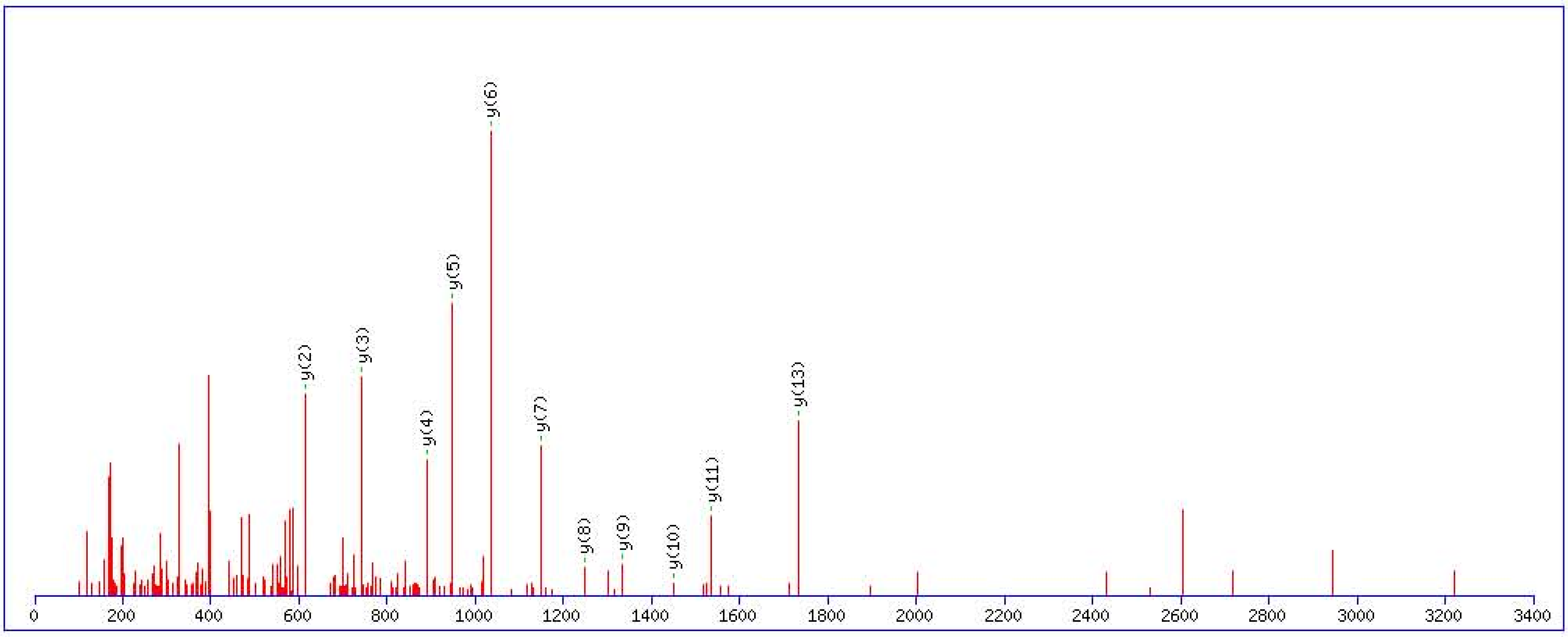
{MATRIX SCIENCE} Mascot Search Results

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

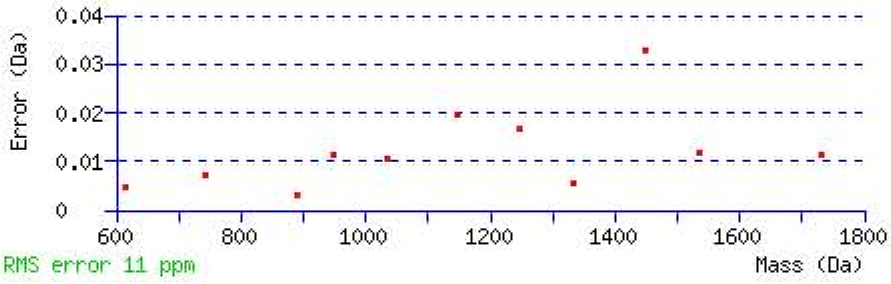
Match to Query 48228: 1931.002692 from(644.674840,3+) rtinseconds(2499) index(28042)
Title: Locus:1.1.1.3012.7 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

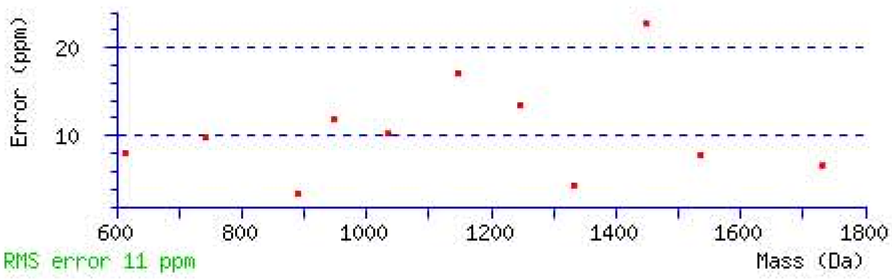
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1930.982254
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 87  Expect: 5.5e-008
Matches : 11/138 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							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





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
87.3	1930.982254	0.020438	SLPVSDSVLSGFEQR

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

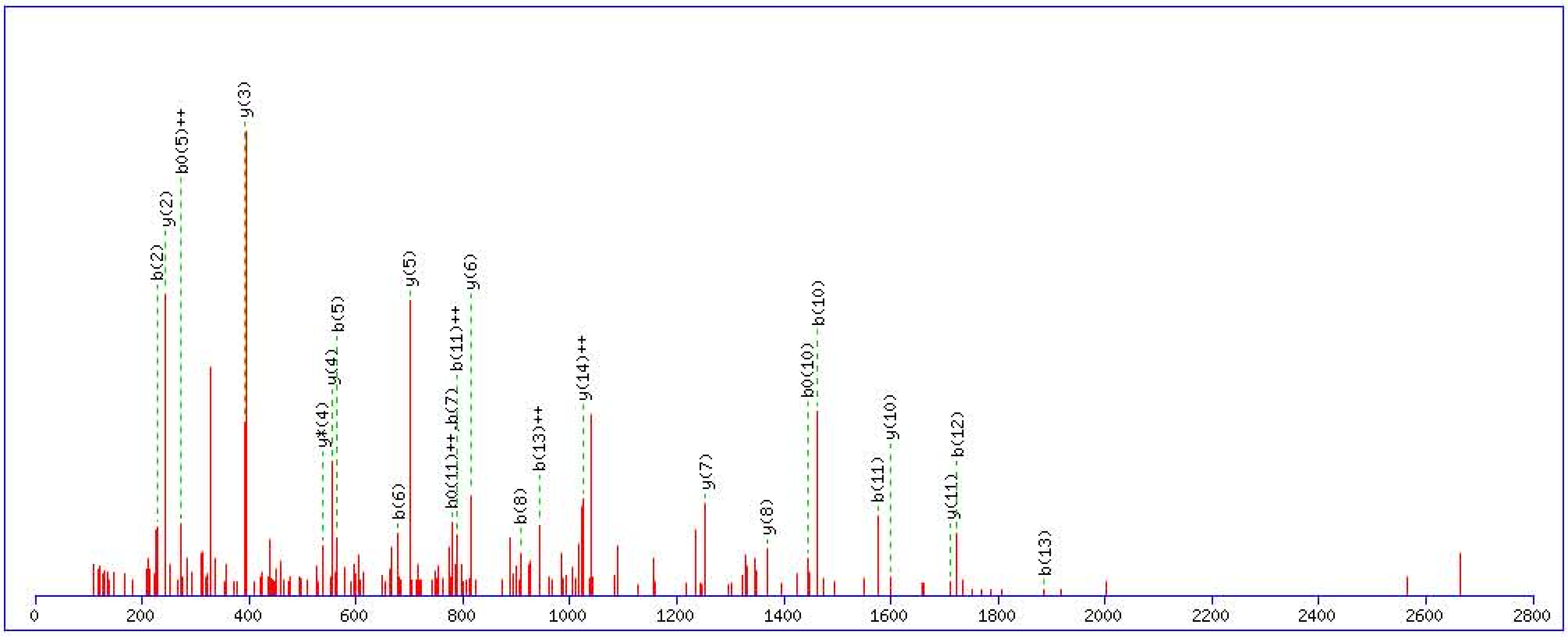
Mascot Search Results

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

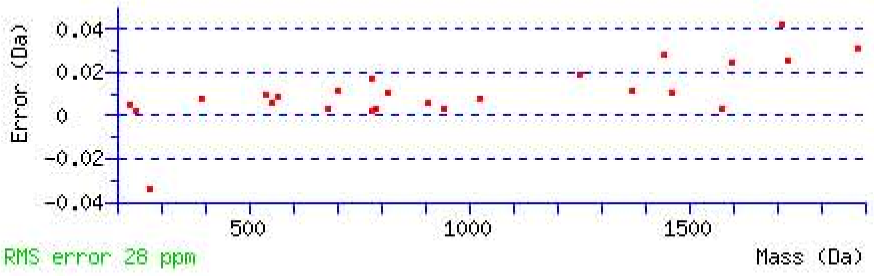
Match to Query 57408: 2275.159482 from(759.393770,3+) rtinseconds(2365) index(27263)
Title: Locus:1.1.1.2965.22 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

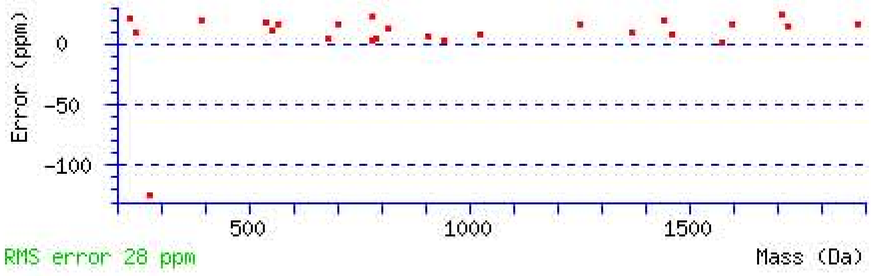
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from [0] to [2800] Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 40 **Expect:** 0.003
Matches : 25/160 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	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
40.1	2275.134720	0.024762	VQEAHLTEDQIFYFPK
15.8	2275.134720	0.024762	VQEAHLTEDQIFYFPK

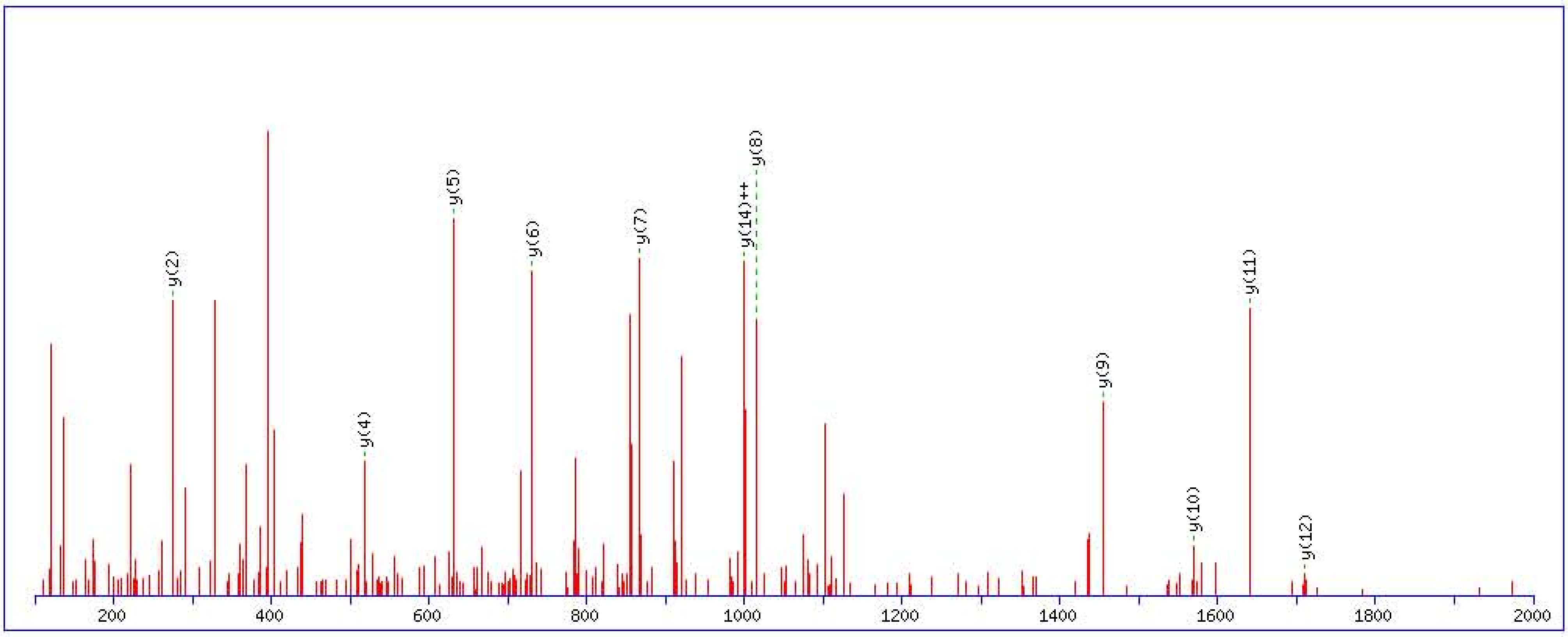
Mascot Search Results

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

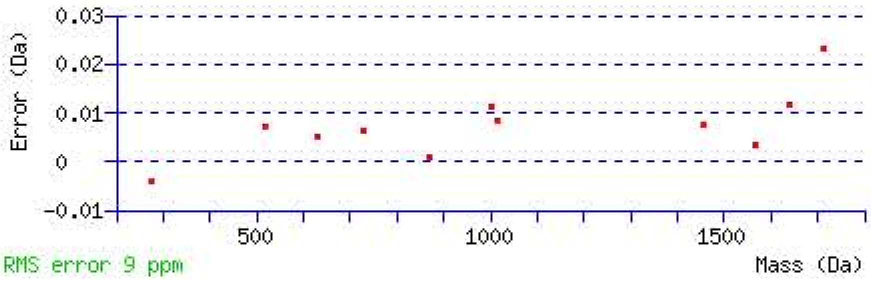
Match to Query 59342: 2366.110392 from(789.710740,3+) rtinseconds(2540) index(28305)
Title: Locus:1.1.1.3026.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

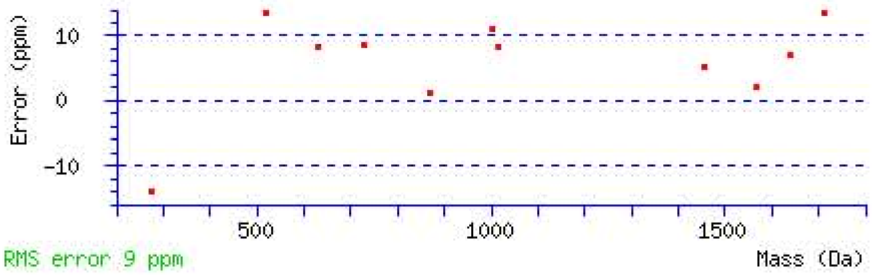
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2366.082382
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 63 **Expect:** 9.7e-006
Matches : 11/164 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	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
62.8	2366.082382	0.028010	YGFCEAADQFHVLDEVR

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

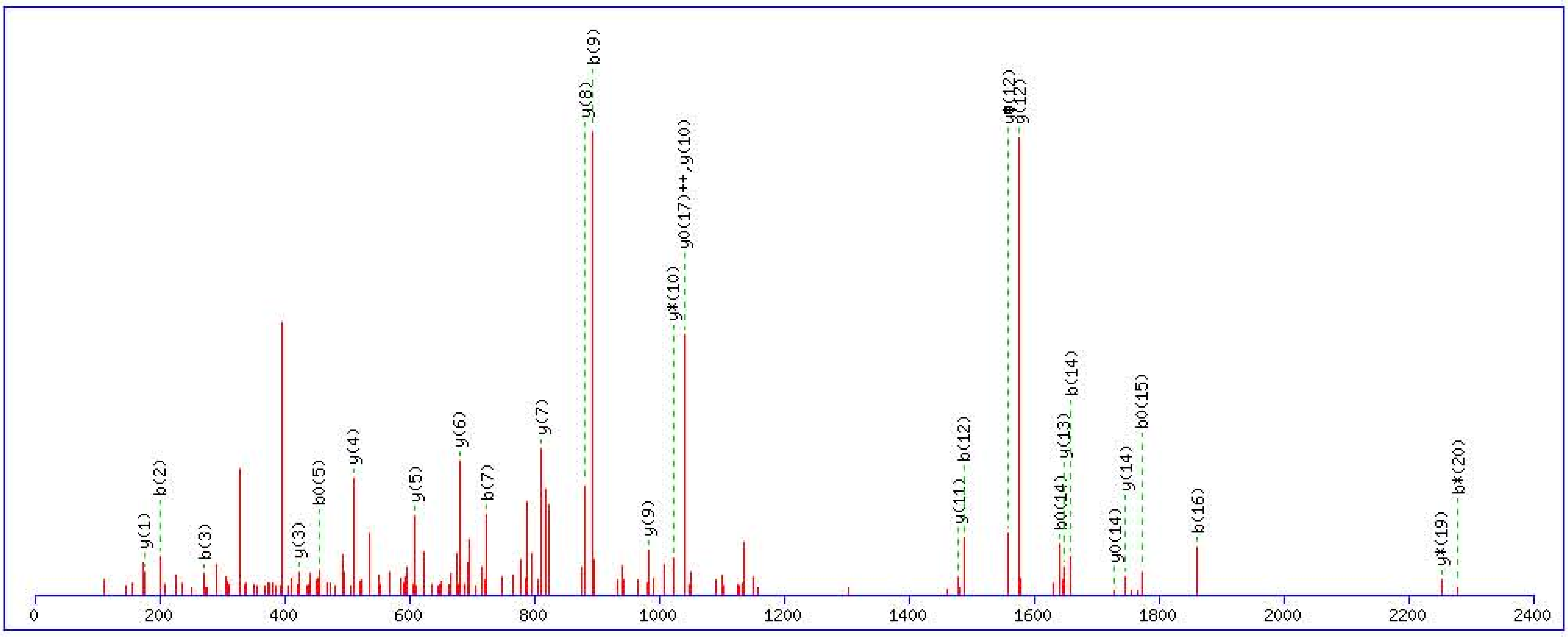
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEATTLHVAPQGTAMAVSTFR**
Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

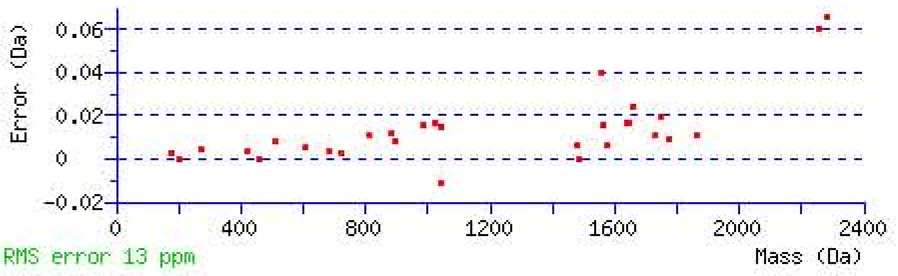
Match to Query 61936: 2469.280152 from(824.100660,3+) rtinseconds(2100) index(25401)
Title: Locus:1.1.1.2873.25 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

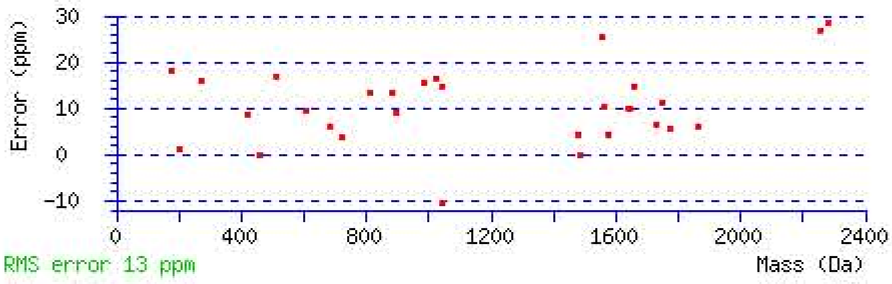
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2469.250839
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 81 **Expect:** 2.5e-008
Matches : 30/214 fragment ions using 49 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	72.044390	36.525833					A							21
2	**201.086983**	101.047130			183.076418	92.041847	E	2399.221002	1200.114139	2382.194453	1191.600864	2381.210437	1191.108856	20
3	**272.124097**	136.565687			254.113532	127.560404	A	2270.178409	1135.592842	2253.151860	1127.079568	2252.167844	1126.587560	19
4	373.171776	187.089526			355.161211	178.084244	T	2199.141295	1100.074285	2182.114746	1091.561011	2181.130730	1091.069003	18
5	474.219455	237.613366			456.208890	228.608083	T	2098.093616	1049.550446	2081.067067	1041.037171	2080.083051	1040.545163	17
6	587.303519	294.155398			569.292954	285.150115	L	1997.045937	999.026606	1980.019388	990.513332	1979.035372	990.021324	16
7	**724.362431**	362.684854			706.351866	353.679571	H	1883.961873	942.484574	1866.935324	933.971300	1865.951308	933.479292	15
8	823.430845	412.219061			805.420280	403.213778	V	***1746.902961***	873.955118	1729.876412	865.441844	1728.892396	864.949836	14
9	**894.467959**	447.737618			876.457394	438.732335	A	***1647.834547***	824.420911	1630.807998	815.907637	1629.823982	815.415629	13
10	991.520723	496.264000			973.510158	487.258717	P	***1576.797433***	788.902355	1559.770884	780.389080	1558.786868	779.897072	12
11	1430.746049	715.876663	1413.719500	707.363388	1412.735484	706.871380	Q	***1479.744669***	740.375972	1462.718120	731.862698	1461.734104	731.370690	11
12	**1487.767513**	744.387395	1470.740964	735.874120	1469.756948	735.382112	G	***1040.519343***	520.763309	1023.492794	512.250035	1022.508778	511.758027	10
13	1588.815192	794.911234	1571.788643	786.397960	1570.804627	785.905952	T	***983.497879***	492.252577	966.471330	483.739303	965.487314	483.247295	9
14	**1659.852306**	830.429791	1642.825757	821.916517	1641.841741	821.424509	A	***882.450200***	441.728738	865.423651	433.215463	864.439635	432.723455	8
15	1790.892791	895.950034	1773.866242	887.436759	1772.882226	886.944751	M	***811.413086***	406.210181	794.386537	397.696906	793.402521	397.204898	7
16	**1861.929905**	931.468591	1844.903356	922.955316	1843.919340	922.463308	A	***680.372601***	340.689938	663.346052	332.176664	662.362036	331.684656	6
17	1960.998319	981.002798	1943.971770	972.489523	1942.987754	971.997515	V	***609.335487***	305.171381	592.308938	296.658107	591.324922	296.166099	5
18	2048.030347	1024.518812	2031.003798	1016.005537	2030.019782	1015.513529	S	***510.267073***	255.637174	493.240524	247.123900	492.256508	246.631892	4
19	2149.078026	1075.042651	2132.051477	1066.529376	2131.067461	1066.037368	T	***423.235045***	212.121160	406.208496	203.607886	405.224480	203.115878	3
20	2296.146440	1148.576858	2279.119891	1140.063583	2278.135875	1139.571575	F	322.187366	161.597321	305.160817	153.084046			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.2	2469.250839	0.029313	AEATTLHVAPQGTAMAVSTFR
0.1	2469.246765	0.033387	LSSQLVEHCQKLEEQMNKLR

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

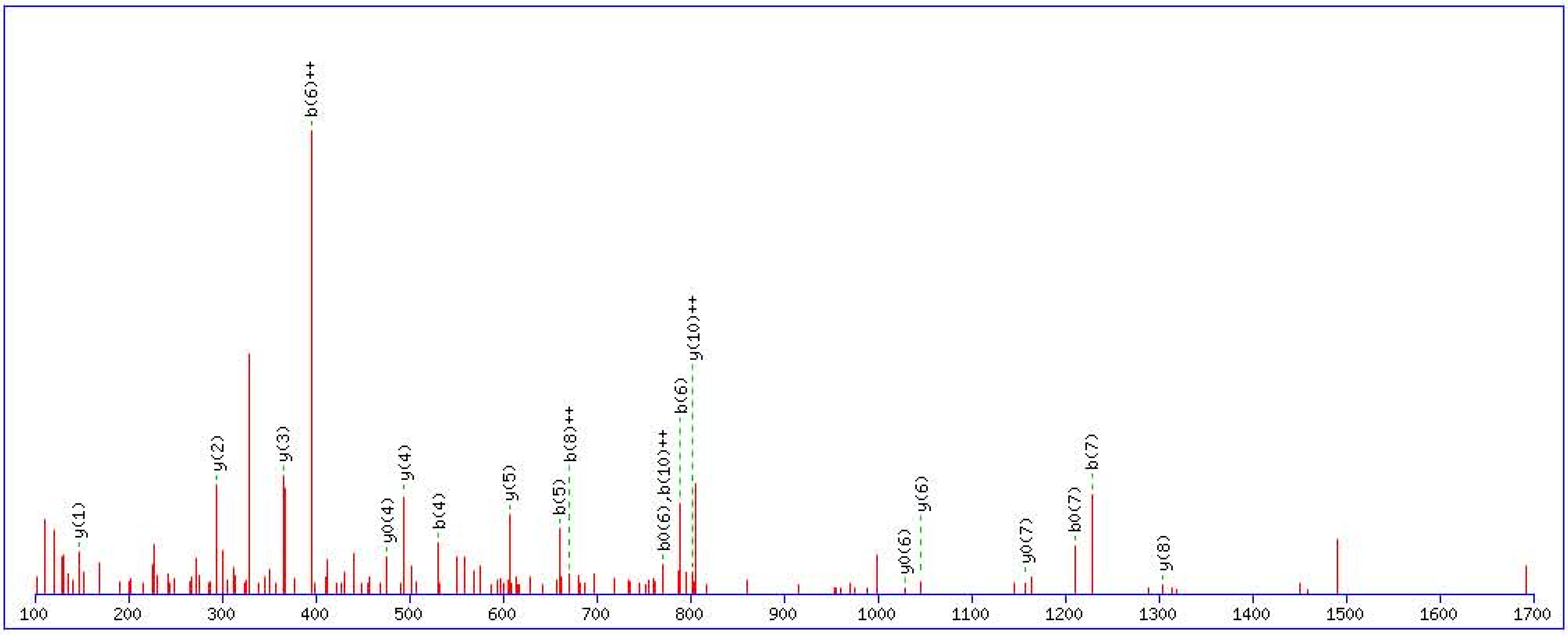
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEHYEEQIEAFK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

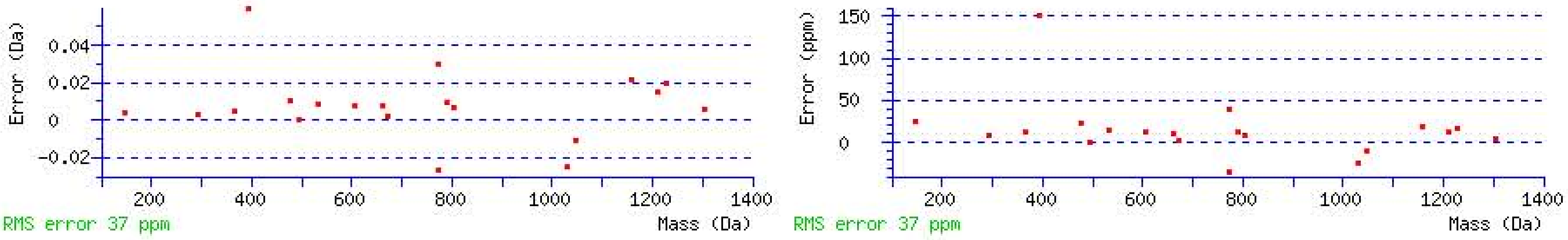
Match to Query 46105: 1833.881292 from(612.301040,3+) rtinseconds(1950) index(41861)
Title: Locus:1.1.1.3128.16 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1833.860703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.055
Matches : 20/114 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	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
26.1	1833.860703	0.020589	TEHYEEQIEAFK

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

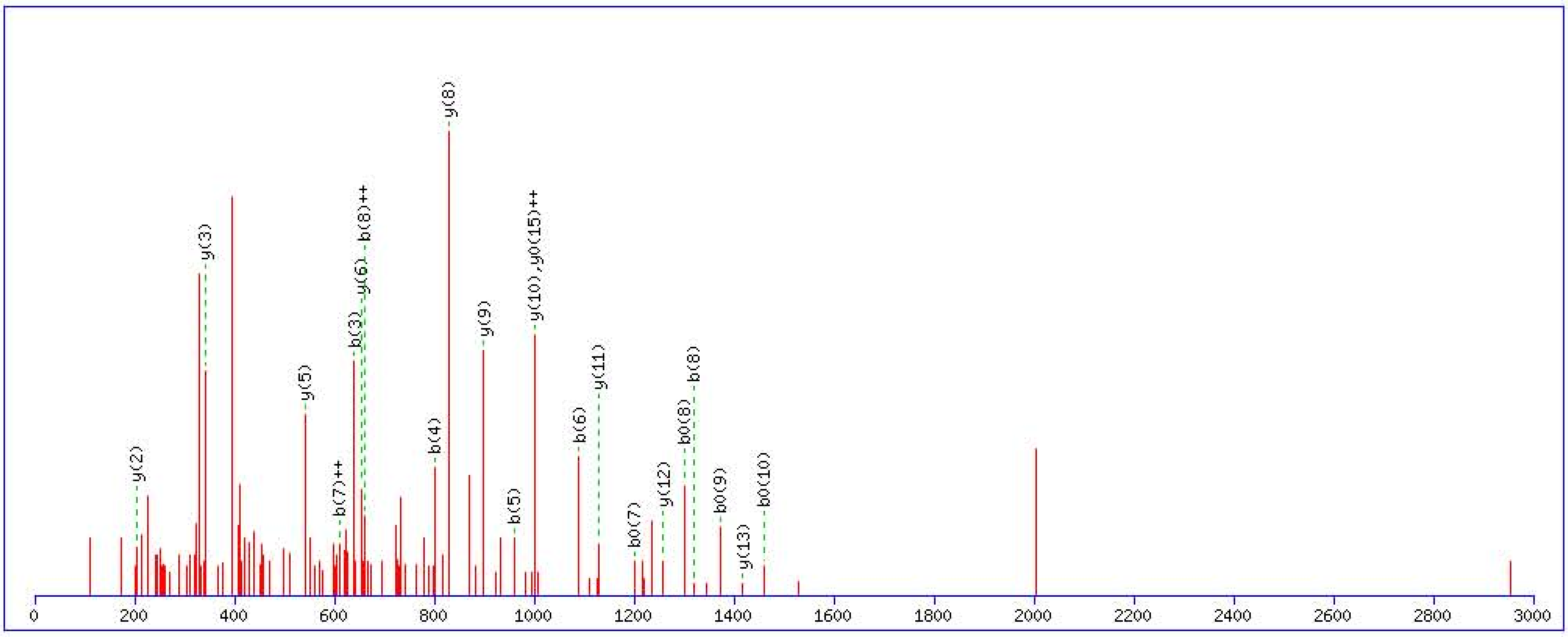
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEQCCEETASSISLHGK**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

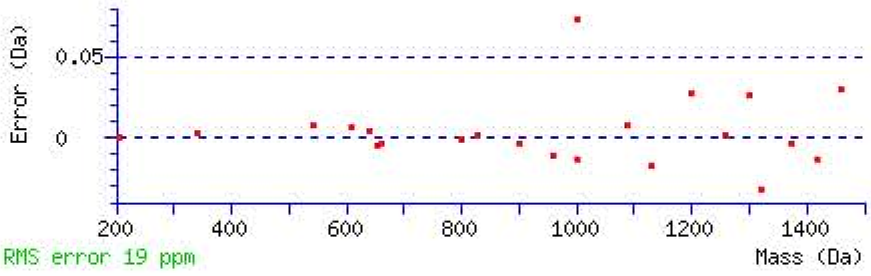
Match to Query 55889: 2217.007872 from(740.009900,3+) rtinseconds(1570) index(39316)
Title: Locus:1.1.1.2996.14 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

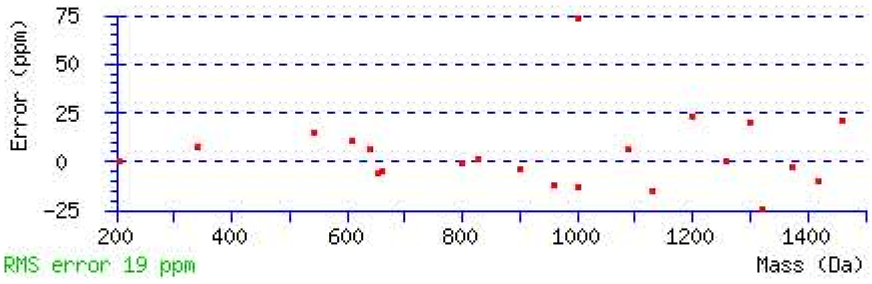
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2216.986404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00011
Matches : 22/178 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	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
50.9	2216.986404	0.021468	AEQCCEETASSISLHGK

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

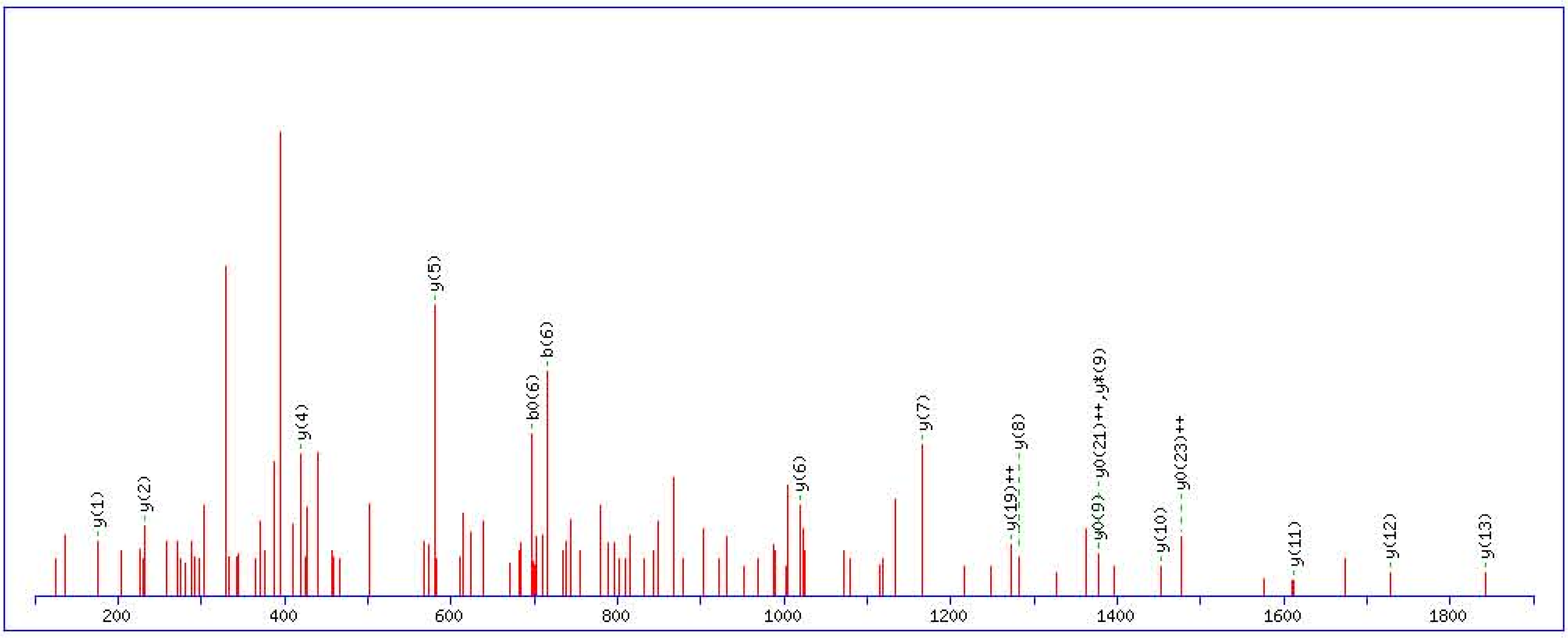
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QCVPTEPCEDAEDDCGNDFQCSTGR**
Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

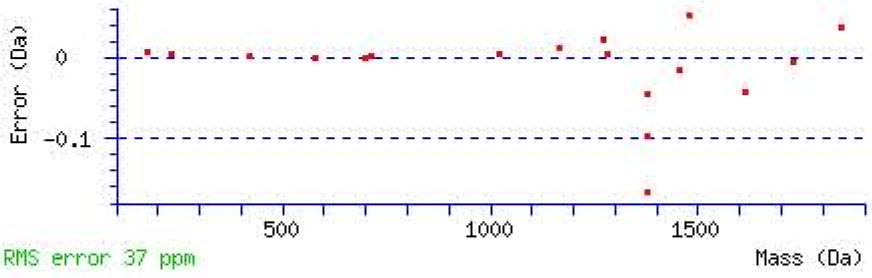
Match to Query 74380: 3257.291856 from(815.330240,4+) rtinseconds(1873) index(41196)
Title: Locus:1.1.1.3101.26 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

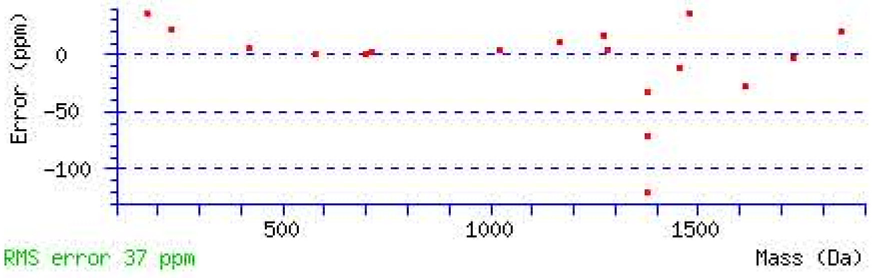
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3257.246475
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20    : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.00082
Matches : 18/276 fragment ions using 47 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							25
2	289.096503	145.051890	272.069954	136.538615			C	3130.195136	1565.601206	3113.168587	1557.087931	3112.184571	1556.595923	24
3	388.164917	194.586097	371.138368	186.072822			V	2970.164487	1485.585881	2953.137938	1477.072607	2952.153922	1476.580599	23
4	485.217681	243.112479	468.191132	234.599204			P	2871.096073	1436.051674	2854.069524	1427.538400	2853.085508	1427.046392	22
5	586.265360	293.636318	569.238811	285.123044	568.254795	284.631036	T	2774.043309	1387.525292	2757.016760	1379.012018	2756.032744	1378.520010	21
6	715.307953	358.157615	698.281404	349.644340	697.297388	349.152332	E	2672.995630	1337.001453	2655.969081	1328.488178	2654.985065	1327.996170	20
7	812.360717	406.683997	795.334168	398.170722	794.350152	397.678714	P	2543.953037	1272.480156	2526.926488	1263.966882	2525.942472	1263.474874	19
8	972.391366	486.699321	955.364817	478.186047	954.380801	477.694039	C	2446.900273	1223.953774	2429.873724	1215.440500	2428.889708	1214.948492	18
9	1101.433959	551.220618	1084.407410	542.707343	1083.423394	542.215335	E	2286.869624	1143.938450	2269.843075	1135.425175	2268.859059	1134.933167	17
10	1216.460902	608.734089	1199.434353	600.220815	1198.450337	599.728807	D	2157.827031	1079.417153	2140.800482	1070.903879	2139.816466	1070.411871	16
11	1287.498016	644.252646	1270.471467	635.739372	1269.487451	635.247364	A	2042.800088	1021.903682	2025.773539	1013.390408	2024.789523	1012.898400	15
12	1416.540609	708.773943	1399.514060	700.260668	1398.530044	699.768660	E	1971.762974	986.385125	1954.736425	977.871851	1953.752409	977.379843	14
13	1531.567552	766.287414	1514.541003	757.774140	1513.556987	757.282132	D	***1842.720381***	921.863828	1825.693832	913.350554	1824.709816	912.858546	13
14	1646.594495	823.800886	1629.567946	815.287611	1628.583930	814.795603	D	***1727.693438***	864.350357	1710.666889	855.837082	1709.682873	855.345074	12
15	1806.625144	903.816210	1789.598595	895.302936	1788.614579	894.810928	C	***1612.666495***	806.836885	1595.639946	798.323611	1594.655930	797.831603	11
16	1863.646608	932.326942	1846.620059	923.813668	1845.636043	923.321660	G	***1452.635846***	726.821561	1435.609297	718.308286	1434.625281	717.816278	10
17	1977.689535	989.348406	1960.662986	980.835131	1959.678970	980.343123	N	1395.614382	698.310829	1378.587833	689.797554	1377.603817	689.305546	9
18	2092.716478	1046.861877	2075.689929	1038.348603	2074.705913	1037.856595	D	***1281.571455***	641.289365	1264.544906	632.776091	1263.560890	632.284083	8
19	2239.784892	1120.396084	2222.758343	1111.882809	2221.774327	1111.390802	F	***1166.544512***	583.775894	1149.517963	575.262619	1148.533947	574.770611	7
20	2679.010218	1340.008747	2661.983669	1331.495473	2660.999653	1331.003465	Q	***1019.476098***	510.241687	1002.449549	501.728412	1001.465533	501.236404	6
21	2839.040867	1420.024072	2822.014318	1411.510797	2821.030302	1411.018789	C	***580.250772***	290.629024	563.224223	282.115749	562.240207	281.623741	5
22	2926.072895	1463.540086	2909.046346	1455.026811	2908.062330	1454.534803	S	***420.220123***	210.613699	403.193574	202.100425	402.209558	201.608417	4
23	3027.120574	1514.063925	3010.094025	1505.550650	3009.110009	1505.058642	T	333.188095	167.097685	316.161546	158.584411	315.177530	158.092403	3
24	3084.142038	1542.574657	3067.115489	1534.061382	3066.131473	1533.569374	G	***232.140416***	116.573846	215.113867	108.060571			2
25							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QCVPTEPCEDAEDDCGNDFQCSTGR
(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	3257.246475	0.045381	QCVPTEPCEDAEDDCGNDFQCSTGR

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

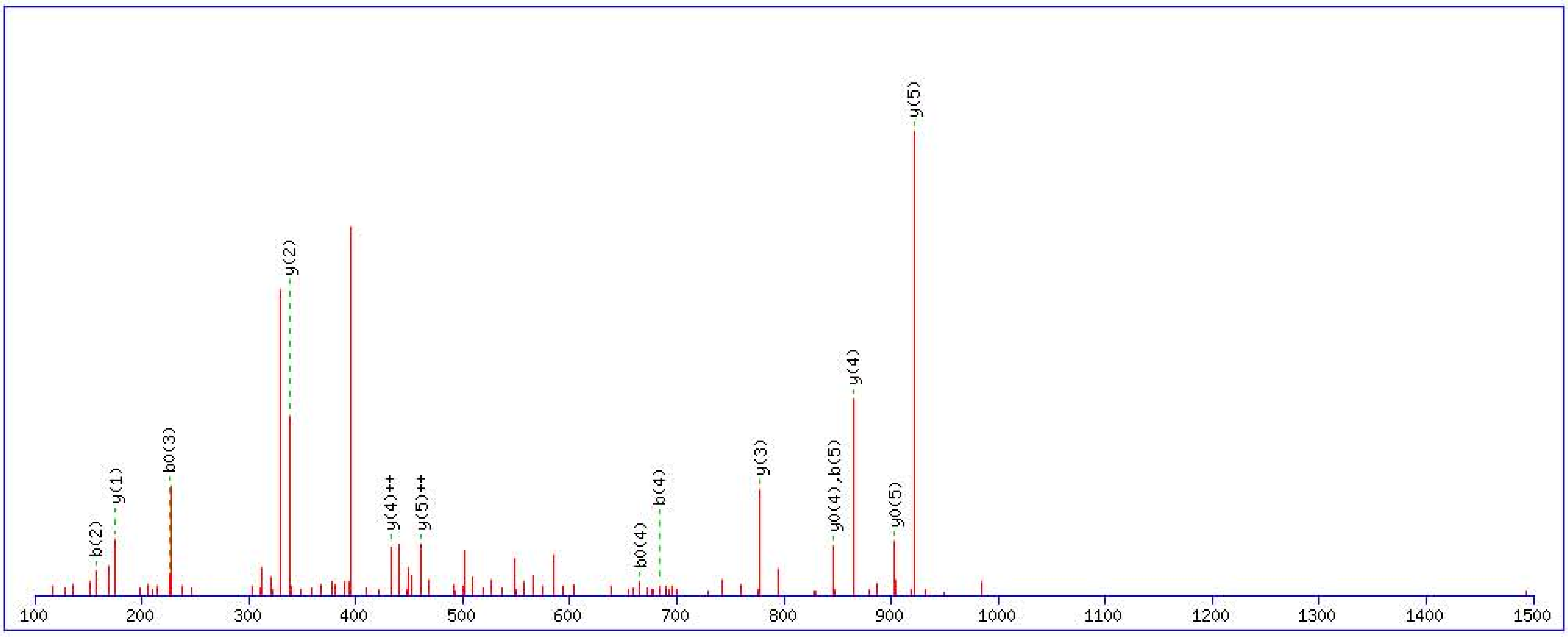
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGSQYR**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

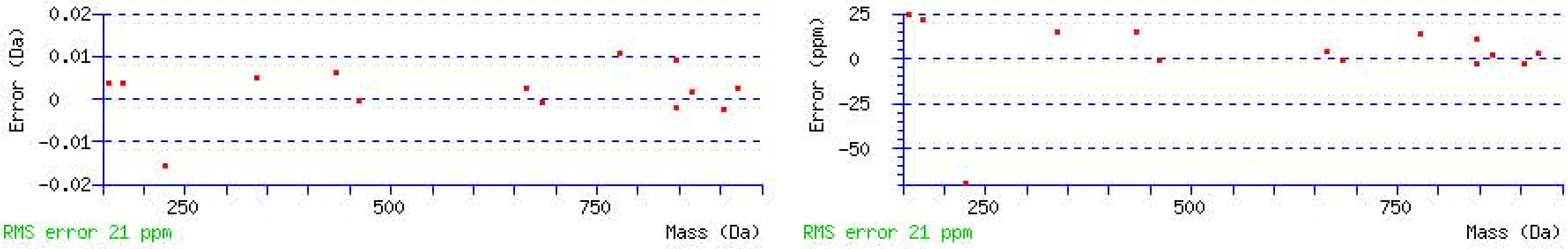
Match to Query 16512: 1019.527488 from(510.771020,2+) rtinseconds(1374) index(2387)
Title: Locus:1.1.1.2732.18 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1019.522232
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.063
Matches : 14/44 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	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
25.2	1019.522232	0.005256	VGSQYR
14.9	1019.539993	-0.012505	VGEAFALTGR
12.2	1019.533447	-0.005959	RSQYR
4.5	1019.533447	-0.005959	QSRYR
3.8	1019.539963	-0.012475	NVILENYR
3.4	1019.533447	-0.005959	RQSYR
3.2	1019.526047	0.001441	SRERGPYR
2.6	1019.525589	0.001899	VMMEVQKR
2.5	1019.539963	-0.012475	IIEAASNFR
2.4	1019.529419	-0.001931	REGLMRSR

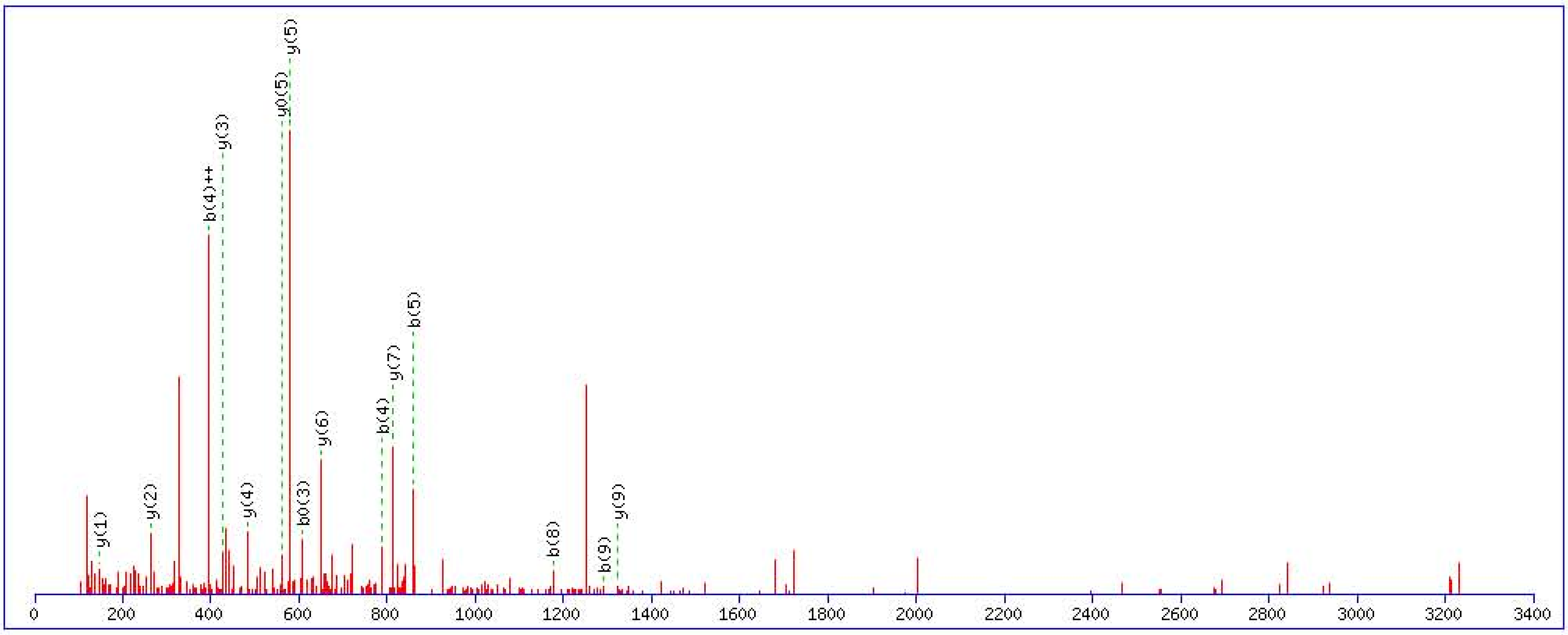
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAQYAPGYDK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

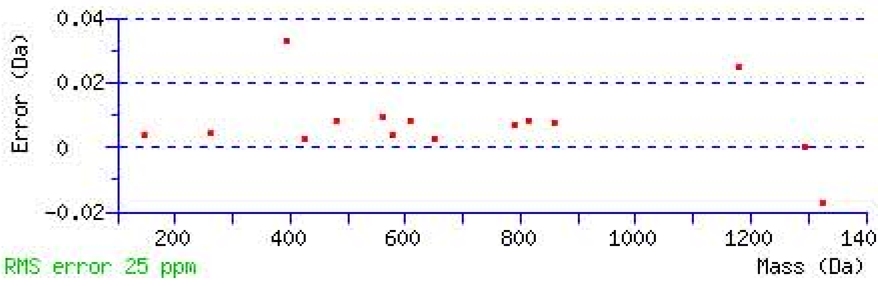
Match to Query 32939: 1437.670128 from(719.842340,2+) rtinseconds(1649) index(4213)
Title: Locus:1.1.1.2828.13 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

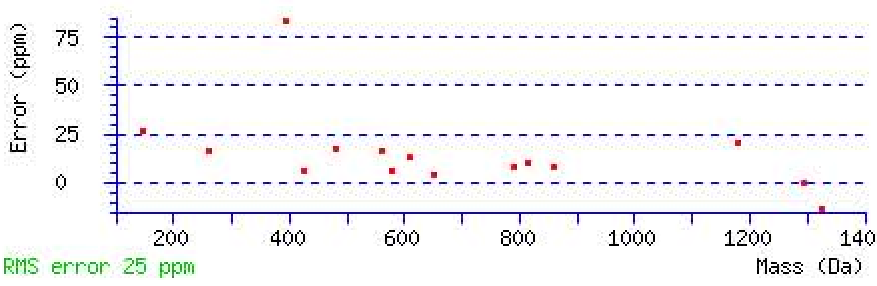
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1437.659836
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.015
Matches : 15/102 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	116.034219	58.520748			98.023654	49.515465	D							10
2	187.071333	94.039304			169.060768	85.034022	A	***1323.640187***	662.323732	1306.613638	653.810457	1305.629622	653.318449	9
3	626.296659	313.651968	609.270110	305.138693	608.286094	304.646685	Q	1252.603073	626.805175	1235.576524	618.291900	1234.592508	617.799892	8
4	**789.359988**	395.183632	772.333439	386.670358	771.349423	386.178350	Y	***813.377747***	407.192512	796.351198	398.679237	795.367182	398.187229	7
5	**860.397102**	430.702189	843.370553	422.188915	842.386537	421.696907	A	***650.314418***	325.660847	633.287869	317.147573	632.303853	316.655565	6
6	957.449866	479.228571	940.423317	470.715297	939.439301	470.223289	P	***579.277304***	290.142290	562.250755	281.629016	561.266739	281.137008	5
7	1014.471330	507.739303	997.444781	499.226029	996.460765	498.734021	G	***482.224540***	241.615908	465.197991	233.102634	464.213975	232.610626	4
8	**1177.534659**	589.270968	1160.508110	580.757693	1159.524094	580.265685	Y	***425.203076***	213.105176	408.176527	204.591902	407.192511	204.099894	3
9	**1292.561602**	646.784439	1275.535053	638.271165	1274.551037	637.779157	D	***262.139747***	131.573512	245.113198	123.060237	244.129182	122.568229	2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.6	1437.659836	0.010292	DAQYAPGYDK
7.2	1437.659164	0.010964	LAEAEQMALMGSR

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

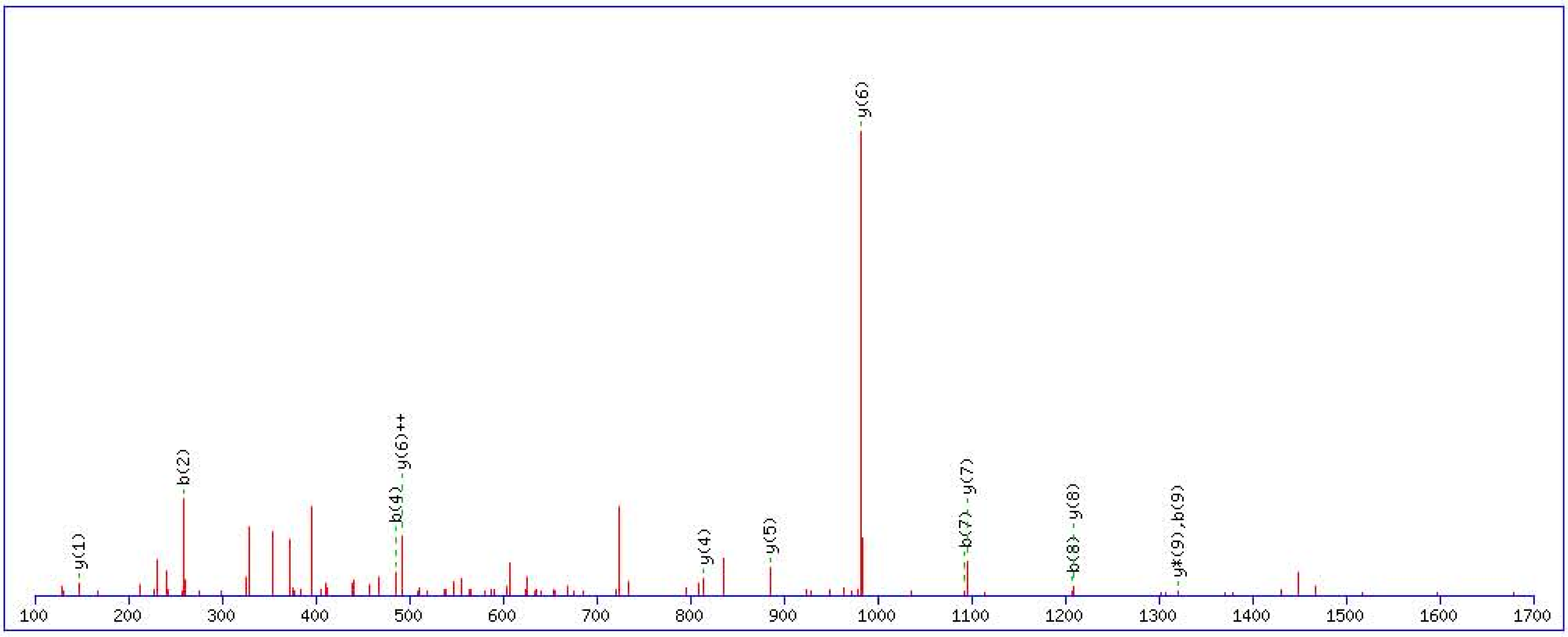
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EELLPAQDIK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

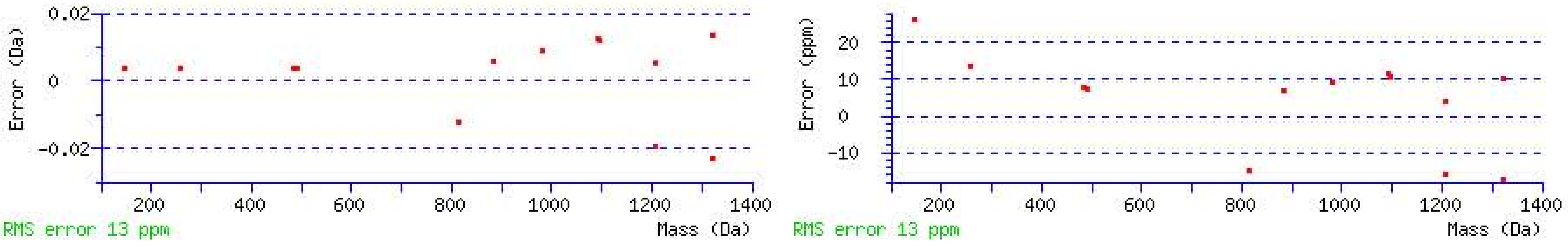
Match to Query 33896: 1465.798028 from(733.906290,2+) rtinseconds(2130) index(79719)
Title: Locus:1.1.1.2092.13 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1465.785019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.0048
Matches : 13/92 fragment ions using 28 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							10
2	*259.092462*	130.049869			241.081897	121.044587	E	1337.749736	669.378506	1320.723187	660.865232	1319.739171	660.373223	9
3	372.176526	186.591901			354.165961	177.586619	L	*1208.707143*	604.857210	1191.680594	596.343935	1190.696578	595.851927	8
4	*485.260590*	243.133933			467.250025	234.128651	L	*1095.623079*	548.315178	1078.596530	539.801903	1077.612514	539.309895	7
5	582.313354	291.660315			564.302789	282.655033	P	*982.539015*	491.773146	965.512466	483.259871	964.528450	482.767863	6
6	653.350468	327.178872			635.339903	318.173590	A	*885.486251*	443.246764	868.459702	434.733489	867.475686	434.241481	5
7	*1092.575794*	546.791535	1075.549245	538.278261	1074.565229	537.786253	Q	*814.449137*	407.728207	797.422588	399.214932	796.438572	398.722924	4
8	*1207.602737*	604.305007	1190.576188	595.791732	1189.592172	595.299724	D	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
9	*1320.686801*	660.847039	1303.660252	652.333764	1302.676236	651.841756	I	260.196868	130.602072	243.170319	122.088797			2
10							K	*147.112804*	74.060040	130.086255	65.546765			1



NCBI **BLAST** search of EELLPAQDIK
(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	1465.785019	0.013009	EELLPAQDIK
6.7	1465.814011	-0.015983	EPIAQDQPKILSK
5.5	1465.813995	-0.015967	SQLKHEILELEK
5.2	1465.804108	-0.006080	SRAFNFLNEIKK
3.9	1465.794235	0.003793	KWGIGYHLSLHR
0.5	1465.788849	0.009179	KQVEHQLEEAKK
0.4	1465.800125	-0.002097	LAQDGAHVVVSSRK
0.4	1465.789734	0.008294	TAAALGMHQKK

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

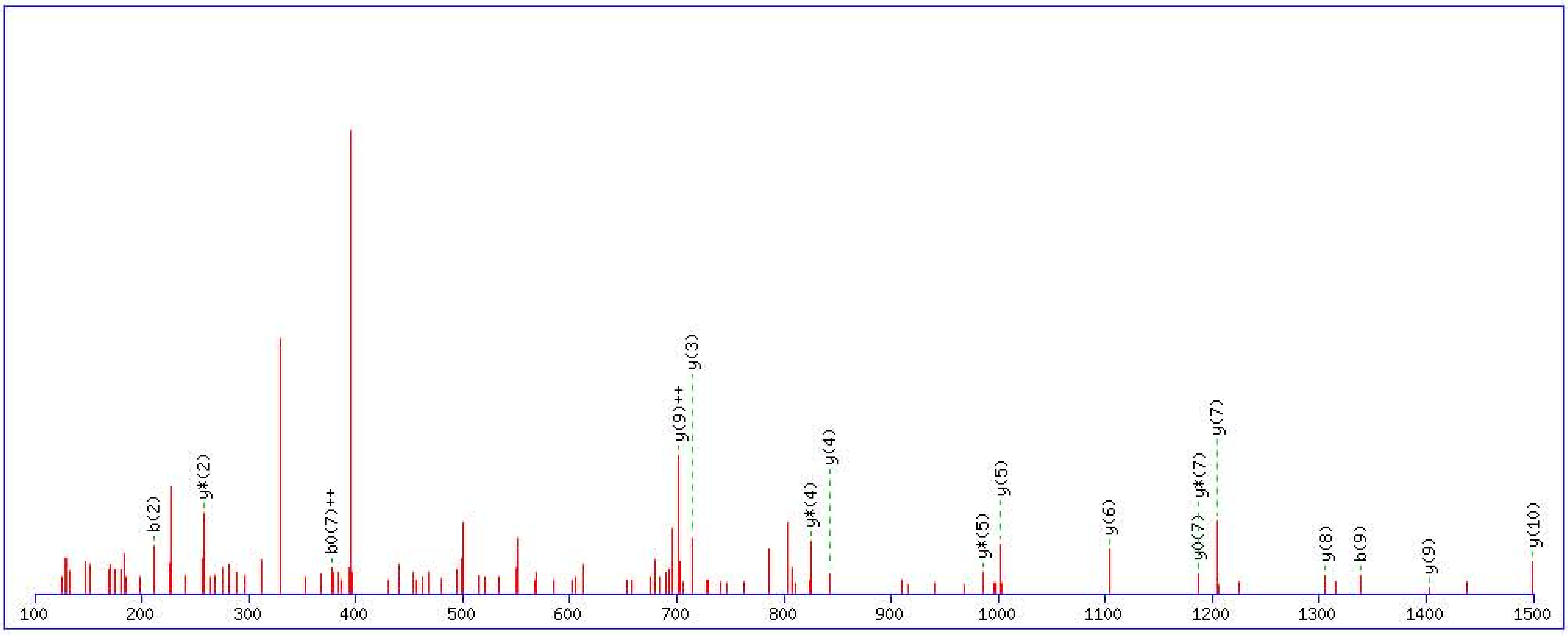
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPPTTTCQQQK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

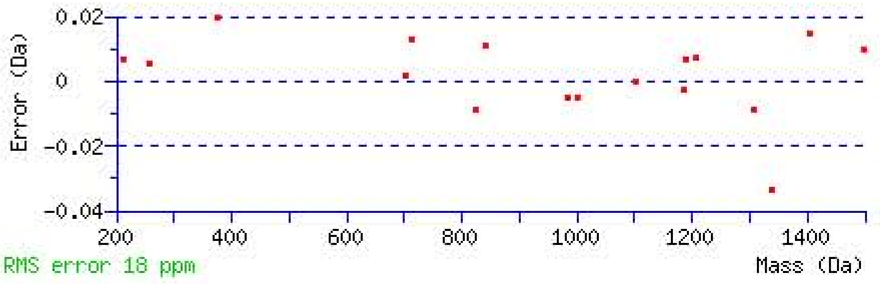
Match to Query 39275: 1611.815112 from(538.278980,3+) rtinseconds(1416) index(2668)
Title: Locus:1.1.1.2747.14 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

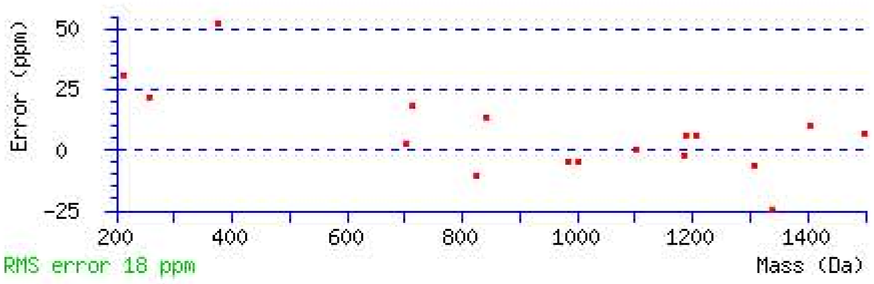
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1611.811295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.01
Matches : 17/90 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	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
34.0	1611.811295	0.003817	LPPTTTCQQQK
34.0	1611.811295	0.003817	LPPTTTCQQQK
31.1	1611.811295	0.003817	LPPTTTCQQQK

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

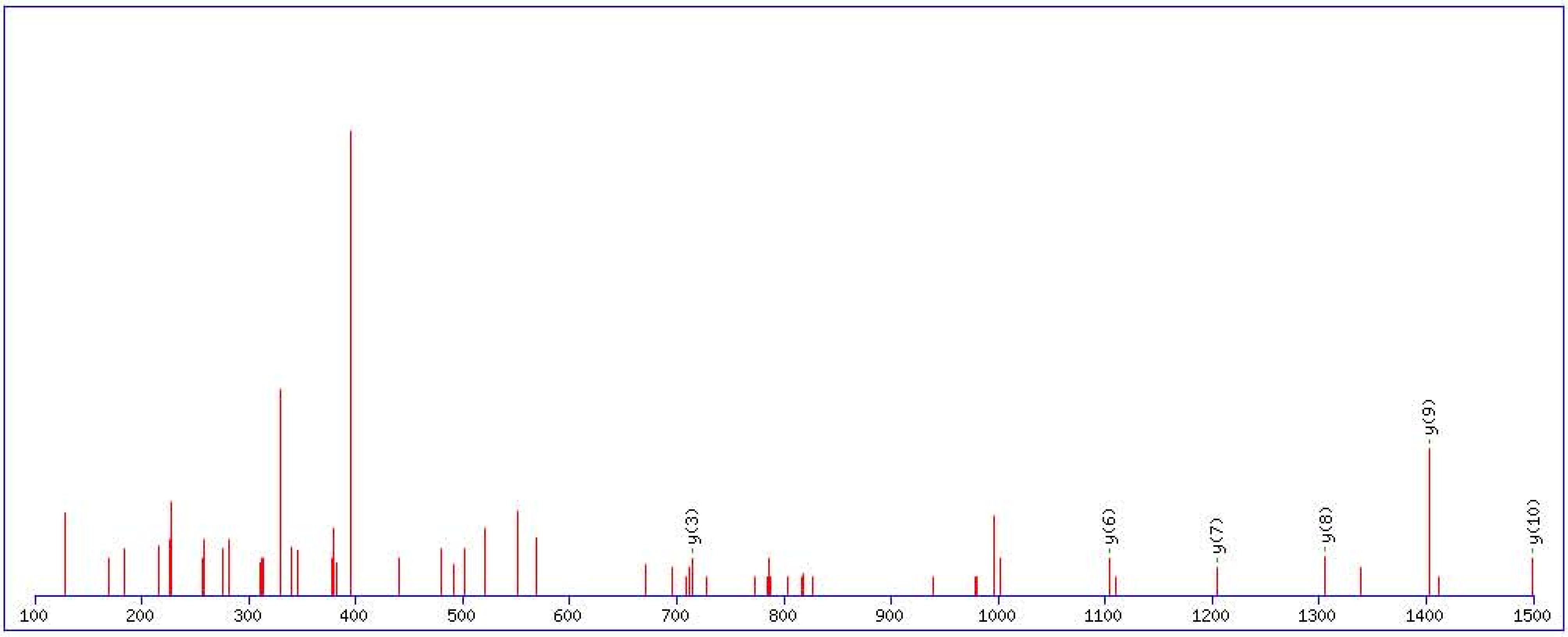
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPPTTTCQQQK**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

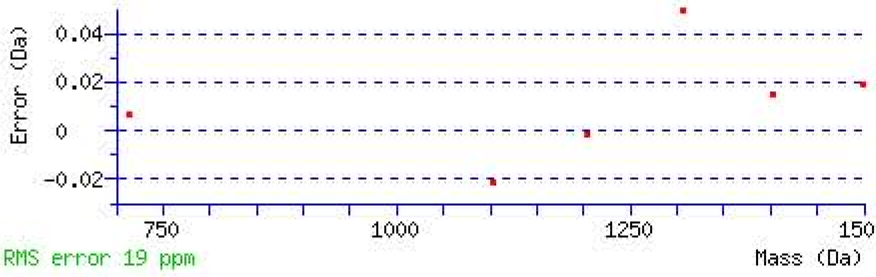
Match to Query 39279: 1611.819912 from(538.280580,3+) rtinseconds(1403) index(74984)
Title: Locus:1.1.1.1839.19 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

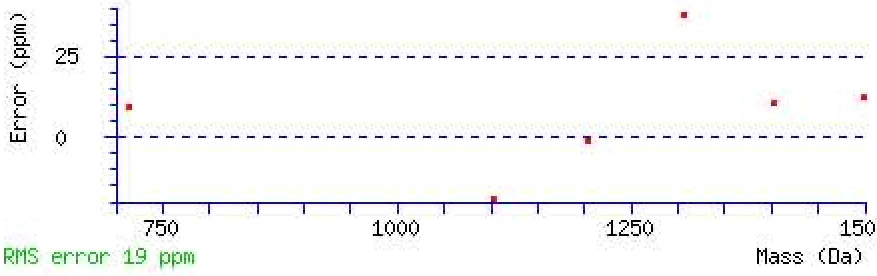
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 27  Expect: 0.0037
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
26.8	1611.811295	0.008617	LPPTTTCQQQK
26.8	1611.811295	0.008617	LPPTTTCQQQK
17.3	1611.811295	0.008617	LPPTTTCQQQK
0.8	1611.803864	0.016048	HQEMEDVIRLAQK

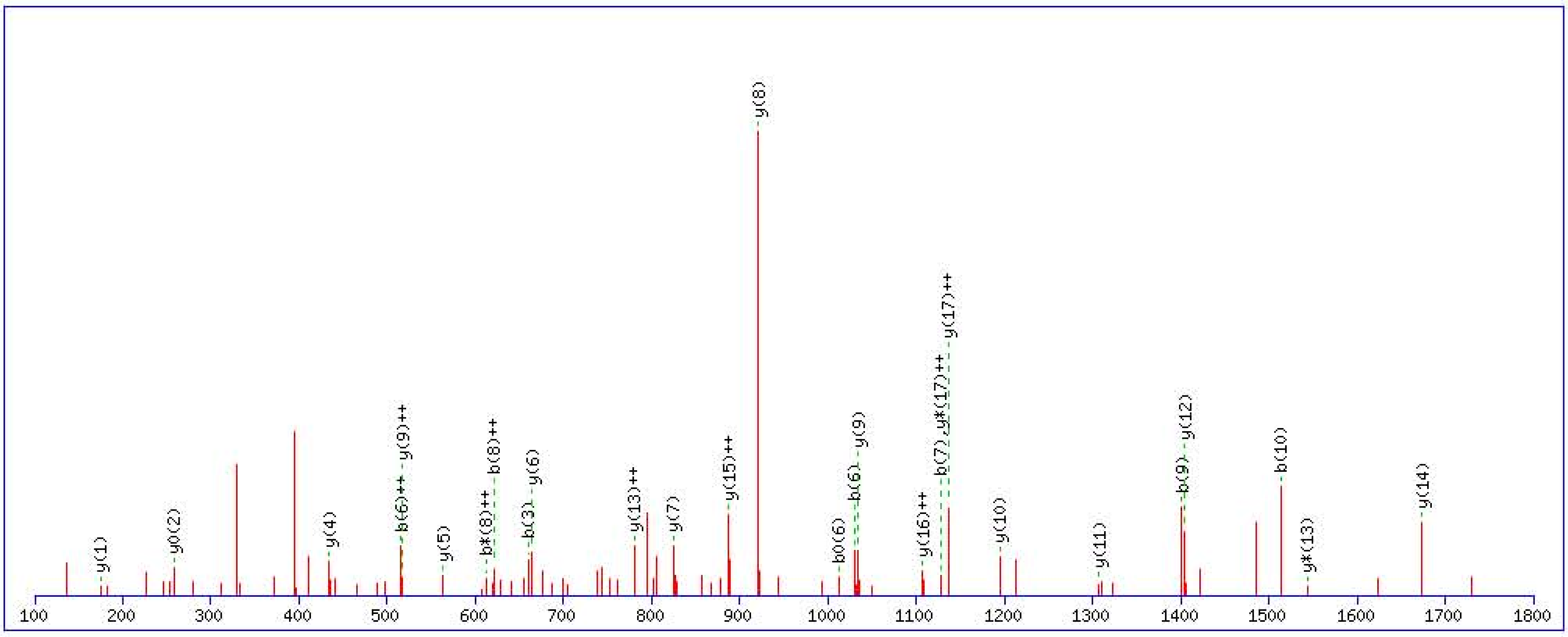
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGQTIRPICLPCTEGTTR**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

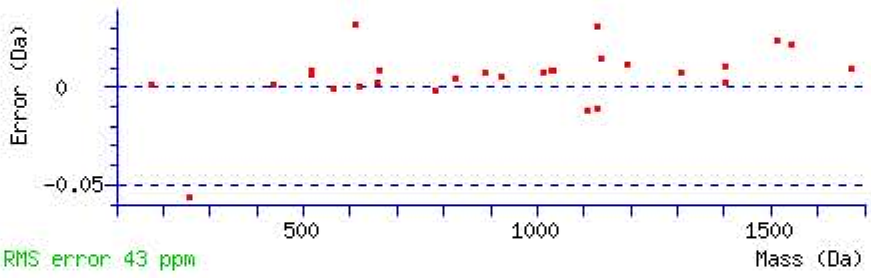
Match to Query 61039: 2433.216342 from(812.079390,3+) rtinseconds(2054) index(79229)
Title: Locus:1.1.1.2065.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

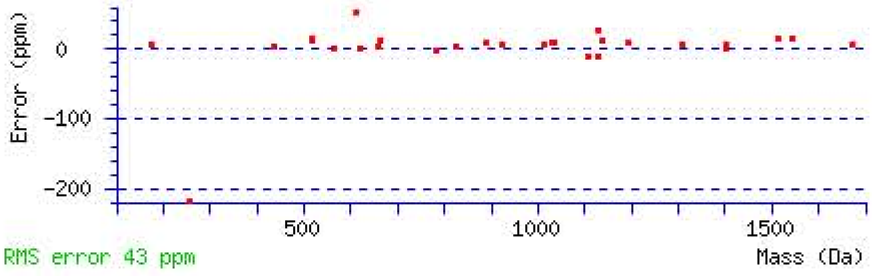
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2433.196701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 9.2e-006
Matches : 28/192 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	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
65.1	2433.196701	0.019641	YGQTIRPICLPCTEGTTR

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

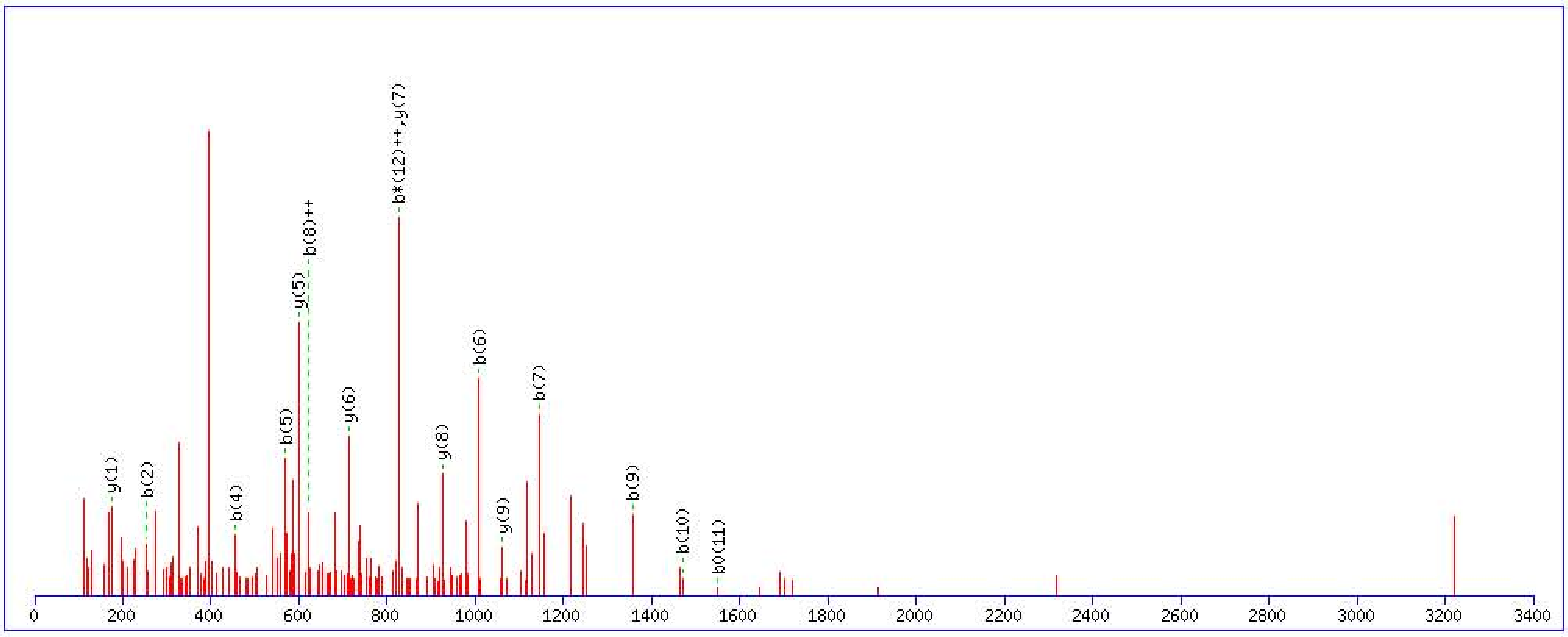
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPDSLQHVLLPVLDR**
Found in **CFAD_HUMAN**, Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5

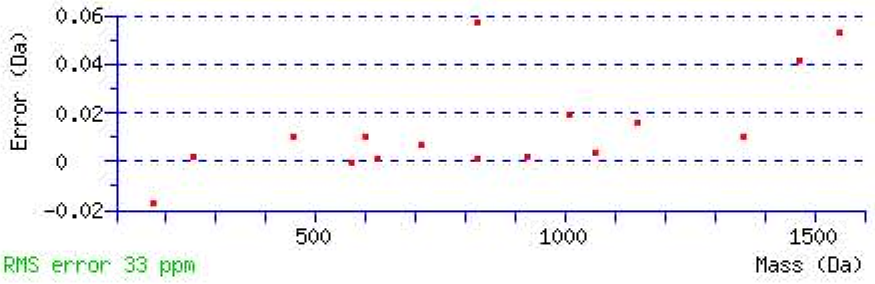
Match to Query 52484: 2068.186812 from(690.402880,3+) rtinseconds(2352) index(27162)
Title: Locus:1.1.1.2961.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

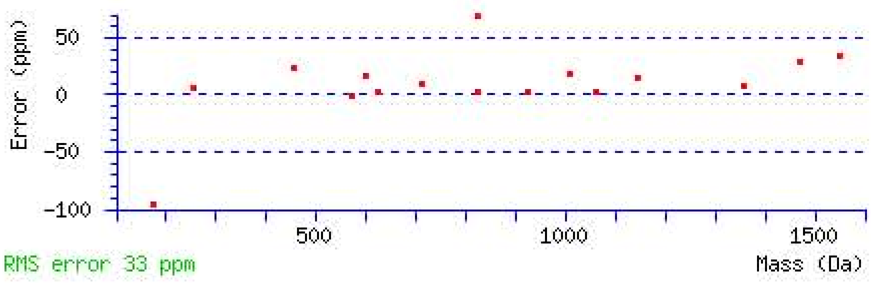
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2068.161545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0056
Matches : 16/162 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	157.108387	79.057831	140.081838	70.544557			R							15
2	***254.161151***	127.584213	237.134602	119.070939			P	1913.067716	957.037496	1896.041167	948.524222	1895.057151	948.032214	14
3	369.188094	185.097685	352.161545	176.584410	351.177529	176.092402	D	1816.014952	908.511114	1798.988403	899.997840	1798.004387	899.505832	13
4	***456.220122***	228.613699	439.193573	220.100425	438.209557	219.608417	S	1700.988009	850.997643	1683.961460	842.484368	1682.977444	841.992360	12
5	***569.304186***	285.155731	552.277637	276.642457	551.293621	276.150449	L	1613.955981	807.481629	1596.929432	798.968354	1595.945416	798.476346	11
6	***1008.529512***	504.768394	991.502963	496.255120	990.518947	495.763112	Q	1500.871917	750.939597	1483.845368	742.426322	1482.861352	741.934314	10
7	***1145.588424***	573.297850	1128.561875	564.784576	1127.577859	564.292568	H	***1061.646591***	531.326934	1044.620042	522.813659	1043.636026	522.321651	9
8	1244.656838	622.832057	1227.630289	614.318783	1226.646273	613.826775	V	***924.587679***	462.797478	907.561130	454.284203	906.577114	453.792195	8
9	***1357.740902***	679.374089	1340.714353	670.860815	1339.730337	670.368807	L	***825.519265***	413.263271	808.492716	404.749996	807.508700	404.257988	7
10	***1470.824966***	735.916121	1453.798417	727.402847	1452.814401	726.910838	L	***712.435201***	356.721239	695.408652	348.207964	694.424636	347.715956	6
11	1567.877730	784.442503	1550.851181	775.929229	1549.867165	775.437220	P	***599.351137***	300.179207	582.324588	291.665932	581.340572	291.173924	5
12	1666.946144	833.976710	1649.919595	825.463436	1648.935579	824.971428	V	502.298373	251.652825	485.271824	243.139550	484.287808	242.647542	4
13	1780.030208	890.518742	1763.003659	882.005468	1762.019643	881.513459	L	403.229959	202.118618	386.203410	193.605343	385.219394	193.113335	3
14	1895.057151	948.032214	1878.030602	939.518939	1877.046586	939.026931	D	290.145895	145.576586	273.119346	137.063311	272.135330	136.571303	2
15							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of RPDSLQHVLLPVLDR
(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	2068.161545	0.025267	RPDSLQHVLLPVLDR

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

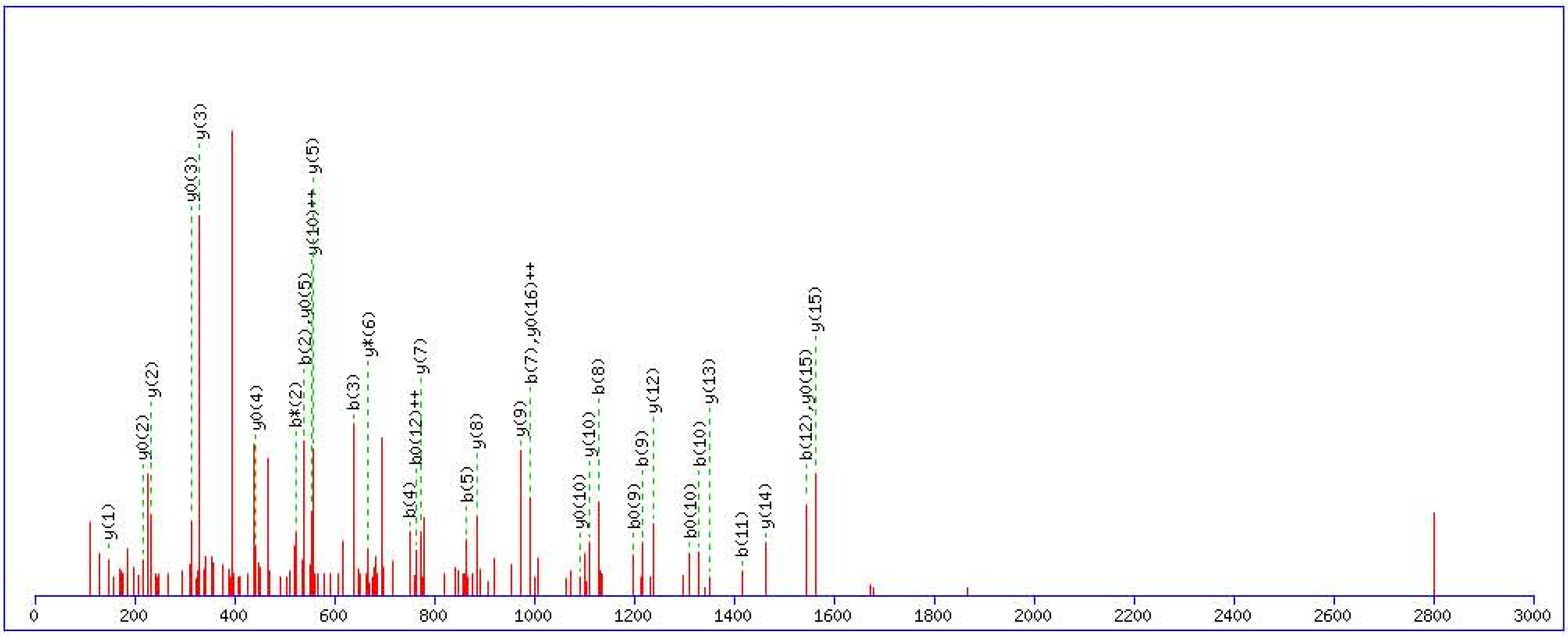
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQVLLGAHSLSQPEPSK**
Found in **CFAD_HUMAN**, Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5

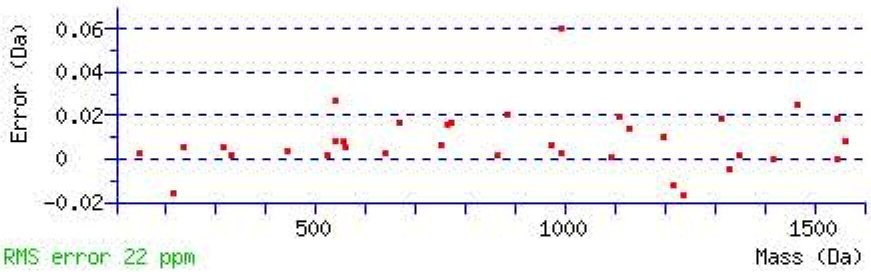
Match to Query 53133: 2100.157302 from(701.059710,3+) rtinseconds(1955) index(78620)
Title: Locus:1.1.1.2031.19 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

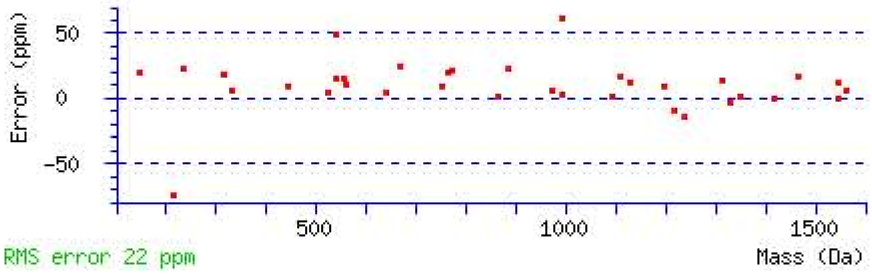
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2100.140137
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 2.5e-006
Matches : 35/172 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	100.075690	50.541483					V							17
2	**539.301016**	270.154146	522.274467	261.640872			Q	2002.079009	1001.543143	1985.052460	993.029868	1984.068444	992.537860	16
3	**638.369430**	319.688353	621.342881	311.175079			V	***1562.853683***	781.930480	1545.827134	773.417205	1544.843118	772.925197	15
4	**751.453494**	376.230385	734.426945	367.717111			L	***1463.785269***	732.396273	1446.758720	723.882998	1445.774704	723.390990	14
5	**864.537558**	432.772417	847.511009	424.259143			L	***1350.701205***	675.854241	1333.674656	667.340966	1332.690640	666.848958	13
6	921.559022	461.283149	904.532473	452.769875			G	***1237.617141***	619.312209	1220.590592	610.798934	1219.606576	610.306926	12
7	**992.596136**	496.801706	975.569587	488.288432			A	1180.595677	590.801477	1163.569128	582.288202	1162.585112	581.796194	11
8	**1129.655048**	565.331162	1112.628499	556.817888			H	***1109.558563***	555.282920	1092.532014	546.769645	1091.547998	546.277637	10
9	**1216.687076**	608.847176	1199.660527	600.333902	1198.676511	599.841894	S	***972.499651***	486.753464	955.473102	478.240189	954.489086	477.748181	9
10	**1329.771140**	665.389208	1312.744591	656.875934	1311.760575	656.383926	L	***885.467623***	443.237450	868.441074	434.724175	867.457058	434.232167	8
11	**1416.803168**	708.905222	1399.776619	700.391948	1398.792603	699.899940	S	***772.383559***	386.695418	755.357010	378.182143	754.372994	377.690135	7
12	**1544.861746**	772.934511	1527.835197	764.421237	1526.851181	763.929229	Q	685.351531	343.179404	668.324982	334.666129	667.340966	334.174121	6
13	1641.914510	821.460893	1624.887961	812.947619	1623.903945	812.455611	P	***557.292953***	279.150115	540.266404	270.636840	539.282388	270.144832	5
14	1770.957103	885.982190	1753.930554	877.468915	1752.946538	876.976907	E	460.240189	230.623733	443.213640	222.110458	442.229624	221.618450	4
15	1868.009867	934.508572	1850.983318	925.995297	1849.999302	925.503289	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
16	1955.041895	978.024586	1938.015346	969.511311	1937.031330	969.019303	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.8	2100.140137	0.017165	VQVLLGAHSLSQPEPSK

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

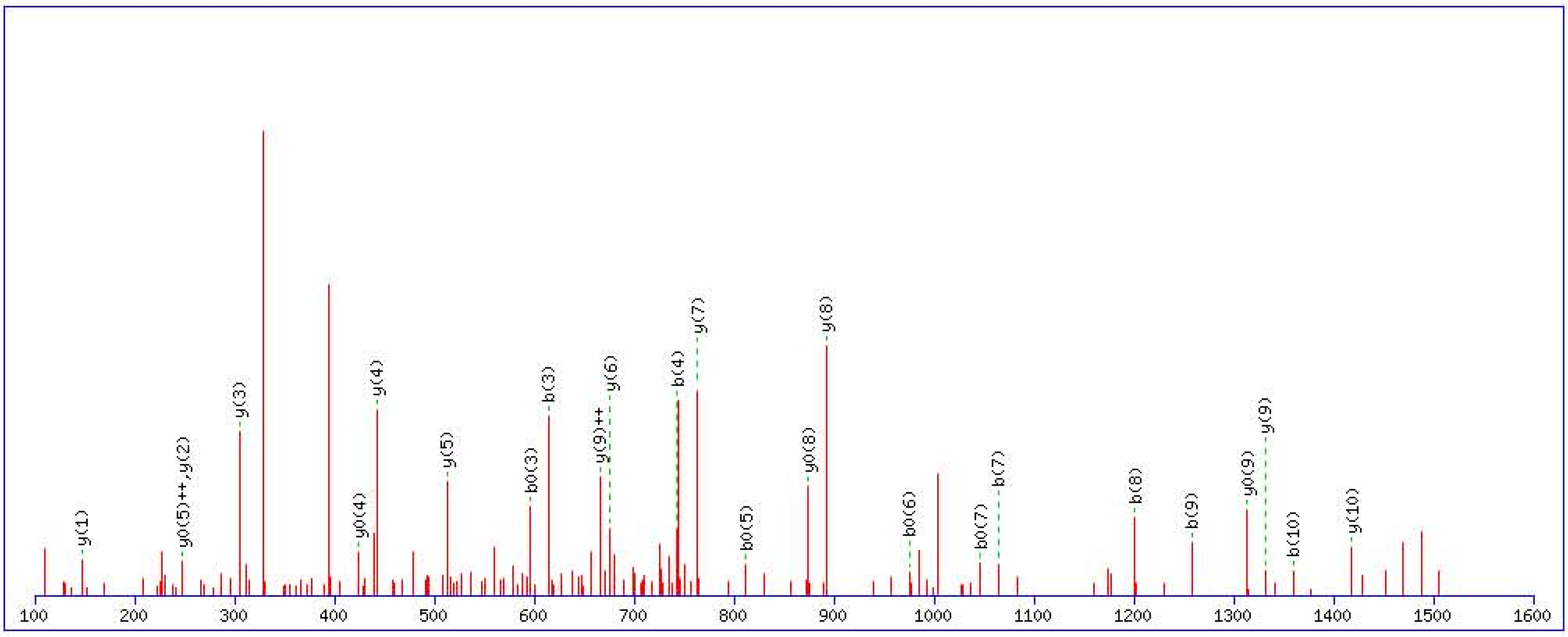
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSQESYAHGTK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

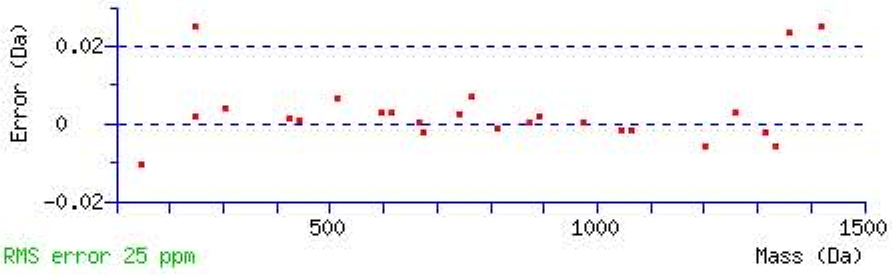
Match to Query 35083: 1504.705248 from(753.359900,2+) rtinseconds(1183) index(18862)
Title: Locus:1.1.1.2554.15 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

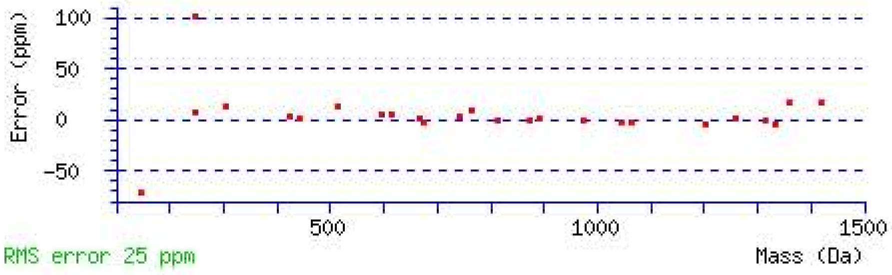
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1504.698013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 72 **Expect:** 1e-006
Matches : 25/114 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	88.039304	44.523290			70.028739	35.518008	S							11
2	175.071332	88.039304			157.060767	79.034021	S	***1418.673277***	709.840276	1401.646728	701.327002	1400.662712	700.834994	10
3	**614.296658**	307.651967	597.270109	299.138692	596.286093	298.646684	Q	***1331.641249***	666.324263	1314.614700	657.810988	1313.630684	657.318980	9
4	**743.339251**	372.173264	726.312702	363.659989	725.328686	363.167981	E	***892.415923***	446.711600	875.389374	438.198325	874.405358	437.706317	8
5	830.371279	415.689278	813.344730	407.176003	812.360714	406.683995	S	***763.373330***	382.190303	746.346781	373.677029	745.362765	373.185021	7
6	993.434608	497.220942	976.408059	488.707668	975.424043	488.215660	Y	***676.341302***	338.674289	659.314753	330.161015	658.330737	329.669007	6
7	**1064.471722**	532.739499	1047.445173	524.226225	1046.461157	523.734217	A	***513.277973***	257.142625	496.251424	248.629350	495.267408	248.137342	5
8	**1201.530634**	601.268955	1184.504085	592.755681	1183.520069	592.263672	H	***442.240859***	221.624067	425.214310	213.110793	424.230294	212.618785	4
9	**1258.552098**	629.779687	1241.525549	621.266413	1240.541533	620.774404	G	***305.181947***	153.094611	288.155398	144.581337	287.171382	144.089329	3
10	**1359.599777**	680.303526	1342.573228	671.790252	1341.589212	671.298244	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SSQESYAHGTK
(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	1504.698013	0.007235	SSQESYAHGTK
9.9	1504.701355	0.003893	KLSMKECEHAEK
5.9	1504.726532	-0.021284	AQELQTETMK
4.7	1504.704544	0.000704	EPSNSIFPVGSEDK
4.0	1504.720474	-0.015226	QYVSGLHMNRER
3.4	1504.720474	-0.015226	NRATGNYDQR
1.1	1504.704544	0.000704	QVFEDGQELESPK
0.2	1504.690140	0.015108	ELQSMADQEK

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

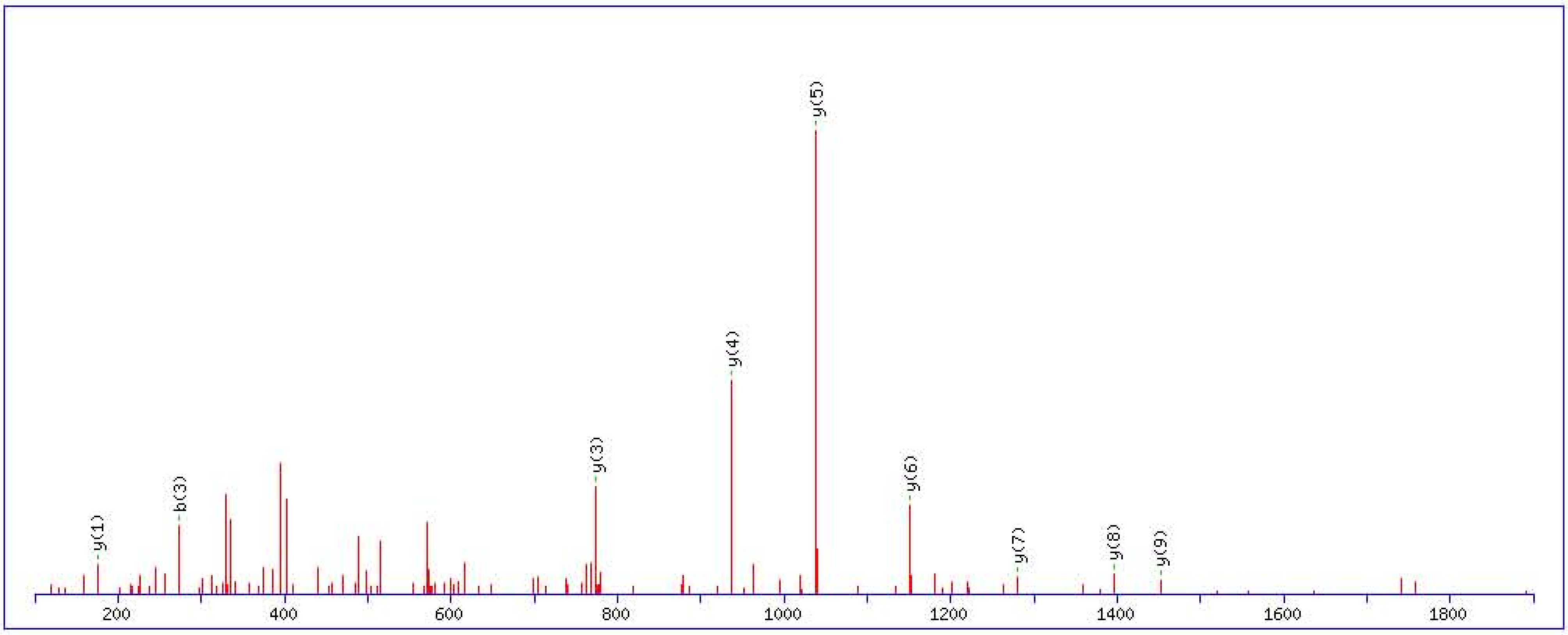
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of TGDEITYQCR
Found in CFAH_HUMAN, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

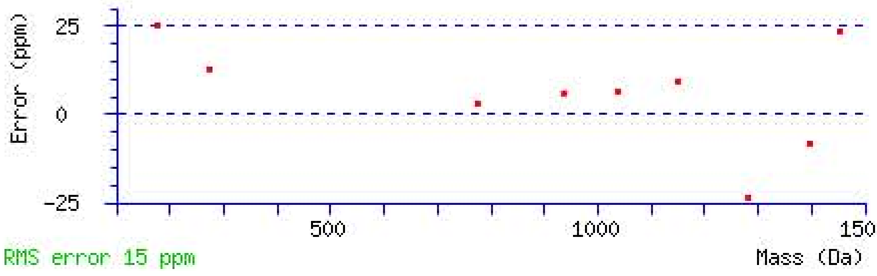
Match to Query 36488: 1552.709848 from(777.362200,2+) rtinseconds(1673) index(22237)
Title: Locus:1.1.1.2725.17 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1552.701401
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 8.3e-006
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
61.0	1552.701401	0.008447	TGDEITYQCR
6.9	1552.715149	-0.005301	LTNGSSSCSGTVEVR
6.1	1552.715820	-0.005972	AVFDALDGDGDGFVR
4.0	1552.712616	-0.002768	NVGMPVAHMESPER

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

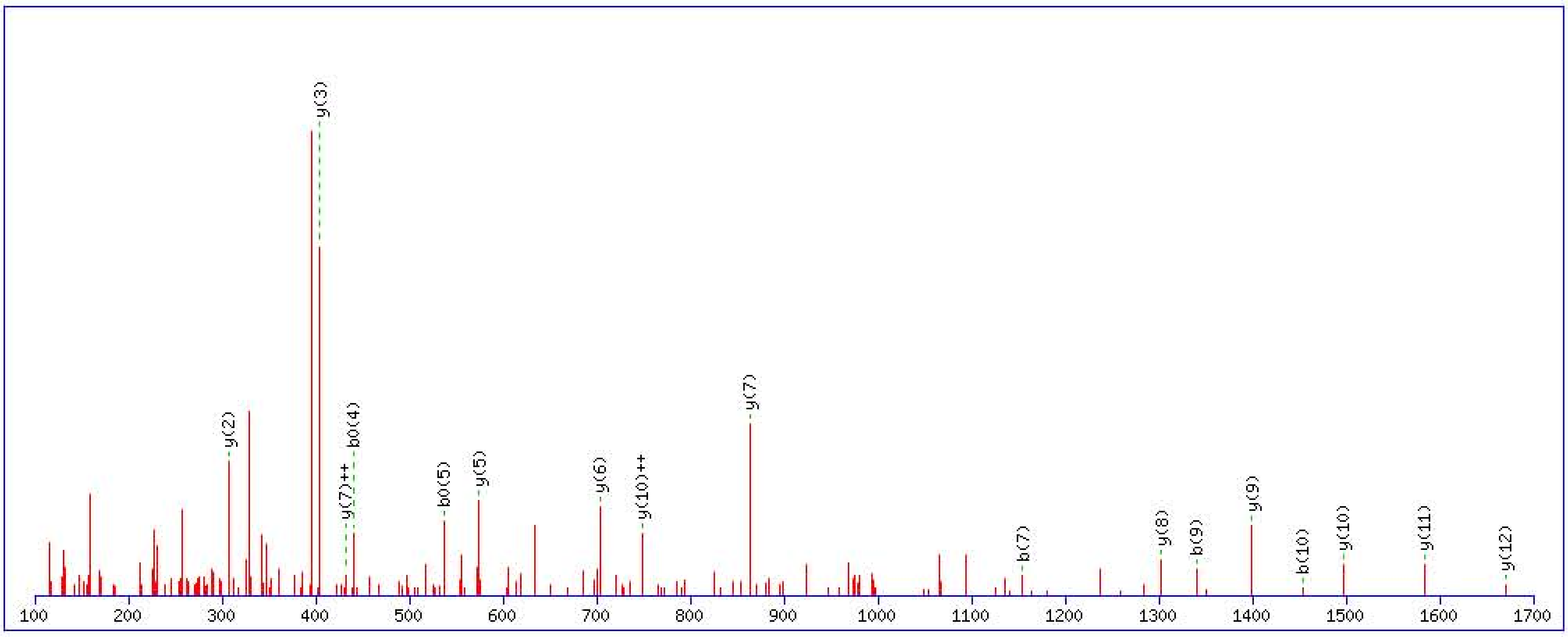
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WSSPPQCEGLPCK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

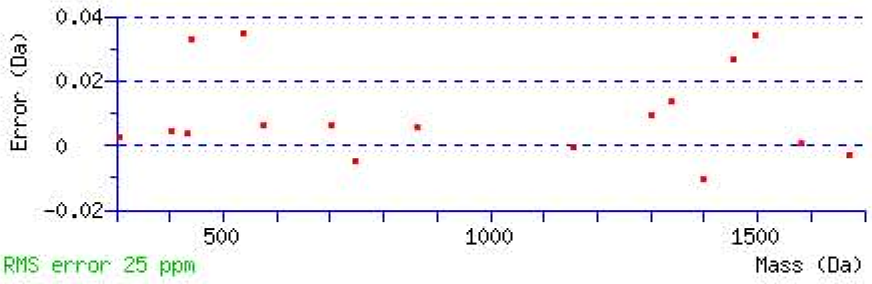
Match to Query 46729: 1855.850862 from(619.624230,3+) rtinseconds(1880) index(23810)
Title: Locus:1.1.1.2797.10 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

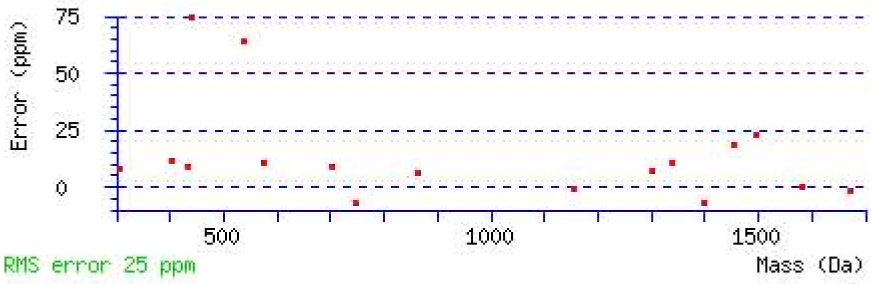
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1855.841934
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 1.5e-006
Matches : 17/122 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	187.086589	94.046932					W							13
2	274.118617	137.562947			256.108052	128.557664	S	***1670.769897***	835.888587	1653.743348	827.375312	1652.759332	826.883304	12
3	361.150645	181.078960			343.140080	172.073678	S	***1583.737869***	792.372573	1566.711320	783.859298	1565.727304	783.367290	11
4	458.203409	229.605343			440.192844	220.600060	P	***1496.705841***	748.856559	1479.679292	740.343284	1478.695276	739.851276	10
5	555.256173	278.131725			537.245608	269.126442	P	***1399.653077***	700.330177	1382.626528	691.816902	1381.642512	691.324894	9
6	994.481499	497.744388	977.454950	489.231113	976.470934	488.739105	Q	***1302.600313***	651.803795	1285.573764	643.290520	1284.589748	642.798512	8
7	**1154.512148**	577.759712	1137.485599	569.246438	1136.501583	568.754430	C	***863.374987***	432.191132	846.348438	423.677857	845.364422	423.185649	7
8	1283.554741	642.281009	1266.528192	633.767734	1265.544176	633.275726	E	***703.344338***	352.175807	686.317789	343.662533	685.333773	343.170525	6
9	**1340.576205**	670.791741	1323.549656	662.278466	1322.565640	661.786458	G	***574.301745***	287.654511	557.275196	279.141236			5
10	**1453.660269**	727.333773	1436.633720	718.820498	1435.649704	718.328490	L	517.280281	259.143779	500.253732	250.630504			4
11	1550.713033	775.860155	1533.686484	767.346880	1532.702468	766.854872	P	***404.196217***	202.601747	387.169668	194.088472			3
12	1710.743682	855.875479	1693.717133	847.362205	1692.733117	846.870197	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 WSSPPQCEGLPCK
(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	1855.841934	0.008928	WSSPPQCEGLPCK
1.7	1855.869568	-0.018706	LMQDDEMNIFINLTK

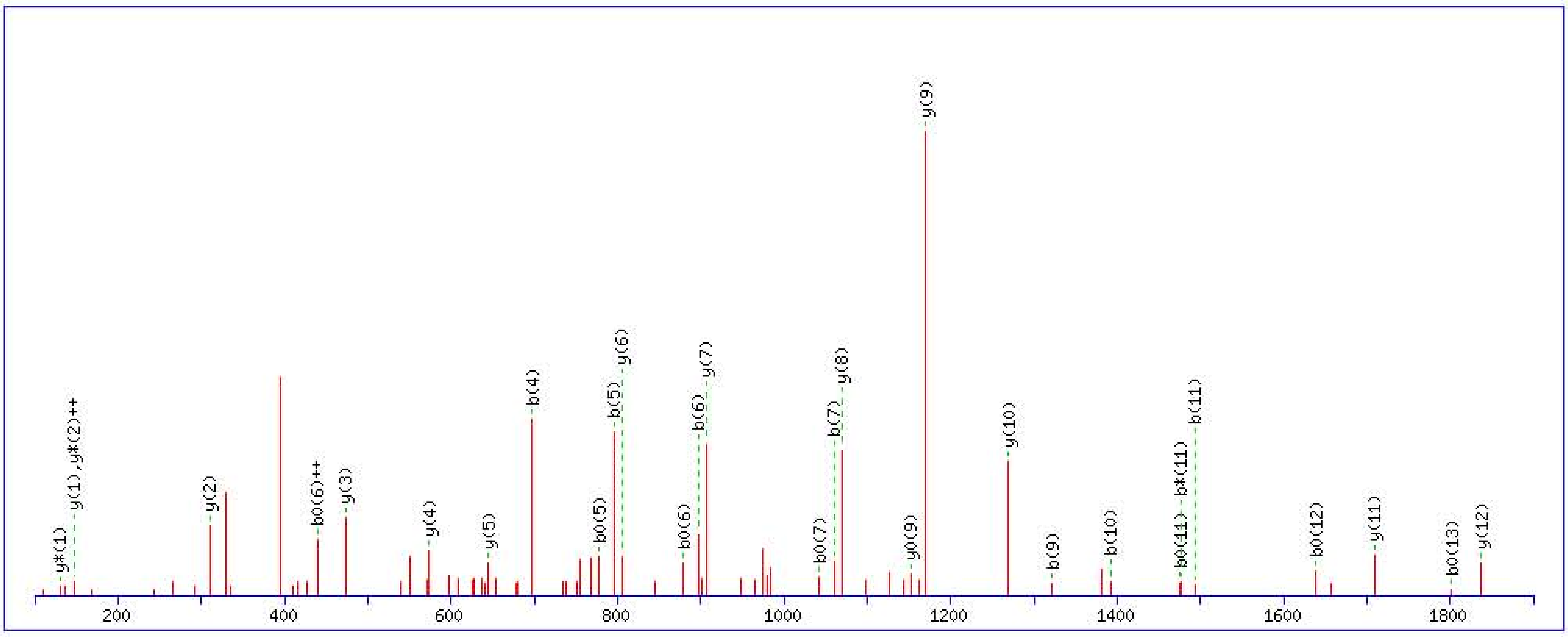
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGEQVTYTCATYYK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

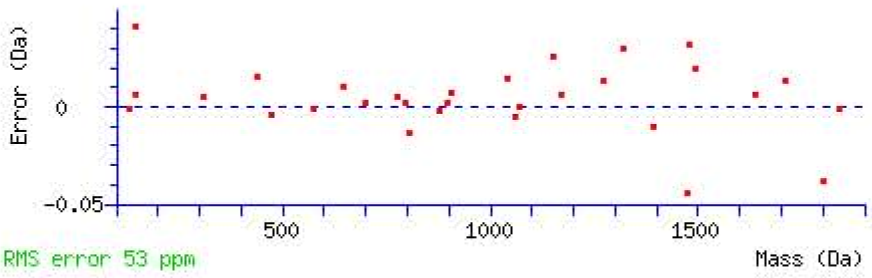
Match to Query 49103: 1964.922208 from(983.468380,2+) rtinseconds(1864) index(23681)
Title: Locus:1.1.1.2791.21 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

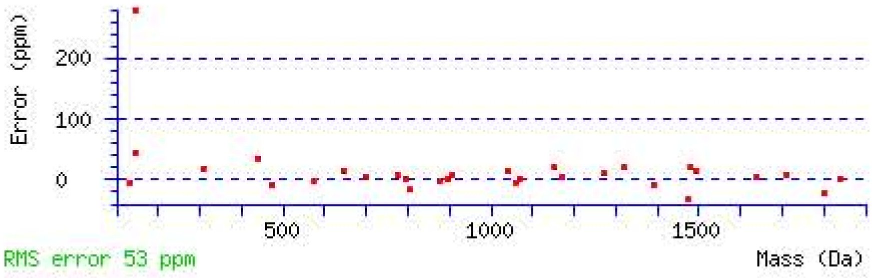
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1964.901215
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 91  Expect: 1.3e-008
Matches : 30/140 fragment ions using 45 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
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
90.8	1964.901215	0.020993	AGEQVTYTCATYYK

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

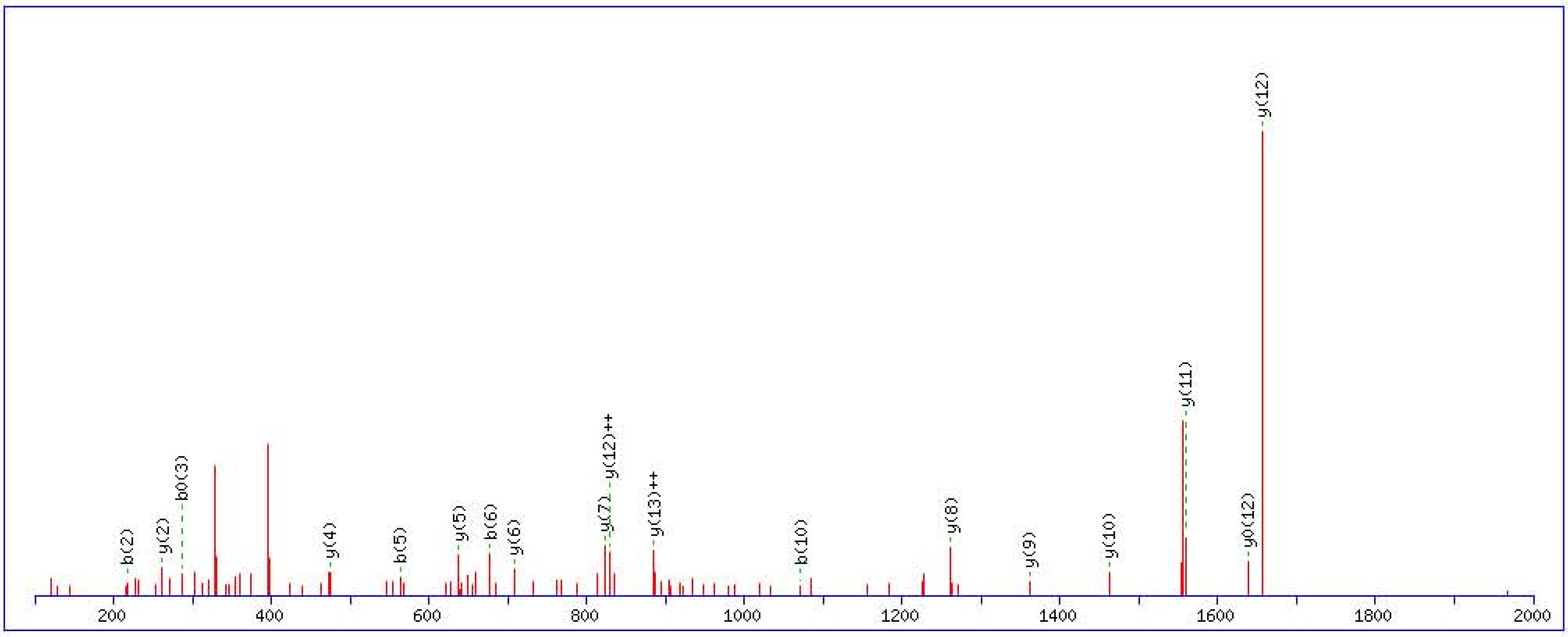
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTSCVNPPTVQNAYIVSR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

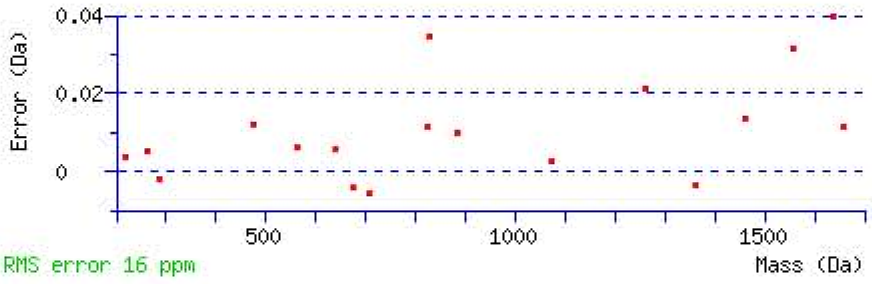
Match to Query 58812: 2331.152382 from(778.058070,3+) rtinseconds(2100) index(25396)
Title: Locus:1.1.1.2873.20 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

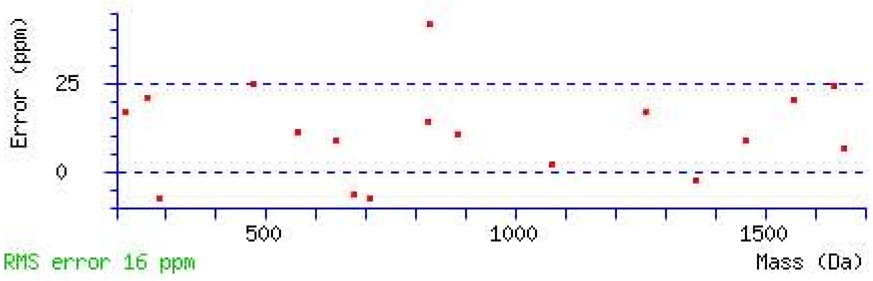
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2331.135147
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 43 **Expect:** 0.0013
Matches : 18/192 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	116.034219	58.520748			98.023654	49.515465	D							18
2	**217.081898**	109.044587			199.071333	100.039304	T	2217.115472	1109.061374	2200.088923	1100.548099	2199.104907	1100.056091	17
3	304.113926	152.560601			286.103361	143.555319	S	2116.067793	1058.537534	2099.041244	1050.024260	2098.057228	1049.532252	16
4	464.144575	232.575925			446.134010	223.570643	C	2029.035765	1015.021521	2012.009216	1006.508246	2011.025200	1006.016238	15
5	**563.212989**	282.110133			545.202424	273.104850	V	1869.005116	935.006196	1851.978567	926.492922	1850.994551	926.000914	14
6	**677.255916**	339.131596	660.229367	330.618321	659.245351	330.126313	N	1769.936702	885.471989	1752.910153	876.958715	1751.926137	876.466707	13
7	774.308680	387.657978	757.282131	379.144703	756.298115	378.652695	P	***1655.893775***	828.450526	1638.867226	819.937251	1637.883210	819.445243	12
8	871.361444	436.184360	854.334895	427.671086	853.350879	427.179078	P	***1558.841011***	779.924144	1541.814462	771.410869	1540.830446	770.918861	11
9	972.409123	486.708200	955.382574	478.194925	954.398558	477.702917	T	***1461.788247***	731.397762	1444.761698	722.884487	1443.777682	722.392479	10
10	**1071.477537**	536.242407	1054.450988	527.729132	1053.466972	527.237124	V	***1360.740568***	680.873922	1343.714019	672.360648	1342.730003	671.868639	9
11	1510.702863	755.855070	1493.676314	747.341795	1492.692298	746.849787	Q	***1261.672154***	631.339715	1244.645605	622.826441	1243.661589	622.334433	8
12	1624.745790	812.876533	1607.719241	804.363259	1606.735225	803.871251	N	***822.446828***	411.727052	805.420279	403.213777	804.436263	402.721769	7
13	1695.782904	848.395090	1678.756355	839.881816	1677.772339	839.389808	A	***708.403901***	354.705588	691.377352	346.192314	690.393336	345.700306	6
14	1858.846233	929.926755	1841.819684	921.413480	1840.835668	920.921472	Y	***637.366787***	319.187031	620.340238	310.673757	619.356222	310.181749	5
15	1971.930297	986.468787	1954.903748	977.955512	1953.919732	977.463504	I	***474.303458***	237.655367	457.276909	229.142092	456.292893	228.650084	4
16	2070.998711	1036.002993	2053.972162	1027.489719	2052.988146	1026.997711	V	361.219394	181.113335	344.192845	172.600060	343.208829	172.108052	3
17	2158.030739	1079.519007	2141.004190	1071.005733	2140.020174	1070.513725	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 DTSCVNPPTVQNAYIVSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.0	2331.135147	0.017235	DTSCVNPPTVQNAYIVSR

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

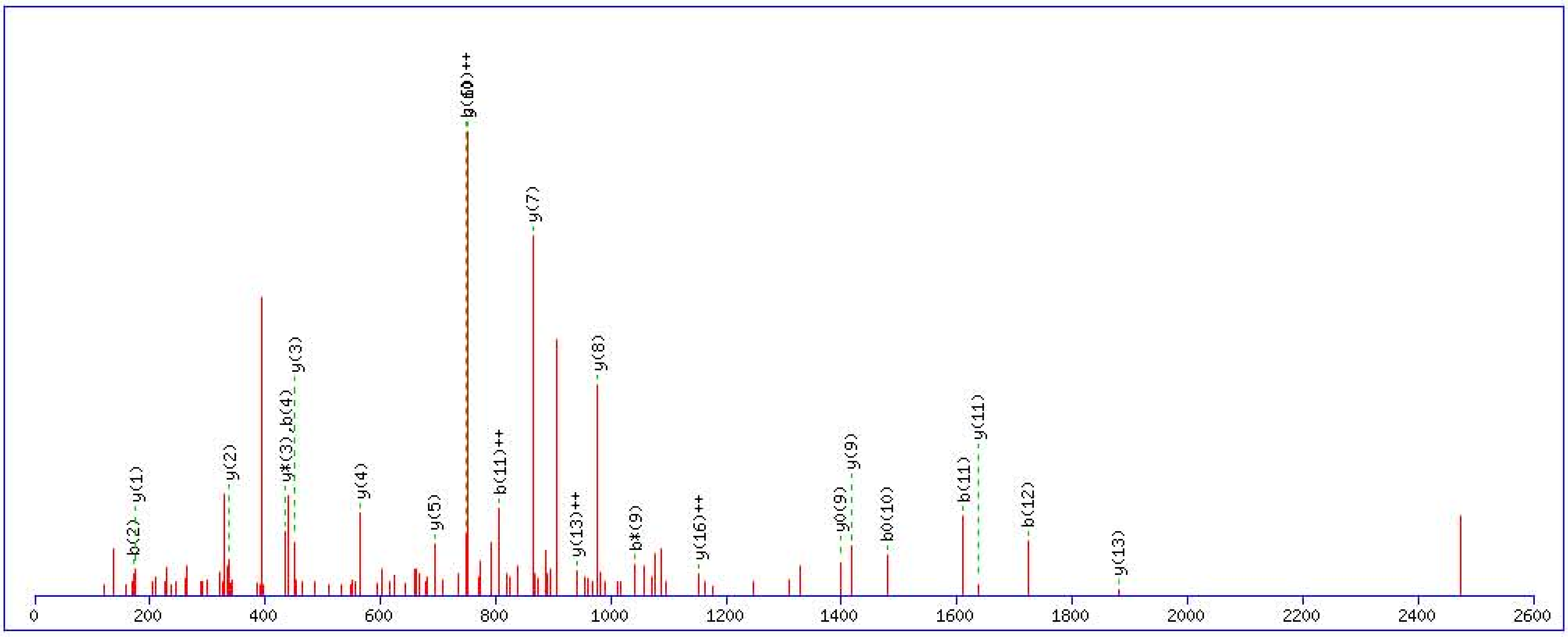
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of AVYTCNEGYQLLGEINYR
Found in CFAH_HUMAN, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

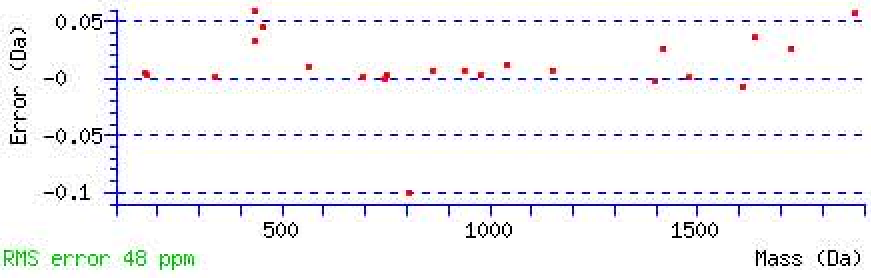
Match to Query 62074: 2473.207392 from(825.409740,3+) rtinseconds(2523) index(28242)
Title: Locus:1.1.1.3020.7 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

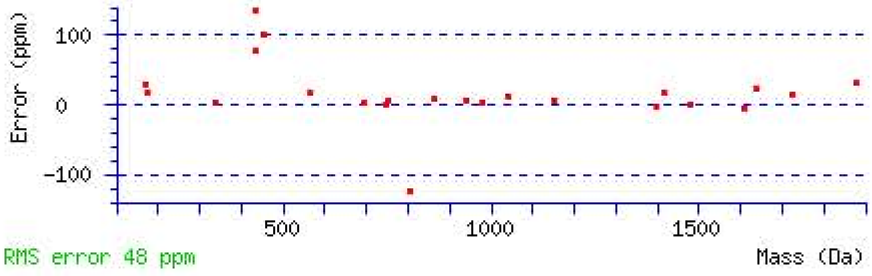
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2473.176971
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 5e-005
Matches : 23/180 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							18
2	**171.112804**	86.060040					V	2403.147167	1202.077221	2386.120618	1193.563947	2385.136602	1193.071939	17
3	334.176133	167.591704					Y	2304.078753	1152.543014	2287.052204	1144.029740	2286.068188	1143.537732	16
4	**435.223812**	218.115544			417.213247	209.110262	T	2141.015424	1071.011350	2123.988875	1062.498075	2123.004859	1062.006067	15
5	595.254461	298.130869			577.243896	289.125586	C	2039.967745	1020.487511	2022.941196	1011.974236	2021.957180	1011.482228	14
6	709.297388	355.152332	692.270839	346.639058	691.286823	346.147050	N	***1879.937096***	940.472186	1862.910547	931.958912	1861.926531	931.466903	13
7	838.339981	419.673629	821.313432	411.160354	820.329416	410.668346	E	1765.894169	883.450722	1748.867620	874.937448	1747.883604	874.445440	12
8	895.361445	448.184361	878.334896	439.671086	877.350880	439.179078	G	***1636.851576***	818.929426	1619.825027	810.416152	1618.841011	809.924144	11
9	1058.424774	529.716025	1041.398225	521.202751	1040.414209	520.710743	Y	1579.830112	790.418694	1562.803563	781.905419	1561.819547	781.413411	10
10	1497.650100	**749.328688**	1480.623551	740.815414	1479.639535	740.323406	Q	***1416.766783***	708.887030	1399.740234	700.373755	1398.756218	699.881747	9
11	**1610.734164**	**805.870720**	1593.707615	797.357446	1592.723599	796.865437	L	***977.541457***	489.274367	960.514908	480.761092	959.530892	480.269084	8
12	**1723.818228**	862.412752	1706.791679	853.899477	1705.807663	853.407469	L	***864.457393***	432.732335	847.430844	424.219060	846.446828	423.727052	7
13	1780.839692	890.923484	1763.813143	882.410209	1762.829127	881.918201	G	***751.373329***	376.190303	734.346780	367.677028	733.362764	367.185020	6
14	1909.882285	955.444780	1892.855736	946.931506	1891.871720	946.439498	E	***694.351865***	347.679571	677.325316	339.166296	676.341300	338.674288	5
15	2022.966349	1011.986812	2005.939800	1003.473538	2004.955784	1002.981530	I	***565.309272***	283.158274	548.282723	274.645000			4
16	2137.009276	1069.008276	2119.982727	1060.495001	2118.998711	1060.002993	N	***452.225208***	226.616242	435.198659	218.102968			3
17	2300.072605	1150.539940	2283.046056	1142.026666	2282.062040	1141.534658	Y	***338.182281***	169.594778	321.155732	161.081504			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.4	2473.176971	0.030421	AVYTCNEGYQLLGEINYR

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

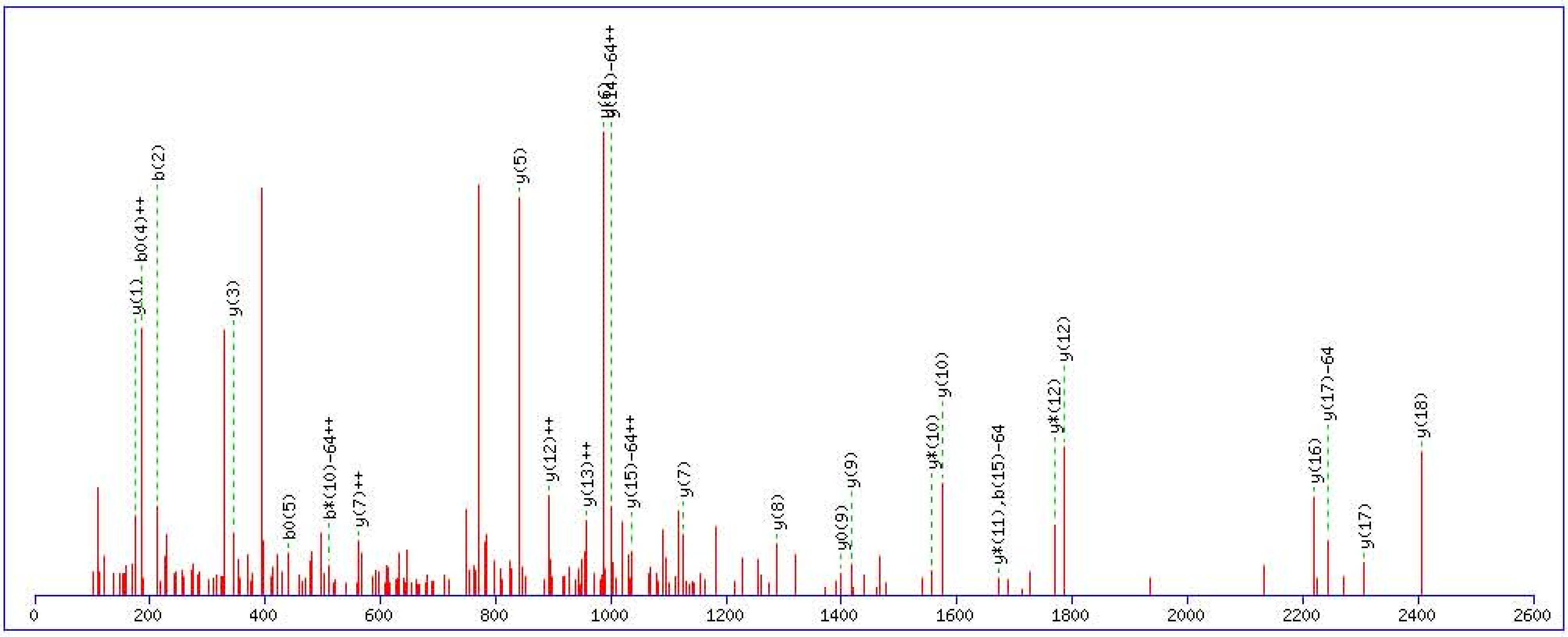
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVSSAMEPDREYHFGQAVR**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

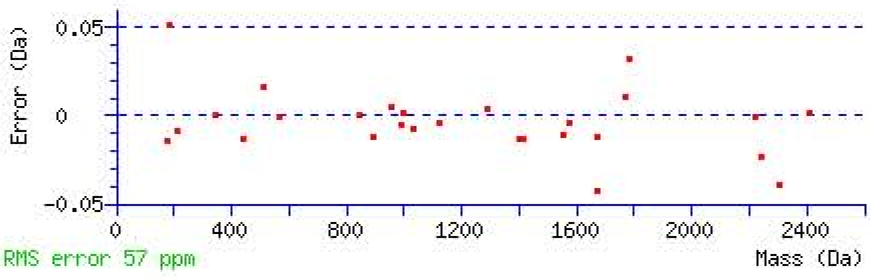
Match to Query 63438: 2518.213336 from(630.560610,4+) rtinseconds(1658) index(22114)
Title: Locus:1.1.1.2720.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

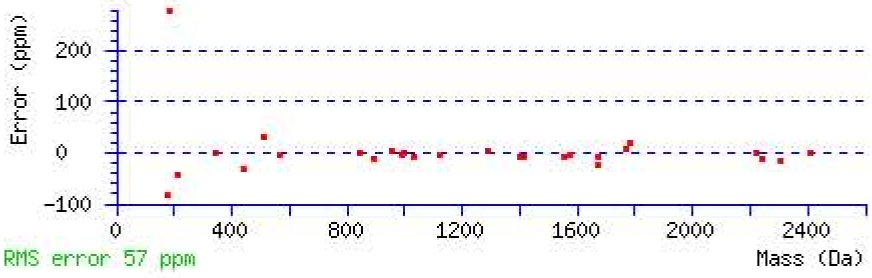
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2518.209686
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
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00031
Matches : 27/278 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	114.091340	57.549308					I							19
2	213.159754	107.083515					V	*2406.132913*	1203.570094	2389.106364	1195.056820	2388.122348	1194.564812	18
3	300.191782	150.599529			282.181217	141.594247	S	*2307.064499*	1154.035887	2290.037950	1145.522613	2289.053934	1145.030605	17
4	387.223810	194.115543			369.213245	185.110261	S	*2220.032471*	1110.519873	2203.005922	1102.006599	2202.021906	1101.514591	16
5	458.260924	229.634100			440.250359	220.628818	A	2133.000443	1067.003859	2115.973894	1058.490585	2114.989878	1057.998577	15
6	605.296324	303.151800			587.285759	294.146518	M	2061.963329	1031.485302	2044.936780	1022.972028	2043.952764	1022.480020	14
7	734.338917	367.673097			716.328352	358.667814	E	1914.927929	957.967603	1897.901380	949.454328	1896.917364	948.962320	13
8	831.391681	416.199479			813.381116	407.194196	P	*1785.885336*	893.446306	1768.858787	884.933032	1767.874771	884.441024	12
9	946.418624	473.712950			928.408059	464.707668	D	1688.832572	844.919924	1671.806023	836.406650	1670.822007	835.914642	11
10	1102.519735	551.763506	1085.493186	543.250231	1084.509170	542.758223	R	*1573.805629*	787.406453	1556.779080	778.893178	1555.795064	778.401170	10
11	1231.562328	616.284802	1214.535779	607.771528	1213.551763	607.279520	E	*1417.704518*	709.355897	1400.677969	700.842623	1399.693953	700.350615	9
12	1394.625657	697.816467	1377.599108	689.303192	1376.615092	688.811184	Y	*1288.661925*	644.834601	1271.635376	636.321326			8
13	1531.684569	766.345923	1514.658020	757.832648	1513.674004	757.340640	H	*1125.598596*	563.302936	1108.572047	554.789662			7
14	1678.752983	839.880130	1661.726434	831.366855	1660.742418	830.874847	F	*988.539684*	494.773480	971.513135	486.260206			6
15	1735.774447	868.390862	1718.747898	859.877587	1717.763882	859.385579	G	*841.471270*	421.239273	824.444721	412.725999			5
16	2174.999773	1088.003524	2157.973224	1079.490250	2156.989208	1078.998242	Q	784.449806	392.728541	767.423257	384.215267			4
17	2246.036887	1123.522082	2229.010338	1115.008807	2228.026322	1114.516799	A	*345.224480*	173.115878	328.197931	164.602603			3
18	2345.105301	1173.056288	2328.078752	1164.543014	2327.094736	1164.051006	V	274.187366	137.597321	257.160817	129.084046			2
19							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.0	2518.209686	0.003650	IVSSAMEPDREYHFGQAVR

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

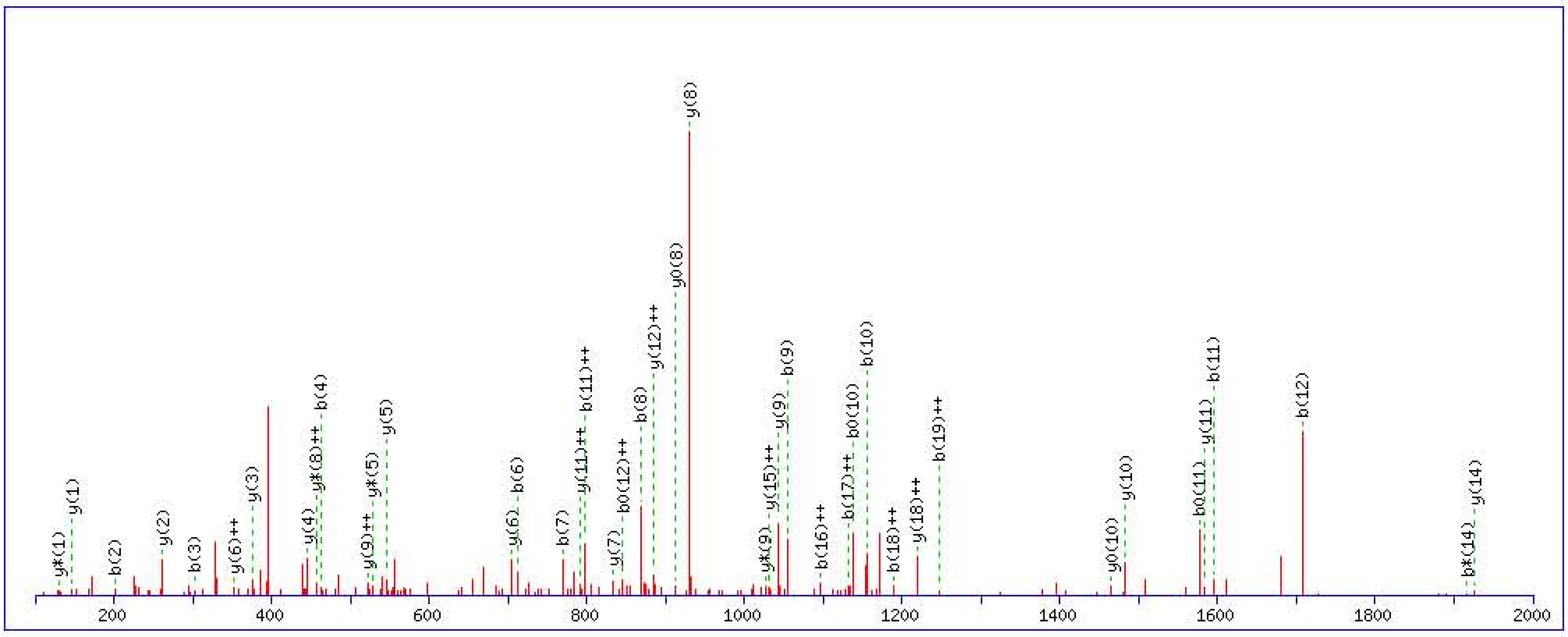
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SITCIHGVWTQLPQCVAIDK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

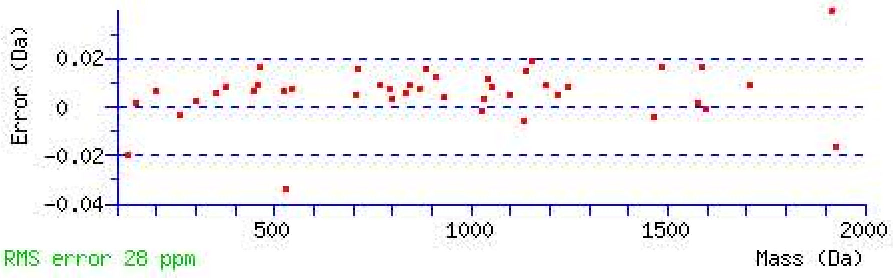
Match to Query 64926: 2636.360772 from(879.794200,3+) rtinseconds(2339) index(27093)
Title: Locus:1.1.1.2956.21 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

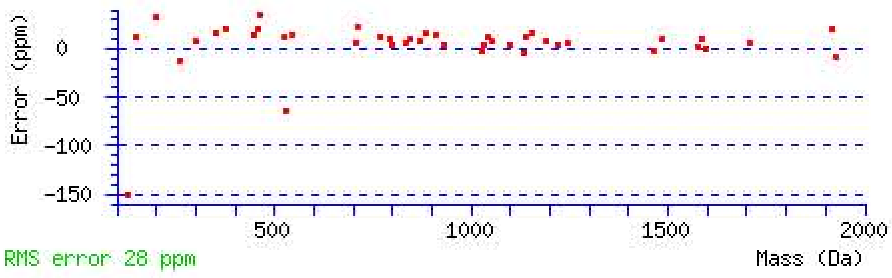
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2636.327728
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 4.4e-005
Matches : 43/206 fragment ions using 116 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							20
2	***201.123368***	101.065322			183.112803	92.060039	I	2550.302958	1275.655117	2533.276409	1267.141842	2532.292393	1266.649834	19
3	***302.171047***	151.589161			284.160482	142.583879	T	2437.218894	1219.113085	2420.192345	1210.599810	2419.208329	1210.107802	18
4	***462.201696***	231.604486			444.191131	222.599204	C	2336.171215	1168.589245	2319.144666	1160.075971	2318.160650	1159.583963	17
5	575.285760	288.146518			557.275195	279.141236	I	2176.140566	1088.573921	2159.114017	1080.060646	2158.130001	1079.568638	16
6	***712.344672***	356.675974			694.334107	347.670692	H	2063.056502	1032.031889	2046.029953	1023.518614	2045.045937	1023.026606	15
7	***769.366136***	385.186706			751.355571	376.181424	G	***1925.997590***	963.502433	1908.971041	954.989159	1907.987025	954.497151	14
8	***868.434550***	434.720913			850.423985	425.715631	V	1868.976126	934.991701	1851.949577	926.478427	1850.965561	925.986419	13
9	***1054.513863***	527.760570			1036.503298	518.755287	W	1769.907712	885.457494	1752.881163	876.944220	1751.897147	876.452211	12
10	***1155.561542***	578.284409			1137.550977	569.279127	T	***1583.828399***	792.417838	1566.801850	783.904563	1565.817834	783.412555	11
11	***1594.786868***	**797.897072**	1577.760319	789.383798	1576.776303	788.891790	Q	***1482.780720***	741.893998	1465.754171	733.380724	1464.770155	732.888715	10
12	***1707.870932***	854.439104	1690.844383	845.925830	1689.860367	845.433822	L	***1043.555394***	522.281335	1026.528845	513.768060	1025.544829	513.276052	9
13	1804.923696	902.965486	1787.897147	894.452212	1786.913131	893.960204	P	***930.471330***	465.739303	913.444781	457.226028	912.460765	456.734020	8
14	1932.982274	966.994775	1915.955725	958.481501	1914.971709	957.989493	Q	***833.418566***	417.212921	816.392017	408.699646	815.408001	408.207638	7
15	2093.012923	1047.010099	2075.986374	1038.496825	2075.002358	1038.004817	C	***705.359988***	353.183632	688.333439	344.670357	687.349423	344.178349	6
16	2192.081337	**1096.544306**	2175.054788	1088.031032	2174.070772	1087.539024	V	***545.329339***	273.168308	528.302790	264.655033	527.318774	264.163025	5
17	2263.118451	**1132.062863**	2246.091902	1123.549589	2245.107886	1123.057581	A	***446.260925***	223.634101	429.234376	215.120826	428.250360	214.628818	4
18	2376.202515	**1188.604895**	2359.175966	1180.091621	2358.191950	1179.599613	I	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
19	2491.229458	**1246.118367**	2474.202909	1237.605092	2473.218893	1237.113084	D	***262.139747***	131.573511	245.113198	123.060237	244.129182	122.568229	2
20							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SITCIHGVWTQLPQCVAIDK
(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	2636.327728	0.033044	SITCIHGVWTQLPQCVAIDK
20.1	2636.327728	0.033044	SITCIHGVWTQLPQCVAIDK
1.2	2636.344574	0.016198	IEGWELTTEPSLTHNSSGLLSPLR

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

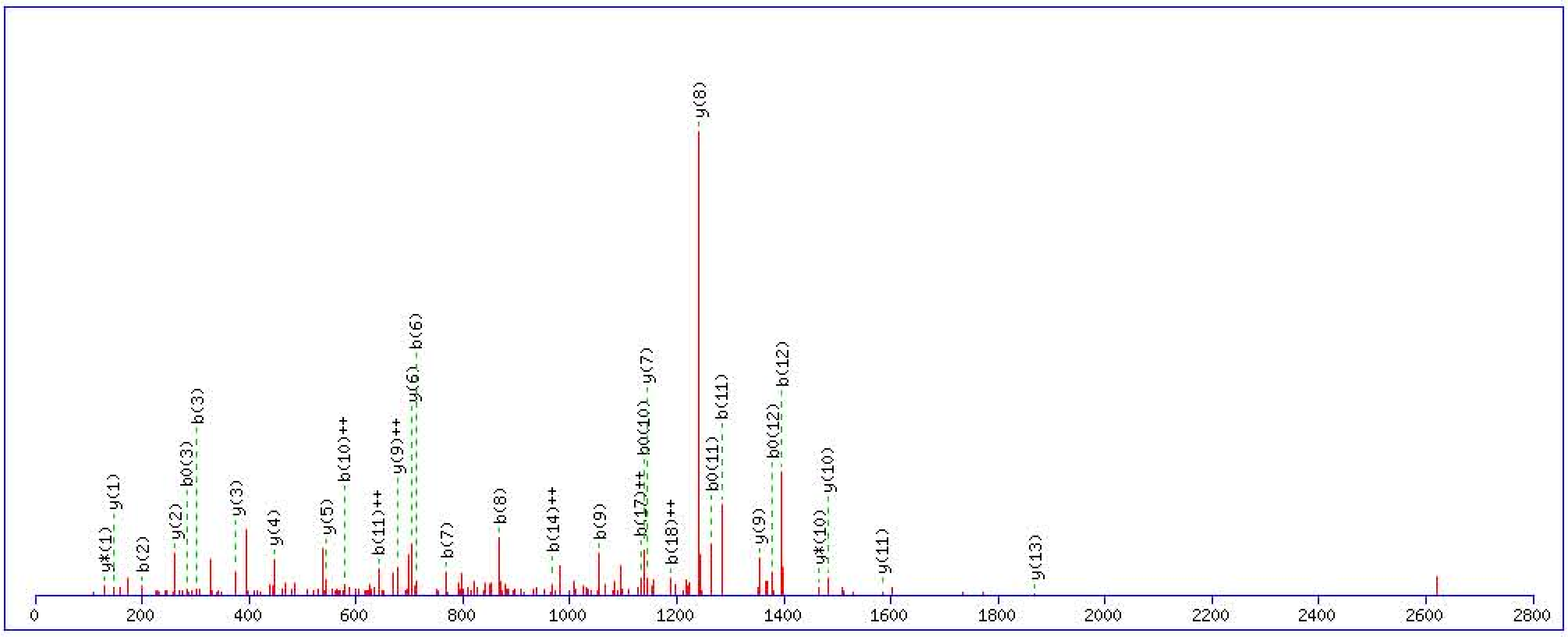
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SITCIHGVWTQLPQCVAIDK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 64927: 2636.360772 from(879.794200,3+) rtinseconds(2365) index(27265)
Title: Locus:1.1.1.2965.24 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 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 ●



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Monoisotopic mass of neutral peptide Mr(calc): 2636.327728
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 1.1e-006
Matches : 32/206 fragment ions using 63 most intense peaks   (help)
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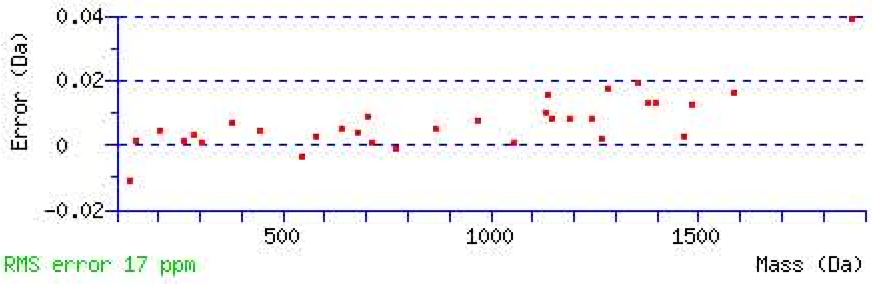
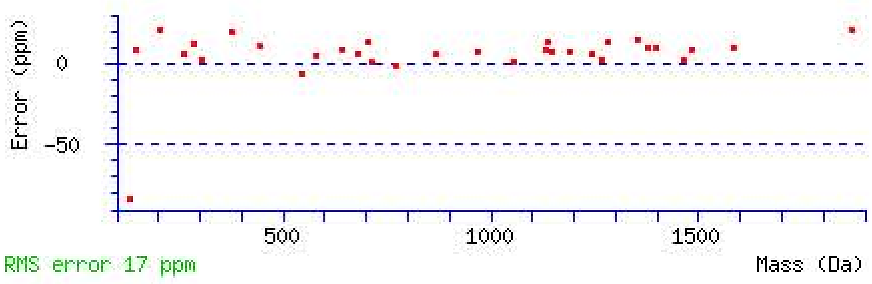
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							20
2	***201.123368***	101.065322			183.112803	92.060039	I	2550.302958	1275.655117	2533.276409	1267.141842	2532.292393	1266.649834	19
3	***302.171047***	151.589161			284.160482	142.583879	T	2437.218894	1219.113085	2420.192345	1210.599810	2419.208329	1210.107802	18
4	462.201696	231.604486			444.191131	222.599204	C	2336.171215	1168.589245	2319.144666	1160.075971	2318.160650	1159.583963	17
5	575.285760	288.146518			557.275195	279.141236	I	2176.140566	1088.573921	2159.114017	1080.060646	2158.130001	1079.568638	16
6	***712.344672***	356.675974			694.334107	347.670692	H	2063.056502	1032.031889	2046.029953	1023.518614	2045.045937	1023.026606	15
7	***769.366136***	385.186706			751.355571	376.181424	G	1925.997590	963.502433	1908.971041	954.989159	1907.987025	954.497151	14
8	***868.434550***	434.720913			850.423985	425.715631	V	***1868.976126***	934.991701	1851.949577	926.478427	1850.965561	925.986419	13
9	***1054.513863***	527.760570			1036.503298	518.755287	W	1769.907712	885.457494	1752.881163	876.944220	1751.897147	876.452211	12
10	1155.561542	**578.284409**			1137.550977	569.279127	T	***1583.828399***	792.417838	1566.801850	783.904563	1565.817834	783.412555	11
11	***1283.620120***	**642.313698**	1266.593571	633.800424	1265.609555	633.308416	Q	***1482.780720***	741.893998	1465.754171	733.380724	1464.770155	732.888715	10
12	***1396.704184***	698.855730	1379.677635	690.342456	1378.693619	689.850448	L	***1354.722142***	677.864709	1337.695593	669.351434	1336.711577	668.859426	9
13	1493.756948	747.382112	1476.730399	738.868838	1475.746383	738.376830	P	***1241.638078***	621.322677	1224.611529	612.809403	1223.627513	612.317394	8
14	1932.982274	**966.994775**	1915.955725	958.481501	1914.971709	957.989493	Q	***1144.585314***	572.796295	1127.558765	564.283021	1126.574749	563.791012	7
15	2093.012923	1047.010099	2075.986374	1038.496825	2075.002358	1038.004817	C	***705.359988***	353.183632	688.333439	344.670357	687.349423	344.178349	6
16	2192.081337	1096.544306	2175.054788	1088.031032	2174.070772	1087.539024	V	***545.329339***	273.168308	528.302790	264.655033	527.318774	264.163025	5
17	2263.118451	**1132.062863**	2246.091902	1123.549589	2245.107886	1123.057581	A	***446.260925***	223.634101	429.234376	215.120826	428.250360	214.628818	4
18	2376.202515	**1188.604895**	2359.175966	1180.091621	2358.191950	1179.599613	I	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
19	2491.229458	1246.118367	2474.202909	1237.605092	2473.218893	1237.113084	D	***262.139747***	131.573511	245.113198	123.060237	244.129182	122.568229	2
20							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.2	2636.327728	0.033044	SITCIHGVWTQLPQCVAIDK
29.8	2636.327728	0.033044	SITCIHGVWTQLPQCVAIDK
0.7	2636.366592	-0.005820	ASKTTDLRIPASVCTMFNVLVDAK

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

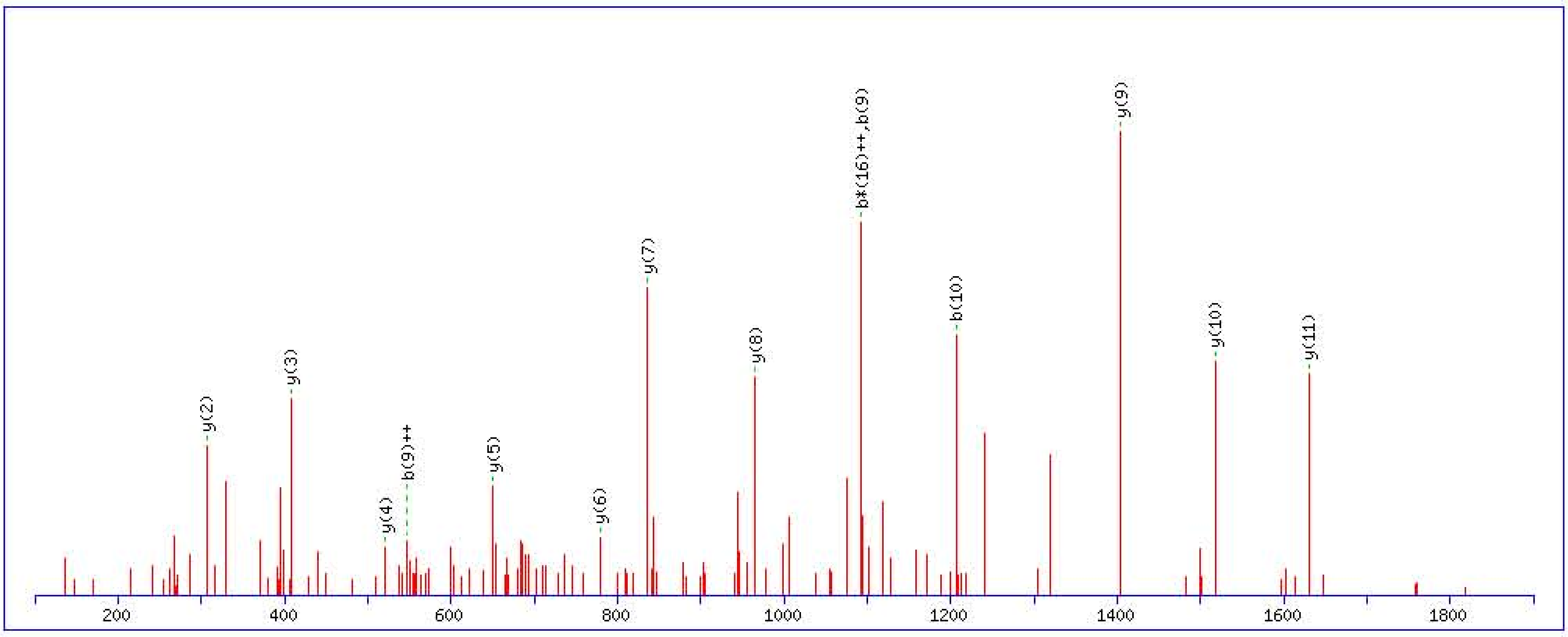
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSVLCQENYLIQEGEEITCK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

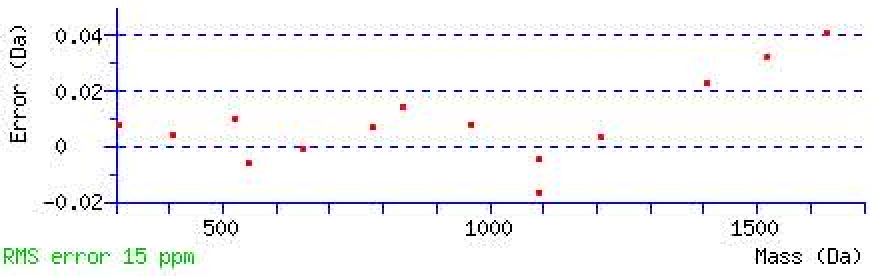
Match to Query 65998: 2722.335312 from(908.452380,3+) rtinseconds(2728) index(29632)
Title: Locus:1.1.1.3090.23 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

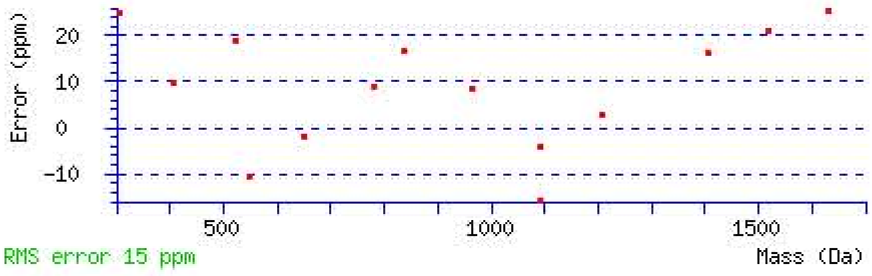
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2722.301590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 1.8e-006
Matches : 14/212 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	100.075690	50.541483					V							20
2	187.107718	94.057497			169.097153	85.052214	S	2624.240475	1312.623875	2607.213926	1304.110601	2606.229910	1303.618593	19
3	286.176132	143.591704			268.165567	134.586422	V	2537.208447	1269.107861	2520.181898	1260.594587	2519.197882	1260.102579	18
4	399.260196	200.133736			381.249631	191.128454	L	2438.140033	1219.573654	2421.113484	1211.060380	2420.129468	1210.568372	17
5	559.290845	280.149061			541.280280	271.143778	C	2325.055969	1163.031622	2308.029420	1154.518348	2307.045404	1154.026340	16
6	687.349423	344.178350	670.322874	335.665075	669.338858	335.173067	Q	2165.025320	1083.016298	2147.998771	1074.503023	2147.014755	1074.011015	15
7	816.392016	408.699646	799.365467	400.186372	798.381451	399.694364	E	2036.966742	1018.987009	2019.940193	1010.473735	2018.956177	1009.981727	14
8	930.434943	465.721110	913.408394	457.207835	912.424378	456.715827	N	1907.924149	954.465713	1890.897600	945.952438	1889.913584	945.460430	13
9	**1093.498272**	547.252774	1076.471723	538.739500	1075.487707	538.247492	Y	1793.881222	897.444249	1776.854673	888.930975	1775.870657	888.438967	12
10	**1206.582336**	603.794806	1189.555787	595.281532	1188.571771	594.789523	L	***1630.817893***	815.912585	1613.791344	807.399310	1612.807328	806.907302	11
11	1319.666400	660.336838	1302.639851	651.823563	1301.655835	651.331555	I	***1517.733829***	759.370553	1500.707280	750.857278	1499.723264	750.365270	10
12	1758.891726	879.949501	1741.865177	871.436227	1740.881161	870.944219	Q	***1404.649765***	702.828521	1387.623216	694.315246	1386.639200	693.823238	9
13	1887.934319	944.470798	1870.907770	935.957523	1869.923754	935.465515	E	***965.424439***	483.215858	948.397890	474.702583	947.413874	474.210575	8
14	1944.955783	972.981530	1927.929234	964.468255	1926.945218	963.976247	G	***836.381846***	418.694561	819.355297	410.181287	818.371281	409.689279	7
15	2073.998376	1037.502826	2056.971827	1028.989551	2055.987811	1028.497543	E	***779.360382***	390.183829	762.333833	381.670555	761.349817	381.178547	6
16	2203.040969	1102.024123	2186.014420	1093.510848	2185.030404	1093.018840	E	***650.317789***	325.662533	633.291240	317.149258	632.307224	316.657250	5
17	2316.125033	1158.566155	2299.098484	1150.052880	2298.114468	1149.560872	I	***521.275196***	261.141236	504.248647	252.627961	503.264631	252.135953	4
18	2417.172712	1209.089994	2400.146163	1200.576719	2399.162147	1200.084711	T	***408.191132***	204.599204	391.164583	196.085929	390.180567	195.593921	3
19	2577.203361	1289.105318	2560.176812	1280.592044	2559.192796	1280.100036	C	***307.143453***	154.075364	290.116904	145.562090			2
20							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.7	2722.301590	0.033722	VSVLCQENYLIQEGEEITCK
65.8	2722.301590	0.033722	VSVLCQENYLIQEGEEITCK
11.6	2722.339783	-0.004471	QDREHLWKLIEGGAHIYVCGDAR
2.1	2722.358841	-0.023529	YEDVKPLETQPAEIAEKETLEYK

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

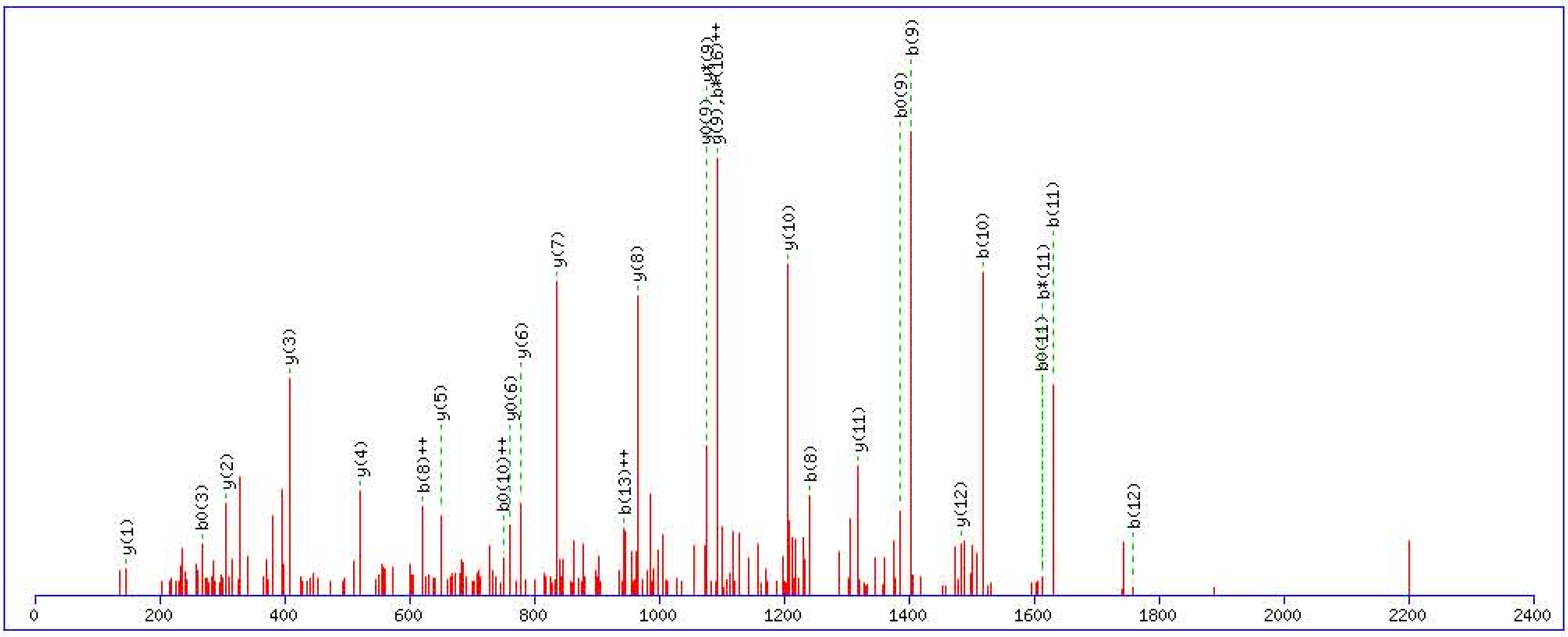
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSVLCQENYLIQEGEEITCK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 65999: 2722.335312 from(908.452380,3+) rtinseconds(2745) index(29764)
Title: Locus:1.1.1.3096.7 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 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 ●



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Monoisotopic mass of neutral peptide Mr(calc): 2722.301590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 1e-005
Matches : 28/212 fragment ions using 50 most intense peaks   (help)
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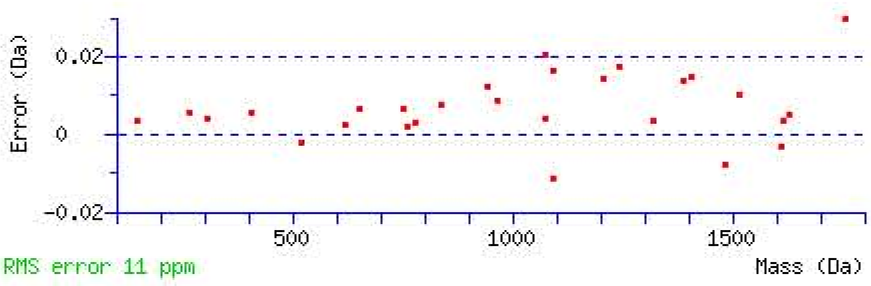
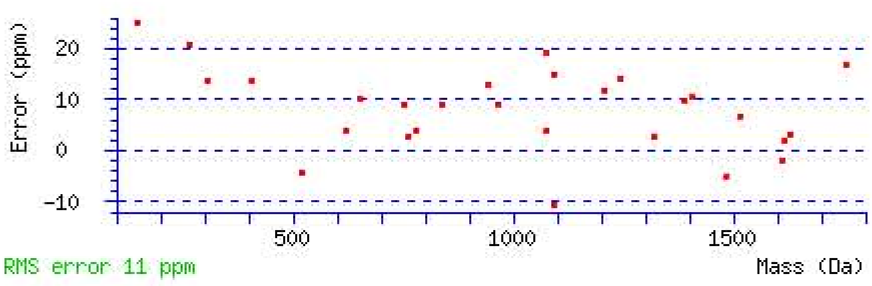
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							20
2	187.107718	94.057497			169.097153	85.052214	S	2624.240475	1312.623875	2607.213926	1304.110601	2606.229910	1303.618593	19
3	286.176132	143.591704			268.165567	134.586422	V	2537.208447	1269.107861	2520.181898	1260.594587	2519.197882	1260.102579	18
4	399.260196	200.133736			381.249631	191.128454	L	2438.140033	1219.573654	2421.113484	1211.060380	2420.129468	1210.568372	17
5	559.290845	280.149061			541.280280	271.143778	C	2325.055969	1163.031622	2308.029420	1154.518348	2307.045404	1154.026340	16
6	998.516171	499.761724	981.489622	491.248449	980.505606	490.756441	Q	2165.025320	1083.016298	2147.998771	1074.503023	2147.014755	1074.011015	15
7	1127.558764	564.283020	1110.532215	555.769746	1109.548199	555.277738	E	1725.799994	863.403635	1708.773445	854.890361	1707.789429	854.398353	14
8	**1241.601691**	**621.304484**	1224.575142	612.791209	1223.591126	612.299201	N	1596.757401	798.882339	1579.730852	790.369064	1578.746836	789.877056	13
9	**1404.665020**	702.836148	1387.638471	694.322874	1386.654455	693.830866	Y	***1482.714474***	741.860875	1465.687925	733.347601	1464.703909	732.855593	12
10	**1517.749084**	759.378180	1500.722535	750.864906	1499.738519	750.372898	L	***1319.651145***	660.329211	1302.624596	651.815936	1301.640580	651.323928	11
11	**1630.833148**	815.920212	1613.806599	807.406938	1612.822583	806.914929	I	***1206.567081***	603.787179	1189.540532	595.273904	1188.556516	594.781896	10
12	**1758.891726**	879.949501	1741.865177	871.436227	1740.881161	870.944219	Q	***1093.483017***	547.245147	1076.456468	538.731872	1075.472452	538.239864	9
13	1887.934319	**944.470798**	1870.907770	935.957523	1869.923754	935.465515	E	***965.424439***	483.215858	948.397890	474.702583	947.413874	474.210575	8
14	1944.955783	972.981530	1927.929234	964.468255	1926.945218	963.976247	G	***836.381846***	418.694561	819.355297	410.181287	818.371281	409.689279	7
15	2073.998376	1037.502826	2056.971827	1028.989551	2055.987811	1028.497543	E	***779.360382***	390.183829	762.333833	381.670555	761.349817	381.178547	6
16	2203.040969	1102.024123	2186.014420	1093.510848	2185.030404	1093.018840	E	***650.317789***	325.662533	633.291240	317.149258	632.307224	316.657250	5
17	2316.125033	1158.566155	2299.098484	1150.052880	2298.114468	1149.560872	I	***521.275196***	261.141236	504.248647	252.627961	503.264631	252.135953	4
18	2417.172712	1209.089994	2400.146163	1200.576719	2399.162147	1200.084711	T	***408.191132***	204.599204	391.164583	196.085929	390.180567	195.593921	3
19	2577.203361	1289.105318	2560.176812	1280.592044	2559.192796	1280.100036	C	***307.143453***	154.075364	290.116904	145.562090			2
20							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.0	2722.301590	0.033722	VSVLCQENYLIQEGEEITCK
58.2	2722.301590	0.033722	VSVLCQENYLIQEGEEITCK
16.1	2722.339783	-0.004471	QDREHLWKLIEGGAHIYVCGDAR

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

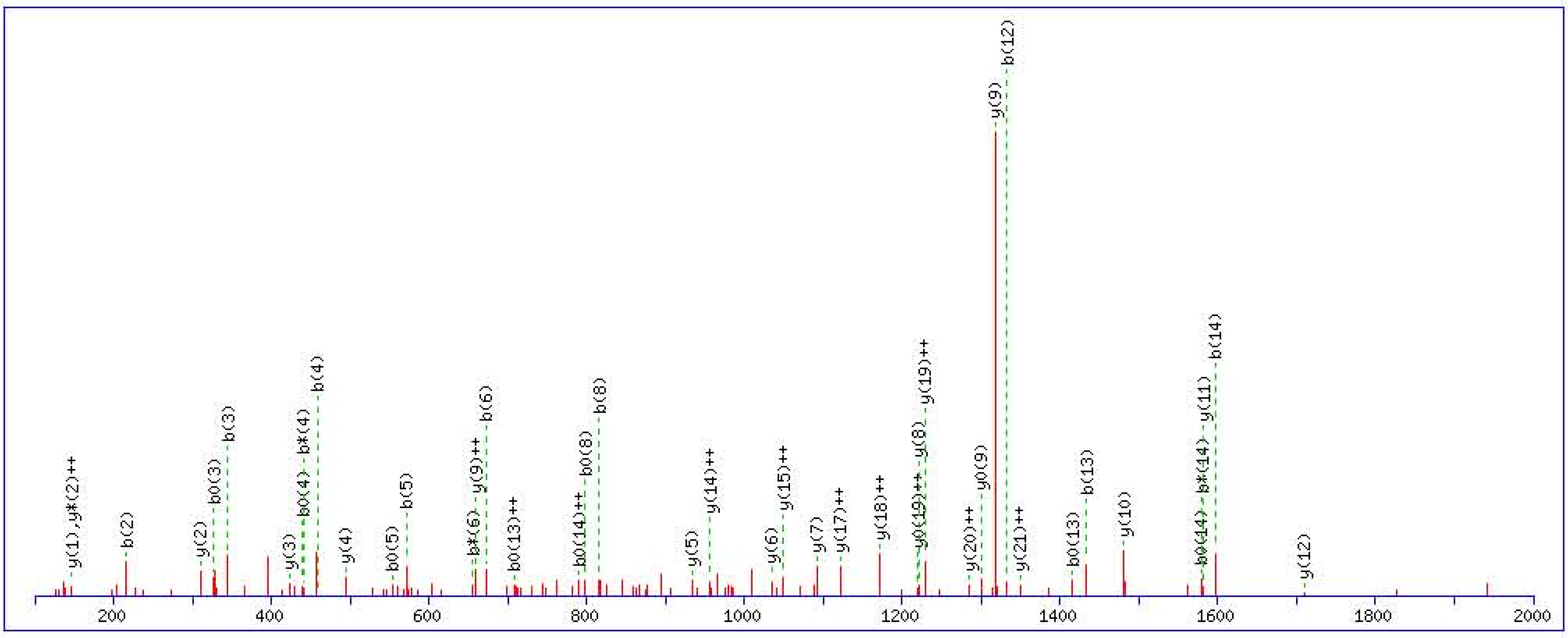
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NTEILTGSWSDQTYPEGTQAIYK**
Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

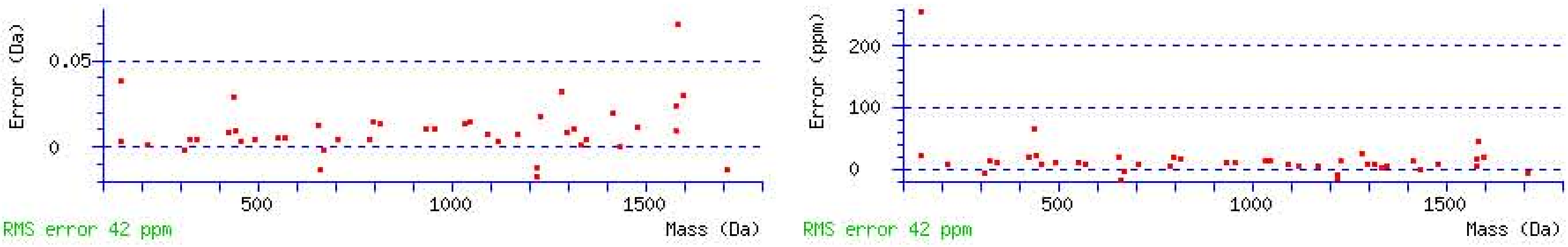
Match to Query 69211: 2912.431062 from(971.817630,3+) rtinseconds(2374) index(27340)
Title: Locus:1.1.1.2968.24 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 2912.390213
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19 : Biotin:Thermo-21345 (Q)
Ions Score: 73 **Expect:** 1.3e-006
Matches : 43/252 fragment ions using 76 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							23
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	T	2799.354578	1400.180927	2782.328029	1391.667652	2781.344013	1391.175644	22
3	**345.140475**	173.073875	328.113926	164.560601	327.129910	164.068593	E	2698.306899	1349.657087	2681.280350	1341.143813	2680.296334	1340.651805	21
4	**458.224539**	229.615907	441.197990	221.102633	440.213974	220.610625	I	2569.264306	1285.135791	2552.237757	1276.622516	2551.253741	1276.130508	20
5	**571.308603**	286.157940	554.282054	277.644665	553.298038	277.152657	L	2456.180242	1228.593759	2439.153693	1220.080484	2438.169677	1219.588476	19
6	**672.356282**	336.681779	655.329733	328.168505	654.345717	327.676497	T	2343.096178	1172.051727	2326.069629	1163.538452	2325.085613	1163.046444	18
7	729.377746	365.192511	712.351197	356.679237	711.367181	356.187229	G	2242.048499	1121.527887	2225.021950	1113.014613	2224.037934	1112.522605	17
8	**816.409774**	408.708525	799.383225	400.195251	798.399209	399.703243	S	2185.027035	1093.017155	2168.000486	1084.503881	2167.016470	1084.011873	16
9	1002.489087	501.748182	985.462538	493.234907	984.478522	492.742899	W	2097.995007	1049.501141	2080.968458	1040.987867	2079.984442	1040.495859	15
10	1089.521115	545.264196	1072.494566	536.750921	1071.510550	536.258913	S	1911.915694	956.461485	1894.889145	947.948211	1893.905129	947.456203	14
11	1204.548058	602.777667	1187.521509	594.264393	1186.537493	593.772385	D	1824.883666	912.945471	1807.857117	904.432197	1806.873101	903.940189	13
12	**1332.606636**	666.806956	1315.580087	658.293682	1314.596071	657.801674	Q	***1709.856723***	855.432000	1692.830174	846.918725	1691.846158	846.426717	12
13	**1433.654315**	717.330796	1416.627766	708.817521	1415.643750	708.325513	T	***1581.798145***	791.402711	1564.771596	782.889436	1563.787580	782.397428	11
14	**1596.717644**	798.862460	1579.691095	790.349186	1578.707079	789.857178	Y	***1480.750466***	740.878871	1463.723917	732.365597	1462.739901	731.873589	10
15	1693.770408	847.388842	1676.743859	838.875568	1675.759843	838.383560	P	***1317.687137***	659.347207	1300.660588	650.833932	1299.676572	650.341924	9
16	1822.813001	911.910139	1805.786452	903.396864	1804.802436	902.904856	E	***1220.634373***	610.820825	1203.607824	602.307550	1202.623808	601.815542	8
17	1879.834465	940.420871	1862.807916	931.907596	1861.823900	931.415588	G	***1091.591780***	546.299528	1074.565231	537.786254	1073.581215	537.294246	7
18	1980.882144	990.944710	1963.855595	982.431436	1962.871579	981.939428	T	***1034.570316***	517.788796	1017.543767	509.275522	1016.559751	508.783514	6
19	2420.107470	1210.557373	2403.080921	1202.044098	2402.096905	1201.552090	Q	***933.522637***	467.264957	916.496088	458.751682			5
20	2491.144584	1246.075930	2474.118035	1237.562655	2473.134019	1237.070648	A	***494.297311***	247.652294	477.270762	239.139019			4
21	2604.228648	1302.617962	2587.202099	1294.104688	2586.218083	1293.612680	I	***423.260197***	212.133737	406.233648	203.620462			3
22	2767.291977	1384.149627	2750.265428	1375.636352	2749.281412	1375.144344	Y	***310.176133***	155.591705	293.149584	147.078430			2
23							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.4	2912.390213	0.040849	NTEILTGSWSDQTYPEGTQAIYK
16.4	2912.390213	0.040849	NTEILTGSWSDQTYPEGTQAIYK

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

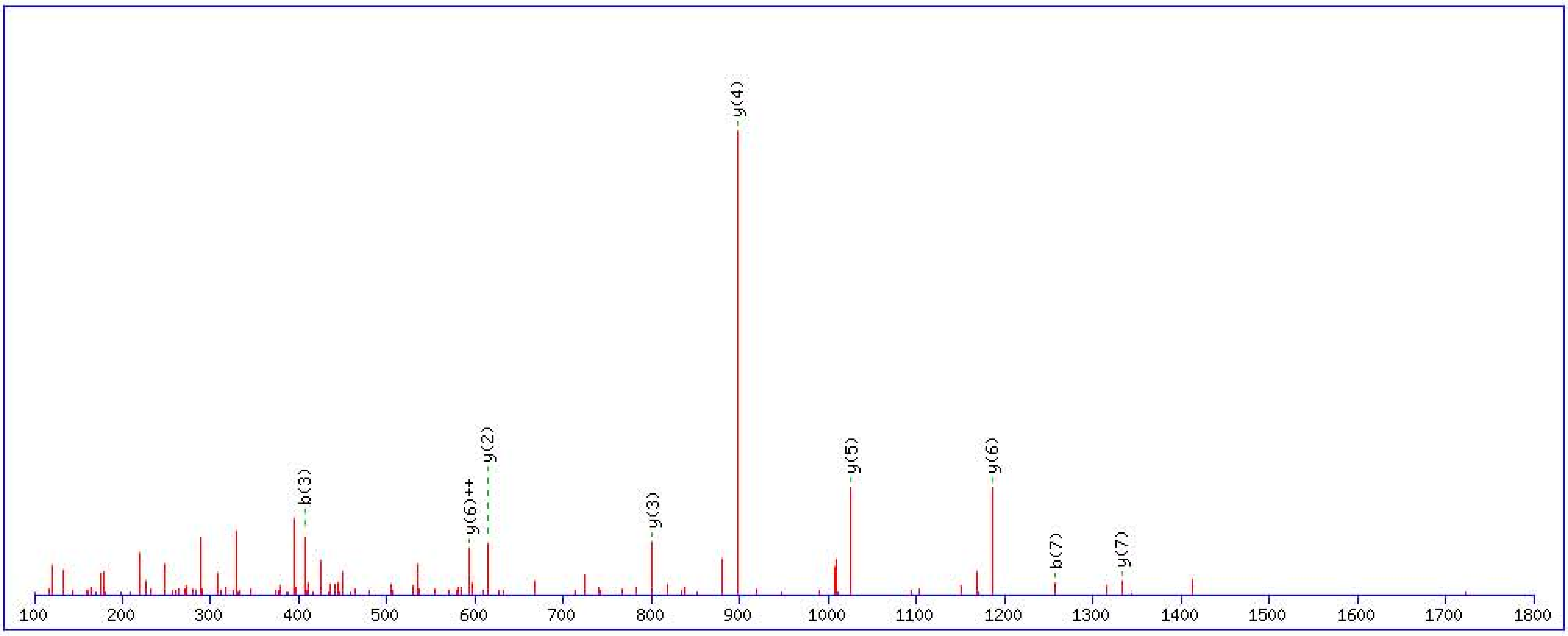
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFCQPWQR**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

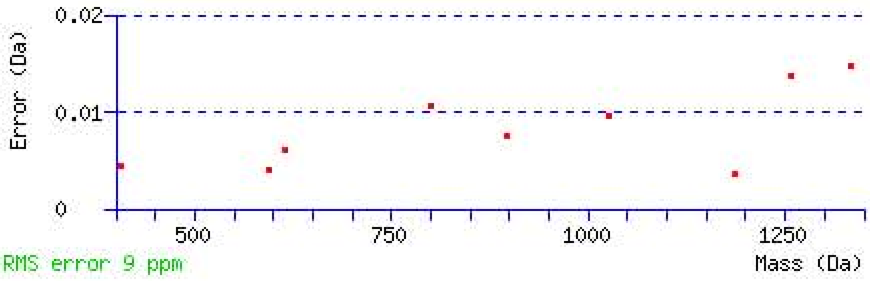
Match to Query 32674: 1430.707748 from(716.361150,2+) rtinseconds(2015) index(78953)
Title: Locus:1.1.1.2052.9 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

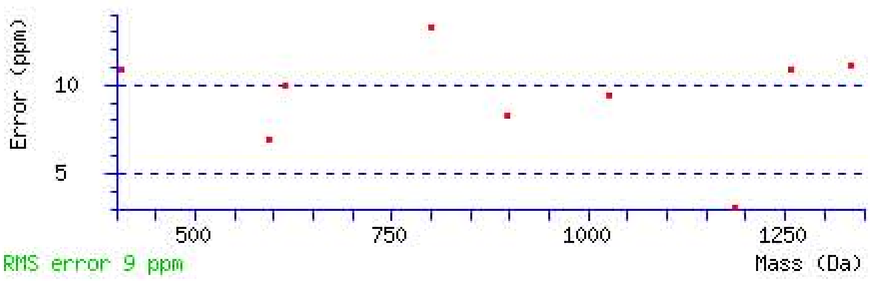
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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	0.012603	VFCQPWQR
8.3	1430.695145	0.012603	VFCQPWQR
2.5	1430.693619	0.014129	QLQTLSMPGGGGNR
1.4	1430.726822	-0.019074	VFDVYLCFLQK
0.7	1430.711319	-0.003571	RAKAEDENETLR
0.4	1430.722565	-0.014817	REAGEAGAATSKQR

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

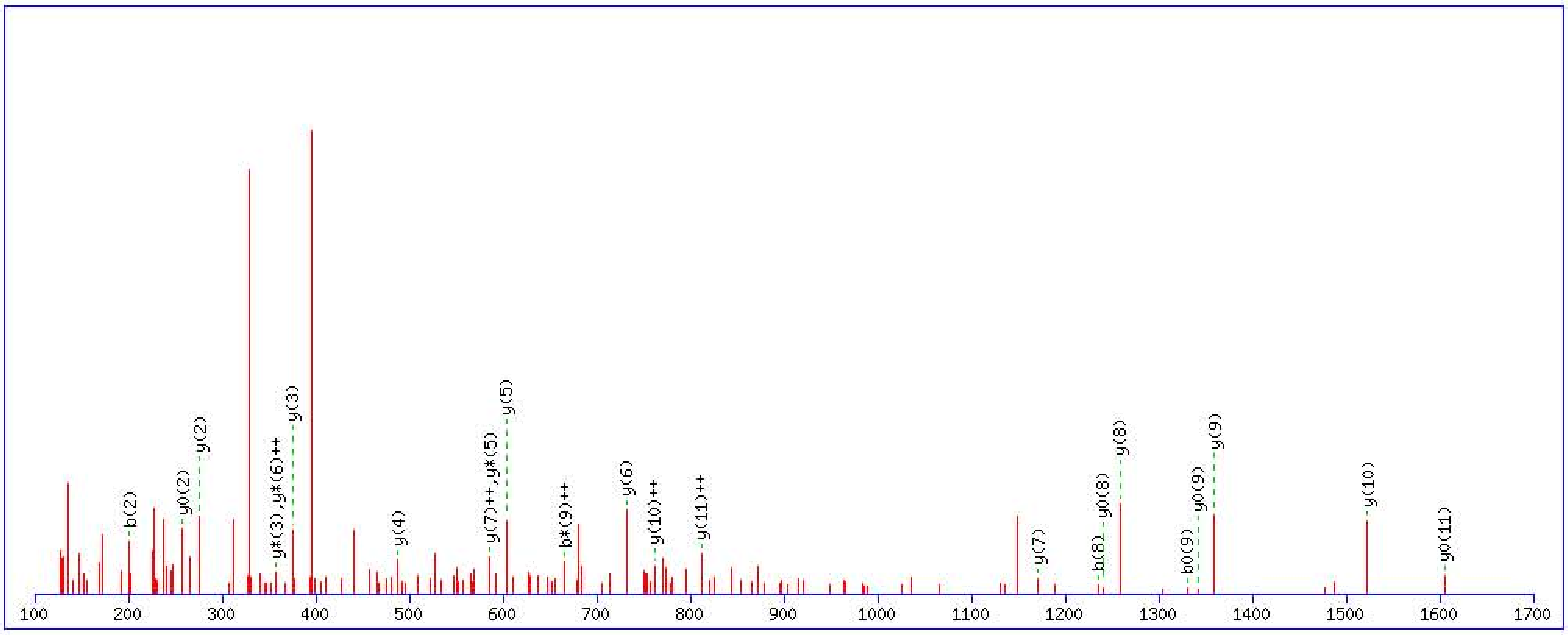
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTYTSQEDLVEK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

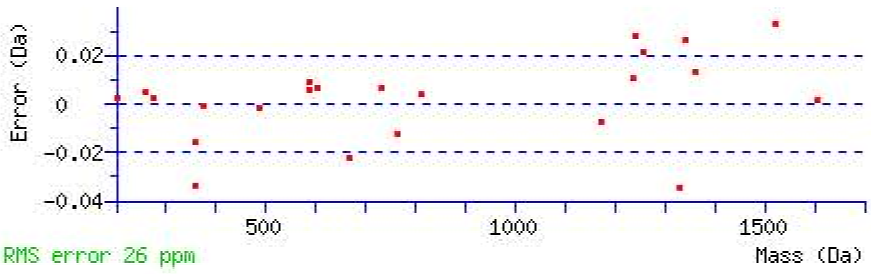
Match to Query 43052: 1721.865822 from(574.962550,3+) rtinseconds(1870) index(77896)
Title: Locus:1.1.1.2002.14 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

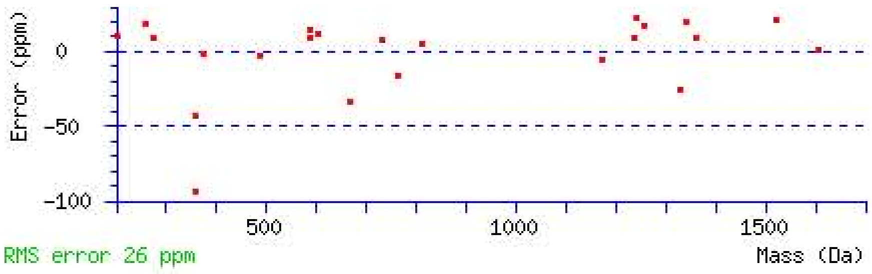
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 35 **Expect:** 0.0074
Matches : 23/118 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							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
35.3	1721.854584	0.011238	VTYTSQEDLVEK

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

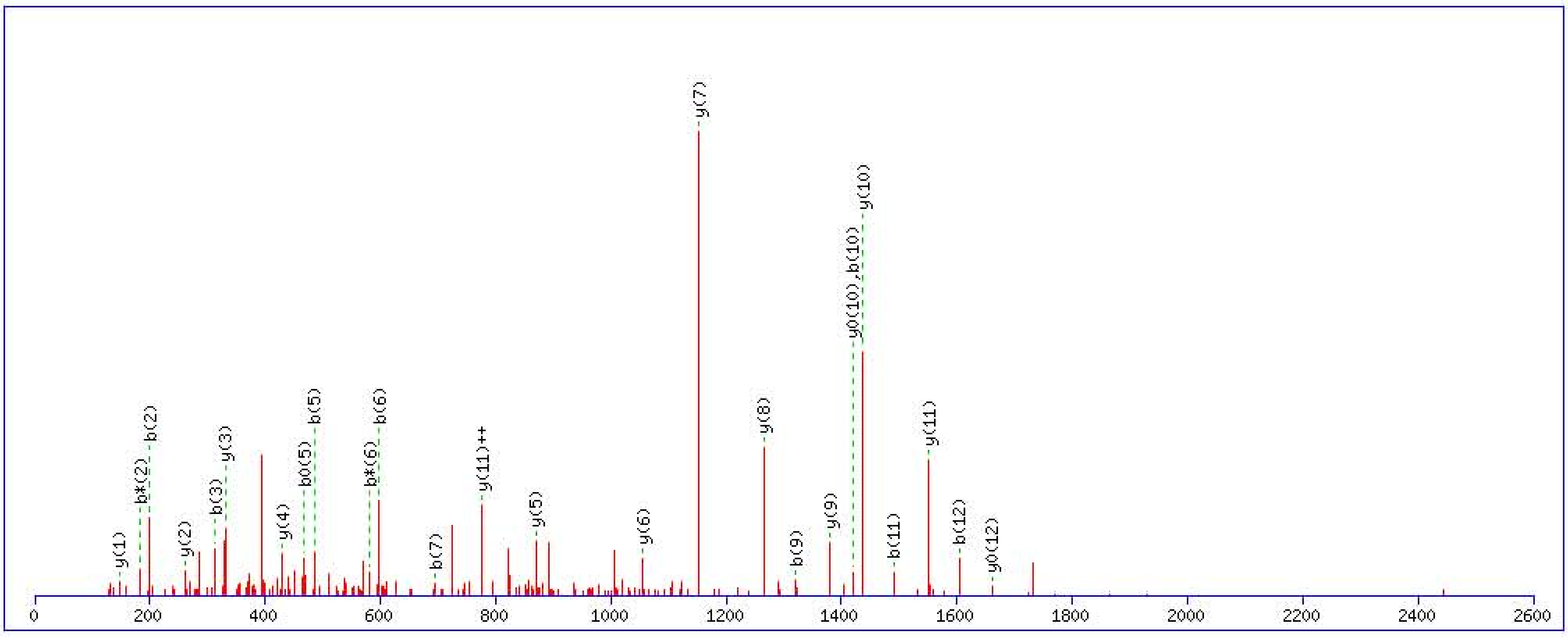
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQLGDLPWQVAIK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

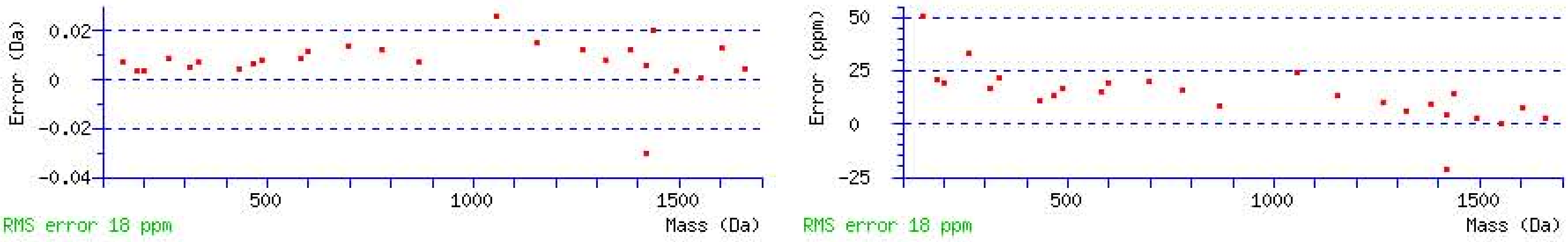
Match to Query 43857: 1748.988508 from(875.501530,2+) rtinseconds(2632) index(82988)
Title: Locus:1.1.1.2266.9 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1748.964737
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 71  Expect: 3.3e-007
Matches : 26/118 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	72.044390	36.525833					A							13
2	**200.102968**	100.555122	183.076419	92.041848			Q	1678.934912	839.971094	1661.908363	831.457820	1660.924347	830.965812	12
3	**313.187032**	157.097154	296.160483	148.583879			L	***1550.876334***	775.941805	1533.849785	767.428531	1532.865769	766.936523	11
4	370.208496	185.607886	353.181947	177.094611			G	***1437.792270***	719.399773	1420.765721	710.886499	1419.781705	710.394491	10
5	**485.235439**	243.121357	468.208890	234.608083	467.224874	234.116075	D	***1380.770806***	690.889041	1363.744257	682.375767	1362.760241	681.883759	9
6	**598.319503**	299.663390	581.292954	291.150115	580.308938	290.658107	L	***1265.743863***	633.375570	1248.717314	624.862295			8
7	**695.372267**	348.189772	678.345718	339.676497	677.361702	339.184489	P	***1152.659799***	576.833538	1135.633250	568.320263			7
8	881.451580	441.229428	864.425031	432.716154	863.441015	432.224146	W	***1055.607035***	528.307156	1038.580486	519.793881			6
9	**1320.676906**	660.842091	1303.650357	652.328817	1302.666341	651.836809	Q	***869.527722***	435.267499	852.501173	426.754225			5
10	**1419.745320**	710.376298	1402.718771	701.863024	1401.734755	701.371016	V	***430.302396***	215.654836	413.275847	207.141561			4
11	**1490.782434**	745.894855	1473.755885	737.381581	1472.771869	736.889573	A	***331.233982***	166.120629	314.207433	157.607354			3
12	**1603.866498**	802.436887	1586.839949	793.923613	1585.855933	793.431605	I	***260.196868***	130.602072	243.170319	122.088797			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.0	1748.964737	0.023771	AQLGDLPWQVAIK
4.3	1748.964737	0.023771	AQLGDLPWQVAIK
1.7	1748.978439	0.010069	YARKISGTTALQEALK
0.1	1748.964523	0.023985	AAAALSLAHRLLDGAGSR

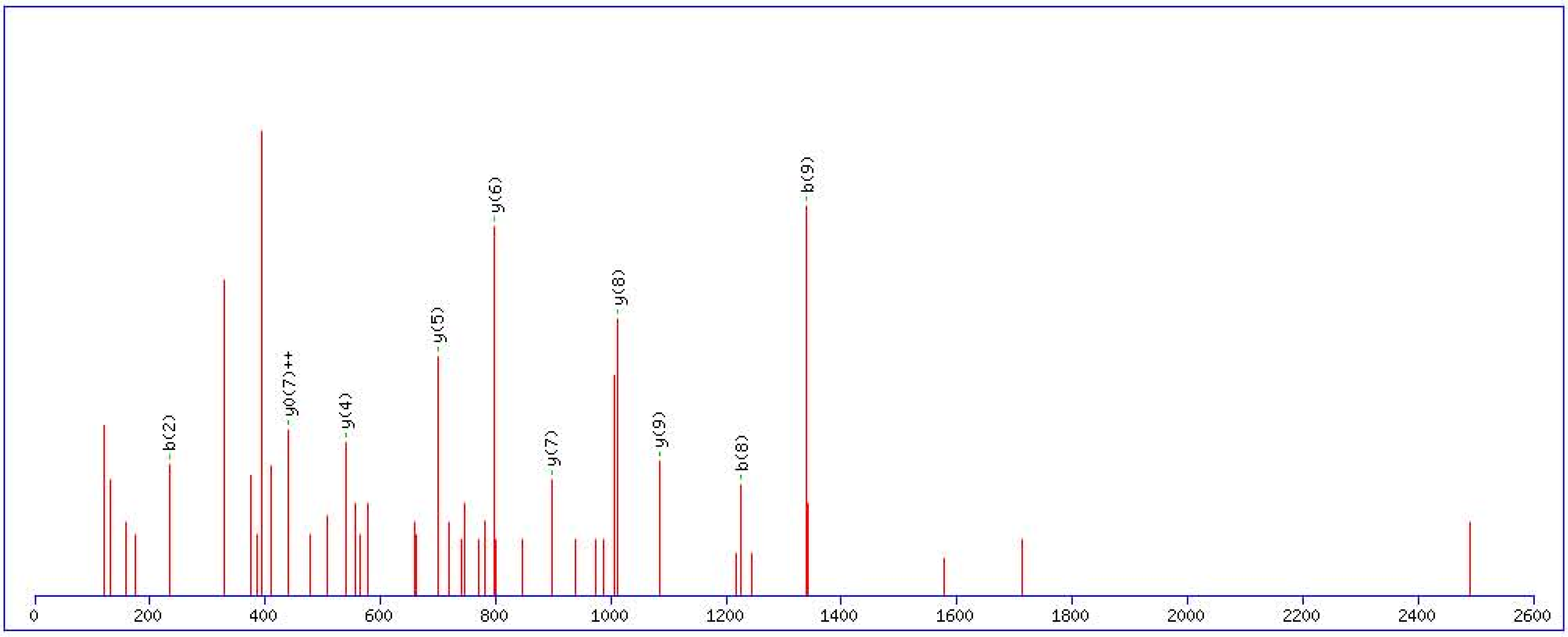
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMGYQDFADVVCYTQK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

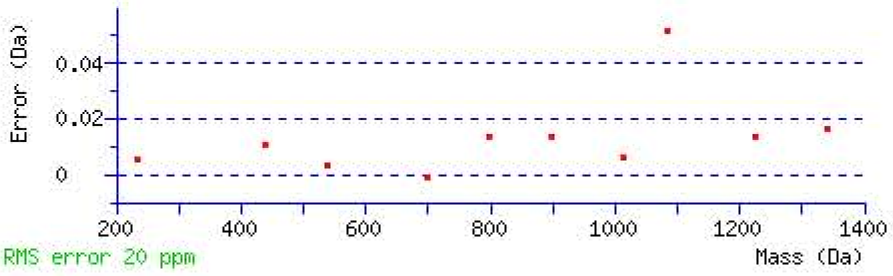
Match to Query 56325: 2236.024512 from(746.348780,3+) rtinseconds(2498) index(82131)
Title: Locus:1.1.1.2220.14 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

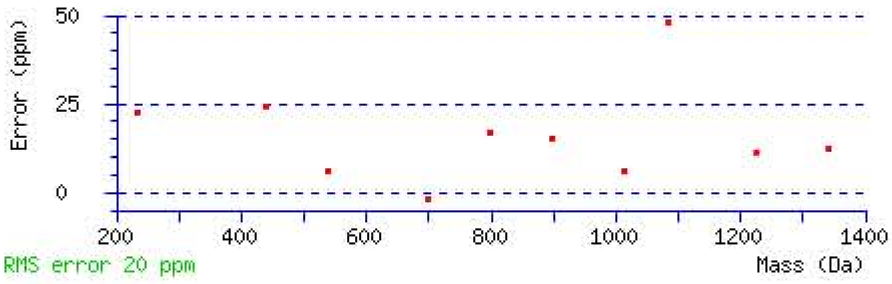
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2236.000305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.004
Matches : 10/168 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	102.054955	51.531116			84.044390	42.525833	T							16
2	**233.095440**	117.051358			215.084875	108.046076	M	2135.959885	1068.483580	2118.933336	1059.970306	2117.949320	1059.478298	15
3	290.116904	145.562090			272.106339	136.556807	G	2004.919400	1002.963338	1987.892851	994.450064	1986.908835	993.958056	14
4	453.180233	227.093754			435.169668	218.088472	Y	1947.897936	974.452606	1930.871387	965.939332	1929.887371	965.447324	13
5	892.405559	446.706418	875.379010	438.193143	874.394994	437.701135	Q	1784.834607	892.920942	1767.808058	884.407667	1766.824042	883.915659	12
6	1007.432502	504.219889	990.405953	495.706615	989.421937	495.214607	D	1345.609281	673.308279	1328.582732	664.795004	1327.598716	664.302996	11
7	1154.500916	577.754096	1137.474367	569.240822	1136.490351	568.748813	F	1230.582338	615.794807	1213.555789	607.281533	1212.571773	606.789525	10
8	**1225.538030**	613.272653	1208.511481	604.759379	1207.527465	604.267370	A	***1083.513924***	542.260600	1066.487375	533.747326	1065.503359	533.255318	9
9	**1340.564973**	670.786125	1323.538424	662.272850	1322.554408	661.780842	D	***1012.476810***	506.742043	995.450261	498.228769	994.466245	497.736761	8
10	1439.633387	720.320332	1422.606838	711.807057	1421.622822	711.315049	V	***897.449867***	449.228572	880.423318	440.715297	879.439302	440.223289	7
11	1538.701801	769.854539	1521.675252	761.341264	1520.691236	760.849256	V	***798.381453***	399.694365	781.354904	391.181090	780.370888	390.689082	6
12	1698.732450	849.869863	1681.705901	841.356589	1680.721885	840.864581	C	***699.313039***	350.160158	682.286490	341.646883	681.302474	341.154875	5
13	1861.795779	931.401528	1844.769230	922.888253	1843.785214	922.396245	Y	***539.282390***	270.144833	522.255841	261.631559	521.271825	261.139551	4
14	1962.843458	981.925367	1945.816909	973.412093	1944.832893	972.920085	T	376.219061	188.613168	359.192512	180.099894	358.208496	179.607886	3
15	2090.902036	1045.954656	2073.875487	1037.441381	2072.891471	1036.949373	Q	275.171382	138.089329	258.144833	129.576054			2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TMGYQDFADVVCYTQK
(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	2236.000305	0.024207	TMGYQDFADVVCYTQK

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

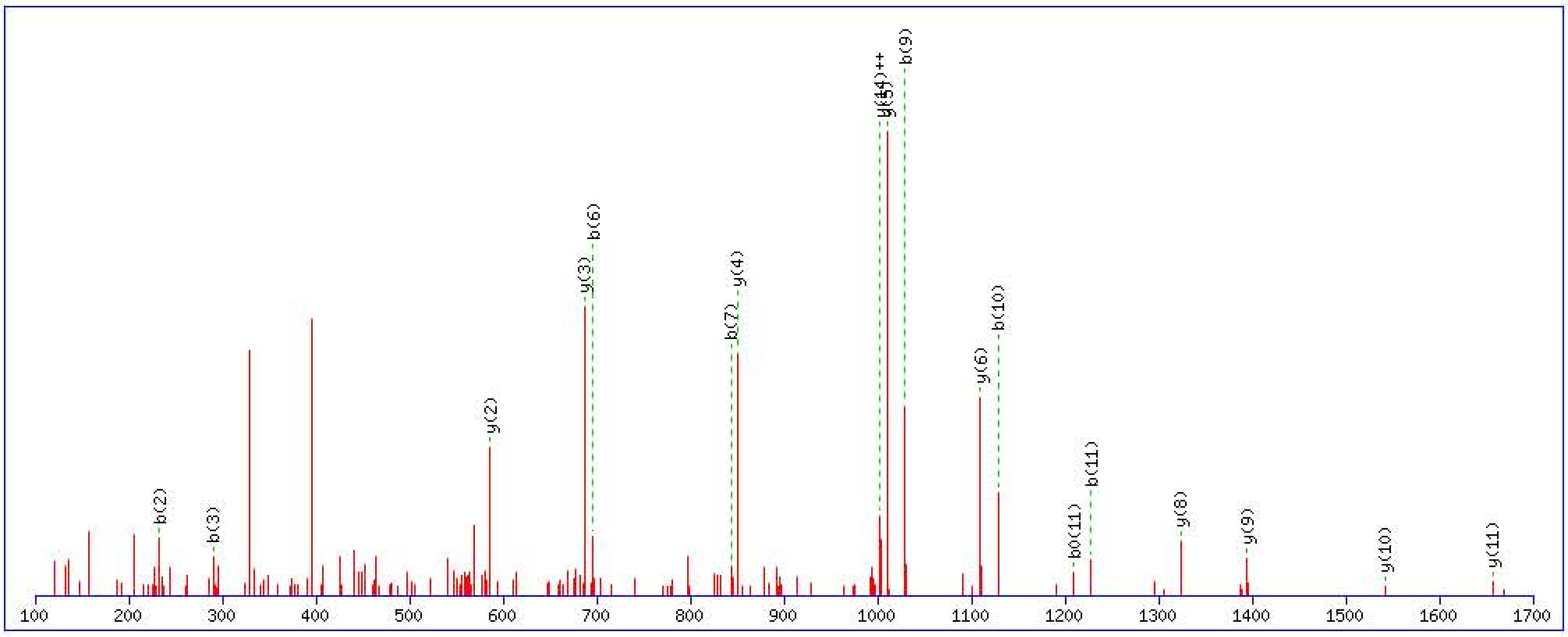
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMGYQDFADVVCYTQK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

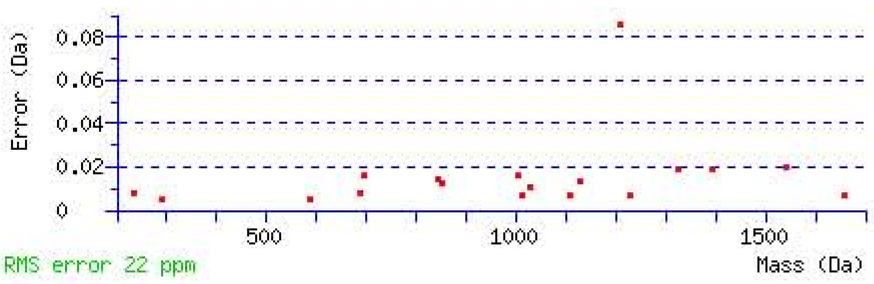
Match to Query 56327: 2236.027272 from(746.349700,3+) rtinseconds(2547) index(82438)
Title: Locus:1.1.1.2237.11 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

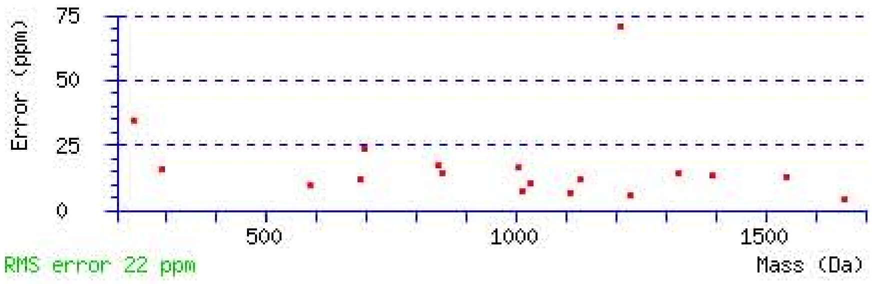
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2236.000305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 2.1e-005
Matches : 18/168 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	102.054955	51.531116			84.044390	42.525833	T							16
2	***233.095440***	117.051358			215.084875	108.046076	M	2135.959885	1068.483580	2118.933336	1059.970306	2117.949320	1059.478298	15
3	***290.116904***	145.562090			272.106339	136.556807	G	2004.919400	1002.963338	1987.892851	994.450064	1986.908835	993.958056	14
4	453.180233	227.093754			435.169668	218.088472	Y	1947.897936	974.452606	1930.871387	965.939332	1929.887371	965.447324	13
5	581.238811	291.123044	564.212262	282.609769	563.228246	282.117761	Q	1784.834607	892.920942	1767.808058	884.407667	1766.824042	883.915659	12
6	***696.265754***	348.636515	679.239205	340.123241	678.255189	339.631233	D	***1656.776029***	828.891653	1639.749480	820.378378	1638.765464	819.886370	11
7	***843.334168***	422.170722	826.307619	413.657447	825.323603	413.165439	F	***1541.749086***	771.378181	1524.722537	762.864907	1523.738521	762.372899	10
8	914.371282	457.689279	897.344733	449.176004	896.360717	448.683996	A	***1394.680672***	697.843974	1377.654123	689.330700	1376.670107	688.838692	9
9	***1029.398225***	515.202750	1012.371676	506.689476	1011.387660	506.197468	D	***1323.643558***	662.325417	1306.617009	653.812143	1305.632993	653.320135	8
10	***1128.466639***	564.736958	1111.440090	556.223683	1110.456074	555.731675	V	1208.616615	604.811946	1191.590066	596.298671	1190.606050	595.806663	7
11	***1227.535053***	614.271165	1210.508504	605.757890	1209.524488	605.265882	V	***1109.548201***	555.277739	1092.521652	546.764464	1091.537636	546.272456	6
12	1387.565702	694.286489	1370.539153	685.773215	1369.555137	685.281207	C	***1010.479787***	505.743532	993.453238	497.230257	992.469222	496.738249	5
13	1550.629031	775.818154	1533.602482	767.304879	1532.618466	766.812871	Y	***850.449138***	425.728207	833.422589	417.214933	832.438573	416.722925	4
14	1651.676710	826.341993	1634.650161	817.828719	1633.666145	817.336711	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
15	2090.902036	1045.954656	2073.875487	1037.441381	2072.891471	1036.949373	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 TMGYQDFADVVCYTQK
(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	2236.000305	0.026967	TMGYQDFADVVCYTQK

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

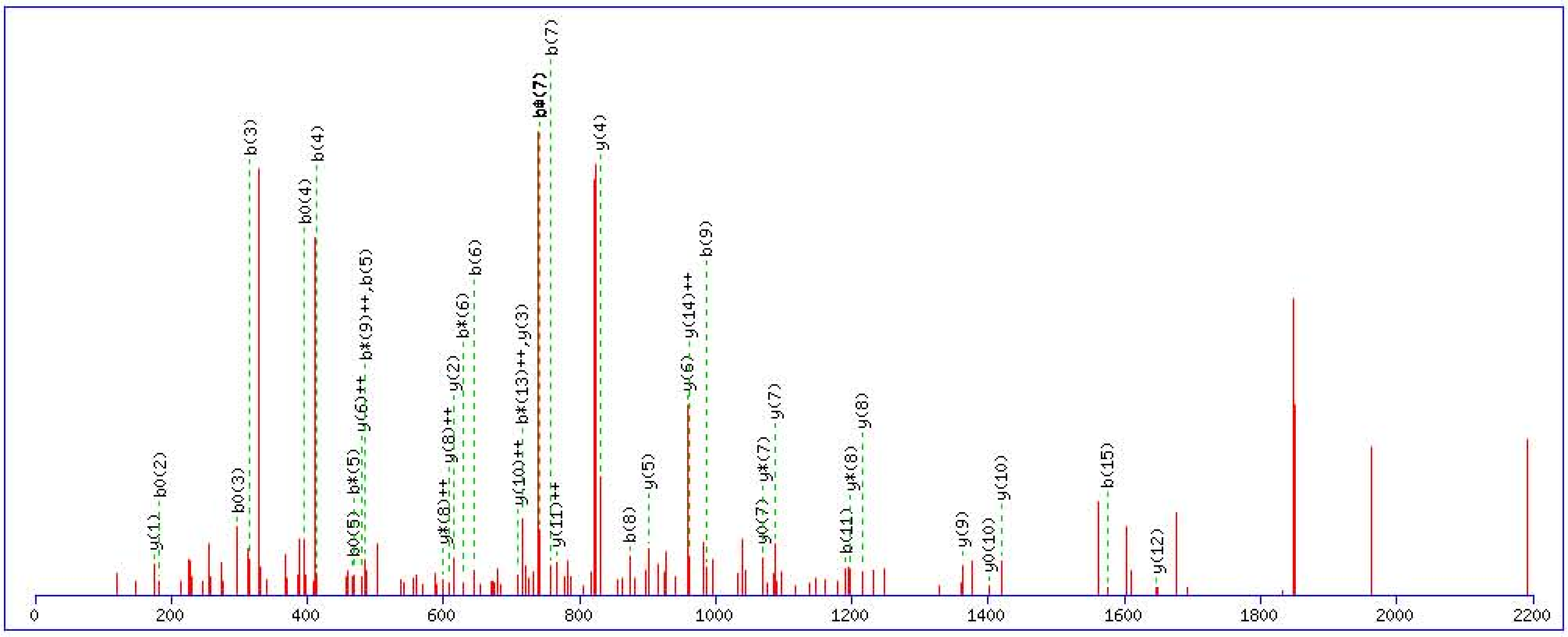
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EANVACLDLGFQQGADTQR**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

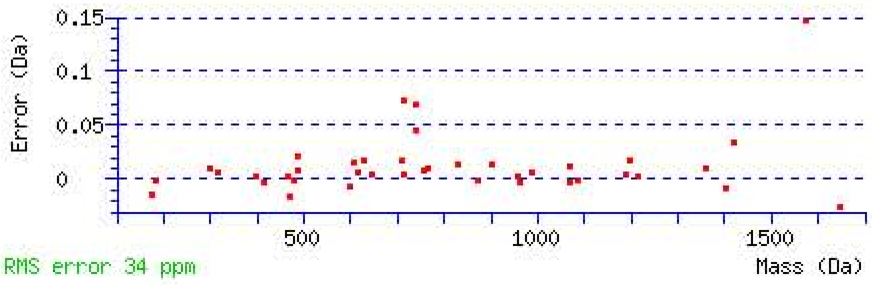
Match to Query 60075: 2403.149742 from(802.057190,3+) rtinseconds(2248) index(80623)
Title: Locus:1.1.1.2133.13 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

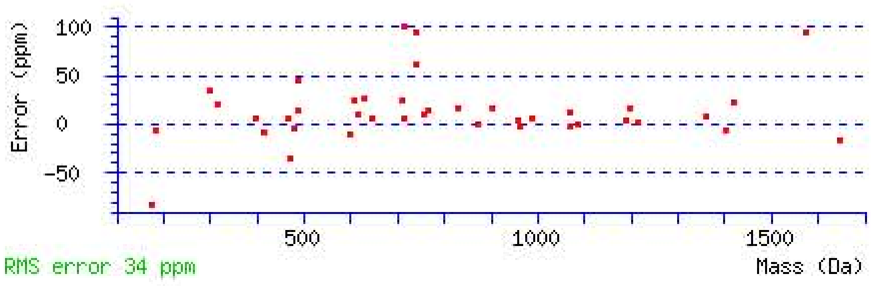
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2403.131119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0074
Matches : 40/208 fragment ions using 119 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	201.086983	101.047130			183.076418	92.041847	A	2275.095801	1138.051538	2258.069252	1129.538264	2257.085236	1129.046256	18
3	***315.129910***	158.068593	298.103361	149.555319	297.119345	149.063311	N	2204.058687	1102.532981	2187.032138	1094.019707	2186.048122	1093.527699	17
4	***414.198324***	207.602800	397.171775	199.089526	396.187759	198.597518	V	2090.015760	1045.511518	2072.989211	1036.998243	2072.005195	1036.506235	16
5	***485.235438***	243.121357	468.208889	234.608082	467.224873	234.116075	A	1990.947346	995.977311	1973.920797	987.464037	1972.936781	986.972029	15
6	***645.266087***	323.136682	628.239538	314.623407	627.255522	314.131399	C	1919.910232	960.458754	1902.883683	951.945480	1901.899667	951.453472	14
7	***758.350151***	379.678714	741.323602	371.165439	740.339586	370.673431	L	1759.879583	880.443430	1742.853034	871.930155	1741.869018	871.438147	13
8	***873.377094***	437.192185	856.350545	428.678911	855.366529	428.186903	D	***1646.795519***	823.901398	1629.768970	815.388123	1628.784954	814.896115	12
9	***986.461158***	493.734217	969.434609	485.220943	968.450593	484.728935	L	1531.768576	766.387926	1514.742027	757.874652	1513.758011	757.382644	11
10	1043.482622	522.244949	1026.456073	513.731675	1025.472057	513.239667	G	***1418.684512***	709.845894	1401.657963	701.332620	1400.673947	700.840612	10
11	***1190.551036***	595.779156	1173.524487	587.265882	1172.540471	586.773874	F	***1361.663048***	681.335162	1344.636499	672.821888	1343.652483	672.329880	9
12	1318.609614	659.808445	1301.583065	651.295171	1300.599049	650.803163	Q	***1214.594634***	607.800955	1197.568085	599.287681	1196.584069	598.795673	8
13	1446.668192	723.837734	1429.641643	715.324460	1428.657627	714.832452	Q	***1086.536056***	543.771666	1069.509507	535.258392	1068.525491	534.766384	7
14	1503.689656	752.348466	1486.663107	743.835192	1485.679091	743.343184	G	***958.477478***	479.742377	941.450929	471.229103	940.466913	470.737095	6
15	***1574.726770***	787.867023	1557.700221	779.353749	1556.716205	778.861741	A	***901.456014***	451.231645	884.429465	442.718371	883.445449	442.226363	5
16	1689.753713	845.380495	1672.727164	836.867220	1671.743148	836.375212	D	***830.418900***	415.713088	813.392351	407.199814	812.408335	406.707806	4
17	1790.801392	895.904334	1773.774843	887.391060	1772.790827	886.899052	T	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
18	2230.026718	1115.516997	2213.000169	1107.003722	2212.016153	1106.511714	Q	***614.344278***	307.675777	597.317729	299.162503			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EANVACLDLGFQQGADTQR
(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	2403.131119	0.018623	EANVACLDLGFQQGADTQR
8.3	2403.131119	0.018623	EANVACLDLGFQQGADTQR
5.9	2403.131119	0.018623	EANVACLDLGFQQGADTQR

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

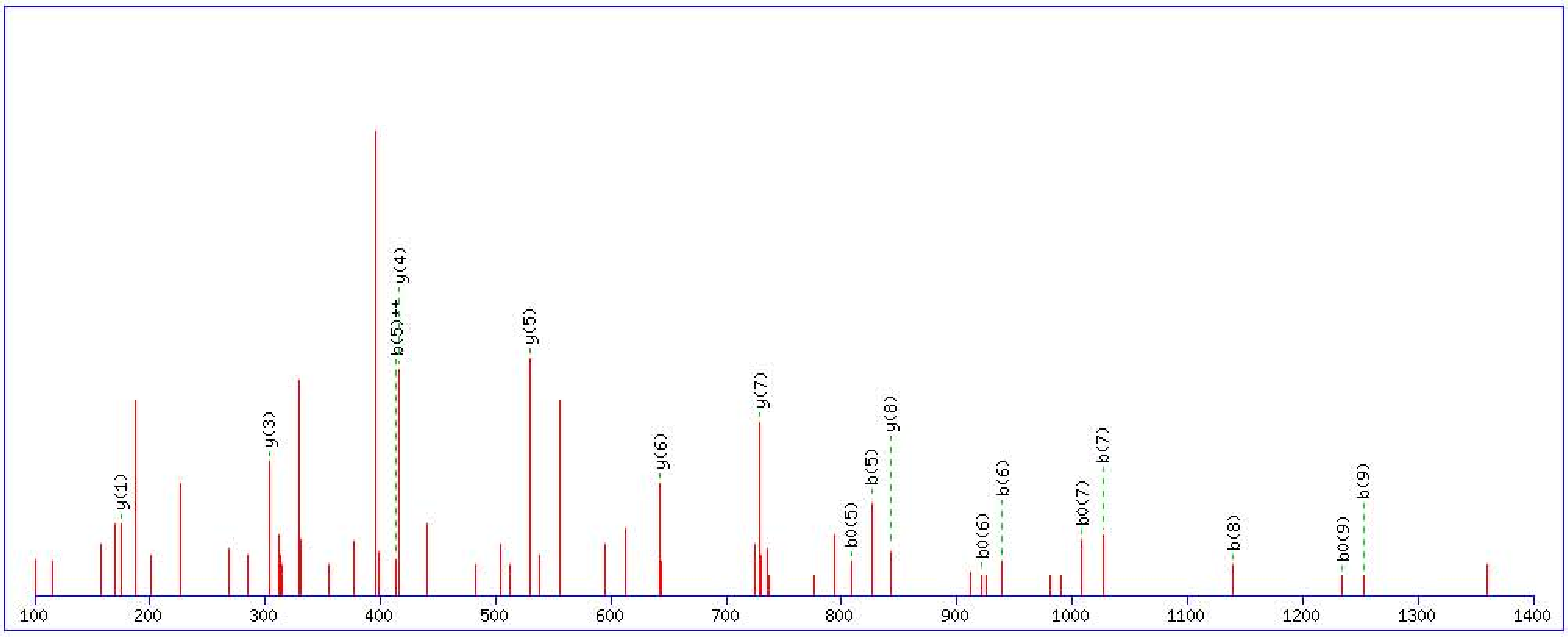
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLGDQLSLLLGAR**
Found in **MRC2_HUMAN**, C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2

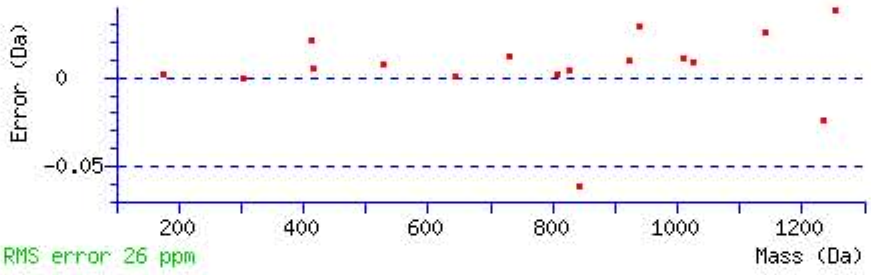
Match to Query 41637: 1666.965282 from(556.662370,3+) rtinseconds(2965) index(49124)
Title: Locus:1.1.1.3478.2 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

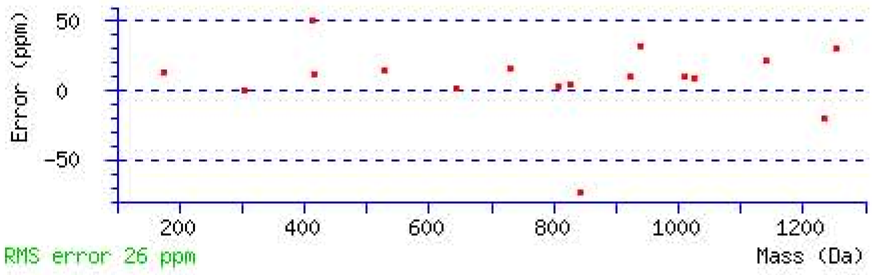
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1666.944000
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.006
Matches : 17/124 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							13
2	215.139019	108.073147			197.128454	99.067865	L	1566.903611	783.955443	1549.877062	775.442169	1548.893046	774.950161	12
3	272.160483	136.583879			254.149918	127.578597	G	1453.819547	727.413411	1436.792998	718.900137	1435.808982	718.408129	11
4	387.187426	194.097351			369.176861	185.092069	D	1396.798083	698.902679	1379.771534	690.389405	1378.787518	689.897397	10
5	**826.412752**	413.710014	809.386203	405.196740	808.402187	404.704732	Q	1281.771140	641.389208	1264.744591	632.875933	1263.760575	632.383925	9
6	**939.496816**	470.252046	922.470267	461.738772	921.486251	461.246764	L	***842.545814***	421.776545	825.519265	413.263270	824.535249	412.771262	8
7	**1026.528844**	513.768060	1009.502295	505.254786	1008.518279	504.762778	S	***729.461750***	365.234513	712.435201	356.721238	711.451185	356.229230	7
8	**1139.612908**	570.310092	1122.586359	561.796818	1121.602343	561.304810	L	***642.429722***	321.718499	625.403173	313.205224			6
9	**1252.696972**	626.852124	1235.670423	618.338850	1234.686407	617.846841	L	***529.345658***	265.176467	512.319109	256.663192			5
10	1365.781036	683.394156	1348.754487	674.880881	1347.770471	674.388873	L	***416.261594***	208.634435	399.235045	200.121160			4
11	1422.802500	711.904888	1405.775951	703.391613	1404.791935	702.899605	G	***303.177530***	152.092403	286.150981	143.579128			3
12	1493.839614	747.423445	1476.813065	738.910170	1475.829049	738.418162	A	246.156066	123.581671	229.129517	115.068396			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.5	1666.944000	0.021282	TLGDQLSLLLGAR
7.4	1666.944016	0.021266	LTNSPTVIVMVGLPAR
5.4	1666.955231	0.010051	RLGIPECILLVTQR
1.8	1666.981033	-0.015751	SYGTIFPIIFLLKR

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

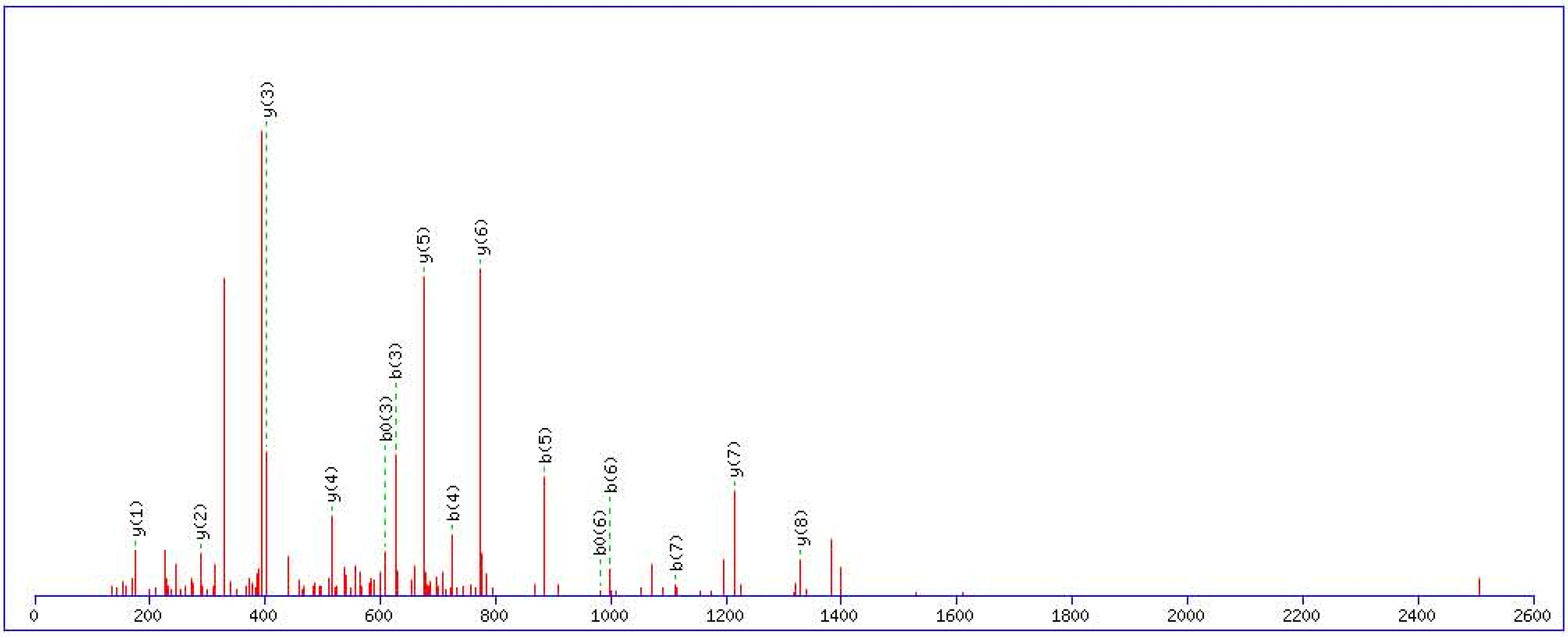
{MATRIX SCIENCE} Mascot Search Results

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

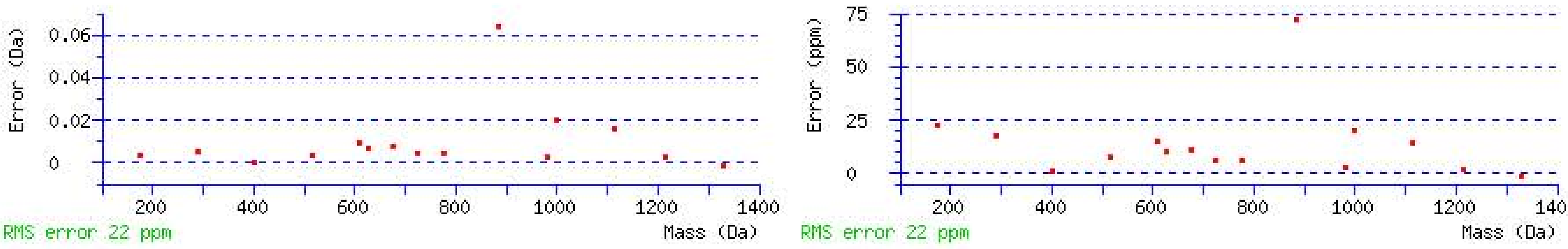
Match to Query 30721: 1398.711428 from(700.362990,2+) rtinseconds(1984) index(24575)
Title: Locus:1.1.1.2833.11 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1398.711166
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 3e-005
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	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
57.5	1398.711166	0.000262	ADQVCINLR
8.8	1398.703781	0.007647	AVVHMNGKEVSGR
8.6	1398.703766	0.007662	GERMADGAPLAGVR
6.5	1398.693878	0.017550	TRHCTQAWAIR
3.6	1398.703766	0.007662	DQAIQSRDR
3.0	1398.728912	-0.017484	QAEATAQTLR
1.9	1398.726227	-0.014799	APGRASGRVCAAAR
1.7	1398.721527	-0.010099	AATASAGAGGIDGKPR

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

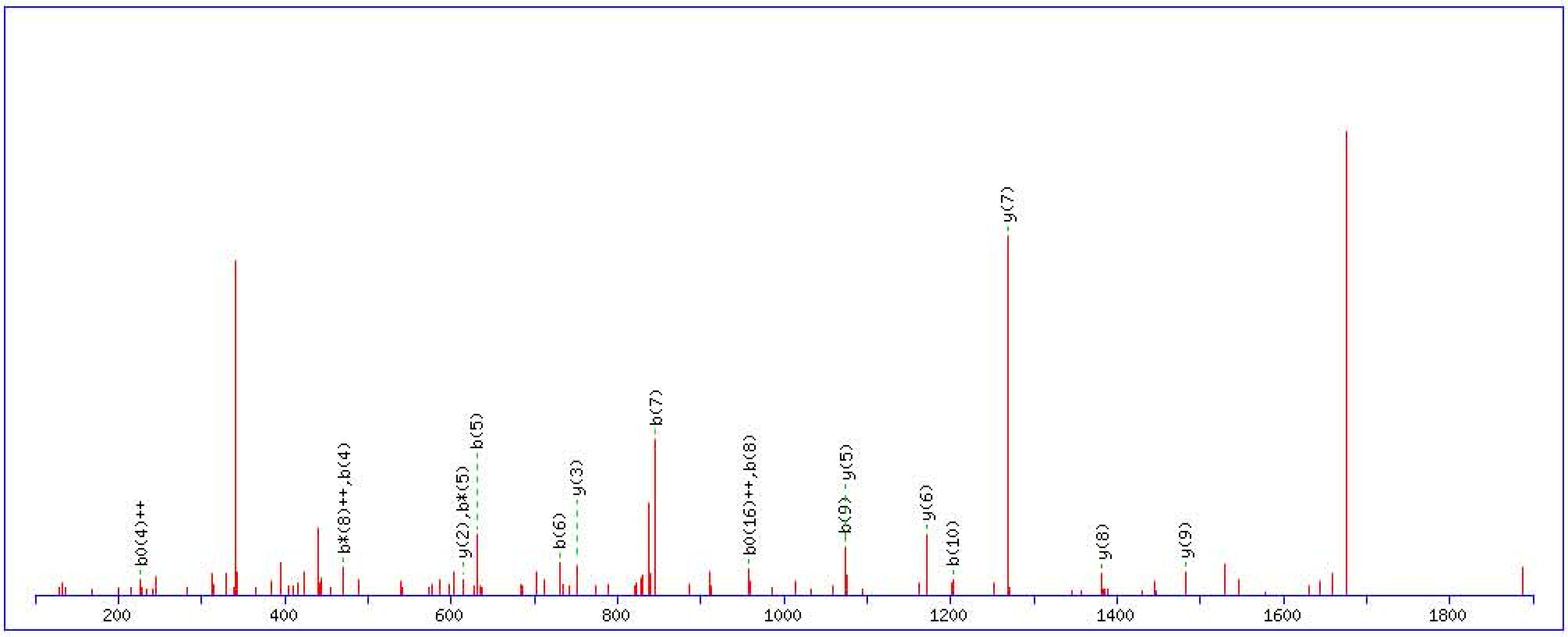
{MATRIX SCIENCE} Mascot Search Results

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

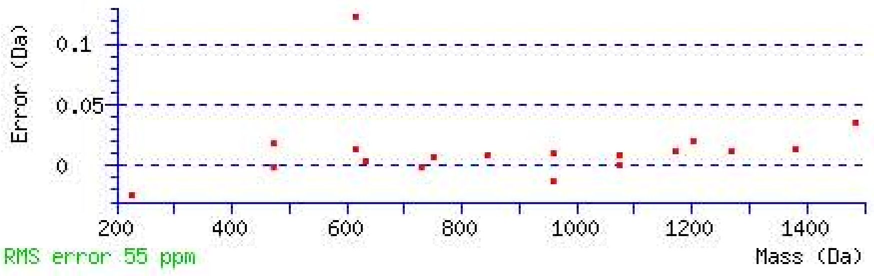
Match to Query 67902: 2843.298296 from(711.831850,4+) rtinseconds(1763) index(40538)
Title: Locus:1.1.1.3063.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

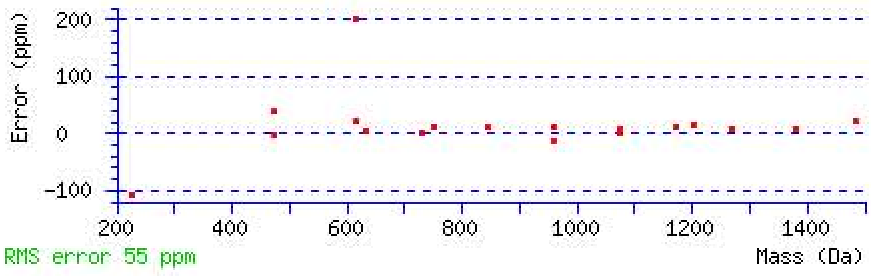
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2843.261169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19     : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00047
Matches : 18/208 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	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





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
43.6	2843.261169	0.037127	RGEQCVDIDECTIPPYCHQR

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

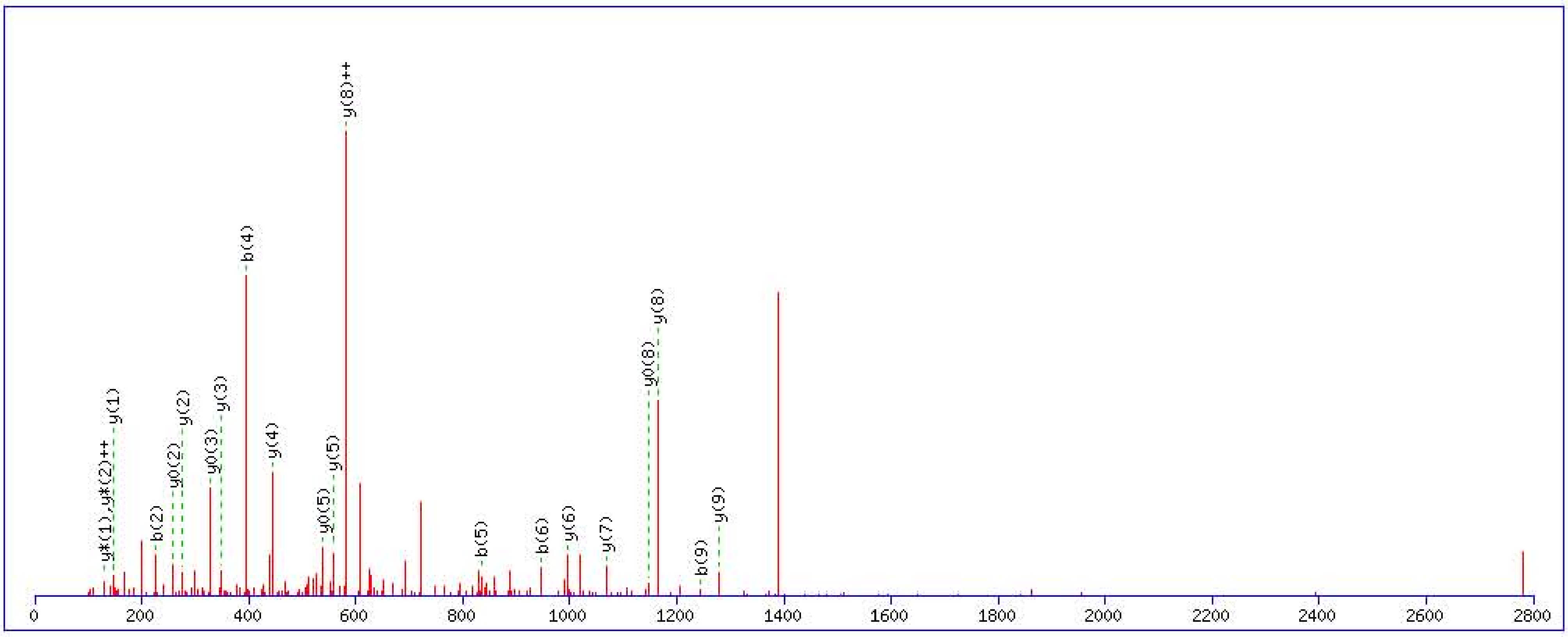
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPAQLPAEK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

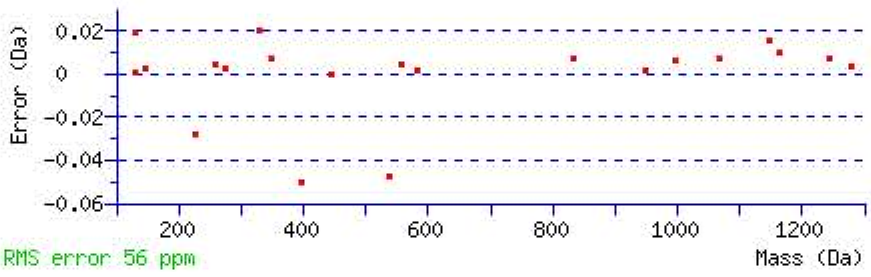
Match to Query 30324: 1389.812328 from(695.913440,2+) rtinseconds(1984) index(24574)
Title: Locus:1.1.1.2833.10 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

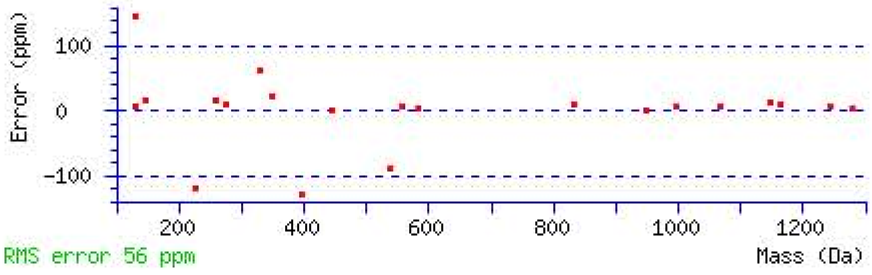
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1389.805359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00023
Matches : 21/82 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	**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
44.4	1389.805359	0.006969	LLPAQLPAEK
5.7	1389.805359	0.006969	LLSSYLQKK
5.4	1389.809189	0.003139	LIKRLDLSYNR
1.4	1389.809204	0.003124	IARVPRLPPDEK
1.2	1389.820450	-0.008122	LINRTHATVPIR
0.8	1389.813232	-0.000904	LIQAPSKFAFLR
0.3	1389.797989	0.014339	LLNLQSLFVTSR
0.3	1389.816605	-0.004277	ILGPLPKHMIQK
0.2	1389.823135	-0.010807	ILIVITDGQKYK

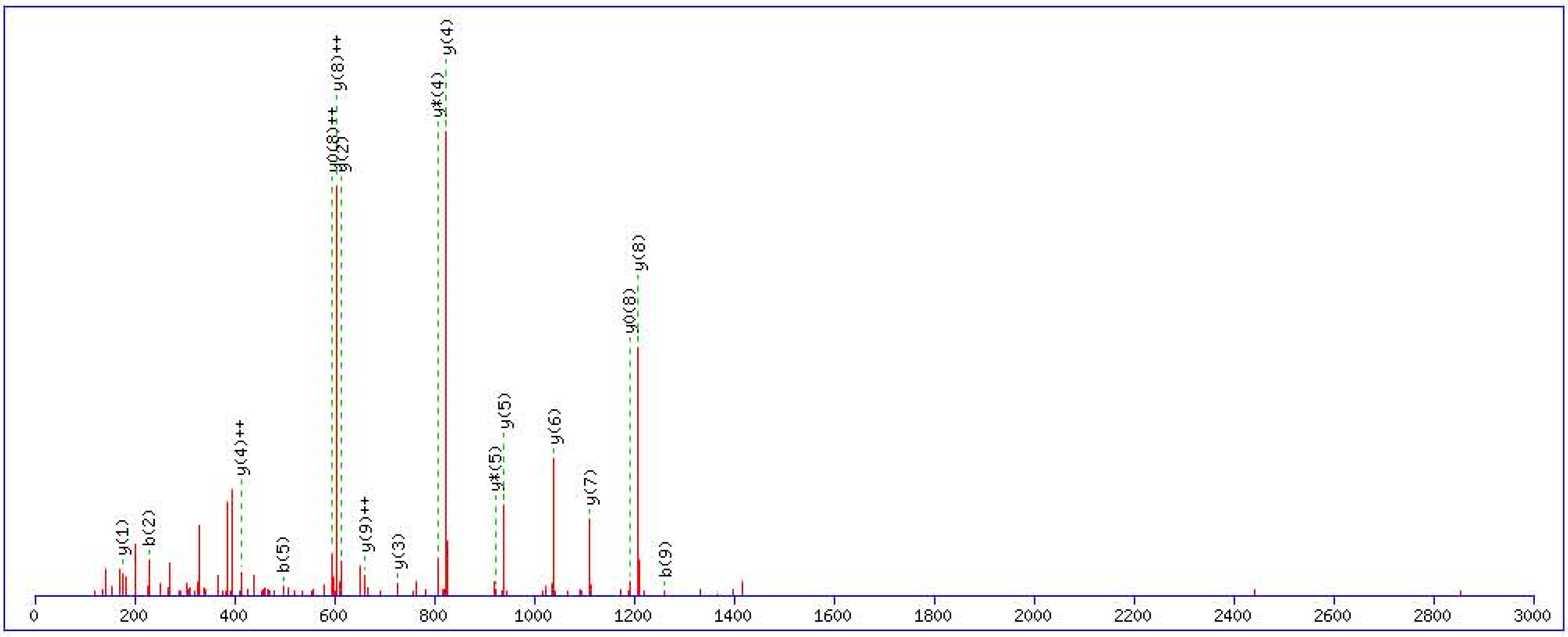
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLPATDPLQR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

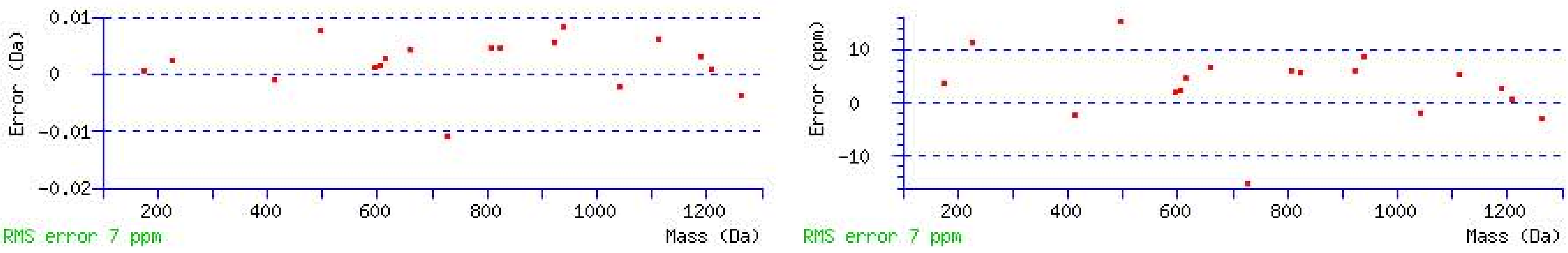
Match to Query 32873: 1434.775768 from(718.395160,2+) rtinseconds(1958) index(24410)
Title: Locus:1.1.1.2824.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1434.765305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0039
Matches : 18/92 fragment ions using 50 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	**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
36.8	1434.765305	0.010463	NLPATDPLQR
11.8	1434.757889	0.017879	NLIRQISSGEYR
5.5	1434.761932	0.013836	NIFPSNLVSAAFR
5.1	1434.757919	0.017849	VQQAELHTGSLPR
4.1	1434.769135	0.006633	INKHVNNDVNLR
1.6	1434.761932	0.013836	NLDYPFGNVLRK
0.8	1434.776520	-0.000752	ARAFLAEVKQMR
0.5	1434.794296	-0.018528	LNHLVDSLQQLR
0.3	1434.761948	0.013820	VQTLPSWKSSFR

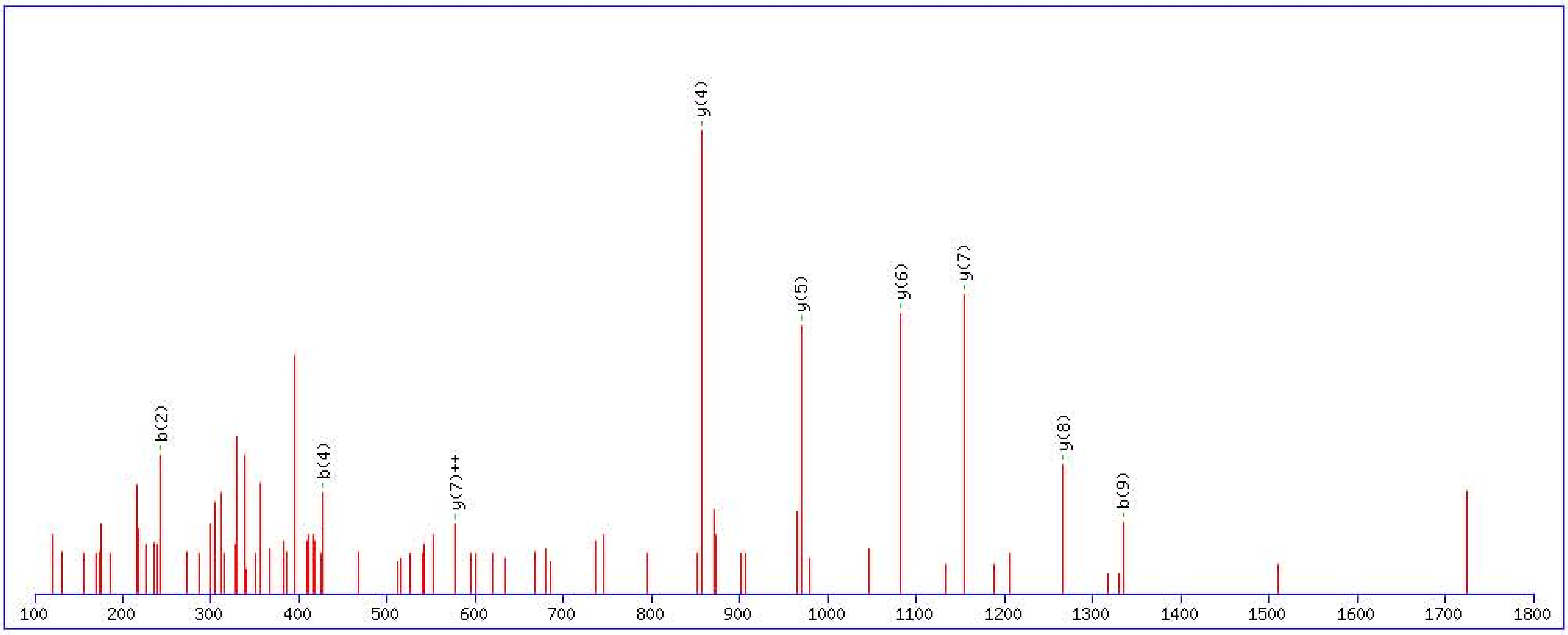
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELLALIQLER**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

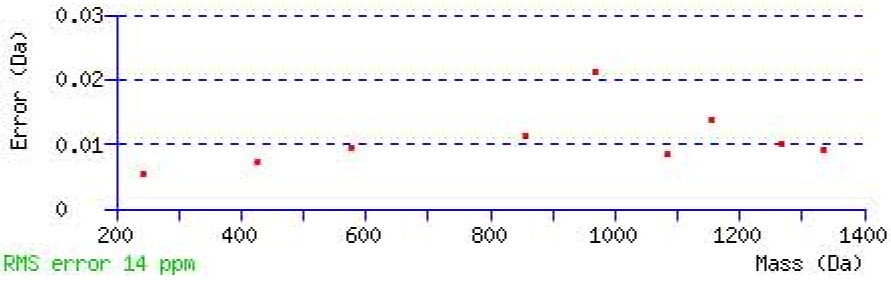
Match to Query 35286: 1507.892088 from(754.953320,2+) rtinseconds(2725) index(11141)
Title: Locus:1.1.1.3202.18 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

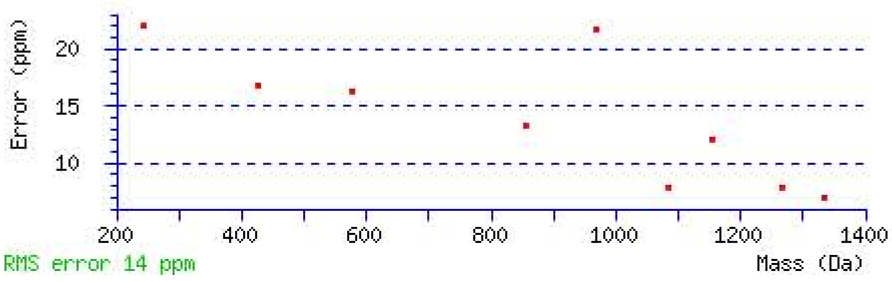


```
Monoisotopic mass of neutral peptide Mr(calc): 1507.879578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0024
Matches : 9/94 fragment ions using 13 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.049869	65.528572			112.039304	56.523290	E							10
2	**243.133933**	122.070605			225.123368	113.065322	L	1379.844305	690.425790	1362.817756	681.912516	1361.833740	681.420508	9
3	356.217997	178.612637			338.207432	169.607354	L	***1266.760241***	633.883759	1249.733692	625.370484	1248.749676	624.878476	8
4	**427.255111**	214.131193			409.244546	205.125911	A	***1153.676177***	577.341727	1136.649628	568.828452	1135.665612	568.336444	7
5	540.339175	270.673226			522.328610	261.667943	L	***1082.639063***	541.823169	1065.612514	533.309895	1064.628498	532.817887	6
6	653.423239	327.215258			635.412674	318.209975	I	***969.554999***	485.281138	952.528450	476.767863	951.544434	476.275855	5
7	1092.648565	546.827921	1075.622016	538.314646	1074.638000	537.822638	Q	***856.470935***	428.739105	839.444386	420.225831	838.460370	419.733823	4
8	1205.732629	603.369953	1188.706080	594.856678	1187.722064	594.364670	L	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
9	**1334.775222**	667.891249	1317.748673	659.377975	1316.764657	658.885966	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
10							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 14 ppm



RMS error 14 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.1	1507.879578	0.012510	ELLALIQLER

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

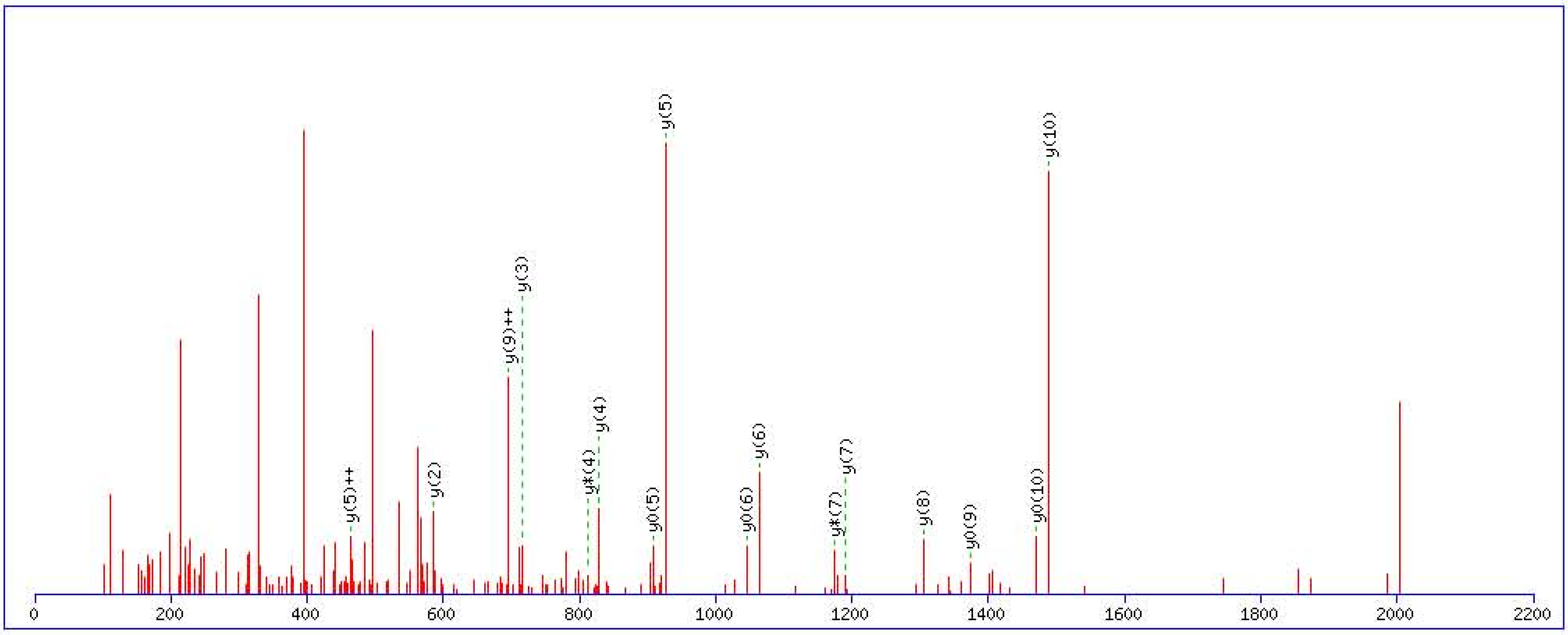
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELPSLQHPNEQK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

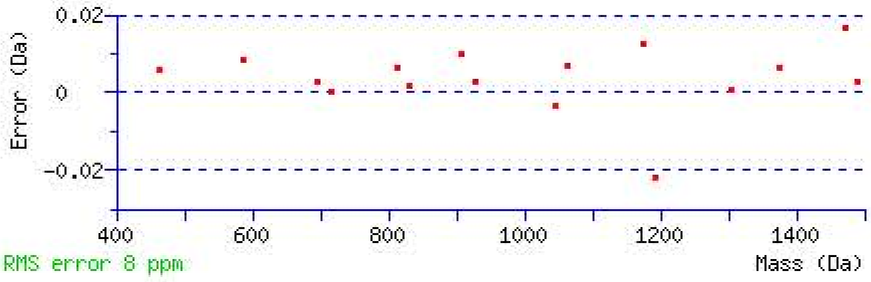
Match to Query 43240: 1729.889922 from(577.637250,3+) rtinseconds(1623) index(4100)
Title: Locus:1.1.1.2819.6 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

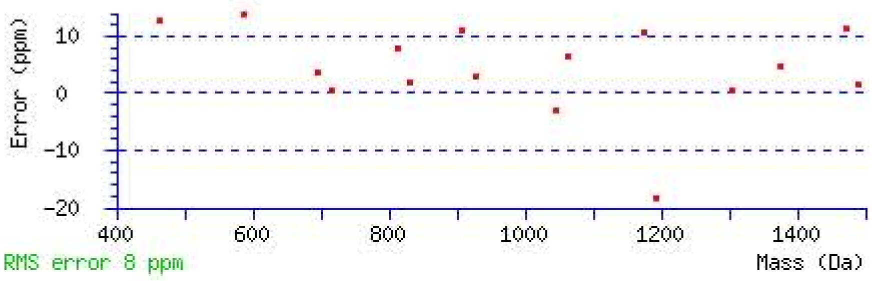


```
Monoisotopic mass of neutral peptide Mr(calc): 1729.882111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.019
Matches : 16/118 fragment ions using 41 most intense peaks   (help)
```

#	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	243.133933	122.070605			225.123368	113.065322	L	1601.846824	801.427050	1584.820275	792.913776	1583.836259	792.421767	11
3	340.186697	170.596987			322.176132	161.591704	P	***1488.762760***	744.885018	1471.736211	736.371744	1470.752195	735.879736	10
4	427.218725	214.113001			409.208160	205.107718	S	1391.709996	696.358636	1374.683447	687.845362	1373.699431	687.353354	9
5	540.302789	270.655033			522.292224	261.649750	L	***1304.677968***	652.842622	1287.651419	644.329348	1286.667403	643.837340	8
6	668.361367	334.684322	651.334818	326.171047	650.350802	325.679039	Q	***1191.593904***	596.300590	1174.567355	587.787316	1173.583339	587.295308	7
7	805.420279	403.213778	788.393730	394.700503	787.409714	394.208495	H	***1063.535326***	532.271301	1046.508777	523.758027	1045.524761	523.266018	6
8	902.473043	451.740160	885.446494	443.226885	884.462478	442.734877	P	***926.476414***	463.741845	909.449865	455.228571	908.465849	454.736563	5
9	1016.515970	508.761623	999.489421	500.248349	998.505405	499.756341	N	***829.423650***	415.215463	812.397101	406.702189	811.413085	406.210181	4
10	1145.558563	573.282920	1128.532014	564.769645	1127.547998	564.277637	E	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
11	1584.783889	792.895583	1567.757340	784.382308	1566.773324	783.890300	Q	***586.338130***	293.672703	569.311581	285.159429			2
12							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 8 ppm



RMS error 8 ppm

NCBI **BLAST** search of ELPSLQHPNEQK
(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	1729.882111	0.007811	ELPSLQHPNEQK

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

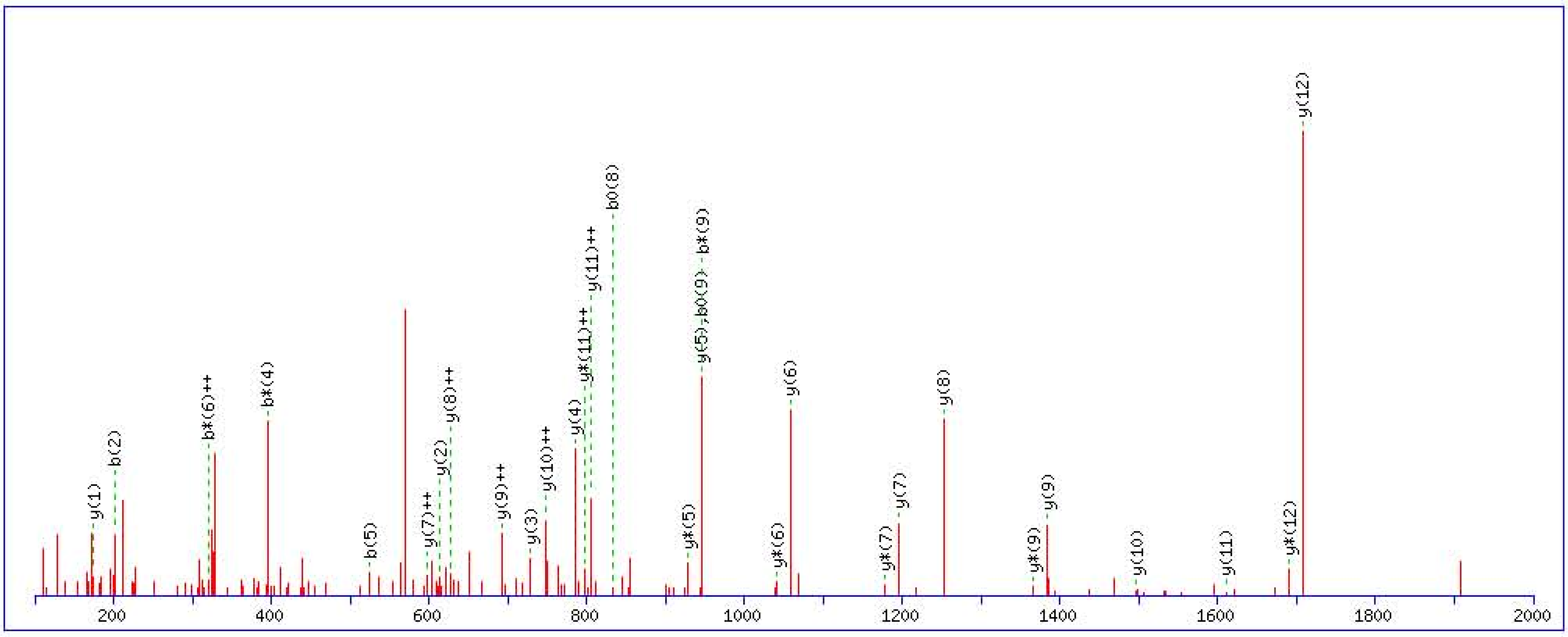
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTPNLMGHLCGNQR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

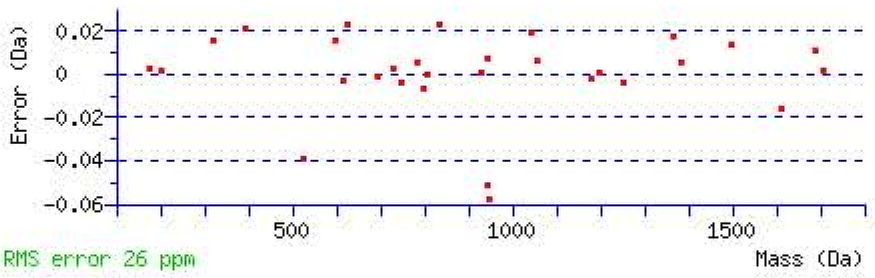
Match to Query 47654: 1906.941792 from(636.654540,3+) rtinseconds(1865) index(23696)
Title: Locus:1.1.1.2792.11 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

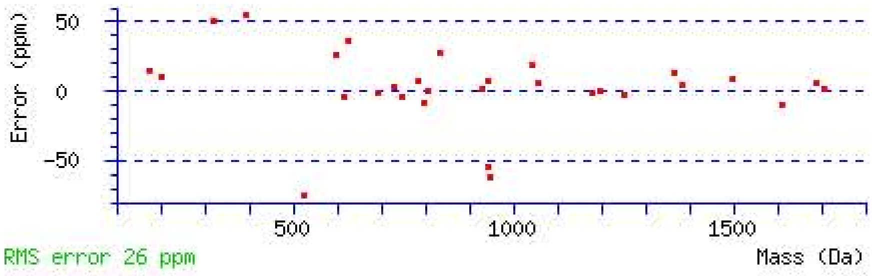
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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 : 30/124 fragment ions using 96 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
41.8	1906.932816	0.008976	VTPNLMGHLCGNQR

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

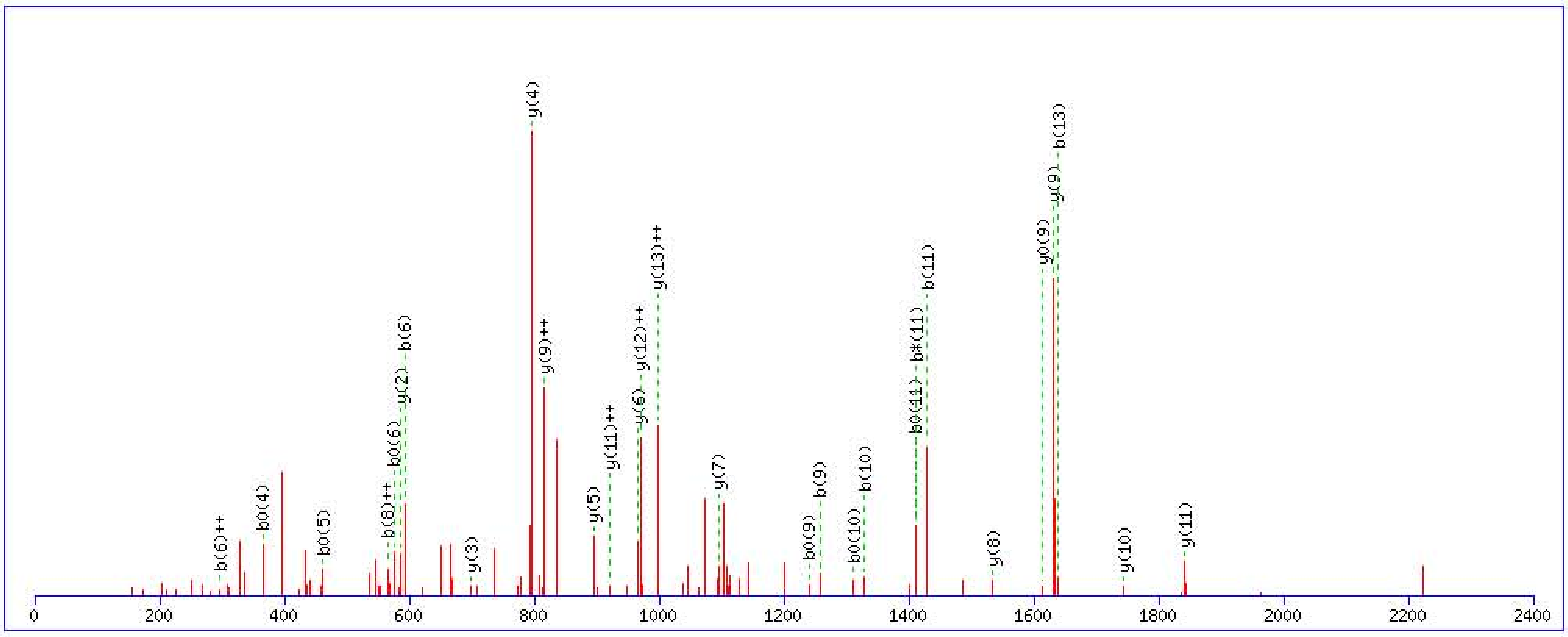
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVGPPLPQEAVPLQK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

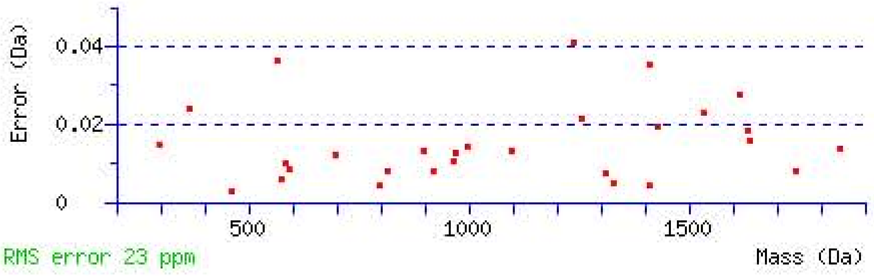
Match to Query 56058: 2223.241928 from(1112.628240,2+) rtinseconds(2426) index(9323)
Title: Locus:1.1.1.3098.17 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

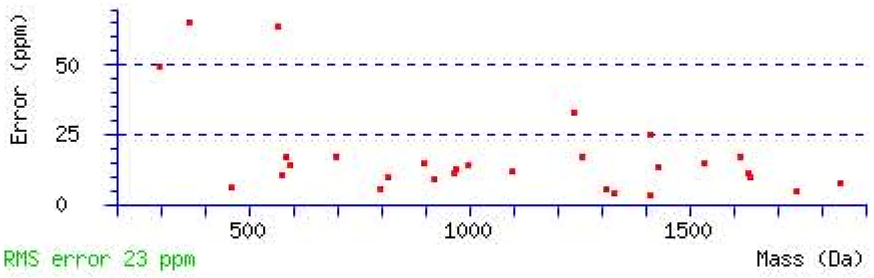
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2223.215942
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Q14    : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0044
Matches : 29/142 fragment ions using 80 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	2095.180639	1048.093957	2078.154090	1039.580683	2077.170074	1039.088675	14
3	286.139747	143.573512			268.129182	134.568229	G	1996.112225	998.559751	1979.085676	990.046476	1978.101660	989.554468	13
4	383.192511	192.099894			365.181946	183.094611	P	1939.090761	970.049019	1922.064212	961.535744	1921.080196	961.043736	12
5	480.245275	240.626276			462.234710	231.620993	P	***1842.037997***	921.522637	1825.011448	913.009362	1824.027432	912.517354	11
6	**593.329339**	**297.168308**			575.318774	288.163025	L	***1744.985233***	872.996255	1727.958684	864.482980	1726.974668	863.990972	10
7	690.382103	345.694690			672.371538	336.689407	P	***1631.901169***	816.454223	1614.874620	807.940948	1613.890604	807.448940	9
8	1129.607429	**565.307353**	1112.580880	556.794078	1111.596864	556.302070	Q	***1534.848405***	767.927841	1517.821856	759.414566	1516.837840	758.922558	8
9	**1258.650022**	629.828649	1241.623473	621.315375	1240.639457	620.823367	E	***1095.623079***	548.315178	1078.596530	539.801903	1077.612514	539.309895	7
10	**1329.687136**	665.347206	1312.660587	656.833932	1311.676571	656.341924	A	***966.580486***	483.793881	949.553937	475.280607			6
11	**1428.755550**	714.881413	1411.729001	706.368139	1410.744985	705.876131	V	***895.543372***	448.275324	878.516823	439.762050			5
12	1525.808314	763.407795	1508.781765	754.894521	1507.797749	754.402513	P	***796.474958***	398.741117	779.448409	390.227843			4
13	**1638.892378**	819.949827	1621.865829	811.436553	1620.881813	810.944545	L	***699.422194***	350.214735	682.395645	341.701461			3
14	2078.117704	1039.562490	2061.091155	1031.049215	2060.107139	1030.557207	Q	***586.338130***	293.672703	569.311581	285.159429			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
33.9	2223.215942	0.025986	EVGPPLPQEAVPLQK

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

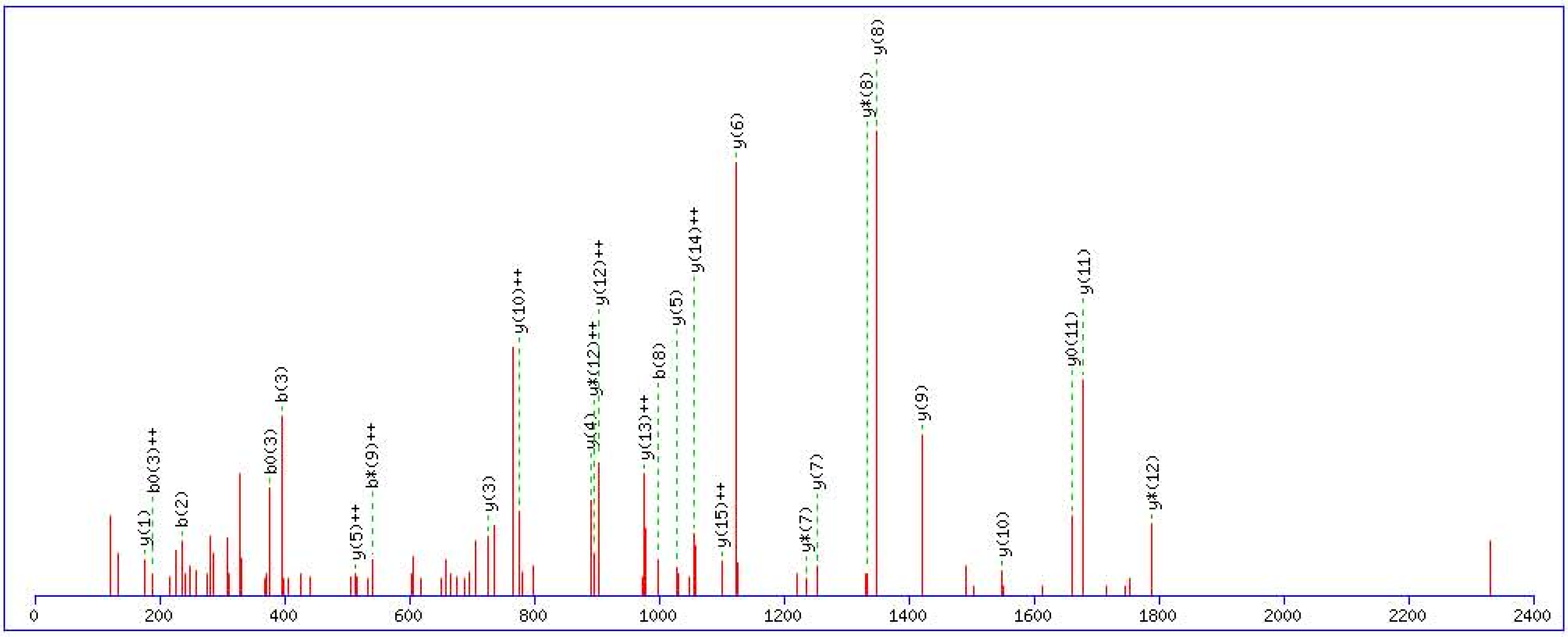
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSCFQEEAPQPHYQLR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

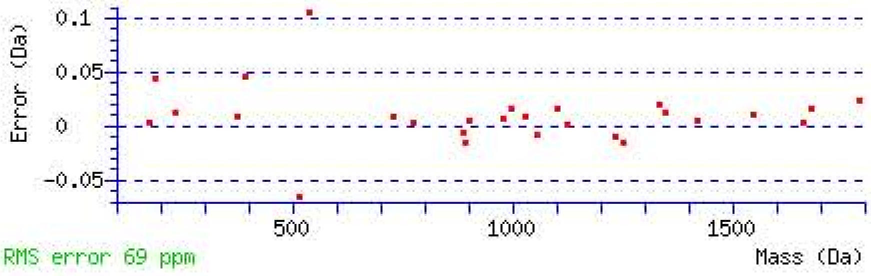
Match to Query 59029: 2347.102662 from(783.374830,3+) rtinseconds(1926) index(6066)
Title: Locus:1.1.1.2924.26 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

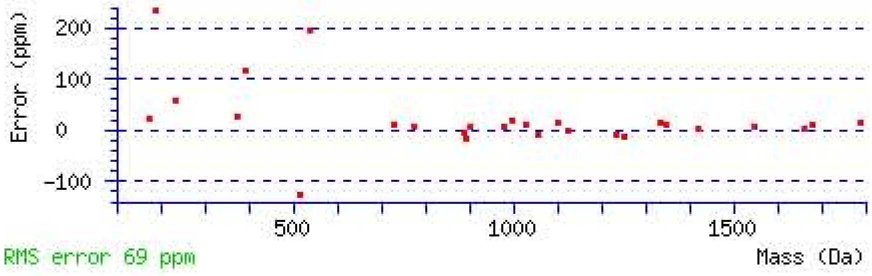
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 47 **Expect:** 4.1e-005
Matches : 27/152 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							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
47.2	2347.087784	0.014878	FSCFQEEAPQPHYQLR
24.7	2347.087784	0.014878	FSCFQEEAPQPHYQLR
0.4	2347.130905	-0.028243	LEQVMAGATLNQMLWCR

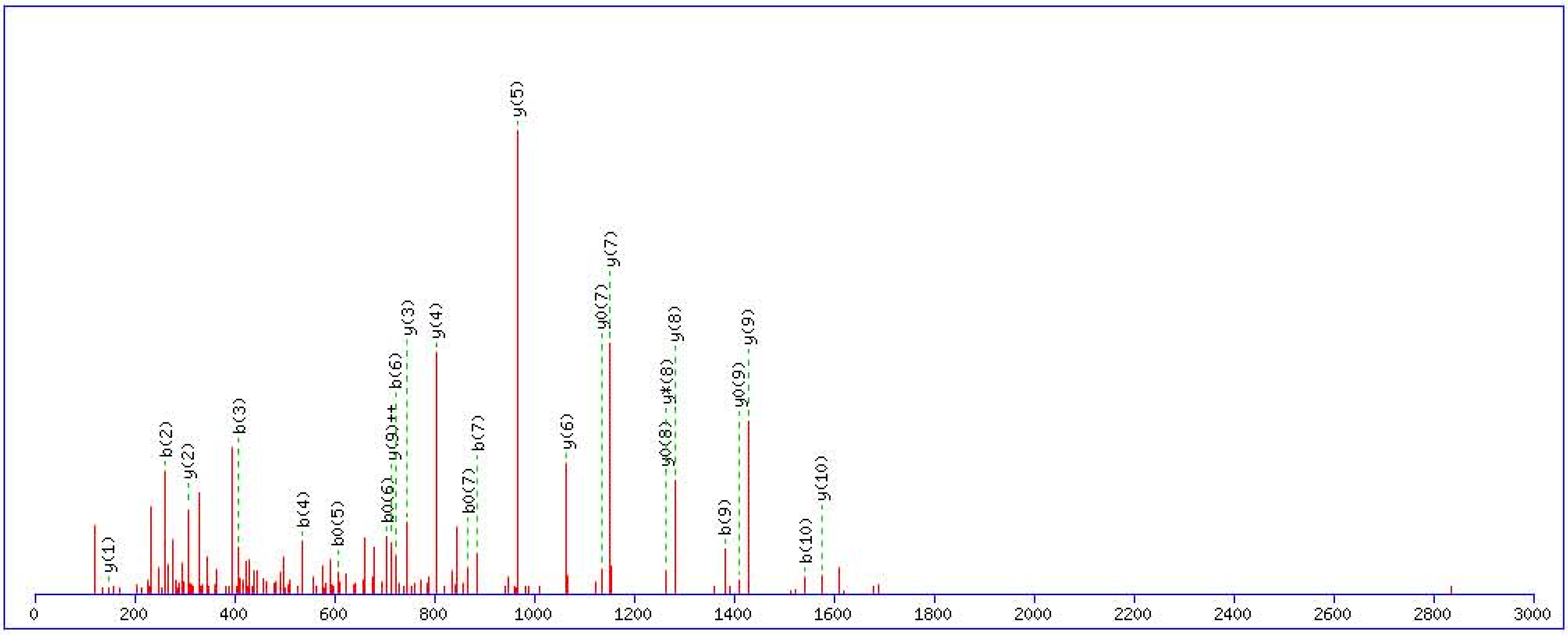
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFFESVYGQCK**
Found in **FETUB_HUMAN**, Fetuin-B OS=Homo sapiens GN=FETUB PE=1 SV=2

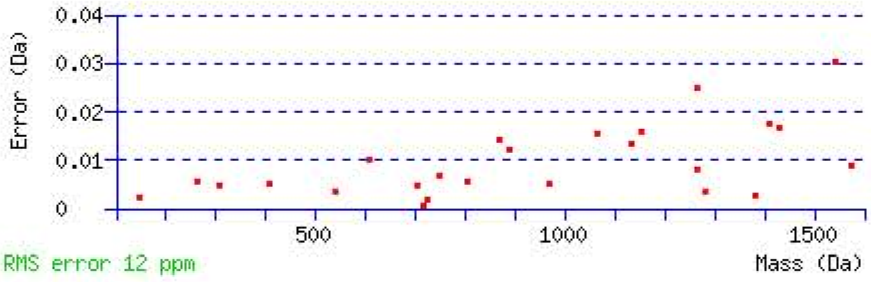
Match to Query 42175: 1687.829688 from(844.922120,2+) rtinseconds(2298) index(80905)
Title: Locus:1.1.1.2150.20 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

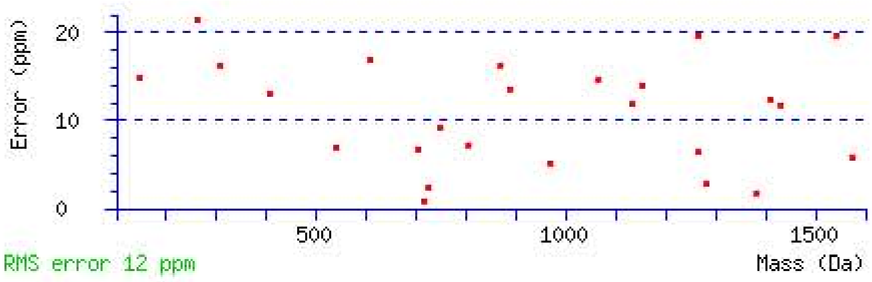
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 48  Expect: 6.5e-005
Matches : 25/86 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	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
47.7	1687.810226	0.019462	IFFESVYGQCK
3.1	1687.831345	-0.001657	MIFSSPACLTASFLK

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

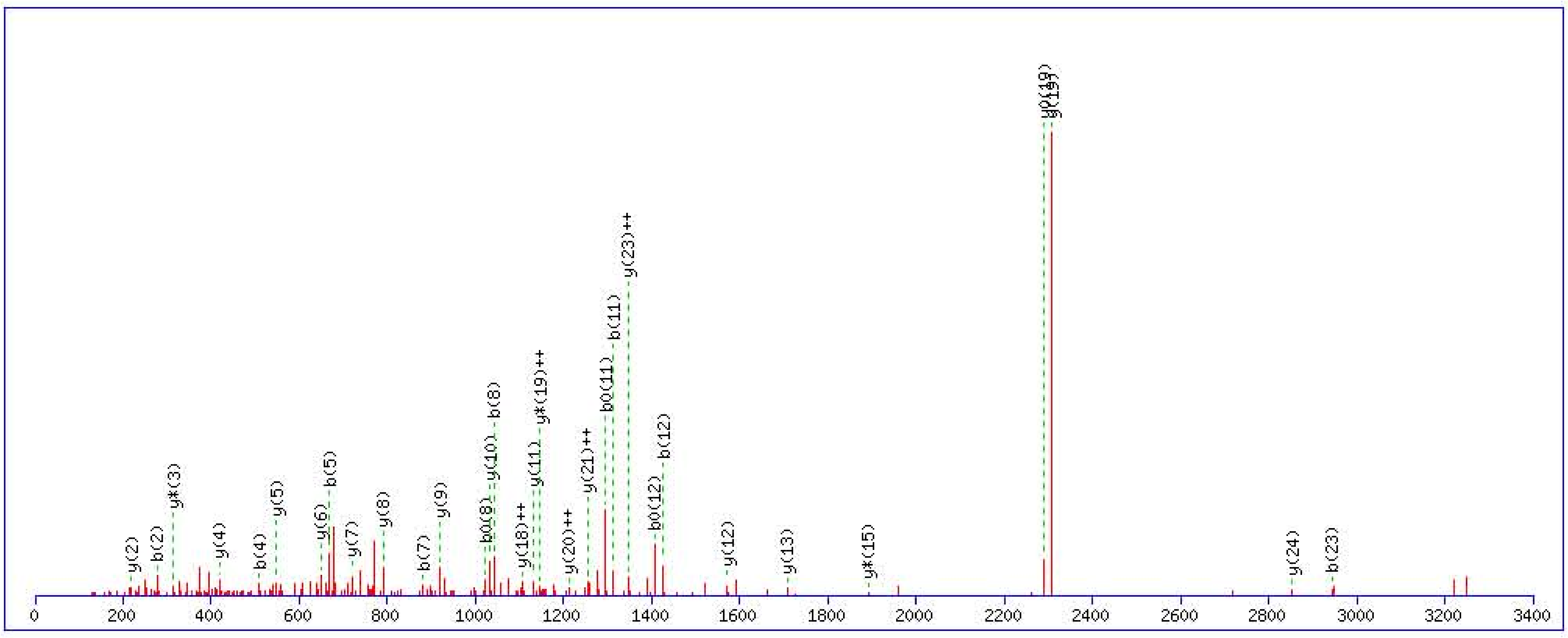
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYMTCPDCPSSIPTDSSNHQVLEAATESLAK**
Found in **FETUB_HUMAN**, Fetuin-B OS=Homo sapiens GN=FETUB PE=1 SV=2

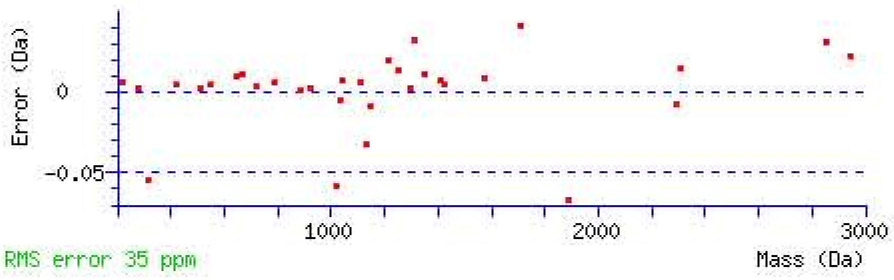
Match to Query 79517: 3732.762336 from(934.197860,4+) rtinseconds(2289) index(80858)
Title: Locus:1.1.1.2147.17 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

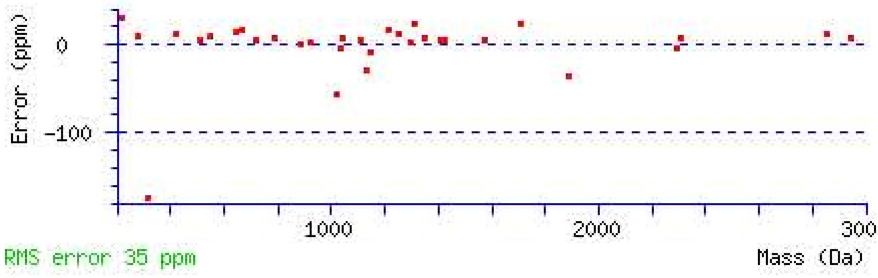
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3732.714340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 2.6e-005
Matches : 32/314 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	114.091340	57.549308					I							31
2	***277.154669***	139.080973					Y	3620.637570	1810.822423	3603.611021	1802.309149	3602.627005	1801.817141	30
3	408.195154	204.601215					M	3457.574241	1729.290759	3440.547692	1720.777484	3439.563676	1720.285476	29
4	***509.242833***	255.125055			491.232268	246.119772	T	3326.533756	1663.770516	3309.507207	1655.257242	3308.523191	1654.765234	28
5	***669.273482***	335.140379			651.262917	326.135097	C	3225.486077	1613.246677	3208.459528	1604.733402	3207.475512	1604.241394	27
6	766.326246	383.666761			748.315681	374.661479	P	3065.455428	1533.231352	3048.428879	1524.718078	3047.444863	1524.226070	26
7	***881.353189***	441.180233			863.342624	432.174950	D	2968.402664	1484.704970	2951.376115	1476.191696	2950.392099	1475.699688	25
8	***1041.383838***	521.195557			1023.373273	512.190274	C	***2853.375721***	1427.191499	2836.349172	1418.678224	2835.365156	1418.186216	24
9	1138.436602	569.721939			1120.426037	560.716657	P	2693.345072	1347.176174	2676.318523	1338.662900	2675.334507	1338.170892	23
10	1225.468630	613.237953			1207.458065	604.232671	S	2596.292308	1298.649792	2579.265759	1290.136518	2578.281743	1289.644510	22
11	***1312.500658***	656.753967			1294.490093	647.748685	S	2509.260280	1255.133778	2492.233731	1246.620504	2491.249715	1246.128496	21
12	***1425.584722***	713.295999			1407.574157	704.290717	I	2422.228252	1211.617764	2405.201703	1203.104490	2404.217687	1202.612482	20
13	1522.637486	761.822381			1504.626921	752.817099	P	***2309.144188***	1155.075732	2292.117639	1146.562458	2291.133623	1146.070450	19
14	1623.685165	812.346221			1605.674600	803.340938	T	2212.091424	1106.549350	2195.064875	1098.036076	2194.080859	1097.544068	18
15	1738.712108	869.859692			1720.701543	860.854410	D	2111.043745	1056.025511	2094.017196	1047.512236	2093.033180	1047.020228	17
16	1825.744136	913.375706			1807.733571	904.370424	S	1996.016802	998.512039	1978.990253	989.998765	1978.006237	989.506757	16
17	1912.776164	956.891720			1894.765599	947.886438	S	1908.984774	954.996025	1891.958225	946.482751	1890.974209	945.990743	15
18	2026.819091	1013.913184	2009.792542	1005.399909	2008.808526	1004.907901	N	1821.952746	911.480011	1804.926197	902.966737	1803.942181	902.474729	14
19	2163.878003	1082.442640	2146.851454	1073.929365	2145.867438	1073.437357	H	***1707.909819***	854.458548	1690.883270	845.945273	1689.899254	845.453265	13
20	2603.103329	1302.055303	2586.076780	1293.542028	2585.092764	1293.050020	Q	***1570.850907***	785.929092	1553.824358	777.415817	1552.840342	776.923809	12
21	2702.171743	1351.589510	2685.145194	1343.076235	2684.161178	1342.584227	V	***1131.625581***	566.316429	1114.599032	557.803154	1113.615016	557.311146	11
22	2815.255807	1408.131542	2798.229258	1399.618267	2797.245242	1399.126259	L	***1032.557167***	516.782222	1015.530618	508.268947	1014.546602	507.776939	10
23	***2944.298400***	1472.652838	2927.271851	1464.139564	2926.287835	1463.647556	E	***919.473103***	460.240190	902.446554	451.726915	901.462538	451.234907	9
24	3015.335514	1508.171395	2998.308965	1499.658121	2997.324949	1499.166113	A	***790.430510***	395.718893	773.403961	387.205619	772.419945	386.713611	8
25	3086.372628	1543.689952	3069.346079	1535.176678	3068.362063	1534.684670	A	***719.393396***	360.200336	702.366847	351.687062	701.382831	351.195054	7
26	3187.420307	1594.213792	3170.393758	1585.700517	3169.409742	1585.208509	T	***648.356282***	324.681779	631.329733	316.168505	630.345717	315.676497	6
27	3316.462900	1658.735088	3299.436351	1650.221814	3298.452335	1649.729806	E	***547.308603***	274.157940	530.282054	265.644665	529.298038	265.152657	5
28	3403.494928	1702.251102	3386.468379	1693.737828	3385.484363	1693.245820	S	***418.266010***	209.636643	401.239461	201.123369	400.255445	200.631361	4
29	3516.578992	1758.793134	3499.552443	1750.279860	3498.568427	1749.787852	L	331.233982	166.120629	314.207433	157.607355			3
30	3587.616106	1794.311691	3570.589557	1785.798417	3569.605541	1785.306409	A	***218.149918***	109.578597	201.123369	101.065323			2
31							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IYMTCPDCPSSIPTDSSNHQVLEAATESLAK
(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	3732.714340	0.047996	IYMTCPDCPSSIPTDSSNHQVLEAATESLAK
2.1	3732.729156	0.033180	QAFDVTIMFLICLNMVTMMVETDDQSPEK
0.1	3732.729156	0.033180	QAFDVTIMFLICLNMVTMMVETDDQSPEK

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

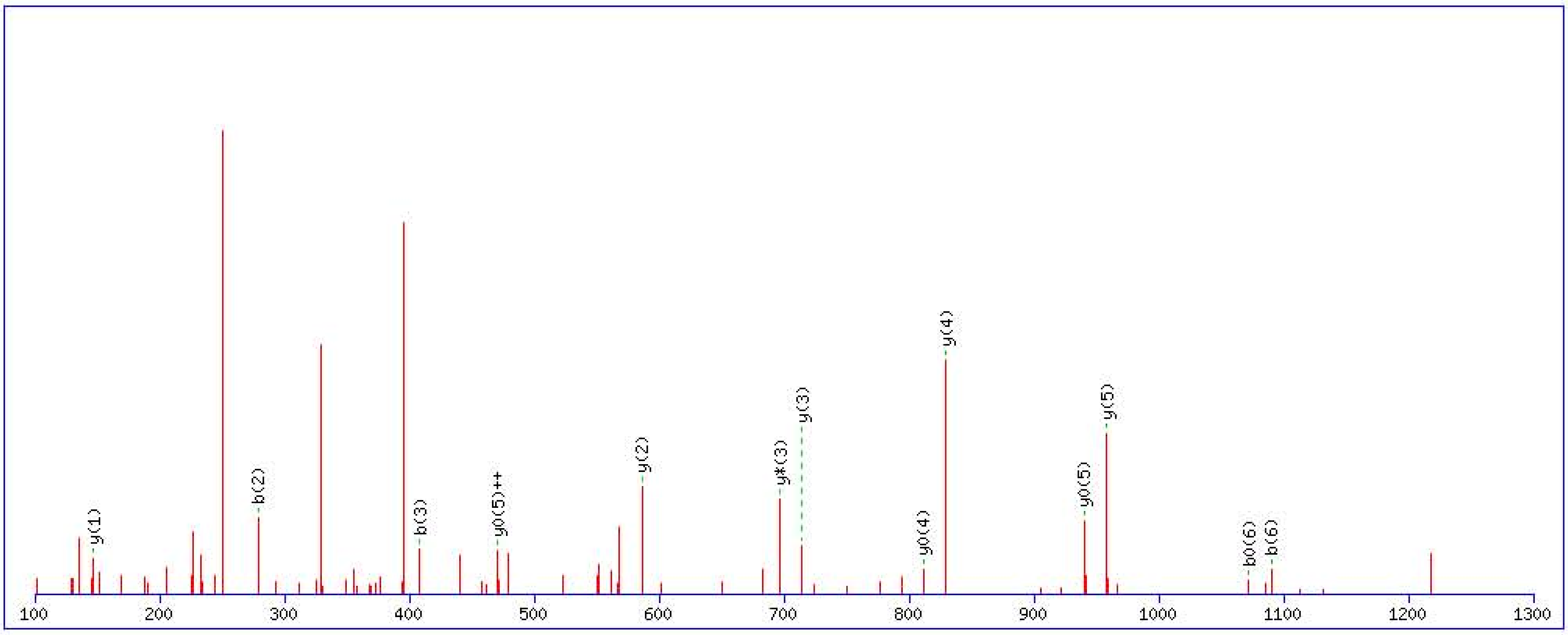
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DYEDQQK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

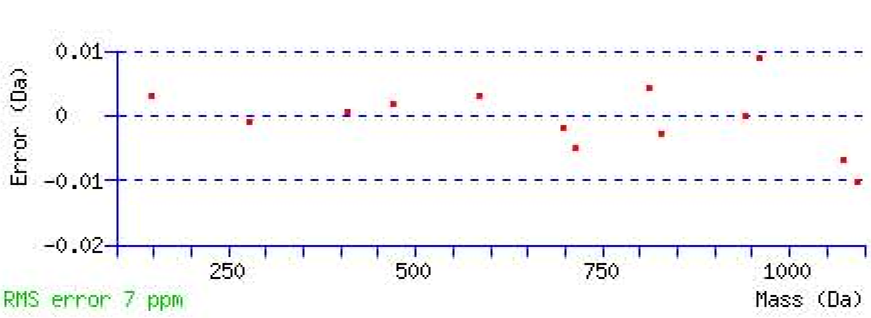
Match to Query 24752: 1235.550948 from(618.782750,2+) rtinseconds(1409) index(20312)
Title: Locus:1.1.1.2633.18 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

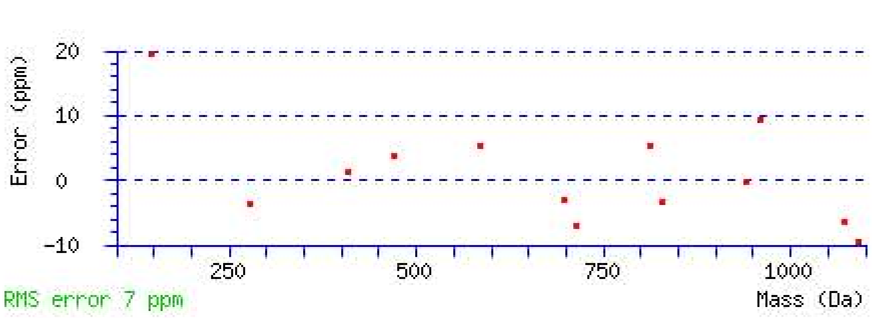
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1235.549225
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.0084
Matches : 13/58 fragment ions using 23 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**							7
2	**279.097548**	140.052412			261.086983	131.047130	**Y**	1121.529573	561.268425	1104.503024	552.755150	1103.519008	552.263142	6
3	**408.140141**	204.573709			390.129576	195.568426	**E**	***958.466244***	479.736760	941.439695	471.223486	940.455679	470.731478	5
4	523.167084	262.087180			505.156519	253.081898	**D**	***829.423651***	415.215464	812.397102	406.702189	811.413086	406.210181	4
5	651.225662	326.116469	634.199113	317.603195	633.215097	317.111187	**Q**	***714.396708***	357.701992	697.370159	349.188718			3
6	**1090.450988**	545.729132	1073.424439	537.215858	1072.440423	536.723850	**Q**	***586.338130***	293.672703	569.311581	285.159429			2
7							**K**	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DYEDQQK
(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	1235.549225	0.001723	DYEDQQK
16.0	1235.549225	0.001723	DYEDQQK
4.0	1235.557098	-0.006150	EGHFQETFNK

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

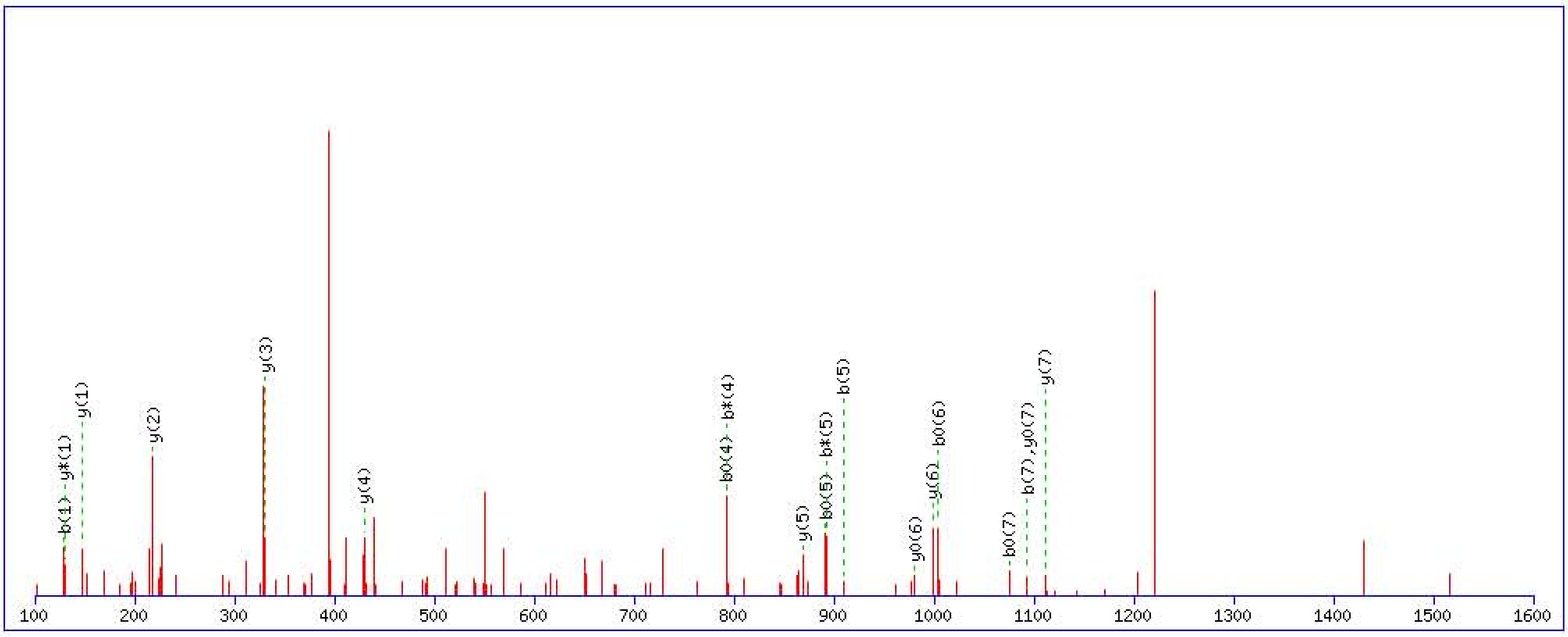
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLEQVIAK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

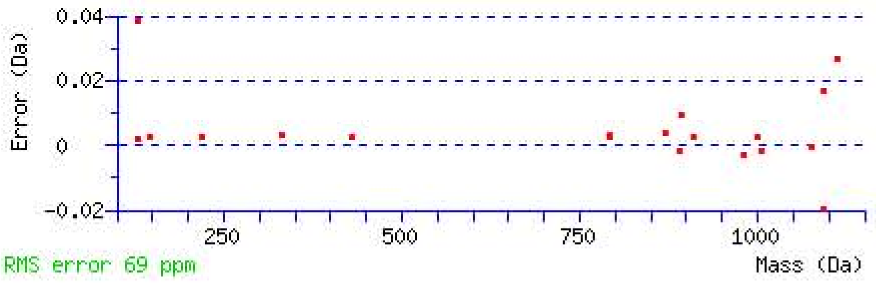
Match to Query 24840: 1238.698968 from(620.356760,2+) rtinseconds(1733) index(22740)
Title: Locus:1.1.1.2746.8 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

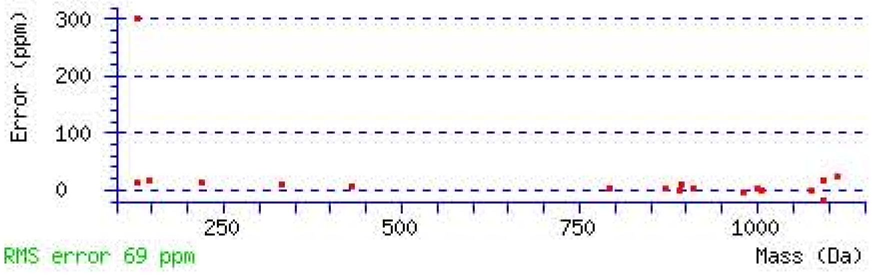
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1238.705658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0017
Matches : 19/70 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	**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
40.3	1238.705658	-0.006690	QLEQVIAK
18.5	1238.687027	0.011941	KEETQPPVALK
12.3	1238.705658	-0.006690	QLEQVIAK
10.7	1238.716904	-0.017936	DRVQVAIK
10.5	1238.698257	0.000711	IHADASSKVLAK
7.8	1238.716888	-0.017920	KRILCPLDPK
7.2	1238.680511	0.018457	EPGRTQIK
5.2	1238.702301	-0.003333	DVFKKGFSIAK
4.7	1238.680496	0.018472	QEVAAAALR
4.0	1238.691040	0.007928	LYKEFIDLAK

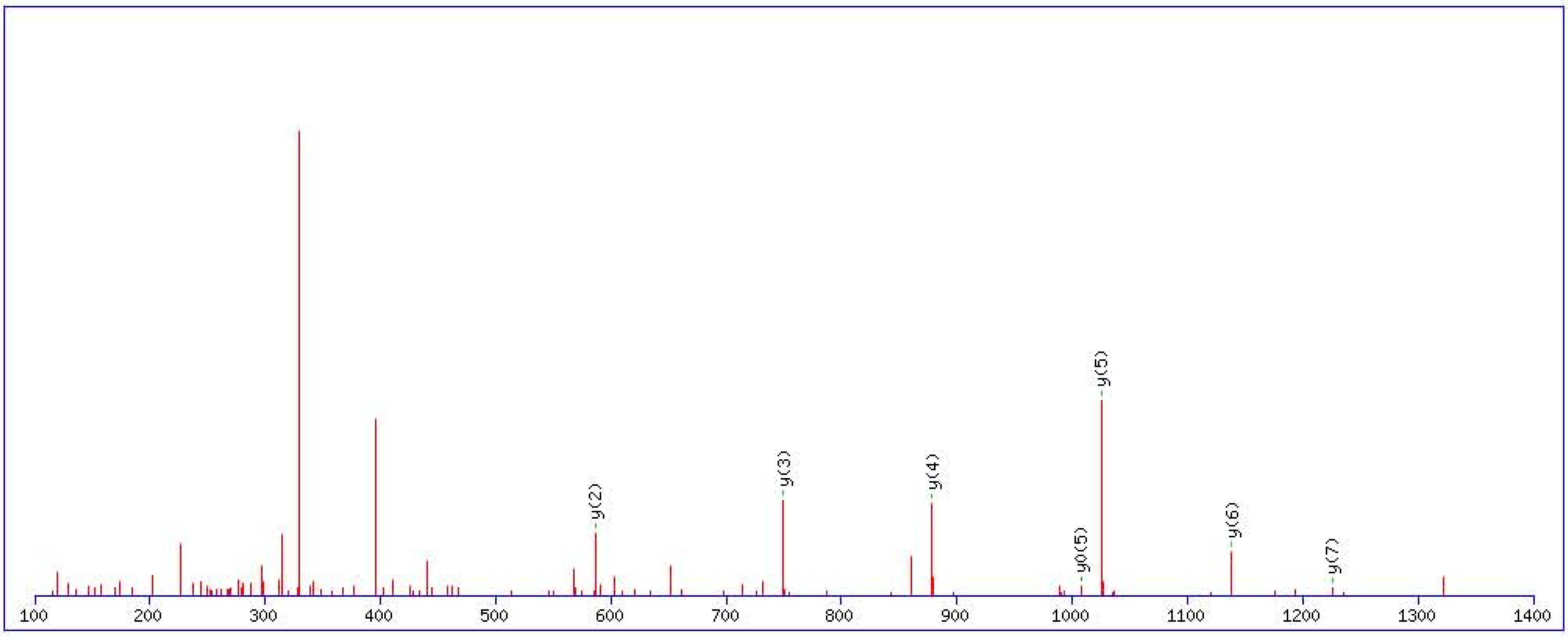
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSLFEYQK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

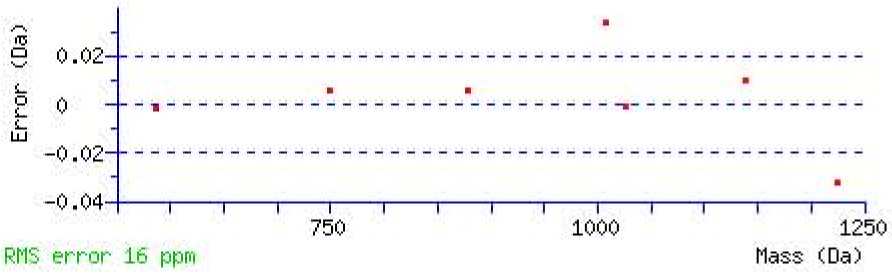
Match to Query 27812: 1338.672928 from(670.343740,2+) rtinseconds(2030) index(24900)
Title: Locus:1.1.1.2849.7 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

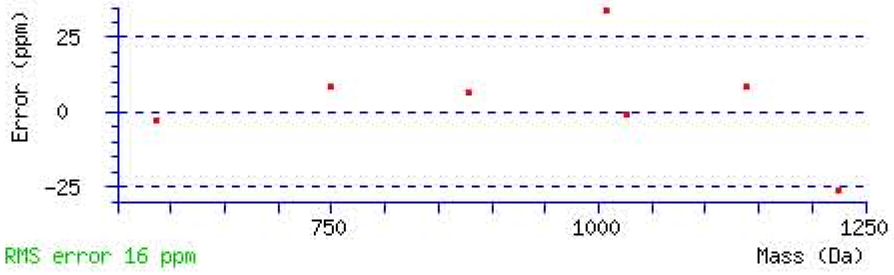
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1338.664185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0026
Matches : 7/76 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
38.5	1338.664185	0.008743	NSLFEYQK
15.9	1338.660172	0.012756	NSMFTAGKGVAEK
5.8	1338.660172	0.012756	BTVYLQMBSLR
1.7	1338.682632	-0.009704	NLSRMQSRFGK
0.9	1338.686188	-0.013260	TVKMMYQK
0.7	1338.660156	0.012772	KEFQKAMEGQK
0.1	1338.671402	0.001526	QGADPQREK

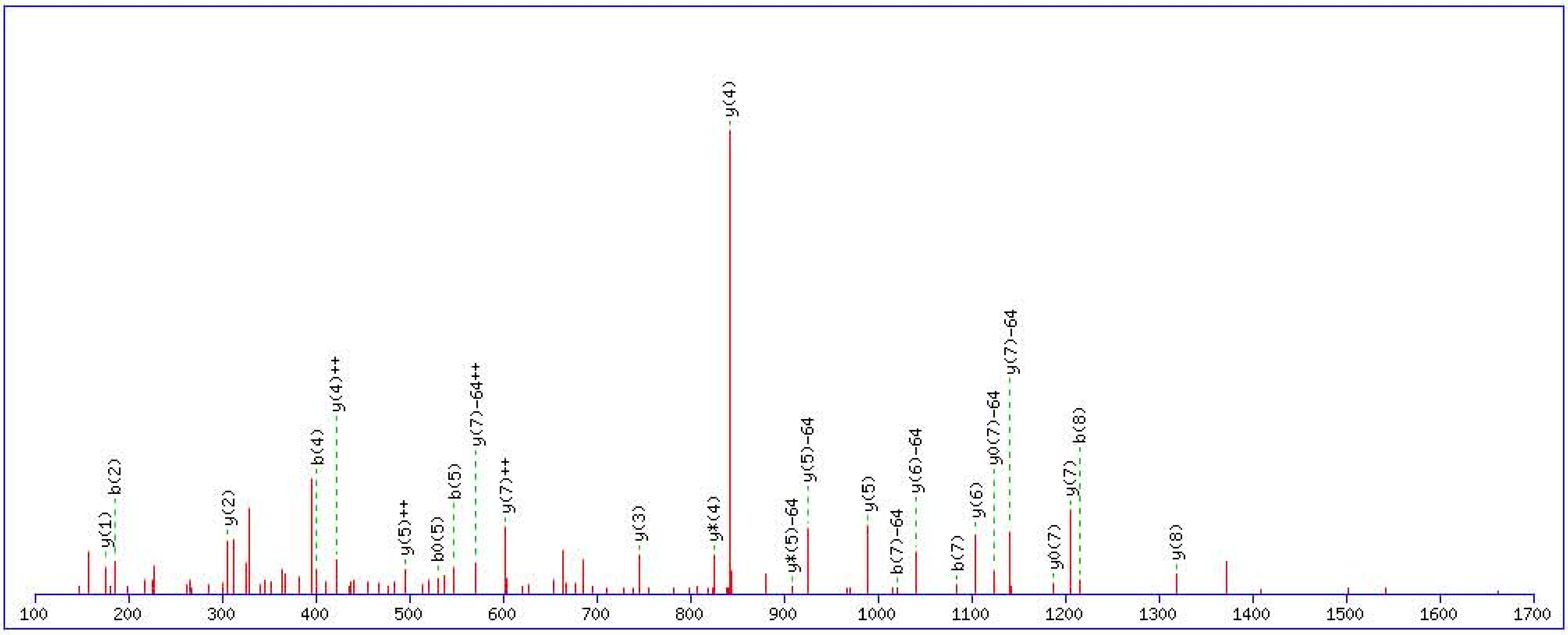
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALTDMPQMR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

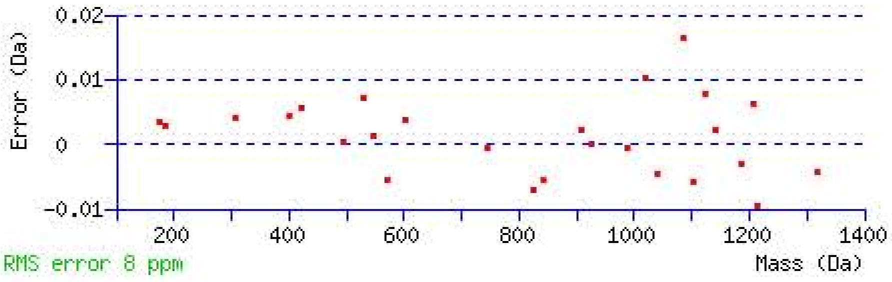
Match to Query 30181: 1388.665028 from(695.339790,2+) rtinseconds(1667) index(22192)
Title: Locus:1.1.1.2723.10 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

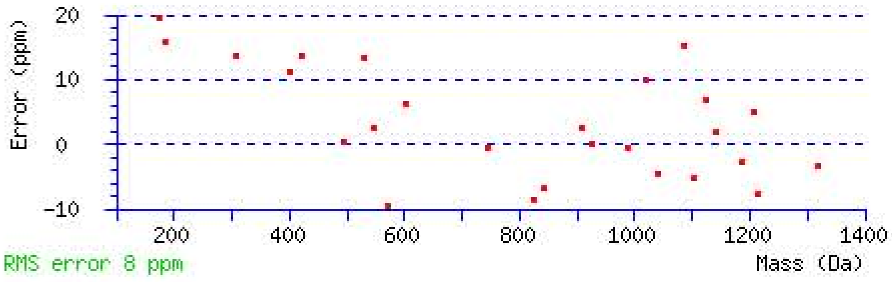
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 51  Expect: 3.2e-005
Matches : 26/112 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	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
50.8	1388.661438	0.003590	ALTDMPQMR
15.4	1388.661438	0.003590	ALTDMPQMR
2.8	1388.660568	0.004460	SEMTASPLVGPER
1.9	1388.646637	0.018391	DREAGSMLPAGNR

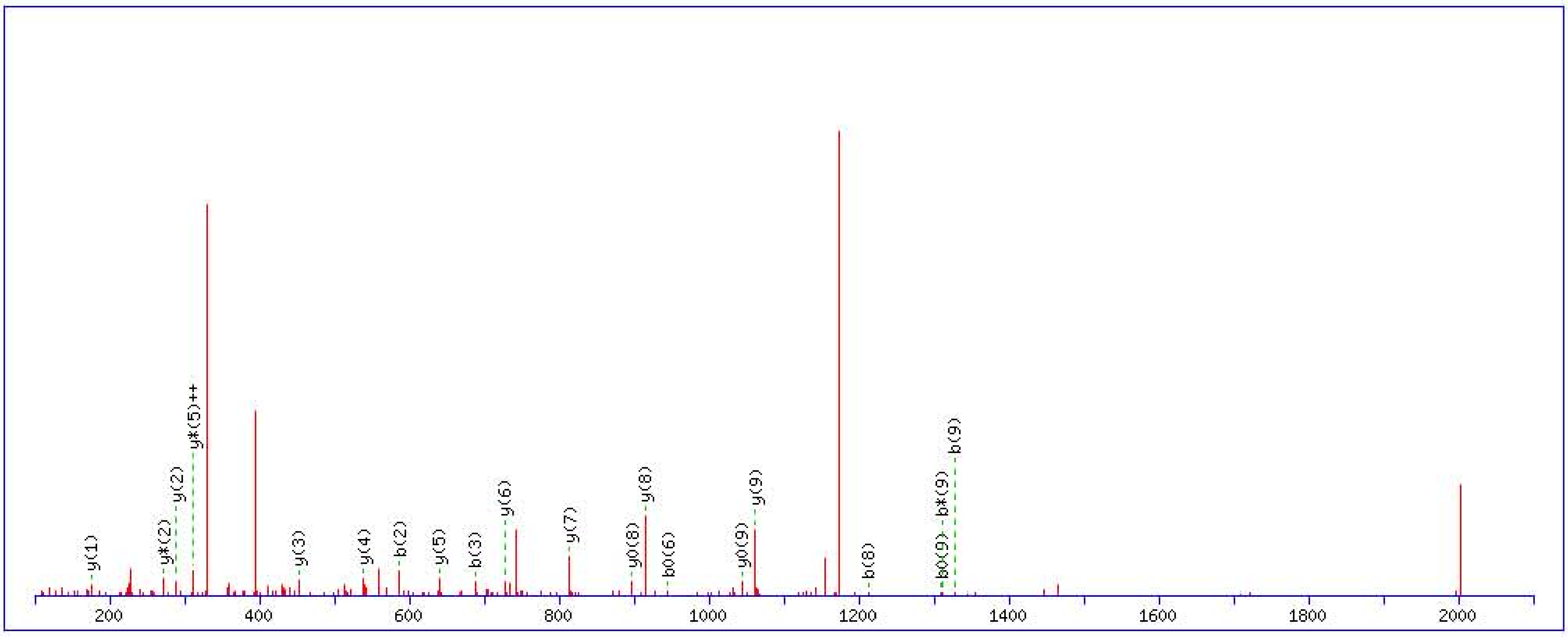
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QFTSSTSYNR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

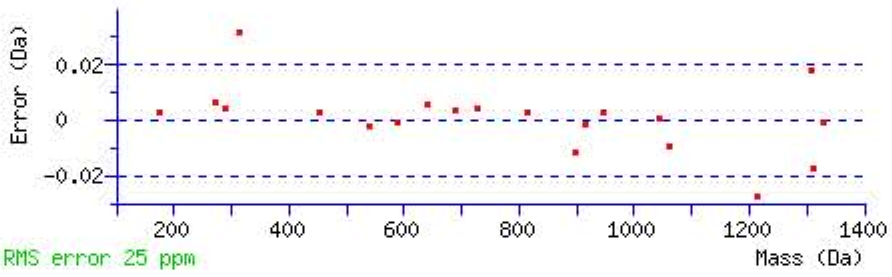
Match to Query 34895: 1500.708348 from(751.361450,2+) rtinseconds(1612) index(21781)
Title: Locus:1.1.1.2704.5 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

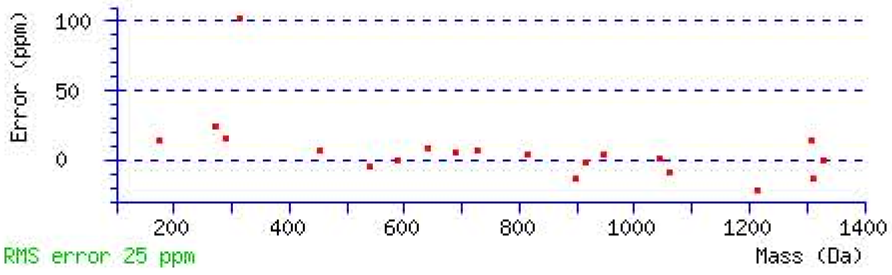
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1500.703110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 4e-005
Matches : 20/98 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	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
54.0	1500.703110	0.005238	QFTSSTSYNR
6.8	1500.699768	0.008580	AEAGSGGPGFTFTFR
6.4	1500.725571	-0.017223	HQSHTAEAGPR
4.0	1500.724869	-0.016521	SKIEDYFPEFAR
3.3	1500.728043	-0.019695	EEARTTPGREEAR
1.6	1500.728256	-0.019908	MVDYYEVLGLQR
1.3	1500.687851	0.020497	MTVLSTAQSDYNR
1.1	1500.725586	-0.017238	IGQICKNDFGGHR

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

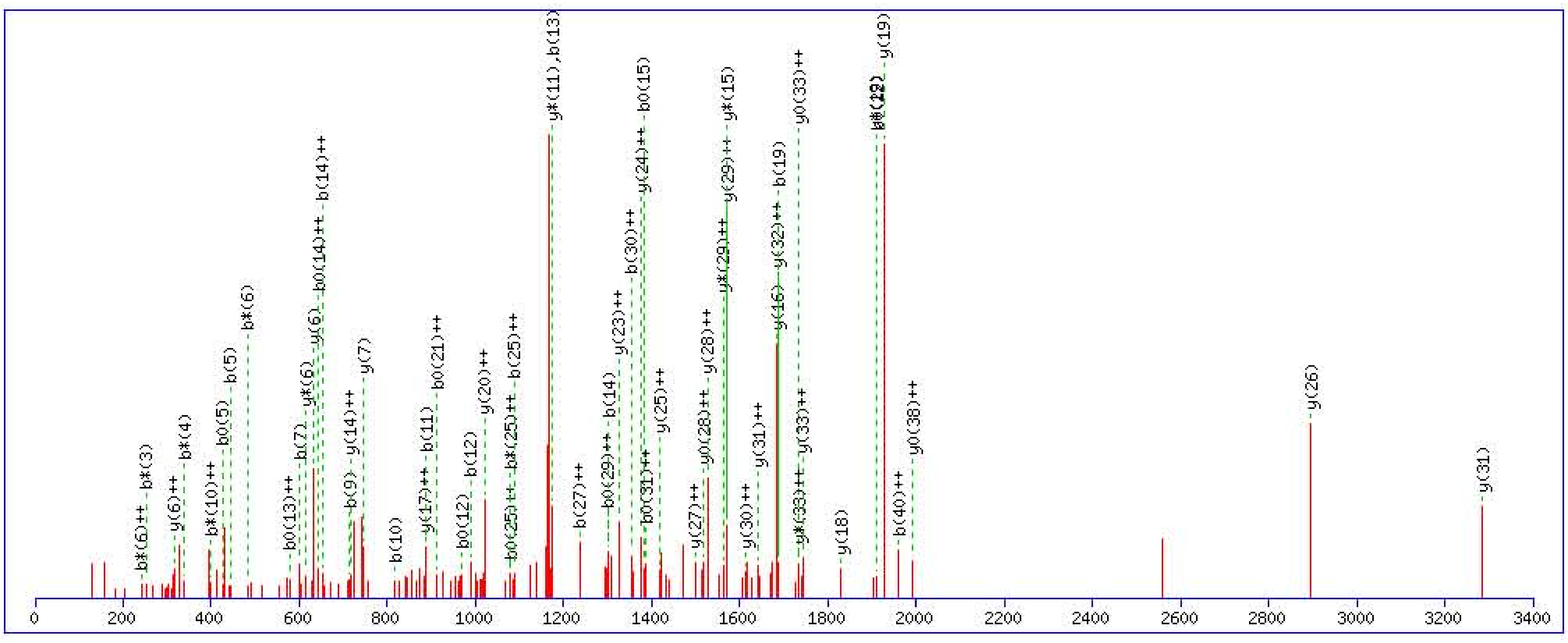
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

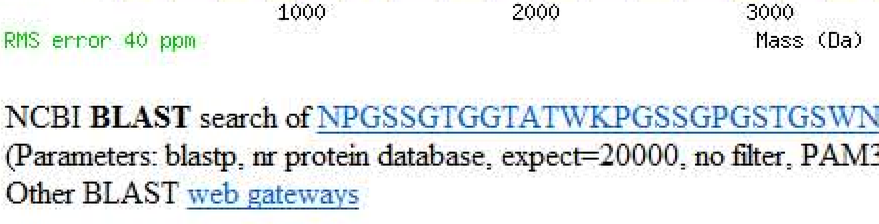
Match to Query 89023: 5844.670470 from(1169.941370,5+) rtinseconds(1740) index(22797)
Title: Locus:1.1.1.2748.25 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 5844.608032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q39     : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 2.8e-005
Matches : 60/688 fragment ions using 113 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
53.4	5844.608032	0.062438	NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER

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

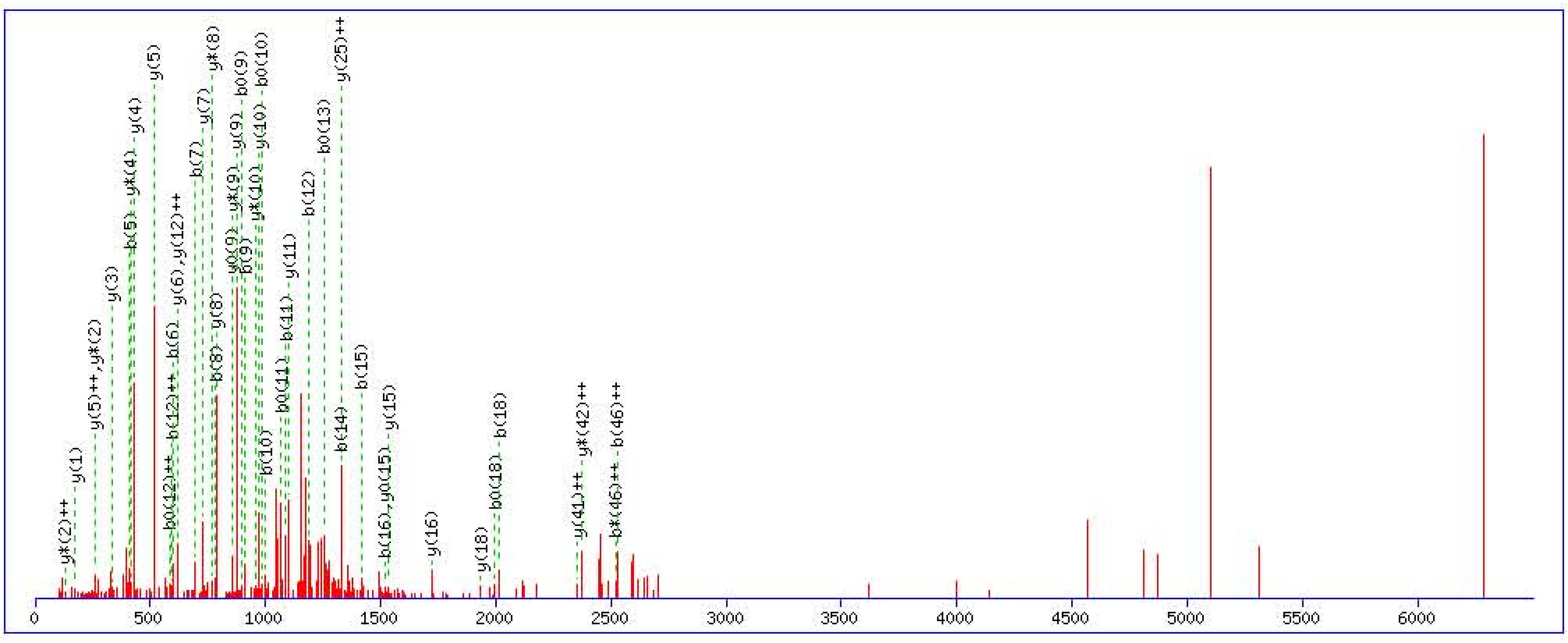
{MATRIX SCIENCE} Mascot Search Results

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 89303: 6284.830644 from(1048.479050,6+) rtinseconds(2051) index(79205)
Title: Locus:1.1.1.2064.24 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 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 ●



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: 35 **Expect:** 0.0014
Matches : 47/646 fragment ions using 126 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							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
35.4	6284.792847	0.037797	GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTR

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

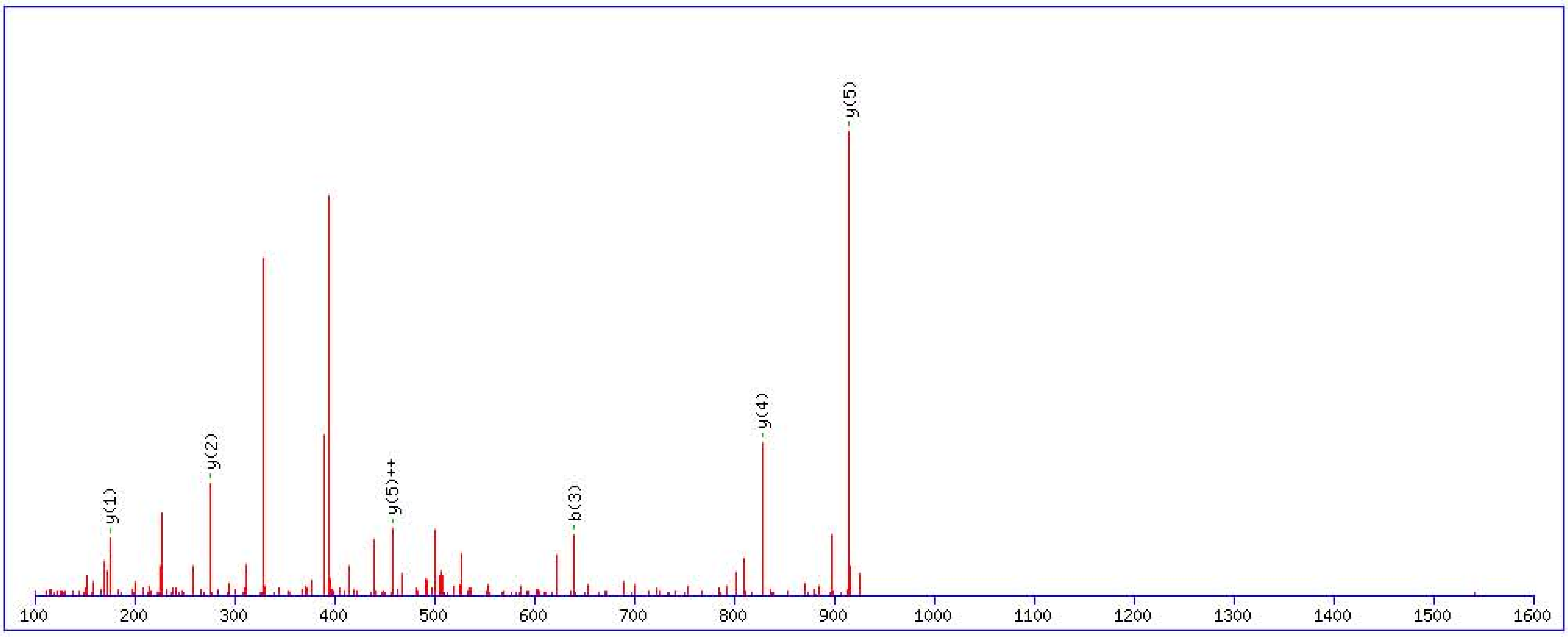
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISQLTR**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

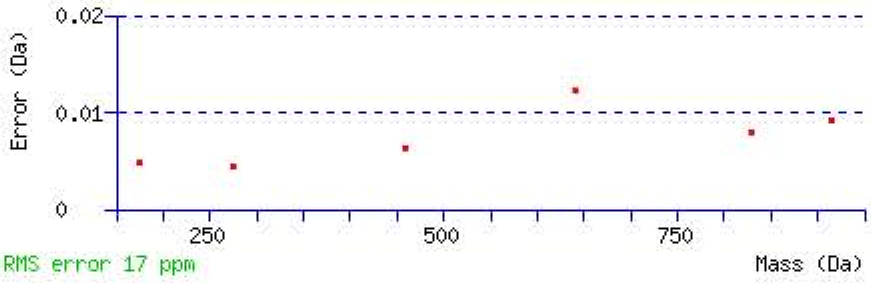
Match to Query 16830: 1027.595308 from(514.804930,2+) rtinseconds(1590) index(57950)
Title: Locus:1.1.1.2977.11 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

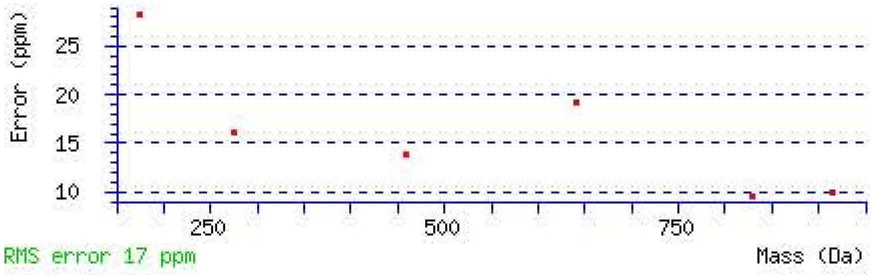
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1027.584824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 25 **Expect:** 0.05
Matches : 6/52 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	114.091340	57.549308					I							6
2	201.123368	101.065322			183.112803	92.060039	S	***915.508049***	458.257663	898.481500	449.744388	897.497484	449.252380	5
3	**640.348694**	320.677985	623.322145	312.164711	622.338129	311.672703	Q	***828.476021***	414.741649	811.449472	406.228374	810.465456	405.736366	4
4	753.432758	377.220017	736.406209	368.706743	735.422193	368.214735	L	389.250695	195.128986	372.224146	186.615711	371.240130	186.123703	3
5	854.480437	427.743857	837.453888	419.230582	836.469872	418.738574	T	***276.166631***	138.586954	259.140082	130.073679	258.156066	129.581671	2
6							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.4	1027.584824	0.010484	ISQLTR
22.3	1027.602585	-0.007277	ISPLVKDTR
22.1	1027.602570	-0.007262	LSAAADLIVR
10.7	1027.584824	0.010484	ILSQTR
10.7	1027.584839	0.010469	LQTVTR
10.7	1027.592682	0.002626	LRLSWPTR
10.6	1027.584808	0.010500	LSKNQK
9.3	1027.584839	0.010469	VTQLTR
8.7	1027.602570	-0.007262	IILQSEGLR
8.2	1027.602554	-0.007246	ILIERQEK

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

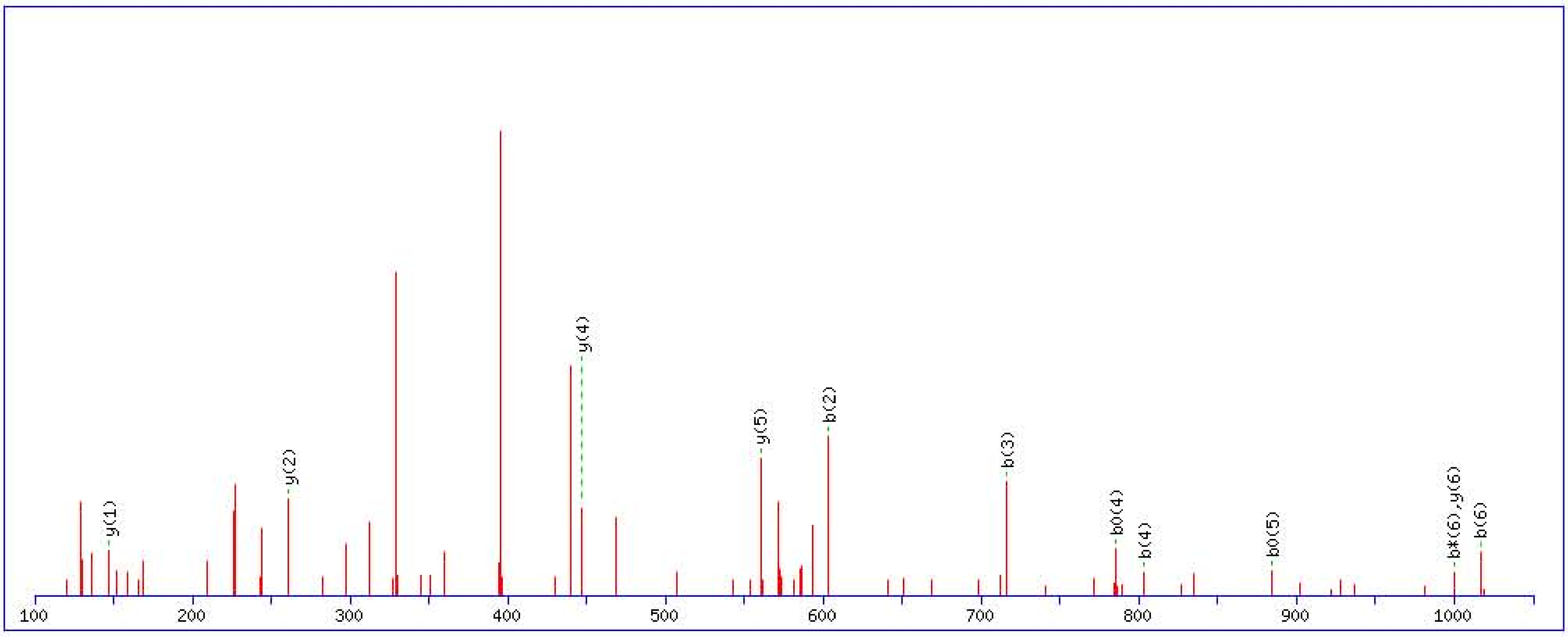
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YQISVNK**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

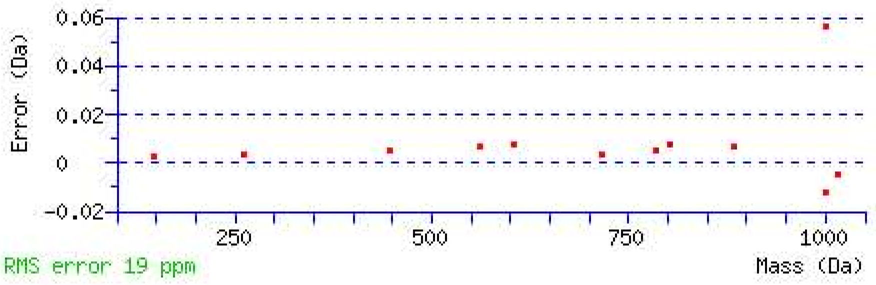
Match to Query 22290: 1161.625748 from(581.820150,2+) rtinseconds(1677) index(4362)
Title: Locus:1.1.1.2838.7 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

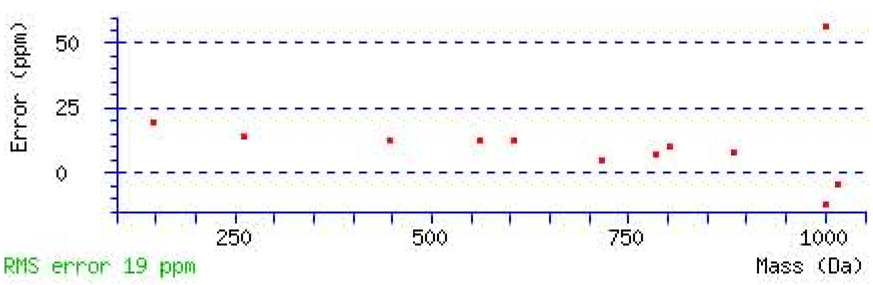
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1161.621597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.024
Matches : 12/58 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	164.070605	82.538940					Y							7
2	*603.295931*	302.151604	586.269382	293.638329			Q	*999.565563*	500.286419	982.539014	491.773145	981.554998	491.281137	6
3	*716.379995*	358.693636	699.353446	350.180361			I	*560.340237*	280.673756	543.313688	272.160482	542.329672	271.668474	5
4	*803.412023*	402.209650	786.385474	393.696375	785.401458	393.204367	S	*447.256173*	224.131724	430.229624	215.618450	429.245608	215.126442	4
5	902.480437	451.743857	885.453888	443.230582	884.469872	442.738574	V	360.224145	180.615710	343.197596	172.102436			3
6	*1016.523364*	508.765320	999.496815	500.252046	998.512799	499.760038	N	*261.155731*	131.081503	244.129182	122.568229			2
7							K	*147.112804*	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.2	1161.621597	0.004151	YQISVNK
23.4	1161.629456	-0.003708	DFALRLWNK
6.3	1161.611694	0.014054	WMIRNWIK
4.5	1161.639359	-0.013611	FLDKDGLINK
3.9	1161.632843	-0.007095	QHLQTPK
3.8	1161.618225	0.007523	KISFPQWEK
3.8	1161.617554	0.008194	KLSRECEIK
3.8	1161.642715	-0.016967	KSLIDPKMSK
3.5	1161.632843	-0.007095	QHLQTPK
2.0	1161.621597	0.004151	QKEAFTK

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

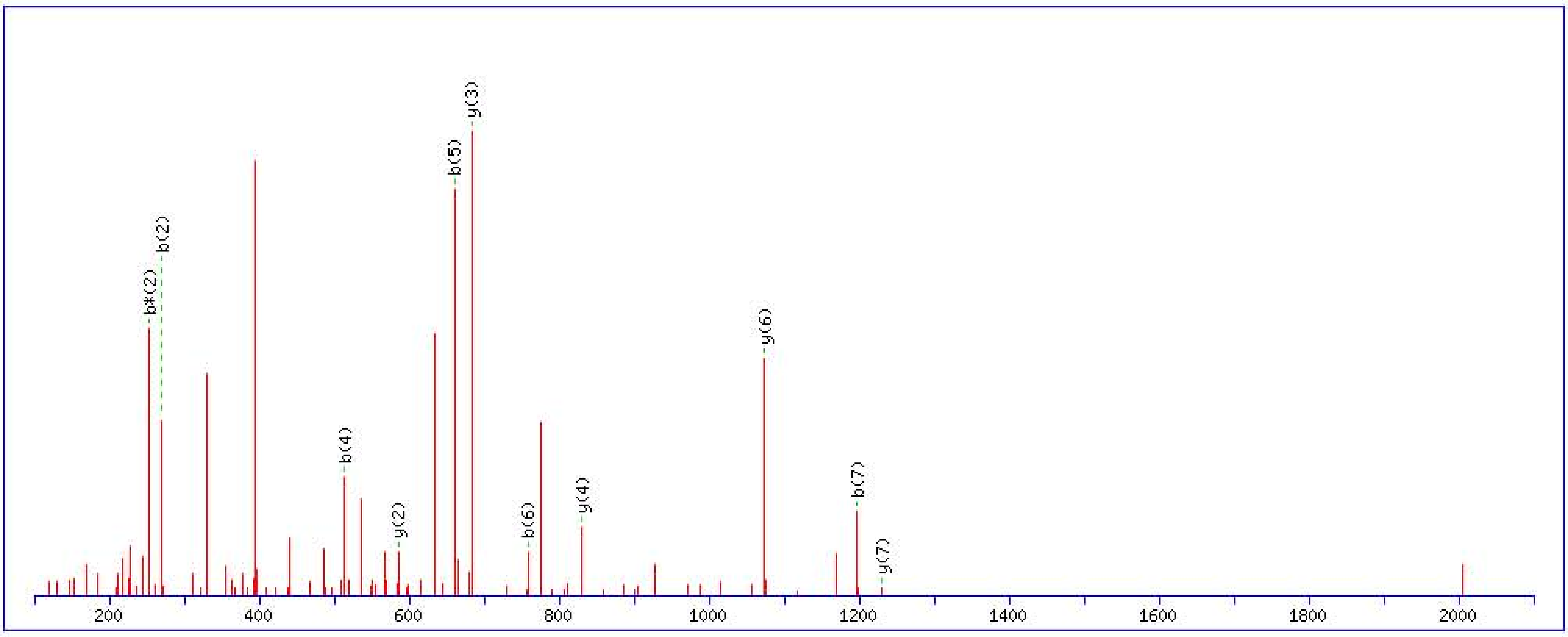
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IRPFFPQQ**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

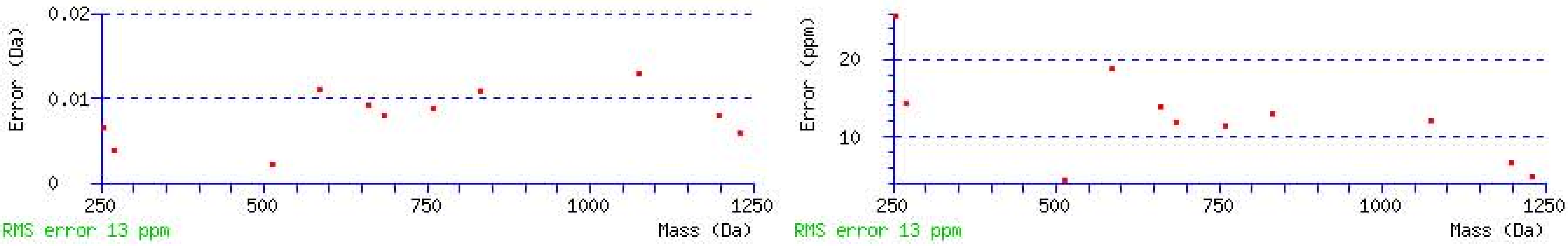
Match to Query 27930: 1342.734748 from(672.374650,2+) rtinseconds(2251) index(8211)
Title: Locus:1.1.1.3038.6 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1342.722000
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.018
Matches : 11/54 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	114.091340	57.549308			I					8
2	*270.192451*	135.599864	253.165902	127.086589	R	*1230.645212*	615.826244	1213.618663	607.312970	7
3	367.245215	184.126245	350.218666	175.612971	P	*1074.544101*	537.775689	1057.517552	529.262414	6
4	*514.313629*	257.660453	497.287080	249.147178	F	977.491337	489.249307	960.464788	480.736032	5
5	*661.382043*	331.194660	644.355494	322.681385	F	*830.422923*	415.715100	813.396374	407.201825	4
6	*758.434807*	379.721042	741.408258	371.207767	P	*683.354509*	342.180893	666.327960	333.667618	3
7	*1197.660133*	599.333705	1180.633584	590.820430	Q	*586.301745*	293.654511	569.275196	285.141236	2
8					Q	147.076419	74.041848	130.049870	65.528573	1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.2	1342.722000	0.012748	IRPFFPQQ
26.0	1342.722000	0.012748	IRPFFPQQ
7.2	1342.716629	0.018119	LLSVTEDQK
6.1	1342.729187	0.005561	QPHRPIER
4.9	1342.743103	-0.008355	IRYVPEQK
3.5	1342.727859	0.006889	ATPTSTAKQK
2.3	1342.746918	-0.012170	RIYNNIPANLR
0.0	1342.735718	-0.000970	EPVFIAAGDIRR

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

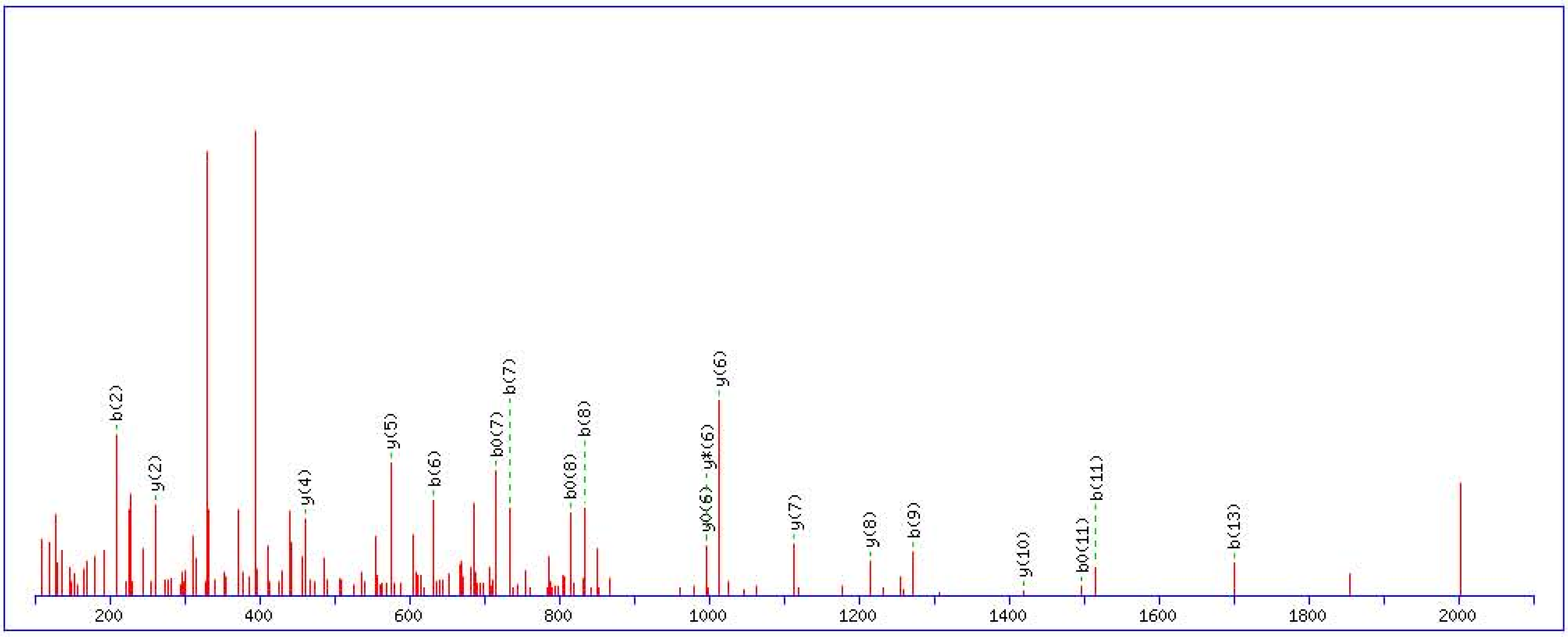
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AHYGGFTVQNEANK**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

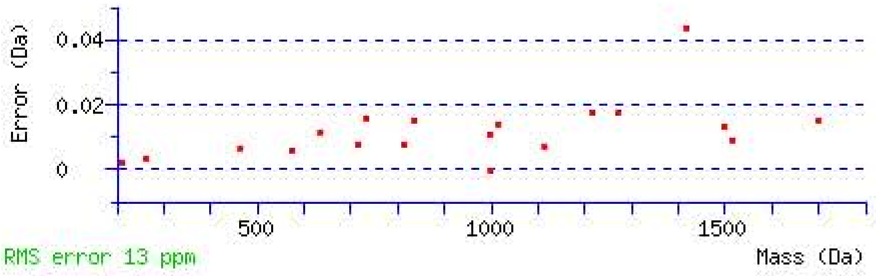
Match to Query 46380: 1845.904812 from(616.308880,3+) rtinseconds(1673) index(58399)
Title: Locus:1.1.1.3006.6 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

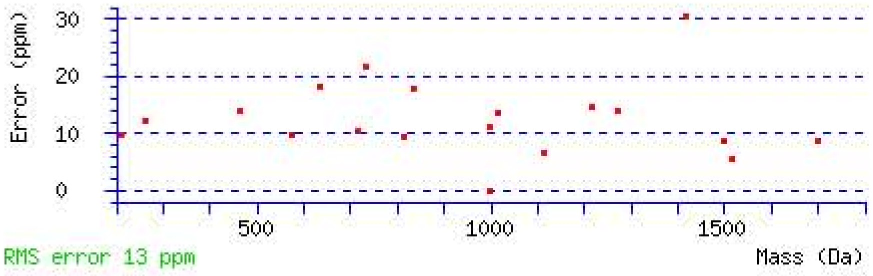
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1845.883194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 9.8e-005
Matches : 19/122 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	72.044390	36.525833					A							14
2	***209.103302***	105.055289					H	1775.853367	888.430321	1758.826818	879.917047	1757.842802	879.425039	13
3	372.166631	186.586953					Y	1638.794455	819.900866	1621.767906	811.387591	1620.783890	810.895583	12
4	429.188095	215.097685					G	1475.731126	738.369201	1458.704577	729.855927	1457.720561	729.363918	11
5	486.209559	243.608417					G	***1418.709662***	709.858469	1401.683113	701.345195	1400.699097	700.853186	10
6	***633.277973***	317.142625					F	1361.688198	681.347737	1344.661649	672.834463	1343.677633	672.342455	9
7	***734.325652***	367.666464			716.315087	358.661182	T	***1214.619784***	607.813530	1197.593235	599.300256	1196.609219	598.808247	8
8	***833.394066***	417.200671			815.383501	408.195388	V	***1113.572105***	557.289691	1096.545556	548.776416	1095.561540	548.284408	7
9	***1272.619392***	636.813334	1255.592843	628.300059	1254.608827	627.808051	Q	***1014.503691***	507.755484	997.477142	499.242209	996.493126	498.750201	6
10	1386.662319	693.834797	1369.635770	685.321523	1368.651754	684.829515	N	***575.278365***	288.142821	558.251816	279.629546	557.267800	279.137538	5
11	***1515.704912***	758.356094	1498.678363	749.842820	1497.694347	749.350811	E	***461.235438***	231.121357	444.208889	222.608083	443.224873	222.116075	4
12	1586.742026	793.874651	1569.715477	785.361377	1568.731461	784.869368	A	332.192845	166.600060	315.166296	158.086786			3
13	***1700.784953***	850.896114	1683.758404	842.382840	1682.774388	841.890832	N	***261.155731***	131.081503	244.129182	122.568229			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AHYGGFTVQNEANK
(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	1845.883194	0.021618	AHYGGFTVQNEANK
12.5	1845.918243	-0.013431	DSKEDQVPYVVEK

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

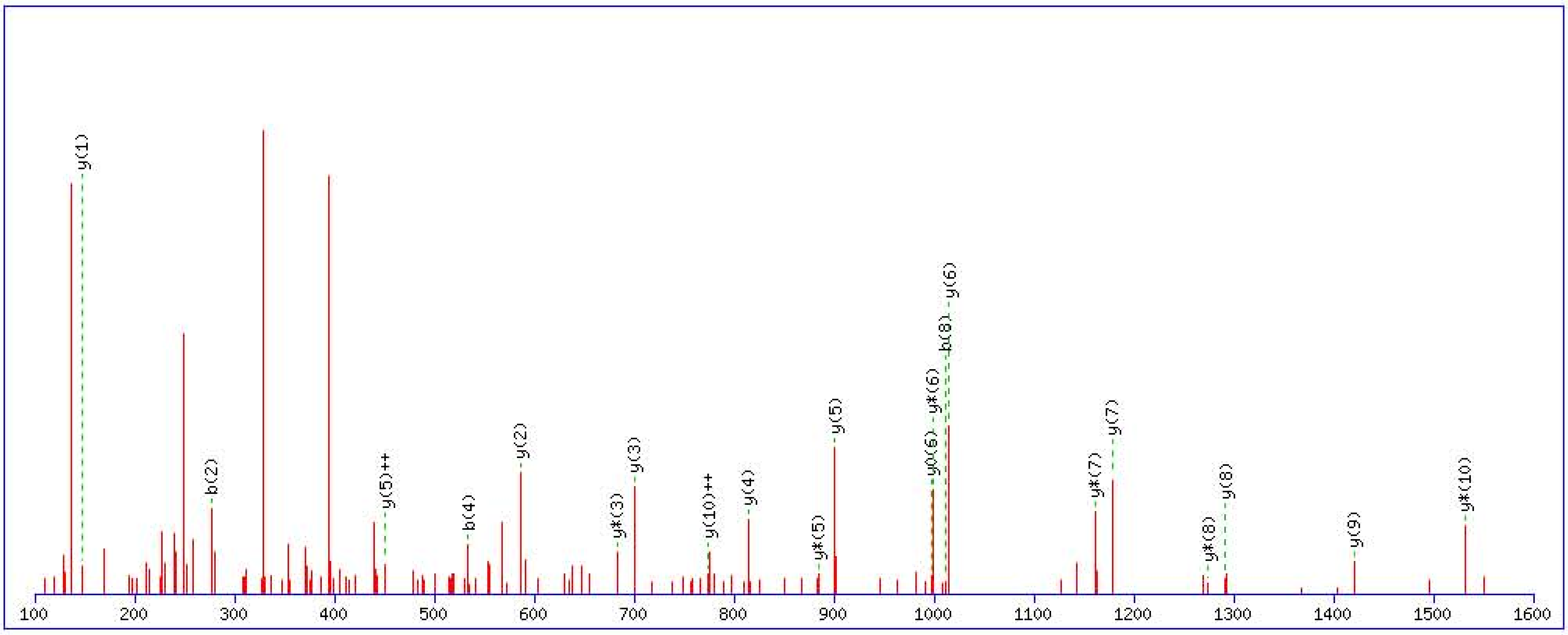
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLQEIYNSNNQK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

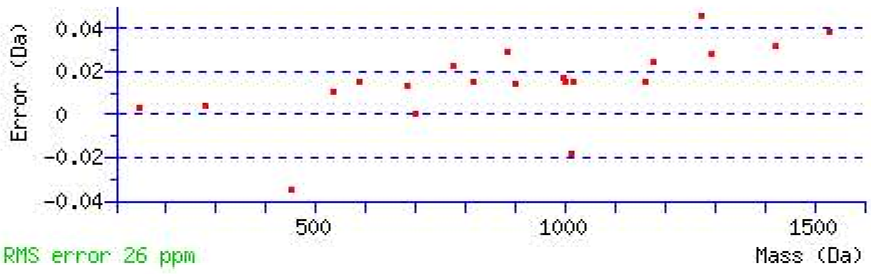
Match to Query 45925: 1823.913732 from(608.978520,3+) rtinseconds(1837) index(59579)
Title: Locus:1.1.1.3063.7 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

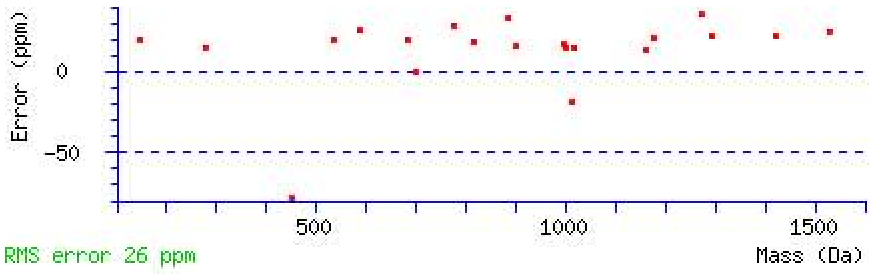
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 35  Expect: 0.0073
Matches : 21/114 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	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
35.4	1823.887573	0.026159	YLQEIYNSNNQK

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

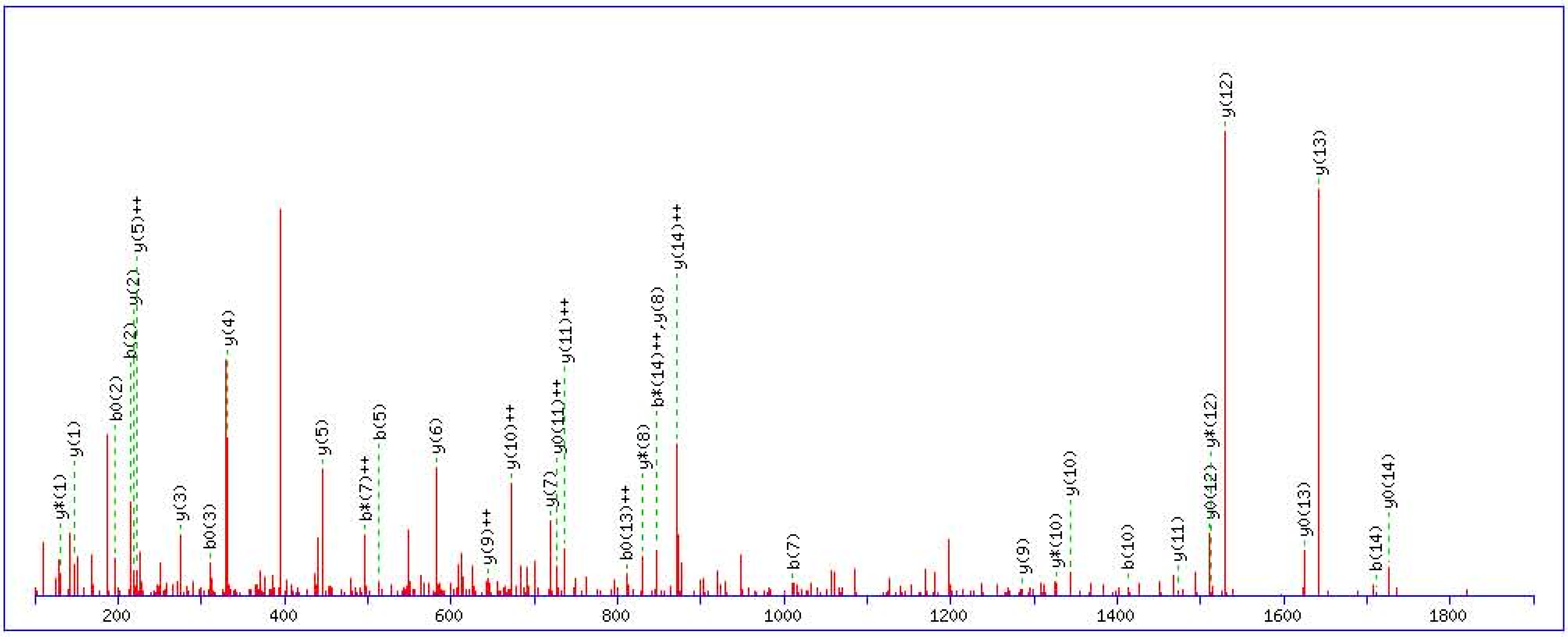
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

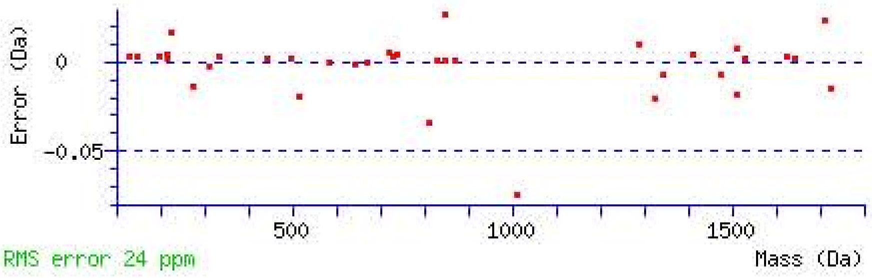
Match to Query 46738: 1855.975812 from(619.665880,3+) rtinseconds(1475) index(20825)
Title: Locus:1.1.1.2656.21 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

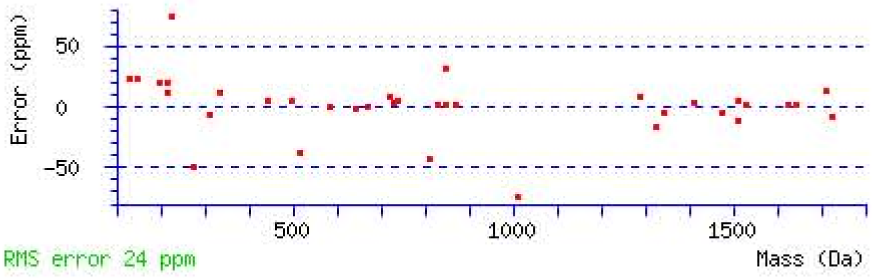
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1855.972687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.0036
Matches : 36/134 fragment ions using 144 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
38.7	1855.972687	0.003125	LTIGEGQQHHLGGAK
29.4	1855.972687	0.003125	LTIGEGQQHHLGGAK

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

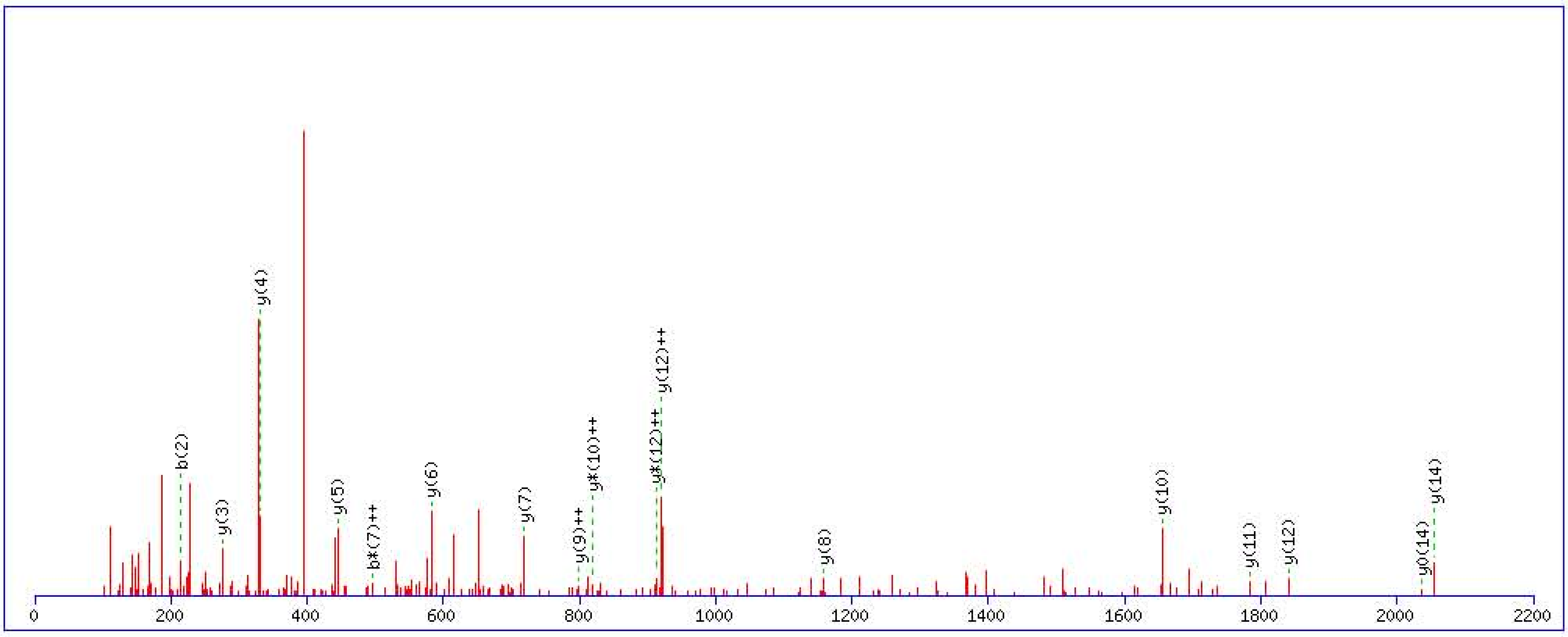
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

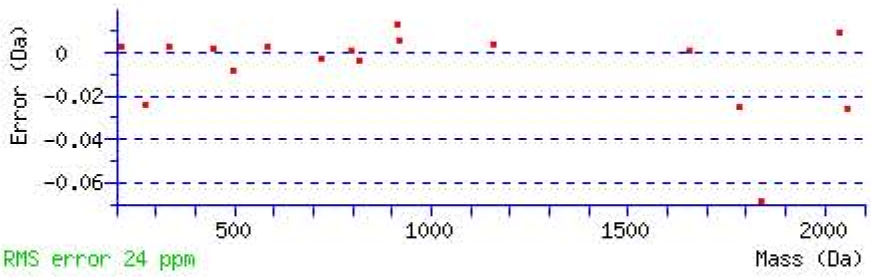
Match to Query 54604: 2167.141376 from(542.792620,4+) rtinseconds(1752) index(22875)
Title: Locus:1.1.1.2753.4 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

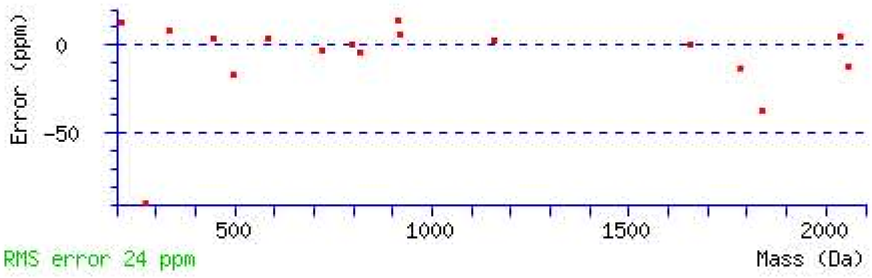
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 29  Expect: 0.035
Matches : 17/134 fragment ions using 55 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
28.5	2167.139435	0.001941	LTIGEGQQHHLGGAK

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

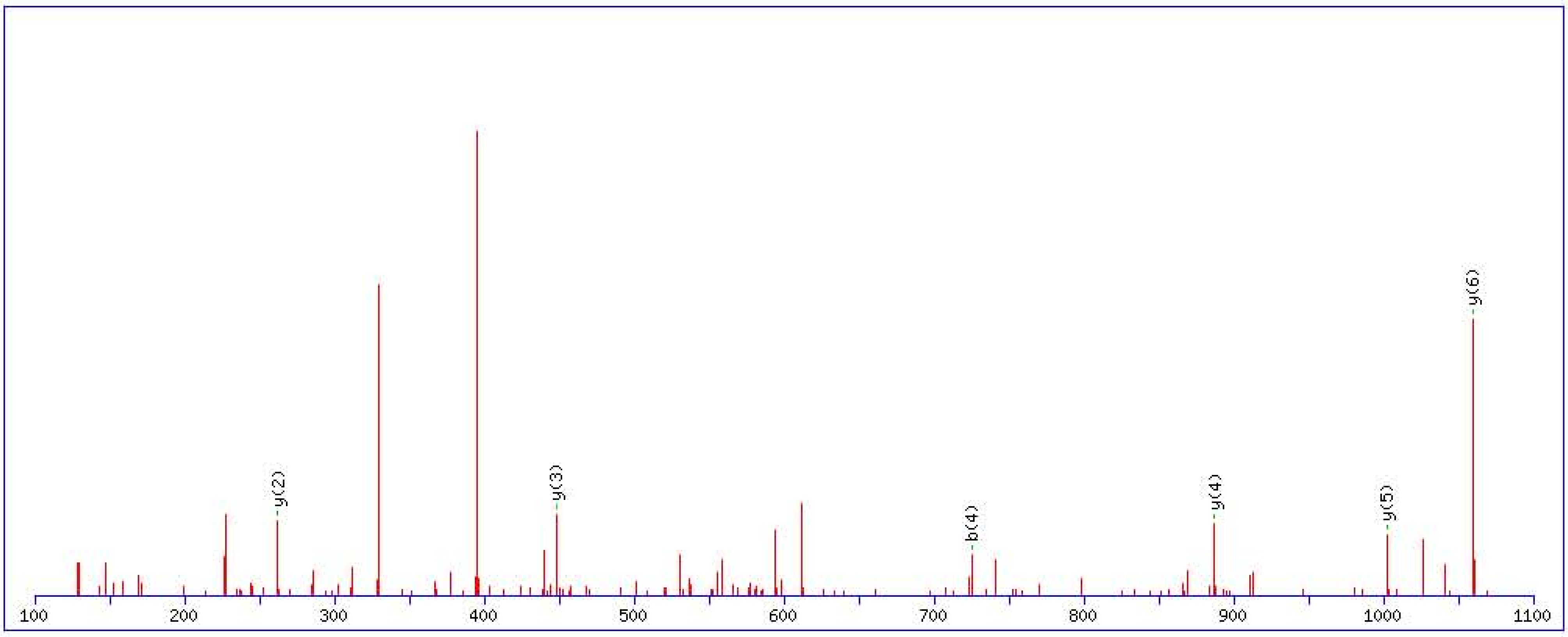
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGDQWDK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

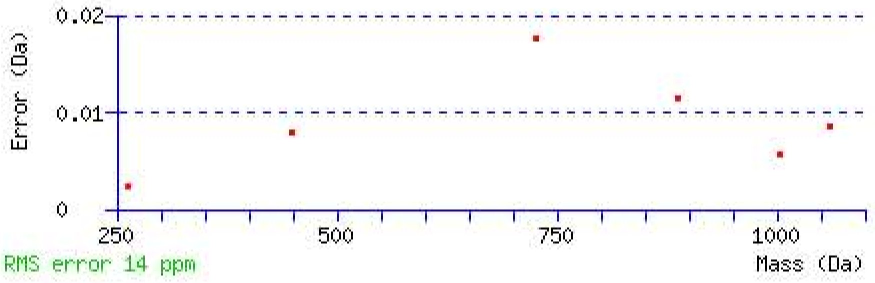
Match to Query 22667: 1171.578288 from(586.796420,2+) rtinseconds(1791) index(40714)
Title: Locus:1.1.1.3073.16 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

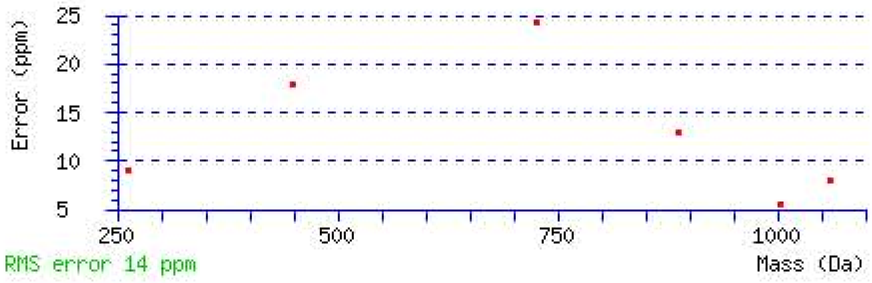
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 31 **Expect:** 0.0046
Matches : 6/60 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							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





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
30.7	1171.569580	0.008708	IGDQWDK
5.5	1171.583328	-0.005040	GEVGDPGQKGTK
5.3	1171.590714	-0.012426	GEVQVSDK
5.0	1171.576096	0.002192	LYFSDATLDK
4.5	1171.590698	-0.012410	LPALSGQDMPK
3.0	1171.569565	0.008723	LGPEWSQPMK
3.0	1171.572067	0.006221	LGSGPDGAEEIK
2.9	1171.573410	0.004878	RAPDPGFQER

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

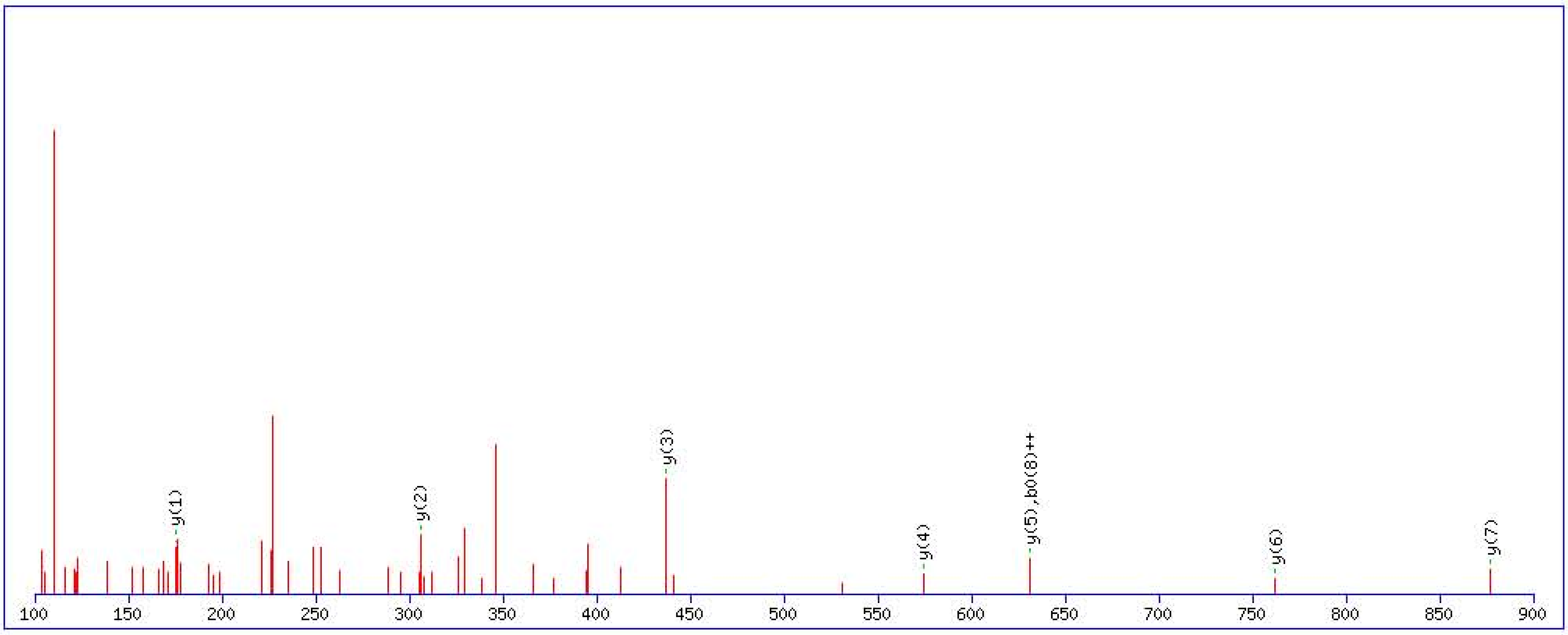
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QHDMGHMMR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

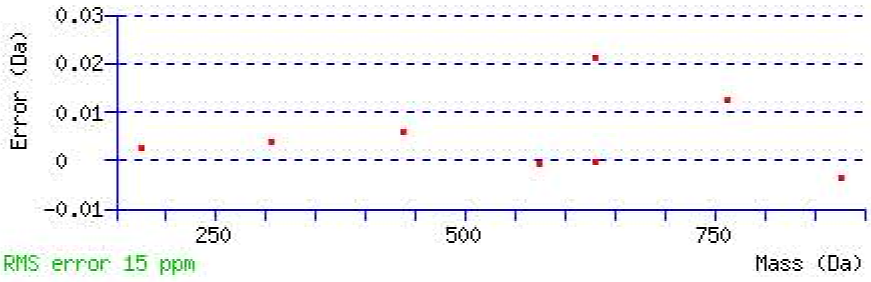
Match to Query 33384: 1452.628496 from(364.164400,4+) rtinseconds(1397) index(37995)
Title: Locus:1.1.1.2936.2 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

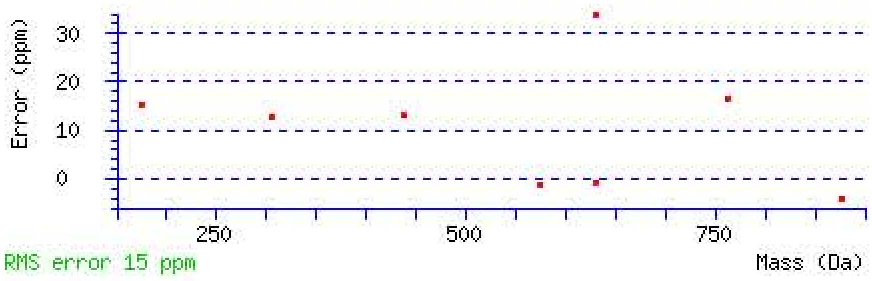
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1452.624680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0023
Matches : 8/80 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	440.232602	220.619939	423.206053	212.106664			Q							9
2	577.291514	289.149395	560.264965	280.636121			H	1014.406638	507.706957	997.380089	499.193682	996.396073	498.701674	8
3	692.318457	346.662867	675.291908	338.149592	674.307892	337.657584	D	***877.347726***	439.177501	860.321177	430.664226	859.337161	430.172218	7
4	823.358942	412.183109	806.332393	403.669834	805.348377	403.177826	M	***762.320783***	381.664030	745.294234	373.150755			6
5	880.380406	440.693841	863.353857	432.180567	862.369841	431.688559	G	***631.280298***	316.143787	614.253749	307.630513			5
6	1017.439318	509.223297	1000.412769	500.710022	999.428753	500.218014	H	***574.258834***	287.633055	557.232285	279.119780			4
7	1148.479803	574.743540	1131.453254	566.230265	1130.469238	565.738257	M	***437.199922***	219.103599	420.173373	210.590324			3
8	1279.520288	640.263782	1262.493739	631.750508	1261.509723	631.258499	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 QHDMGHMMR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.4	1452.624680	0.003816	QHDMGHMMR

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

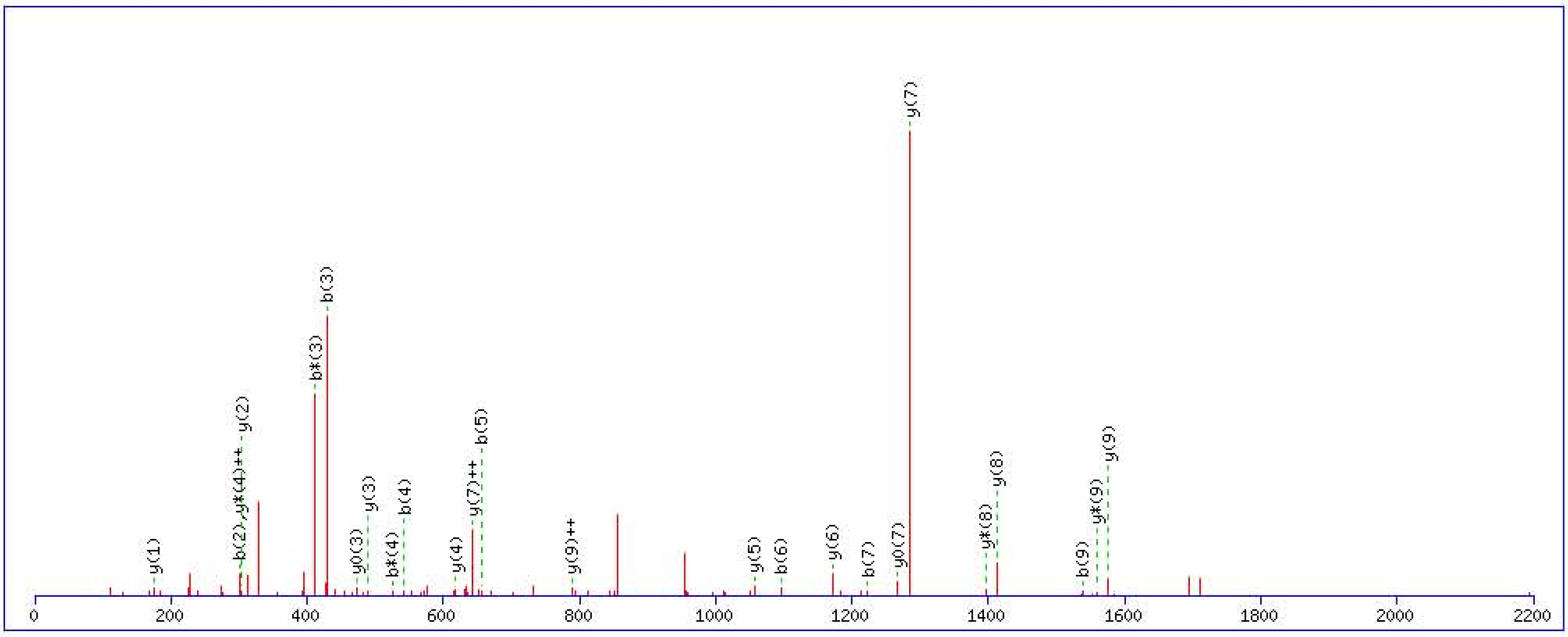
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HYQINQQWER**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

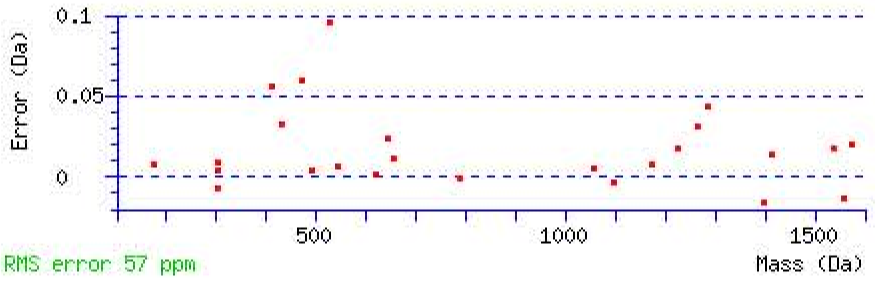
Match to Query 42792: 1711.850728 from(856.932640,2+) rtinseconds(1754) index(40466)
Title: Locus:1.1.1.3060.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

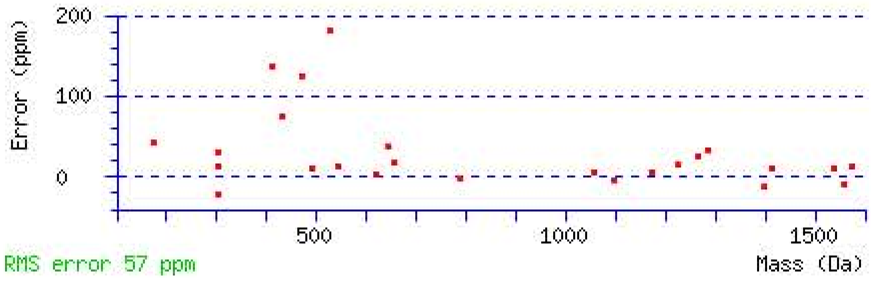
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1711.825272
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.0056
Matches : 25/86 fragment ions using 77 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	**301.129517**	151.068397					Y	***1575.773660***	788.390468	1558.747111	779.877194	1557.763095	779.385186	9
3	**429.188095**	215.097686	412.161546	206.584411			Q	***1412.710331***	706.858804	1395.683782	698.345529	1394.699766	697.853521	8
4	**542.272159**	271.639718	525.245610	263.126443			I	***1284.651753***	642.829514	1267.625204	634.316240	1266.641188	633.824232	7
5	**656.315086**	328.661181	639.288537	320.147907			N	***1171.567689***	586.287483	1154.541140	577.774208	1153.557124	577.282200	6
6	**1095.540412**	548.273844	1078.513863	539.760570			Q	***1057.524762***	529.266019	1040.498213	520.752745	1039.514197	520.260737	5
7	**1223.598990**	612.303133	1206.572441	603.789859			Q	***618.299436***	309.653356	601.272887	301.140082	600.288871	300.648074	4
8	1409.678303	705.342790	1392.651754	696.829515			W	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	3
9	**1538.720896**	769.864086	1521.694347	761.350812	1520.710331	760.858804	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of HYQINQQWER
(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	1711.825272	0.025456	HYQINQQWER
23.0	1711.825272	0.025456	HYQINQQWER
2.7	1711.871368	-0.020640	AQTQEGAGARAGAQAVAR
2.0	1711.848938	0.001790	TVTQVVPAEGQENGQR
1.0	1711.825272	0.025456	HYQINQQWER
0.3	1711.856293	-0.005565	LLQGQEKDGEER
0.1	1711.867538	-0.016810	QVMKDEDKPPDRVR

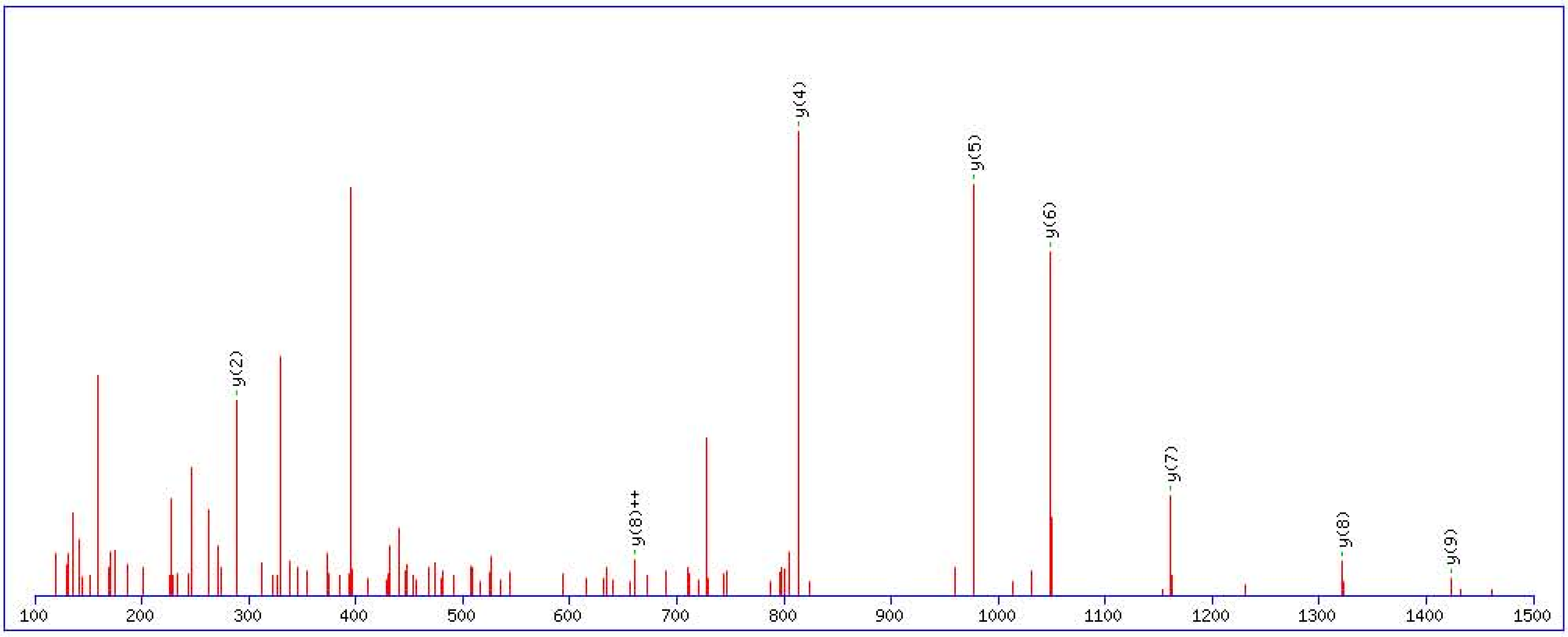
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEWTCIAYSQLR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

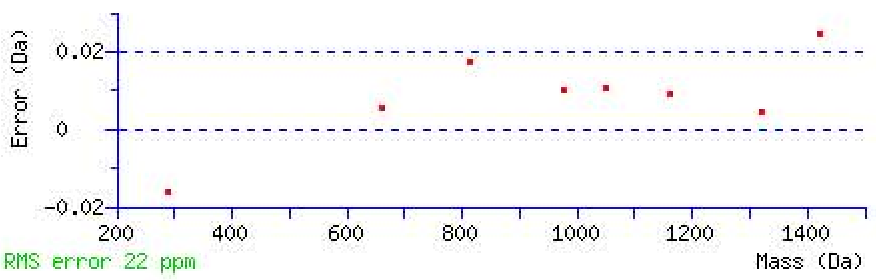
Match to Query 45118: 1793.882652 from(598.968160,3+) rtinseconds(2349) index(44617)
Title: Locus:1.1.1.3267.9 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

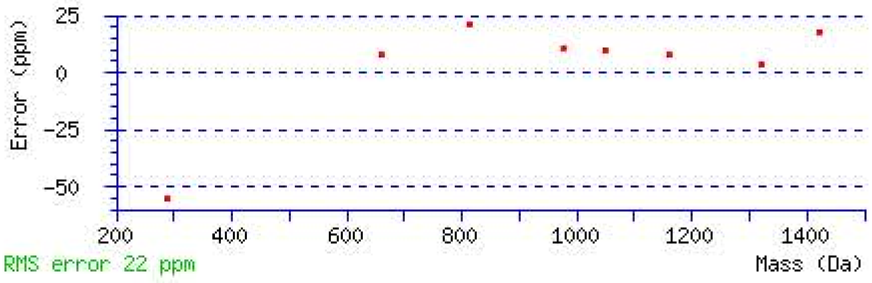
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1793.859283
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00027
Matches : 8/106 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	58.028740	29.518008					G							12
2	187.071333	94.039305			169.060768	85.034022	E	1737.845111	869.426194	1720.818562	860.912919	1719.834546	860.420911	11
3	373.150646	187.078961			355.140081	178.073679	W	1608.802518	804.904897	1591.775969	796.391623	1590.791953	795.899614	10
4	474.198325	237.602801			456.187760	228.597518	T	***1422.723205***	711.865241	1405.696656	703.351966	1404.712640	702.859958	9
5	634.228974	317.618125			616.218409	308.612843	C	***1321.675526***	661.341401	1304.648977	652.828127	1303.664961	652.336119	8
6	747.313038	374.160157			729.302473	365.154875	I	***1161.644877***	581.326077	1144.618328	572.812802	1143.634312	572.320794	7
7	818.350152	409.678714			800.339587	400.673432	A	***1048.560813***	524.784044	1031.534264	516.270770	1030.550248	515.778762	6
8	981.413481	491.210379			963.402916	482.205096	Y	***977.523699***	489.265488	960.497150	480.752213	959.513134	480.260205	5
9	1068.445509	534.726393			1050.434944	525.721110	S	***814.460370***	407.733823	797.433821	399.220549	796.449805	398.728541	4
10	1507.670835	754.339056	1490.644286	745.825781	1489.660270	745.333773	Q	727.428342	364.217809	710.401793	355.704534			3
11	1620.754899	810.881088	1603.728350	802.367813	1602.744334	801.875805	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 GEWTCIAYSQLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.7	1793.859283	0.023369	GEWTCIAYSQLR
4.4	1793.865158	0.017494	ACLECELTSKDVTLR
2.8	1793.865158	0.017494	EDVNLMMSSGQILGIR
1.4	1793.873016	0.009636	DQKLFVSESRMPDSR

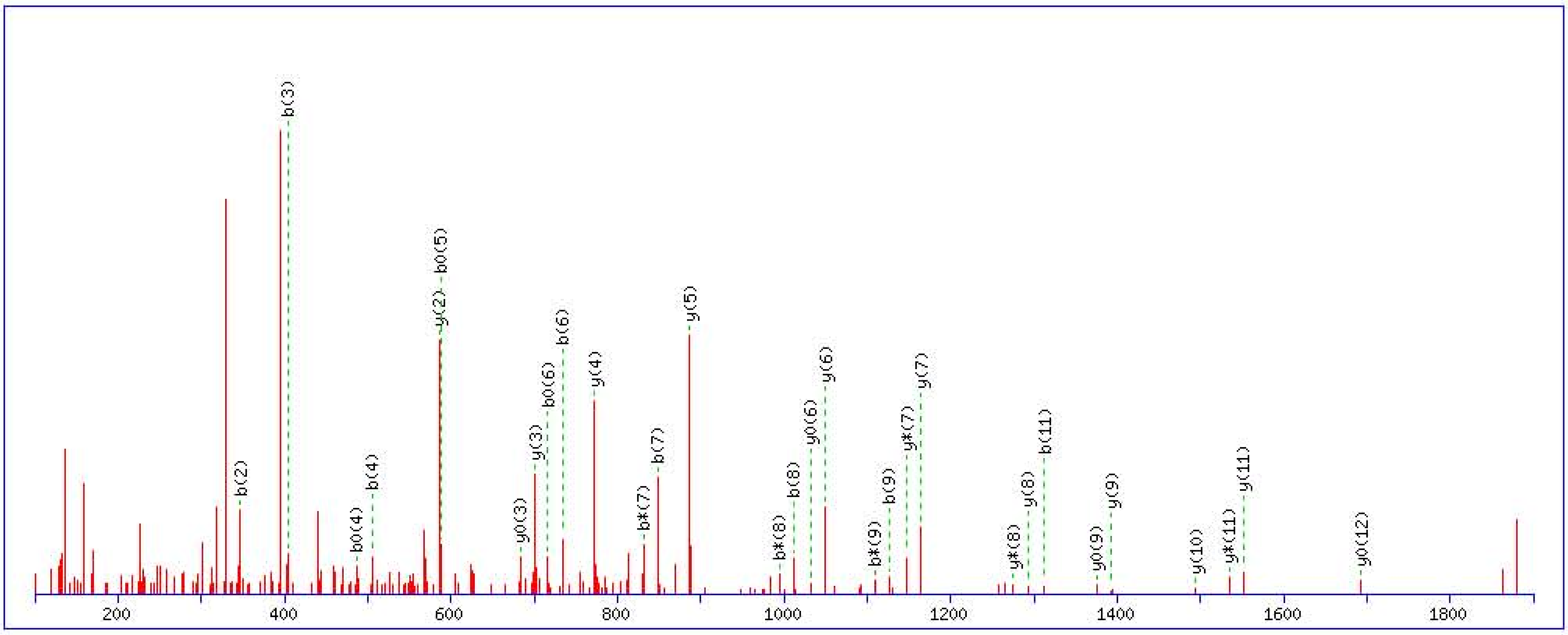
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WCGTTQNYDADQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

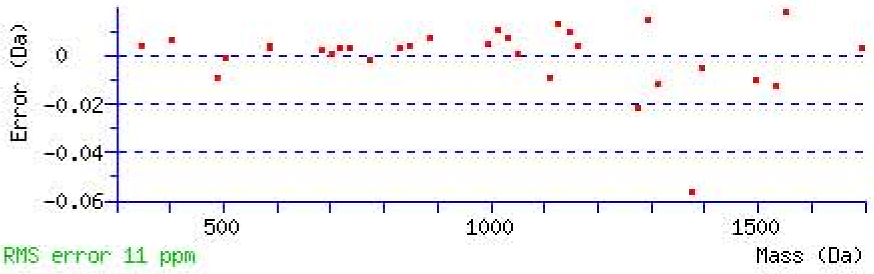
Match to Query 47421: 1896.827862 from(633.283230,3+) rtinseconds(1665) index(39833)
Title: Locus:1.1.1.3029.13 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

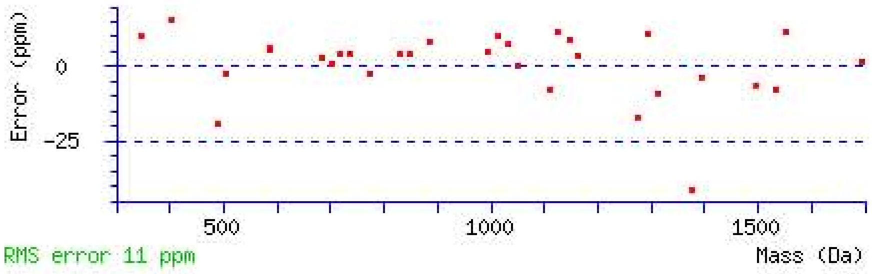
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1896.813477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 2.2e-005
Matches : 31/124 fragment ions using 58 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
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
53.5	1896.813477	0.014385	WCGTTQNYDADQK

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

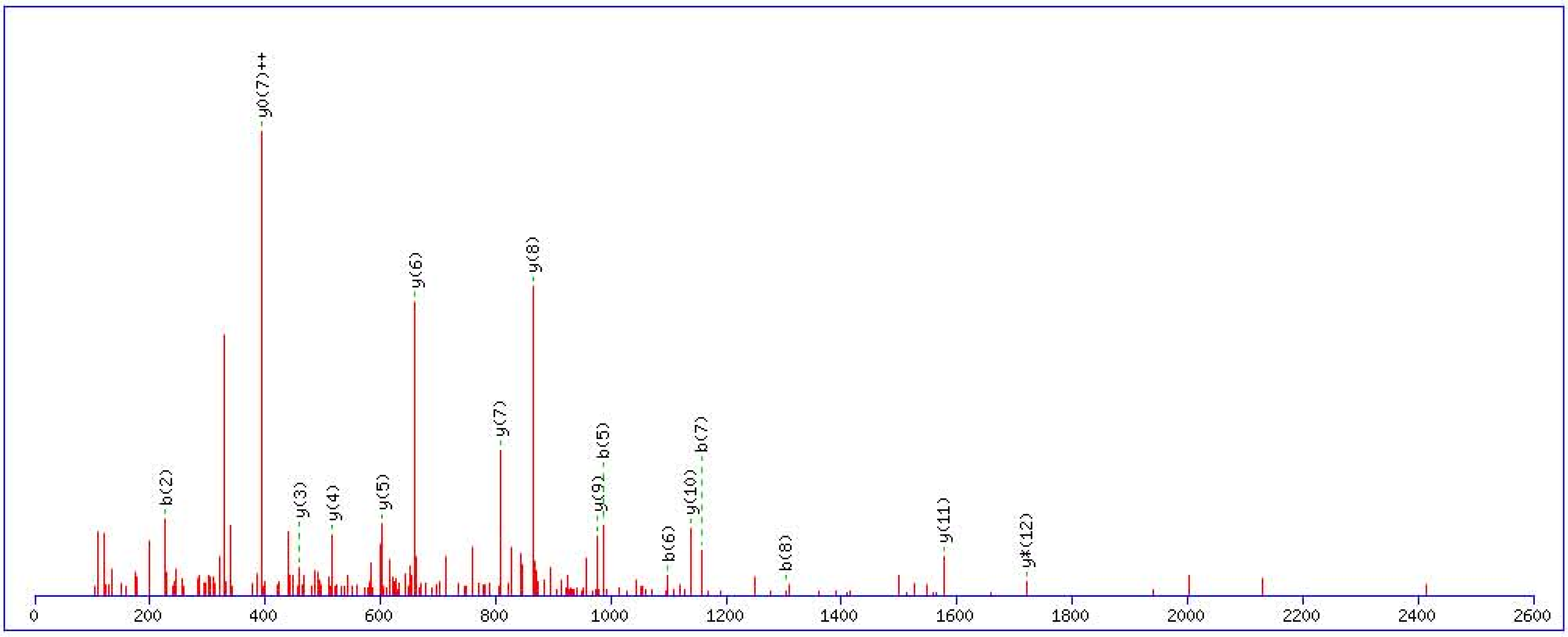
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLCQCLGFGSGHFR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

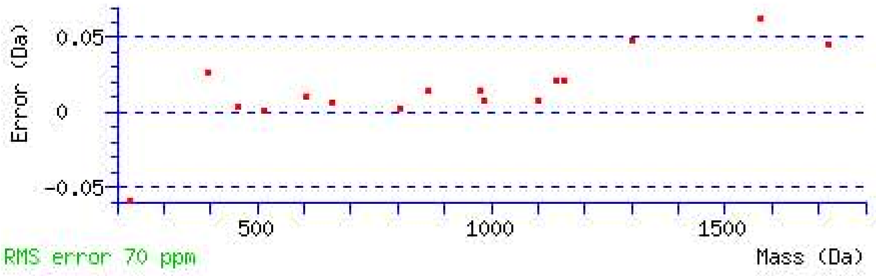
Match to Query 48969: 1961.965182 from(654.995670,3+) rtinseconds(2154) index(43282)
Title: Locus:1.1.1.3199.14 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

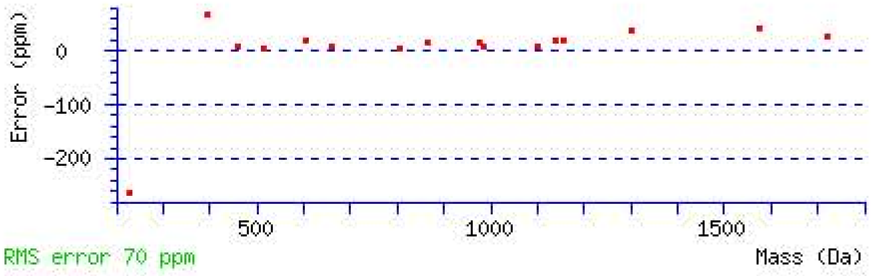
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1961.942673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 3.6e-005
Matches : 16/124 fragment ions using 33 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
47.4	1961.942673	0.022509	LLCQCLGFGSGHFR
0.0	1961.970779	-0.005597	DAGREGLRSDVFPGPSFR

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

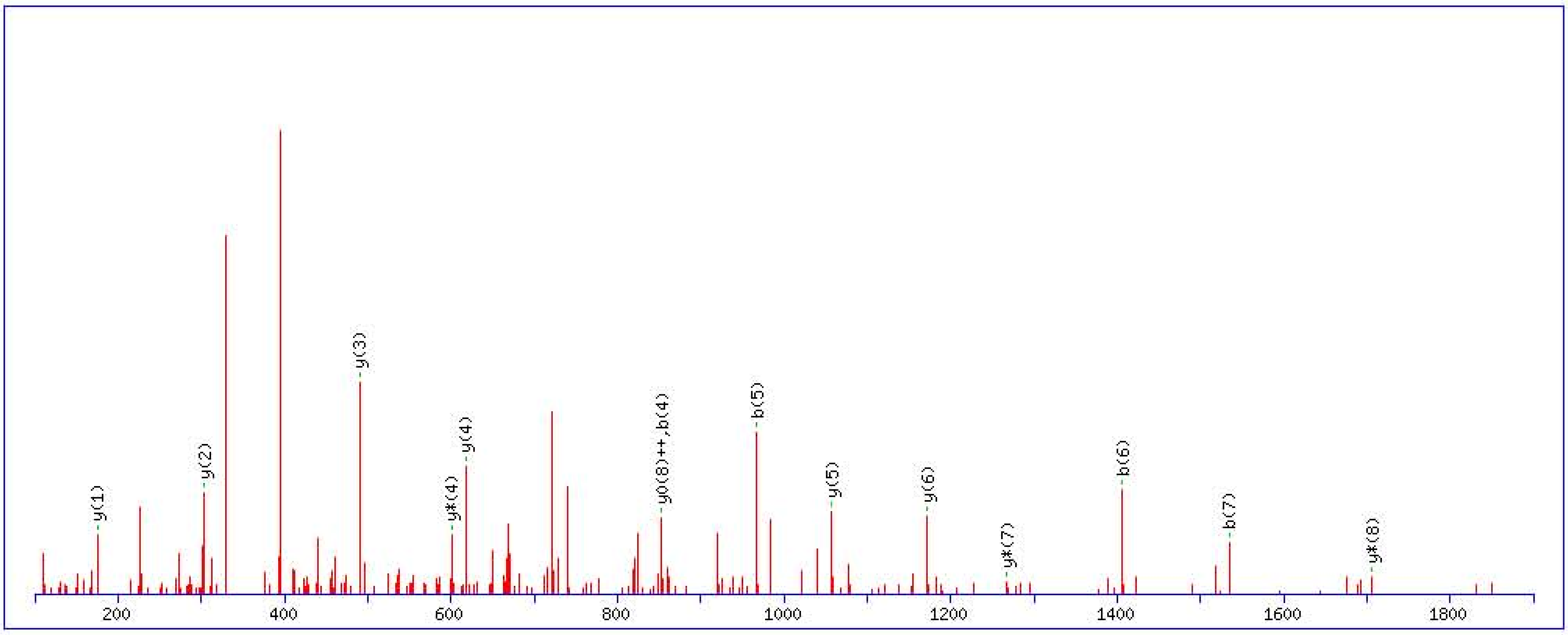
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HYQINQQWER**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

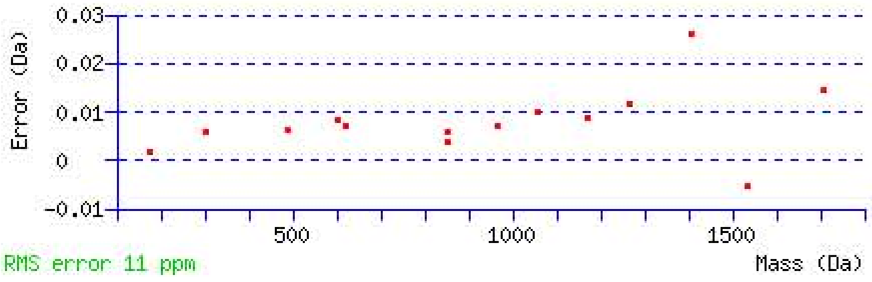
Match to Query 51354: 2023.014132 from(675.345320,3+) rtinseconds(1993) index(42184)
Title: Locus:1.1.1.3143.10 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

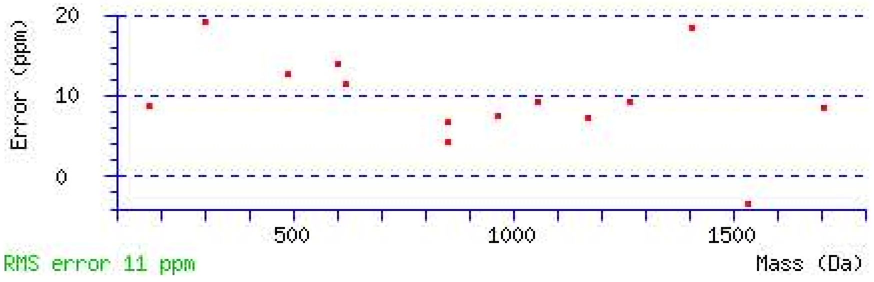
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2022.992020
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0017
Matches : 14/86 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	138.066188	69.536732					H							10
2	301.129517	151.068397					Y	1886.940408	943.973842	1869.913859	935.460568	1868.929843	934.968560	9
3	740.354843	370.681060	723.328294	362.167785			Q	1723.877079	862.442178	1706.850530	853.928903	1705.866514	853.436895	8
4	**853.438907**	427.223092	836.412358	418.709817			I	1284.651753	642.829515	1267.625204	634.316240	1266.641188	633.824232	7
5	**967.481834**	484.244555	950.455285	475.731281			N	***1171.567689***	586.287483	1154.541140	577.774208	1153.557124	577.282200	6
6	**1406.707160**	703.857218	1389.680611	695.343944			Q	***1057.524762***	529.266019	1040.498213	520.752745	1039.514197	520.260737	5
7	**1534.765738**	767.886507	1517.739189	759.373233			Q	***618.299436***	309.653356	601.272887	301.140082	600.288871	300.648074	4
8	1720.845051	860.926164	1703.818502	852.412889			W	***490.240858***	245.624067	473.214309	237.110792	472.230293	236.618784	3
9	1849.887644	925.447460	1832.861095	916.934186	1831.877079	916.442178	E	***304.161545***	152.584410	287.134996	144.071136	286.150980	143.579128	2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of HYQINQQWER
(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	2022.992020	0.022112	HYQINQQWER
20.7	2022.992020	0.022112	HYQINQQWER
7.3	2023.023682	-0.009550	ILDQYLYKEGWER
0.6	2023.038284	-0.024152	EVNKFQMAYSNLLR

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

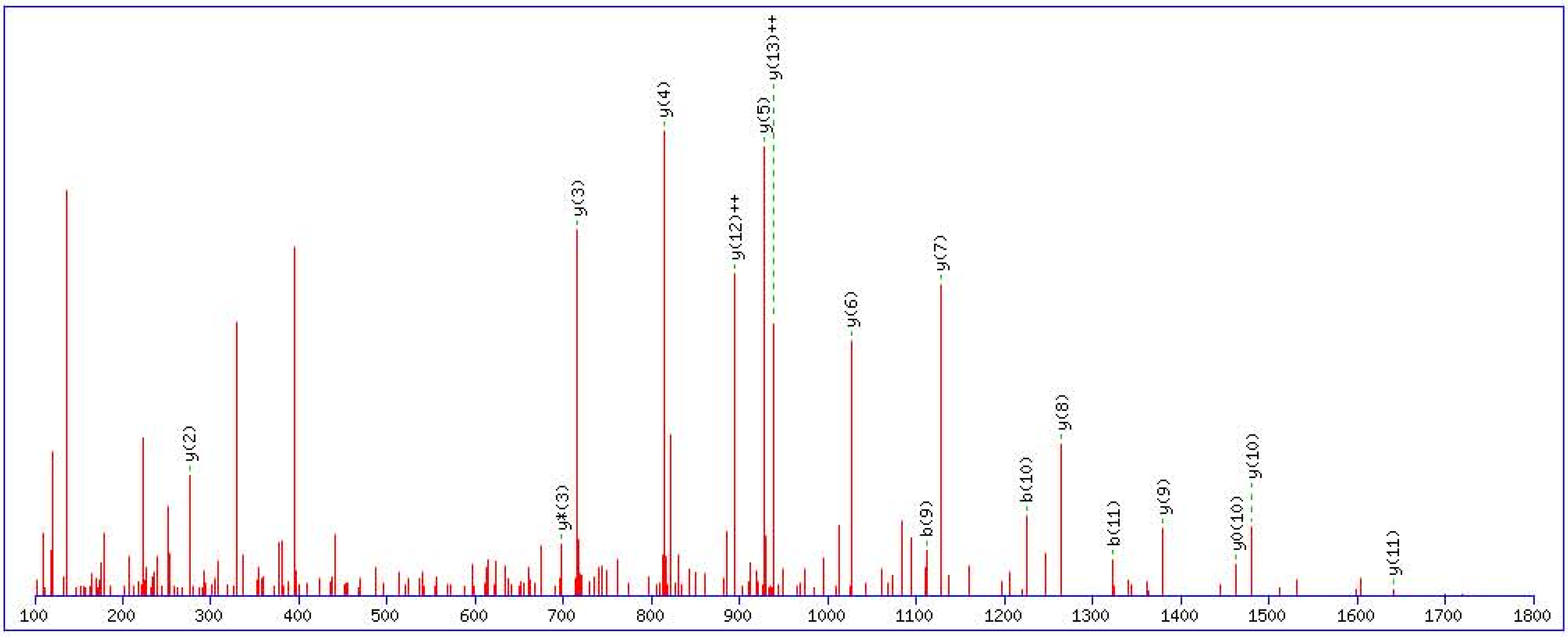
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSFCTDHTVLVQTR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

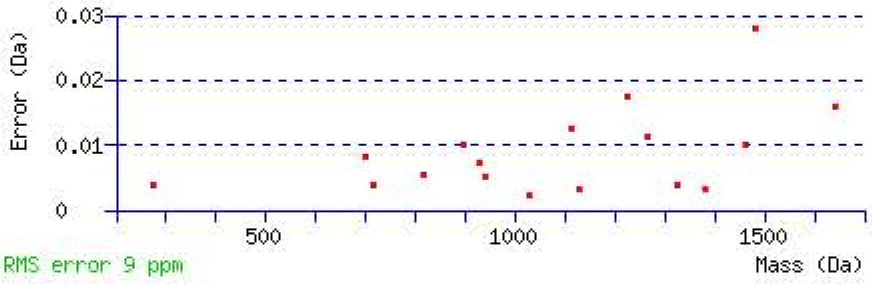
Match to Query 51688: 2037.005142 from(680.008990,3+) rtinseconds(1999) index(42215)
Title: Locus:1.1.1.3145.12 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

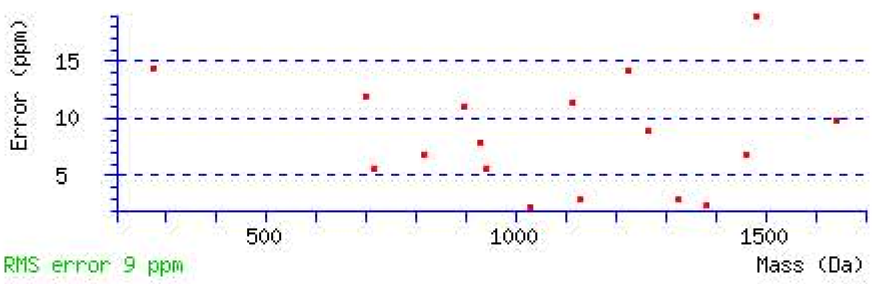
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 57  Expect: 4.6e-005
Matches : 17/130 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	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
56.9	2036.981232	0.023910	YSFCTDHTVLVQTR

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

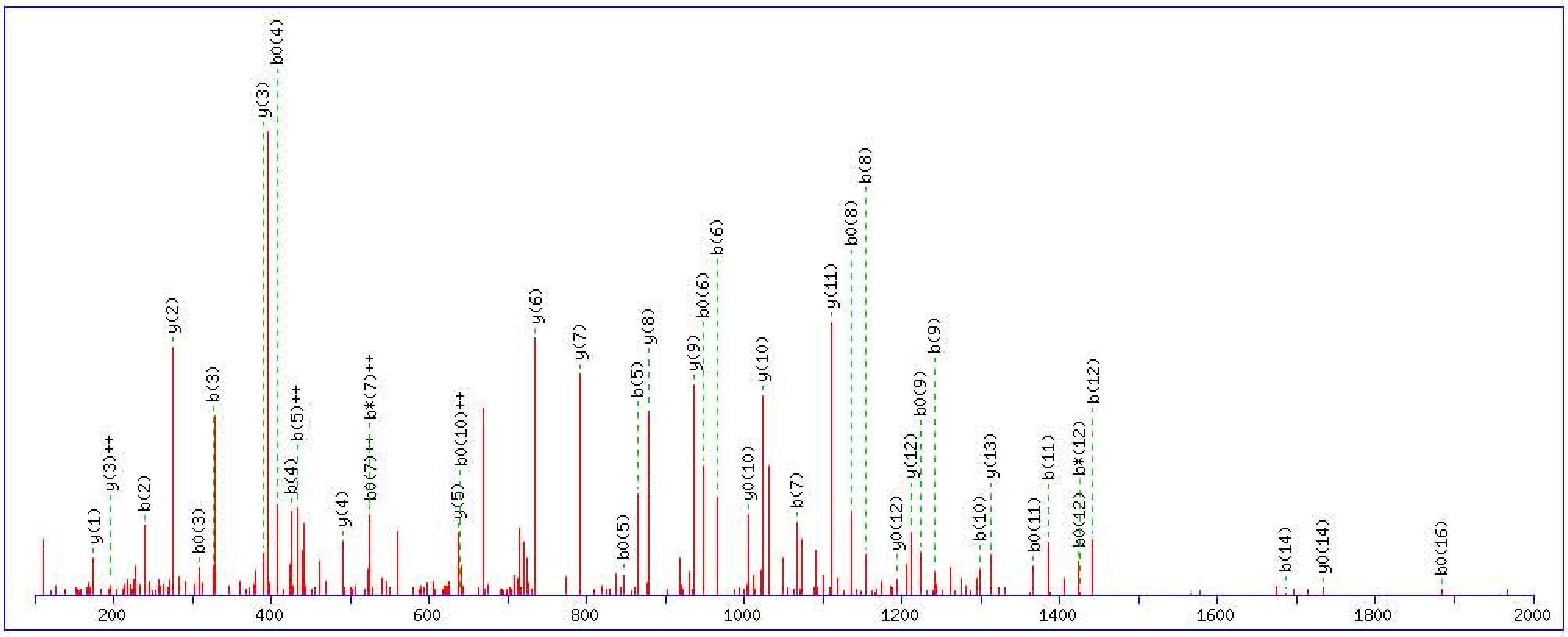
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HTSVQTTSSGSGPFTDVR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

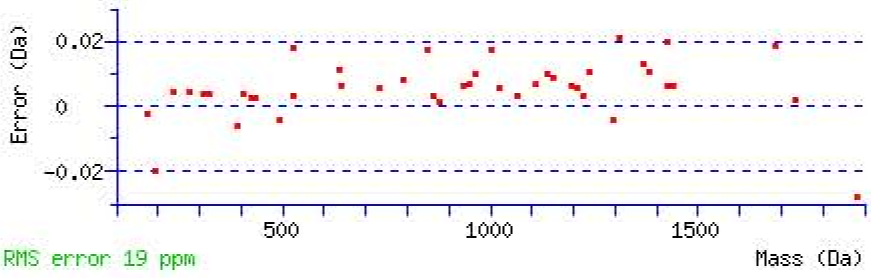
Match to Query 54774: 2174.063862 from(725.695230,3+) rtinseconds(1674) index(39890)
Title: Locus:1.1.1.3032.16 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

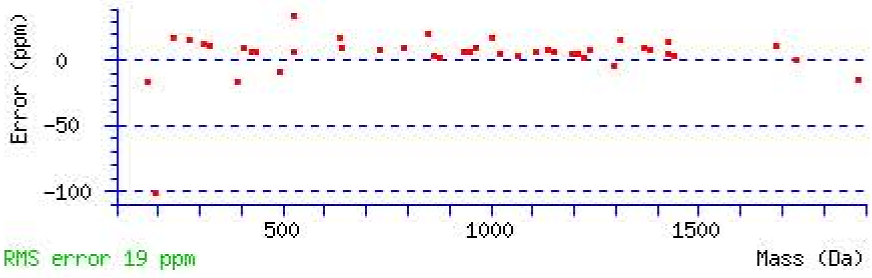
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2174.042664
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 79  Expect: 7.5e-008
Matches : 43/190 fragment ions using 78 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
78.8	2174.042664	0.021198	HTSVQTTSSGSGPFTDVR
2.8	2174.034729	0.029133	QNKAEGLGMVTEEGSGEK

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

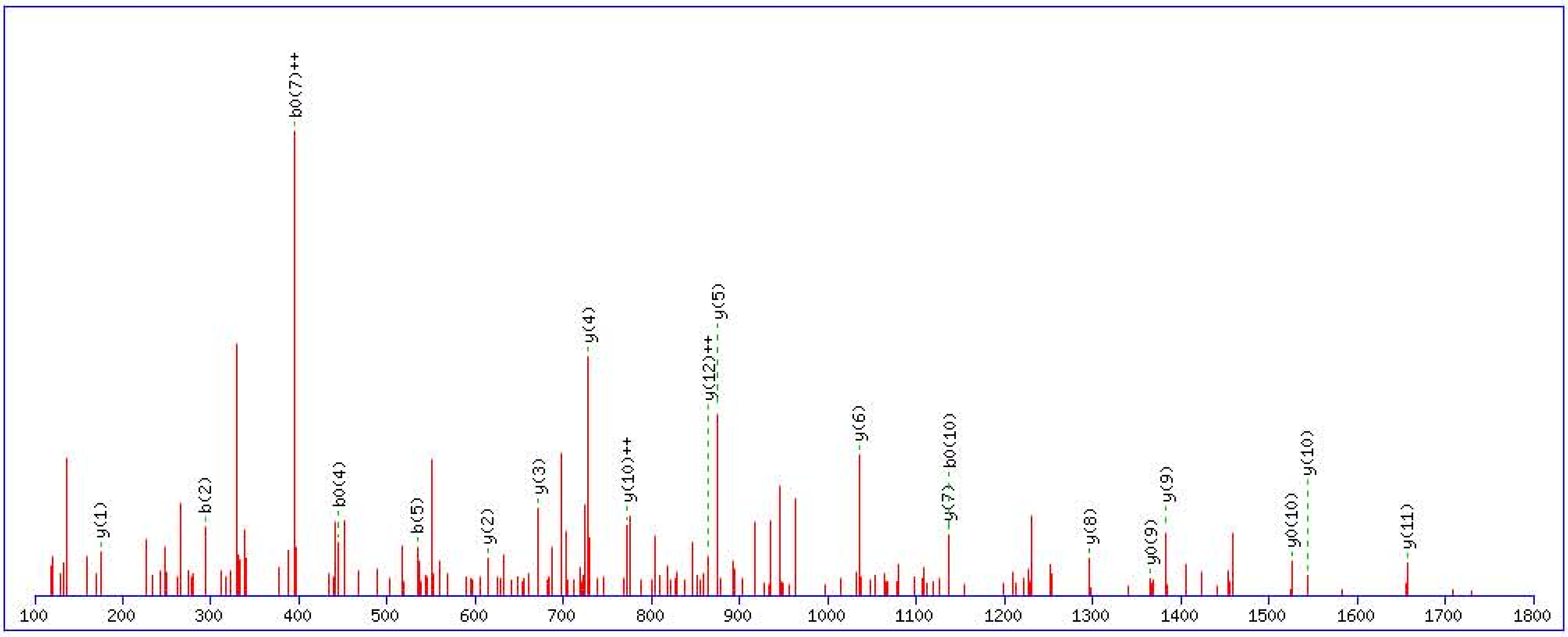
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYLGAICSCTCFGGQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

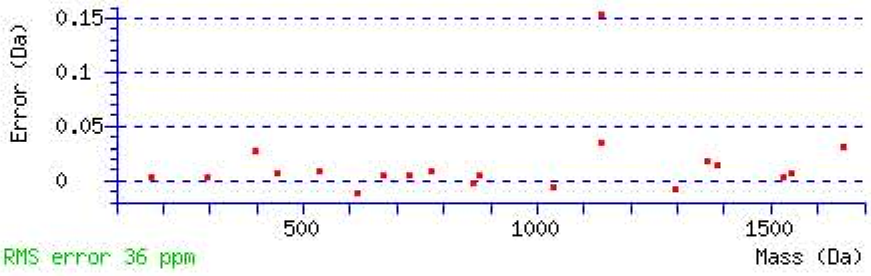
Match to Query 55128: 2188.981452 from(730.667760,3+) rtinseconds(2155) index(43286)
Title: Locus:1.1.1.3199.18 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

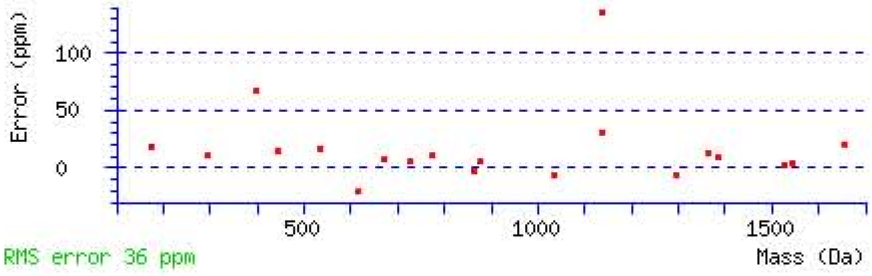
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2188.952637
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0021
Matches : 20/140 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							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
36.7	2188.952637	0.028815	EYLGAICSCTCFGGQR

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

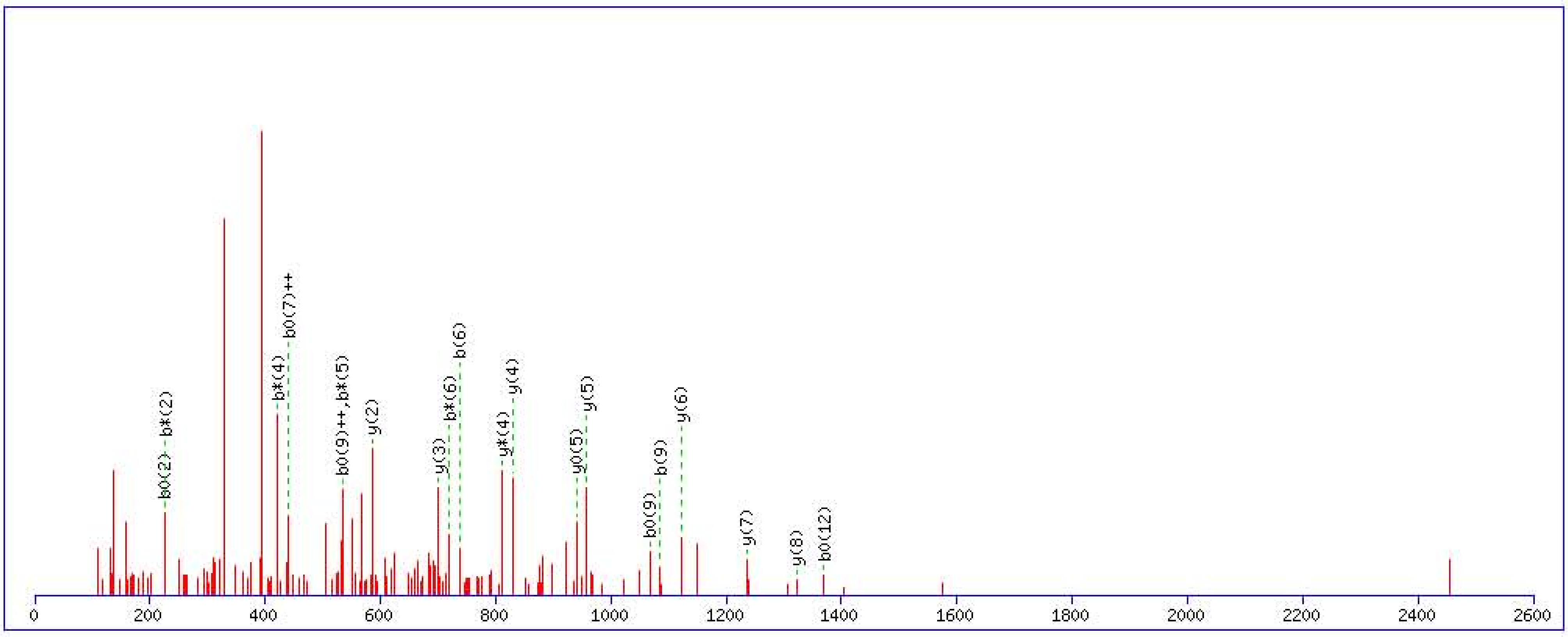
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDGHLWCSTTSNYEQDQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

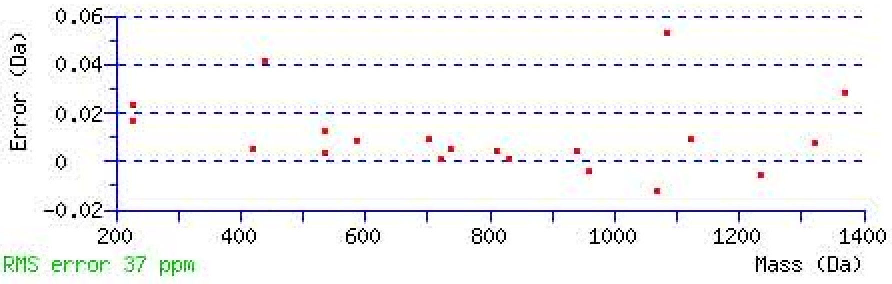
Match to Query 63232: 2507.110016 from(627.784780,4+) rtinseconds(1763) index(40534)
Title: Locus:1.1.1.3063.16 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

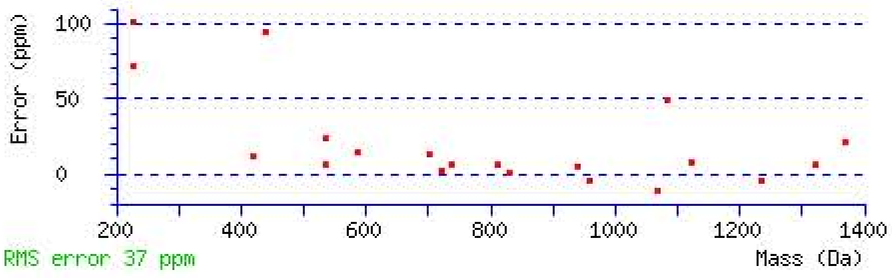
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 36  Expect: 0.0015
Matches : 20/198 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	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
36.4	2507.084564	0.025452	QDGHLWCSTTSNYEQDQK
20.9	2507.084564	0.025452	QDGHLWCSTTSNYEQDQK

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

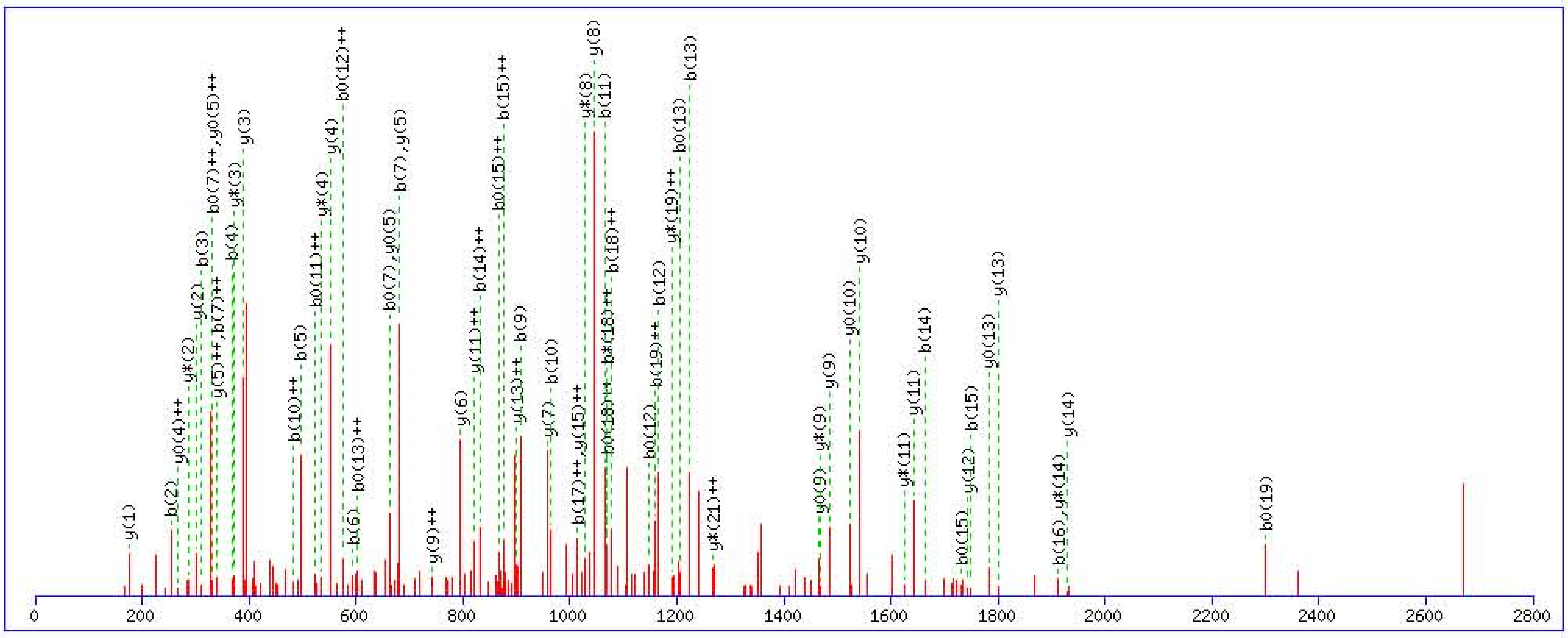
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

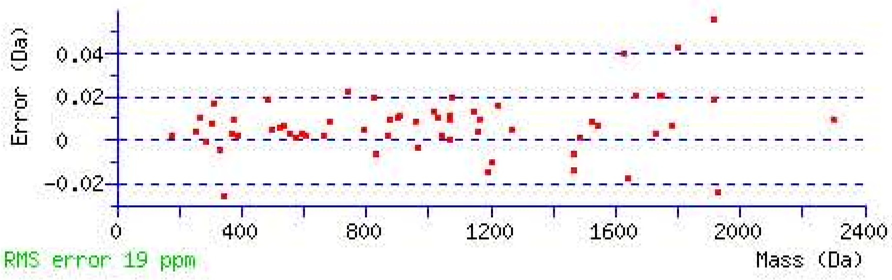
Match to Query 65722: 2706.282312 from(903.101380,3+) rtinseconds(1516) index(38898)
Title: Locus:1.1.1.2977.17 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

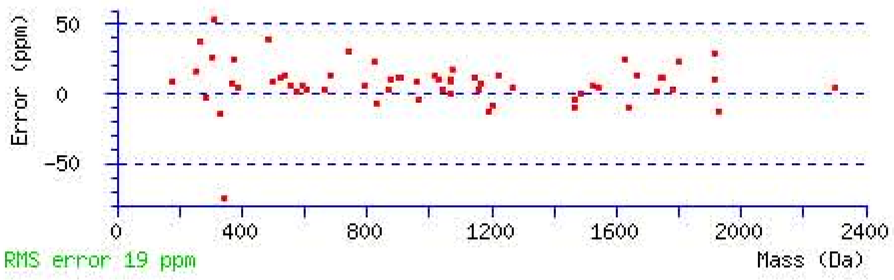
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 72 **Expect:** 1.3e-006
Matches : 67/240 fragment ions using 131 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
71.7	2706.245621	0.036691	RPGGEPSPEGTTGQSYNQYSQR
71.6	2706.245621	0.036691	RPGGEPSPEGTTGQSYNQYSQR
43.2	2706.245621	0.036691	RPGGEPSPEGTTGQSYNQYSQR

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

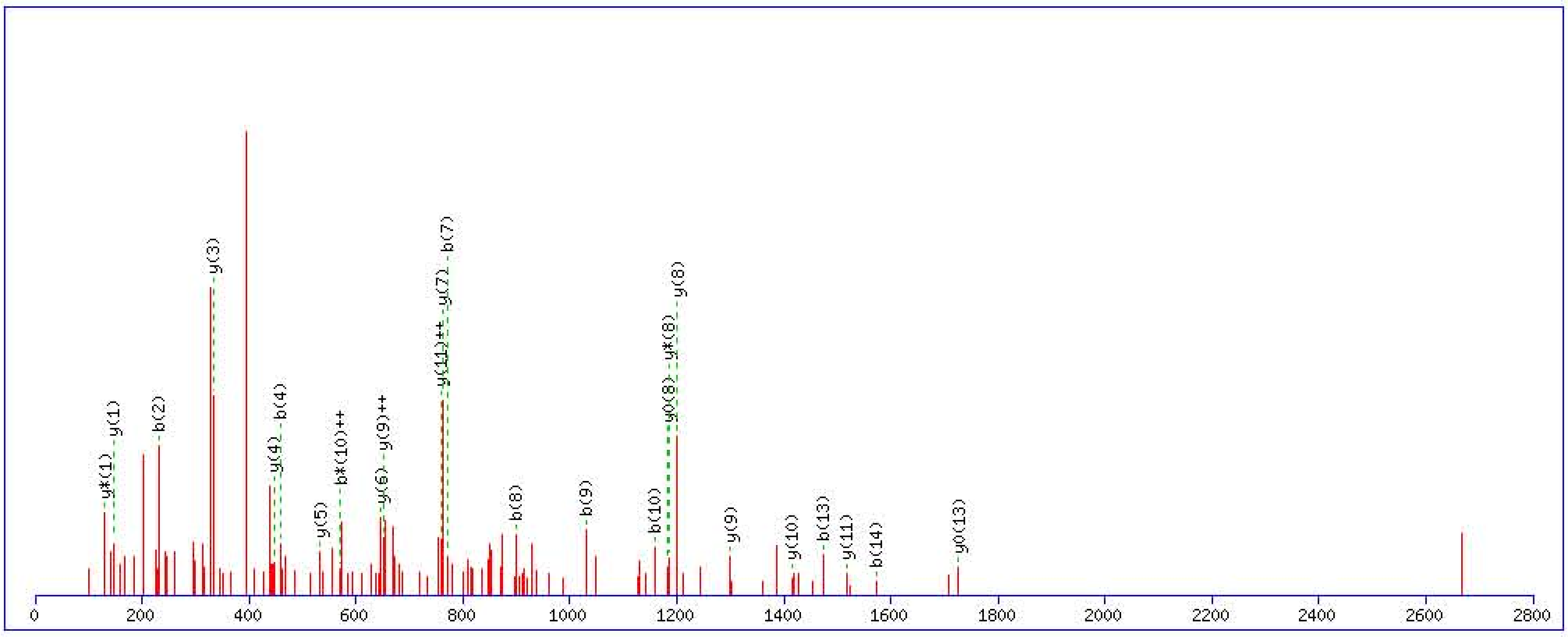
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEIDKPSQMQVTDVQDNSISVK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

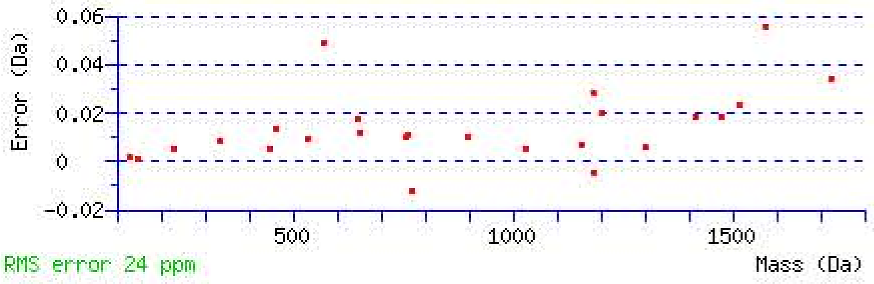
Match to Query 66716: 2772.399616 from(694.107180,4+) rtinseconds(1953) index(41890)
Title: Locus:1.1.1.3129.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

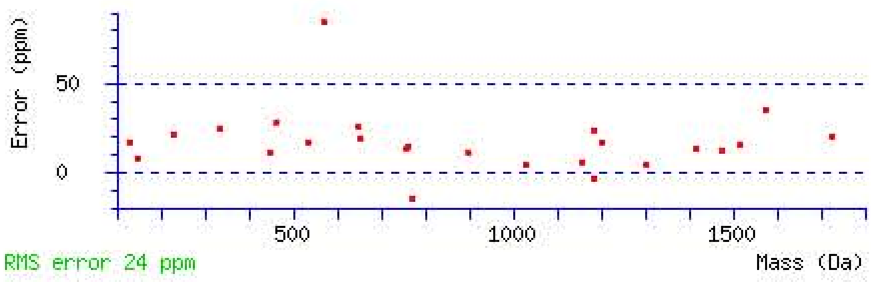
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2772.367386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 48 **Expect:** 0.00046
Matches : 25/240 fragment ions using 61 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							22
2	***231.097548***	116.052412			213.086983	107.047130	E	2672.326980	1336.667128	2655.300431	1328.153854	2654.316415	1327.661846	21
3	344.181612	172.594444			326.171047	163.589162	I	2543.284387	1272.145832	2526.257838	1263.632557	2525.273822	1263.140549	20
4	***459.208555***	230.107916			441.197990	221.102633	D	2430.200323	1215.603799	2413.173774	1207.090525	2412.189758	1206.598517	19
5	587.303518	294.155397	570.276969	285.642123	569.292953	285.150115	K	2315.173380	1158.090328	2298.146831	1149.577053	2297.162815	1149.085046	18
6	684.356282	342.681779	667.329733	334.168505	666.345717	333.676497	P	2187.078417	1094.042847	2170.051868	1085.529572	2169.067852	1085.037564	17
7	***771.388310***	386.197793	754.361761	377.684519	753.377745	377.192511	S	2090.025653	1045.516465	2072.999104	1037.003190	2072.015088	1036.511182	16
8	***899.446888***	450.227082	882.420339	441.713808	881.436323	441.221800	Q	2002.993625	1002.000451	1985.967076	993.487176	1984.983060	992.995168	15
9	***1030.487373***	515.747325	1013.460824	507.234050	1012.476808	506.742042	M	1874.935047	937.971162	1857.908498	929.457887	1856.924482	928.965879	14
10	***1158.545951***	579.776614	1141.519402	571.263339	1140.535386	570.771331	Q	1743.894562	872.450919	1726.868013	863.937645	1725.883997	863.445637	13
11	1257.614365	629.310821	1240.587816	620.797546	1239.603800	620.305538	V	1615.835984	808.421630	1598.809435	799.908356	1597.825419	799.416348	12
12	1358.662044	679.834660	1341.635495	671.321386	1340.651479	670.829378	T	***1516.767570***	758.887423	1499.741021	750.374149	1498.757005	749.882141	11
13	***1473.688987***	737.348132	1456.662438	728.834857	1455.678422	728.342849	D	***1415.719891***	708.363584	1398.693342	699.850309	1397.709326	699.358301	10
14	***1572.757401***	786.882339	1555.730852	778.369064	1554.746836	777.877056	V	***1300.692948***	650.850112	1283.666399	642.336838	1282.682383	641.844830	9
15	2011.982727	1006.495002	1994.956178	997.981727	1993.972162	997.489719	Q	***1201.624534***	601.315905	1184.597985	592.802631	1183.613969	592.310623	8
16	2127.009670	1064.008473	2109.983121	1055.495199	2108.999105	1055.003191	D	***762.399208***	381.703242	745.372659	373.189968	744.388643	372.697960	7
17	2241.052597	1121.029937	2224.026048	1112.516662	2223.042032	1112.024654	N	***647.372265***	324.189771	630.345716	315.676496	629.361700	315.184488	6
18	2328.084625	1164.545951	2311.058076	1156.032676	2310.074060	1155.540668	S	***533.329338***	267.168307	516.302789	258.655033	515.318773	258.163025	5
19	2441.168689	1221.087983	2424.142140	1212.574708	2423.158124	1212.082700	I	***446.297310***	223.652293	429.270761	215.139019	428.286745	214.647011	4
20	2528.200717	1264.603997	2511.174168	1256.090722	2510.190152	1255.598714	S	***333.213246***	167.110261	316.186697	158.596986	315.202681	158.104978	3
21	2627.269131	1314.138204	2610.242582	1305.624929	2609.258566	1305.132921	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 TEIDKPSQMQVTDVQDNSISVK
(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	2772.367386	0.032230	TEIDKPSQMQVTDVQDNSISVK
10.2	2772.367386	0.032230	TEIDKPSQMQVTDVQDNSISVK

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

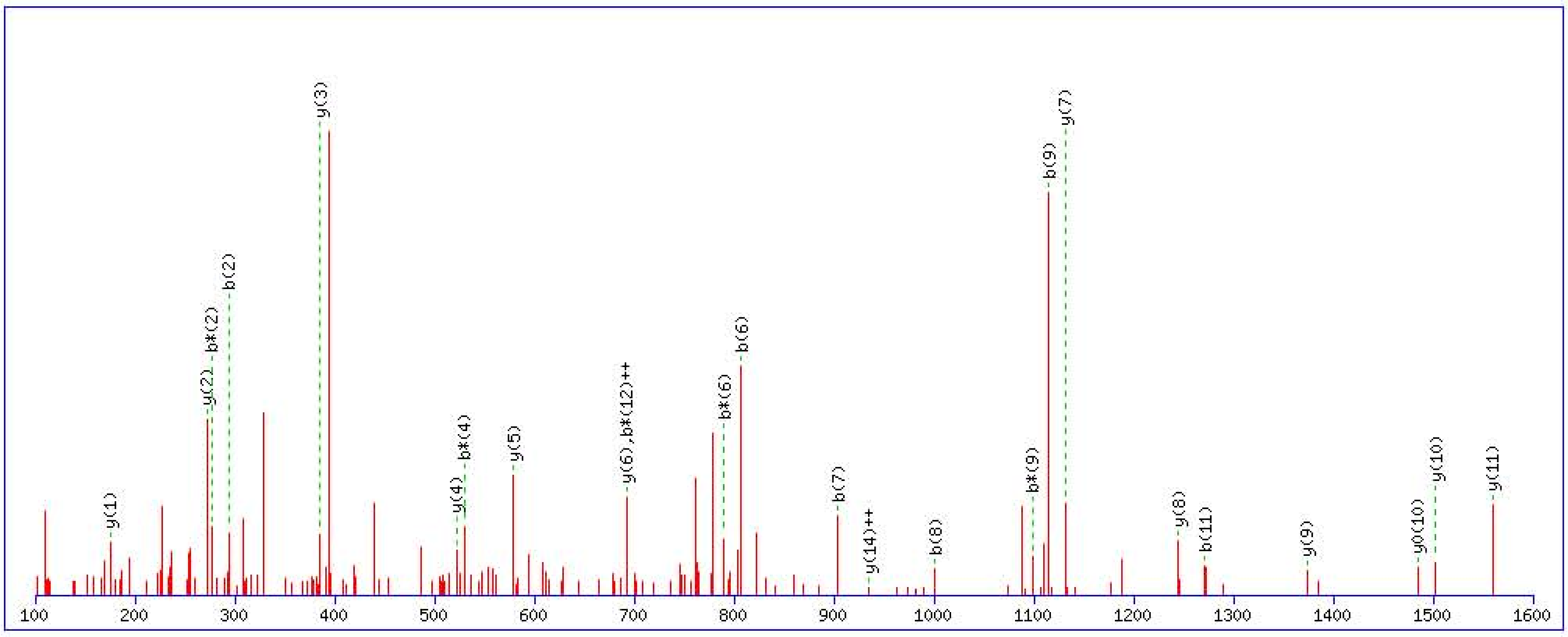
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HRPRPYPPNVGEEIQIGHIPR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

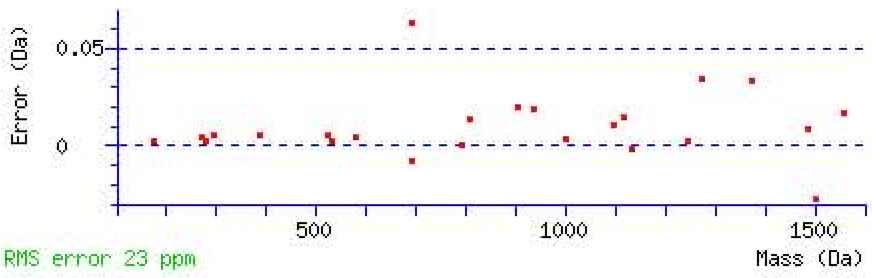
Match to Query 66722: 2772.499770 from(555.507230,5+) rtinseconds(1757) index(40481)
Title: Locus:1.1.1.3061.13 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

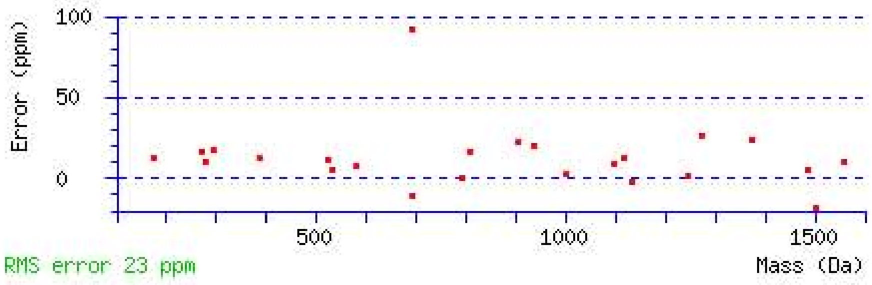
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2772.475815
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00022
Matches : 24/200 fragment ions using 55 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
48.5	2772.475815	0.023955	HRPRPYPPNVGEEIQIGHIPR

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

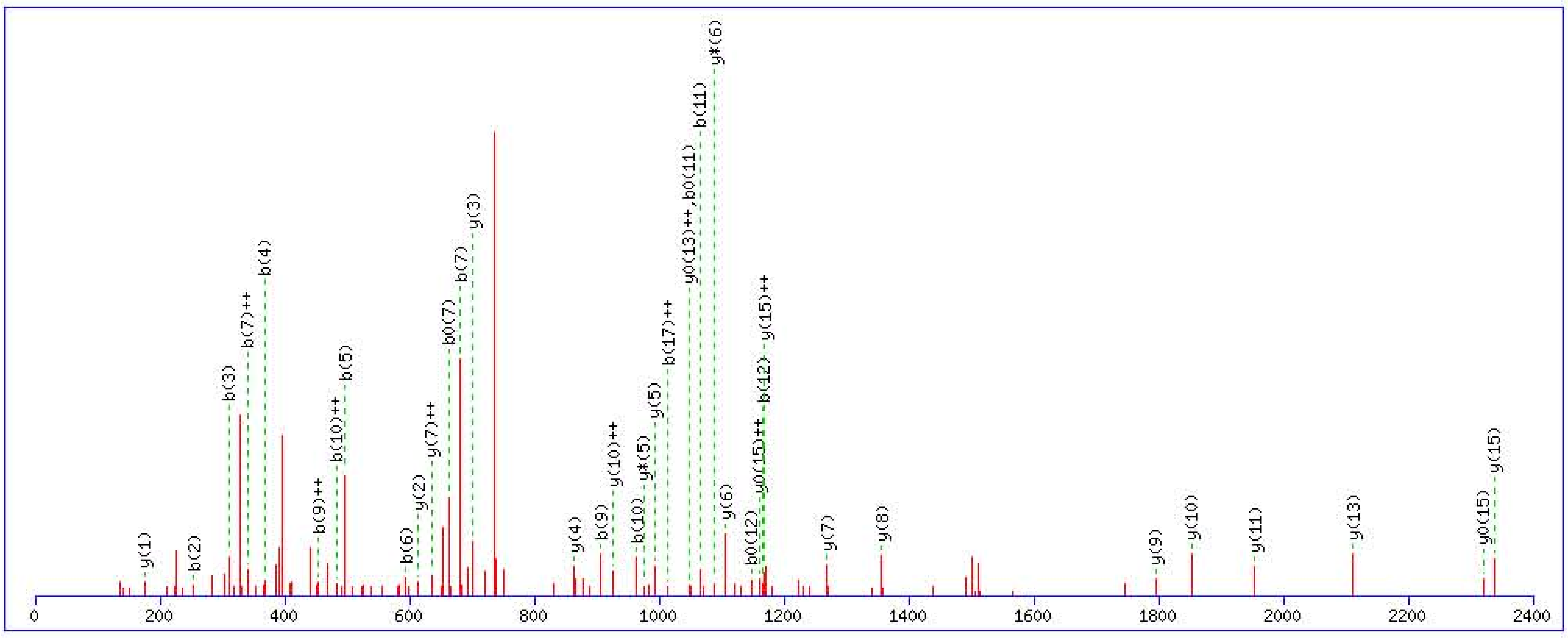
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

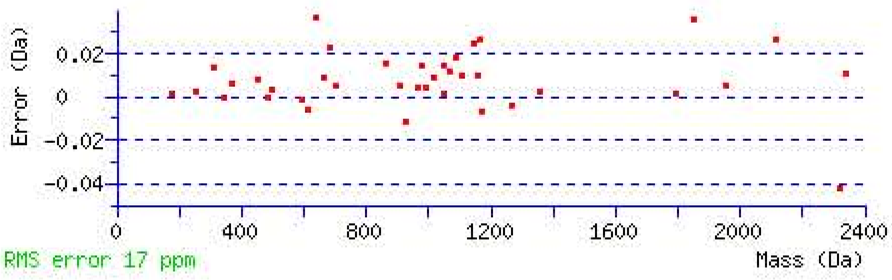
Match to Query 70547: 3017.448856 from(755.369490,4+) rtinseconds(1795) index(40743)
Title: Locus:1.1.1.3074.21 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

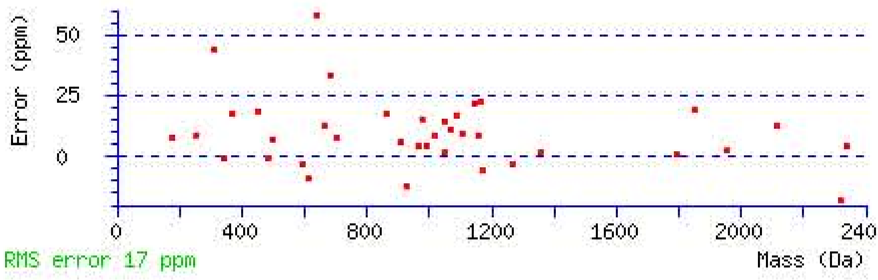
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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)
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 7.9e-006
Matches : 38/240 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	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
64.6	3017.412369	0.036487	RPGGEPSPEGTTGQSYNQYSQR
58.4	3017.412369	0.036487	RPGGEPSPEGTTGQSYNQYSQR
34.4	3017.412369	0.036487	RPGGEPSPEGTTGQSYNQYSQR

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

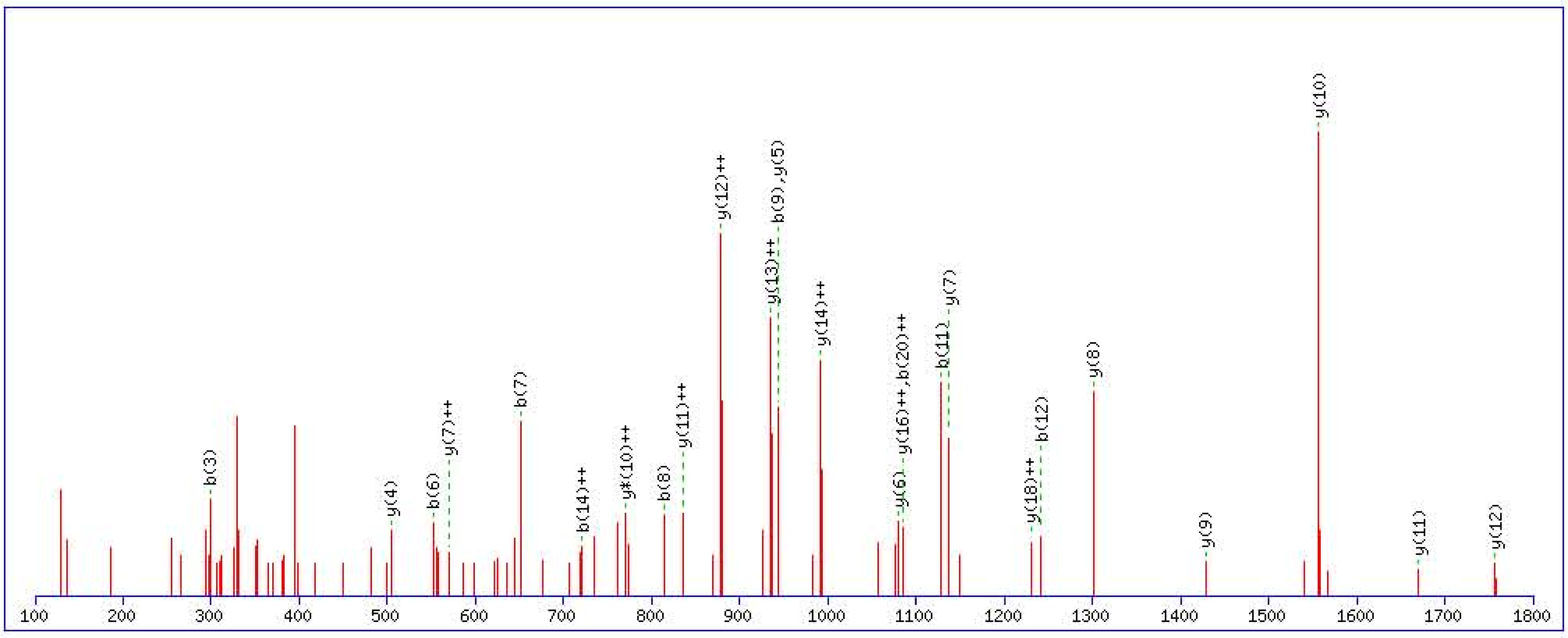
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLKPGVVYEGQLISIQQYGHQEVTR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

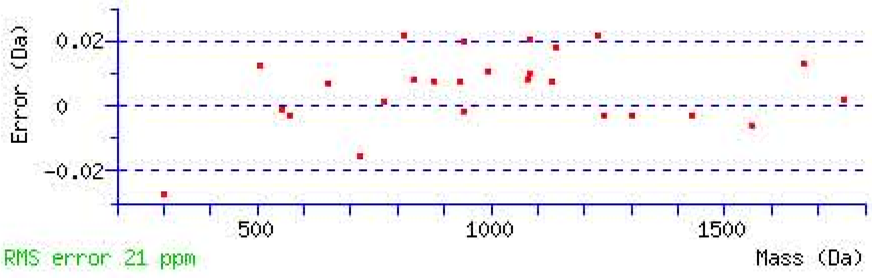
Match to Query 71423: 3109.681016 from(778.427530,4+) rtinseconds(2169) index(43413)
Title: Locus:1.1.1.3204.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

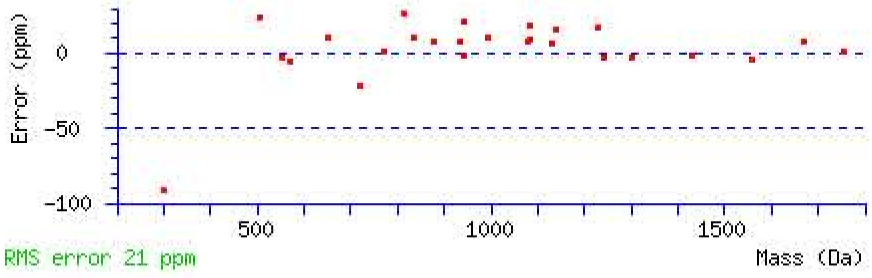
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3109.638275
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21    : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 2.8e-005
Matches : 26/266 fragment ions using 43 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							25
2	171.112804	86.060040					L	3053.624092	1527.315684	3036.597543	1518.802409	3035.613527	1518.310401	24
3	***299.207767***	150.107521	282.181218	141.594247			K	2940.540028	1470.773652	2923.513479	1462.260377	2922.529463	1461.768369	23
4	396.260531	198.633903	379.233982	190.120629			P	2812.445065	1406.726170	2795.418516	1398.212896	2794.434500	1397.720888	22
5	453.281995	227.144635	436.255446	218.631361			G	2715.392301	1358.199788	2698.365752	1349.686514	2697.381736	1349.194506	21
6	***552.350409***	276.678843	535.323860	268.165568			V	2658.370837	1329.689056	2641.344288	1321.175782	2640.360272	1320.683774	20
7	***651.418823***	326.213050	634.392274	317.699775			V	2559.302423	1280.154849	2542.275874	1271.641575	2541.291858	1271.149567	19
8	***814.482152***	407.744714	797.455603	399.231440			Y	2460.234009	1230.620642	2443.207460	1222.107368	2442.223444	1221.615360	18
9	***943.524745***	472.266011	926.498196	463.752736	925.514180	463.260728	E	2297.170680	1149.088978	2280.144131	1140.575703	2279.160115	1140.083695	17
10	1000.546209	500.776743	983.519660	492.263468	982.535644	491.771460	G	2168.128087	1084.567681	2151.101538	1076.054407	2150.117522	1075.562399	16
11	***1128.604787***	564.806032	1111.578238	556.292757	1110.594222	555.800749	Q	2111.106623	1056.056949	2094.080074	1047.543675	2093.096058	1047.051667	15
12	***1241.688851***	621.348063	1224.662302	612.834789	1223.678286	612.342781	L	1983.048045	992.027660	1966.021496	983.514386	1965.037480	983.022378	14
13	1354.772915	677.890095	1337.746366	669.376821	1336.762350	668.884813	I	1869.963981	935.485628	1852.937432	926.972354	1851.953416	926.480346	13
14	1441.804943	**721.406109**	1424.778394	712.892835	1423.794378	712.400827	S	***1756.879917***	878.943597	1739.853368	870.430322	1738.869352	869.938314	12
15	1554.889007	777.948141	1537.862458	769.434867	1536.878442	768.942859	I	***1669.847889***	835.427582	1652.821340	826.914308	1651.837324	826.422300	11
16	1682.947585	841.977430	1665.921036	833.464156	1664.937020	832.972148	Q	***1556.763825***	778.885551	1539.737276	770.372276	1538.753260	769.880268	10
17	1811.006163	906.006719	1793.979614	897.493445	1792.995598	897.001437	Q	***1428.705247***	714.856262	1411.678698	706.342987	1410.694682	705.850979	9
18	1974.069492	987.538384	1957.042943	979.025109	1956.058927	978.533101	Y	***1300.646669***	650.826973	1283.620120	642.313698	1282.636104	641.821690	8
19	2031.090956	1016.049116	2014.064407	1007.535841	2013.080391	1007.043833	G	***1137.583340***	569.295308	1120.556791	560.782034	1119.572775	560.290025	7
20	2168.149868	**1084.578572**	2151.123319	1076.065297	2150.139303	1075.573289	H	***1080.561876***	540.784576	1063.535327	532.271302	1062.551311	531.779293	6
21	2607.375194	1304.191235	2590.348645	1295.677960	2589.364629	1295.185952	Q	***943.502964***	472.255120	926.476415	463.741846	925.492399	463.249838	5
22	2736.417787	1368.712531	2719.391238	1360.199257	2718.407222	1359.707249	E	***504.277638***	252.642457	487.251089	244.129182	486.267073	243.637174	4
23	2835.486201	1418.246738	2818.459652	1409.733464	2817.475636	1409.241456	V	375.235045	188.121160	358.208496	179.607886	357.224480	179.115878	3
24	2936.533880	1468.770578	2919.507331	1460.257303	2918.523315	1459.765295	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.7	3109.638275	0.042741	GLKPGVVYEGQLISIQQYGHQEVTR
29.9	3109.638275	0.042741	GLKPGVVYEGQLISIQQYGHQEVTR
24.5	3109.638275	0.042741	GLKPGVVYEGQLISIQQYGHQEVTR
0.3	3109.638275	0.042741	GLKPGVVYEGQLISIQQYGHQEVTR

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

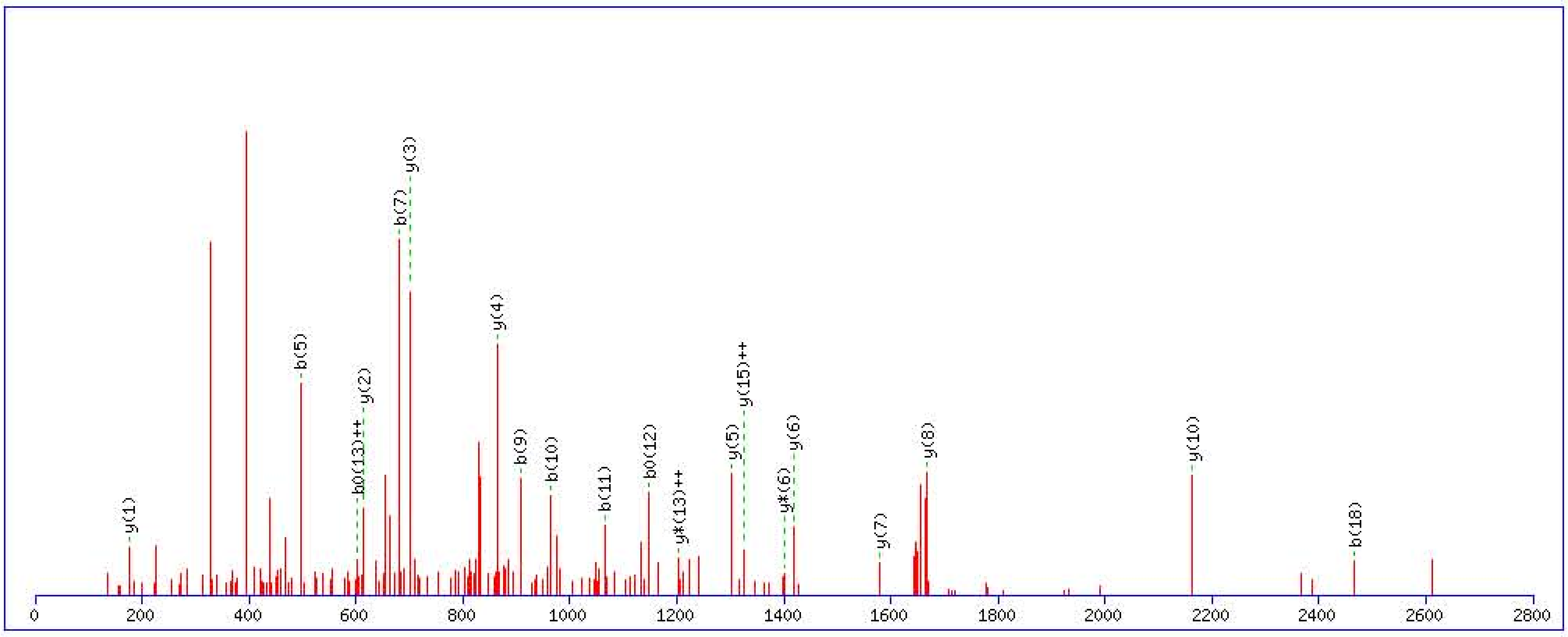
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPEGTTGQSYNQYSQR**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

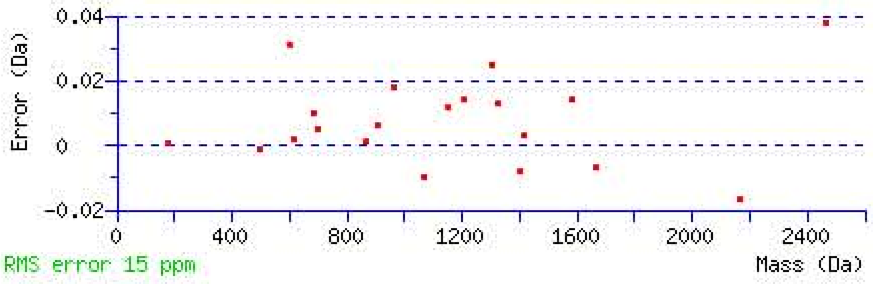
Match to Query 75495: 3328.628616 from(833.164430,4+) rtinseconds(2009) index(42272)
Title: Locus:1.1.1.3148.16 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

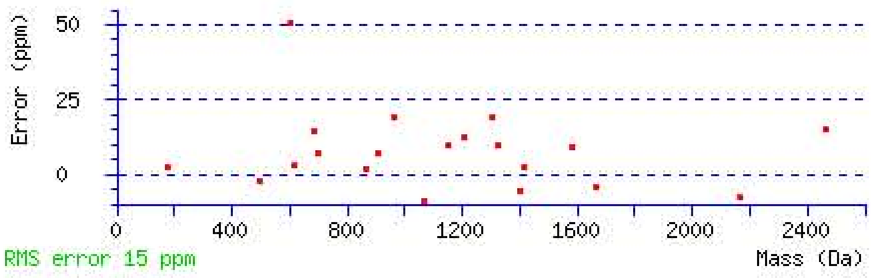
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3328.579117
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Q18     : Biotin:Thermo-21345 (Q)
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00072
Matches : 20/240 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	157.108387	79.057831	140.081838	70.544557			R							22
2	254.161151	127.584213	237.134602	119.070939			P	3173.485291	1587.246283	3156.458742	1578.733009	3155.474726	1578.241001	21
3	311.182615	156.094945	294.156066	147.581671			G	3076.432527	1538.719901	3059.405978	1530.206627	3058.421962	1529.714619	20
4	368.204079	184.605677	351.177530	176.092403			G	3019.411063	1510.209169	3002.384514	1501.695895	3001.400498	1501.203887	19
5	***497.246672***	249.126974	480.220123	240.613700	479.236107	240.121692	E	2962.389599	1481.698438	2945.363050	1473.185163	2944.379034	1472.693155	18
6	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	P	2833.347006	1417.177141	2816.320457	1408.663866	2815.336441	1408.171858	17
7	***681.331464***	341.169370	664.304915	332.656095	663.320899	332.164087	S	2736.294242	1368.650759	2719.267693	1360.137484	2718.283677	1359.645476	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	2649.262214	1325.134745	2632.235665	1316.621470	2631.251649	1316.129462	15
9	***907.426821***	454.217049	890.400272	445.703774	889.416256	445.211766	E	2552.209450	1276.608363	2535.182901	1268.095088	2534.198885	1267.603080	14
10	***964.448285***	482.727781	947.421736	474.214506	946.437720	473.722498	G	2423.166857	1212.087066	2406.140308	1203.573792	2405.156292	1203.081784	13
11	***1065.495964***	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	2366.145393	1183.576334	2349.118844	1175.063060	2348.134828	1174.571052	12
12	1166.543643	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	2265.097714	1133.052495	2248.071165	1124.539220	2247.087149	1124.047212	11
13	1223.565107	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	***2164.050035***	1082.528655	2147.023486	1074.015381	2146.039470	1073.523373	10
14	1662.790433	831.898854	1645.763884	823.385580	1644.779868	822.893572	Q	2107.028571	1054.017924	2090.002022	1045.504649	2089.018006	1045.012641	9
15	1749.822461	875.414869	1732.795912	866.901594	1731.811896	866.409586	S	***1667.803245***	834.405261	1650.776696	825.891986	1649.792680	825.399978	8
16	1912.885790	956.946533	1895.859241	948.433259	1894.875225	947.941251	Y	***1580.771217***	790.889247	1563.744668	782.375972	1562.760652	781.883964	7
17	2026.928717	1013.967997	2009.902168	1005.454722	2008.918152	1004.962714	N	***1417.707888***	709.357582	1400.681339	700.844308	1399.697323	700.352300	6
18	***2466.154043***	1233.580659	2449.127494	1225.067385	2448.143478	1224.575377	Q	***1303.664961***	652.336119	1286.638412	643.822844	1285.654396	643.330836	5
19	2629.217372	1315.112324	2612.190823	1306.599049	2611.206807	1306.107041	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
20	2716.249400	1358.628338	2699.222851	1350.115063	2698.238835	1349.623056	S	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
21	3155.474726	1578.241001	3138.448177	1569.727727	3137.464161	1569.235719	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
45.6	3328.579117	0.049499	RPGGEPSPEGTTGQSYNQYSQR

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

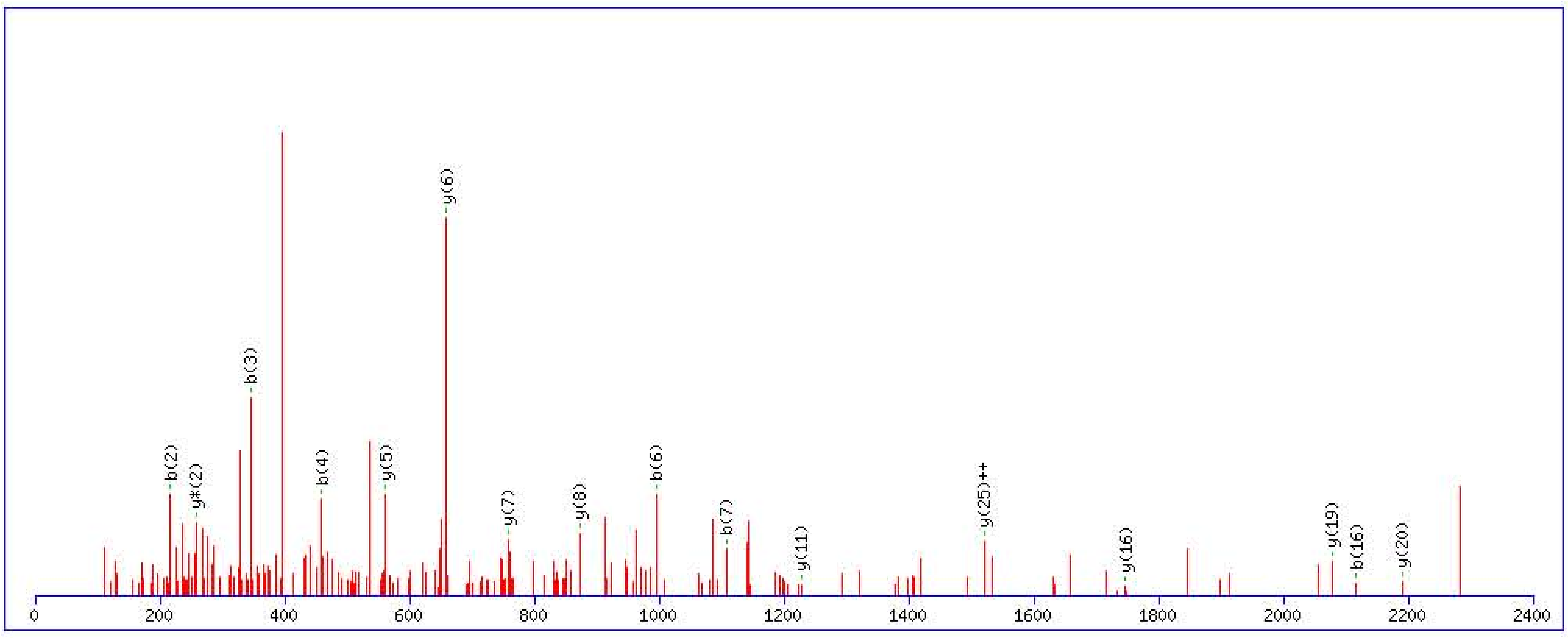
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDELPQLVTLPHPNLHGPEILDVPSTVQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

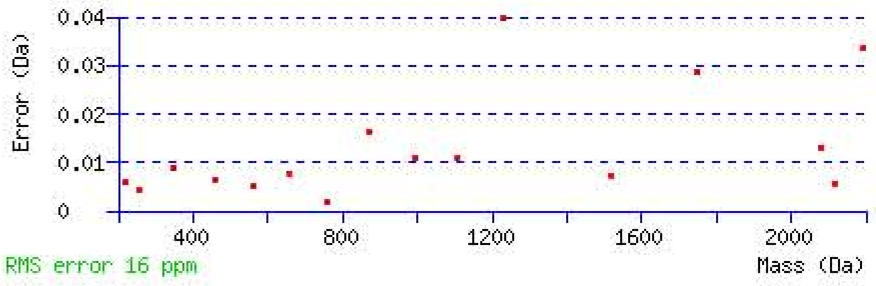
Match to Query 77376: 3497.910870 from(700.589450,5+) rtinseconds(2575) index(46084)
Title: Locus:1.1.1.3345.9 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

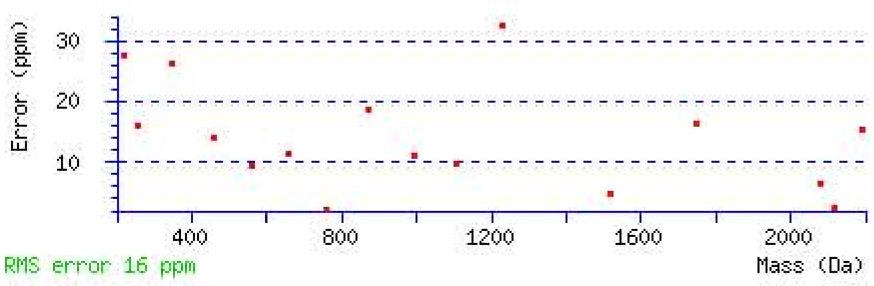
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3497.859238
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.011
Matches : 16/320 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	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
28.5	3497.859238	0.051632	TDELPQLVTLPHPNLHGPEILDVPSTVQK

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

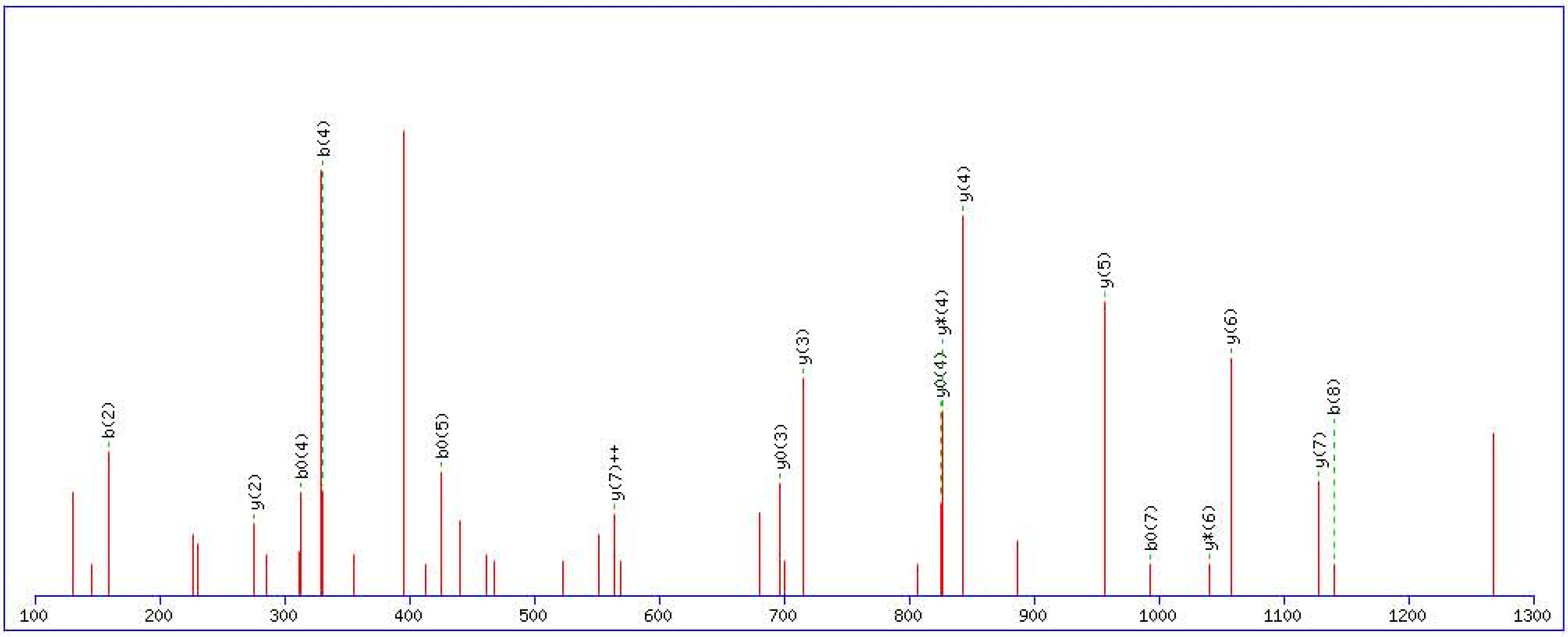
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAATLQQEK**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

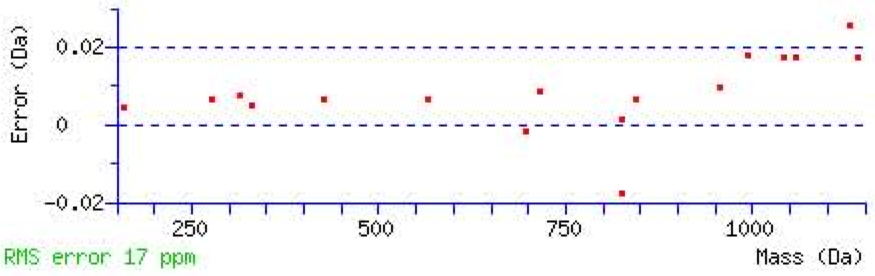
Match to Query 26585: 1285.682228 from(643.848390,2+) rtinseconds(1488) index(38686)
Title: Locus:1.1.1.2967.24 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

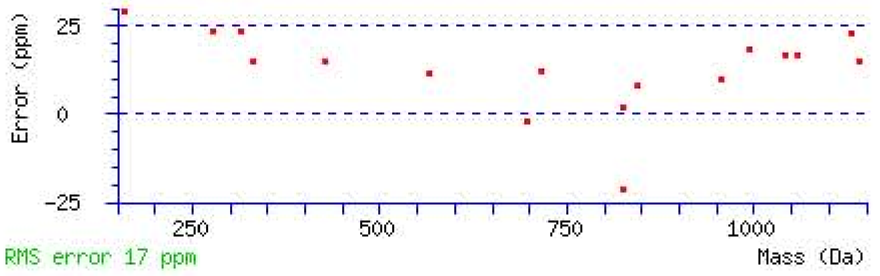
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1285.669998
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.0067
Matches : 17/84 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							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
33.9	1285.669998	0.012230	SAATLQQEK
22.3	1285.669998	0.012230	SAATLQQEK
10.3	1285.699860	-0.017632	RCSQLLAK
8.3	1285.688614	-0.006386	SMANQLLAK
5.9	1285.669998	0.012230	ASLDQGKEK
3.8	1285.681244	0.000984	QEQSTRVK

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

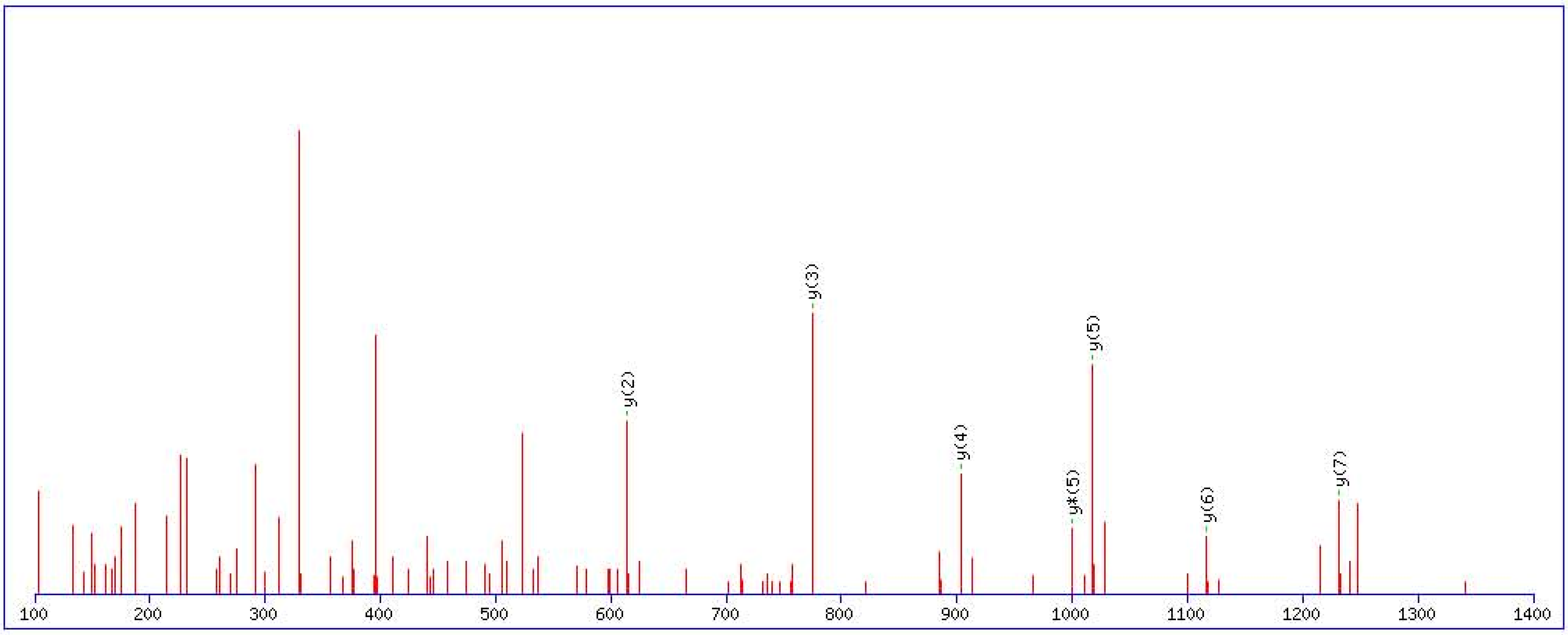
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCVDVNECQR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

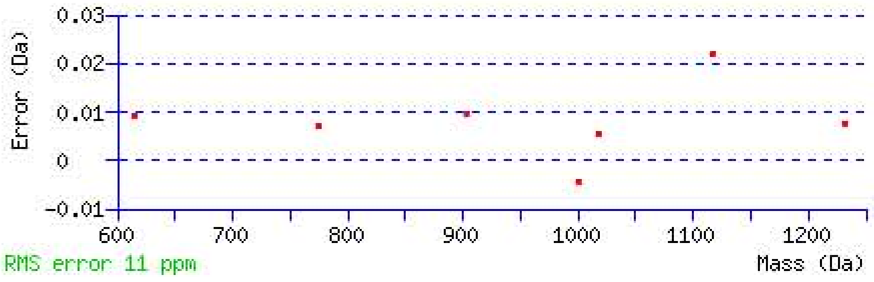
Match to Query 39645: 1620.696702 from(541.239510,3+) rtinseconds(1719) index(40185)
Title: Locus:1.1.1.3048.13 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

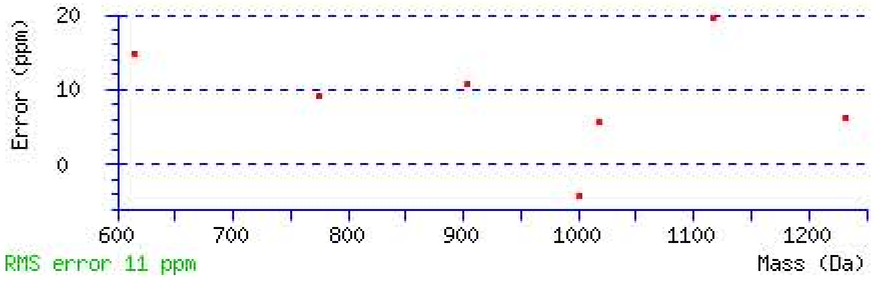
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1620.688080
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0027
Matches : 7/86 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	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
32.6	1620.688080	0.008622	MCVDVNECQR

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

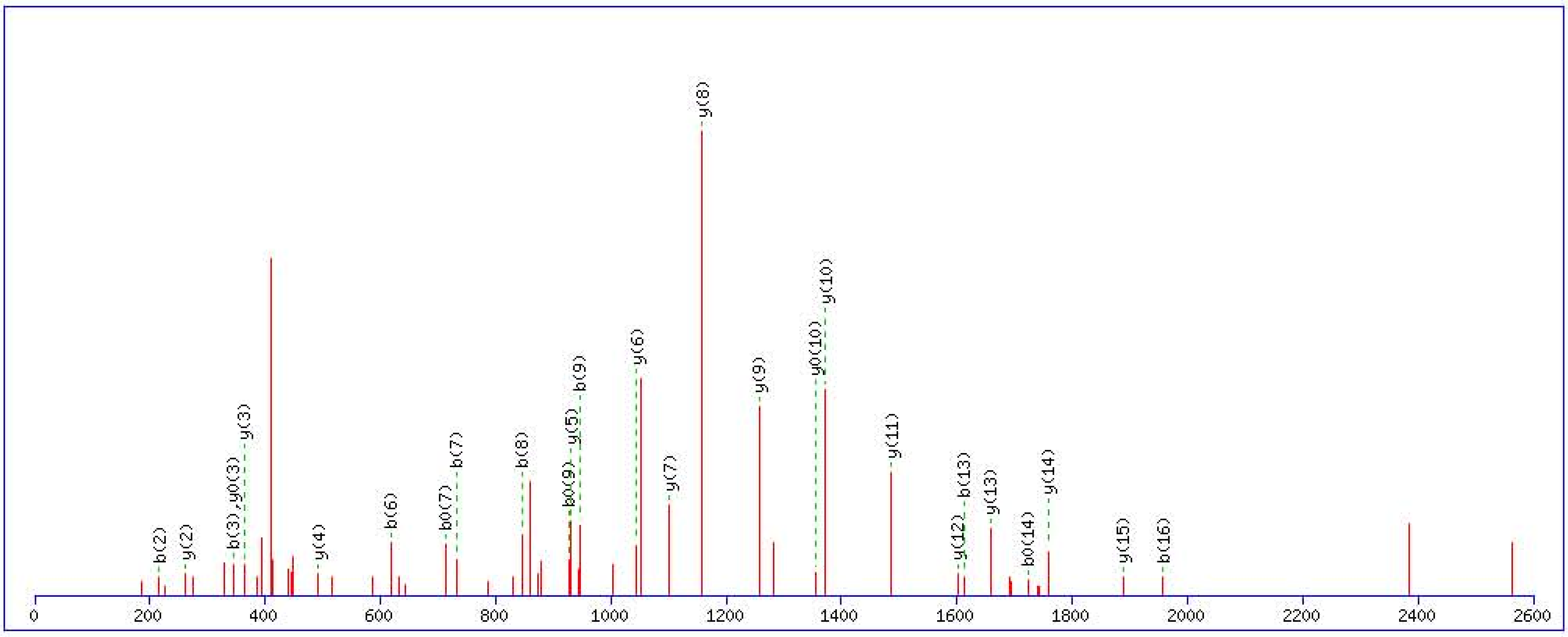
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQETGDLDVGGLQETDK**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

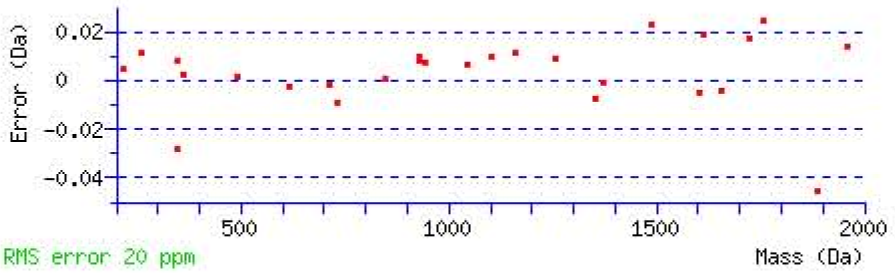
Match to Query 53170: 2102.014448 from(1052.014500,2+) rtinseconds(2020) index(42349)
Title: Locus:1.1.1.3152.21 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

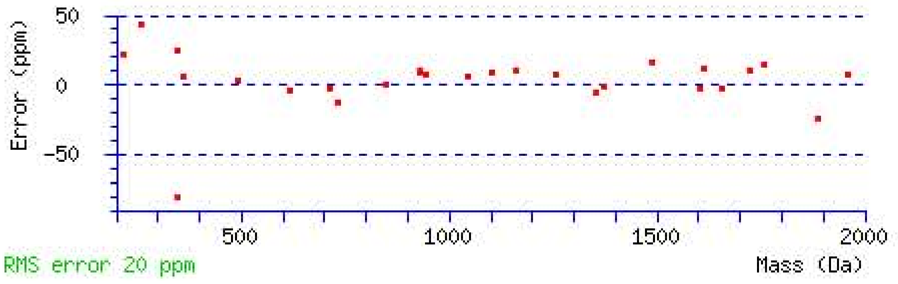
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2101.983780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 111 **Expect:** 4e-011
Matches : 27/188 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	88.039304	44.523290			70.028739	35.518008	S							17
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	Q	2015.959015	1008.483146	1998.932466	999.969871	1997.948450	999.477863	16
3	**345.140475**	173.073875	328.113926	164.560601	327.129910	164.068593	E	***1887.900437***	944.453857	1870.873888	935.940582	1869.889872	935.448574	15
4	446.188154	223.597715	429.161605	215.084441	428.177589	214.592433	T	***1758.857844***	879.932560	1741.831295	871.419286	1740.847279	870.927278	14
5	503.209618	252.108447	486.183069	243.595172	485.199053	243.103164	G	***1657.810165***	829.408721	1640.783616	820.895446	1639.799600	820.403438	13
6	**618.236561**	309.621919	601.210012	301.108644	600.225996	300.616636	D	***1600.788701***	800.897989	1583.762152	792.384714	1582.778136	791.892706	12
7	**731.320625**	366.163951	714.294076	357.650676	713.310060	357.158668	L	***1485.761758***	743.384517	1468.735209	734.871243	1467.751193	734.379235	11
8	**846.347568**	423.677422	829.321019	415.164148	828.337003	414.672140	D	***1372.677694***	686.842485	1355.651145	678.329211	1354.667129	677.837203	10
9	**945.415982**	473.211629	928.389433	464.698354	927.405417	464.206347	V	***1257.650751***	629.329014	1240.624202	620.815739	1239.640186	620.323731	9
10	1002.437446	501.722361	985.410897	493.209087	984.426881	492.717079	G	***1158.582337***	579.794807	1141.555788	571.281532	1140.571772	570.789524	8
11	1059.458910	530.233093	1042.432361	521.719819	1041.448345	521.227811	G	***1101.560873***	551.284075	1084.534324	542.770800	1083.550308	542.278792	7
12	1172.542974	586.775125	1155.516425	578.261851	1154.532409	577.769842	L	***1044.539409***	522.773343	1027.512860	514.260068	1026.528844	513.768060	6
13	**1611.768300**	806.387788	1594.741751	797.874514	1593.757735	797.382505	Q	***931.455345***	466.231311	914.428796	457.718036	913.444780	457.226028	5
14	1740.810893	870.909085	1723.784344	862.395810	1722.800328	861.903802	E	***492.230019***	246.618648	475.203470	238.105373	474.219454	237.613365	4
15	1841.858572	921.432924	1824.832023	912.919650	1823.848007	912.427642	T	***363.187426***	182.097351	346.160877	173.584077	345.176861	173.092069	3
16	**1956.885515**	978.946396	1939.858966	970.433121	1938.874950	969.941113	D	***262.139747***	131.573512	245.113198	123.060237	244.129182	122.568229	2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
111.0	2101.983780	0.030668	SQETGDLDVGGLQETDK
0.1	2101.988480	0.025968	MQQVGGNSQTESSLPGR

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

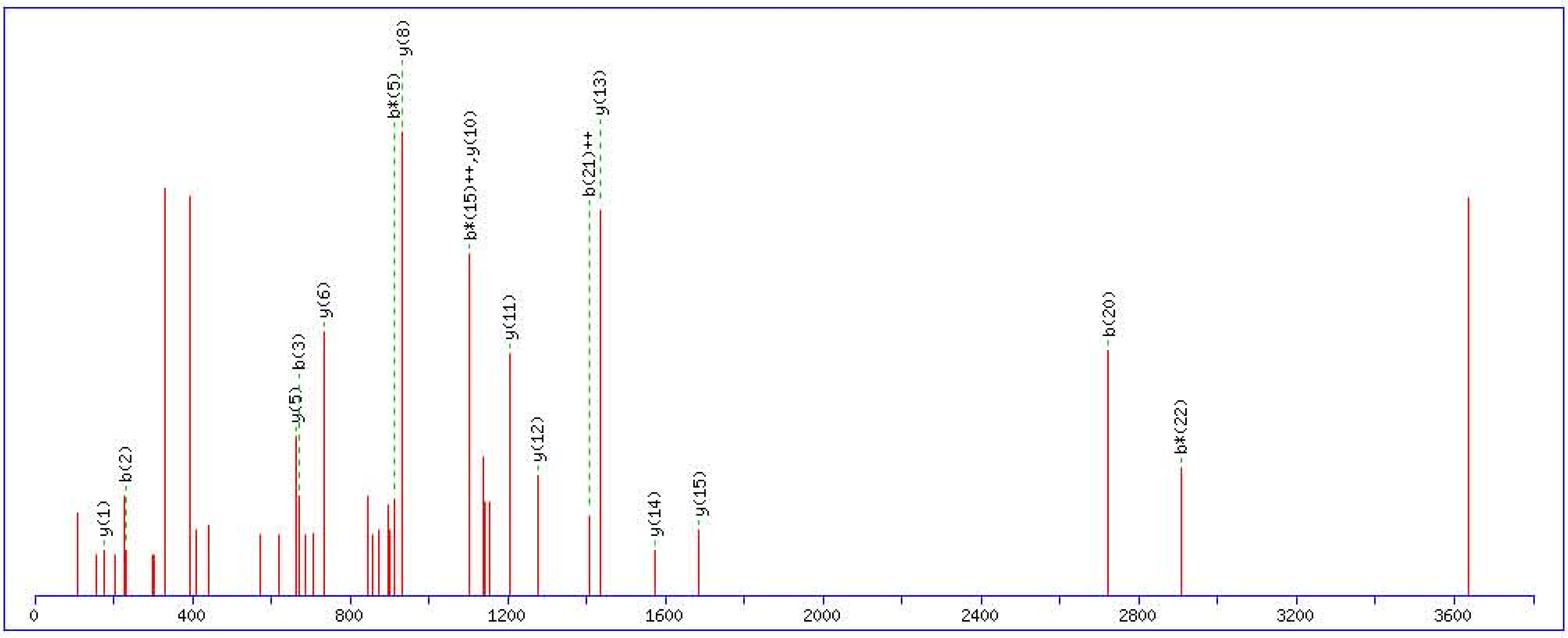
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

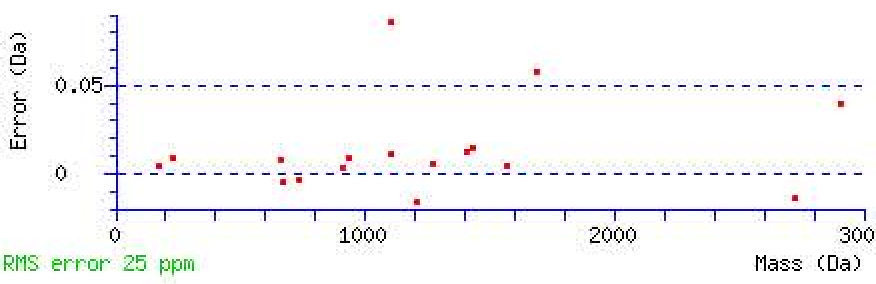
Match to Query 79025: 3653.658496 from(914.421900,4+) rtinseconds(1956) index(78627)
Title: Locus:1.1.1.2031.26 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

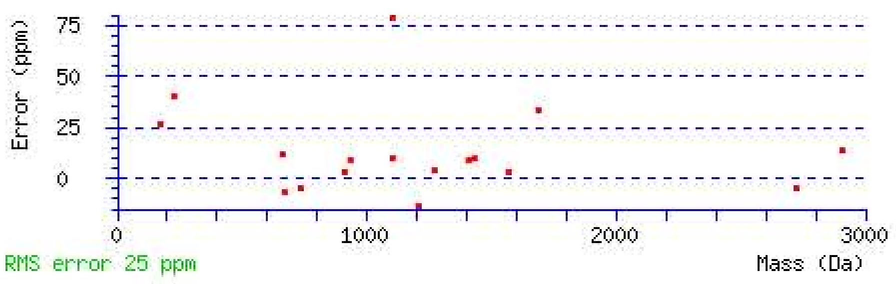
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 6.5e-005
Matches : 17/312 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	**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
52.4	3653.615311	0.043185	MVQEQCCHSQLEELHCATGISLANEQDR
50.0	3653.615311	0.043185	MVQEQCCHSQLEELHCATGISLANEQDR
50.0	3653.615311	0.043185	MVQEQCCHSQLEELHCATGISLANEQDR

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

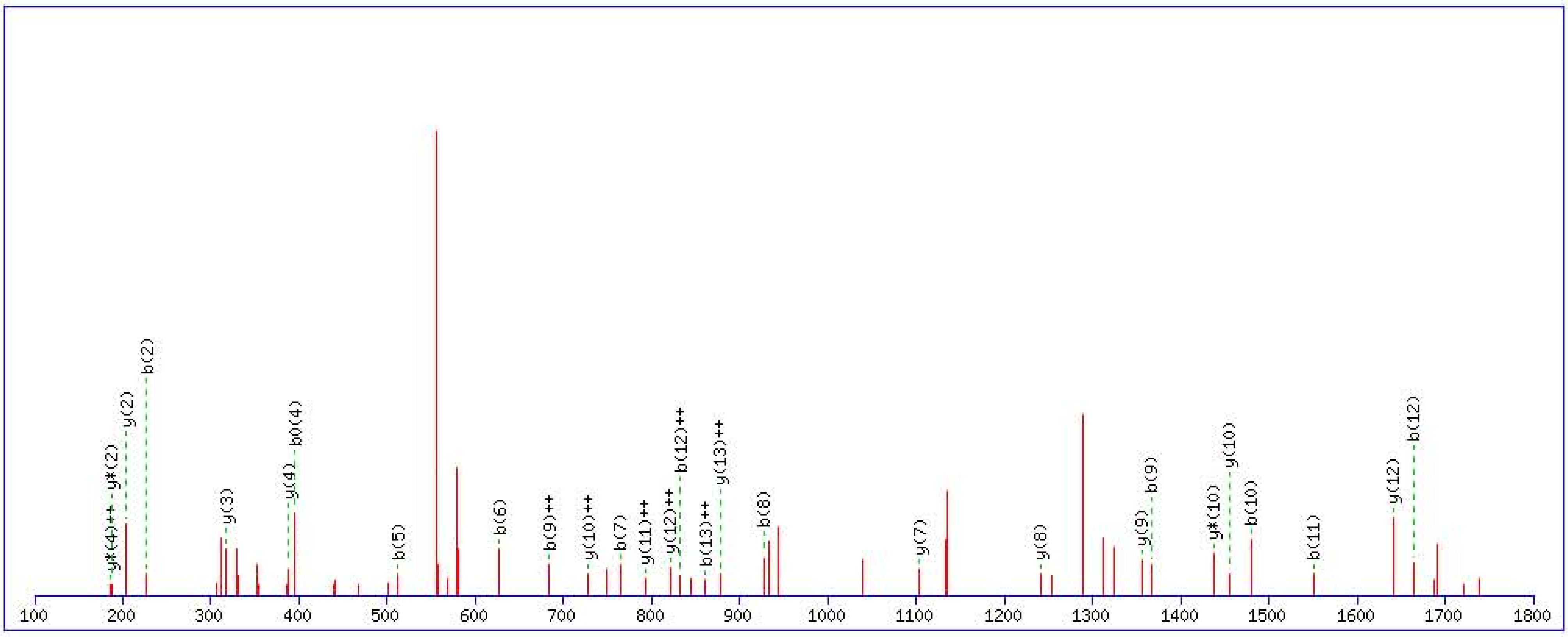
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLGEVDHYQLALGK**
Found in **FCN3_HUMAN**, Ficolin-3 OS=Homo sapiens GN=FCN3 PE=1 SV=2

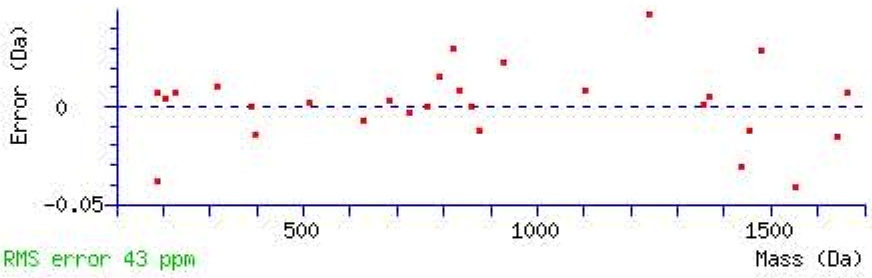
Match to Query 46900: 1866.025448 from(934.020000,2+) rtinseconds(2175) index(25962)
Title: Locus:1.1.1.2899.15 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

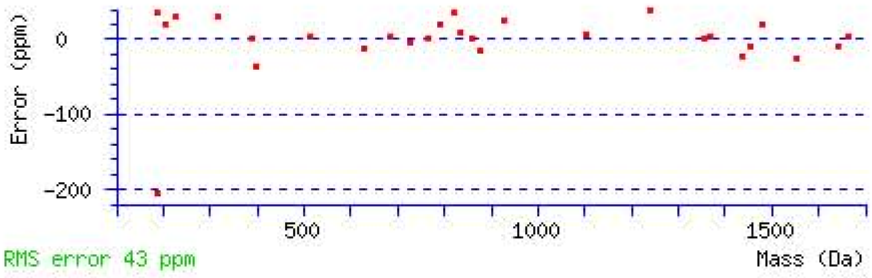
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1866.007324
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.004
Matches : 28/118 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	114.091340	57.549308					L							14
2	***227.175404***	114.091340					L	1753.930555	877.468916	1736.904006	868.955641	1735.919990	868.463633	13
3	284.196868	142.602072					G	**1640.846491**	820.926884	1623.819942	812.413609	1622.835926	811.921601	12
4	413.239461	207.123369			395.228896	198.118086	E	1583.825027	792.416152	1566.798478	783.902877	1565.814462	783.410869	11
5	***512.307875***	256.657576			494.297310	247.652293	V	**1454.782434**	727.894855	1437.755885	719.381581	1436.771869	718.889572	10
6	***627.334818***	314.171047			609.324253	305.165765	D	**1355.714020**	678.360648	1338.687471	669.847374	1337.703455	669.355366	9
7	***764.393730***	382.700503			746.383165	373.695221	H	**1240.687077**	620.847177	1223.660528	612.333902			8
8	***927.457059***	464.232168			909.446494	455.226885	Y	**1103.628165**	552.317721	1086.601616	543.804446			7
9	***1366.682385***	**683.844831**	1349.655836	675.331556	1348.671820	674.839548	Q	940.564836	470.786056	923.538287	462.272782			6
10	***1479.766449***	740.386863	1462.739900	731.873588	1461.755884	731.381580	L	501.339510	251.173393	484.312961	242.660118			5
11	***1550.803563***	775.905420	1533.777014	767.392145	1532.792998	766.900137	A	**388.255446**	194.631361	371.228897	186.118086			4
12	***1663.887627***	**832.447452**	1646.861078	823.934177	1645.877062	823.442169	L	**317.218332**	159.112804	300.191783	150.599529			3
13	1720.909091	**860.958184**	1703.882542	852.444909	1702.898526	851.952901	G	**204.134268**	102.570772	187.107719	94.057497			2
14							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLGEVDHYQLALGK
(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	1866.007324	0.018124	LLGEVDHYQLALGK

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

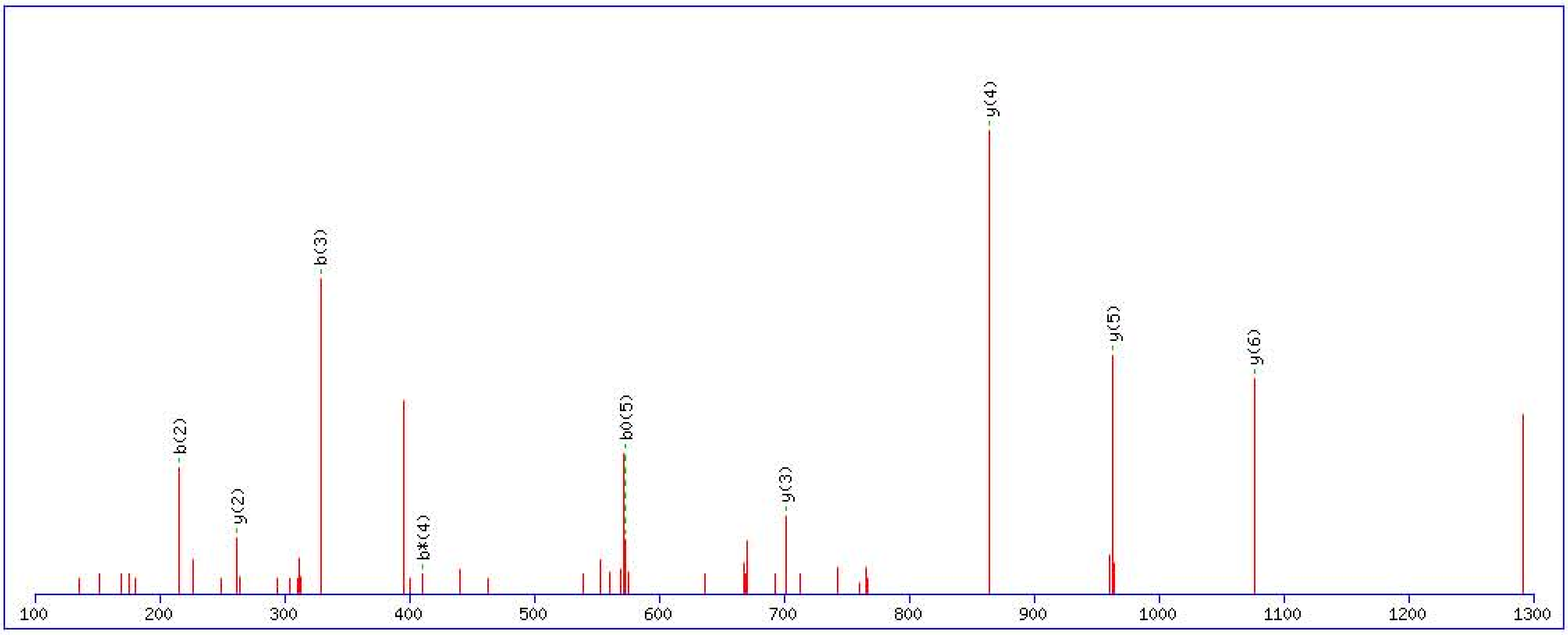
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQLVYQSR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

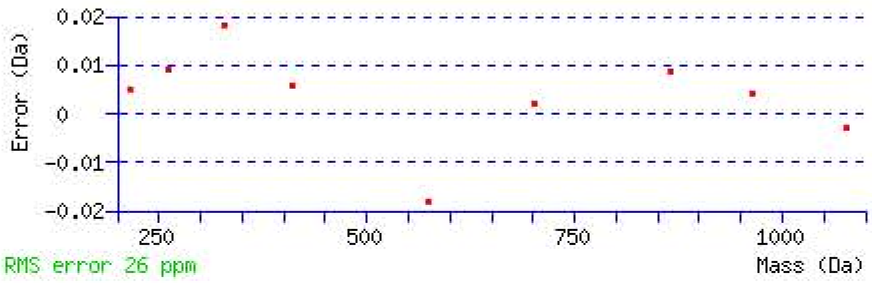
Match to Query 26728: 1290.675348 from(646.344950,2+) rtinseconds(1682) index(39943)
Title: Locus:1.1.1.3035.8 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

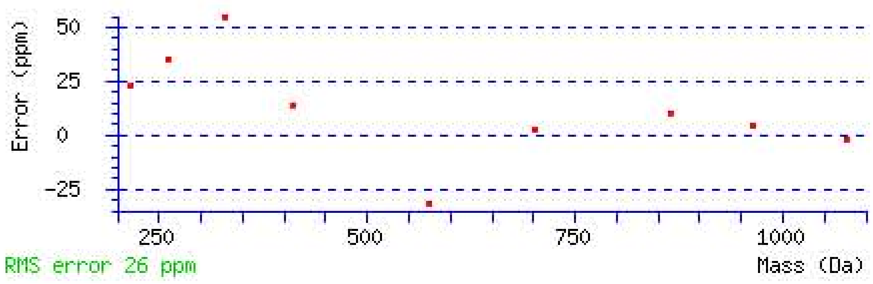
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1290.675430
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.0073
Matches : 9/80 fragment ions using 18 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							8
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	Q	1204.650691	602.828984	1187.624142	594.315709	1186.640126	593.823701	7
3	**329.181946**	165.094611	312.155397	156.581336	311.171381	156.089328	L	***1076.592113***	538.799695	1059.565564	530.286420	1058.581548	529.794412	6
4	428.250360	214.628818	411.223811	206.115544	410.239795	205.623536	V	***963.508049***	482.257663	946.481500	473.744388	945.497484	473.252380	5
5	591.313689	296.160483	574.287140	287.647208	573.303124	287.155200	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
6	1030.539015	515.773146	1013.512466	507.259871	1012.528450	506.767863	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
7	1117.571043	559.289160	1100.544494	550.775885	1099.560478	550.283877	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
26.8	1290.675430	-0.000082	SQLVYQSR
4.0	1290.693176	-0.017828	EAVKVAIDAGYR
3.9	1290.685303	-0.009955	SQISELNLLMK

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

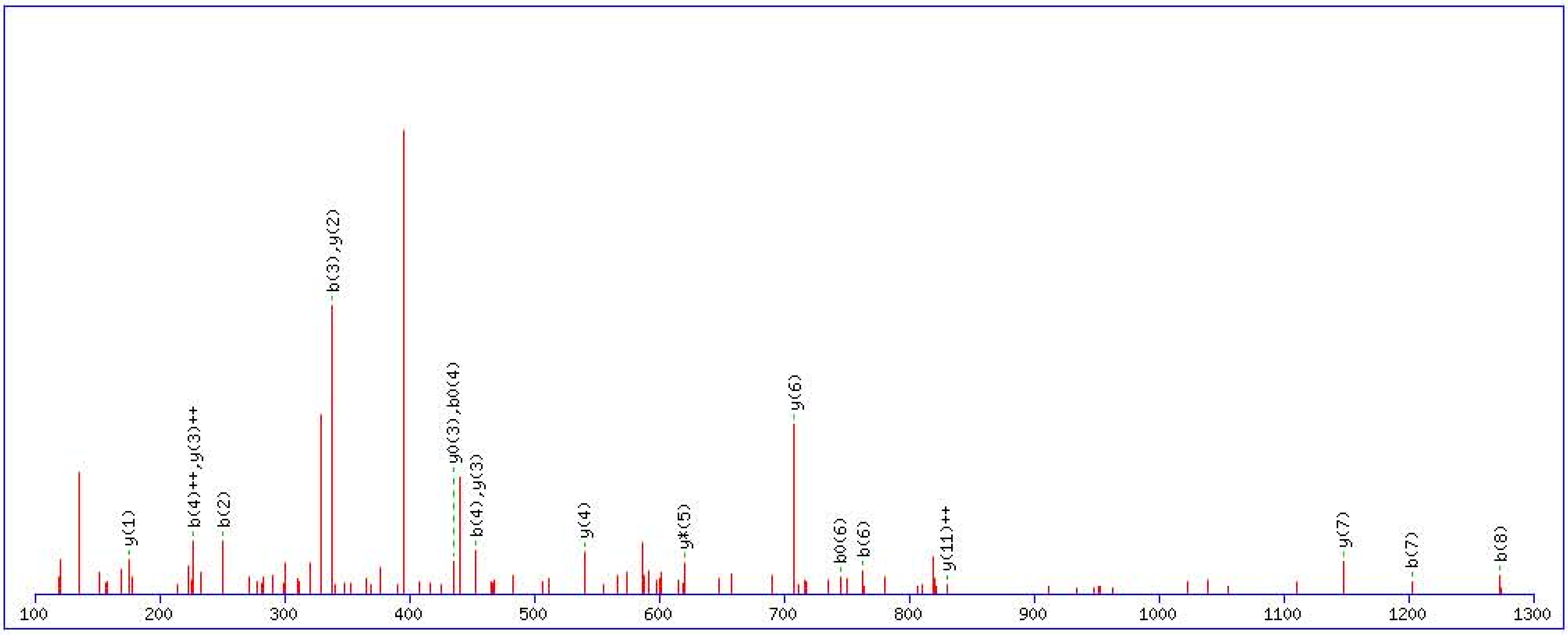
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSSDYFQAPSDYR**
Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

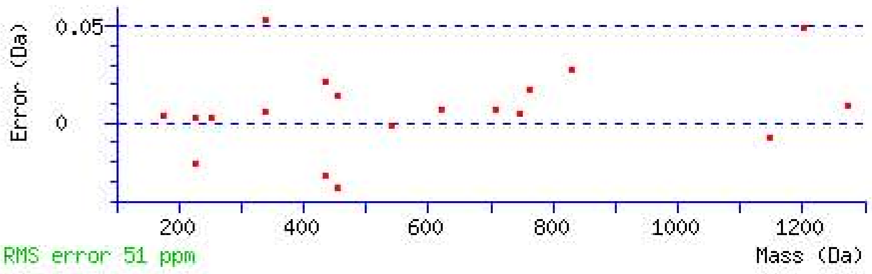
Match to Query 47714: 1908.858972 from(637.293600,3+) rtinseconds(2076) index(42755)
Title: Locus:1.1.1.3172.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

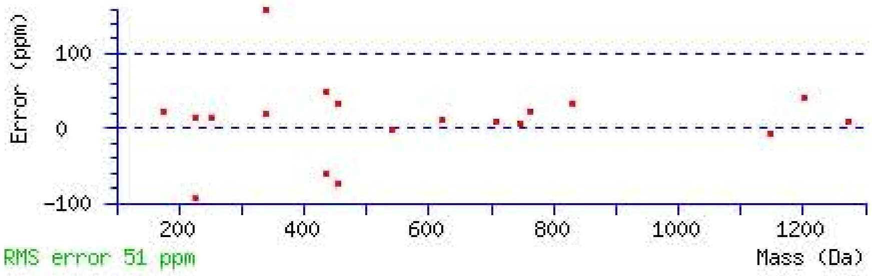
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1908.835236
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.022
Matches : 19/126 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							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
26.2	1908.835236	0.023736	YSSDYFQAPSDYR

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

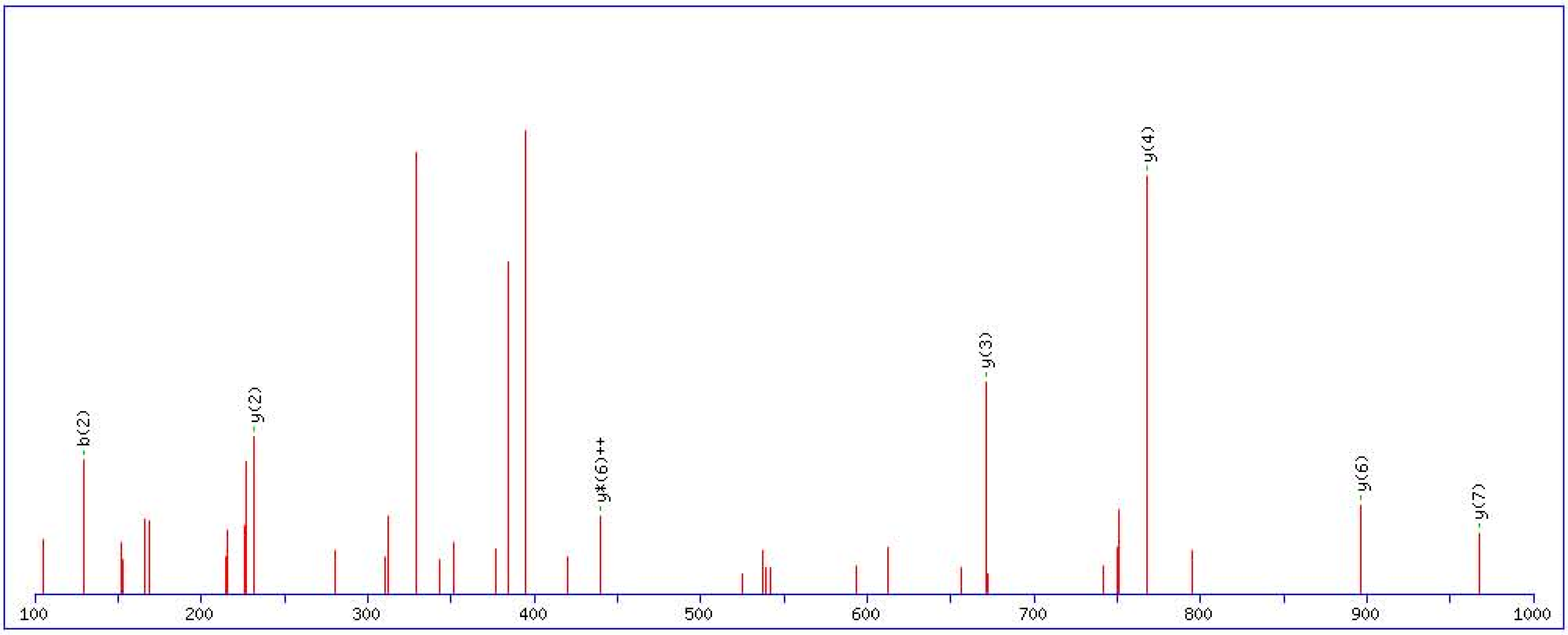
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GASQAGAPQGR**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

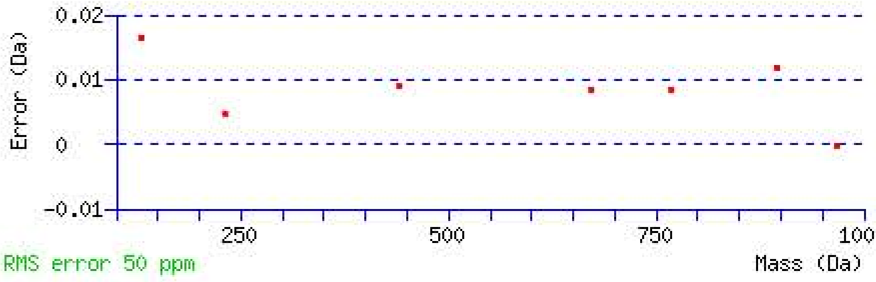
Match to Query 27154: 1309.662432 from(437.561420,3+) rtinseconds(1244) index(1558)
Title: Locus:1.1.1.2687.13 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

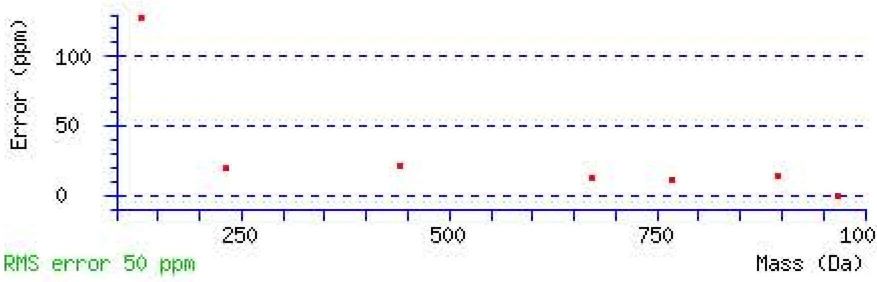
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1309.656097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0038
Matches : 7/94 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							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
37.3	1309.656097	0.006335	GASQAGAPQGR

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

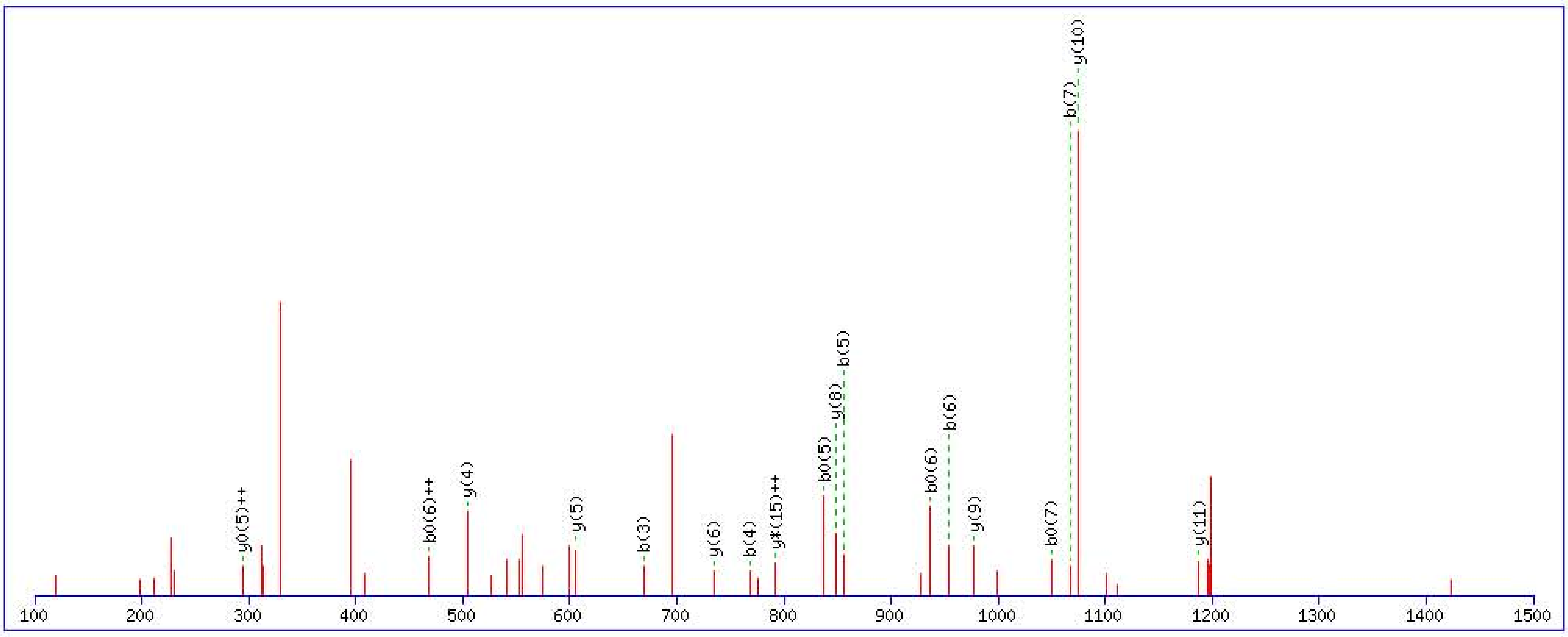
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QTQVSVLPEGGETPLFK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

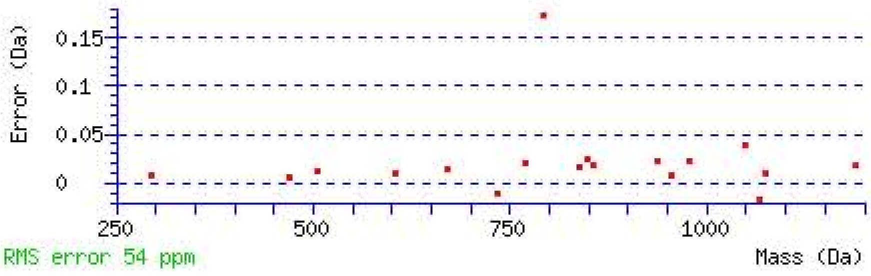
Match to Query 32558: 2140.137552 from(714.386460,3+) rtinseconds(2398) index(9164)
Title: Locus:1.1.1.3089.6 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

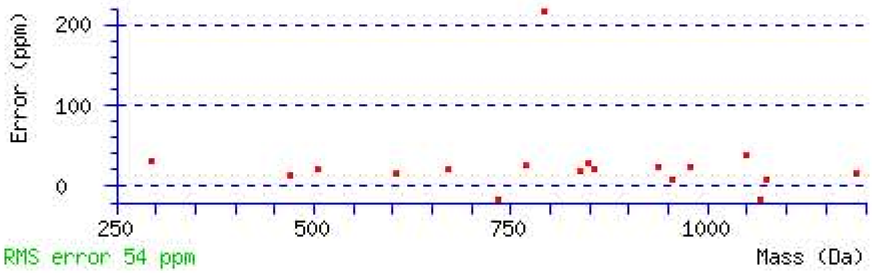
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2140.123840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.0021
Matches : 19/182 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	440.232602	220.619939	423.206053	212.106664			Q							17
2	541.280281	271.143779	524.253732	262.630504	523.269716	262.138496	T	1701.905780	851.456528	1684.879231	842.943254	1683.895215	842.451246	16
3	***669.338859***	335.173068	652.312310	326.659793	651.328294	326.167785	Q	1600.858101	800.932689	1583.831552	792.419414	1582.847536	791.927406	15
4	***768.407273***	384.707275	751.380724	376.194000	750.396708	375.701992	V	1472.799523	736.903399	1455.772974	728.390125	1454.788958	727.898117	14
5	***855.439301***	428.223289	838.412752	419.710014	837.428736	419.218006	S	1373.731109	687.369193	1356.704560	678.855918	1355.720544	678.363910	13
6	***954.507715***	477.757496	937.481166	469.244221	936.497150	468.752213	V	1286.699081	643.853179	1269.672532	635.339904	1268.688516	634.847896	12
7	***1067.591779***	534.299527	1050.565230	525.786253	1049.581214	525.294245	L	***1187.630667***	594.318972	1170.604118	585.805697	1169.620102	585.313689	11
8	1164.644543	582.825909	1147.617994	574.312635	1146.633978	573.820627	P	***1074.546603***	537.776940	1057.520054	529.263665	1056.536038	528.771657	10
9	1293.687136	647.347206	1276.660587	638.833931	1275.676571	638.341923	E	***977.493839***	489.250558	960.467290	480.737283	959.483274	480.245275	9
10	1350.708600	675.857938	1333.682051	667.344663	1332.698035	666.852655	G	***848.451246***	424.729261	831.424697	416.215987	830.440681	415.723979	8
11	1407.730064	704.368670	1390.703515	695.855395	1389.719499	695.363387	G	791.429782	396.218529	774.403233	387.705255	773.419217	387.213247	7
12	1536.772657	768.889966	1519.746108	760.376692	1518.762092	759.884684	E	***734.408318***	367.707797	717.381769	359.194523	716.397753	358.702515	6
13	1637.820336	819.413806	1620.793787	810.900531	1619.809771	810.408523	T	***605.365725***	303.186501	588.339176	294.673226	587.355160	294.181218	5
14	1734.873100	867.940188	1717.846551	859.426913	1716.862535	858.934905	P	***504.318046***	252.662661	487.291497	244.149387			4
15	1847.957164	924.482220	1830.930615	915.968945	1829.946599	915.476937	L	407.265282	204.136279	390.238733	195.623005			3
16	1995.025578	998.016427	1977.999029	989.503152	1977.015013	989.011144	F	***294.181218***	147.594247	277.154669	139.080973			2
17							K	147.112804	74.060040	130.086255	65.546766			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
45.5	2140.123840	0.013712	QTQVSVLPEGGETPLFK
43.7	2140.123840	0.013712	QTQVSVLPEGGETPLFK

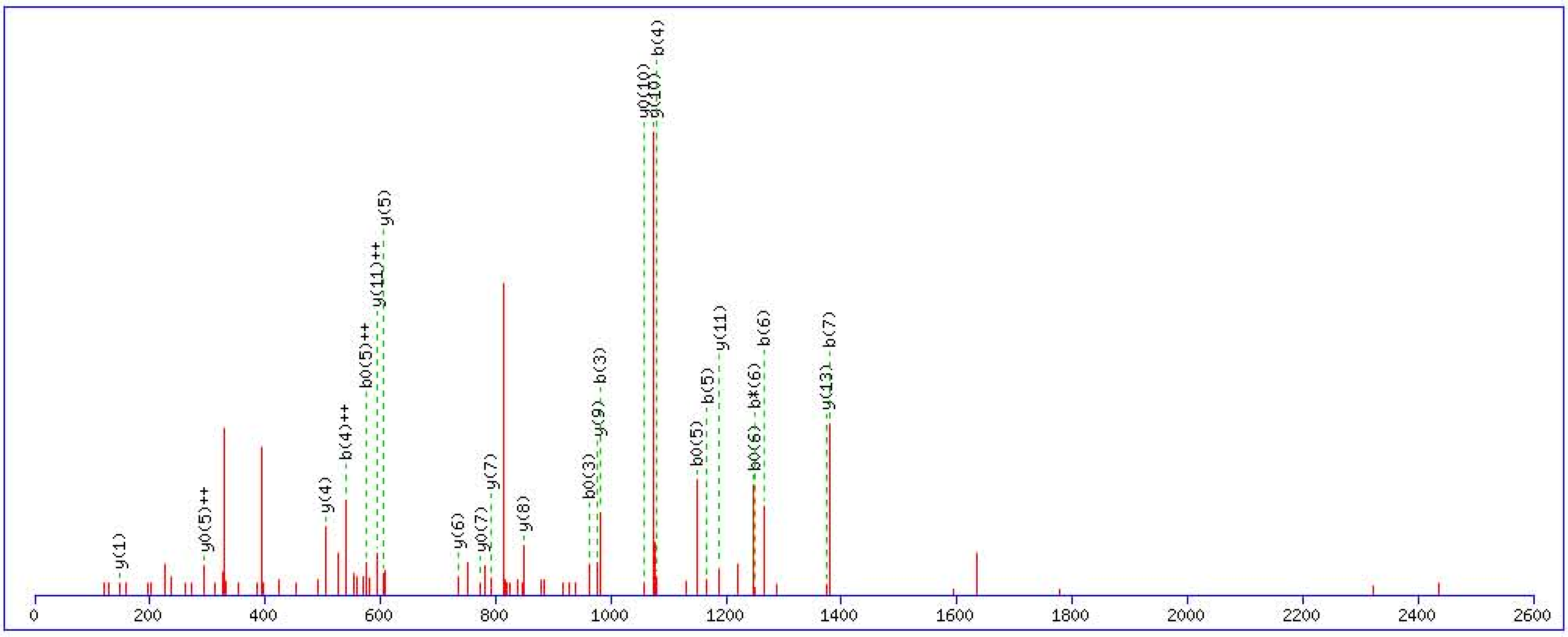
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QTQVSVLPEGGETPLFK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

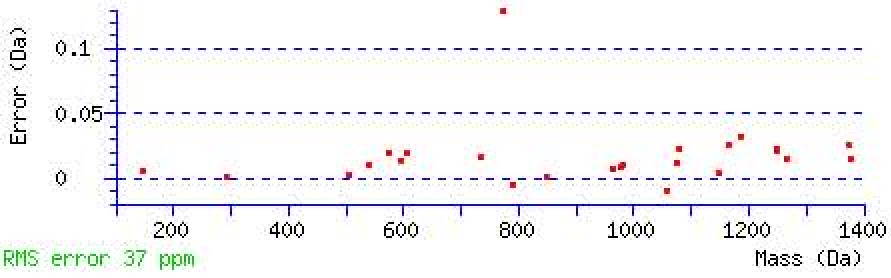
Match to Query 61423: 2451.321072 from(818.114300,3+) rtinseconds(2584) index(10260)
Title: Locus:1.1.1.3153.21 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

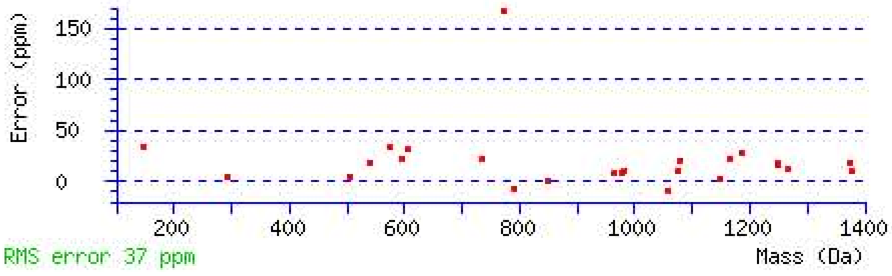
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 36  Expect: 0.00047
Matches : 26/182 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	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
36.3	2451.290588	0.030484	QTQVSVLPEGGETPLFK
0.8	2451.301590	0.019482	ATKRISHMPSRPELSAVATDLR
0.2	2451.357254	-0.036182	LLQRLHSLNGSILWIPAFMAR

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

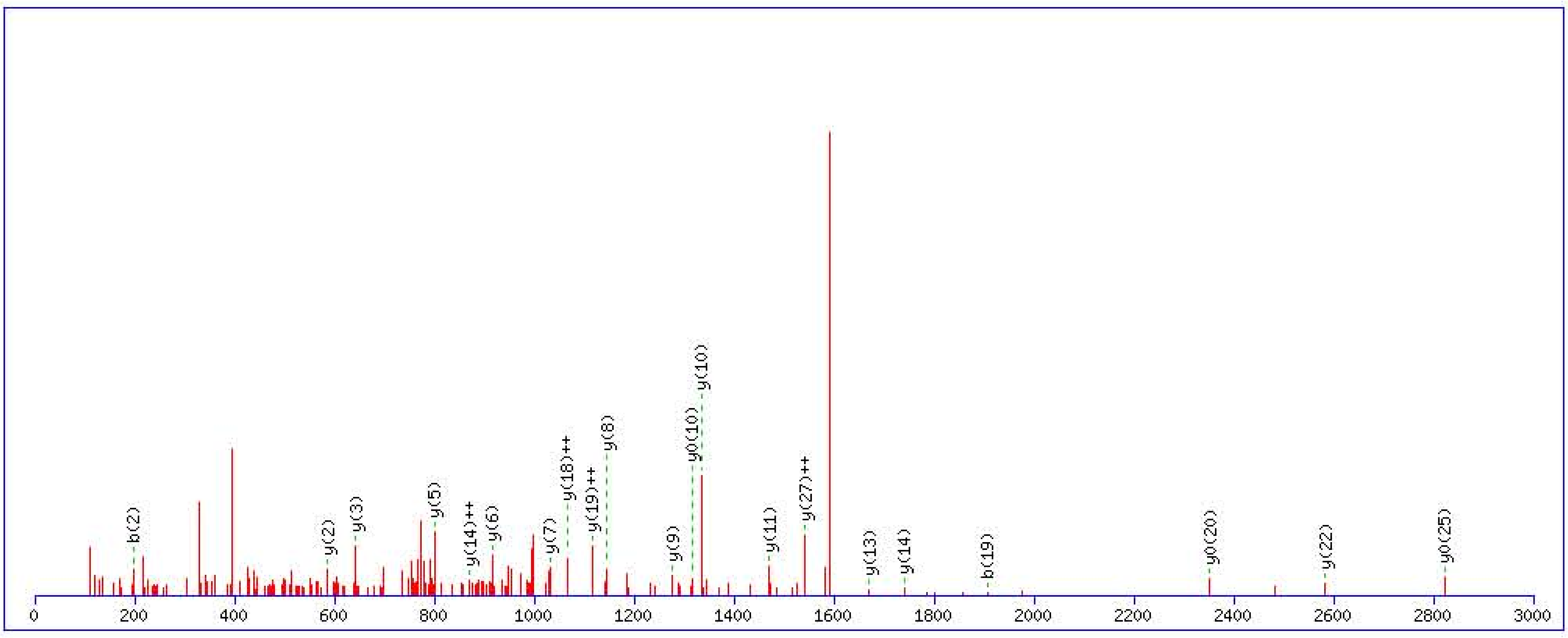
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPFDAATLHTSTAMAAQHGMDDDGTGQK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

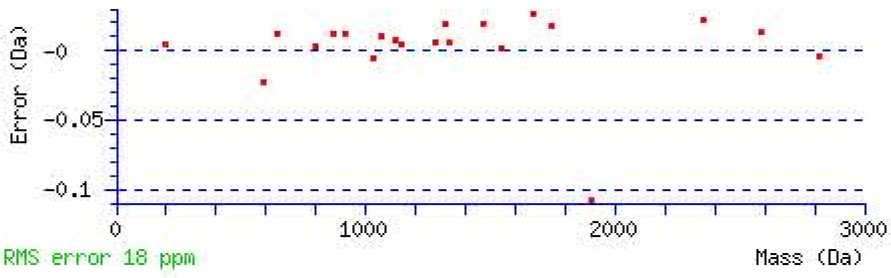
Match to Query 72166: 3183.471816 from(796.875230,4+) rtinseconds(1946) index(6200)
Title: Locus:1.1.1.2931.13 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

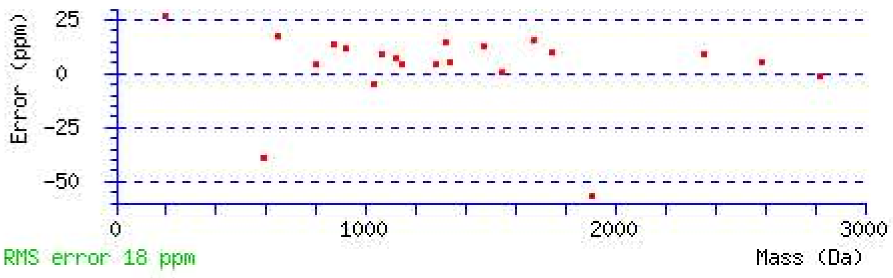
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3183.442383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q27 : Biotin:Thermo-21345 (Q)
Ions Score: 43 **Expect:** 0.00067
Matches : 21/280 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	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
43.3	3183.442383	0.029433	VPFDAATLHTSTAMAAQHGMDDDGTGQK
8.7	3183.442383	0.029433	VPFDAATLHTSTAMAAQHGMDDDGTGQK

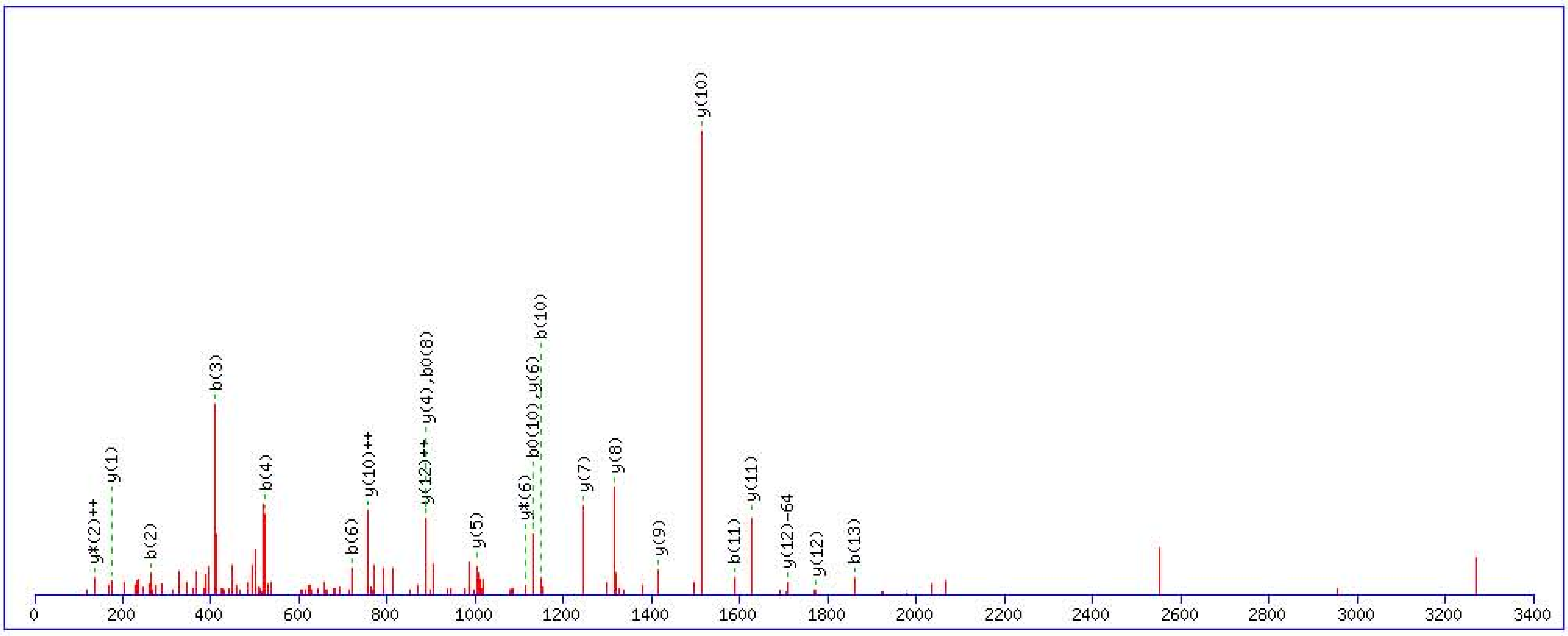
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVMLPVADQDQCIR**
Found in **HPT_HUMAN**, Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1

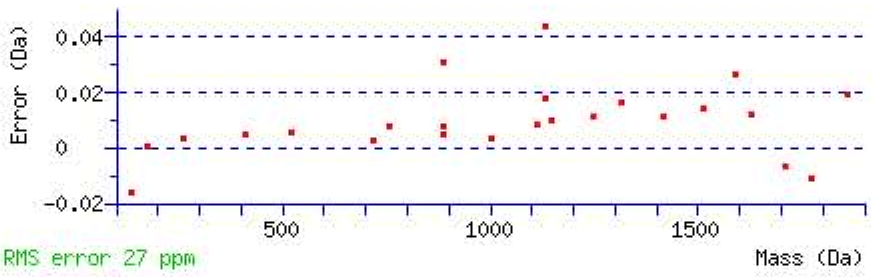
Match to Query 51627: 2034.003828 from(1018.009190,2+) rtinseconds(2126) index(25573)
Title: Locus:1.1.1.2882.21 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

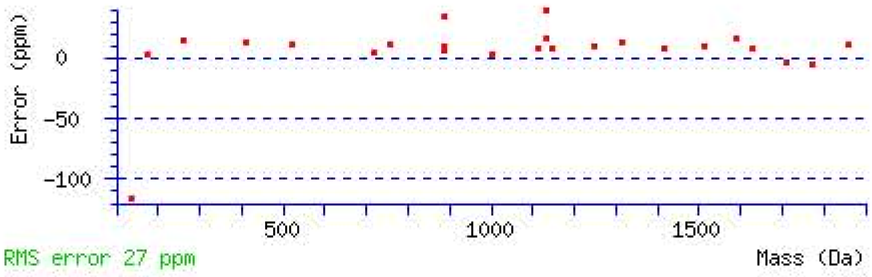
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2033.973679
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 1e-005
Matches : 24/174 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	164.070605	82.538940					Y							14
2	**263.139019**	132.073148					V	1871.917625	936.462450	1854.891076	927.949176	1853.907060	927.457168	13
3	**410.174419**	205.590848					M	***1772.849211***	886.928244	1755.822662	878.414969	1754.838646	877.922961	12
4	**523.258483**	262.132880					L	***1625.813811***	813.410543	1608.787262	804.897269	1607.803246	804.405261	11
5	620.311247	310.659262					P	***1512.729747***	756.868511	1495.703198	748.355237	1494.719182	747.863229	10
6	**719.379661**	360.193469					V	***1415.676983***	708.342129	1398.650434	699.828855	1397.666418	699.336847	9
7	790.416775	395.712026					A	***1316.608569***	658.807922	1299.582020	650.294648	1298.598004	649.802640	8
8	905.443718	453.225497			887.433153	444.220215	D	***1245.571455***	623.289366	1228.544906	614.776091	1227.560890	614.284083	7
9	1033.502296	517.254786	1016.475747	508.741511	1015.491731	508.249503	Q	***1130.544512***	565.775894	1113.517963	557.262620	1112.533947	556.770611	6
10	**1148.529239**	574.768258	1131.502690	566.254983	1130.518674	565.762975	D	***1002.485934***	501.746605	985.459385	493.233331	984.475369	492.741323	5
11	**1587.754565**	794.380921	1570.728016	785.867646	1569.744000	785.375638	Q	***887.458991***	444.233134	870.432442	435.719859			4
12	1747.785214	874.396245	1730.758665	865.882971	1729.774649	865.390963	C	448.233665	224.620470	431.207116	216.107196			3
13	**1860.869278**	930.938277	1843.842729	922.425003	1842.858713	921.932994	I	288.203016	144.605146	271.176467	136.091871			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.0	2033.973679	0.030149	YVMLPVADQDQCIR
47.0	2033.973679	0.030149	YVMLPVADQDQCIR
13.7	2034.006516	-0.002688	KGYDRVSVMRPQPGDTGR

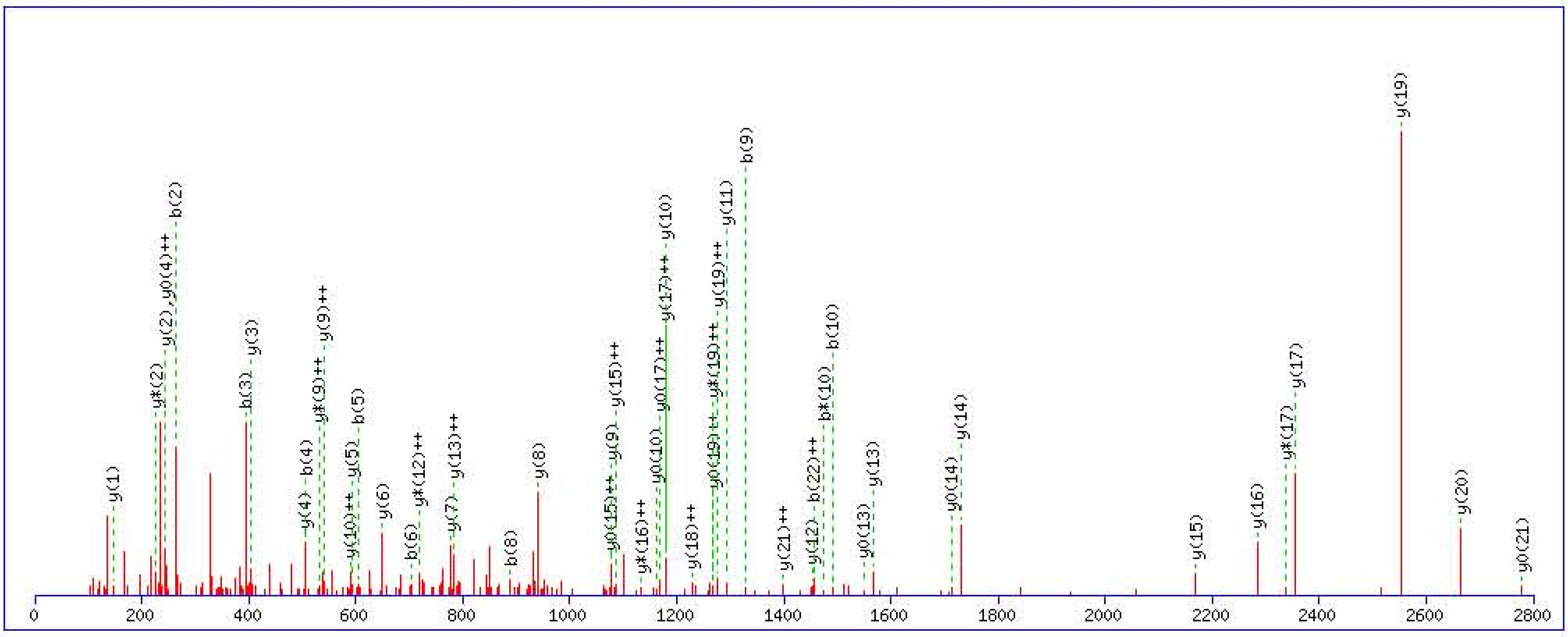
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVMLPVADQYDCITHYEGSTCPK**
Found in **HPTR_HUMAN**, Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2

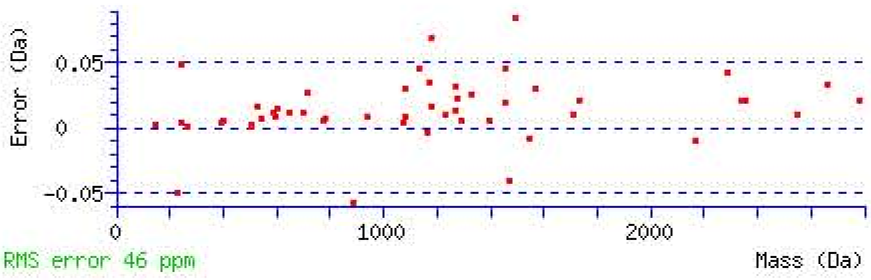
Match to Query 70931: 3057.411376 from(765.360120,4+) rtinseconds(2428) index(27601)
Title: Locus:1.1.1.2987.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

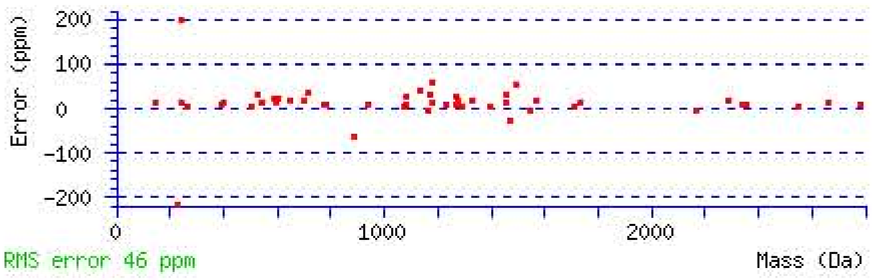
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 82  Expect: 1e-007
Matches : 51/228 fragment ions using 132 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							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
81.7	3057.374466	0.036910	YVMLPVADQYDCITHYEGSTCPK

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

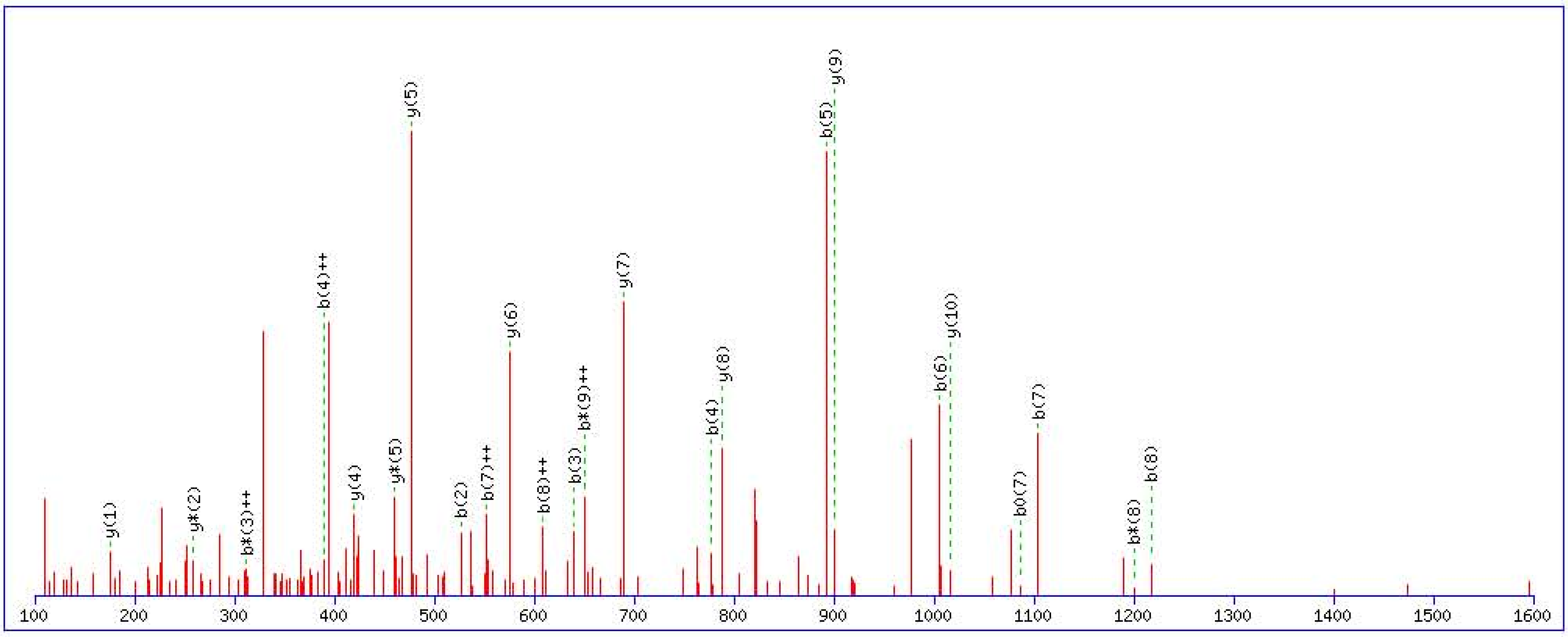
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQIHDIVLVGGSTR**
Found in **HSP7C_HUMAN**, Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

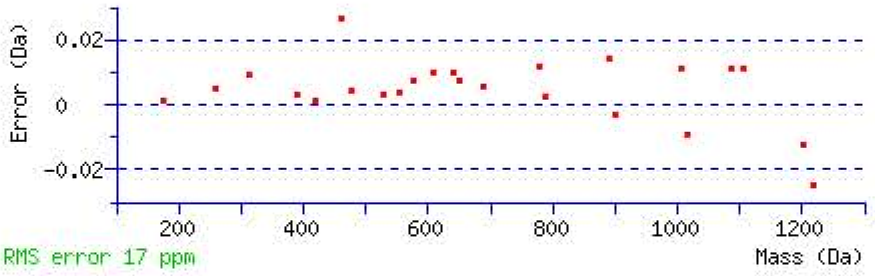
Match to Query 45090: 1791.984282 from(598.335370,3+) rtinseconds(1987) index(78816)
Title: Locus:1.1.1.2042.10 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

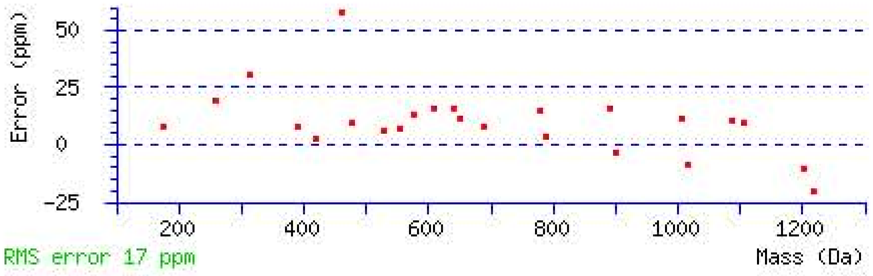
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1791.966553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0066
Matches : 24/152 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	88.039304	44.523290			70.028739	35.518008	S							14
2	***527.264630***	264.135953	510.238081	255.622679	509.254065	255.130671	Q	1705.941788	853.474532	1688.915239	844.961257	1687.931223	844.469249	13
3	***640.348694***	320.677985	623.322145	312.164711	622.338129	311.672703	I	1266.716462	633.861869	1249.689913	625.348595	1248.705897	624.856587	12
4	***777.407606***	**389.207441**	760.381057	380.694166	759.397041	380.202159	H	1153.632398	577.319837	1136.605849	568.806563	1135.621833	568.314554	11
5	***892.434549***	446.720913	875.408000	438.207638	874.423984	437.715630	D	***1016.573486***	508.790381	999.546937	500.277107	998.562921	499.785099	10
6	***1005.518613***	503.262945	988.492064	494.749670	987.508048	494.257662	I	***901.546543***	451.276910	884.519994	442.763635	883.535978	442.271627	9
7	***1104.587027***	**552.797152**	1087.560478	544.283877	1086.576462	543.791869	V	***788.462479***	394.734878	771.435930	386.221603	770.451914	385.729595	8
8	***1217.671091***	**609.339183**	1200.644542	600.825909	1199.660526	600.333901	L	***689.394065***	345.200671	672.367516	336.687396	671.383500	336.195388	7
9	1316.739505	658.873391	1299.712956	650.360116	1298.728940	649.868108	V	***576.310001***	288.658639	559.283452	280.145364	558.299436	279.653356	6
10	1373.760969	687.384122	1356.734420	678.870848	1355.750404	678.378840	G	***477.241587***	239.124431	460.215038	230.611157	459.231022	230.119149	5
11	1430.782433	715.894854	1413.755884	707.381580	1412.771868	706.889572	G	***420.220123***	210.613699	403.193574	202.100425	402.209558	201.608417	4
12	1517.814461	759.410868	1500.787912	750.897594	1499.803896	750.405586	S	363.198659	182.102968	346.172110	173.589693	345.188094	173.097685	3
13	1618.862140	809.934708	1601.835591	801.421434	1600.851575	800.929425	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 SQIHDIVLVGGSTR
(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	1791.966553	0.017729	SQIHDIVLVGGSTR

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

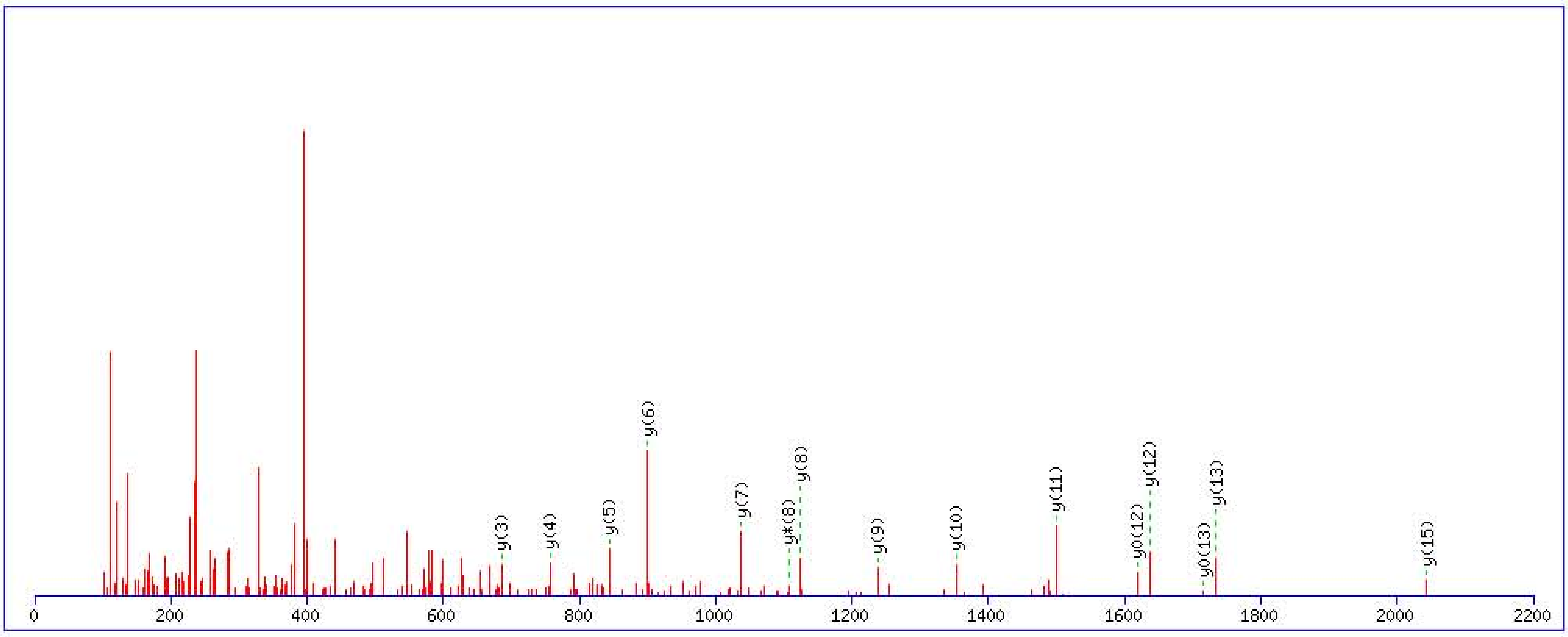
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYFPHFDLSHGSAQVK**
Found in **HBA_HUMAN**, Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2

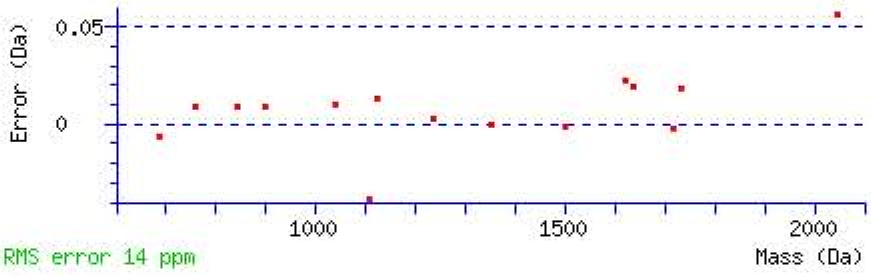
Match to Query 54001: 2144.069536 from(537.024660,4+) rtinseconds(2056) index(6857)
Title: Locus:1.1.1.2970.8 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

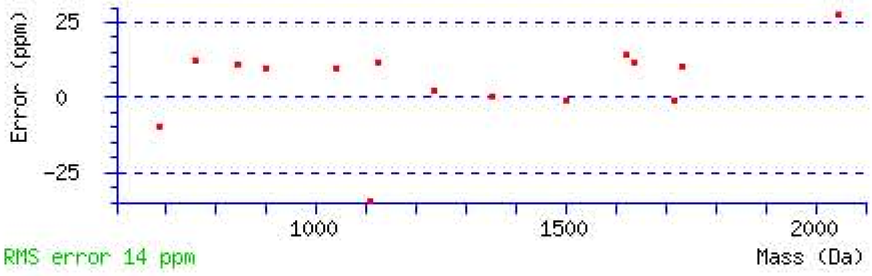
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2144.051346
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14    : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 9.3e-006
Matches : 15/146 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	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
64.7	2144.051346	0.018190	TYFPHFDLSHGSAQVK

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

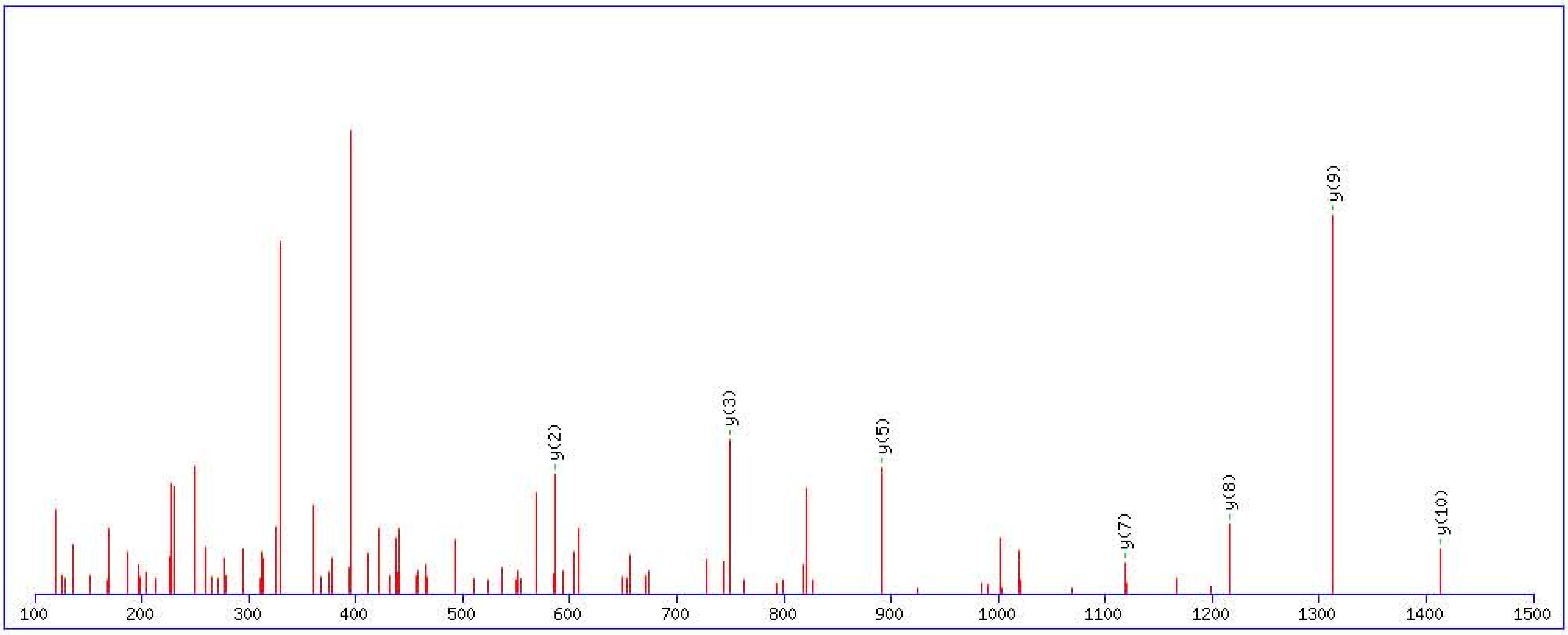
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFTPPVQAAYQK**
Found in **HBB_HUMAN**, Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2

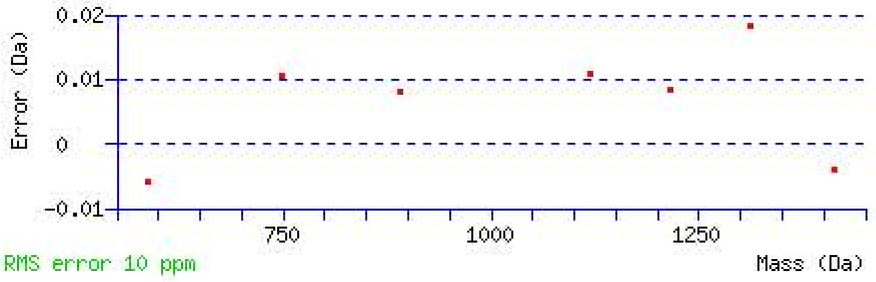
Match to Query 42191: 1688.873952 from(563.965260,3+) rtinseconds(1984) index(6437)
Title: Locus:1.1.1.2945.5 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

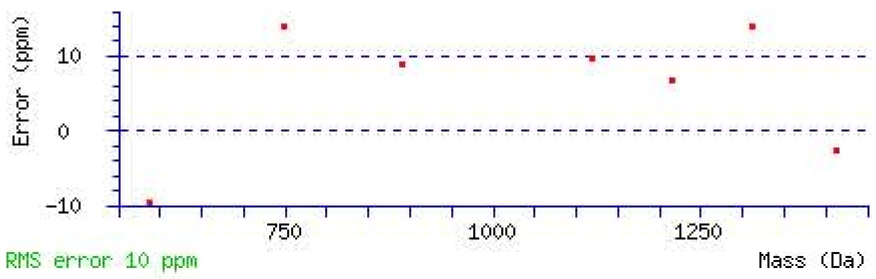
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1688.859604
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.002
Matches : 7/102 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	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
41.0	1688.859604	0.014348	EFTPPVQAAYQK
10.4	1688.859604	0.014348	EFTPPVQAAYQK

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

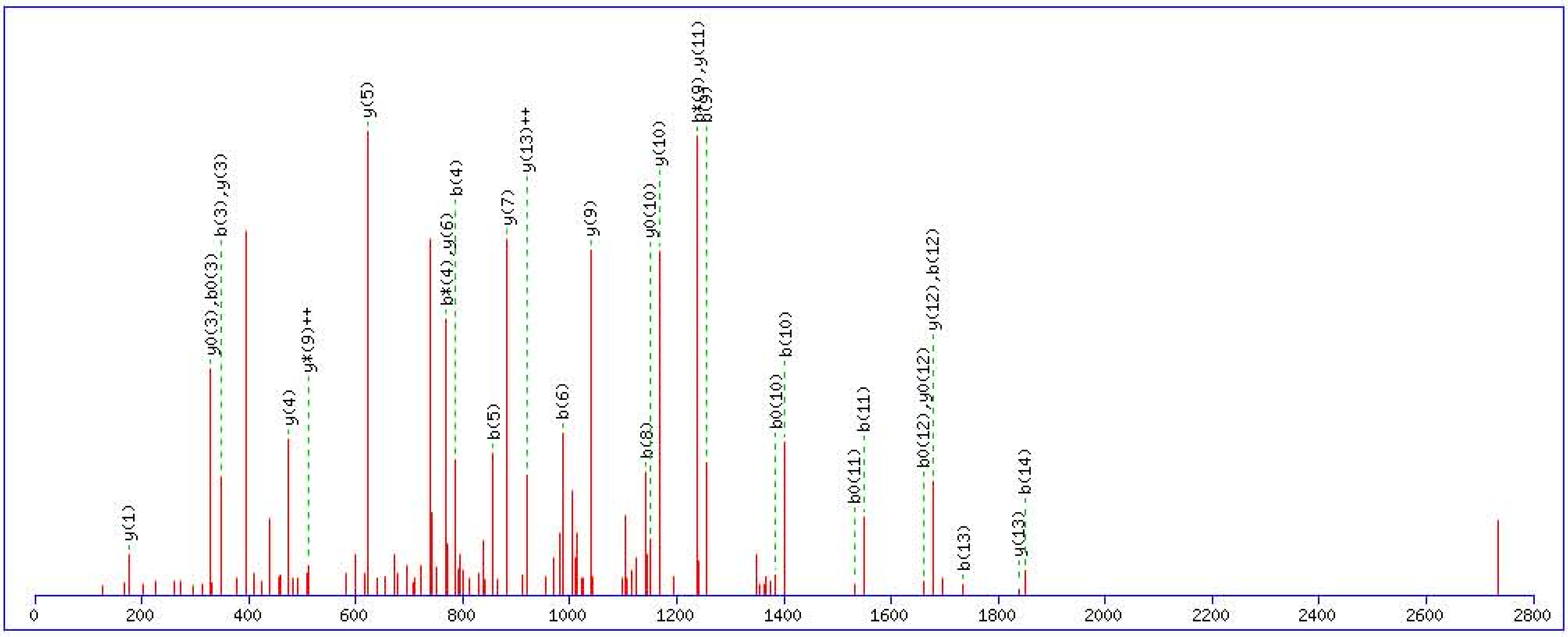
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GECQAEGVLFFQGDR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

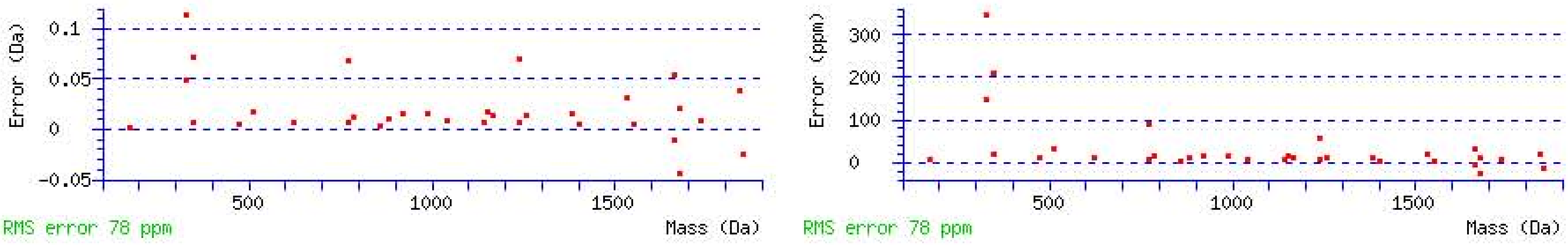
Match to Query 51349: 2022.953308 from(1012.483930,2+) rtinseconds(2384) index(81488)
Title: Locus:1.1.1.2180.11 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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: 69  Expect: 1.7e-006
Matches : 33/158 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	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
69.4	2022.929184	0.024124	GECQAEGVLFFQGDR
18.3	2022.929184	0.024124	GECQAEGVLFFQGDR
7.7	2022.950317	0.002991	NMSFVNDLTVTQDGR
4.2	2022.980133	-0.026825	QHMEQKEQTAR
0.4	2022.980133	-0.026825	QHMEQKEQTAR

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

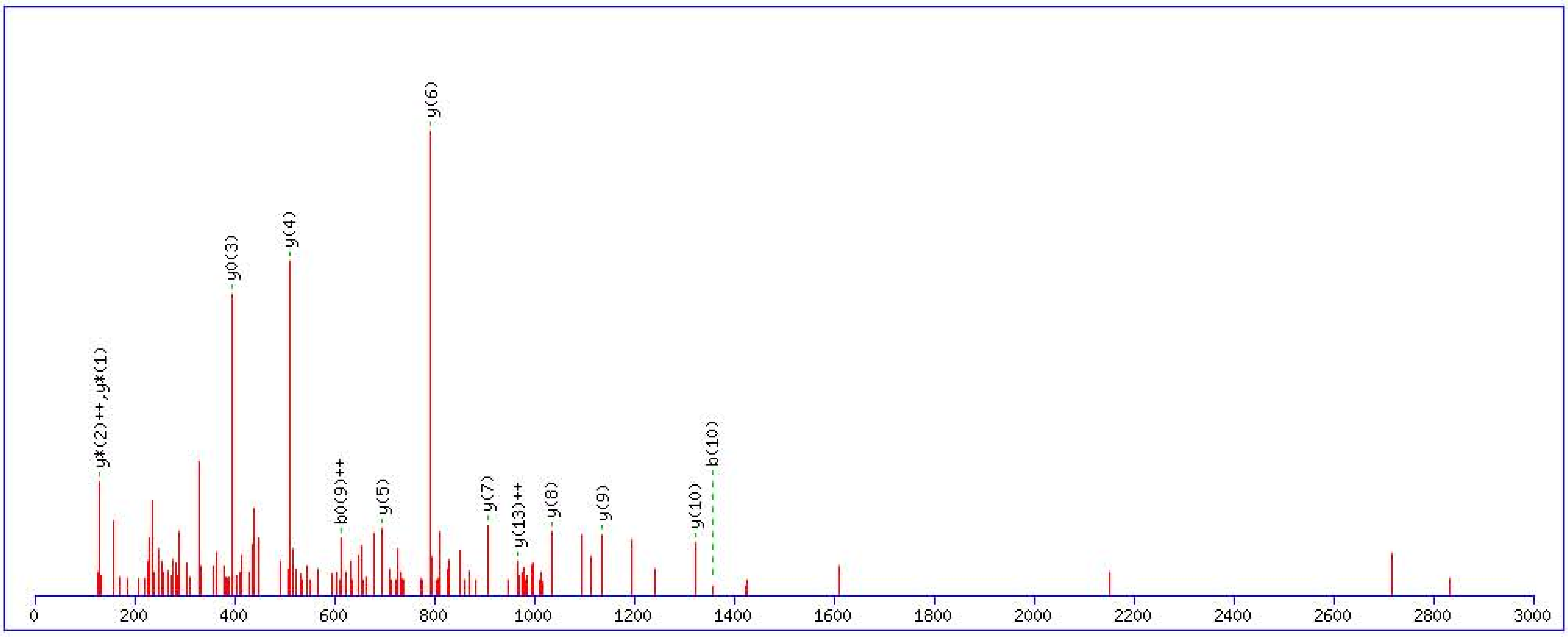
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGAQATWTELPWPHEK**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

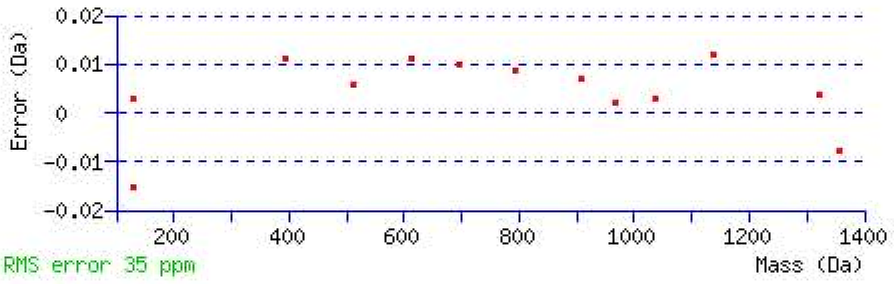
Match to Query 54072: 2148.068142 from(717.029990,3+) rtinseconds(2279) index(80802)
Title: Locus:1.1.1.2144.13 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

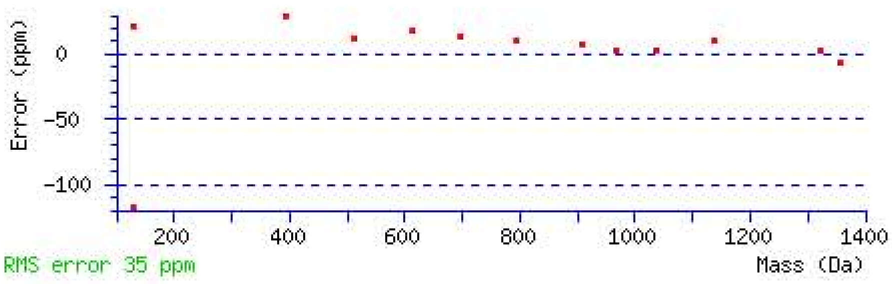
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2148.046234
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0019
Matches : 13/172 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							16
2	145.060768	73.034022			127.050203	64.028740	G	2062.021496	1031.514386	2044.994947	1023.001111	2044.010931	1022.509103	15
3	216.097882	108.552579			198.087317	99.547296	A	2005.000032	1003.003654	1987.973483	994.490380	1986.989467	993.998372	14
4	655.323208	328.165242	638.296659	319.651968	637.312643	319.159960	Q	1933.962918	967.485097	1916.936369	958.971823	1915.952353	958.479815	13
5	726.360322	363.683799	709.333773	355.170525	708.349757	354.678517	A	1494.737592	747.872434	1477.711043	739.359160	1476.727027	738.867152	12
6	827.408001	414.207639	810.381452	405.694364	809.397436	405.202356	T	1423.700478	712.353877	1406.673929	703.840603	1405.689913	703.348595	11
7	1013.487314	507.247295	996.460765	498.734020	995.476749	498.242012	W	***1322.652799***	661.830038	1305.626250	653.316763	1304.642234	652.824755	10
8	1114.534993	557.771135	1097.508444	549.257860	1096.524428	548.765852	T	***1136.573486***	568.790381	1119.546937	560.277107	1118.562921	559.785099	9
9	1243.577586	622.292431	1226.551037	613.779157	1225.567021	613.287149	E	***1035.525807***	518.266542	1018.499258	509.753267	1017.515242	509.261259	8
10	1356.661650	678.834463	1339.635101	670.321189	1338.651085	669.829181	L	***906.483214***	453.745245	889.456665	445.231971	888.472649	444.739963	7
11	1453.714414	727.360845	1436.687865	718.847571	1435.703849	718.355563	P	***793.399150***	397.203213	776.372601	388.689939	775.388585	388.197931	6
12	1639.793727	820.400502	1622.767178	811.887227	1621.783162	811.395219	W	***696.346386***	348.676831	679.319837	340.163557	678.335821	339.671549	5
13	1736.846491	868.926884	1719.819942	860.413609	1718.835926	859.921601	P	***510.267073***	255.637175	493.240524	247.123900	492.256508	246.631892	4
14	1873.905403	937.456340	1856.878854	928.943065	1855.894838	928.451057	H	413.214309	207.110793	396.187760	198.597518	395.203744	198.105510	3
15	2002.947996	1001.977636	1985.921447	993.464362	1984.937431	992.972354	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SGAQATWTELPWPHEK
(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	2148.046234	0.021908	SGAQATWTELPWPHEK

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

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 65413: 2674.355742 from(892.459190,3+) rtinseconds(2652) index(83080)
Title: Locus:1.1.1.2273.22 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\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): 2674.324722
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 75  Expect: 9.1e-007
Matches : 30/224 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					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
75.0	2674.324722	0.031020	LLQDEFPGIPSPLDAAVECHR

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

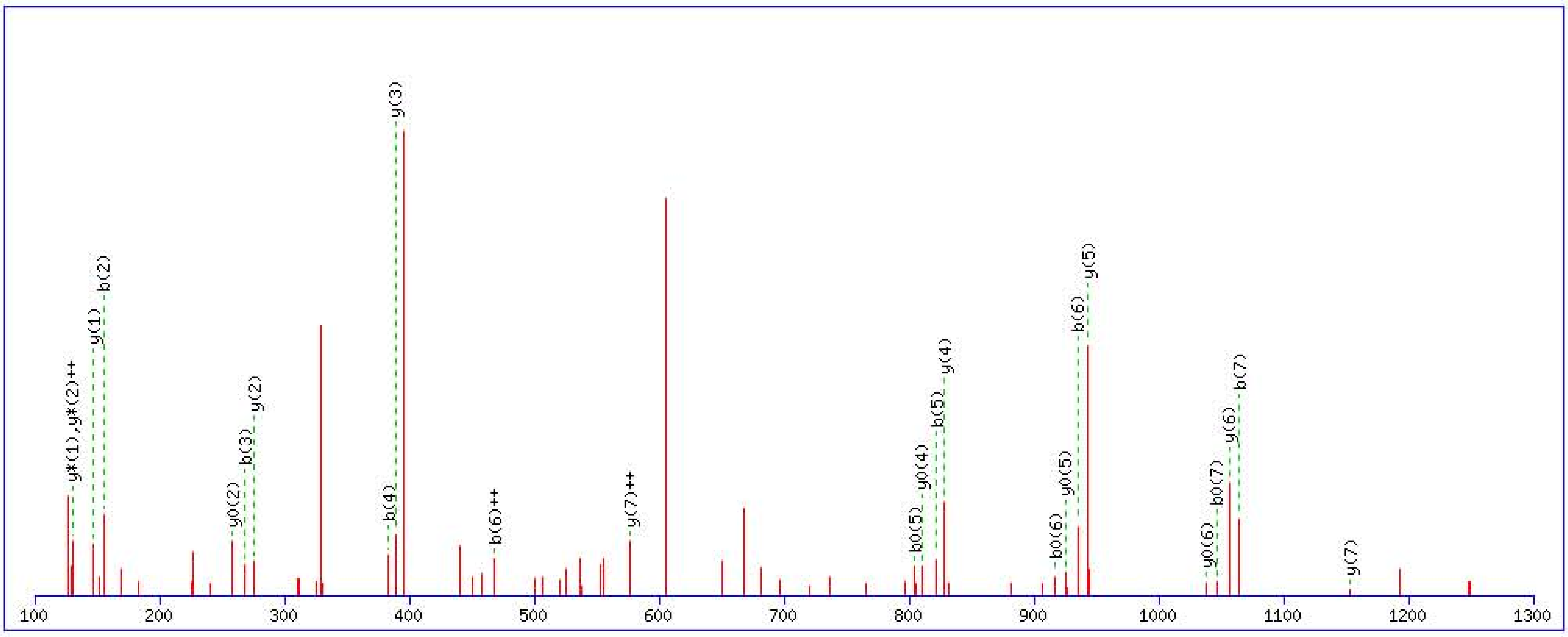
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPLDQLEK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

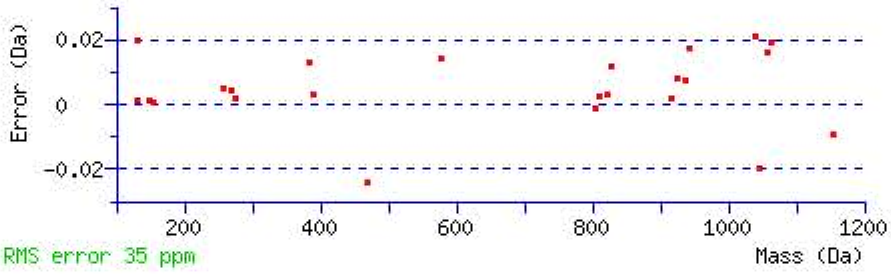
Match to Query 23988: 1209.656308 from(605.835430,2+) rtinseconds(2076) index(42754)
Title: Locus:1.1.1.3172.10 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

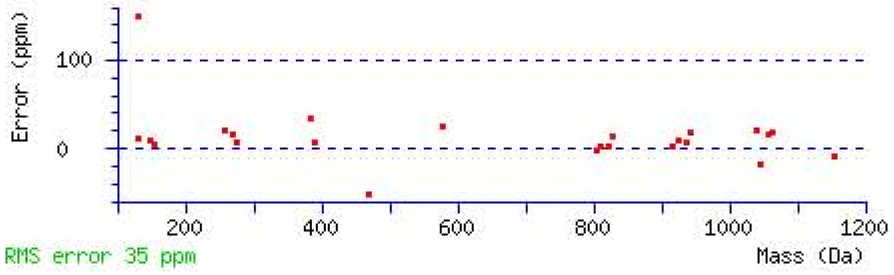
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1209.642731
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0021
Matches : 24/68 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							8
2	**155.081504**	78.044390					P	***1153.628558***	577.317917	1136.602009	568.804643	1135.617993	568.312635	7
3	**268.165568**	134.586422					L	***1056.575794***	528.791535	1039.549245	520.278261	1038.565229	519.786253	6
4	**383.192511**	192.099894			365.181946	183.094611	D	***943.491730***	472.249503	926.465181	463.736228	925.481165	463.244220	5
5	**822.417837**	411.712557	805.391288	403.199282	804.407272	402.707274	Q	***828.464787***	414.736032	811.438238	406.222757	810.454222	405.730749	4
6	**935.501901**	468.254589	918.475352	459.741314	917.491336	459.249306	L	***389.239461***	195.123368	372.212912	186.610094	371.228896	186.118086	3
7	**1064.544494**	532.775885	1047.517945	524.262611	1046.533929	523.770603	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GPLDQLEK
(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	1209.642731	0.013577	GPLDQLEK
13.3	1209.646545	0.009763	EHNRLATELK
4.3	1209.639343	0.016965	AFAKGFLAEEK
4.2	1209.665192	-0.008884	GQGKPREK
3.3	1209.642731	0.013577	GTGEFIKALMK
2.3	1209.653976	0.002332	GPDGLKGQK
1.6	1209.642731	0.013577	LQPSTPEK

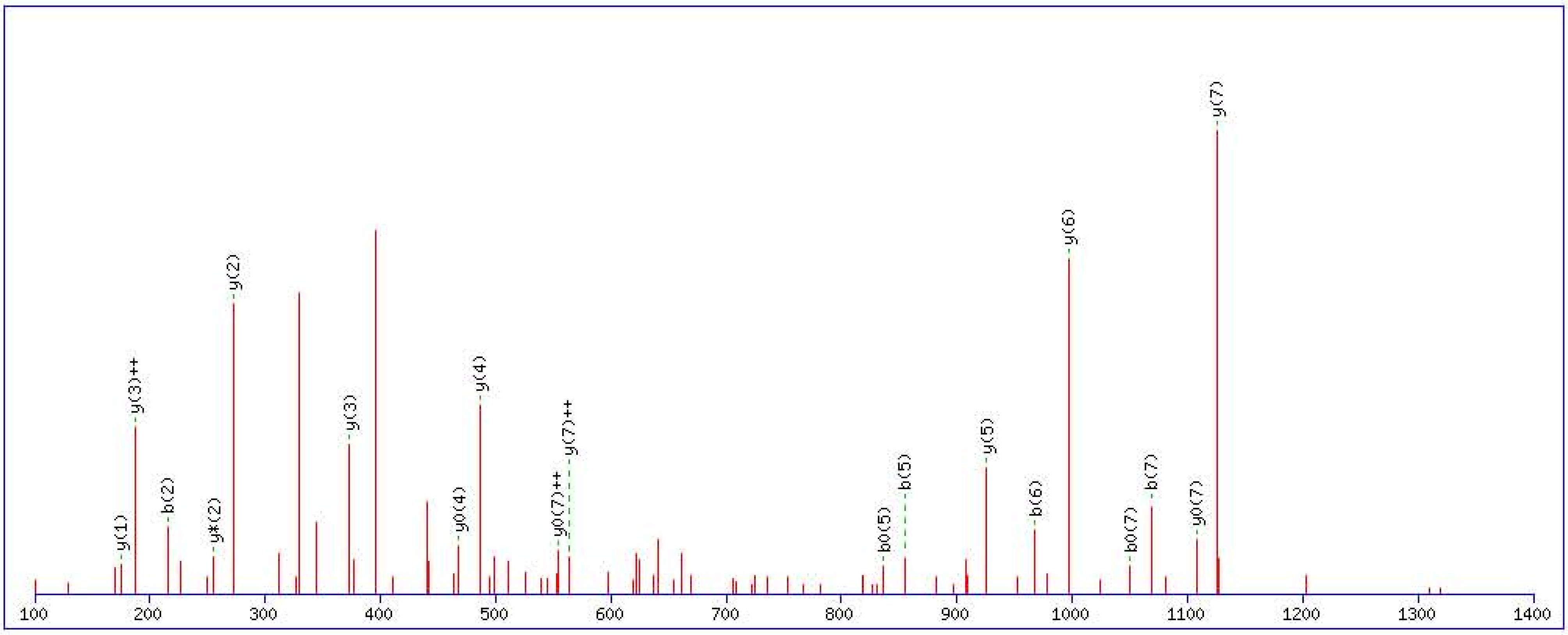
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLEAQLTPR**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

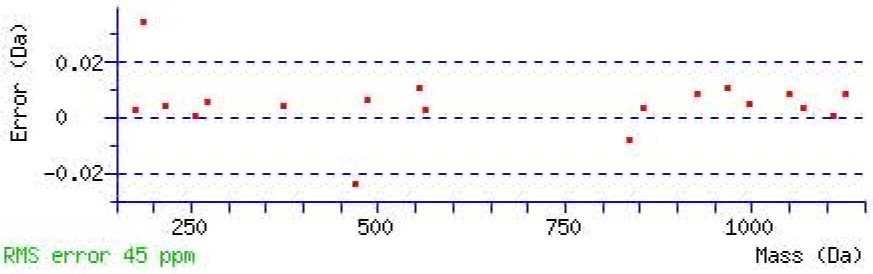
Match to Query 27821: 1338.748728 from(670.381640,2+) rtinseconds(1942) index(41791)
Title: Locus:1.1.1.3125.21 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

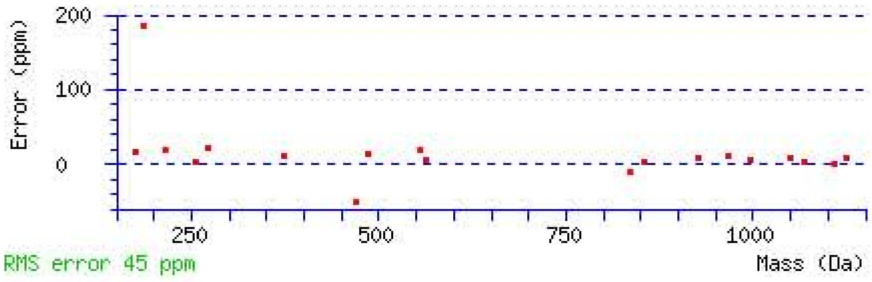
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1338.732941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0016
Matches : 19/84 fragment ions using 36 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							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
39.4	1338.732941	0.015787	TLEAQLTPR
9.1	1338.732956	0.015772	VDLQSLPTR
0.8	1338.761932	-0.013204	LTVLREDQIPR

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

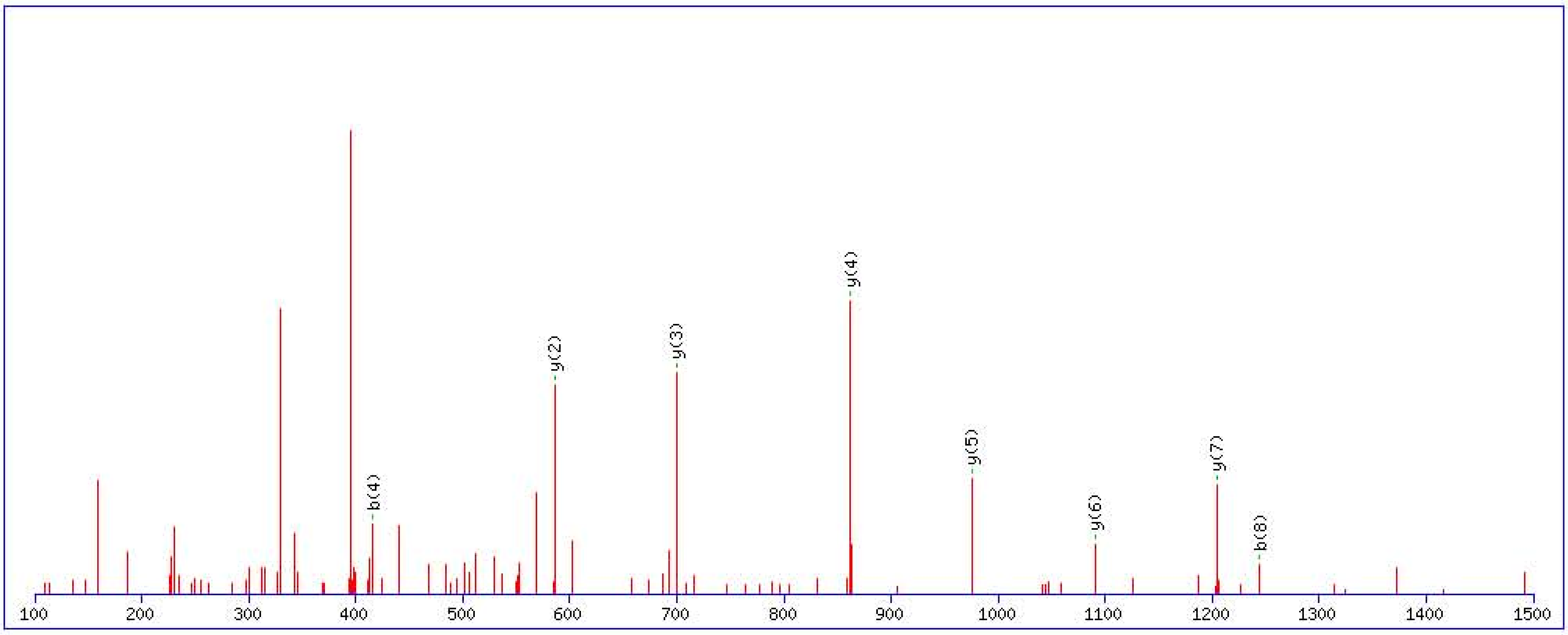
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVNDLYIQK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

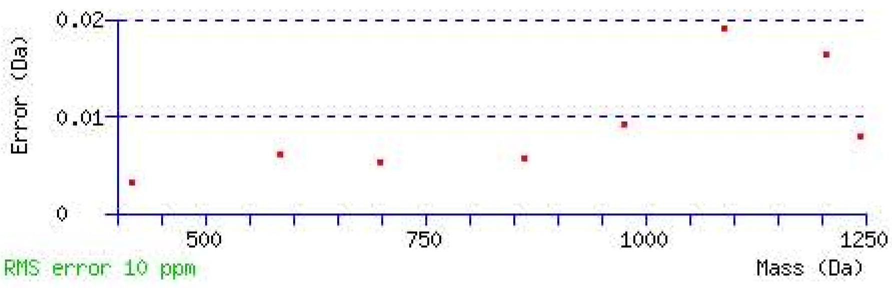
Match to Query 30321: 1389.749008 from(695.881780,2+) rtinseconds(1951) index(41866)
Title: Locus:1.1.1.3128.21 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

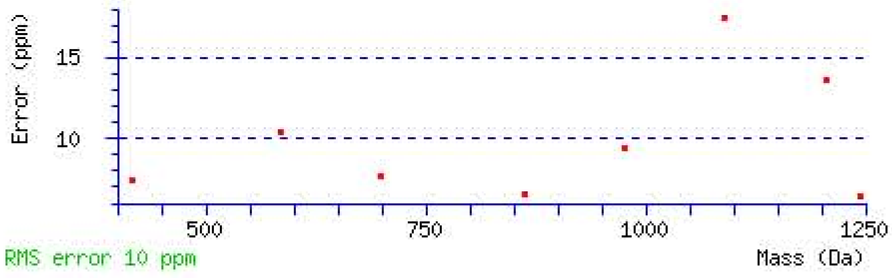
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1389.732605
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 42 **Expect:** 0.00062
Matches : 8/82 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							9
2	187.107718	94.057497			169.097153	85.052214	V	1303.707871	652.357573	1286.681322	643.844299	1285.697306	643.352291	8
3	301.150645	151.078960	284.124096	142.565686	283.140080	142.073678	N	***1204.639457***	602.823367	1187.612908	594.310092	1186.628892	593.818084	7
4	**416.177588**	208.592432	399.151039	200.079158	398.167023	199.587150	D	***1090.596530***	545.801903	1073.569981	537.288629	1072.585965	536.796621	6
5	529.261652	265.134464	512.235103	256.621190	511.251087	256.129182	L	***975.569587***	488.288432	958.543038	479.775157			5
6	692.324981	346.666129	675.298432	338.152854	674.314416	337.660846	Y	***862.485523***	431.746400	845.458974	423.233125			4
7	805.409045	403.208161	788.382496	394.694886	787.398480	394.202878	I	***699.422194***	350.214735	682.395645	341.701461			3
8	**1244.634371**	622.820823	1227.607822	614.307549	1226.623806	613.815541	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 SVNDLYIQK
(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	1389.732605	0.016403	SVNDLYIQK
7.6	1389.728577	0.020431	NMLTESLVALQR
5.0	1389.761612	-0.012604	SGVGNIFVKNLDK
4.4	1389.746307	0.002701	SEKATSLQAKAEK
3.8	1389.735107	0.013901	SQSILDSLETVAK

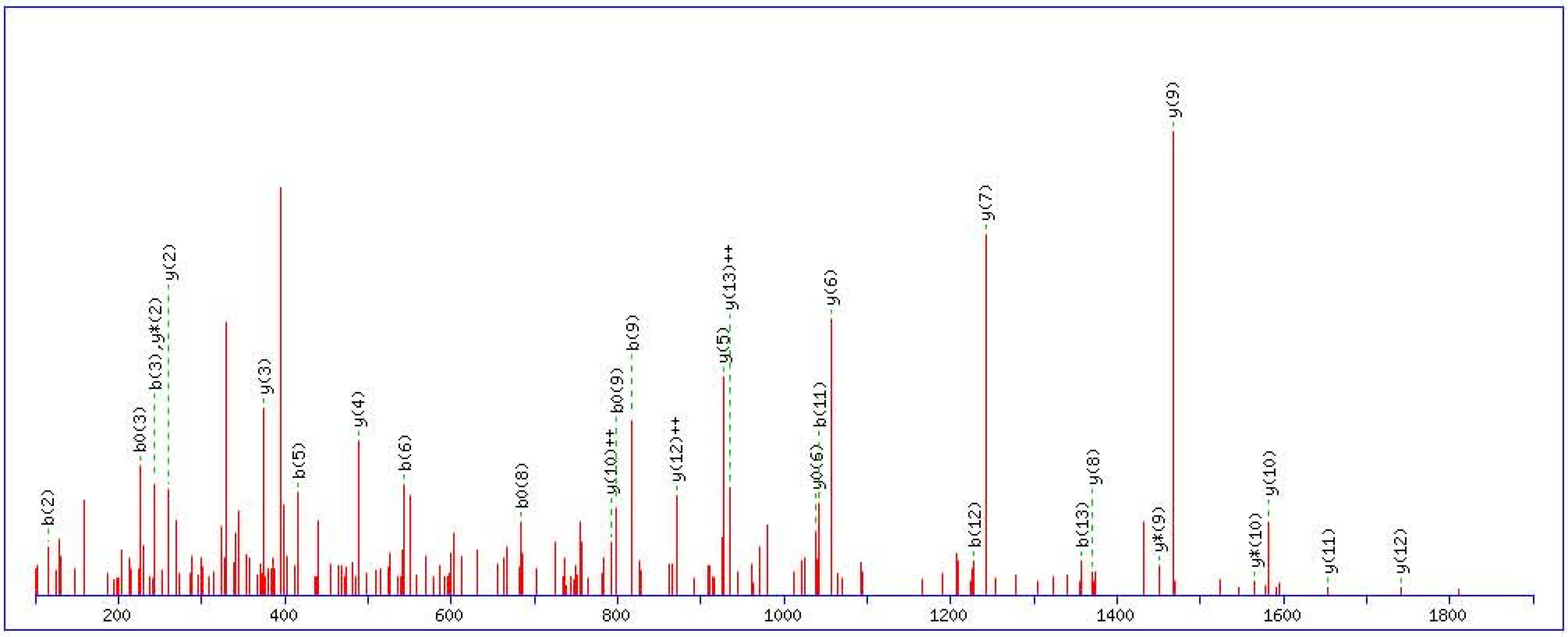
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

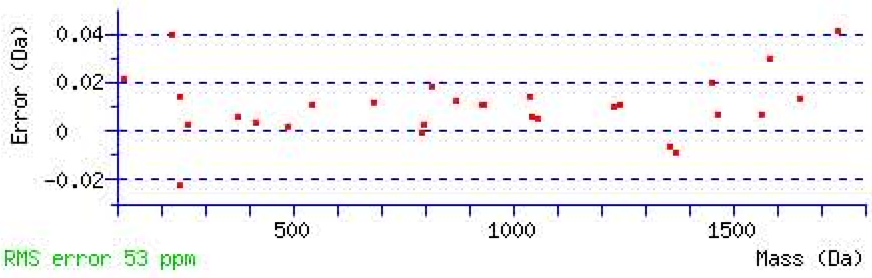
Match to Query 57584: 2283.079122 from(762.033650,3+) rtinseconds(1919) index(41592)
Title: Locus:1.1.1.3117.22 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

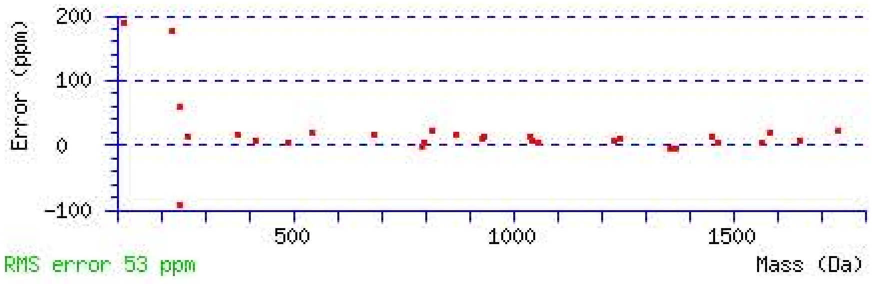
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2283.058975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 2.3e-006
Matches : 29/180 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	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	***544.236168***	272.621722	527.209619	264.108448	526.225603	263.616440	Q	1868.895959	934.951618	1851.869410	926.438343	1850.885394	925.946335	13
7	631.268196	316.137736	614.241647	307.624462	613.257631	307.132454	S	***1740.837381***	870.922329	1723.810832	862.409054	1722.826816	861.917046	12
8	702.305310	351.656293	685.278761	343.143019	684.294745	342.651011	A	***1653.805353***	827.406315	1636.778804	818.893040	1635.794788	818.401032	11
9	***817.332253***	409.169765	800.305704	400.656490	799.321688	400.164482	D	***1582.768239***	791.887758	1565.741690	783.374483	1564.757674	782.882475	10
10	914.385017	457.696147	897.358468	449.182872	896.374452	448.690864	P	***1467.741296***	734.374286	1450.714747	725.861012	1449.730731	725.369004	9
11	***1042.443595***	521.725436	1025.417046	513.212161	1024.433030	512.720153	Q	***1370.688532***	685.847904	1353.661983	677.334630	1352.677967	676.842622	8
12	***1228.522908***	614.765092	1211.496359	606.251818	1210.512343	605.759809	W	***1242.629954***	621.818615	1225.603405	613.305341	1224.619389	612.813333	7
13	***1357.565501***	679.286388	1340.538952	670.773114	1339.554936	670.281106	E	***1056.550641***	528.778959	1039.524092	520.265684	1038.540076	519.773676	6
14	1796.790827	898.899052	1779.764278	890.385777	1778.780262	889.893769	Q	***927.508048***	464.257662	910.481499	455.744388			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
68.7	2283.058975	0.020147	GGETAQSADPQWEQLNNK
33.6	2283.058975	0.020147	GGETAQSADPQWEQLNNK

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

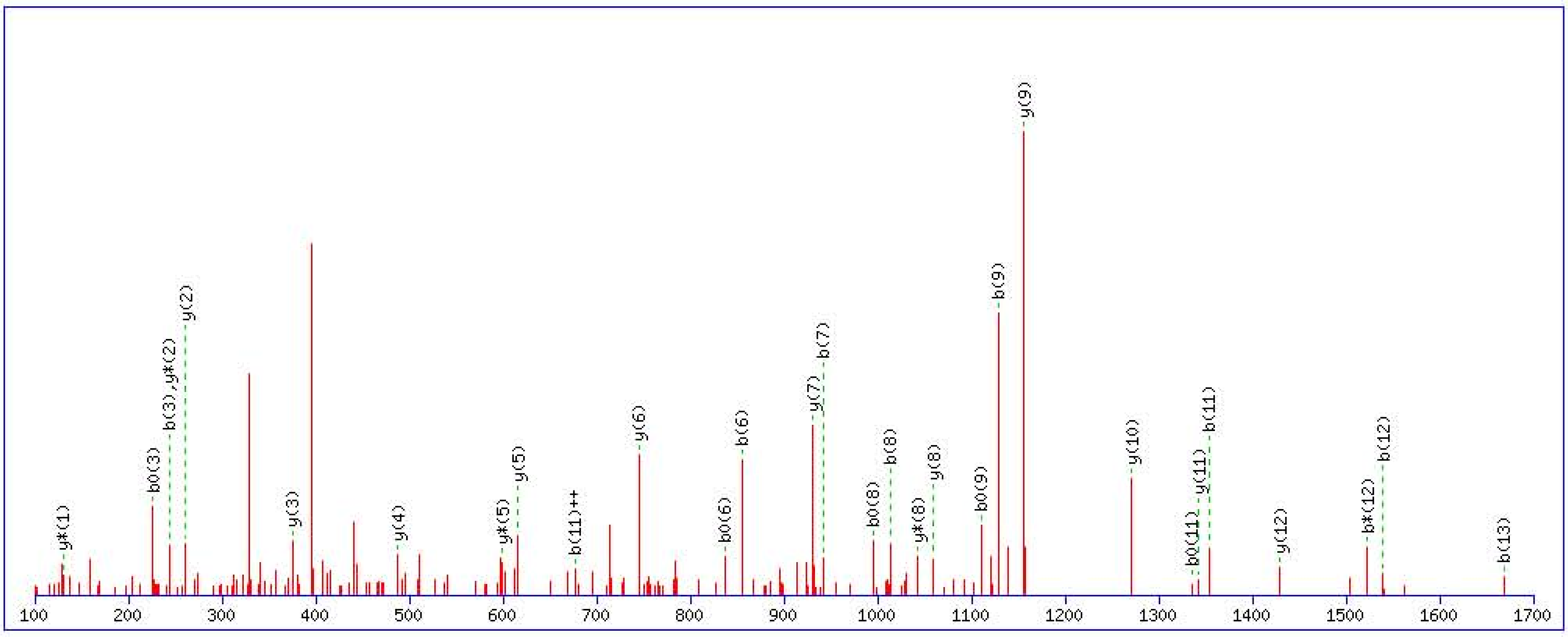
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNK**
Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

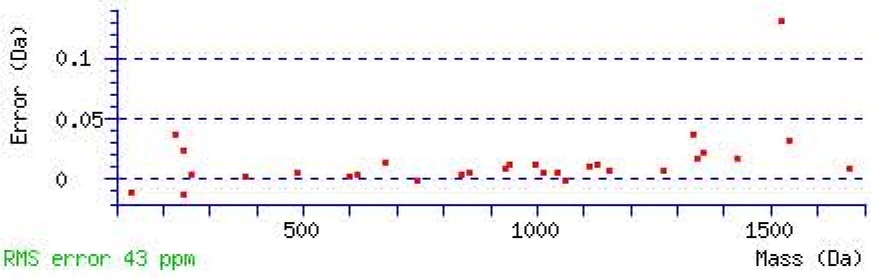
Match to Query 57588: 2283.090162 from(762.037330,3+) rtinseconds(1896) index(41395)
Title: Locus:1.1.1.3109.25 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

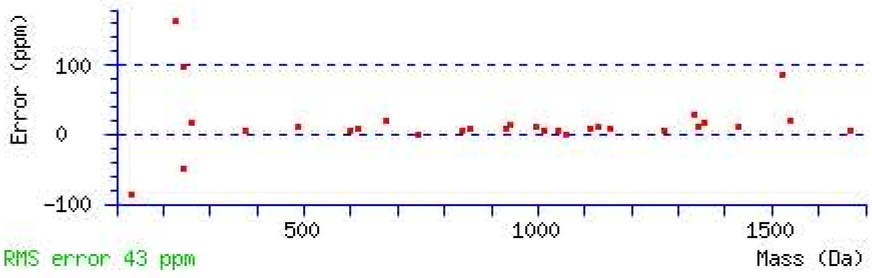
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 73  Expect: 2e-007
Matches : 30/180 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							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
72.5	2283.058975	0.031187	GGETAQSADPQWEQLNNK
14.7	2283.058975	0.031187	GGETAQSADPQWEQLNNK
1.1	2283.080109	0.010053	RGVEKMVDPGEEQPTQENPK

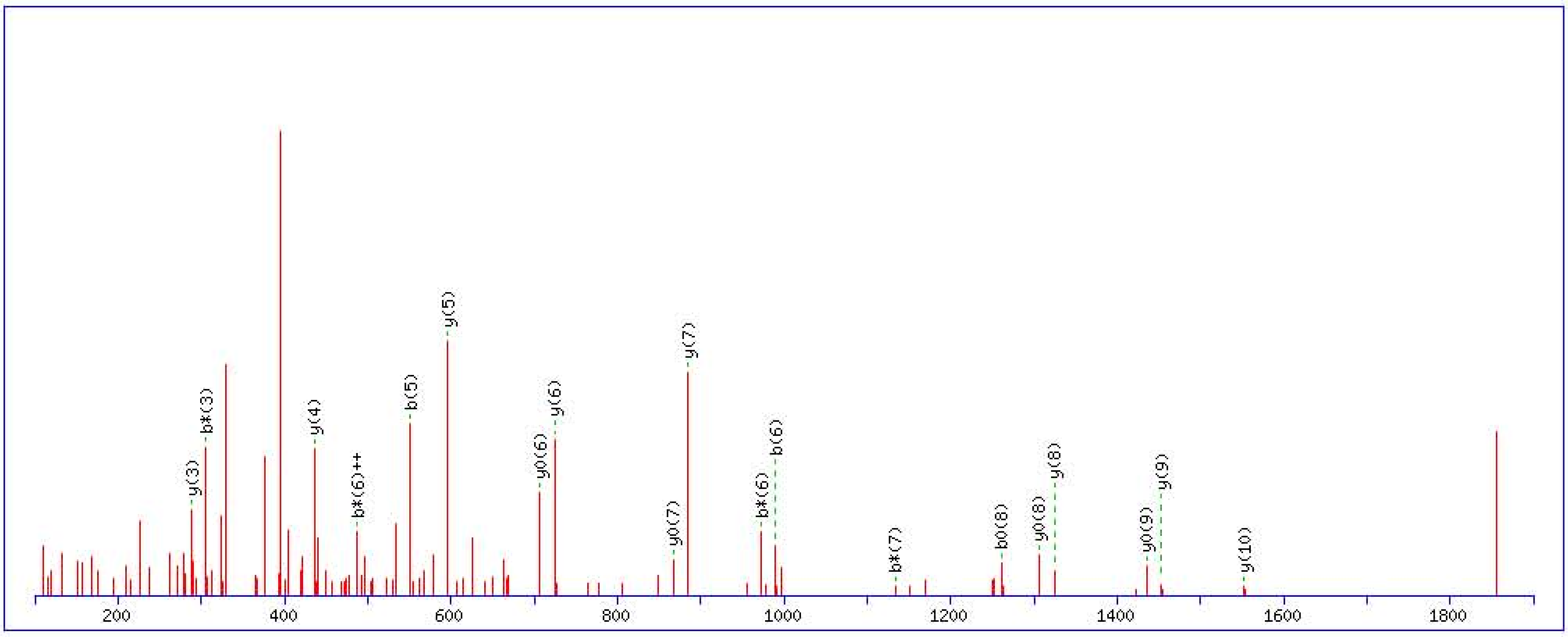
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGHVEQCECFGGR**
Found in **HGFA_HUMAN**, Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1

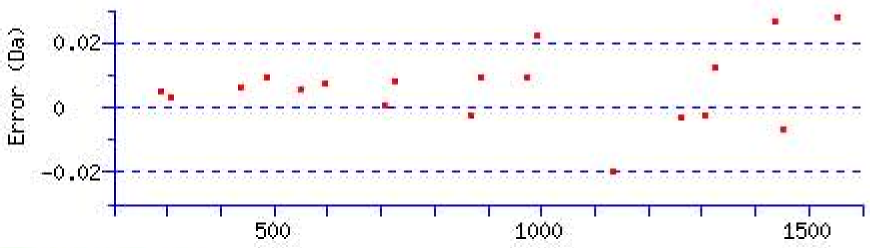
Match to Query 47051: 1873.820172 from(625.614000,3+) rtinseconds(1494) index(38734)
Title: Locus:1.1.1.2969.23 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

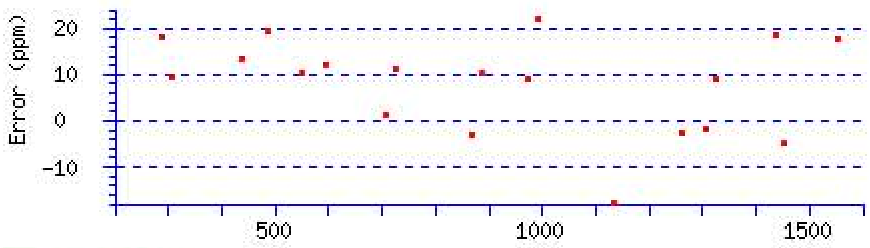


```
Monoisotopic mass of neutral peptide Mr(calc): 1873.802216
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 2.2e-005
Matches : 19/126 fragment ions using 28 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							13
2	186.087318	93.547297	169.060769	85.034023			G	1746.750894	873.879085	1729.724345	865.365811	1728.740329	864.873803	12
3	323.146230	162.076753	306.119681	153.563479			H	1689.729430	845.368353	1672.702881	836.855079	1671.718865	836.363071	11
4	422.214644	211.610960	405.188095	203.097686			V	***1552.670518***	776.838897	1535.643969	768.325623	1534.659953	767.833615	10
5	**551.257237**	276.132257	534.230688	267.618982	533.246672	267.126974	E	***1453.602104***	727.304690	1436.575555	718.791416	1435.591539	718.299408	9
6	**990.482563**	495.744920	973.456014	487.231645	972.471998	486.739637	Q	***1324.559511***	662.783394	1307.532962	654.270119	1306.548946	653.778111	8
7	1150.513212	575.760244	1133.486663	567.246970	1132.502647	566.754962	C	***885.334185***	443.170731	868.307636	434.657456	867.323620	434.165448	7
8	1279.555805	640.281541	1262.529256	631.768266	1261.545240	631.276258	E	***725.303536***	363.155406	708.276987	354.642132	707.292971	354.150124	6
9	1439.586454	720.296865	1422.559905	711.783591	1421.575889	711.291583	C	***596.260943***	298.634110	579.234394	290.120835			5
10	1586.654868	793.831072	1569.628319	785.317798	1568.644303	784.825790	F	***436.230294***	218.618785	419.203745	210.105510			4
11	1643.676332	822.341804	1626.649783	813.828530	1625.665767	813.336522	G	***289.161880***	145.084578	272.135331	136.571303			3
12	1700.697796	850.852536	1683.671247	842.339262	1682.687231	841.847254	G	232.140416	116.573846	215.113867	108.060571			2
13							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 12 ppm



RMS error 12 ppm

NCBI **BLAST** search of QGHVEQCECFGGR
(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	1873.802216	0.017956	QGHVEQCECFGGR
20.1	1873.802216	0.017956	QGHVEQCECFGGR

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

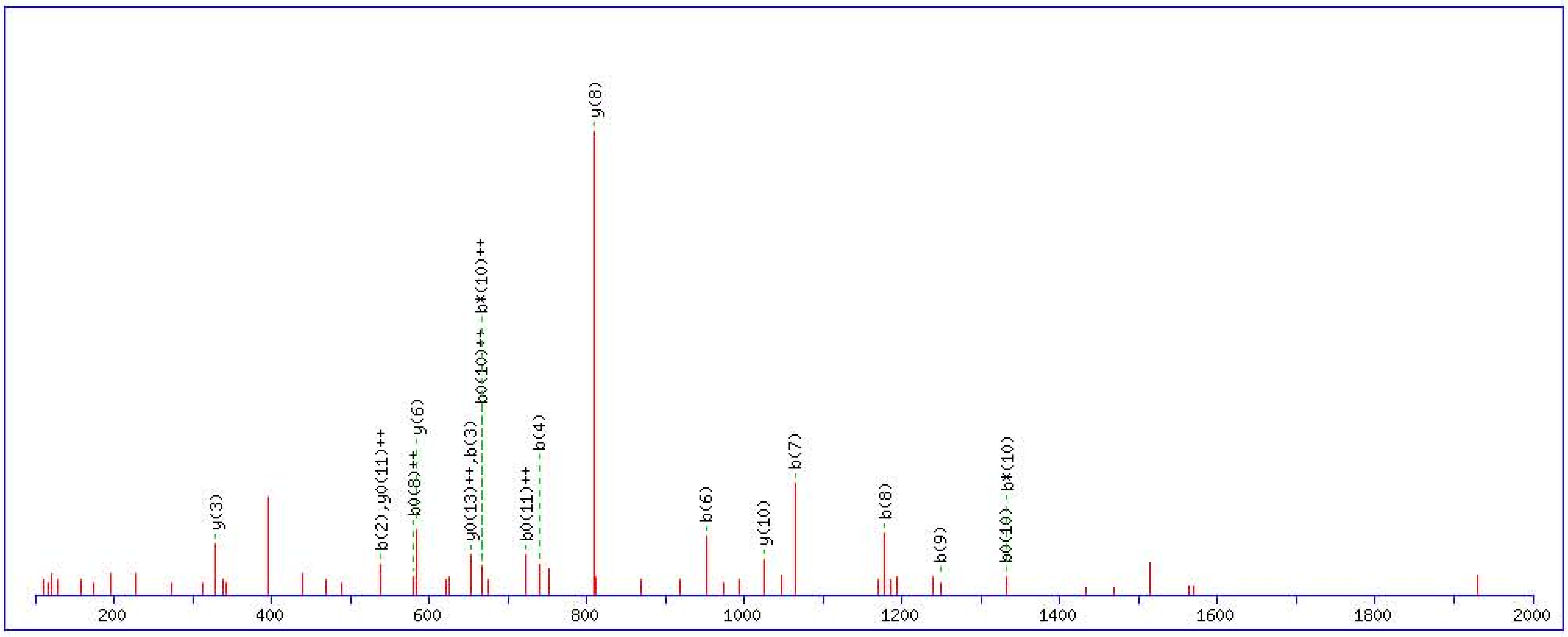
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQLSPDLLATLPEPASPGR**
Found in **HGFA_HUMAN**, Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1

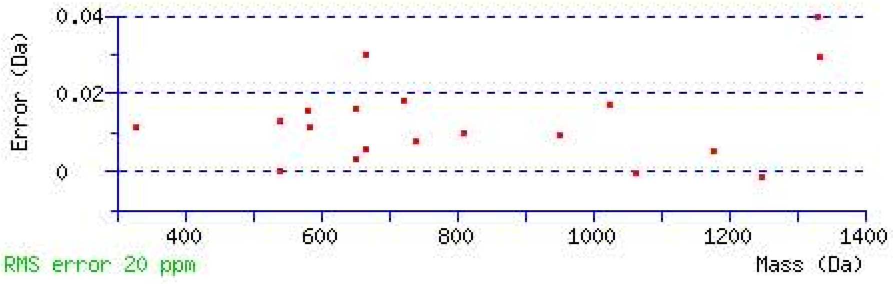
Match to Query 57272: 2271.228522 from(758.083450,3+) rtinseconds(2660) index(46675)
Title: Locus:1.1.1.3374.21 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

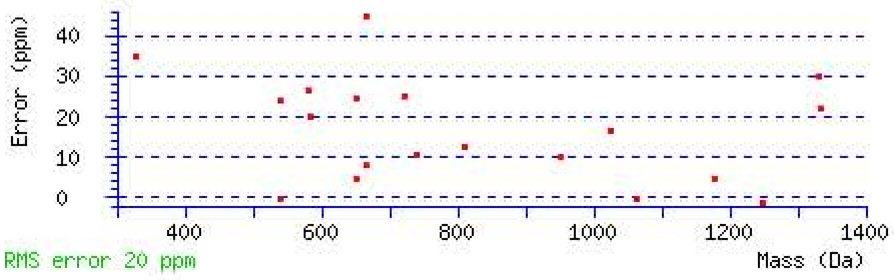
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2271.229675
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.043
Matches : 19/202 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							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
26.5	2271.229675	-0.001153	VQLSPDLLATLPEPASPGR

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

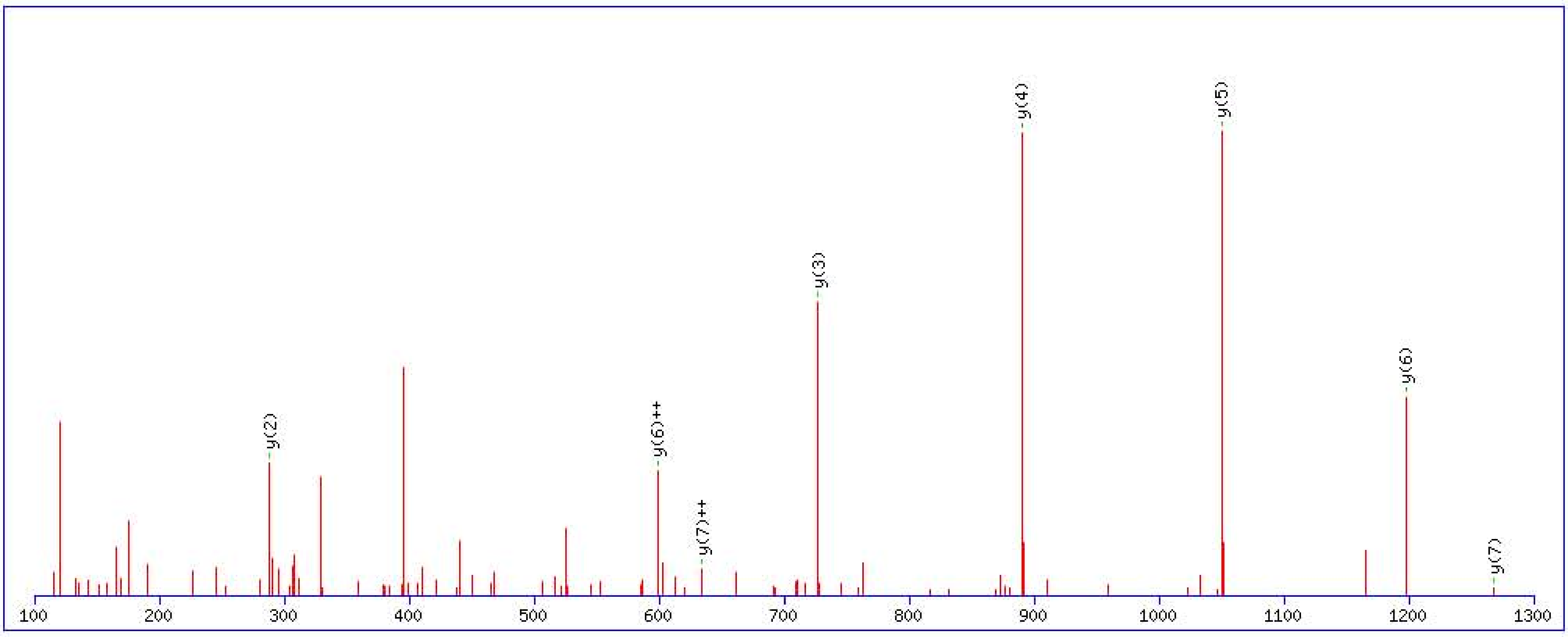
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAFCYQIR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

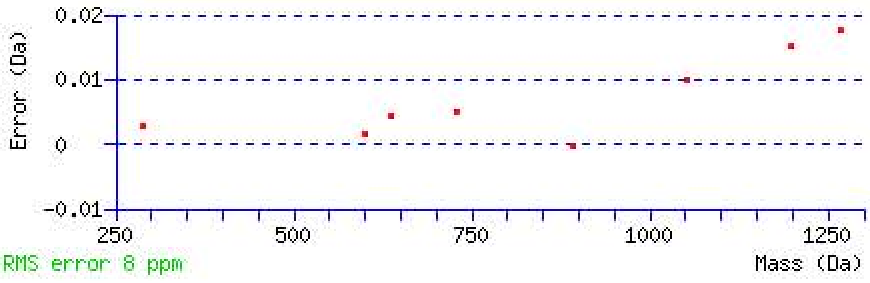
Match to Query 27811: 1338.668728 from(670.341640,2+) rtinseconds(2010) index(78923)
Title: Locus:1.1.1.2050.14 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

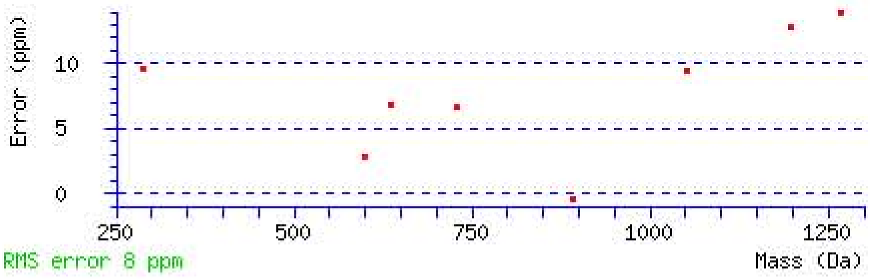
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1338.657669
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00074
Matches : 8/46 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					8
2	143.081504	72.044390			A	***1268.627848***	634.817562	1251.601299	626.304288	7
3	290.149918	145.578597			F	***1197.590734***	599.299005	1180.564185	590.785731	6
4	450.180567	225.593922			C	***1050.522320***	525.764798	1033.495771	517.251524	5
5	613.243896	307.125586			Y	***890.491671***	445.749474	873.465122	437.236199	4
6	1052.469222	526.738249	1035.442673	518.224975	Q	***727.428342***	364.217809	710.401793	355.704534	3
7	1165.553286	583.280281	1148.526737	574.767007	I	***288.203016***	144.605146	271.176467	136.091871	2
8					R	175.118952	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.4	1338.657669	0.011059	AAFCYQIR
9.4	1338.657669	0.011059	AAFLQYCR
3.7	1338.656784	0.011944	ATNYVESNWKK
3.6	1338.671402	-0.002674	AIQSNQPDR
2.6	1338.678787	-0.010059	AEPPMSLQR
1.6	1338.660156	0.008572	AAEEPQQQK
1.6	1338.660156	0.008572	AAEEPQQQK
1.6	1338.660156	0.008572	AAEEPQQQK

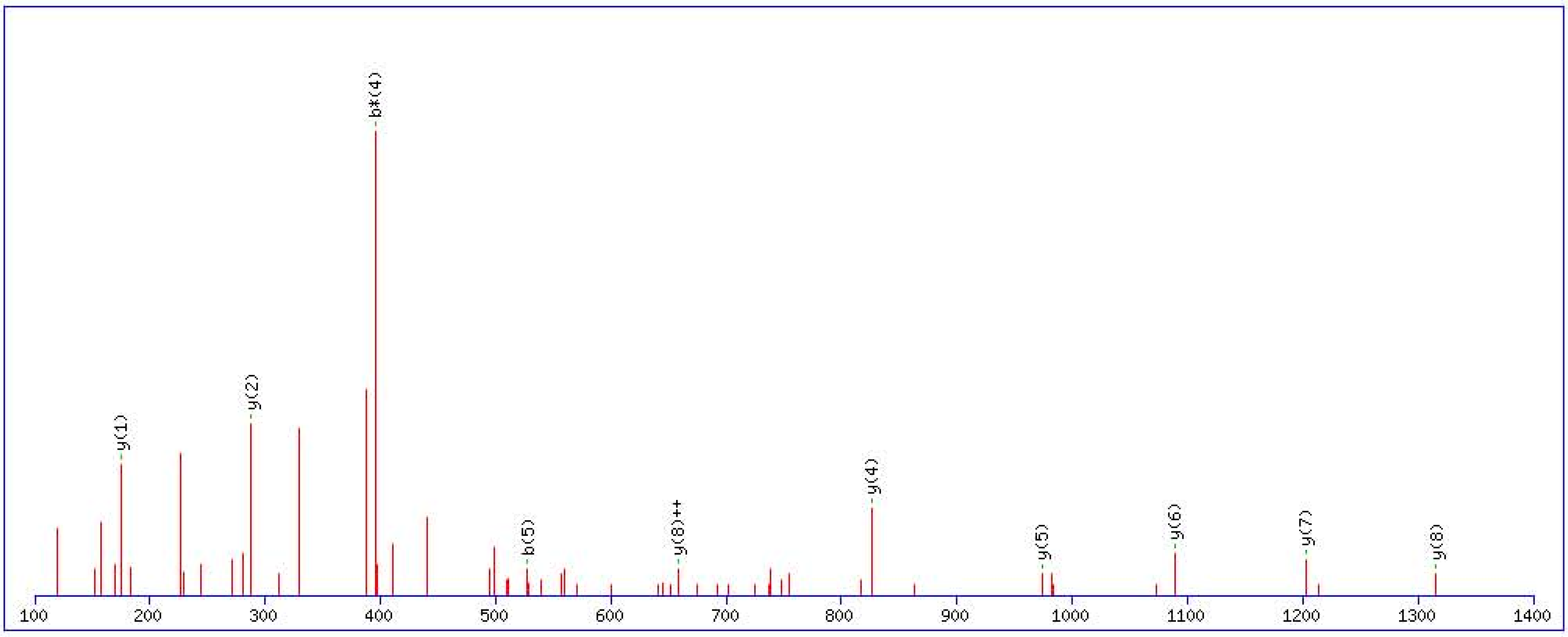
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPLNDFQVLR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

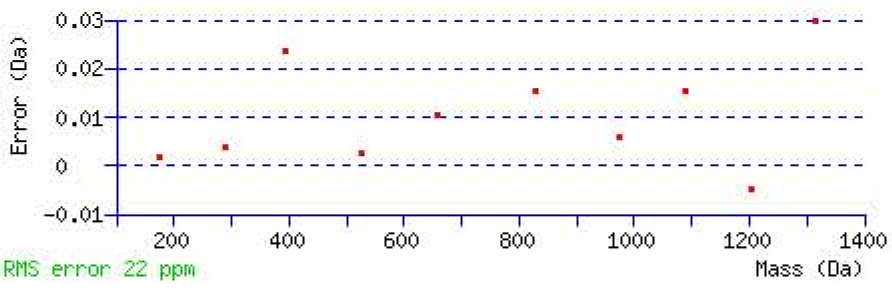
Match to Query 34860: 1498.811532 from(500.611120,3+) rtinseconds(2353) index(81273)
Title: Locus:1.1.1.2170.7 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

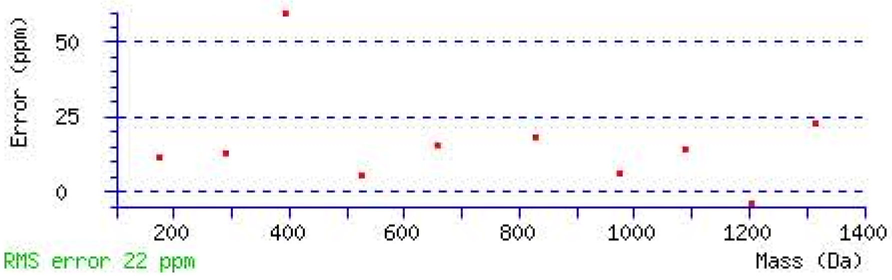
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1498.796616
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 2.2e-005
Matches : 10/92 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	88.039304	44.523290			70.028739	35.518008	S							10
2	185.092068	93.049672			167.081503	84.044389	P	1412.771868	706.889572	1395.745319	698.376298	1394.761303	697.884290	9
3	298.176132	149.591704			280.165567	140.586422	L	***1315.719104***	658.363190	1298.692555	649.849916	1297.708539	649.357908	8
4	412.219059	206.613168	395.192510	198.099893	394.208494	197.607885	N	***1202.635040***	601.821158	1185.608491	593.307884	1184.624475	592.815876	7
5	**527.246002**	264.126639	510.219453	255.613365	509.235437	255.121357	D	***1088.592113***	544.799695	1071.565564	536.286420	1070.581548	535.794412	6
6	674.314416	337.660846	657.287867	329.147572	656.303851	328.655564	F	***973.565170***	487.286223	956.538621	478.772949			5
7	1113.539742	557.273509	1096.513193	548.760235	1095.529177	548.268227	Q	***826.496756***	413.752016	809.470207	405.238742			4
8	1212.608156	606.807716	1195.581607	598.294442	1194.597591	597.802434	V	387.271430	194.139353	370.244881	185.626078			3
9	1325.692220	663.349748	1308.665671	654.836474	1307.681655	654.344466	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 SPLNDFQVLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.9	1498.796616	0.014916	SPLNDFQVLR
12.2	1498.792572	0.018960	ALNITSLQMHSLR
4.3	1498.799103	0.012429	ALLNLPGTQTSGEAK
2.9	1498.807831	0.003701	MRSGLPAPWISLR
2.8	1498.832993	-0.021461	QAFKPTDILR
0.8	1498.817749	-0.006217	LQGLPIVAGTMDIR
0.5	1498.832962	-0.021430	LRLDKYYMLIR
0.0	1498.815674	-0.004142	YRYLPERPHLR

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

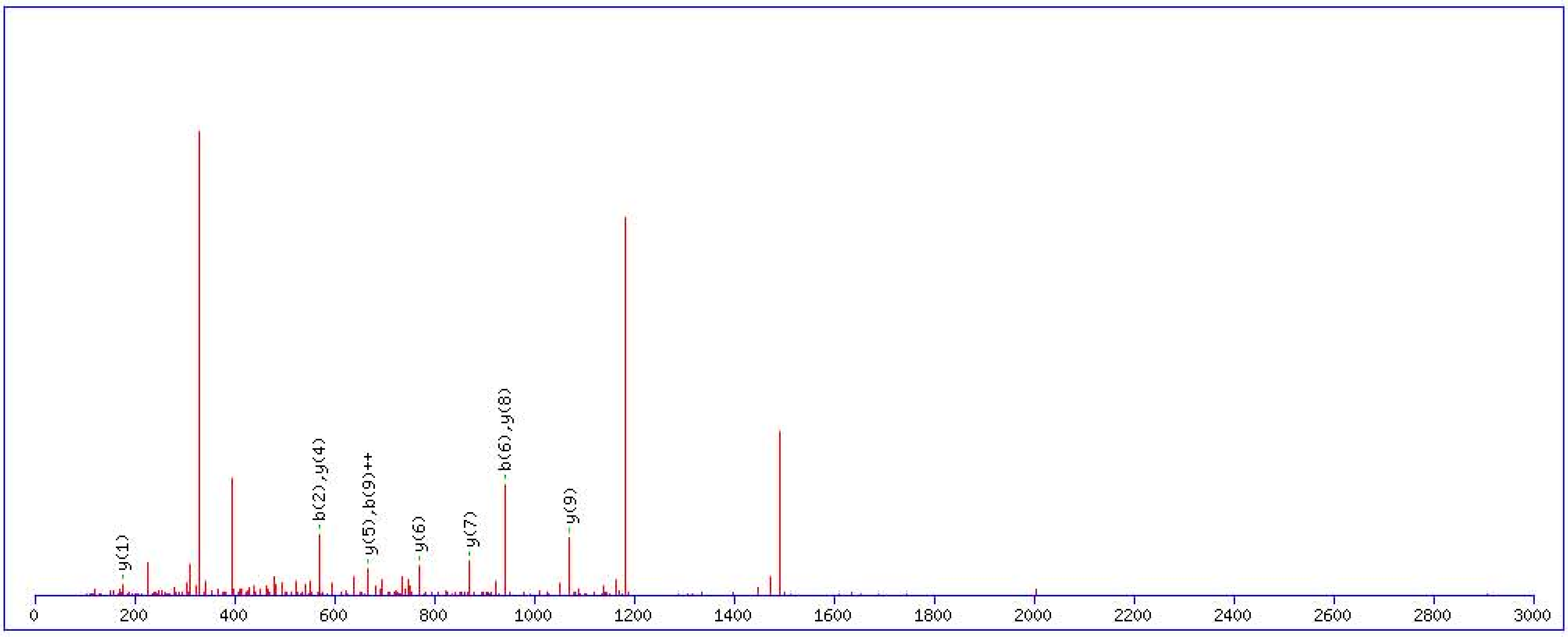
Mascot Search Results

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

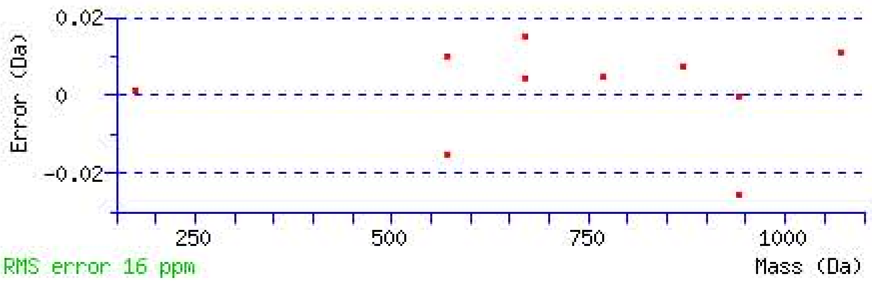
Match to Query 35329: 1508.723308 from(755.368930,2+) rtinseconds(1744) index(77200)
Title: Locus:1.1.1.1958.8 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

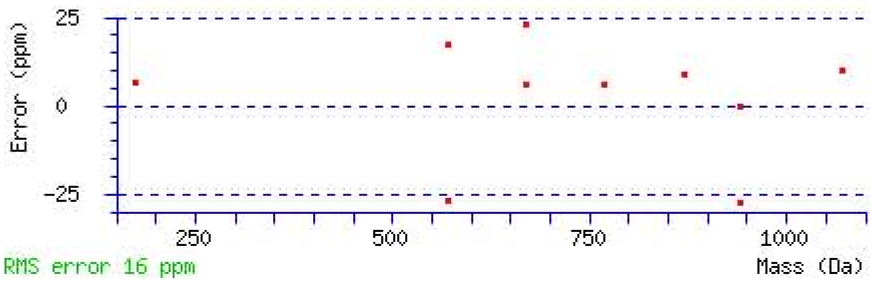


Monoisotopic mass of neutral peptide Mr(calc): 1508.711578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 44 **Expect:** 0.00059
Matches : 10/100 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 16 ppm



RMS error 16 ppm

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
44.2	1508.711578	0.011730	QEATTVSCFR
9.2	1508.711380	0.011928	RTASGGRTEQGMSR
7.2	1508.726624	-0.003316	RDGQLQRMNYGR
5.7	1508.744385	-0.021077	VSNQQSNLAQHQR
4.8	1508.733154	-0.009846	APGSRLSSGGTNYSR
2.7	1508.708191	0.015117	EYGSMYTVHLGPR
2.1	1508.741180	-0.017872	SKLAYYDPHPYR
2.1	1508.703461	0.019847	LKSFTYEYEDSK
1.8	1508.727295	-0.003987	ESSHKHTFFHPR
1.5	1508.740540	-0.017232	EQHEDKSAVR

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

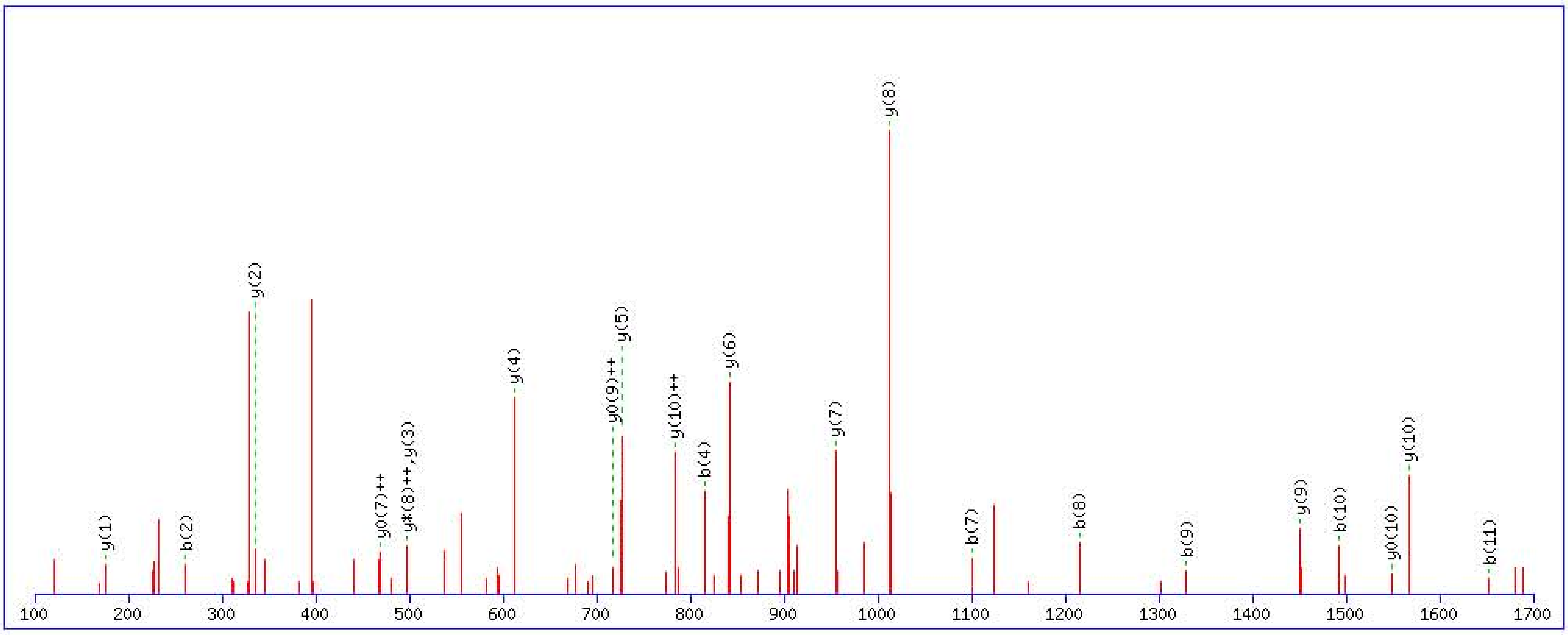
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLDQGLDDNYCR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

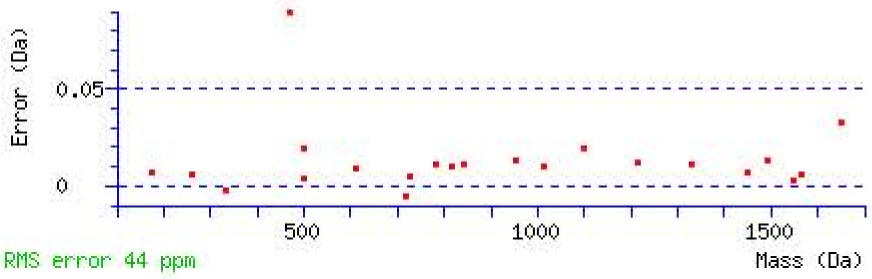
Match to Query 45938: 1825.830628 from(913.922590,2+) rtinseconds(2145) index(79835)
Title: Locus:1.1.1.2097.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

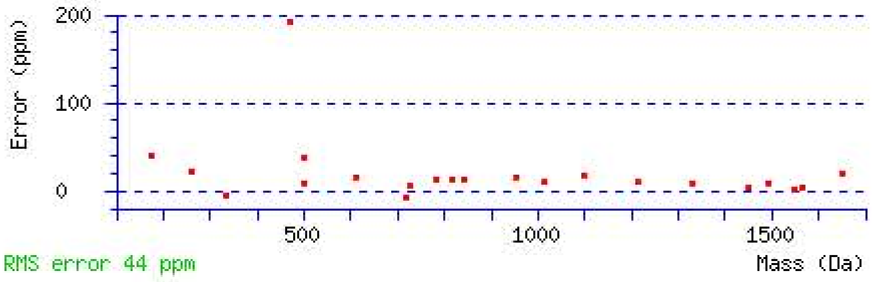
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1825.812744
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 3.7e-006
Matches : 22/114 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	148.075690	74.541483					F							12
2	**261.159754**	131.083515					L	1679.751604	840.379440	1662.725055	831.866166	1661.741039	831.374158	11
3	376.186697	188.596986			358.176132	179.591704	D	***1566.667540***	783.837408	1549.640991	775.324134	1548.656975	774.832126	10
4	**815.412023**	408.209650	798.385474	399.696375	797.401458	399.204367	Q	***1451.640597***	726.323937	1434.614048	717.810662	1433.630032	717.318654	9
5	872.433487	436.720382	855.406938	428.207107	854.422922	427.715099	G	***1012.415271***	506.711274	995.388722	498.197999	994.404706	497.705991	8
6	985.517551	493.262414	968.491002	484.749139	967.506986	484.257131	L	***955.393807***	478.200542	938.367258	469.687267	937.383242	469.195259	7
7	**1100.544494**	550.775885	1083.517945	542.262611	1082.533929	541.770603	D	***842.309743***	421.658510	825.283194	413.145235	824.299178	412.653227	6
8	**1215.571437**	608.289357	1198.544888	599.776082	1197.560872	599.284074	D	***727.282800***	364.145038	710.256251	355.631764	709.272235	355.139756	5
9	**1329.614364**	665.310820	1312.587815	656.797546	1311.603799	656.305538	N	***612.255857***	306.631567	595.229308	298.118292			4
10	**1492.677693**	746.842485	1475.651144	738.329210	1474.667128	737.837202	Y	***498.212930***	249.610103	481.186381	241.096829			3
11	**1652.708342**	826.857809	1635.681793	818.344535	1634.697777	817.852527	C	***335.149601***	168.078438	318.123052	159.565164			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.0	1825.812744	0.017884	FLDQGLDDNYCR
0.1	1825.823944	0.006684	QNSWKGYSENMR

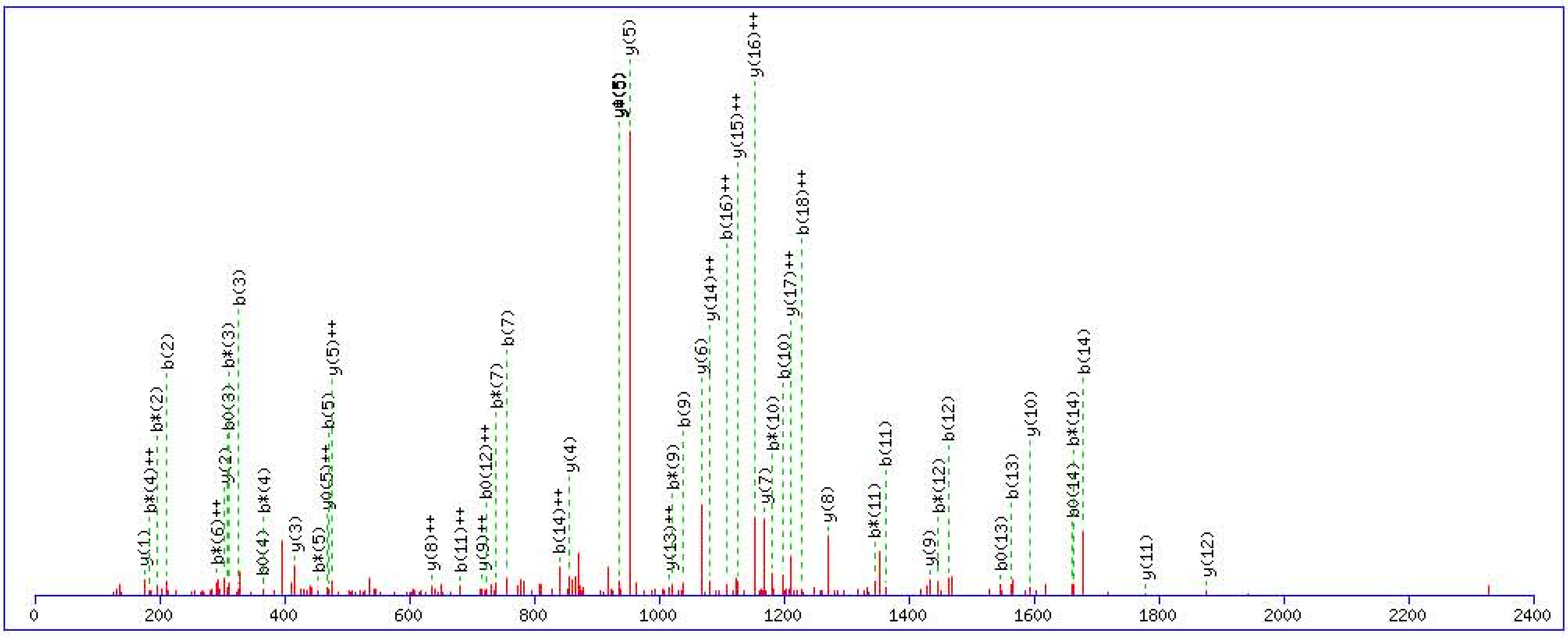
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of NPDGSERPWCYTTDPQIER
Found in HGFL_HUMAN, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

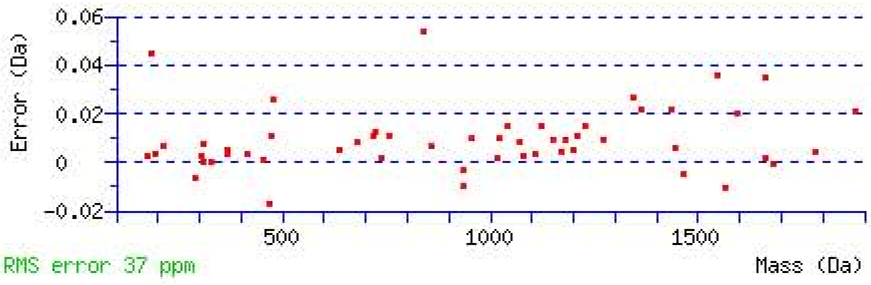
Match to Query 64878: 2631.206262 from(878.076030,3+) rtinseconds(1999) index(78875)
Title: Locus:1.1.1.2046.12 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

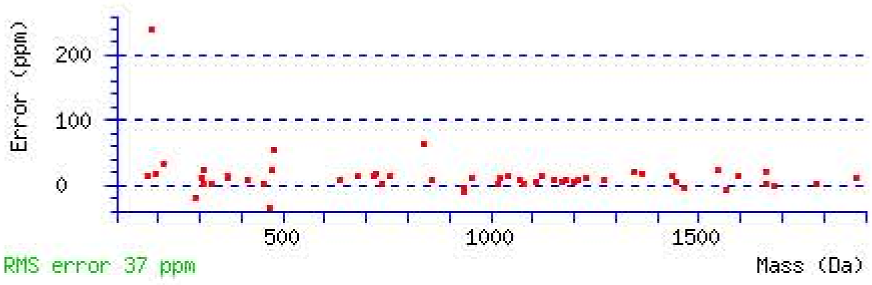
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2631.184601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 4.1e-005
Matches : 54/210 fragment ions using 113 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							19
2	**212.102967**	106.555121	195.076418	98.041847			P	2518.148958	1259.578117	2501.122409	1251.064842	2500.138393	1250.572834	18
3	**327.129910**	164.068593	310.103361	155.555319	309.119345	155.063311	D	2421.096194	1211.051735	2404.069645	1202.538460	2403.085629	1202.046452	17
4	384.151374	192.579325	367.124825	184.066050	366.140809	183.574042	G	2306.069251	1153.538263	2289.042702	1145.024989	2288.058686	1144.532981	16
5	**471.183402**	236.095339	454.156853	227.582064	453.172837	227.090056	S	2249.047787	1125.027531	2232.021238	1116.514257	2231.037222	1116.022249	15
6	600.225995	300.616636	583.199446	292.103361	582.215430	291.611353	E	2162.015759	1081.511517	2144.989210	1072.998243	2144.005194	1072.506235	14
7	**756.327106**	378.667191	739.300557	370.153916	738.316541	369.661908	R	2032.973166	1016.990221	2015.946617	1008.476947	2014.962601	1007.984939	13
8	853.379870	427.193573	836.353321	418.680298	835.369305	418.188290	P	***1876.872055***	938.939666	1859.845506	930.426391	1858.861490	929.934383	12
9	**1039.459183**	520.233229	1022.432634	511.719955	1021.448618	511.227947	W	***1779.819291***	890.413284	1762.792742	881.900009	1761.808726	881.408001	11
10	**1199.489832**	600.248554	1182.463283	591.735280	1181.479267	591.243271	C	***1593.739978***	797.373627	1576.713429	788.860353	1575.729413	788.368345	10
11	**1362.553161**	**681.780219**	1345.526612	673.266944	1344.542596	672.774936	Y	***1433.709329***	717.358303	1416.682780	708.845028	1415.698764	708.353020	9
12	**1463.600840**	732.304058	1446.574291	723.790784	1445.590275	723.298776	T	***1270.646000***	635.826638	1253.619451	627.313364	1252.635435	626.821356	8
13	**1564.648519**	782.827898	1547.621970	774.314623	1546.637954	773.822615	T	***1169.598321***	585.302799	1152.571772	576.789524	1151.587756	576.297516	7
14	**1679.675462**	**840.341369**	1662.648913	831.828095	1661.664897	831.336087	D	***1068.550642***	534.778959	1051.524093	526.265685	1050.540077	525.773677	6
15	1776.728226	888.867751	1759.701677	880.354477	1758.717661	879.862469	P	***953.523699***	477.265488	936.497150	468.752213	935.513134	468.260205	5
16	2215.953552	**1108.480414**	2198.927003	1099.967139	2197.942987	1099.475131	Q	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
17	2329.037616	1165.022446	2312.011067	1156.509171	2311.027051	1156.017163	I	***417.245609***	209.126443	400.219060	200.613168	399.235044	200.121160	3
18	2458.080209	**1229.543743**	2441.053660	1221.030468	2440.069644	1220.538460	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.0	2631.184601	0.021661	NPDGSERPWCYTTDPQIER

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

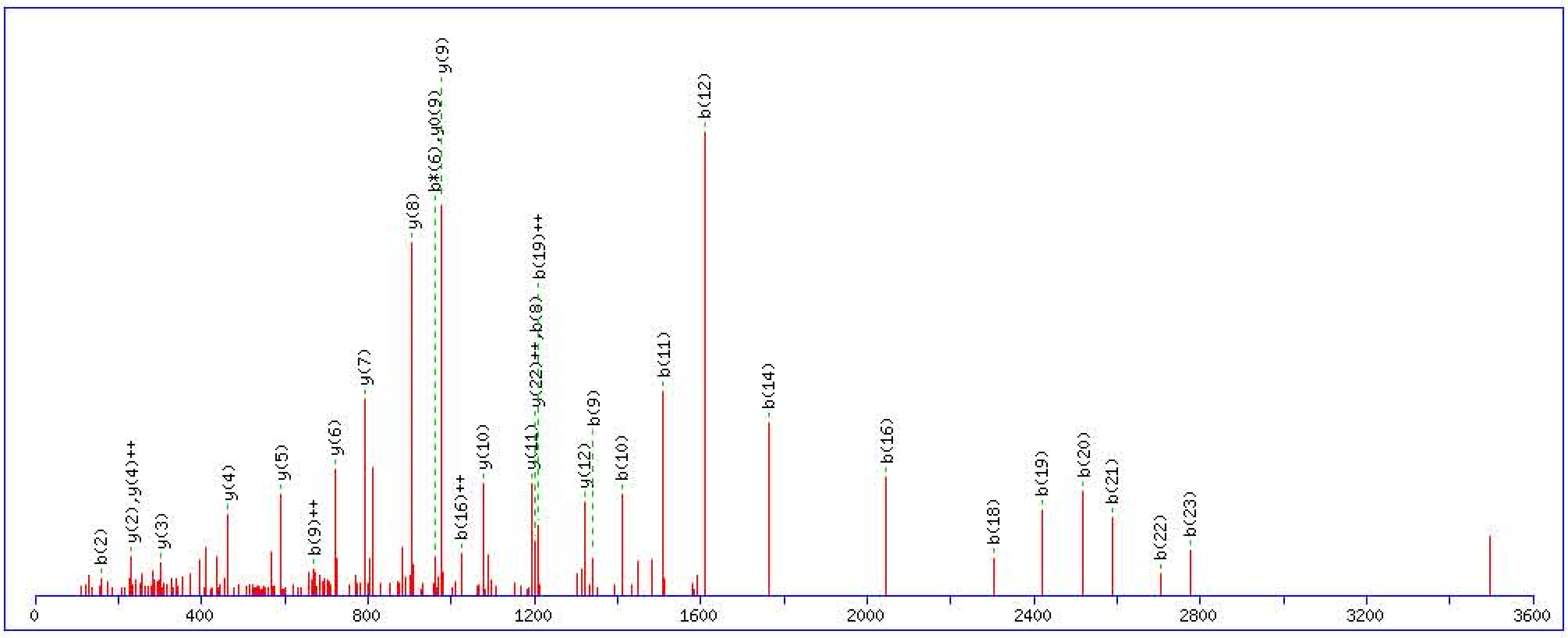
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTELQHLLHAVVPGPWQEDVADAEECAGR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

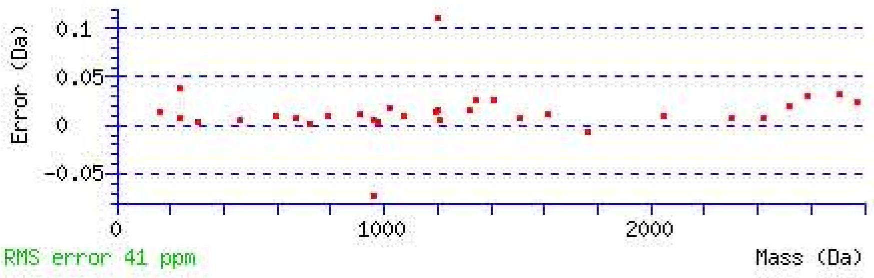
Match to Query 77303: 3494.708496 from(874.684400,4+) rtinseconds(2782) index(84141)
Title: Locus:1.1.1.2317.19 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

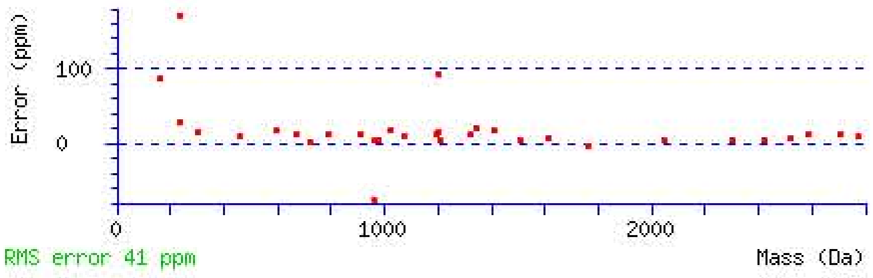


```
Monoisotopic mass of neutral peptide Mr(calc): 3494.671112
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 104  Expect: 1.8e-010
Matches : 32/318 fragment ions using 40 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							29
2	***159.076419***	80.041847			141.065854	71.036565	T	3438.656925	1719.832100	3421.630376	1711.318826	3420.646360	1710.826818	28
3	288.119012	144.563144			270.108447	135.557862	E	3337.609246	1669.308261	3320.582697	1660.794986	3319.598681	1660.302978	27
4	401.203076	201.105176			383.192511	192.099894	L	3208.566653	1604.786964	3191.540104	1596.273690	3190.556088	1595.781682	26
5	840.428402	420.717839	823.401853	412.204565	822.417837	411.712557	Q	3095.482589	1548.244932	3078.456040	1539.731658	3077.472024	1539.239650	25
6	977.487314	489.247295	960.460765	480.734021	959.476749	480.242013	H	2656.257263	1328.632269	2639.230714	1320.118995	2638.246698	1319.626987	24
7	1090.571378	545.789327	1073.544829	537.276053	1072.560813	536.784045	L	2519.198351	1260.102813	2502.171802	1251.589539	2501.187786	1251.097531	23
8	***1203.655442***	602.331359	1186.628893	593.818085	1185.644877	593.326077	L	2406.114287	1203.560781	2389.087738	1195.047507	2388.103722	1194.555499	22
9	***1340.714354***	**670.860815**	1323.687805	662.347541	1322.703789	661.855532	H	2293.030223	1147.018749	2276.003674	1138.505475	2275.019658	1138.013467	21
10	***1411.751468***	706.379372	1394.724919	697.866098	1393.740903	697.374089	A	2155.971311	1078.489293	2138.944762	1069.976019	2137.960746	1069.484011	20
11	***1510.819882***	755.913579	1493.793333	747.400305	1492.809317	746.908297	V	2084.934197	1042.970736	2067.907648	1034.457462	2066.923632	1033.965454	19
12	***1609.888296***	805.447786	1592.861747	796.934512	1591.877731	796.442504	V	1985.865783	993.436530	1968.839234	984.923255	1967.855218	984.431247	18
13	1706.941060	853.974168	1689.914511	845.460894	1688.930495	844.968886	P	1886.797369	943.902323	1869.770820	935.389048	1868.786804	934.897040	17
14	***1763.962524***	882.484900	1746.935975	873.971626	1745.951959	873.479618	G	1789.744605	895.375941	1772.718056	886.862666	1771.734040	886.370658	16
15	1861.015288	931.011282	1843.988739	922.498008	1843.004723	922.006000	P	1732.723141	866.865209	1715.696592	858.351934	1714.712576	857.859926	15
16	***2047.094601***	**1024.050939**	2030.068052	1015.537664	2029.084036	1015.045656	W	1635.670377	818.338827	1618.643828	809.825552	1617.659812	809.333544	14
17	2175.153179	1088.080227	2158.126630	1079.566953	2157.142614	1079.074945	Q	1449.591064	725.299170	1432.564515	716.785896	1431.580499	716.293888	13
18	***2304.195772***	1152.601524	2287.169223	1144.088249	2286.185207	1143.596241	E	***1321.532486***	661.269881	1304.505937	652.756607	1303.521921	652.264599	12
19	***2419.222715***	**1210.114995**	2402.196166	1201.601721	2401.212150	1201.109713	D	***1192.489893***	596.748585	1175.463344	588.235310	1174.479328	587.743302	11
20	***2518.291129***	1259.649202	2501.264580	1251.135928	2500.280564	1250.643920	V	***1077.462950***	539.235113	1060.436401	530.721839	1059.452385	530.229831	10
21	***2589.328243***	1295.167759	2572.301694	1286.654485	2571.317678	1286.162477	A	***978.394536***	489.700906	961.367987	481.187632	960.383971	480.695624	9
22	***2704.355186***	1352.681231	2687.328637	1344.167956	2686.344621	1343.675948	D	***907.357422***	454.182349	890.330873	445.669075	889.346857	445.177067	8
23	***2775.392300***	1388.199788	2758.365751	1379.686513	2757.381735	1379.194505	A	***792.330479***	396.668878	775.303930	388.155603	774.319914	387.663595	7
24	2904.434893	1452.721085	2887.408344	1444.207810	2886.424328	1443.715802	E	***721.293365***	361.150321	704.266816	352.637046	703.282800	352.145038	6
25	3033.477486	1517.242381	3016.450937	1508.729106	3015.466921	1508.237099	E	***592.250772***	296.629024	575.224223	288.115750	574.240207	287.623742	5
26	3193.508135	1597.257705	3176.481586	1588.744431	3175.497570	1588.252423	C	***463.208179***	232.107727	446.181630	223.594453			4
27	3264.545249	1632.776263	3247.518700	1624.262988	3246.534684	1623.770980	A	***303.177530***	152.092403	286.150981	143.579129			3
28	3321.566713	1661.286995	3304.540164	1652.773720	3303.556148	1652.281712	G	***232.140416***	116.573846	215.113867	108.060571			2
29							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 41 ppm



RMS error 41 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
104.4	3494.671112	0.037384	GTELQHLLHAVVPGPWQEDVADAEECAGR
47.5	3494.671112	0.037384	GTELQHLLHAVVPGPWQEDVADAEECAGR
0.4	3494.727249	-0.018753	ETVAQLLKEMTNADSQNEGLLTMEQFNTVLK

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

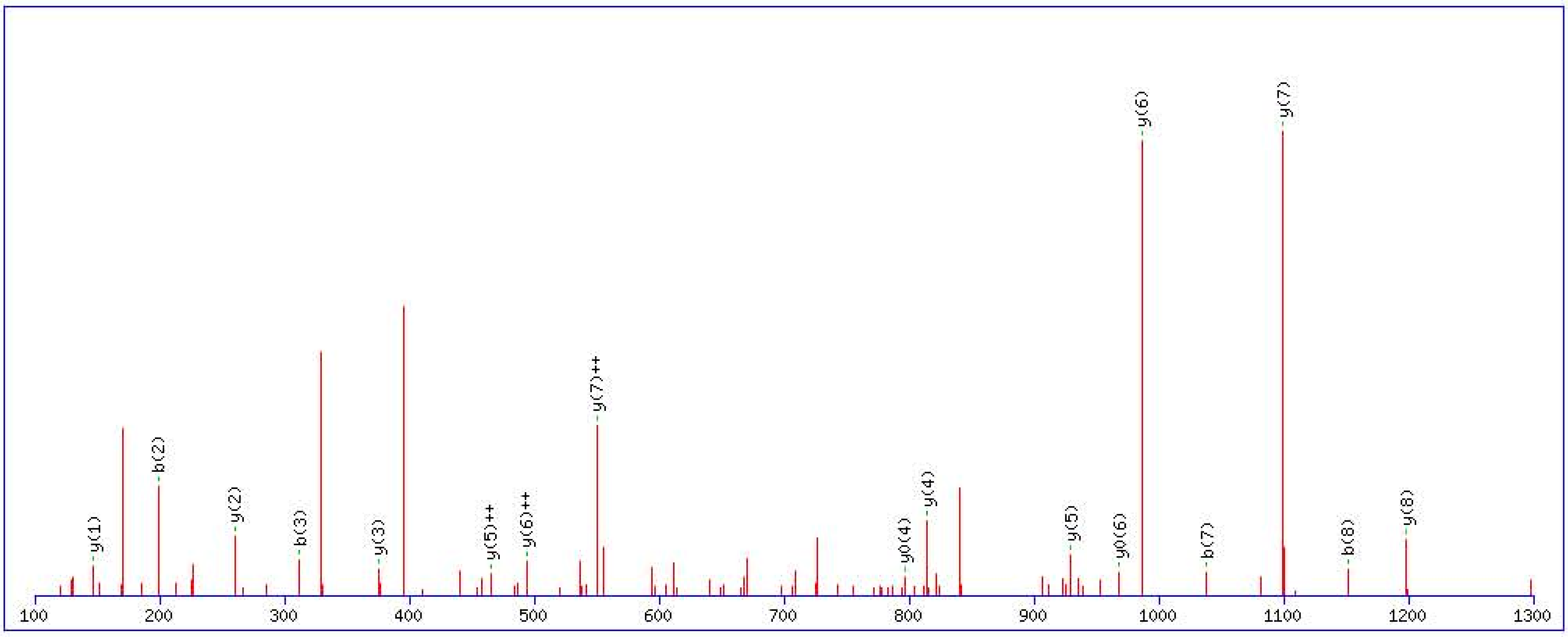
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLGDQDLK**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

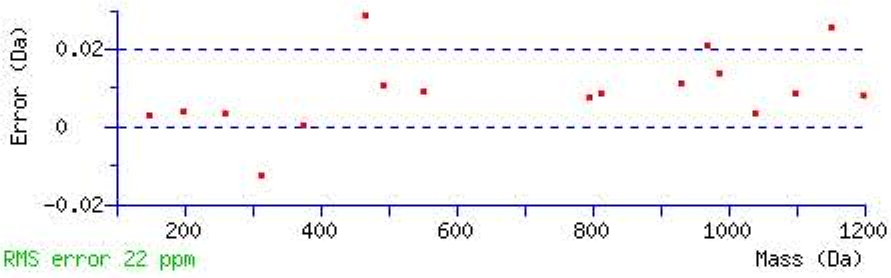
Match to Query 26851: 1296.728928 from(649.371740,2+) rtinseconds(1954) index(60464)
Title: Locus:1.1.1.3103.15 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

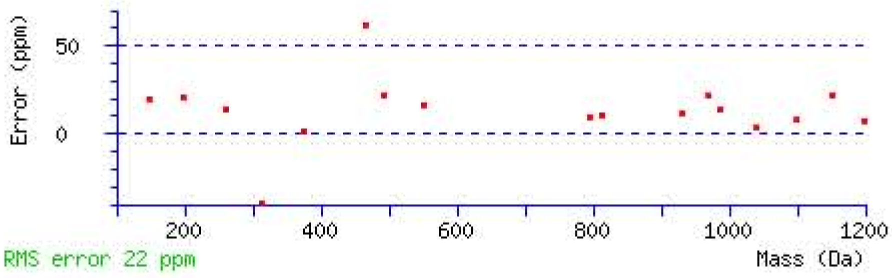
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1296.711166
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00011
Matches : 17/74 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	100.075690	50.541483					V							9
2	**199.144104**	100.075690					V	***1198.650022***	599.828649	1181.623473	591.315374	1180.639457	590.823366	8
3	**312.228168**	156.617722					L	***1099.581608***	550.294442	1082.555059	541.781168	1081.571043	541.289159	7
4	369.249632	185.128454					G	***986.497544***	493.752410	969.470995	485.239135	968.486979	484.747127	6
5	484.276575	242.641925			466.266010	233.636643	D	***929.476080***	465.241678	912.449531	456.728403	911.465515	456.236395	5
6	923.501901	462.254589	906.475352	453.741314	905.491336	453.249306	Q	***814.449137***	407.728206	797.422588	399.214932	796.438572	398.722924	4
7	**1038.528844**	519.768060	1021.502295	511.254785	1020.518279	510.762777	D	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
8	**1151.612908**	576.310092	1134.586359	567.796817	1133.602343	567.304809	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 VVLGDQDLK
(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	1296.711166	0.017762	VVLGDQDLK
6.5	1296.711136	0.017792	QEVQELLK
6.3	1296.719025	0.009903	VVSIHQDPKFK
5.6	1296.747513	-0.018585	QDEKLLLK
2.8	1296.733612	-0.004684	QRIITGGNK
2.8	1296.711136	0.017792	ELCGLPPIASLK
2.1	1296.714996	0.013932	KPGSAGGPKVGGASK
1.9	1296.740112	-0.011184	QIIEATPERIK

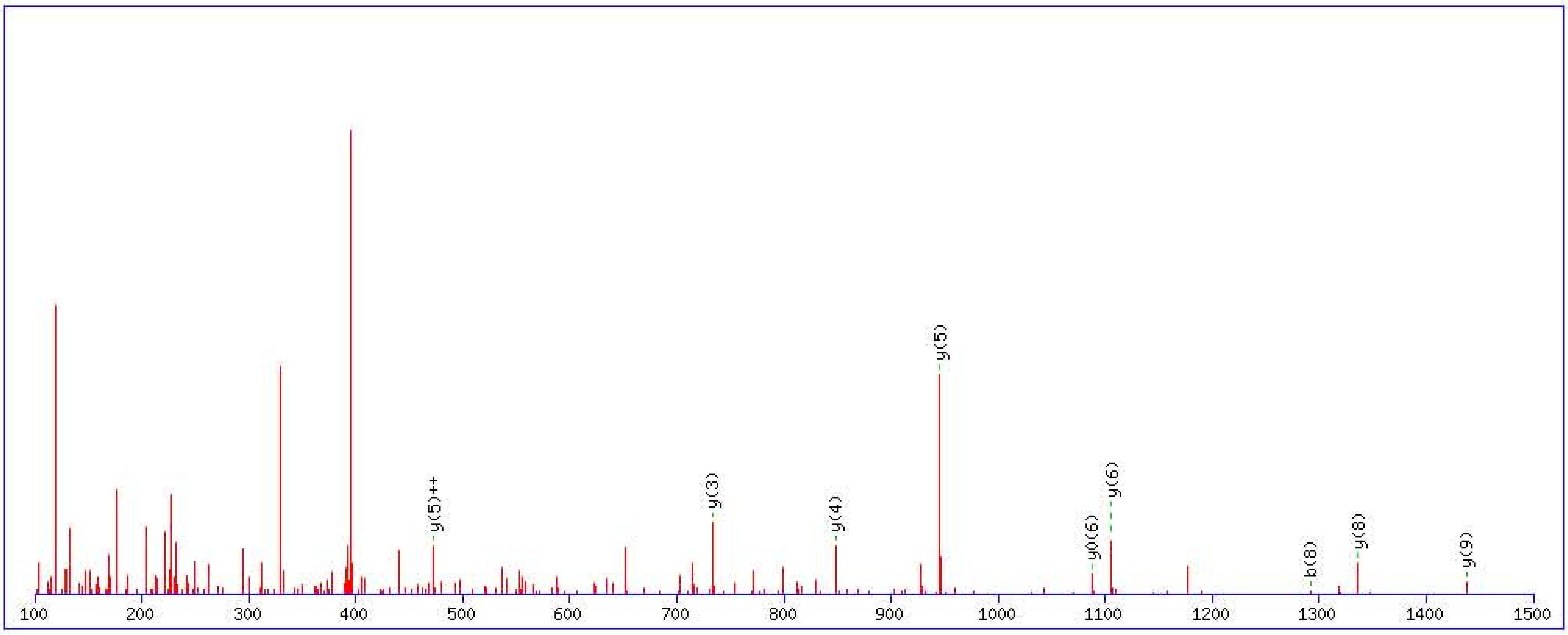
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FTCACPDQFK**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

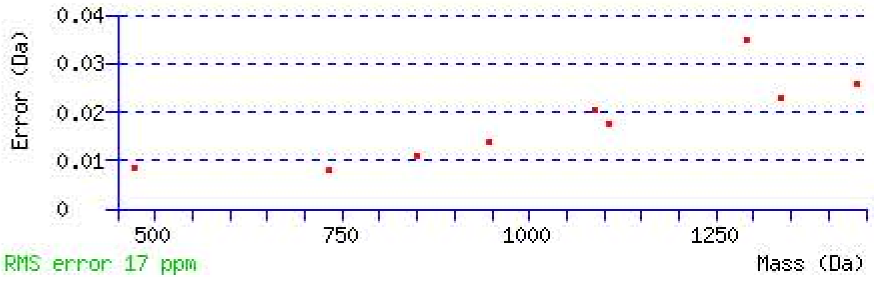
Match to Query 37912: 1583.713332 from(528.911720,3+) rtinseconds(1852) index(59645)
Title: Locus:1.1.1.3068.7 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

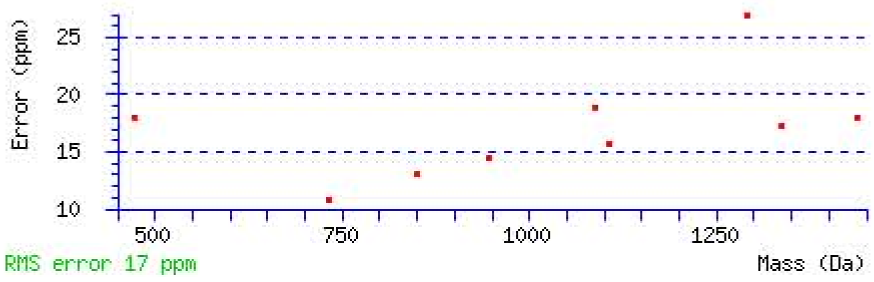
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1583.693497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.0031
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	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
34.5	1583.693497	0.019835	FTCACPDQFK

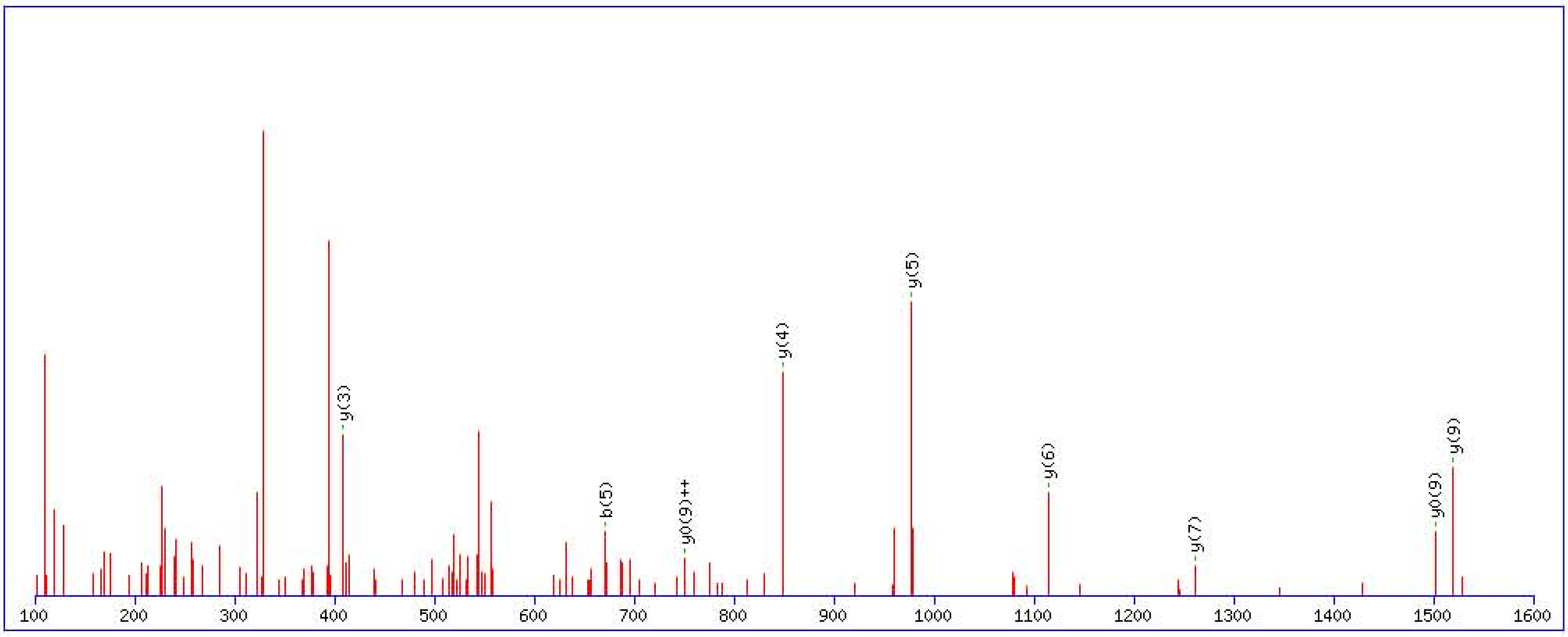
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KEEFHEQSFR**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

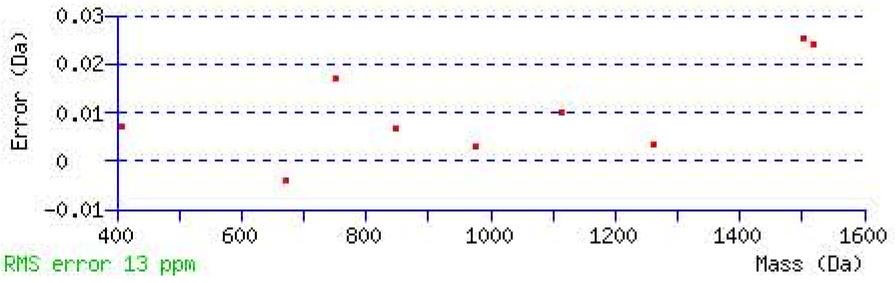
Match to Query 41080: 1646.809662 from(549.943830,3+) rtinseconds(1502) index(57282)
Title: Locus:1.1.1.2946.14 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

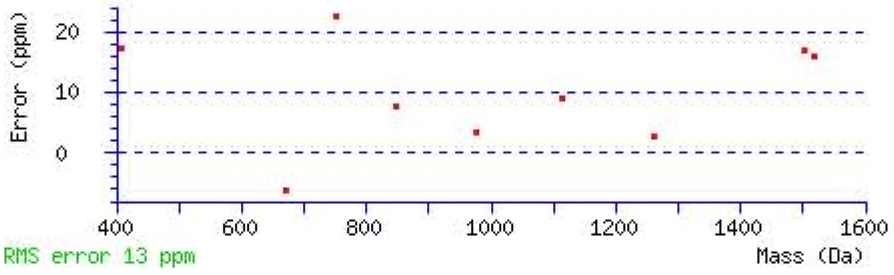
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1646.787491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.011
Matches : 9/102 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							10
2	258.144832	129.576054	241.118283	121.062780	240.134267	120.570772	E	***1519.699825***	760.353551	1502.673276	751.840276	1501.689260	751.348268	9
3	387.187425	194.097351	370.160876	185.584076	369.176860	185.092068	E	1390.657232	695.832254	1373.630683	687.318980	1372.646667	686.826972	8
4	534.255839	267.631558	517.229290	259.118283	516.245274	258.626275	F	***1261.614639***	631.310958	1244.588090	622.797683	1243.604074	622.305675	7
5	671.314751	336.161014	654.288202	327.647739	653.304186	327.155731	H	***1114.546225***	557.776751	1097.519676	549.263476	1096.535660	548.771468	6
6	800.357344	400.682310	783.330795	392.169036	782.346779	391.677028	E	***977.487313***	489.247295	960.460764	480.734020	959.476748	480.242012	5
7	1239.582670	620.294973	1222.556121	611.781699	1221.572105	611.289691	Q	***848.444720***	424.725998	831.418171	416.212724	830.434155	415.720716	4
8	1326.614698	663.810987	1309.588149	655.297713	1308.604133	654.805705	S	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	3
9	1473.683112	737.345194	1456.656563	728.831920	1455.672547	728.339912	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 KEEFHEQSFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.5	1646.787491	0.022171	KEEFHEQSFR
10.2	1646.818497	-0.008835	QLDDAKEGEMALLSK
6.7	1646.812469	-0.002807	QEERLGRGGLDDFR
6.5	1646.819824	-0.010162	QREEYERAQK
1.6	1646.793365	0.016297	GDQQDKLLESLNCK

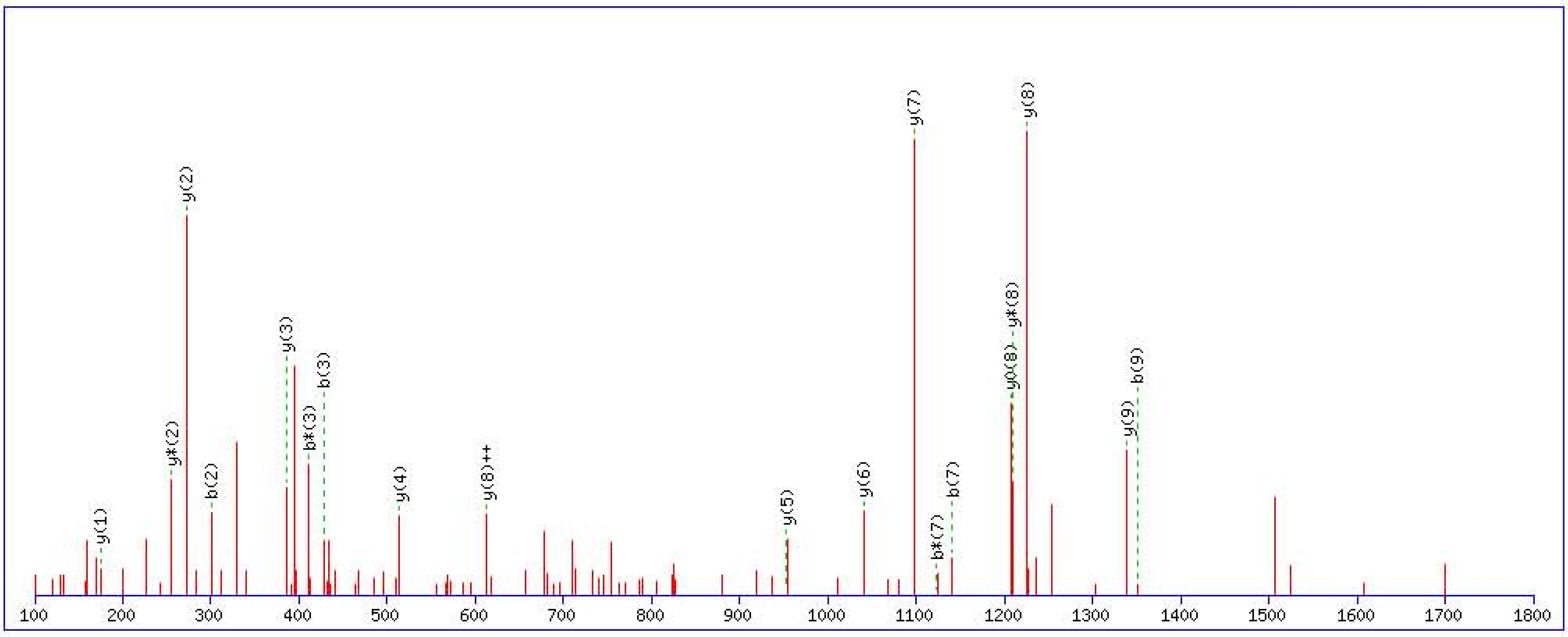
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLQGSQELPR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

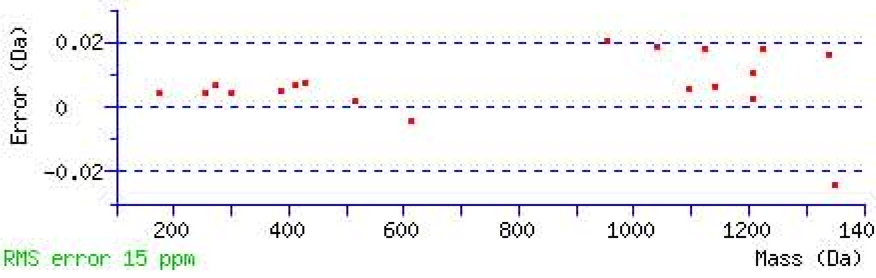
Match to Query 35837: 1523.813348 from(762.913950,2+) rtinseconds(2045) index(42531)
Title: Locus:1.1.1.3161.15 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

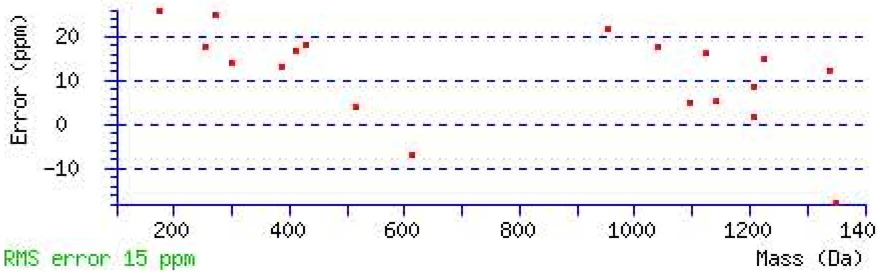
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1523.791855
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 0.00016
Matches : 19/90 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	187.086589	94.046932					W							10
2	**300.170653**	150.588965					L	***1338.719833***	669.863554	1321.693284	661.350280	1320.709268	660.858272	9
3	**428.229231**	214.618254	411.202682	206.104979			Q	***1225.635769***	613.321522	1208.609220	604.808248	1207.625204	604.316240	8
4	485.250695	243.128986	468.224146	234.615711			G	***1097.577191***	549.292233	1080.550642	540.778959	1079.566626	540.286951	7
5	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	S	***1040.555727***	520.781501	1023.529178	512.268227	1022.545162	511.776219	6
6	1011.508049	506.257663	994.481500	497.744388	993.497484	497.252380	Q	***953.523699***	477.265487	936.497150	468.752213	935.513134	468.260205	5
7	**1140.550642**	570.778959	1123.524093	562.265685	1122.540077	561.773676	E	***514.298373***	257.652824	497.271824	249.139550	496.287808	248.647542	4
8	1253.634706	627.320991	1236.608157	618.807716	1235.624141	618.315708	L	***385.255780***	193.131528	368.229231	184.618253			3
9	**1350.687470**	675.847373	1333.660921	667.334098	1332.676905	666.842090	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 WLQGSQELPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.2	1523.791855	0.021493	WLQGSQELPR
21.9	1523.791855	0.021493	WLQGSQELPR
12.9	1523.816833	-0.003485	KGLGEGVPSSQRGPR
4.0	1523.812988	0.000360	EGQGIKTDIPR
3.7	1523.795227	0.018121	GAQMQPISLPR
3.7	1523.795227	0.018121	GAQMQPISLPR
2.8	1523.824219	-0.010871	SVQIRTEAGPR
2.1	1523.813644	-0.000296	WIPTSNPLPQPFK
1.9	1523.820831	-0.007483	GNPAPELRASFLPR
1.8	1523.805603	0.007745	LSATLGGLLQDHGSR

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

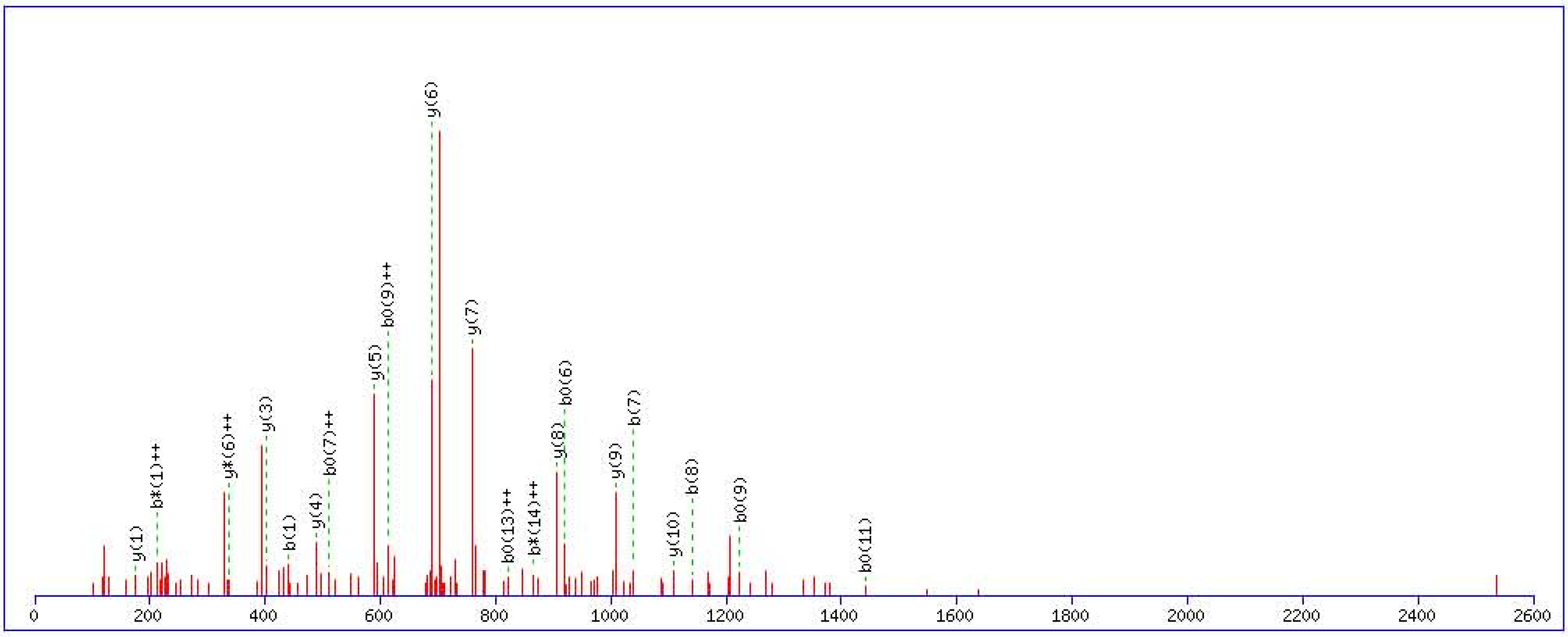
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEPSQGTTTFAVTSILR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

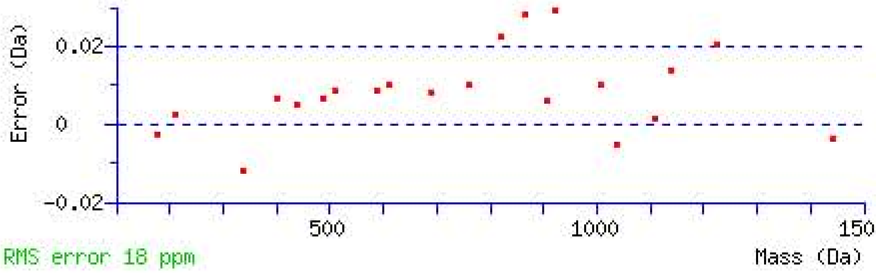
Match to Query 54025: 2146.131912 from(716.384580,3+) rtinseconds(2468) index(9537)
Title: Locus:1.1.1.3113.18 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

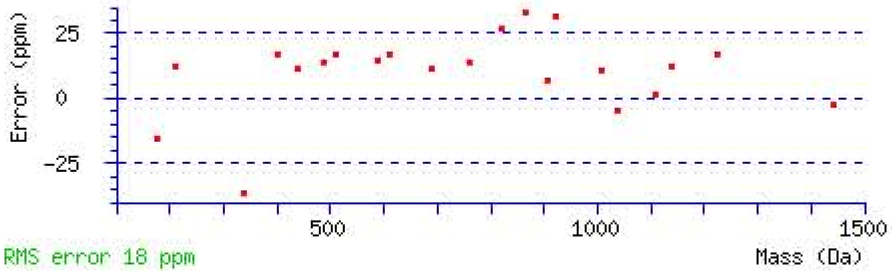
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2146.109253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 42 **Expect:** 0.0015
Matches : 21/184 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							17
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	E	1707.891193	854.449235	1690.864644	845.935960	1689.880628	845.443952	16
3	666.327959	333.667618	649.301410	325.154343	648.317394	324.662335	P	1578.848600	789.927938	1561.822051	781.414664	1560.838035	780.922656	15
4	753.359987	377.183632	736.333438	368.670357	735.349422	368.178349	S	1481.795836	741.401556	1464.769287	732.888282	1463.785271	732.396274	14
5	881.418565	441.212921	864.392016	432.699646	863.408000	432.207638	Q	1394.763808	697.885542	1377.737259	689.372268	1376.753243	688.880260	13
6	938.440029	469.723653	921.413480	461.210378	920.429464	460.718370	G	1266.705230	633.856253	1249.678681	625.342979	1248.694665	624.850971	12
7	**1039.487708**	520.247492	1022.461159	511.734218	1021.477143	511.242210	T	1209.683766	605.345521	1192.657217	596.832247	1191.673201	596.340239	11
8	**1140.535387**	570.771332	1123.508838	562.258057	1122.524822	561.766049	T	***1108.636087***	554.821682	1091.609538	546.308407	1090.625522	545.816399	10
9	1241.583066	621.295171	1224.556517	612.781897	1223.572501	612.289889	T	***1007.588408***	504.297842	990.561859	495.784568	989.577843	495.292560	9
10	1388.651480	694.829378	1371.624931	686.316104	1370.640915	685.824096	F	***906.540729***	453.774003	889.514180	445.260728	888.530164	444.768720	8
11	1459.688594	730.347935	1442.662045	721.834661	1441.678029	721.342653	A	***759.472315***	380.239796	742.445766	371.726521	741.461750	371.234513	7
12	1558.757008	779.882142	1541.730459	771.368868	1540.746443	770.876860	V	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
13	1659.804687	830.405982	1642.778138	821.892707	1641.794122	821.400699	T	***589.366787***	295.187032	572.340238	286.673757	571.356222	286.181749	5
14	1746.836715	873.921996	1729.810166	865.408721	1728.826150	864.916713	S	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
15	1859.920779	930.464028	1842.894230	921.950753	1841.910214	921.458745	I	***401.287080***	201.147178	384.260531	192.633903			3
16	1973.004843	987.006060	1955.978294	978.492785	1954.994278	978.000777	L	288.203016	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of QEPSQGTTTFAVTSILR
(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	2146.109253	0.022659	QEPSQGTTTFAVTSILR
40.5	2146.109253	0.022659	QEPSQGTTTFAVTSILR

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

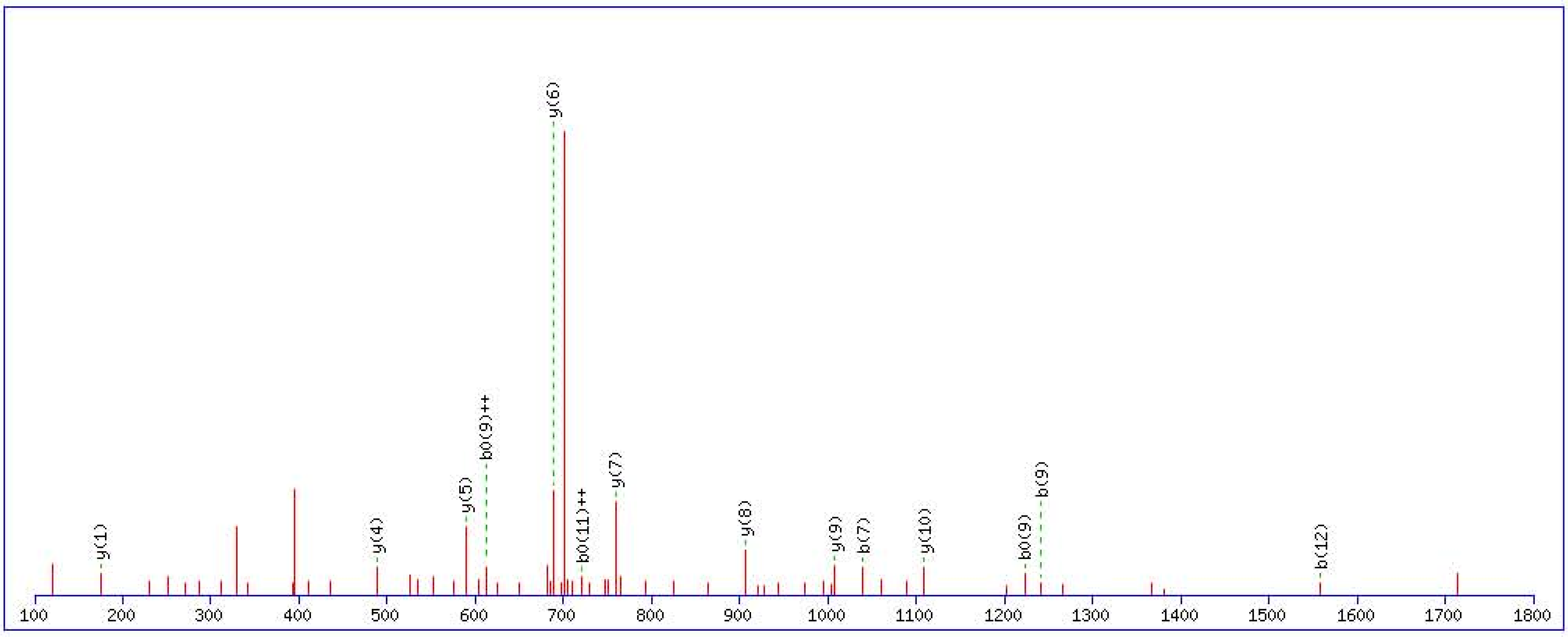
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEPSQGTTTFAVTSILR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

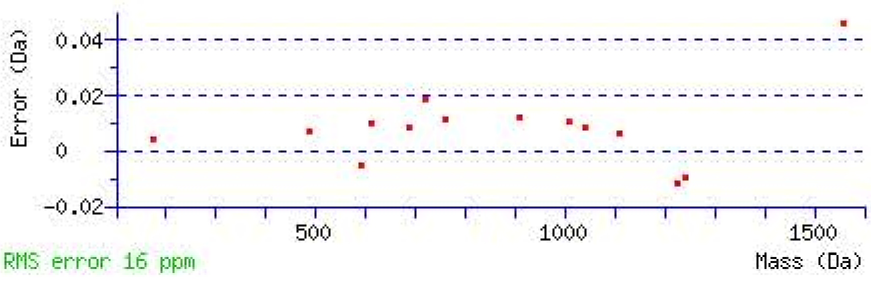
Match to Query 54026: 2146.133352 from(716.385060,3+) rtinseconds(2483) index(82006)
Title: Locus:1.1.1.2215.14 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

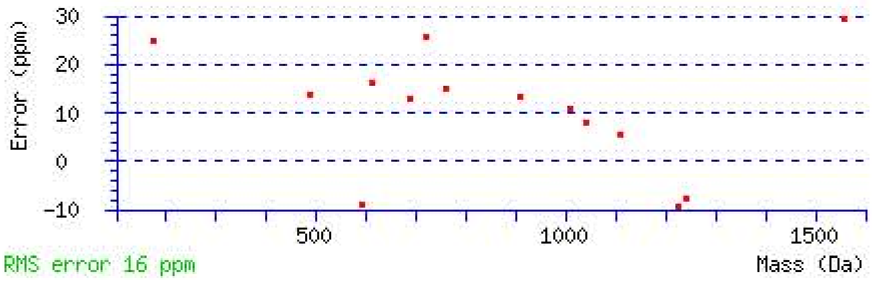
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2146.109253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.00048
Matches : 14/184 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	129.065854	65.036565	112.039305	56.523291			Q							17
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	E	2019.057941	1010.032609	2002.031392	1001.519334	2001.047376	1001.027326	16
3	355.161211	178.084244	338.134662	169.570969	337.150646	169.078961	P	1890.015348	945.511312	1872.988799	936.998038	1872.004783	936.506030	15
4	442.193239	221.600258	425.166690	213.086983	424.182674	212.594975	S	1792.962584	896.984930	1775.936035	888.471656	1774.952019	887.979648	14
5	881.418565	441.212921	864.392016	432.699646	863.408000	432.207638	Q	1705.930556	853.468916	1688.904007	844.955642	1687.919991	844.463634	13
6	938.440029	469.723653	921.413480	461.210378	920.429464	460.718370	G	1266.705230	633.856253	1249.678681	625.342979	1248.694665	624.850971	12
7	**1039.487708**	520.247492	1022.461159	511.734218	1021.477143	511.242210	T	1209.683766	605.345521	1192.657217	596.832247	1191.673201	596.340239	11
8	1140.535387	570.771332	1123.508838	562.258057	1122.524822	561.766049	T	***1108.636087***	554.821682	1091.609538	546.308407	1090.625522	545.816399	10
9	**1241.583066**	621.295171	1224.556517	612.781897	1223.572501	612.289889	T	***1007.588408***	504.297842	990.561859	495.784568	989.577843	495.292560	9
10	1388.651480	694.829378	1371.624931	686.316104	1370.640915	685.824096	F	***906.540729***	453.774003	889.514180	445.260728	888.530164	444.768720	8
11	1459.688594	730.347935	1442.662045	721.834661	1441.678029	721.342653	A	***759.472315***	380.239796	742.445766	371.726521	741.461750	371.234513	7
12	**1558.757008**	779.882142	1541.730459	771.368868	1540.746443	770.876860	V	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
13	1659.804687	830.405982	1642.778138	821.892707	1641.794122	821.400699	T	***589.366787***	295.187032	572.340238	286.673757	571.356222	286.181749	5
14	1746.836715	873.921996	1729.810166	865.408721	1728.826150	864.916713	S	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
15	1859.920779	930.464028	1842.894230	921.950753	1841.910214	921.458745	I	401.287080	201.147178	384.260531	192.633903			3
16	1973.004843	987.006060	1955.978294	978.492785	1954.994278	978.000777	L	288.203016	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.4	2146.109253	0.024099	QEPSQGTTTFAVTSILR
39.4	2146.109253	0.024099	QEPSQGTTTFAVTSILR
3.9	2146.164688	-0.031336	VQEDIILLRELHVNHYR
2.5	2146.130997	0.002355	VNFPENGFLSPDKLSLLEK

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

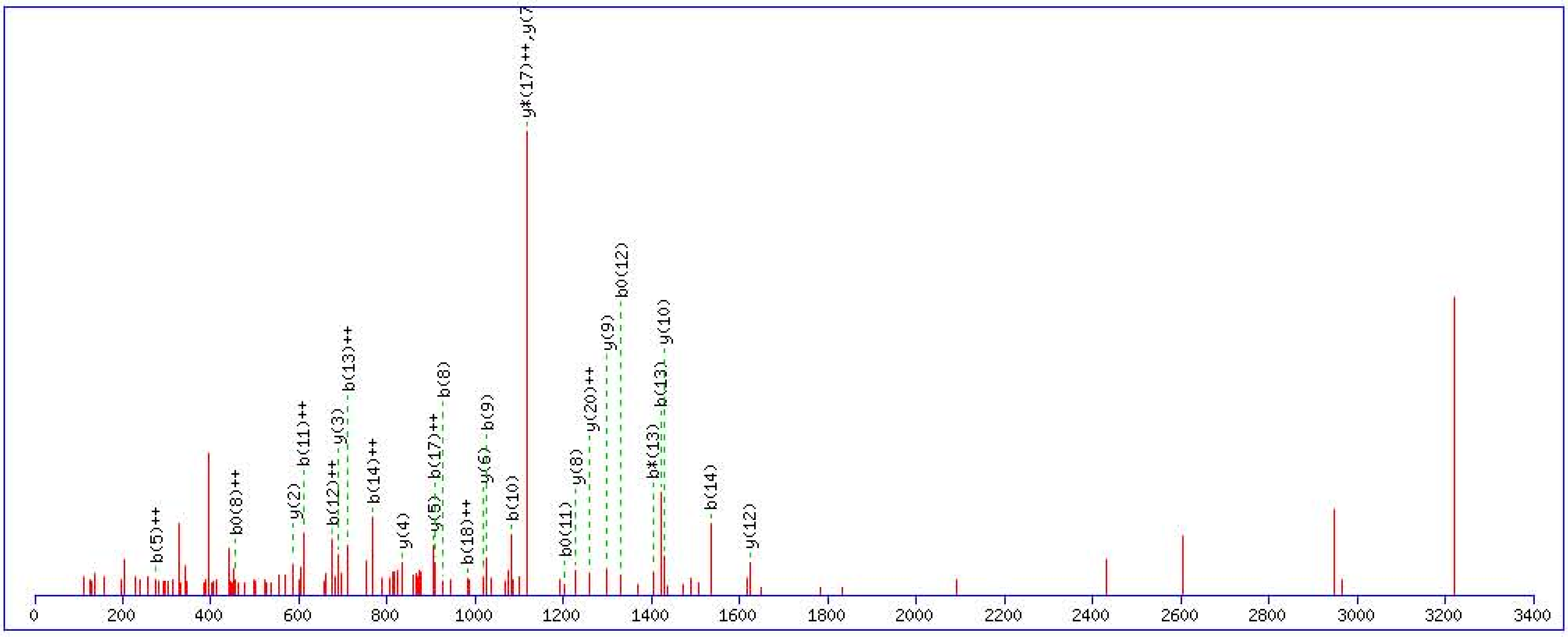
{MATRIX SCIENCE} Mascot Search Results

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

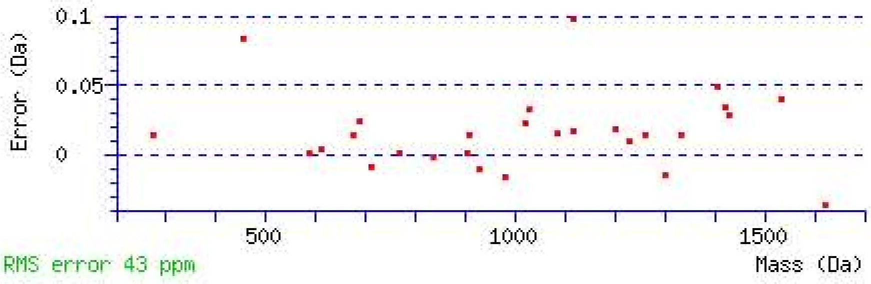
Match to Query 65071: 2647.328202 from(883.450010,3+) rtinseconds(2335) index(81163)
Title: Locus:1.1.1.2163.16 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

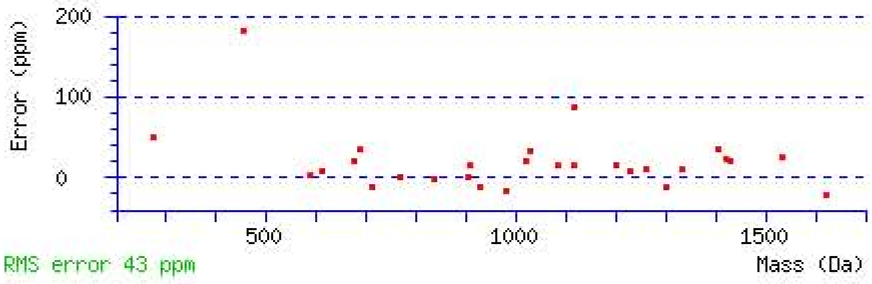
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2647.296082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.011
Matches : 28/232 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	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
34.7	2647.296082	0.032120	KGDTFSCMVGHEALPLAFTQK

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

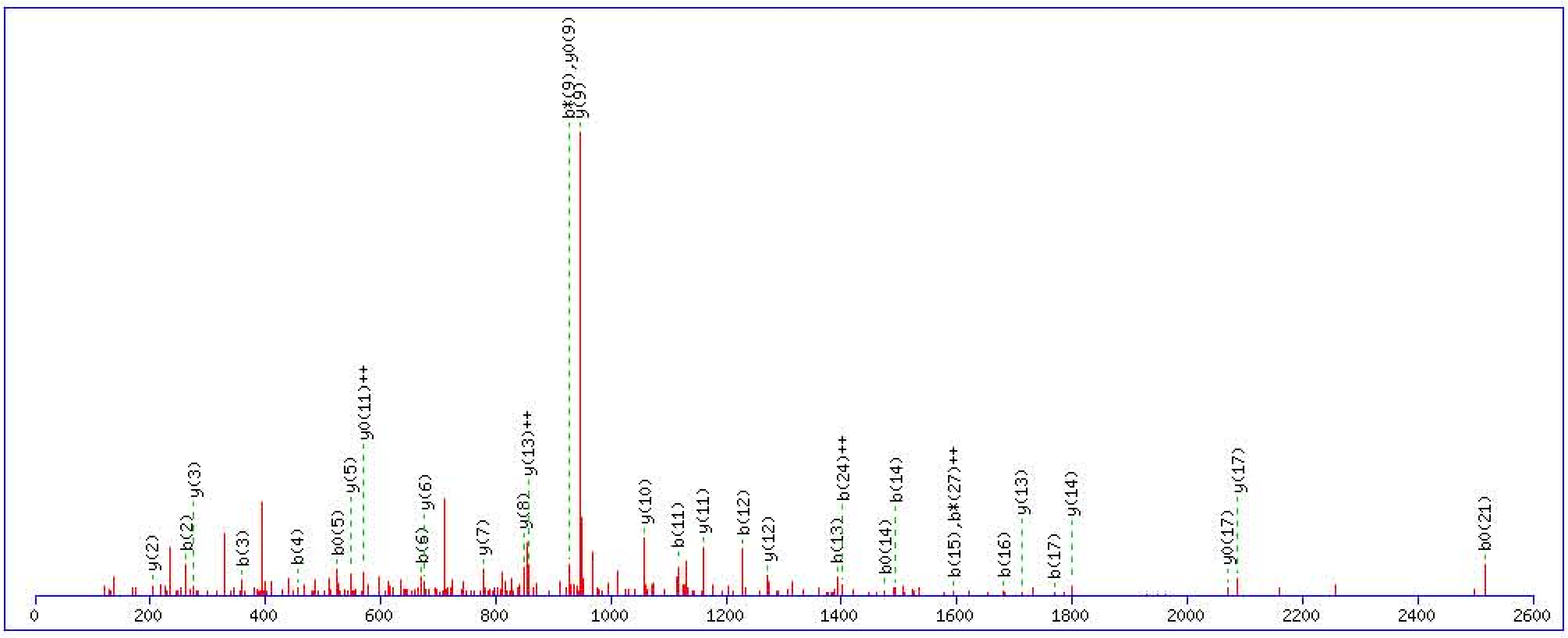
Mascot Search Results

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

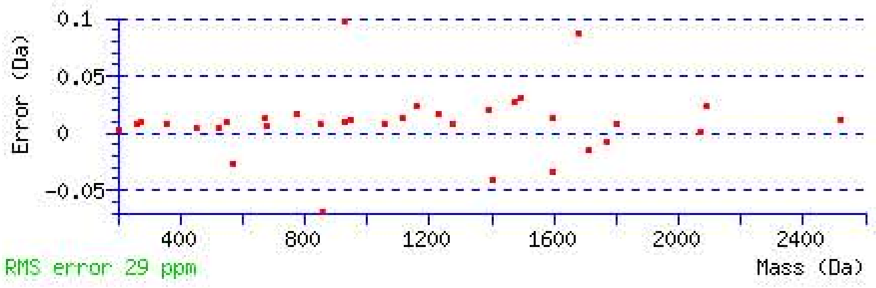
Match to Query 77079: 3478.720136 from(870.687310,4+) rtinseconds(2486) index(9662)
Title: Locus:1.1.1.3119.11 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

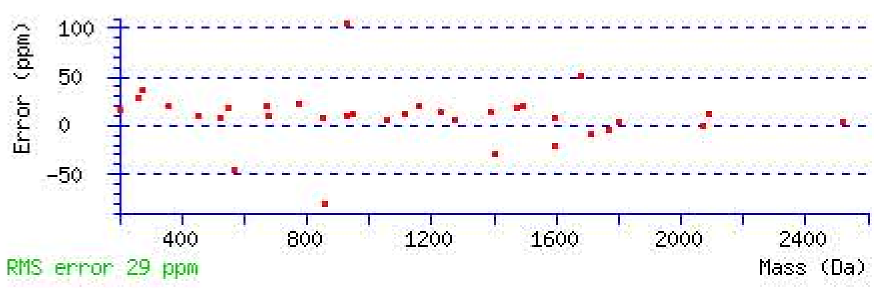
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3478.674866
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 0.00013
Matches : 34/328 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	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
53.1	3478.674866	0.045270	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
18.2	3478.674866	0.045270	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
14.7	3478.674866	0.045270	NFPPSQDASGDLYTTSSQLTLPATQCLAGK

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

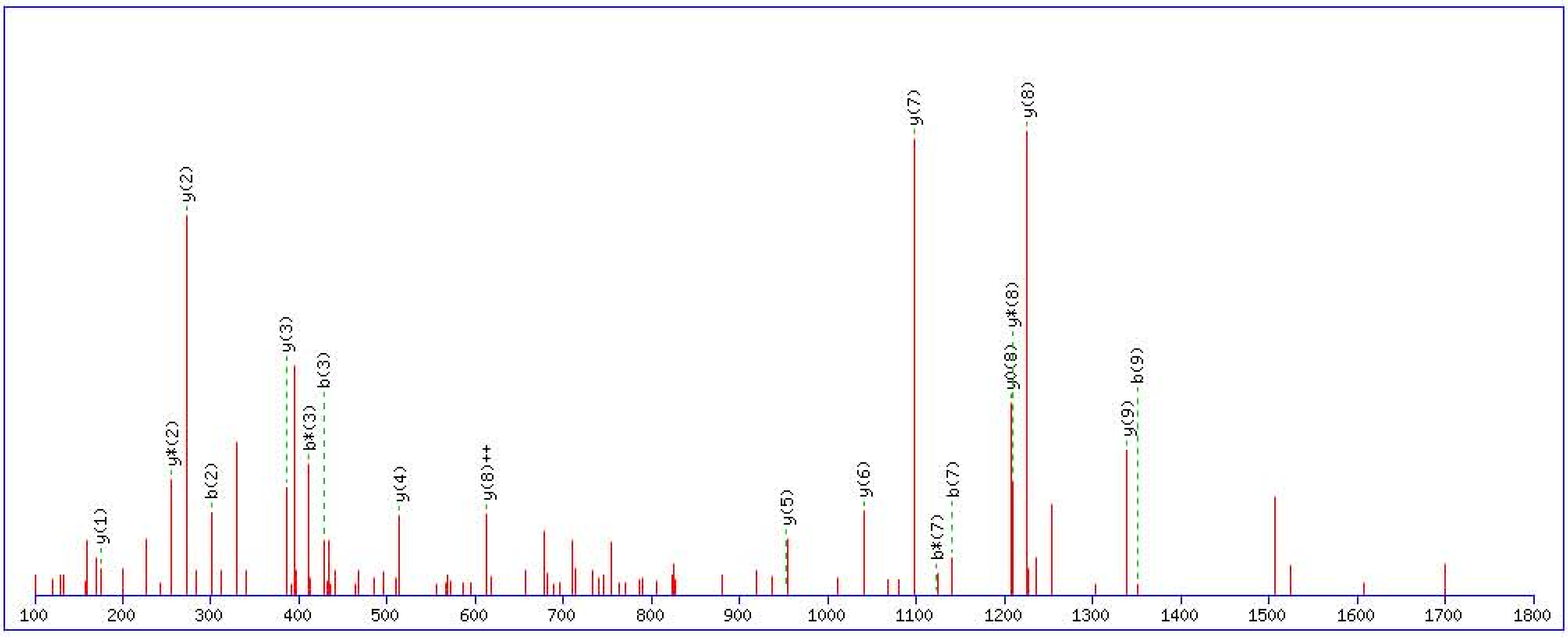
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLQGSQELPR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

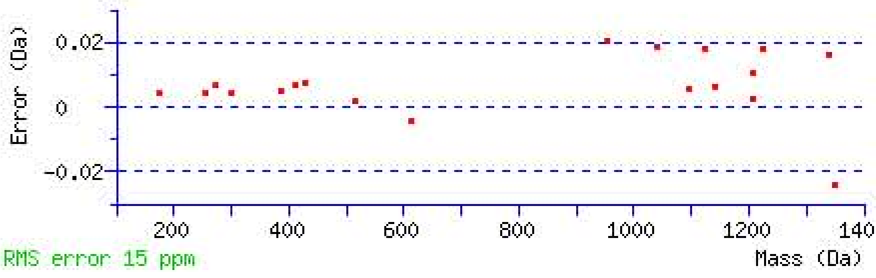
Match to Query 35837: 1523.813348 from(762.913950,2+) rtinseconds(2045) index(42531)
Title: Locus:1.1.1.3161.15 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

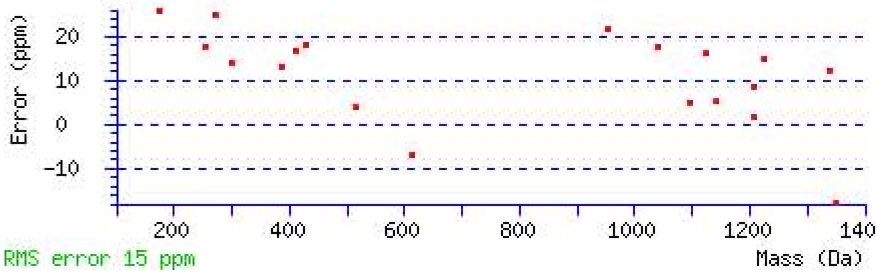
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1523.791855
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 0.00016
Matches : 19/90 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	187.086589	94.046932					W							10
2	**300.170653**	150.588965					L	***1338.719833***	669.863554	1321.693284	661.350280	1320.709268	660.858272	9
3	**428.229231**	214.618254	411.202682	206.104979			Q	***1225.635769***	613.321522	1208.609220	604.808248	1207.625204	604.316240	8
4	485.250695	243.128986	468.224146	234.615711			G	***1097.577191***	549.292233	1080.550642	540.778959	1079.566626	540.286951	7
5	572.282723	286.645000	555.256174	278.131725	554.272158	277.639717	S	***1040.555727***	520.781501	1023.529178	512.268227	1022.545162	511.776219	6
6	1011.508049	506.257663	994.481500	497.744388	993.497484	497.252380	Q	***953.523699***	477.265487	936.497150	468.752213	935.513134	468.260205	5
7	**1140.550642**	570.778959	1123.524093	562.265685	1122.540077	561.773676	E	***514.298373***	257.652824	497.271824	249.139550	496.287808	248.647542	4
8	1253.634706	627.320991	1236.608157	618.807716	1235.624141	618.315708	L	***385.255780***	193.131528	368.229231	184.618253			3
9	**1350.687470**	675.847373	1333.660921	667.334098	1332.676905	666.842090	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 WLQGSQELPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.2	1523.791855	0.021493	WLQGSQELPR
21.9	1523.791855	0.021493	WLQGSQELPR
12.9	1523.816833	-0.003485	KGLGEGVPSSQRGPR
4.0	1523.812988	0.000360	EGQGIKTDIPR
3.7	1523.795227	0.018121	GAQMQPISLPR
3.7	1523.795227	0.018121	GAQMQPISLPR
2.8	1523.824219	-0.010871	SVQIRTEAGPR
2.1	1523.813644	-0.000296	WIPTSNPLPQPFK
1.9	1523.820831	-0.007483	GNPAPELRASFLPR
1.8	1523.805603	0.007745	LSATLGGLLQDHGSR

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

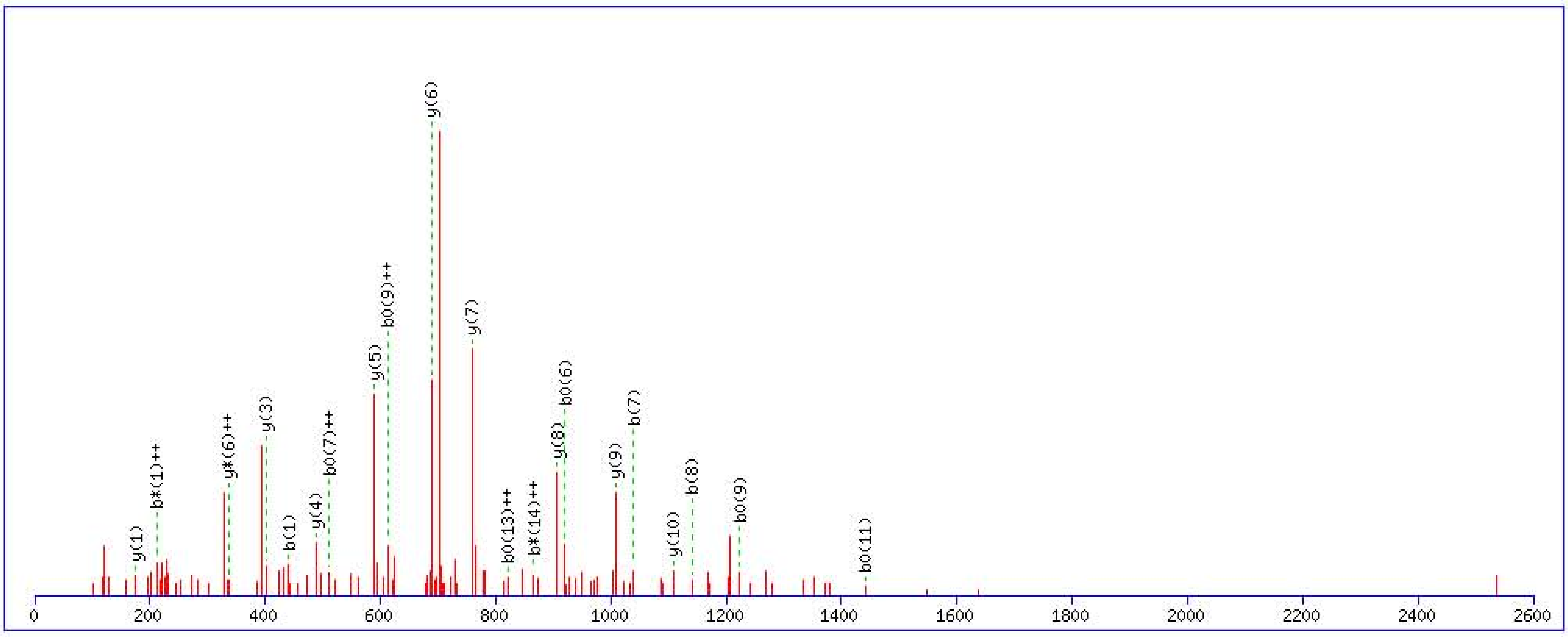
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEPSQGTTTFAVTSILR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

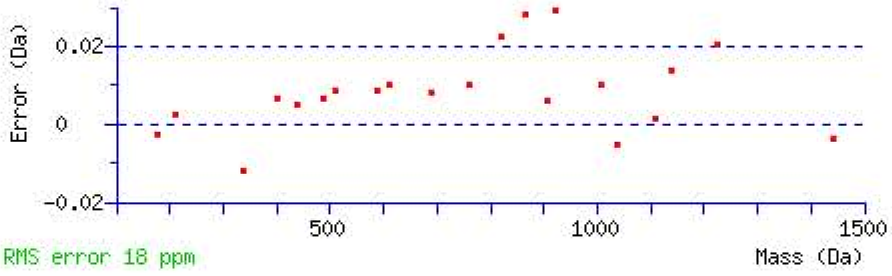
Match to Query 54025: 2146.131912 from(716.384580,3+) rtinseconds(2468) index(9537)
Title: Locus:1.1.1.3113.18 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

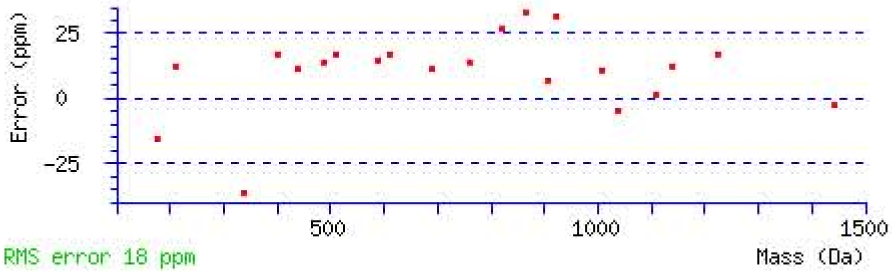


Monoisotopic mass of neutral peptide Mr(calc): 2146.109253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 42 **Expect:** 0.0015
Matches : 21/184 fragment ions using 42 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	**440.232602**	220.619939	423.206053	212.106664			Q							17
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	E	1707.891193	854.449235	1690.864644	845.935960	1689.880628	845.443952	16
3	666.327959	333.667618	649.301410	325.154343	648.317394	324.662335	P	1578.848600	789.927938	1561.822051	781.414664	1560.838035	780.922656	15
4	753.359987	377.183632	736.333438	368.670357	735.349422	368.178349	S	1481.795836	741.401556	1464.769287	732.888282	1463.785271	732.396274	14
5	881.418565	441.212921	864.392016	432.699646	863.408000	432.207638	Q	1394.763808	697.885542	1377.737259	689.372268	1376.753243	688.880260	13
6	938.440029	469.723653	921.413480	461.210378	920.429464	460.718370	G	1266.705230	633.856253	1249.678681	625.342979	1248.694665	624.850971	12
7	**1039.487708**	520.247492	1022.461159	511.734218	1021.477143	511.242210	T	1209.683766	605.345521	1192.657217	596.832247	1191.673201	596.340239	11
8	**1140.535387**	570.771332	1123.508838	562.258057	1122.524822	561.766049	T	***1108.636087***	554.821682	1091.609538	546.308407	1090.625522	545.816399	10
9	1241.583066	621.295171	1224.556517	612.781897	1223.572501	612.289889	T	***1007.588408***	504.297842	990.561859	495.784568	989.577843	495.292560	9
10	1388.651480	694.829378	1371.624931	686.316104	1370.640915	685.824096	F	***906.540729***	453.774003	889.514180	445.260728	888.530164	444.768720	8
11	1459.688594	730.347935	1442.662045	721.834661	1441.678029	721.342653	A	***759.472315***	380.239796	742.445766	371.726521	741.461750	371.234513	7
12	1558.757008	779.882142	1541.730459	771.368868	1540.746443	770.876860	V	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
13	1659.804687	830.405982	1642.778138	821.892707	1641.794122	821.400699	T	***589.366787***	295.187032	572.340238	286.673757	571.356222	286.181749	5
14	1746.836715	873.921996	1729.810166	865.408721	1728.826150	864.916713	S	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
15	1859.920779	930.464028	1842.894230	921.950753	1841.910214	921.458745	I	***401.287080***	201.147178	384.260531	192.633903			3
16	1973.004843	987.006060	1955.978294	978.492785	1954.994278	978.000777	L	288.203016	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549840			1



RMS error 18 ppm



RMS error 18 ppm

NCBI **BLAST** search of QEPSQGTTTFAVTSILR
(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	2146.109253	0.022659	QEPSQGTTTFAVTSILR
40.5	2146.109253	0.022659	QEPSQGTTTFAVTSILR

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

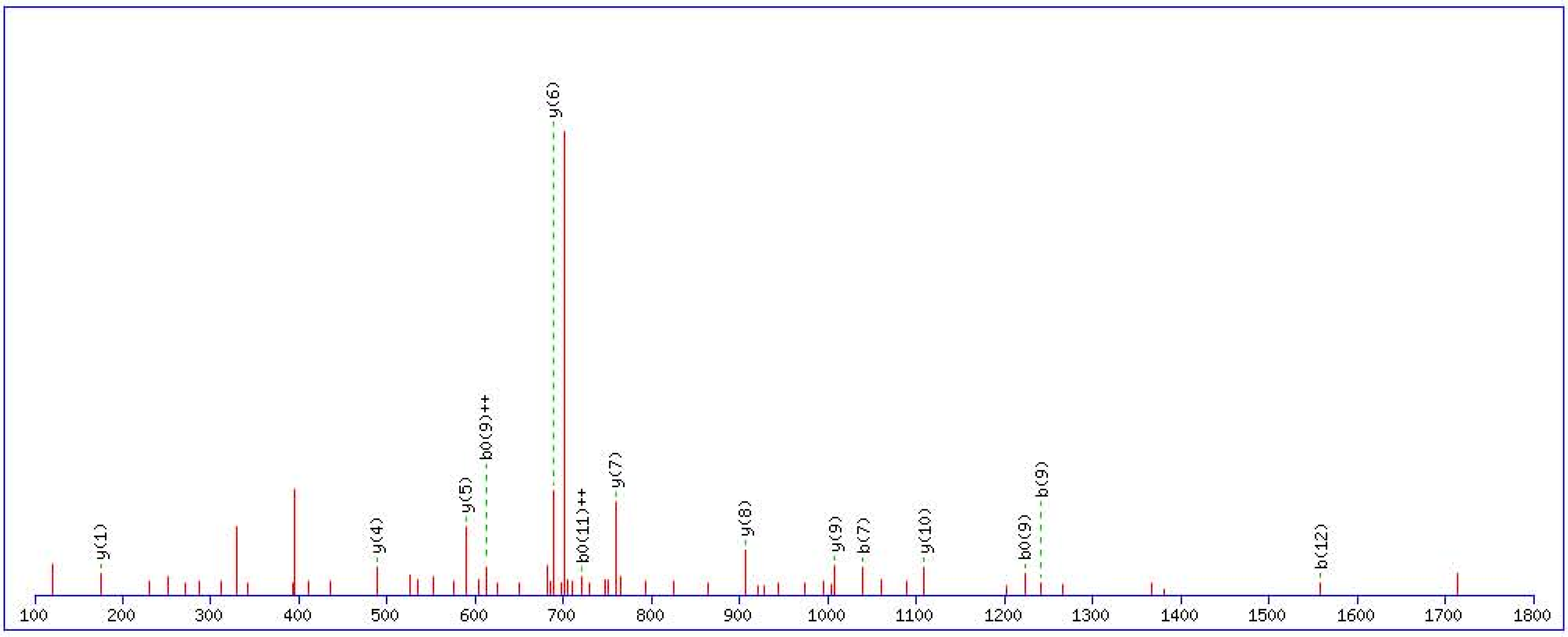
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEPSQGTTTFAVTSILR**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

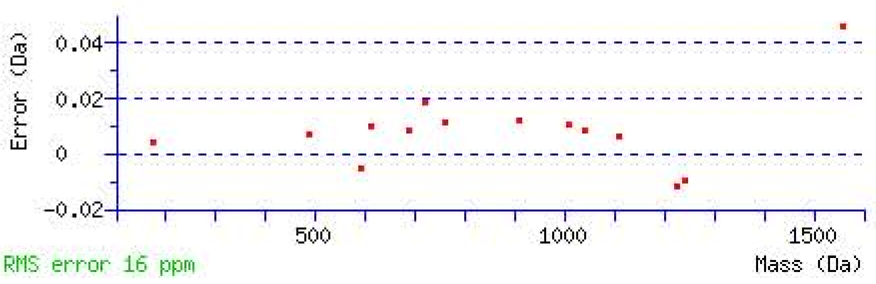
Match to Query 54026: 2146.133352 from(716.385060,3+) rtinseconds(2483) index(82006)
Title: Locus:1.1.1.2215.14 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

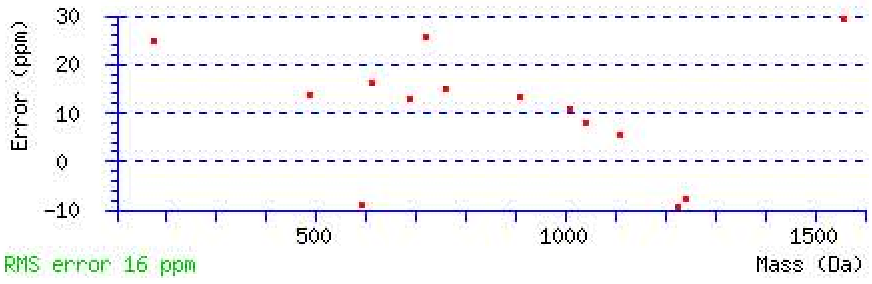
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2146.109253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.00048
Matches : 14/184 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	129.065854	65.036565	112.039305	56.523291			Q							17
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	E	2019.057941	1010.032609	2002.031392	1001.519334	2001.047376	1001.027326	16
3	355.161211	178.084244	338.134662	169.570969	337.150646	169.078961	P	1890.015348	945.511312	1872.988799	936.998038	1872.004783	936.506030	15
4	442.193239	221.600258	425.166690	213.086983	424.182674	212.594975	S	1792.962584	896.984930	1775.936035	888.471656	1774.952019	887.979648	14
5	881.418565	441.212921	864.392016	432.699646	863.408000	432.207638	Q	1705.930556	853.468916	1688.904007	844.955642	1687.919991	844.463634	13
6	938.440029	469.723653	921.413480	461.210378	920.429464	460.718370	G	1266.705230	633.856253	1249.678681	625.342979	1248.694665	624.850971	12
7	**1039.487708**	520.247492	1022.461159	511.734218	1021.477143	511.242210	T	1209.683766	605.345521	1192.657217	596.832247	1191.673201	596.340239	11
8	1140.535387	570.771332	1123.508838	562.258057	1122.524822	561.766049	T	***1108.636087***	554.821682	1091.609538	546.308407	1090.625522	545.816399	10
9	**1241.583066**	621.295171	1224.556517	612.781897	1223.572501	612.289889	T	***1007.588408***	504.297842	990.561859	495.784568	989.577843	495.292560	9
10	1388.651480	694.829378	1371.624931	686.316104	1370.640915	685.824096	F	***906.540729***	453.774003	889.514180	445.260728	888.530164	444.768720	8
11	1459.688594	730.347935	1442.662045	721.834661	1441.678029	721.342653	A	***759.472315***	380.239796	742.445766	371.726521	741.461750	371.234513	7
12	**1558.757008**	779.882142	1541.730459	771.368868	1540.746443	770.876860	V	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
13	1659.804687	830.405982	1642.778138	821.892707	1641.794122	821.400699	T	***589.366787***	295.187032	572.340238	286.673757	571.356222	286.181749	5
14	1746.836715	873.921996	1729.810166	865.408721	1728.826150	864.916713	S	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
15	1859.920779	930.464028	1842.894230	921.950753	1841.910214	921.458745	I	401.287080	201.147178	384.260531	192.633903			3
16	1973.004843	987.006060	1955.978294	978.492785	1954.994278	978.000777	L	288.203016	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.4	2146.109253	0.024099	QEPSQGTTTFAVTSILR
39.4	2146.109253	0.024099	QEPSQGTTTFAVTSILR
3.9	2146.164688	-0.031336	VQEDIILLRELHVNHYR
2.5	2146.130997	0.002355	VNFPENGFLSPDKLSLLEK

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

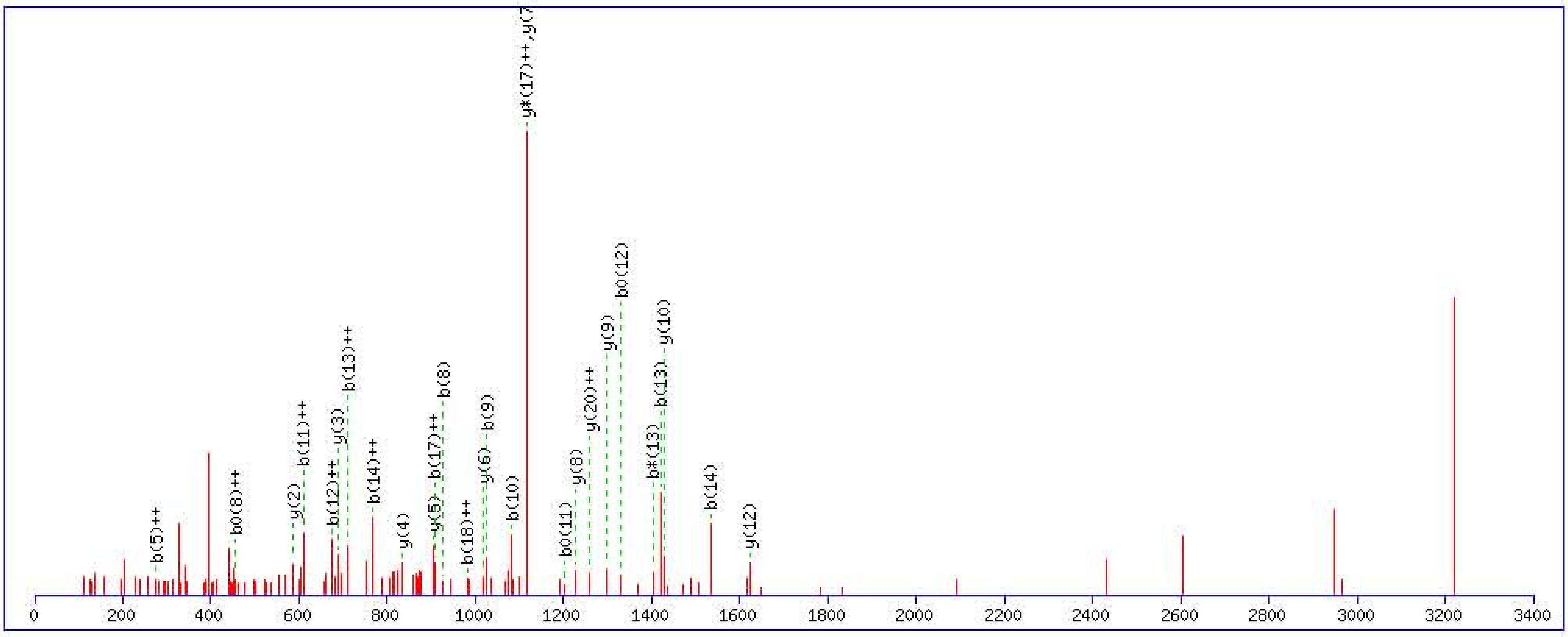
{MATRIX SCIENCE} Mascot Search Results

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

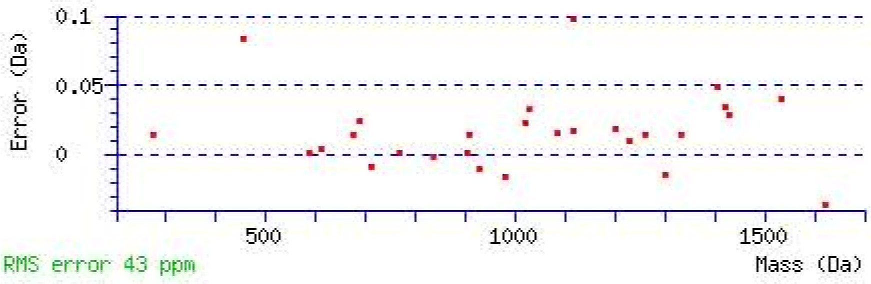
Match to Query 65071: 2647.328202 from(883.450010,3+) rtinseconds(2335) index(81163)
Title: Locus:1.1.1.2163.16 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

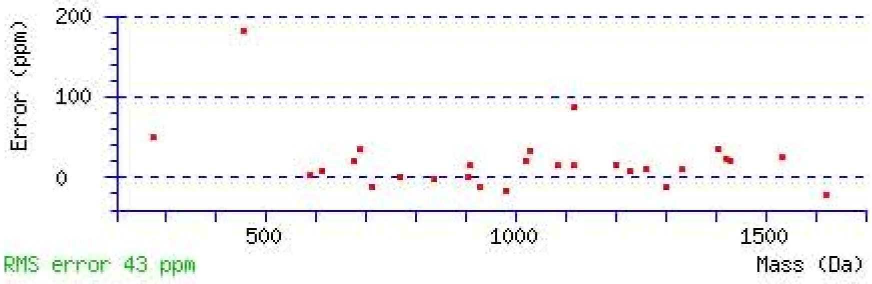
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2647.296082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.011
Matches : 28/232 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	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
34.7	2647.296082	0.032120	KGDTFSCMVGHEALPLAFTQK

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

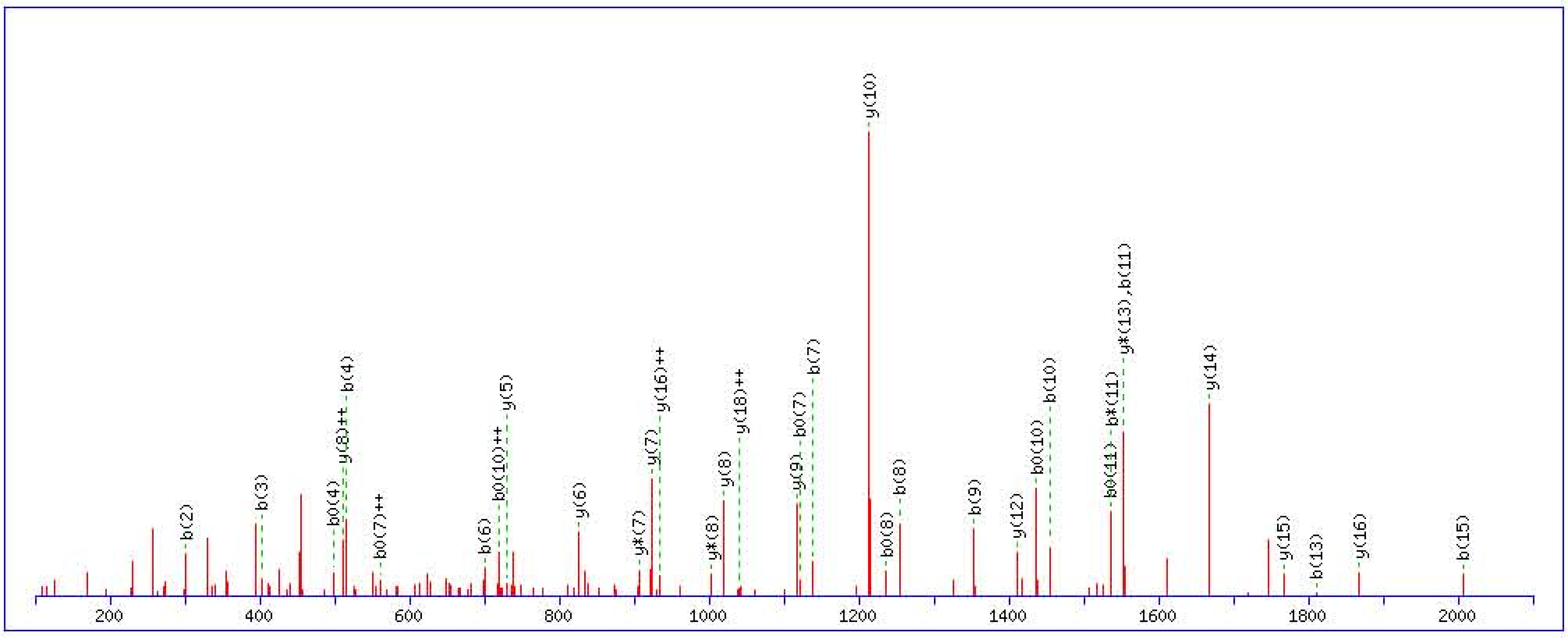
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HYTNPSQDVTVPCPVPPPPPCCHPR**
Found in **IGHA2_HUMAN**, Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 SV=3

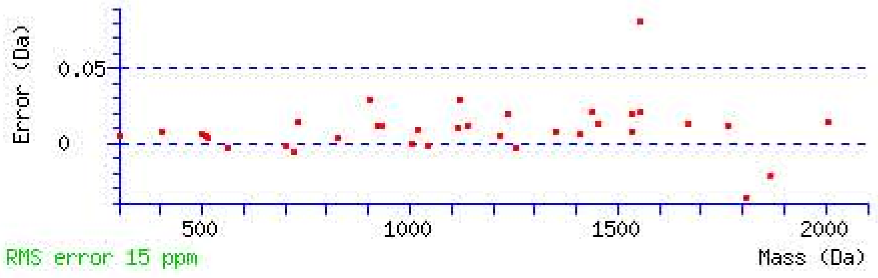
Match to Query 73087: 3219.509896 from(805.884750,4+) rtinseconds(1790) index(5160)
Title: Locus:1.1.1.2877.21 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

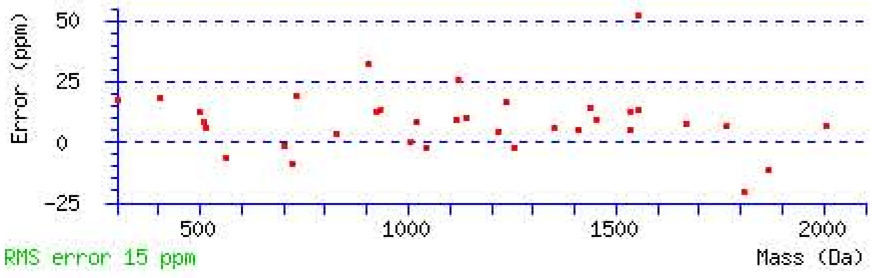
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3219.487518
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 59 **Expect:** 2.5e-005
Matches : 35/248 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	138.066188	69.536732					H							25
2	***301.129517***	151.068397					Y	3083.435840	1542.221558	3066.409291	1533.708283	3065.425275	1533.216275	24
3	***402.177196***	201.592236			384.166631	192.586954	T	2920.372511	1460.689893	2903.345962	1452.176619	2902.361946	1451.684611	23
4	***516.220123***	258.613700	499.193574	250.100425	498.209558	249.608417	N	2819.324832	1410.166054	2802.298283	1401.652779	2801.314267	1401.160771	22
5	613.272887	307.140082	596.246338	298.626807	595.262322	298.134799	P	2705.281905	1353.144590	2688.255356	1344.631316	2687.271340	1344.139308	21
6	***700.304915***	350.656096	683.278366	342.142821	682.294350	341.650813	S	2608.229141	1304.618208	2591.202592	1296.104934	2590.218576	1295.612926	20
7	***1139.530241***	570.268759	1122.503692	561.755484	1121.519676	561.263476	Q	2521.197113	1261.102194	2504.170564	1252.588920	2503.186548	1252.096912	19
8	***1254.557184***	627.782230	1237.530635	619.268956	1236.546619	618.776948	D	2081.971787	1041.489531	2064.945238	1032.976257	2063.961222	1032.484249	18
9	***1353.625598***	677.316437	1336.599049	668.803163	1335.615033	668.311155	V	1966.944844	983.976060	1949.918295	975.462786	1948.934279	974.970778	17
10	***1454.673277***	727.840277	1437.646728	719.327002	1436.662712	718.834994	T	***1867.876430***	934.441853	1850.849881	925.928579	1849.865865	925.436571	16
11	***1553.741691***	777.374484	1536.715142	768.861209	1535.731126	768.369201	V	***1766.828751***	883.918014	1749.802202	875.404739			15
12	1650.794455	825.900866	1633.767906	817.387591	1632.783890	816.895583	P	***1667.760337***	834.383806	1650.733788	825.870532			14
13	***1810.825104***	905.916190	1793.798555	897.402916	1792.814539	896.910908	C	1570.707573	785.857424	1553.681024	777.344150			13
14	1907.877868	954.442572	1890.851319	945.929298	1889.867303	945.437290	P	***1410.676924***	705.842100	1393.650375	697.328825			12
15	***2006.946282***	1003.976779	1989.919733	995.463505	1988.935717	994.971497	V	1313.624160	657.315718	1296.597611	648.802443			11
16	2103.999046	1052.503161	2086.972497	1043.989887	2085.988481	1043.497879	P	***1214.555746***	607.781511	1197.529197	599.268236			10
17	2201.051810	1101.029543	2184.025261	1092.516269	2183.041245	1092.024261	P	***1117.502982***	559.255129	1100.476433	550.741854			9
18	2298.104574	1149.555925	2281.078025	1141.042651	2280.094009	1140.550643	P	***1020.450218***	510.728747	1003.423669	502.215472			8
19	2395.157338	1198.082307	2378.130789	1189.569033	2377.146773	1189.077025	P	***923.397454***	462.202365	906.370905	453.689090			7
20	2492.210102	1246.608689	2475.183553	1238.095415	2474.199537	1237.603407	P	***826.344690***	413.675983	809.318141	405.162708			6
21	2652.240751	1326.624014	2635.214202	1318.110739	2634.230186	1317.618731	C	***729.291926***	365.149601	712.265377	356.636326			5
22	2812.271400	1406.639338	2795.244851	1398.126063	2794.260835	1397.634055	C	569.261277	285.134276	552.234728	276.621002			4
23	2949.330312	1475.168794	2932.303763	1466.655519	2931.319747	1466.163511	H	409.230628	205.118952	392.204079	196.605677			3
24	3046.383076	1523.695176	3029.356527	1515.181901	3028.372511	1514.689893	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 HYTNPSQDVTVPCPVPPPPPCCHPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.7	3219.487518	0.022378	HYTNPSQDVTVPCPVPPPPPCCHPR

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

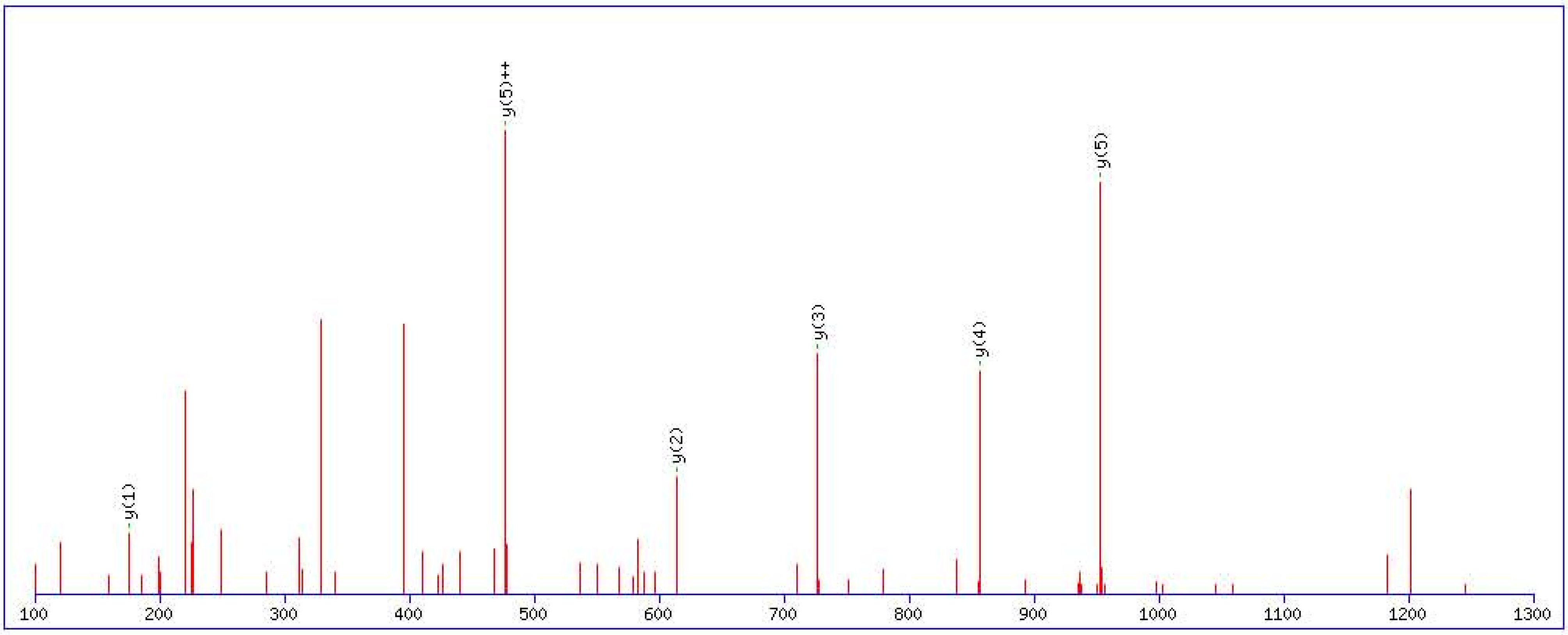
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFPEIQR**
Found in **IGHD_HUMAN**, Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2

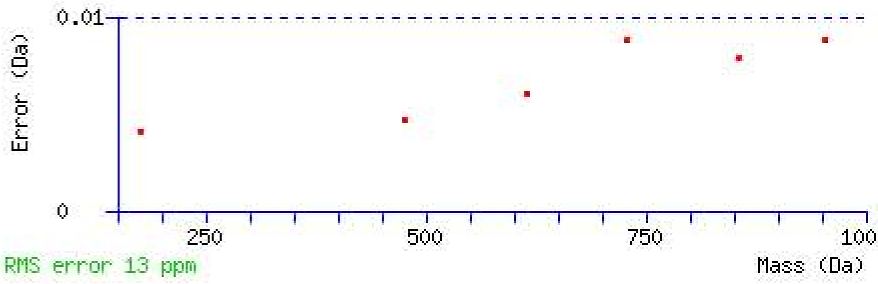
Match to Query 23718: 1200.642488 from(601.328520,2+) rtinseconds(1961) index(78669)
Title: Locus:1.1.1.2033.18 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

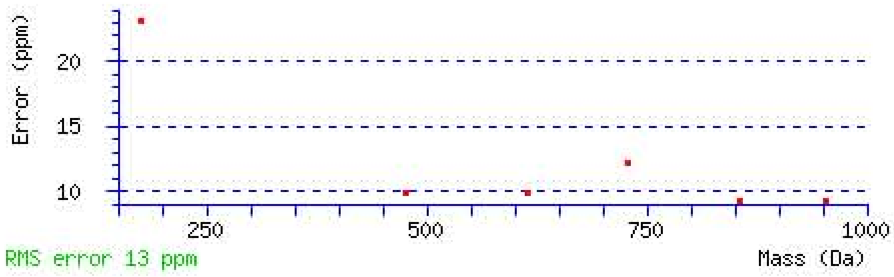
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1200.632507
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0032
Matches : 6/56 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	102.054955	51.531116			84.044390	42.525833	**T**							7
2	249.123369	125.065322			231.112804	116.060040	**F**	1100.592113	550.799695	1083.565564	542.286420	1082.581548	541.794412	6
3	346.176133	173.591704			328.165568	164.586422	**P**	***953.523699***	477.265488	936.497150	468.752213	935.513134	468.260205	5
4	475.218726	238.113001			457.208161	229.107719	**E**	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
5	588.302790	294.655033			570.292225	285.649751	**I**	***727.428342***	364.217809	710.401793	355.704535			3
6	1027.528116	514.267696	1010.501567	505.754422	1009.517551	505.262414	**Q**	***614.344278***	307.675777	597.317729	299.162503			2
7							**R**	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.3	1200.632507	0.009981	TFPEIQR
7.4	1200.628464	0.014024	LLQLQEMGNR
4.0	1200.636353	0.006135	TFTQKGNLHR
2.6	1200.650269	-0.007781	ETDKPPFVIR

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

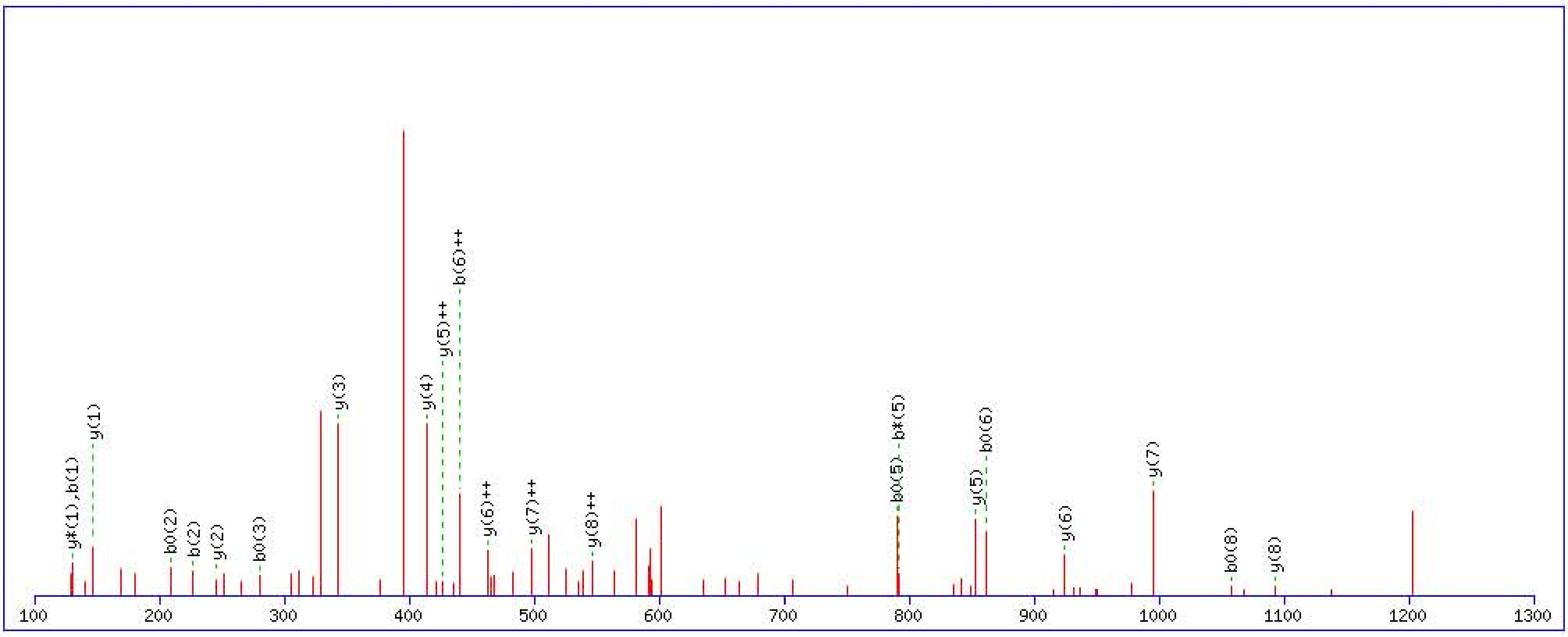
{MATRIX SCIENCE} Mascot Search Results

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

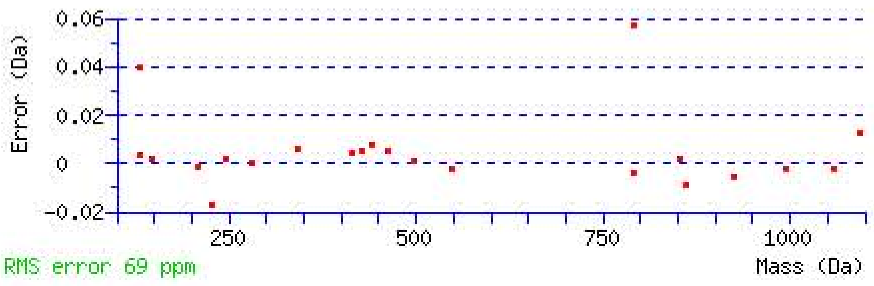
Match to Query 24220: 1220.661148 from(611.337850,2+) rtinseconds(1428) index(20481)
Title: Locus:1.1.1.2640.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

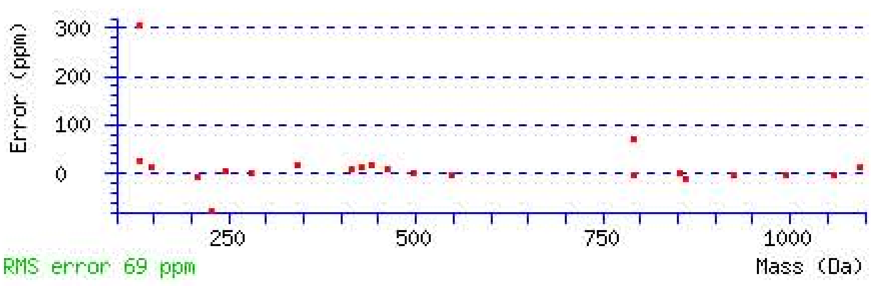
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1220.658707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0018
Matches : 22/72 fragment ions using 55 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
39.7	1220.658707	0.002441	EPAAQAPVK
9.8	1220.658722	0.002426	EQNVPVPK
7.1	1220.676468	-0.015320	EKAATVFNTLK
4.8	1220.676468	-0.015320	AEPPPSKPTVAK
2.8	1220.669952	-0.008804	QTGKKPFKCK
2.2	1220.669937	-0.008789	EQHLQKK
1.5	1220.654663	0.006485	QASKKTAMAAAK
1.0	1220.666580	-0.005432	EPAIVRFFSR
1.0	1220.651306	0.009842	ILSHTEEHKK
0.6	1220.651321	0.009827	GQVLIAASSYGR

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

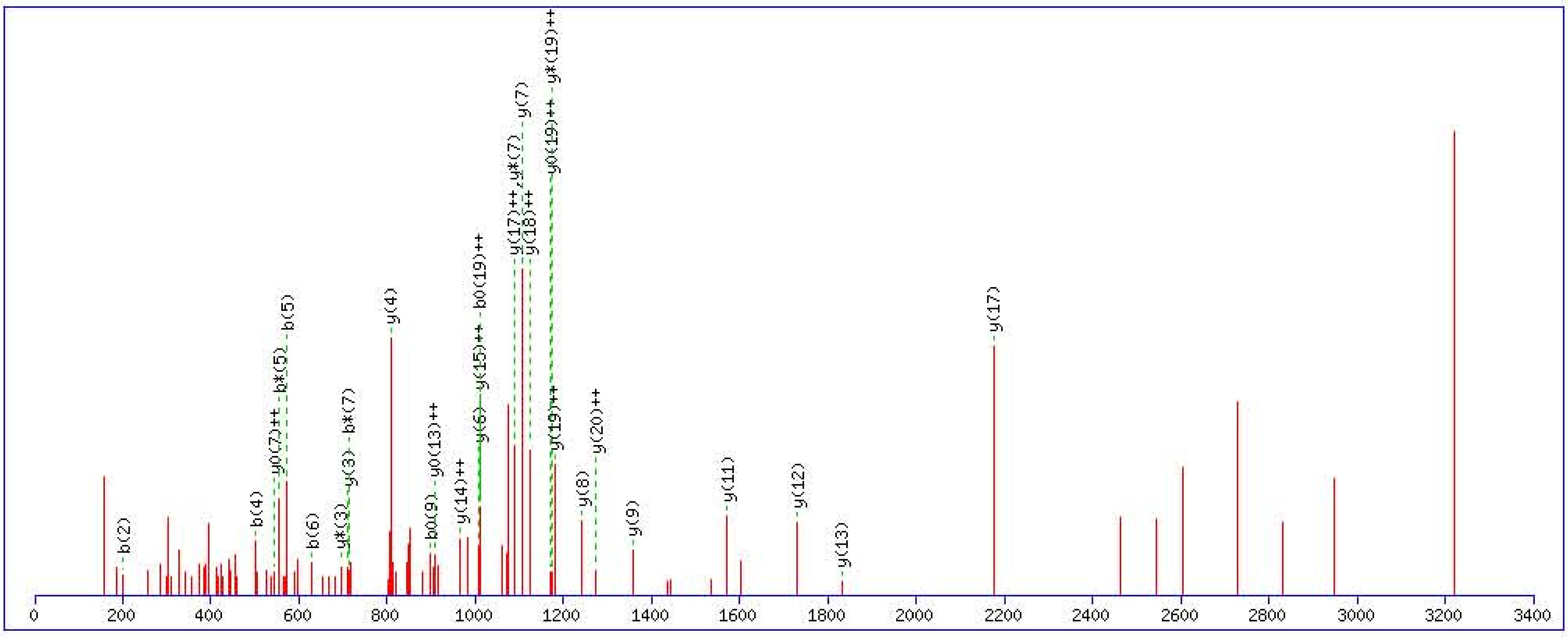
Mascot Search Results

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

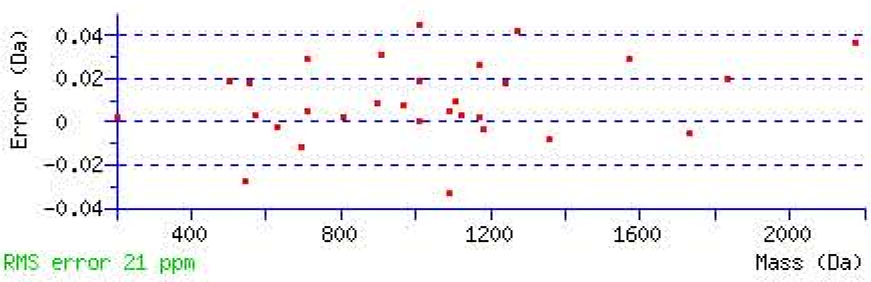
Match to Query 66321: 2746.393272 from(916.471700,3+) rtinseconds(2229) index(80480)
Title: Locus:1.1.1.2126.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

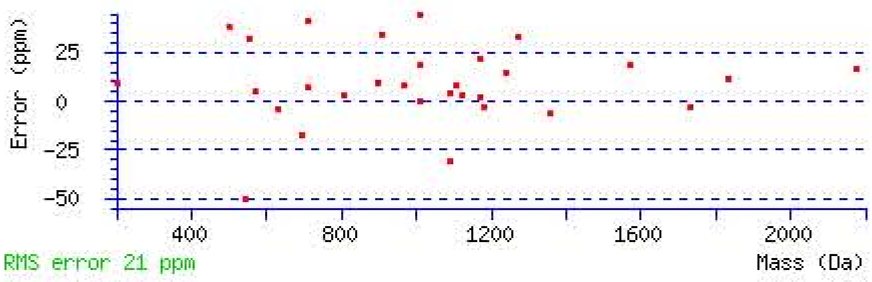
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2746.368332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21    : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.0015
Matches : 30/236 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							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
42.9	2746.368332	0.024940	SLWNAGTSVTCTLNHPSLPPQR

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

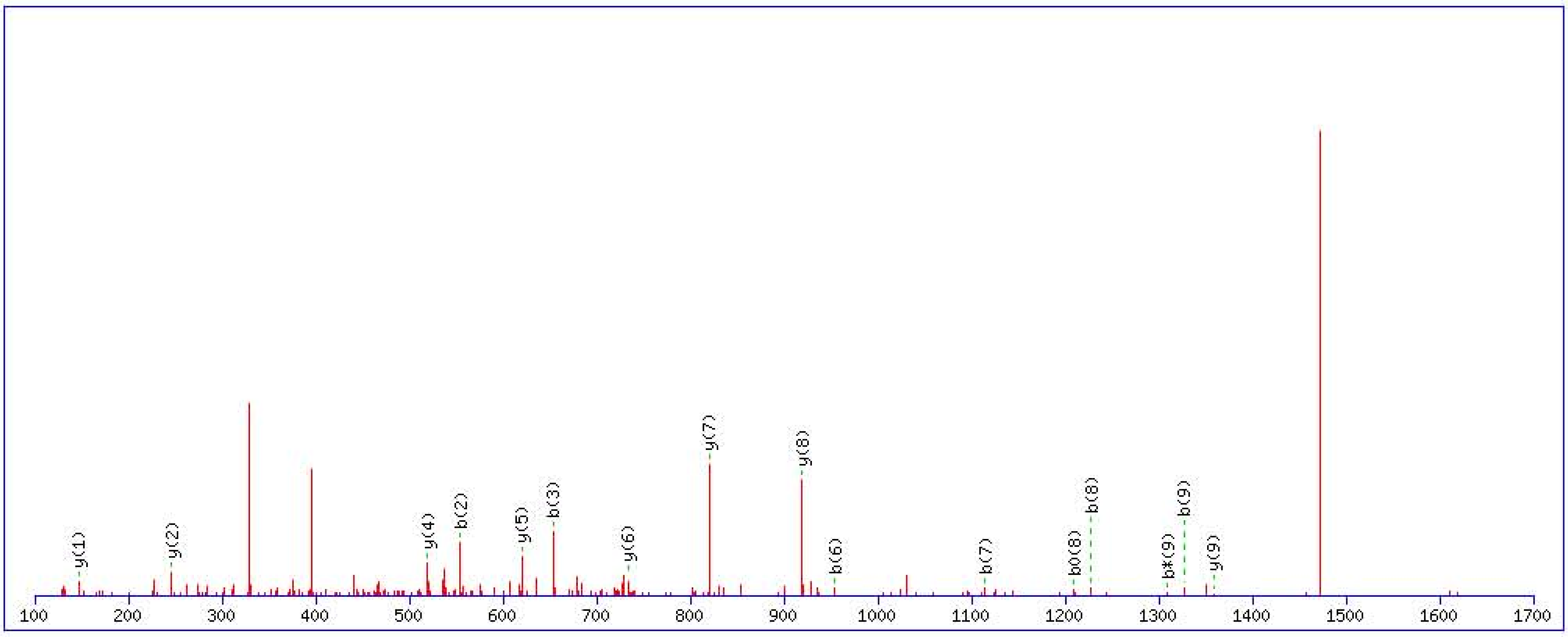
Mascot Search Results

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

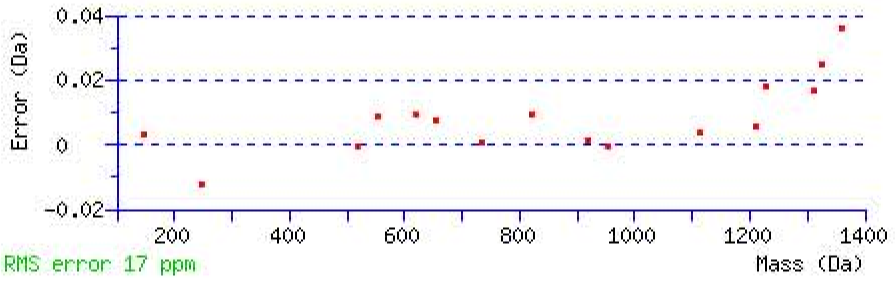
Match to Query 34049: 1471.797908 from(736.906230,2+) rtinseconds(2210) index(80321)
Title: Locus:1.1.1.2120.10 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

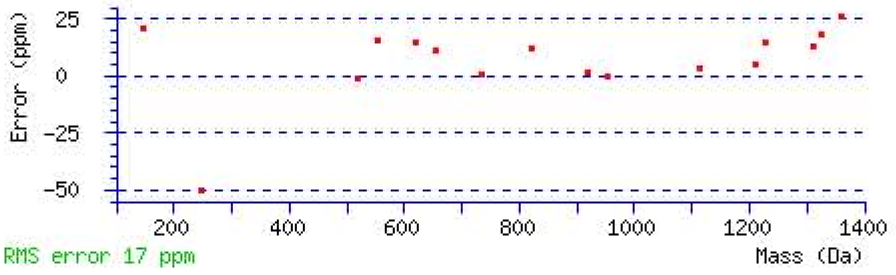
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 3.2e-005
Matches : 16/94 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	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
53.1	1471.789093	0.008815	NQVSLTCLVK
4.9	1471.777847	0.020061	QLDMELVSVK
4.7	1471.806808	-0.008900	ESLLQIPRIEMK
3.6	1471.799438	-0.001530	EVELDRLRDTVK
0.8	1471.797592	0.000316	KYFWDRAFLVK
0.2	1471.792221	0.005687	NESIIPLSPFEVK

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

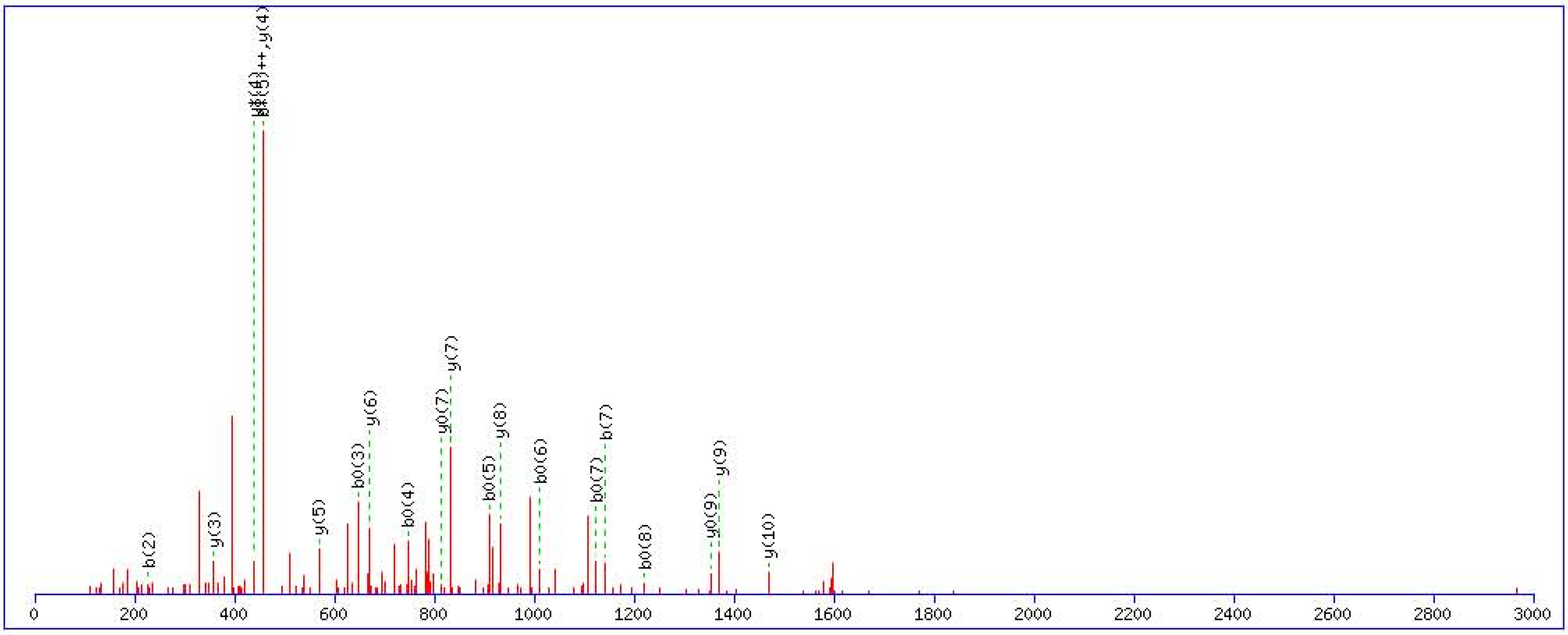
Mascot Search Results

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

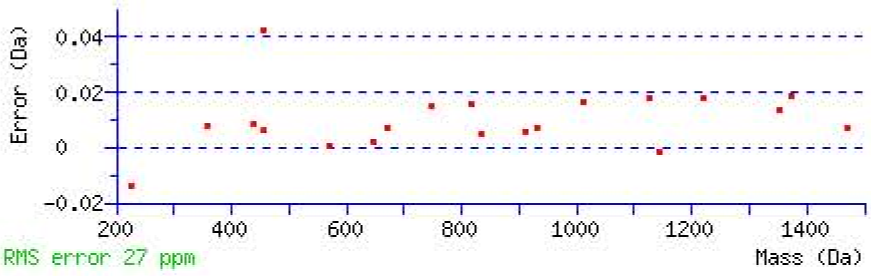
Match to Query 38657: 1596.846108 from(799.430330,2+) rtinseconds(1935) index(78451)
Title: Locus:1.1.1.2024.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

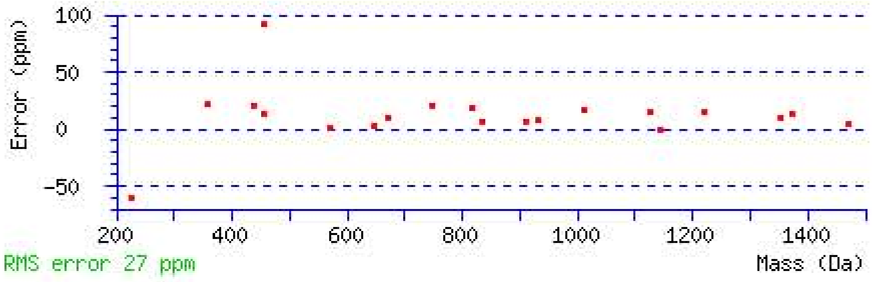
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0024
Matches : 20/114 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	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
40.9	1596.833389	0.012719	EPQVYTLPPSR

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

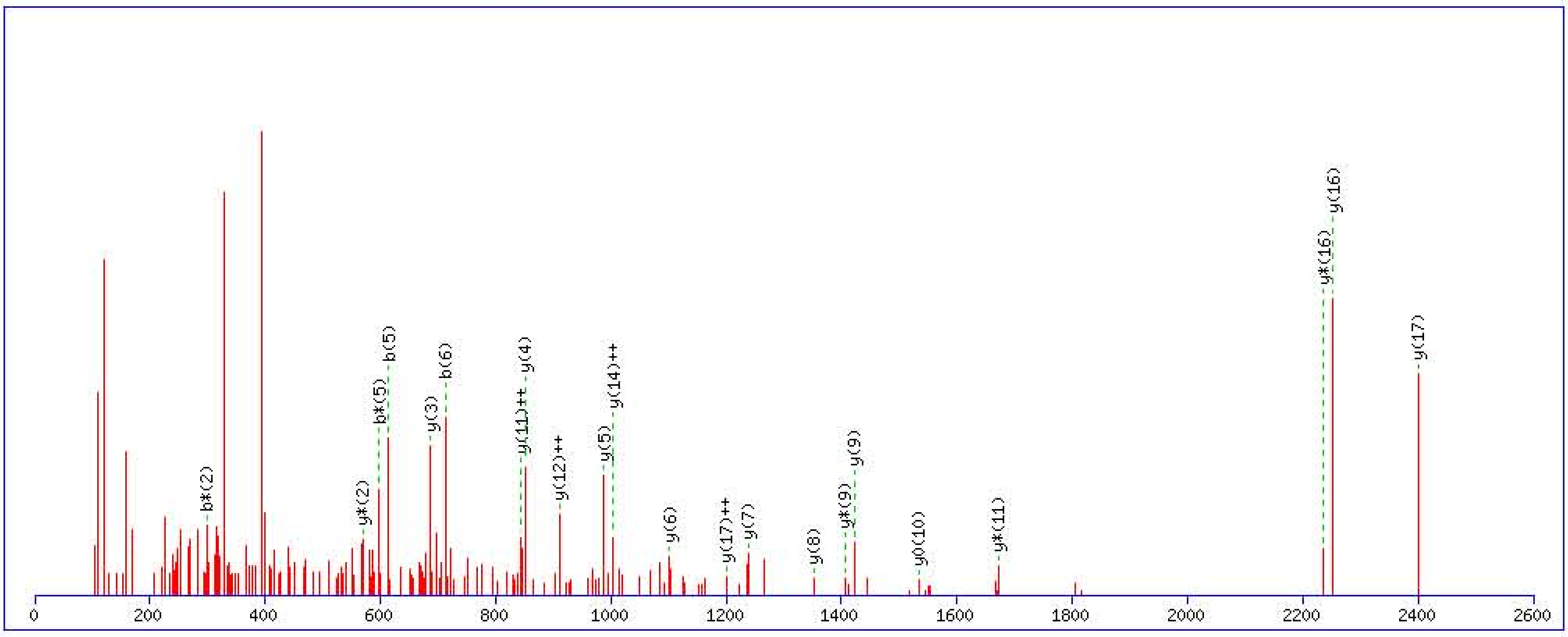
Mascot Search Results

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

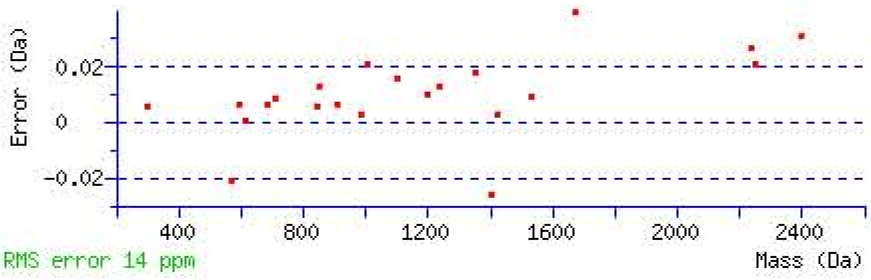
Match to Query 71430: 3111.450670 from(623.297410,5+) rtinseconds(2026) index(79027)
Title: Locus:1.1.1.2056.7 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

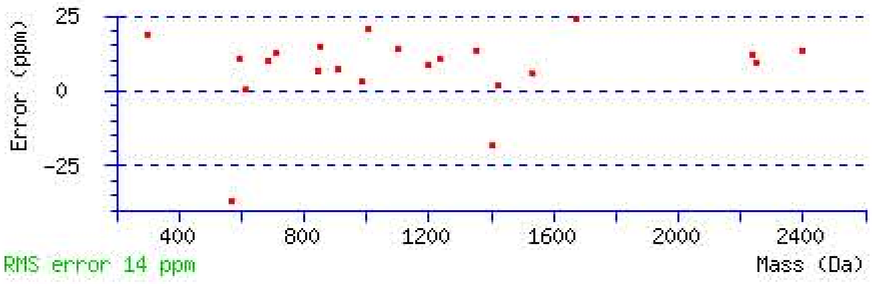
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 43 **Expect:** 0.00088
Matches : 22/244 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	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
42.7	3111.426590	0.024080	WQQGNVFSCSVMHEALHNHYTQK

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

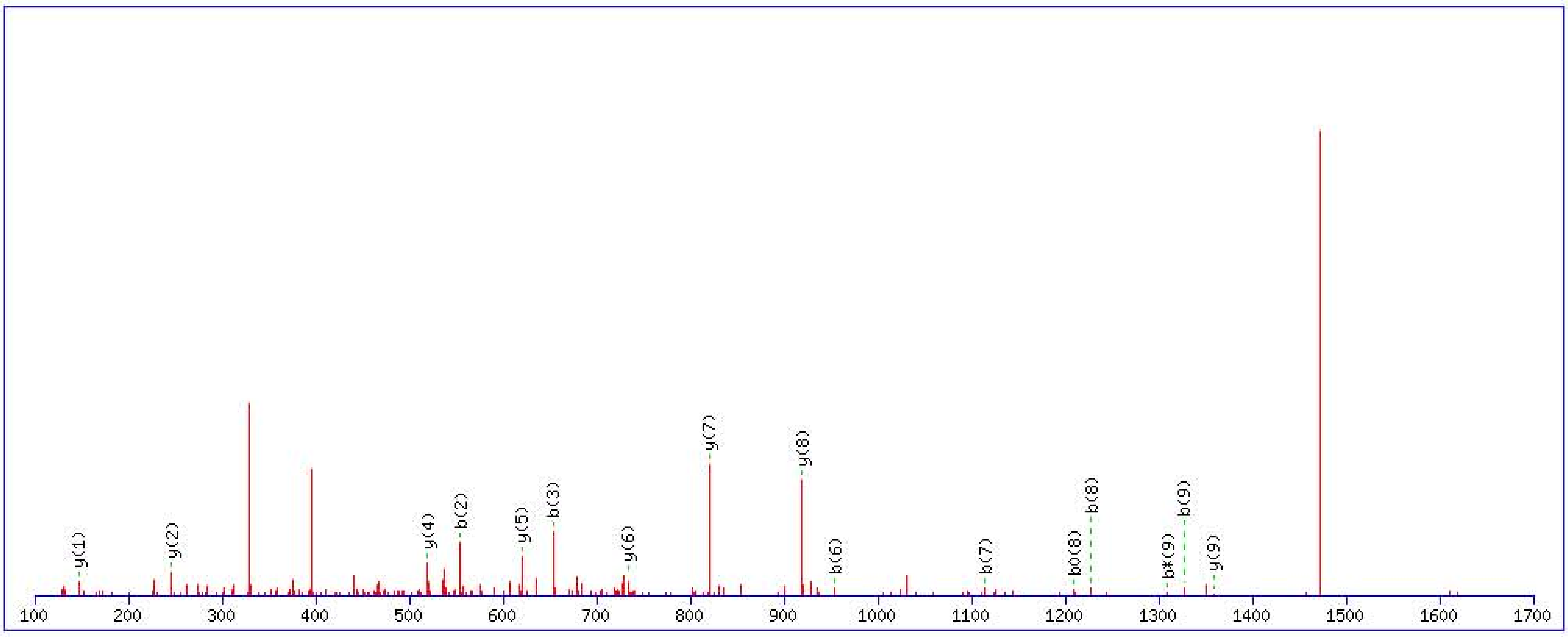
Mascot Search Results

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

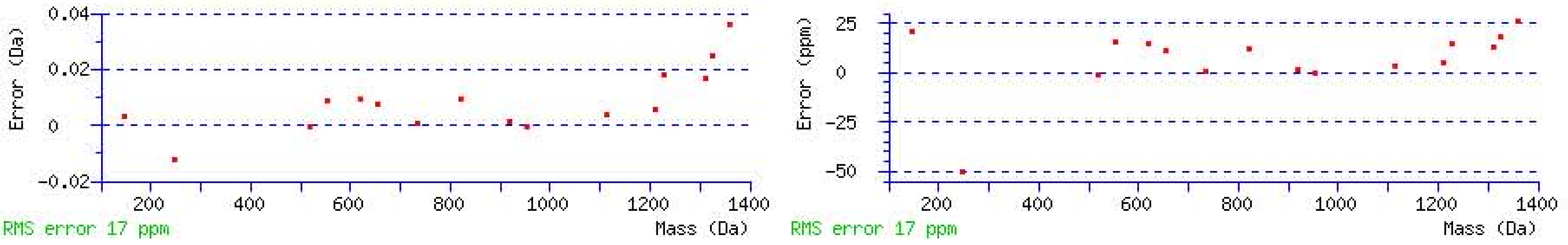
Match to Query 34049: 1471.797908 from(736.906230,2+) rtinseconds(2210) index(80321)
Title: Locus:1.1.1.2120.10 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 3.2e-005
Matches : 16/94 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	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
53.1	1471.789093	0.008815	NQVSLTCLVK
4.9	1471.777847	0.020061	QLDMELVSVK
4.7	1471.806808	-0.008900	ESLLQIPRIEMK
3.6	1471.799438	-0.001530	EVELDRLRDTVK
0.8	1471.797592	0.000316	KYFWDRAFLVK
0.2	1471.792221	0.005687	NESIIPLSPFEVK

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

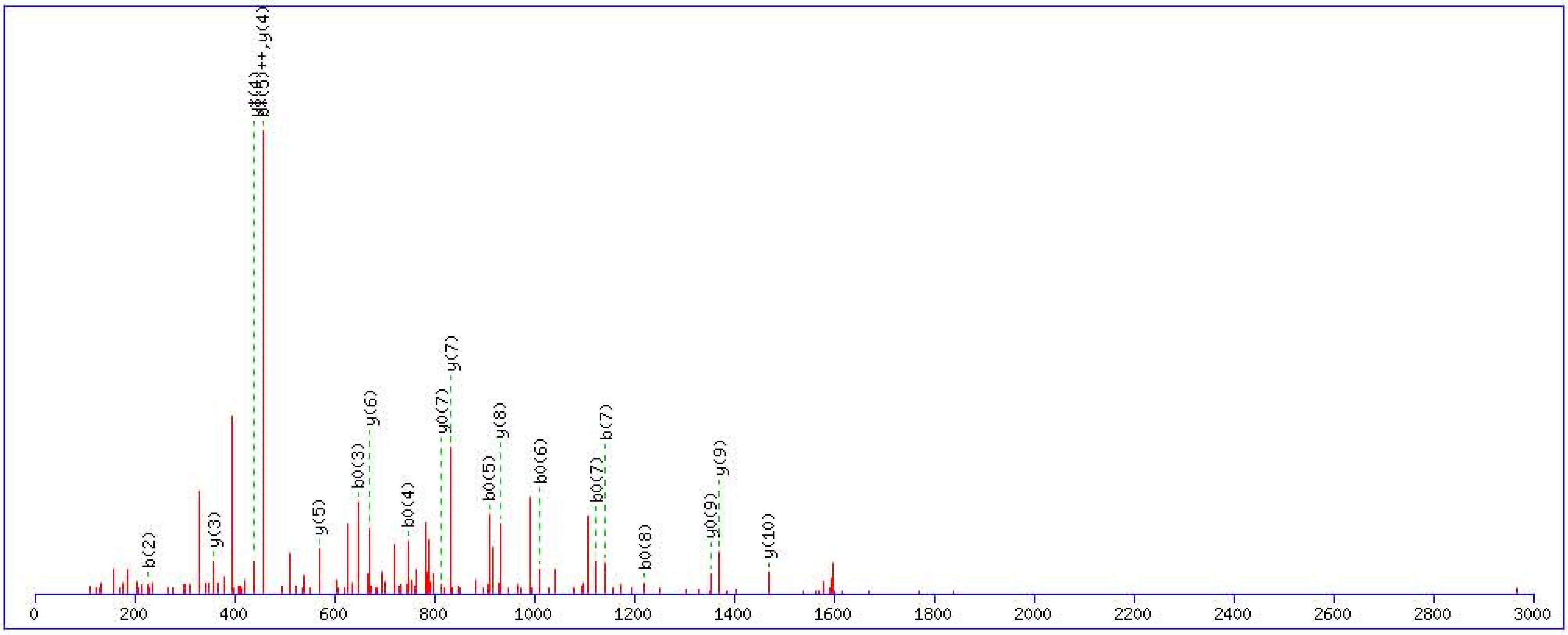
{MATRIX SCIENCE} Mascot Search Results

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

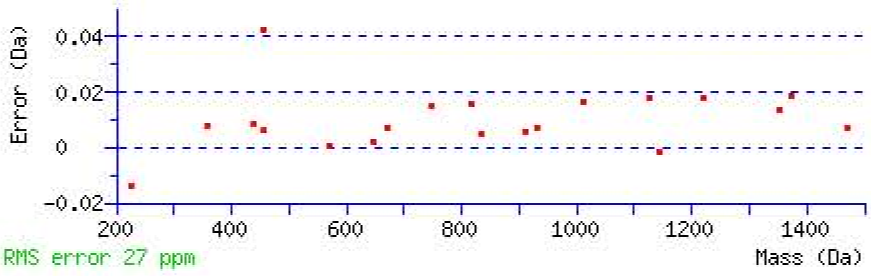
Match to Query 38657: 1596.846108 from(799.430330,2+) rtinseconds(1935) index(78451)
Title: Locus:1.1.1.2024.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

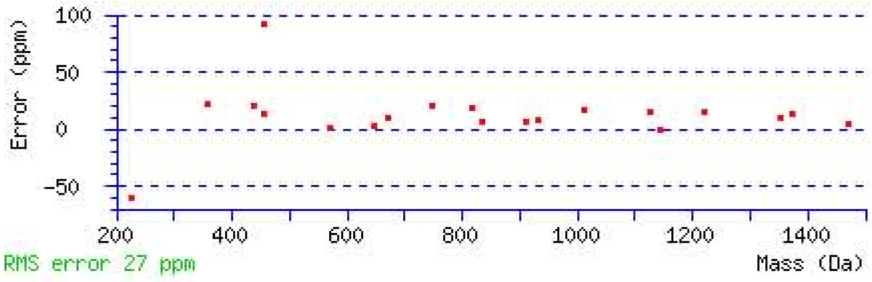
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0024
Matches : 20/114 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	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
40.9	1596.833389	0.012719	EPQVYTLPPSR

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

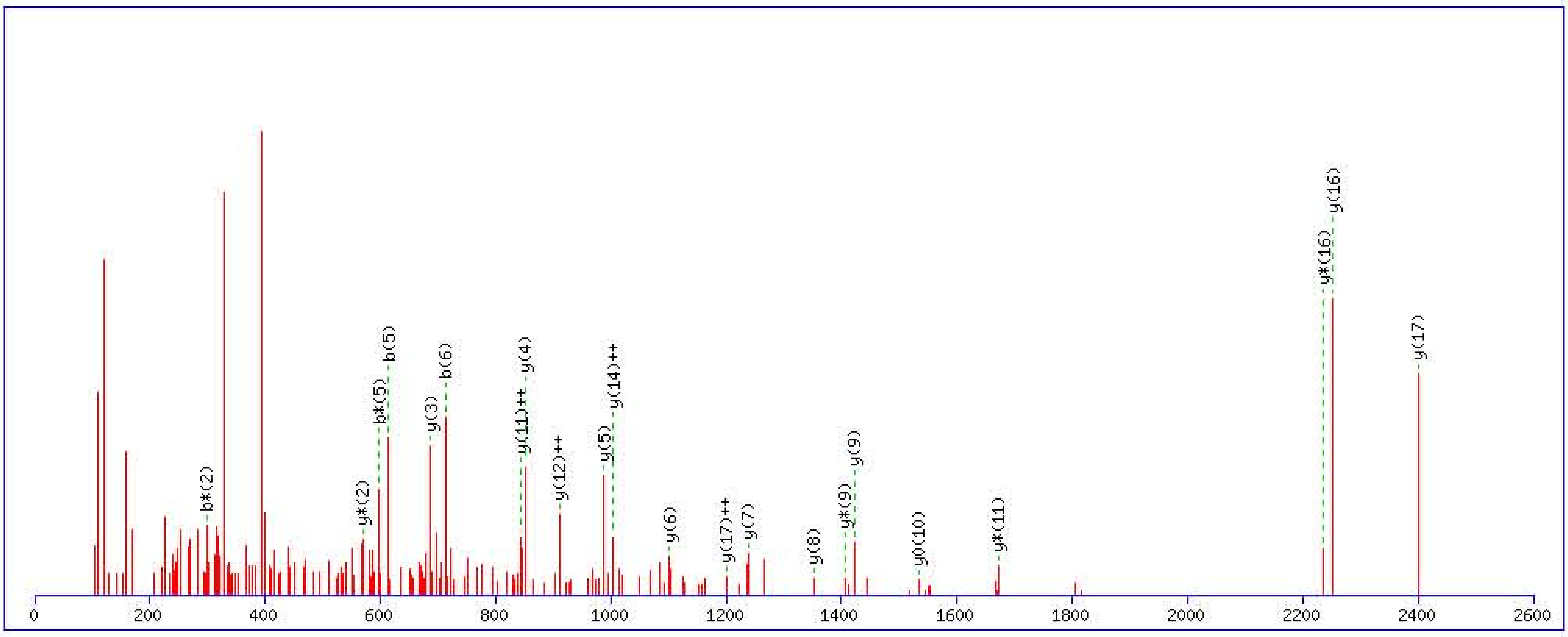
Mascot Search Results

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

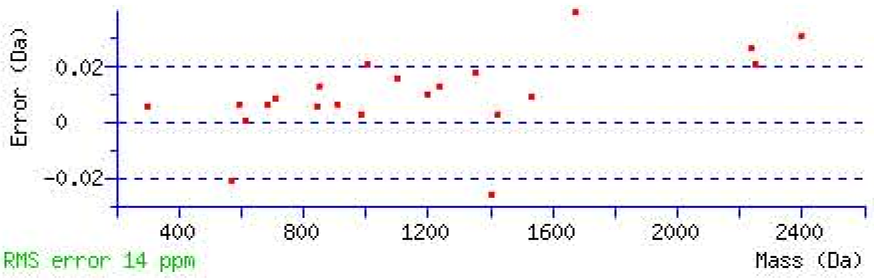
Match to Query 71430: 3111.450670 from(623.297410,5+) rtinseconds(2026) index(79027)
Title: Locus:1.1.1.2056.7 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

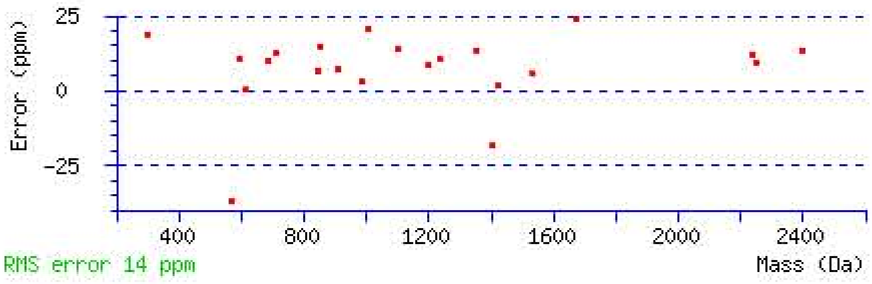
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
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: 43  Expect: 0.00088
Matches : 22/244 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	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
42.7	3111.426590	0.024080	WQQGNVFSCSVMHEALHNHYTQK

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

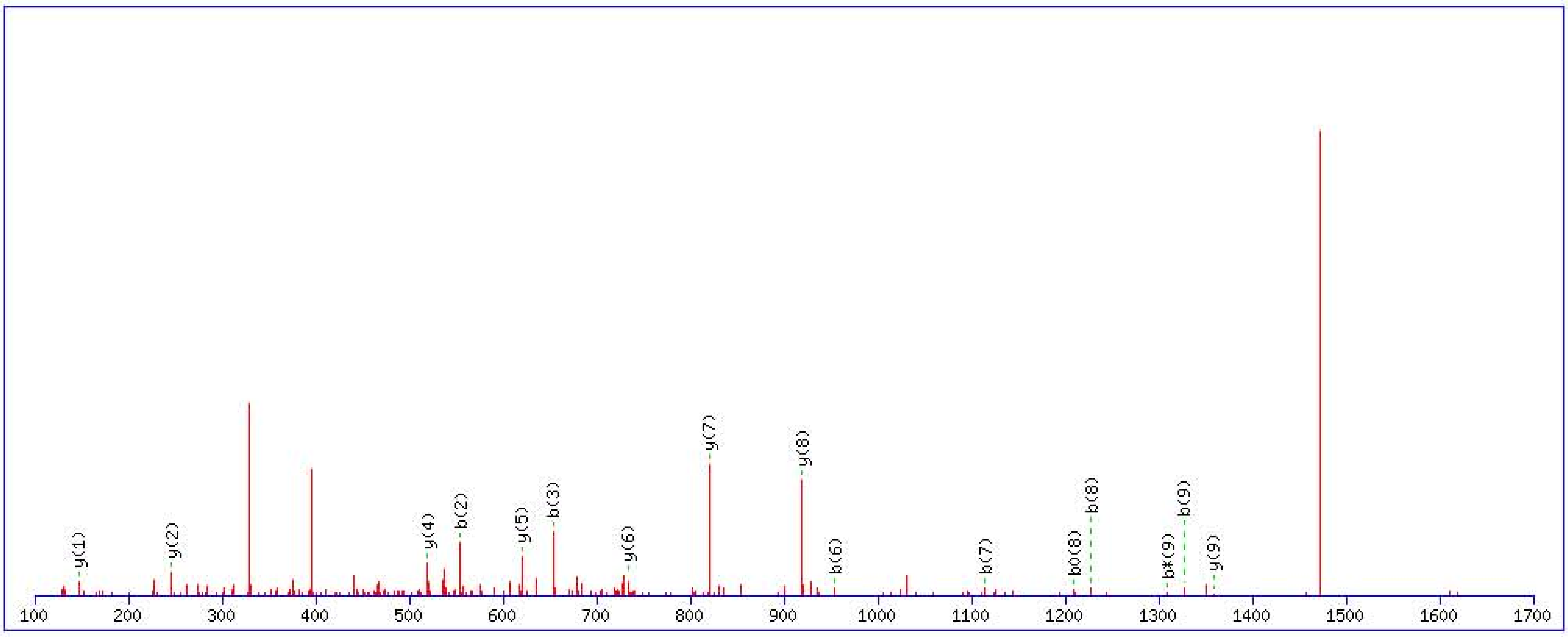
{MATRIX SCIENCE} Mascot Search Results

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

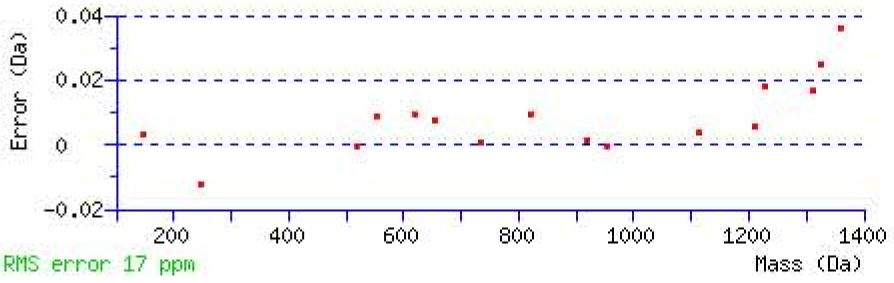
Match to Query 34049: 1471.797908 from(736.906230,2+) rtinseconds(2210) index(80321)
Title: Locus:1.1.1.2120.10 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

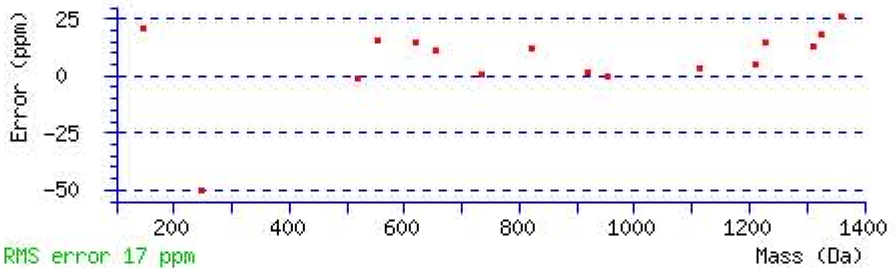
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 3.2e-005
Matches : 16/94 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	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
53.1	1471.789093	0.008815	NQVSLTCLVK
4.9	1471.777847	0.020061	QLDMELVSVK
4.7	1471.806808	-0.008900	ESLLQIPRIEMK
3.6	1471.799438	-0.001530	EVELDRLRDTVK
0.8	1471.797592	0.000316	KYFWDRAFLVK
0.2	1471.792221	0.005687	NESIIPLSPFEVK

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

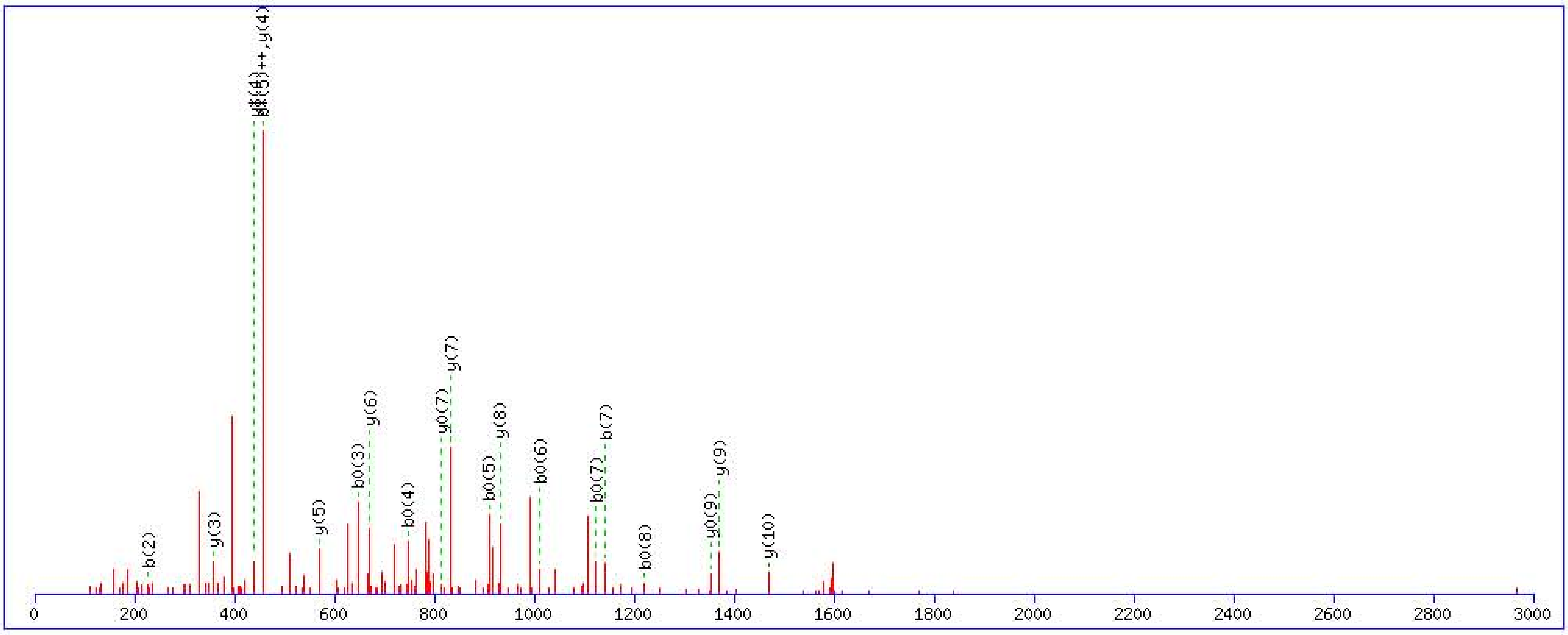
{MATRIX SCIENCE} Mascot Search Results

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

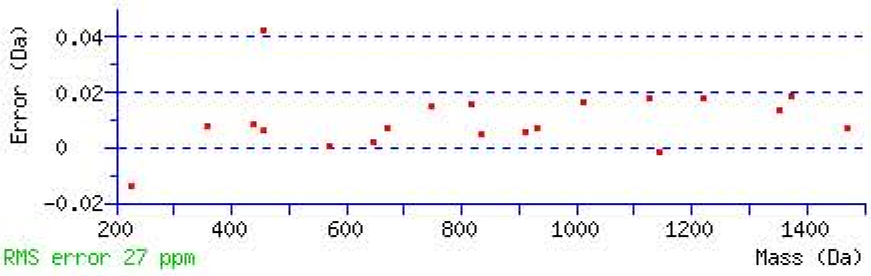
Match to Query 38657: 1596.846108 from(799.430330,2+) rtinseconds(1935) index(78451)
Title: Locus:1.1.1.2024.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

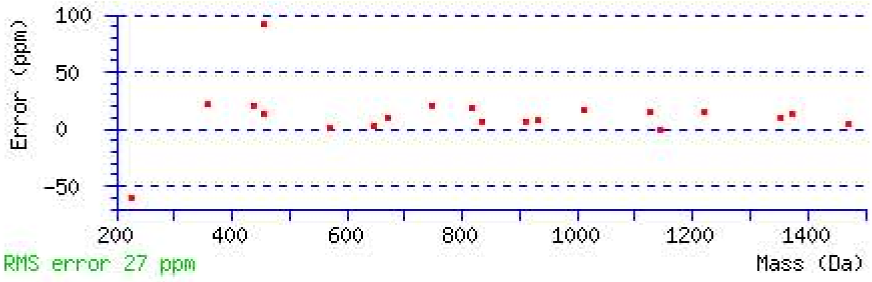
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.0024
Matches : 20/114 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	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
40.9	1596.833389	0.012719	EPQVYTLPPSR

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

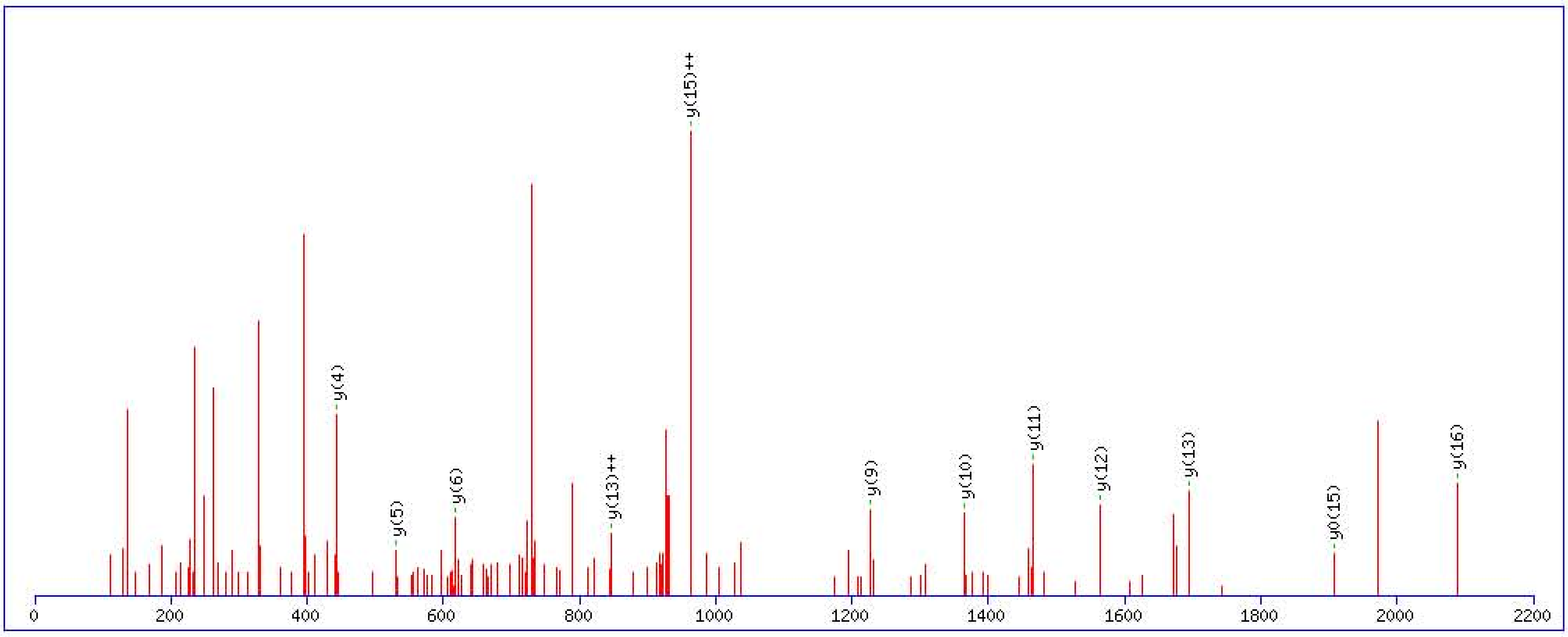
Mascot Search Results

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

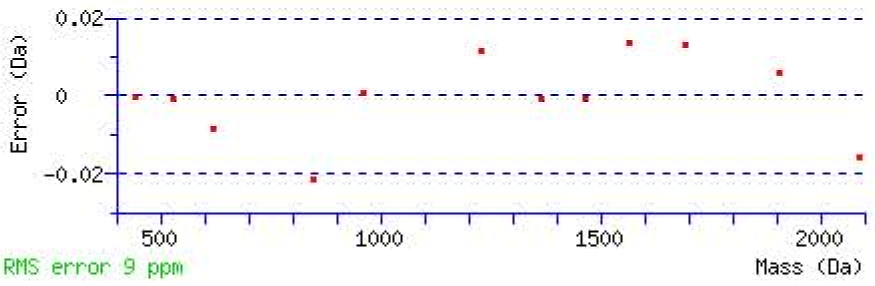
Match to Query 55072: 2186.101062 from(729.707630,3+) rtinseconds(1724) index(22668)
Title: Locus:1.1.1.2743.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

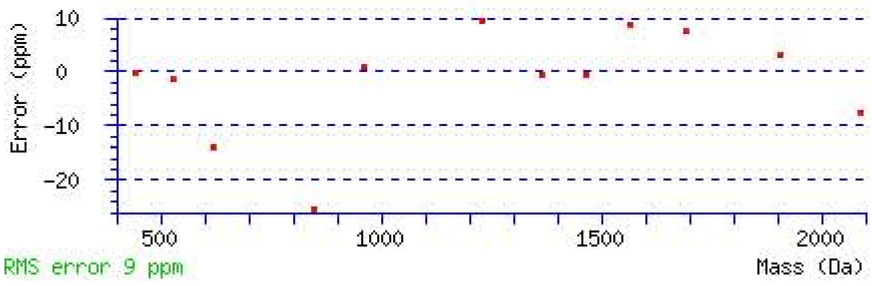
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 55  Expect: 8.8e-005
Matches : 12/166 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	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
55.1	2186.086411	0.014651	VYACEVTHQGLSSPVTK

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

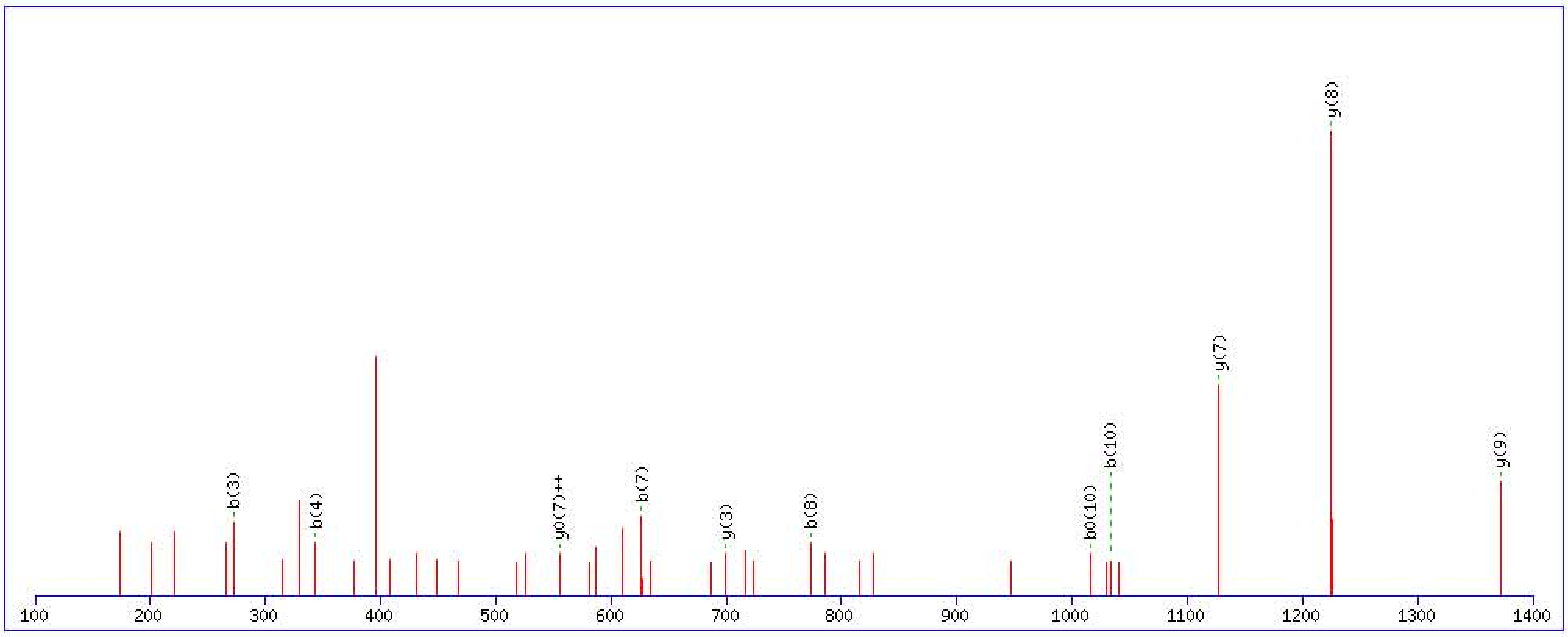
Mascot Search Results

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

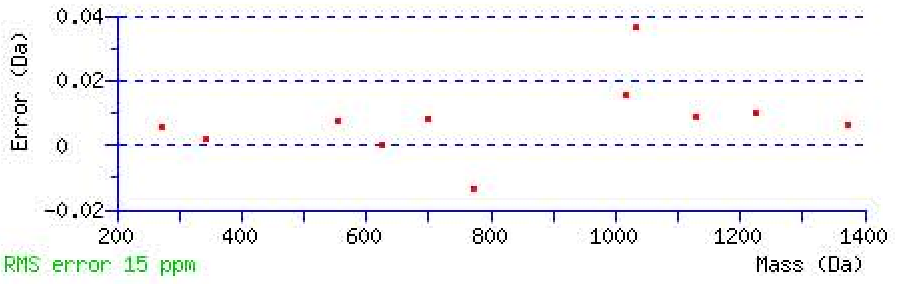
Match to Query 56792: 2256.208692 from(753.076840,3+) rtinseconds(2709) index(29473)
Title: Locus:1.1.1.3084.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

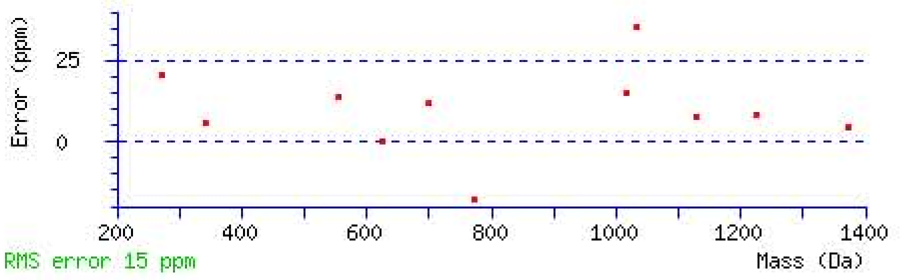
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2256.186432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.045
Matches : 11/168 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	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
26.8	2256.186432	0.022260	TVAAPSVFIFPPSDEQLK

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

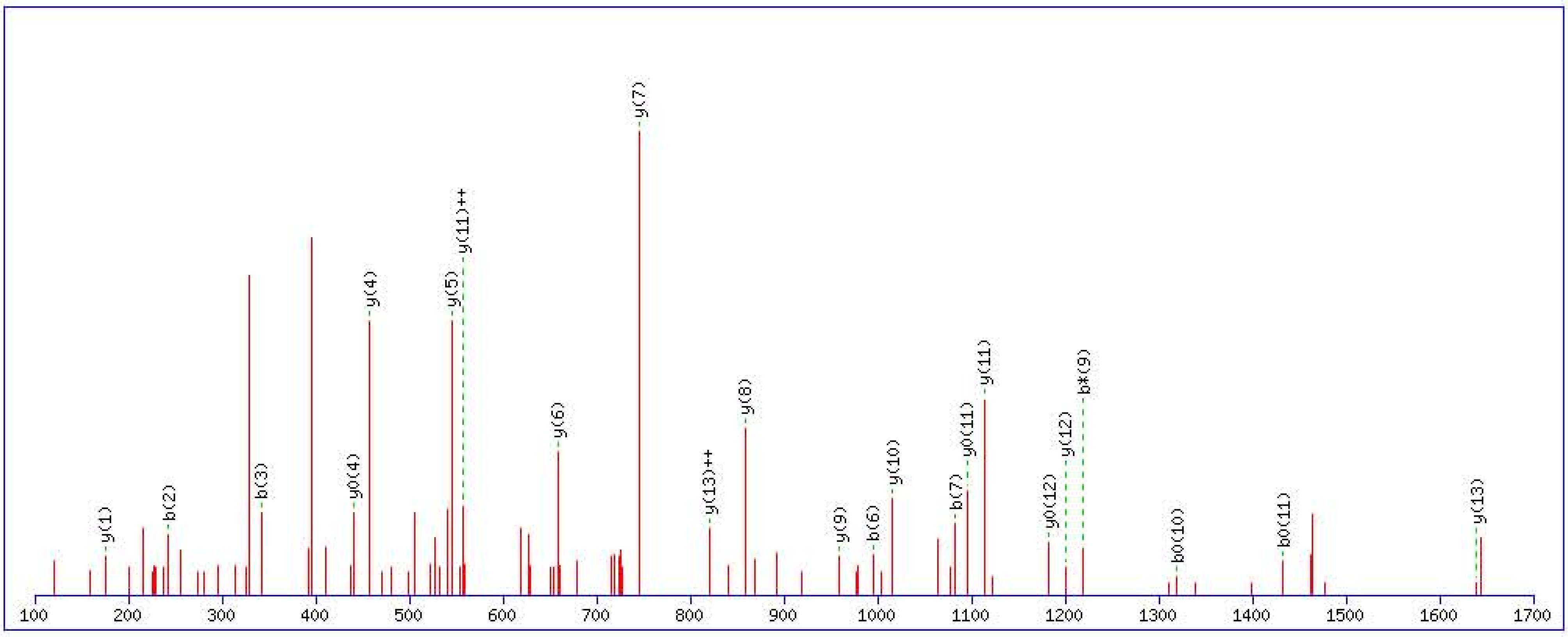
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIVLTQSPGTLSLSPGER**
Found in **KV302_HUMAN**, Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1

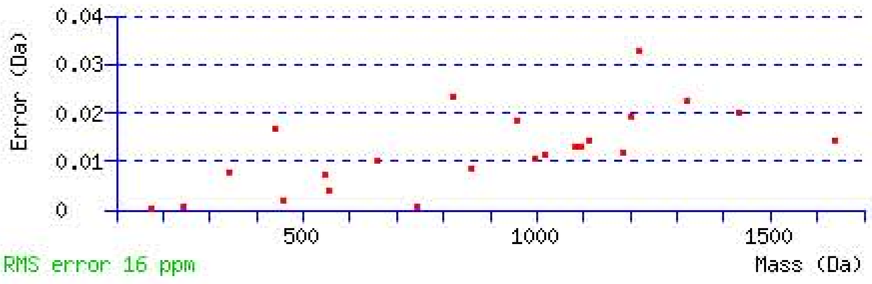
Match to Query 55258: 2194.190352 from(732.404060,3+) rtinseconds(2317) index(81017)
Title: Locus:1.1.1.2157.15 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

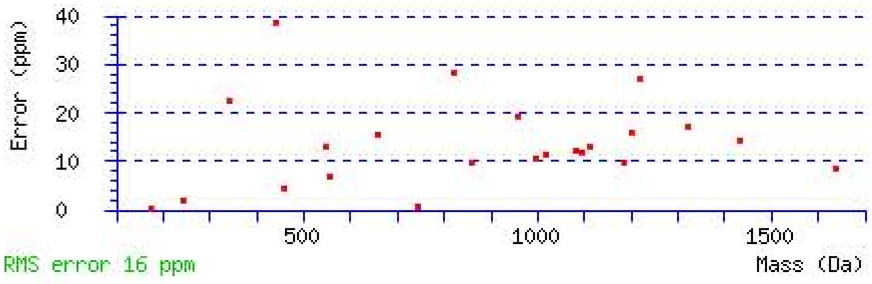
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2194.166748
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 7.7e-006
Matches : 23/192 fragment ions using 42 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							18
2	**243.133933**	122.070605			225.123368	113.065322	I	2066.131439	1033.569357	2049.104890	1025.056083	2048.120874	1024.564075	17
3	**342.202347**	171.604812			324.191782	162.599529	V	1953.047375	977.027326	1936.020826	968.514051	1935.036810	968.022043	16
4	455.286411	228.146844			437.275846	219.141561	L	1853.978961	927.493119	1836.952412	918.979844	1835.968396	918.487836	15
5	556.334090	278.670683			538.323525	269.665401	T	1740.894897	870.951087	1723.868348	862.437812	1722.884332	861.945804	14
6	**995.559416**	498.283346	978.532867	489.770072	977.548851	489.278064	Q	***1639.847218***	820.427247	1622.820669	811.913973	1621.836653	811.421965	13
7	**1082.591444**	541.799360	1065.564895	533.286086	1064.580879	532.794078	S	***1200.621892***	600.814584	1183.595343	592.301310	1182.611327	591.809302	12
8	1179.644208	590.325742	1162.617659	581.812468	1161.633643	581.320460	P	***1113.589864***	557.298570	1096.563315	548.785296	1095.579299	548.293288	11
9	1236.665672	618.836474	1219.639123	610.323200	1218.655107	609.831192	G	***1016.537100***	508.772188	999.510551	500.258914	998.526535	499.766906	10
10	1337.713351	669.360314	1320.686802	660.847039	1319.702786	660.355031	T	***959.515636***	480.261456	942.489087	471.748182	941.505071	471.256174	9
11	1450.797415	725.902346	1433.770866	717.389071	1432.786850	716.897063	L	***858.467957***	429.737617	841.441408	421.224342	840.457392	420.732334	8
12	1537.829443	769.418360	1520.802894	760.905085	1519.818878	760.413077	S	***745.383893***	373.195585	728.357344	364.682310	727.373328	364.190302	7
13	1650.913507	825.960392	1633.886958	817.447117	1632.902942	816.955109	L	***658.351865***	329.679571	641.325316	321.166296	640.341300	320.674288	6
14	1737.945535	869.476406	1720.918986	860.963131	1719.934970	860.471123	S	***545.267801***	273.137539	528.241252	264.624264	527.257236	264.132256	5
15	1834.998299	918.002788	1817.971750	909.489513	1816.987734	908.997505	P	***458.235773***	229.621524	441.209224	221.108250	440.225208	220.616242	4
16	1892.019763	946.513520	1874.993214	938.000245	1874.009198	937.508237	G	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
17	2021.062356	1011.034816	2004.035807	1002.521542	2003.051791	1002.029534	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EIVLTQSPGTLSLSPGER
(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	2194.166748	0.023604	EIVLTQSPGTLSLSPGER
64.3	2194.166748	0.023604	ZIVLTZSPGTLSLSPGZR
47.9	2194.166748	0.023604	ZIVLTZSPGTLSLSPGZR

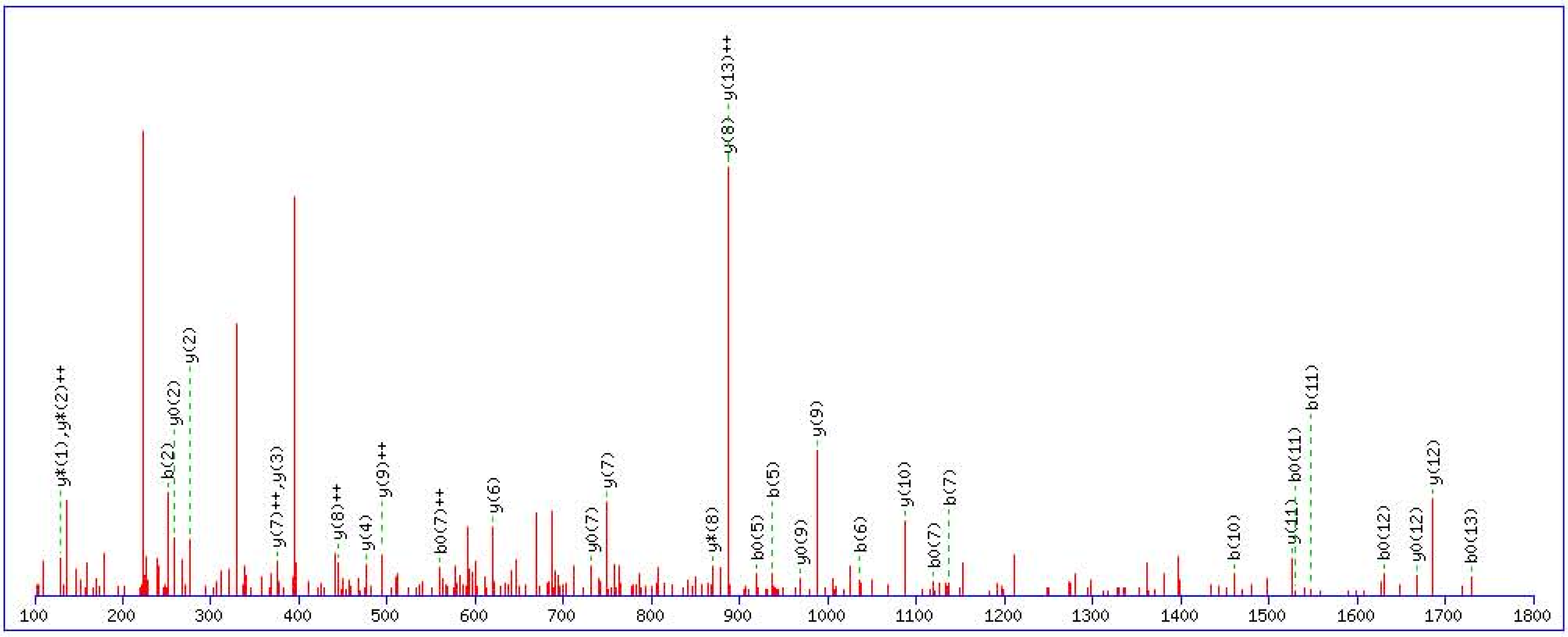
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYSCQVTHEGSTVEK**
Found in **IGLL5_HUMAN**, Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2

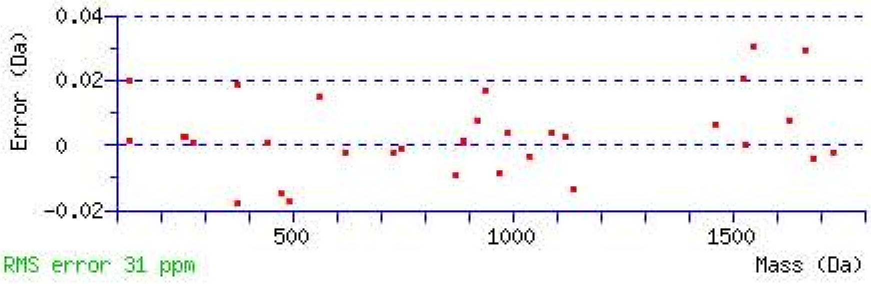
Match to Query 51317: 2021.925162 from(674.982330,3+) rtinseconds(1397) index(20223)
Title: Locus:1.1.1.2629.11 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

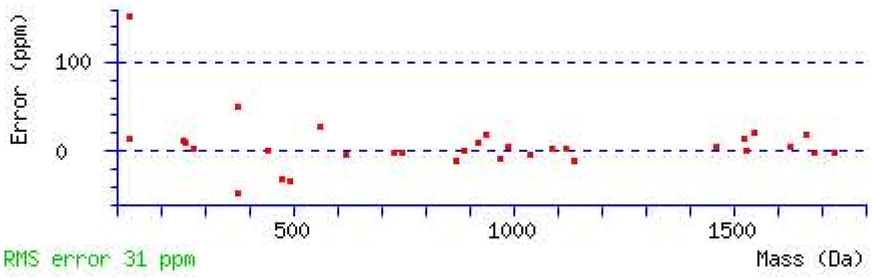
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2021.918671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00071
Matches : 33/158 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	88.039304	44.523290			70.028739	35.518008	S							15
2	**251.102633**	126.054954			233.092068	117.049672	Y	1935.893912	968.450594	1918.867363	959.937320	1917.883347	959.445312	14
3	338.134661	169.570968			320.124096	160.565686	S	1772.830583	886.918930	1755.804034	878.405655	1754.820018	877.913647	13
4	498.165310	249.586293			480.154745	240.581011	C	***1685.798555***	843.402916	1668.772006	834.889641	1667.787990	834.397633	12
5	**937.390636**	469.198956	920.364087	460.685682	919.380071	460.193674	Q	***1525.767906***	763.387591	1508.741357	754.874317	1507.757341	754.382309	11
6	**1036.459050**	518.733163	1019.432501	510.219889	1018.448485	509.727881	V	***1086.542580***	543.774928	1069.516031	535.261654	1068.532015	534.769646	10
7	**1137.506729**	569.257003	1120.480180	560.743728	1119.496164	560.251720	T	***987.474166***	494.240721	970.447617	485.727447	969.463601	485.235439	9
8	1274.565641	637.786459	1257.539092	629.273184	1256.555076	628.781176	H	***886.426487***	443.716882	869.399938	435.203607	868.415922	434.711599	8
9	1403.608234	702.307755	1386.581685	693.794481	1385.597669	693.302473	E	***749.367575***	375.187426	732.341026	366.674151	731.357010	366.182143	7
10	**1460.629698**	730.818487	1443.603149	722.305213	1442.619133	721.813204	G	***620.324982***	310.666129	603.298433	302.152855	602.314417	301.660847	6
11	**1547.661726**	774.334501	1530.635177	765.821227	1529.651161	765.329219	S	563.303518	282.155397	546.276969	273.642123	545.292953	273.150115	5
12	1648.709405	824.858341	1631.682856	816.345066	1630.698840	815.853058	T	***476.271490***	238.639383	459.244941	230.126109	458.260925	229.634101	4
13	1747.777819	874.392548	1730.751270	865.879273	1729.767254	865.387265	V	***375.223811***	188.115544	358.197262	179.602269	357.213246	179.110261	3
14	1876.820412	938.913844	1859.793863	930.400570	1858.809847	929.908562	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SYSCQVTHEGSTVEK
(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	2021.918671	0.006491	SYSCQVTHEGSTVEK

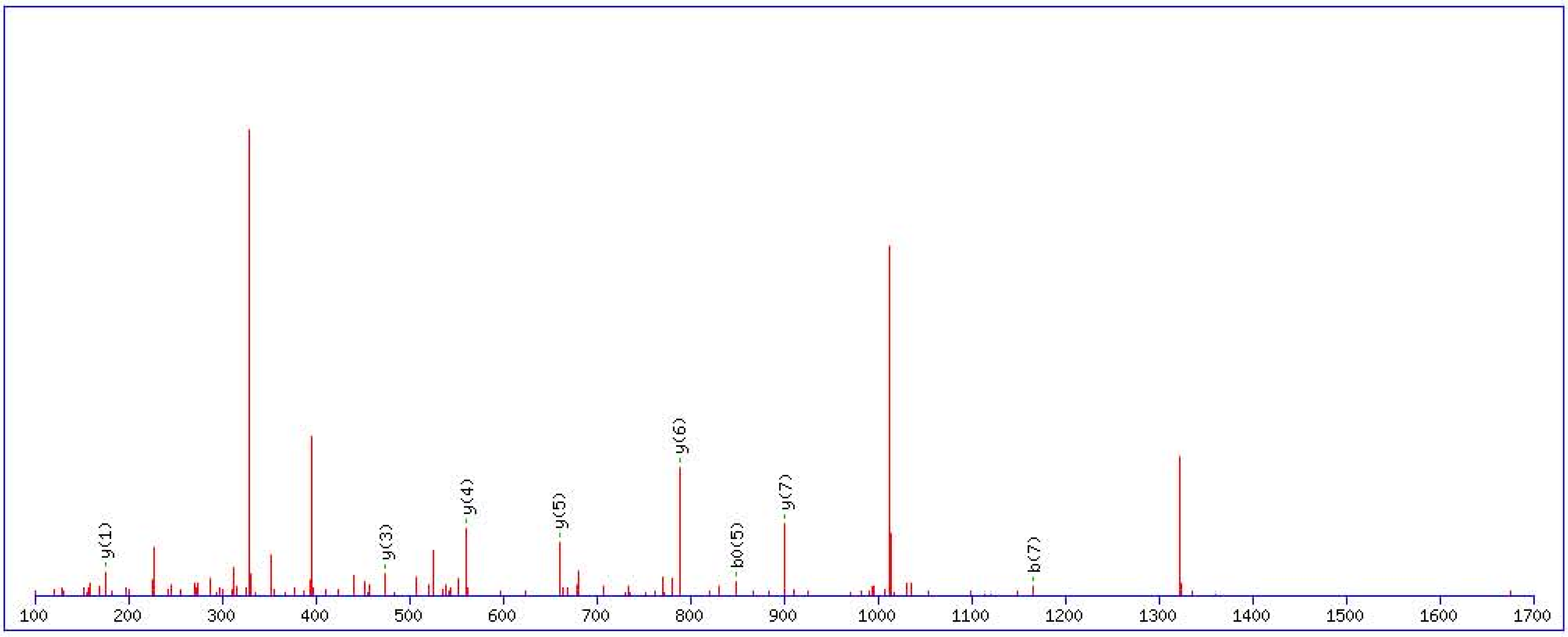
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QIQVSWLR**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

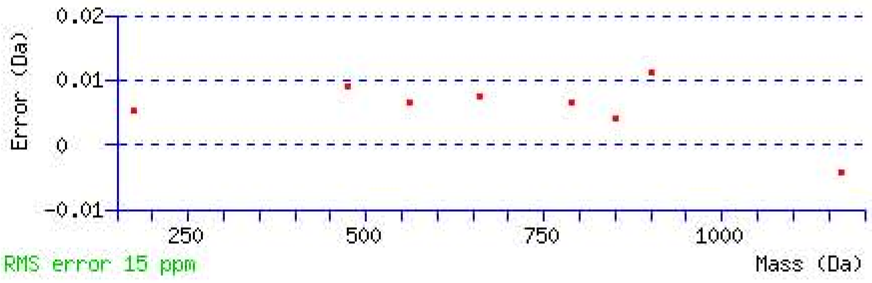
Match to Query 27849: 1339.761288 from(670.887920,2+) rtinseconds(2315) index(44368)
Title: Locus:1.1.1.3255.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

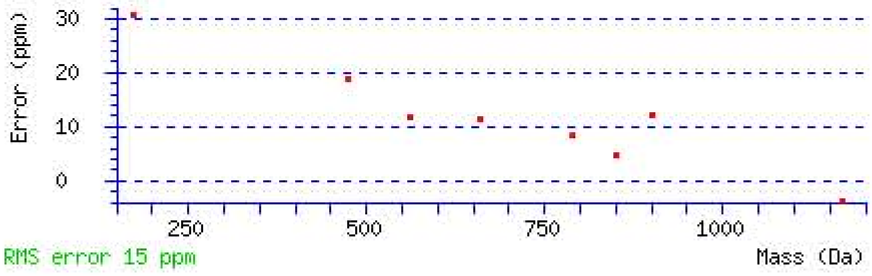
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1339.743454
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00076
Matches : 8/70 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	440.232602	220.619939	423.206053	212.106664			Q							8
2	553.316666	277.161971	536.290117	268.648697			I	***901.525413***	451.266344	884.498864	442.753070	883.514848	442.261062	7
3	681.375244	341.191260	664.348695	332.677986			Q	***788.441349***	394.724312	771.414800	386.211038	770.430784	385.719030	6
4	780.443658	390.725467	763.417109	382.212193			V	***660.382771***	330.695023	643.356222	322.181749	642.372206	321.689741	5
5	867.475686	434.241481	850.449137	425.728207	849.465121	425.236199	S	***561.314357***	281.160816	544.287808	272.647542	543.303792	272.155534	4
6	1053.554999	527.281138	1036.528450	518.767863	1035.544434	518.275855	W	***474.282329***	237.644802	457.255780	229.131528			3
7	**1166.639063**	583.823169	1149.612514	575.309895	1148.628498	574.817887	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 QIQVSWLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.3	1339.743454	0.017834	QIQVSWLR
16.2	1339.743454	0.017834	QIQVSWLR
12.0	1339.765915	-0.004627	QRLRFGPR
9.8	1339.753326	0.007962	QLQISIAEK
7.7	1339.764557	-0.003269	AKETIQALR
6.3	1339.745941	0.015347	QVTAPELNSIIR
6.2	1339.754669	0.006619	QASIRLWR
6.1	1339.775787	-0.014499	QLRSIEKR
6.1	1339.743439	0.017849	QLSWLINR
6.1	1339.743454	0.017834	QLTWLVNR

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

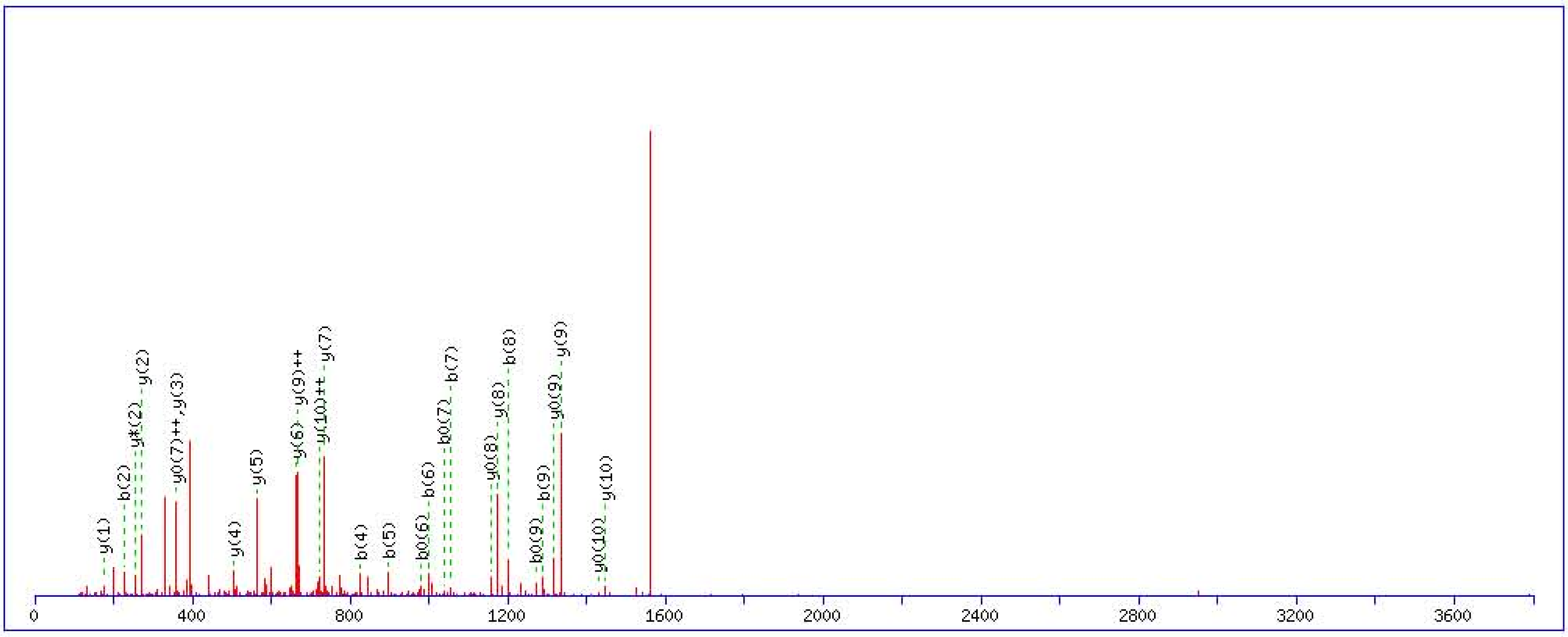
{MATRIX SCIENCE} Mascot Search Results

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

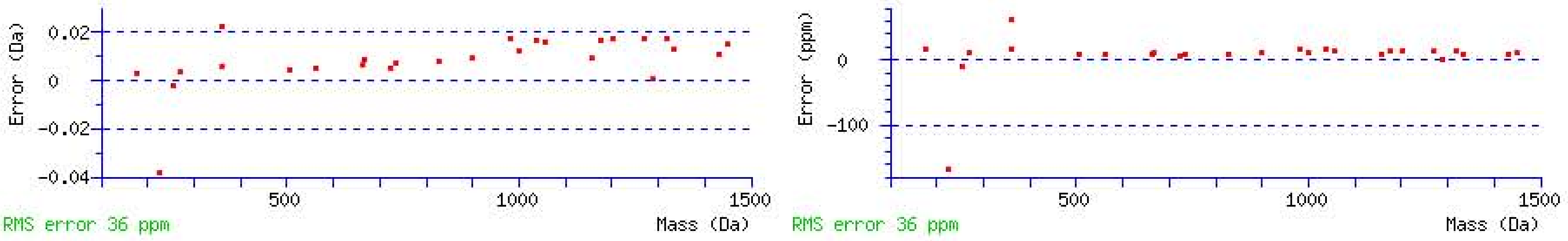
Match to Query 36675: 1559.816868 from(780.915710,2+) rtinseconds(1965) index(41990)
Title: Locus:1.1.1.3133.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1559.795242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 70 **Expect:** 2.7e-006
Matches : 27/100 fragment ions using 45 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
69.8	1559.795242	0.021626	LICQATGFSPR
10.0	1559.820190	-0.003322	MTRSATQAAKQVPR
5.1	1559.808960	0.007908	LDRLSGLADQMVAR
3.7	1559.808975	0.007893	LLDRDACDTVRVK
3.1	1559.838120	-0.021252	LILQYLDSER

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

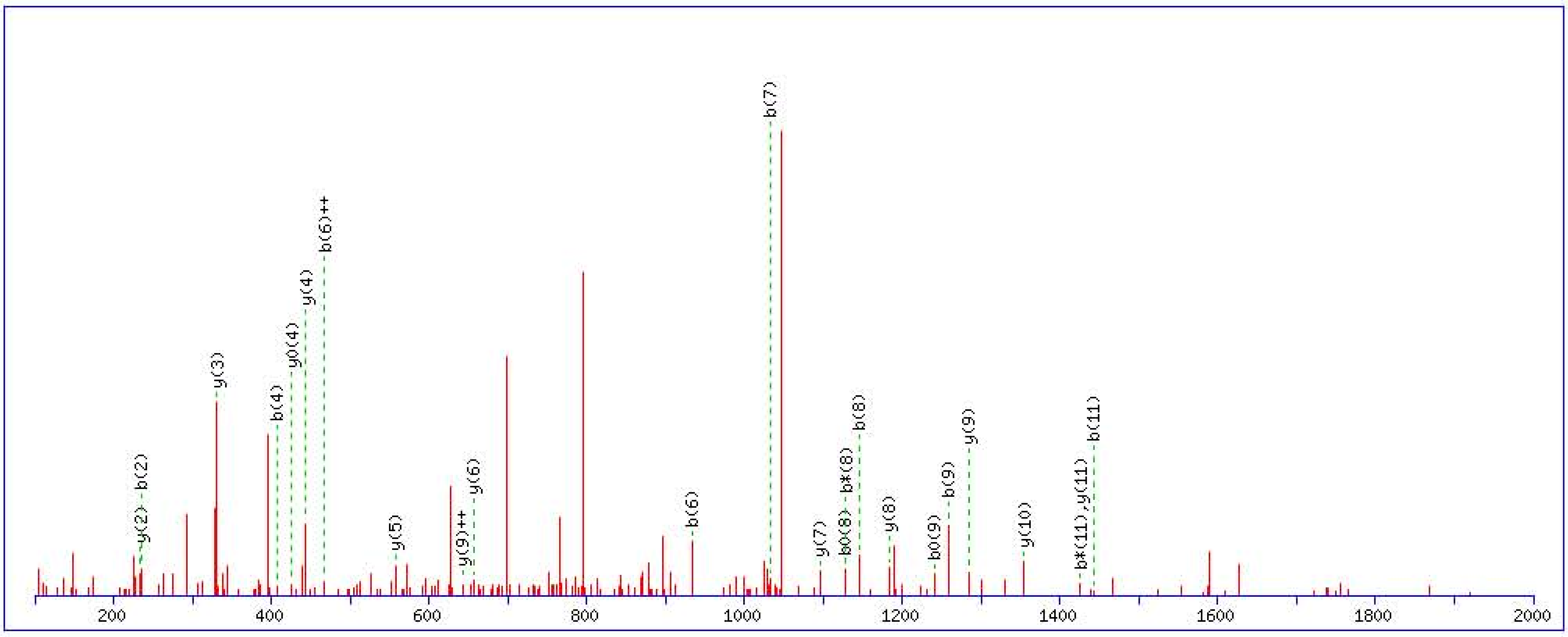
Mascot Search Results

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

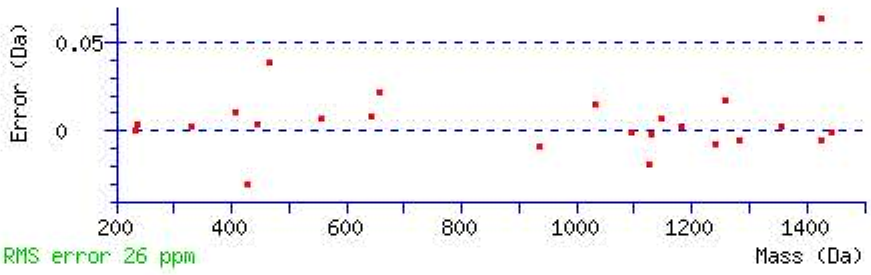
Match to Query 38104: 1587.859728 from(794.937140,2+) rtinseconds(1996) index(24664)
Title: Locus:1.1.1.2837.17 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

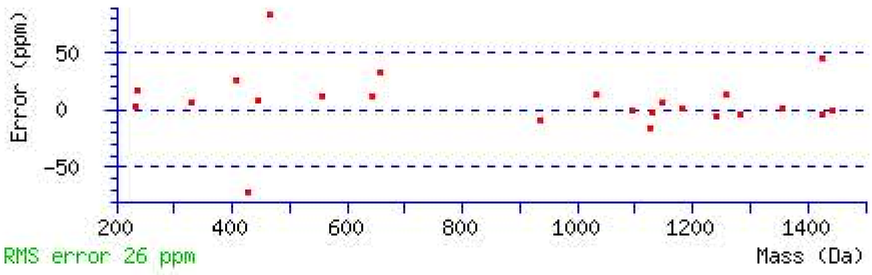
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1587.869431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.026
Matches : 24/114 fragment ions using 81 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	**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





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
29.6	1587.869431	-0.009703	YAATSQVLLPSK
13.1	1587.841599	0.018129	QSTHLKDHRR
4.1	1587.836884	0.022844	NLESIDPQFTIRR
3.6	1587.862045	-0.002317	VTGQNQEQFLLLAK
2.5	1587.840286	0.019442	DATRVLQMVLDGVR

{MATRIX}
{SCIENCE}

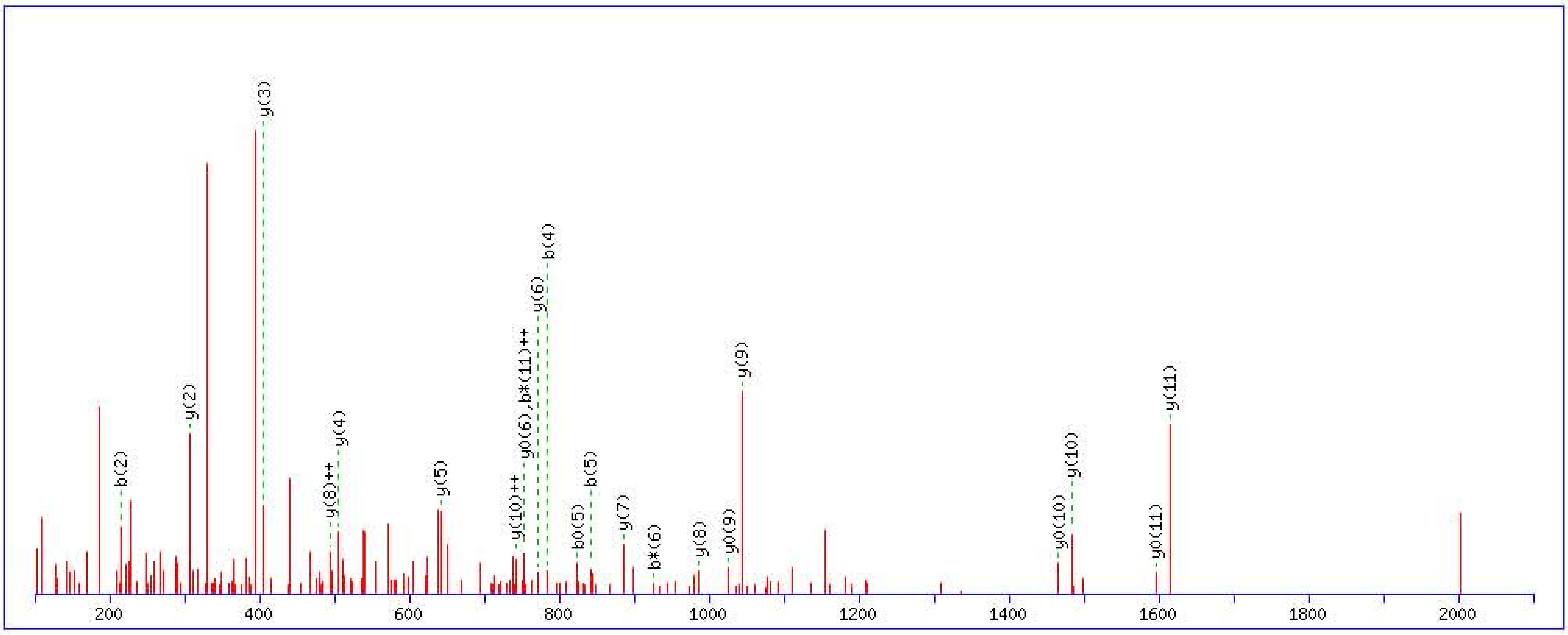
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVMQGTDEHVVCK**
Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

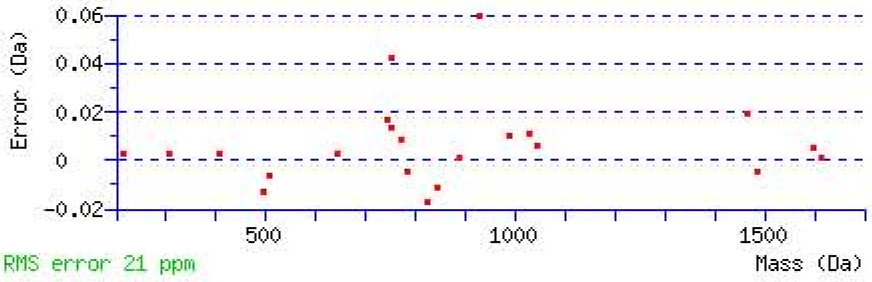
Match to Query 46002: 1827.844302 from(610.288710,3+) rtinseconds(1620) index(39592)
Title: Locus:1.1.1.3013.10 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

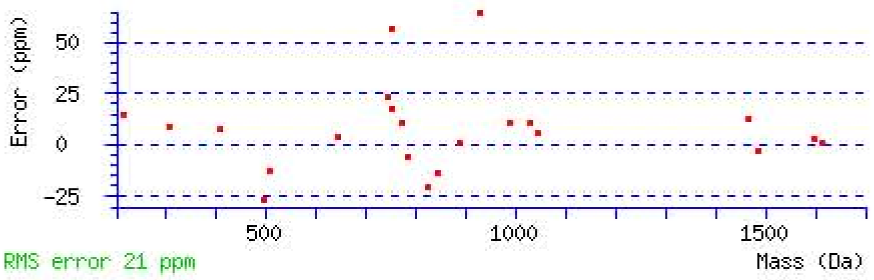
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1827.831787
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0059
Matches : 22/128 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	116.034219	58.520748			98.023654	49.515465	D							13
2	**215.102633**	108.054954			197.092068	99.049672	V	1713.812097	857.409687	1696.785548	848.896412	1695.801532	848.404404	12
3	346.143118	173.575197			328.132553	164.569915	M	***1614.743683***	807.875480	1597.717134	799.362205	1596.733118	798.870197	11
4	**785.368444**	393.187860	768.341895	384.674586	767.357879	384.182578	Q	***1483.703198***	742.355237	1466.676649	733.841963	1465.692633	733.349955	10
5	**842.389908**	421.698592	825.363359	413.185318	824.379343	412.693310	G	***1044.477872***	522.742574	1027.451323	514.229300	1026.467307	513.737292	9
6	943.437587	472.222432	926.411038	463.709157	925.427022	463.217149	T	***987.456408***	494.231842	970.429859	485.718568	969.445843	485.226560	8
7	1058.464530	529.735903	1041.437981	521.222629	1040.453965	520.730621	D	***886.408729***	443.708003	869.382180	435.194728	868.398164	434.702720	7
8	1187.507123	594.257200	1170.480574	585.743925	1169.496558	585.251917	E	***771.381786***	386.194531	754.355237	377.681257	753.371221	377.189249	6
9	1324.566035	662.786656	1307.539486	654.273381	1306.555470	653.781373	H	***642.339193***	321.673235	625.312644	313.159960			5
10	1423.634449	712.320863	1406.607900	703.807588	1405.623884	703.315580	V	***505.280281***	253.143779	488.253732	244.630504			4
11	1522.702863	761.855070	1505.676314	753.341795	1504.692298	752.849787	V	***406.211867***	203.609572	389.185318	195.096297			3
12	1682.733512	841.870394	1665.706963	833.357120	1664.722947	832.865112	C	***307.143453***	154.075365	290.116904	145.562090			2
13							K	147.112804	74.060040	130.086255	65.546765			1



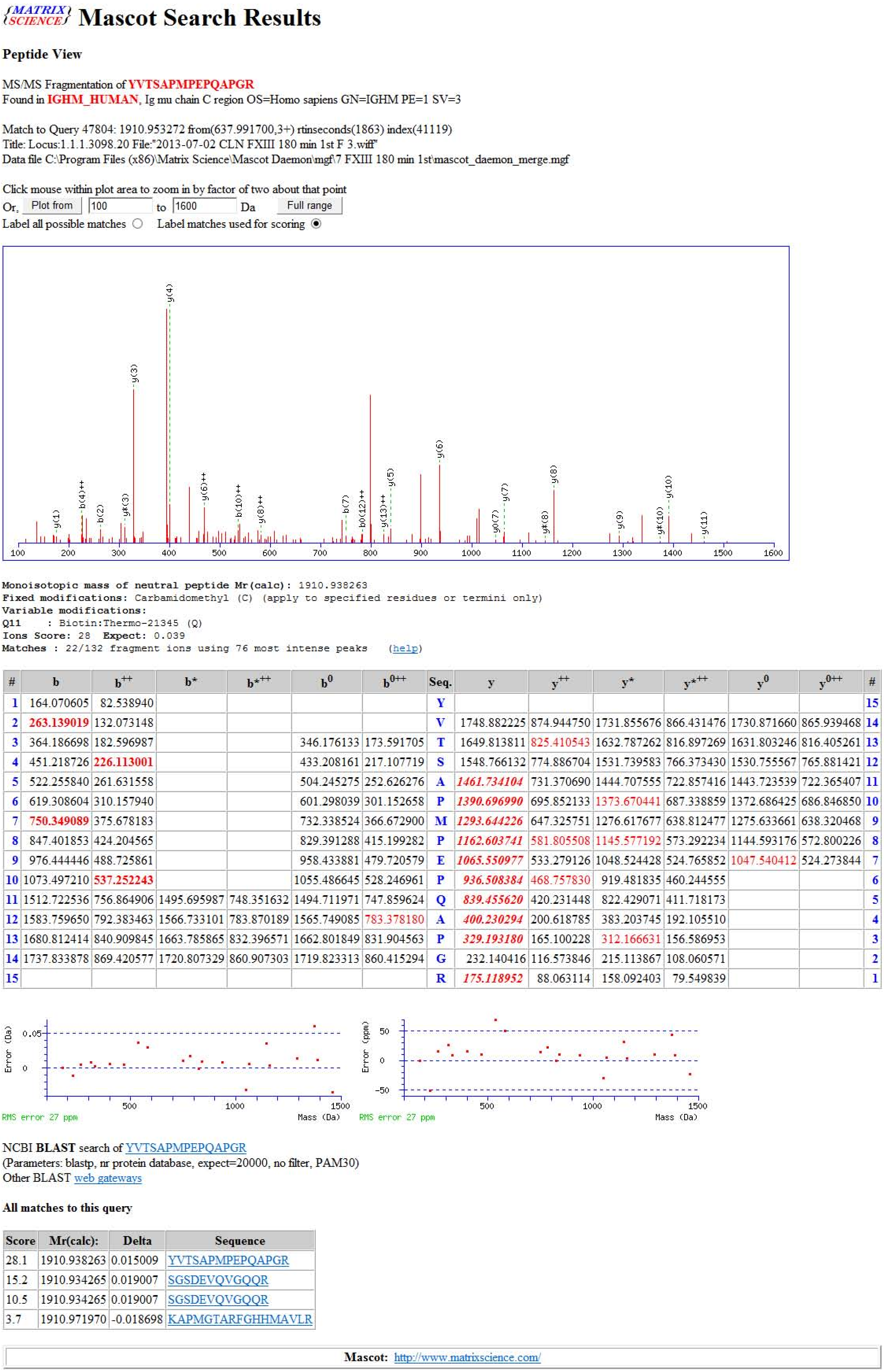


NCBI **BLAST** search of DVMQGTDEHVVCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.3	1827.831787	0.012515	DVMQGTDEHVVCK

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 47804: 1910.953272 from(637.991700,3+) rtinseconds(1863) index(41119)
Title: Locus:1.1.1.3098.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\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): 1910.938263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.039
Matches : 22/132 fragment ions using 76 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
28.1	1910.938263	0.015009	YVTSAPMPEPQAPGR
15.2	1910.934265	0.019007	SGSDEVQVGQQR
10.5	1910.934265	0.019007	SGSDEVQVGQQR
3.7	1910.971970	-0.018698	KAPMGTARFGHHMAVLR

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

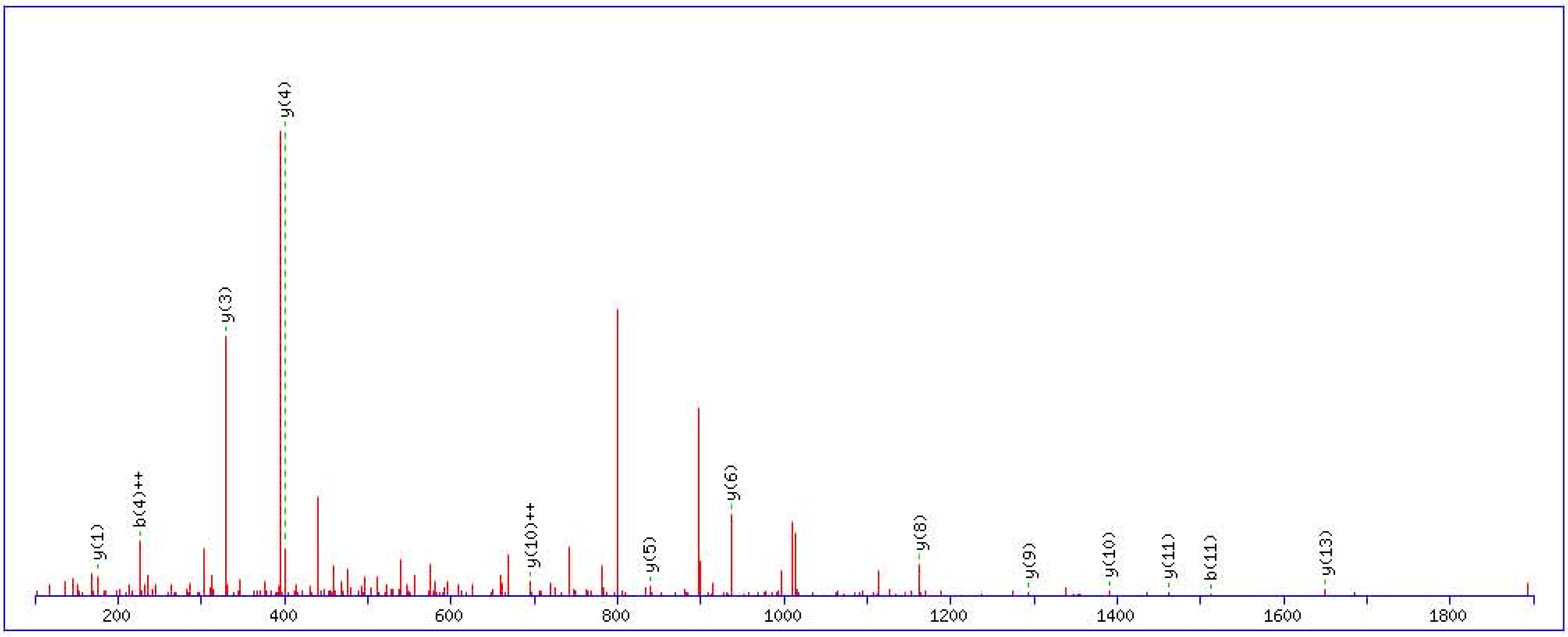
{MATRIX SCIENCE} Mascot Search Results

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

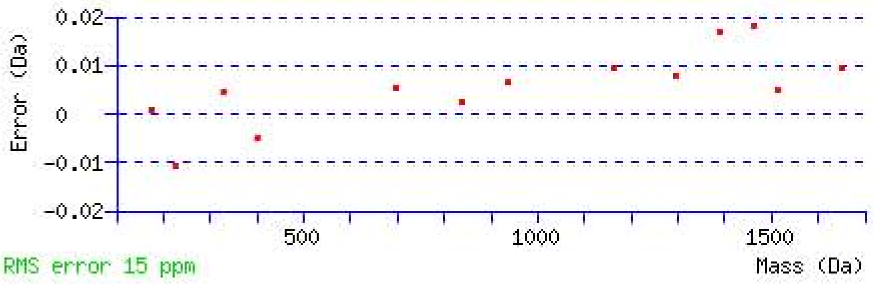
Match to Query 47805: 1910.953272 from(637.991700,3+) rtinseconds(1872) index(41194)
Title: Locus:1.1.1.3101.24 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

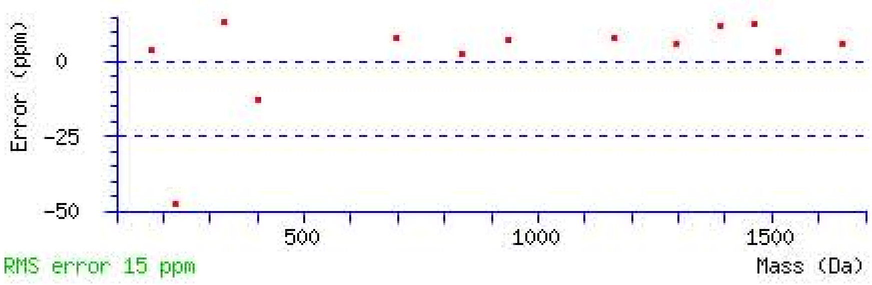
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1910.938263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.028
Matches : 13/132 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	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



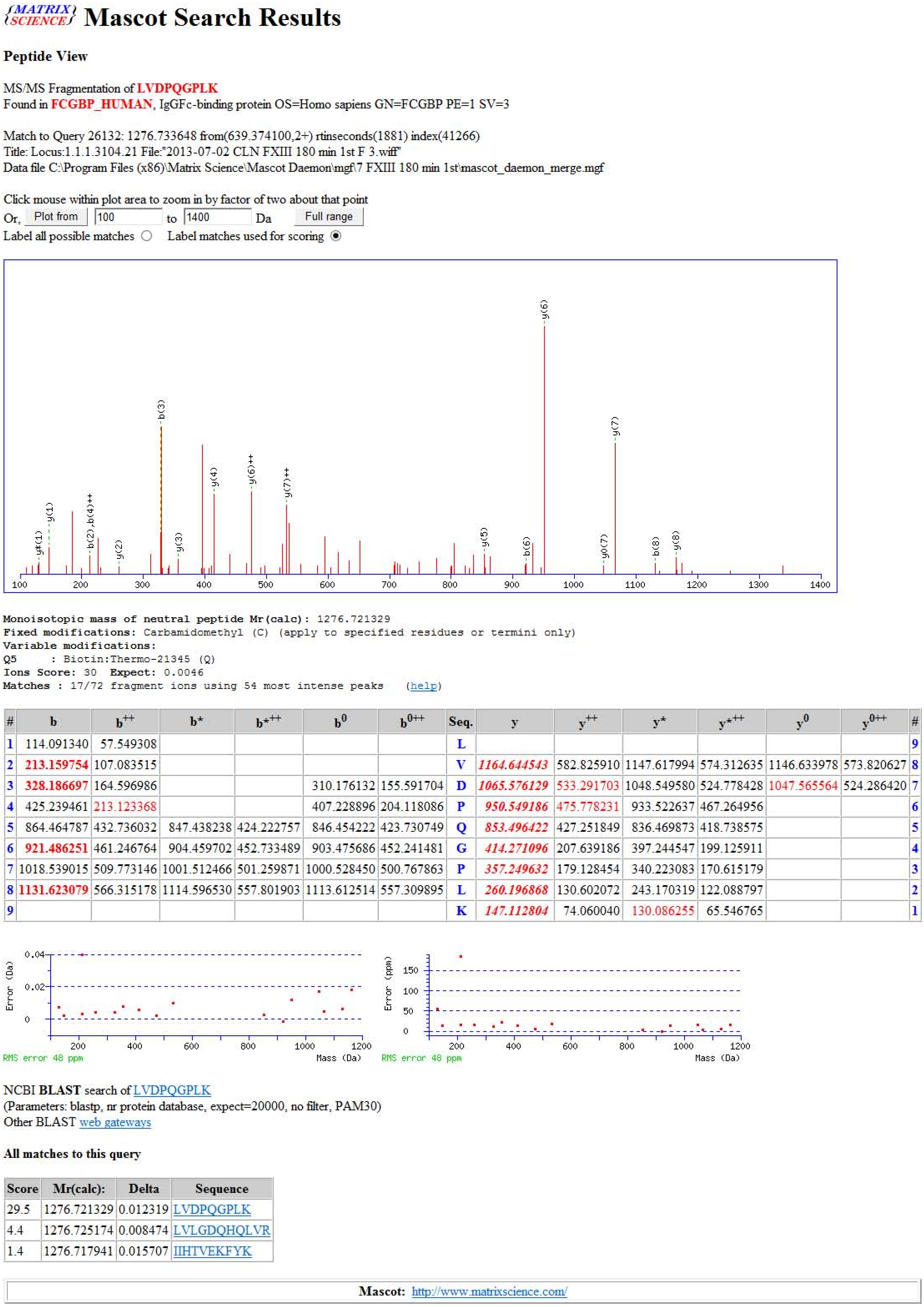


NCBI **BLAST** search of YVTSAPMPEPQAPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.5	1910.938263	0.015009	YVTSAPMPEPQAPGR
26.4	1910.934265	0.019007	SGSDEVQVGQQR
20.8	1910.934265	0.019007	SGSDEVQVGQQR

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



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVDPQGPLK**
Found in **FCGBP_HUMAN**, IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

Match to Query 26132: 1276.733648 from(639.374100,2+) rtinseconds(1881) index(41266)
Title: Locus:1.1.1.3104.21 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\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): 1276.721329
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.0046
Matches : 17/72 fragment ions using 54 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	**213.159754**	107.083515					V	***1164.644543***	582.825910	1147.617994	574.312635	1146.633978	573.820627	8
3	**328.186697**	164.596986			310.176132	155.591704	D	***1065.576129***	533.291703	1048.549580	524.778428	1047.565564	524.286420	7
4	425.239461	213.123368			407.228896	204.118086	P	***950.549186***	475.778231	933.522637	467.264956			6
5	864.464787	432.736032	847.438238	424.222757	846.454222	423.730749	Q	***853.496422***	427.251849	836.469873	418.738575			5
6	**921.486251**	461.246764	904.459702	452.733489	903.475686	452.241481	G	***414.271096***	207.639186	397.244547	199.125911			4
7	1018.539015	509.773146	1001.512466	501.259871	1000.528450	500.767863	P	***357.249632***	179.128454	340.223083	170.615179			3
8	**1131.623079**	566.315178	1114.596530	557.801903	1113.612514	557.309895	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 LVDPQGPLK
(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	1276.721329	0.012319	LVDPQGPLK
4.4	1276.725174	0.008474	LVLGDQHQLVR
1.4	1276.717941	0.015707	IIHTVEKFYK

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

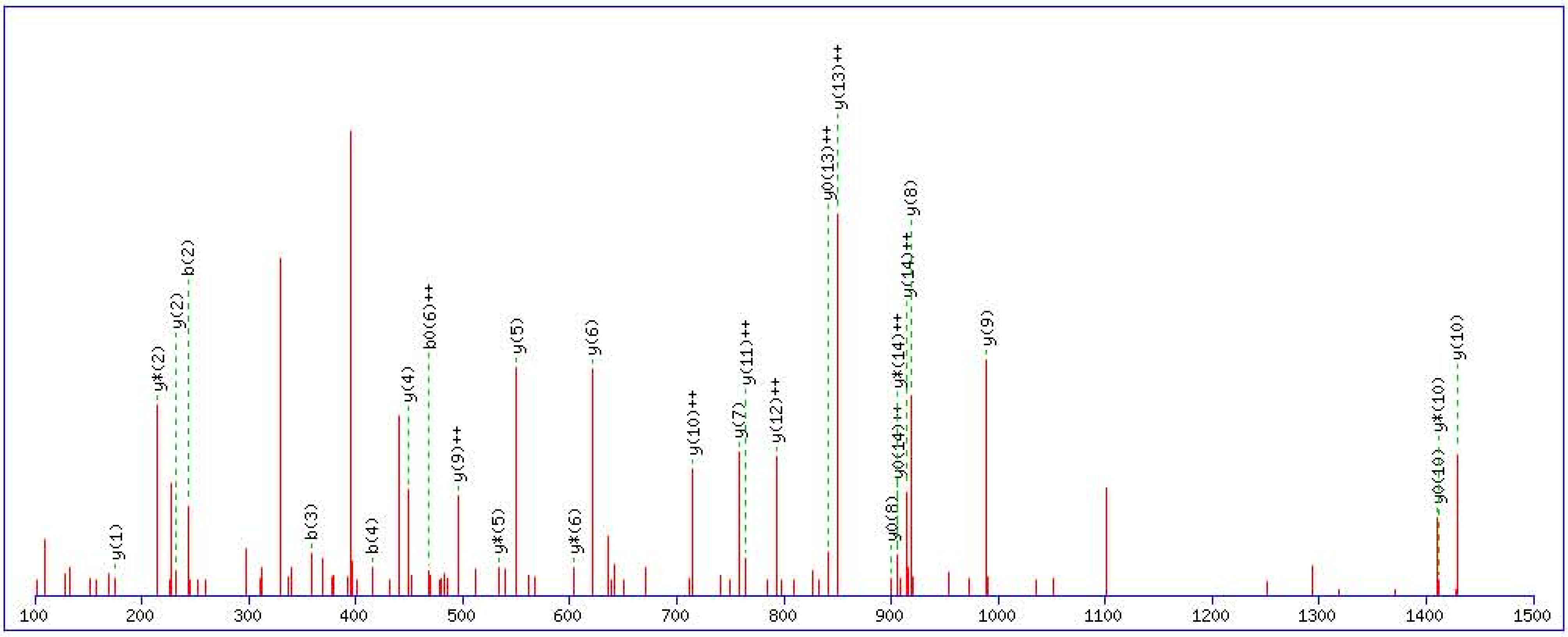
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEDGVQACHATGCGR**
Found in **FCGBP_HUMAN**, IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

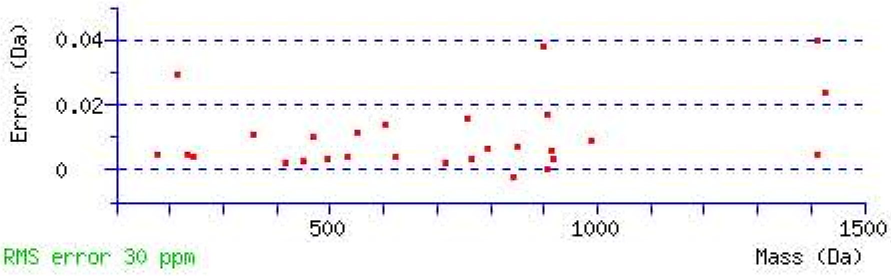
Match to Query 48492: 1940.884452 from(647.968760,3+) rtinseconds(1419) index(38119)
Title: Locus:1.1.1.2943.15 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

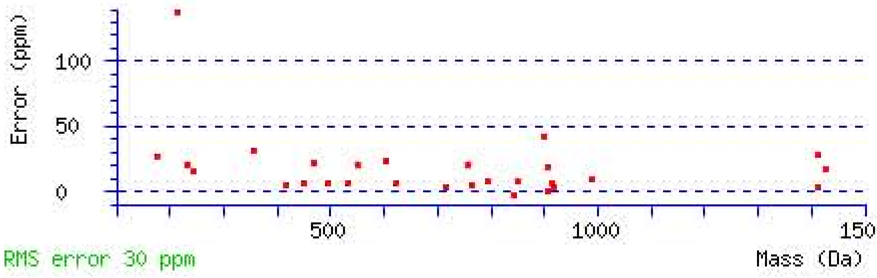
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1940.865540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 0.00011
Matches : 28/148 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	114.091340	57.549308					L							15
2	**243.133933**	122.070605			225.123368	113.065322	E	1828.788737	914.898006	1811.762188	906.384732	1810.778172	905.892724	14
3	**358.160876**	179.584076			340.150311	170.578794	D	1699.746144	850.376710	1682.719595	841.863435	1681.735579	841.371427	13
4	**415.182340**	208.094808			397.171775	199.089526	G	1584.719201	792.863238	1567.692652	784.349964	1566.708636	783.857956	12
5	514.250754	257.629015			496.240189	248.623733	V	1527.697737	764.352506	1510.671188	755.839232	1509.687172	755.347224	11
6	953.476080	477.241678	936.449531	468.728404	935.465515	468.236396	Q	***1428.629323***	714.818299	1411.602774	706.305025	1410.618758	705.813017	10
7	1024.513194	512.760235	1007.486645	504.246960	1006.502629	503.754952	A	***989.403997***	495.205636	972.377448	486.692362	971.393432	486.200354	9
8	1184.543843	592.775559	1167.517294	584.262285	1166.533278	583.770277	C	***918.366883***	459.687079	901.340334	451.173805	900.356318	450.681797	8
9	1321.602755	661.305015	1304.576206	652.791741	1303.592190	652.299733	H	***758.336234***	379.671755	741.309685	371.158480	740.325669	370.666472	7
10	1392.639869	696.823572	1375.613320	688.310298	1374.629304	687.818290	A	***621.277322***	311.142299	604.250773	302.629024	603.266757	302.137016	6
11	1493.687548	747.347412	1476.660999	738.834138	1475.676983	738.342129	T	***550.240208***	275.623742	533.213659	267.110467	532.229643	266.618459	5
12	1550.709012	775.858144	1533.682463	767.344869	1532.698447	766.852861	G	***449.192529***	225.099902	432.165980	216.586628			4
13	1710.739661	855.873468	1693.713112	847.360194	1692.729096	846.868186	C	392.171065	196.589170	375.144516	188.075896			3
14	1767.761125	884.384200	1750.734576	875.870926	1749.750560	875.378918	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 LEDGVQACHATGCGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.1	1940.865540	0.018912	LEDGVQACHATGCGR

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

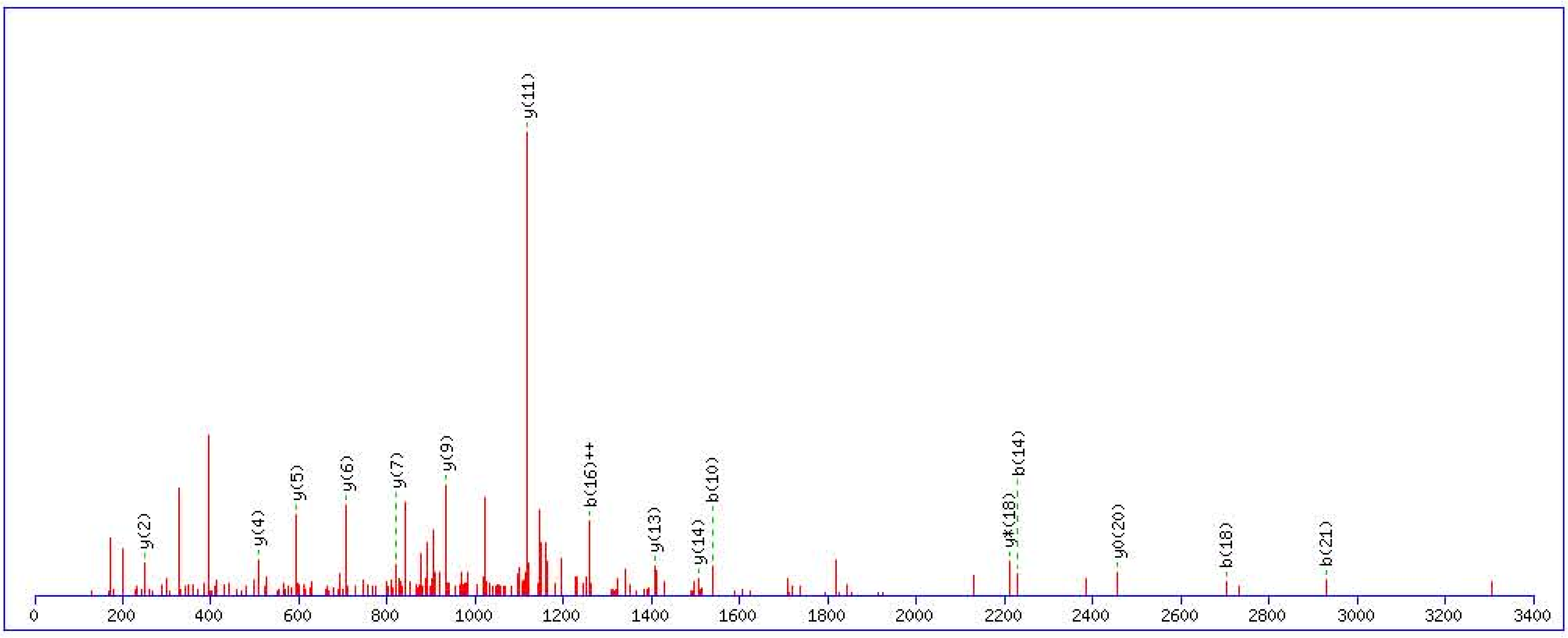
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVVCQEHSCKPGQVCQPSGGILSCVTK**
Found in **FCGBP_HUMAN**, IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

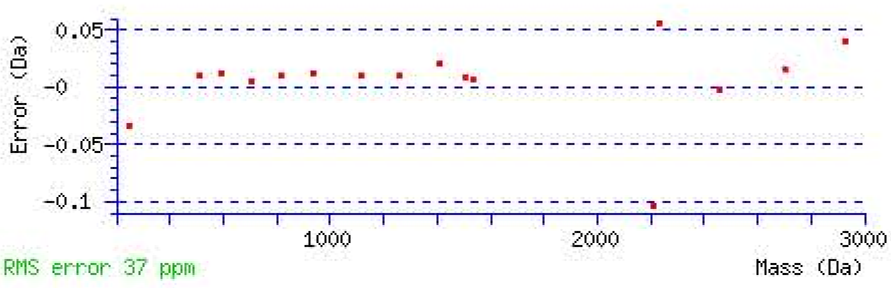
Match to Query 78887: 3635.810816 from(909.959980,4+) rtinseconds(1977) index(42094)
Title: Locus:1.1.1.3137.24 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

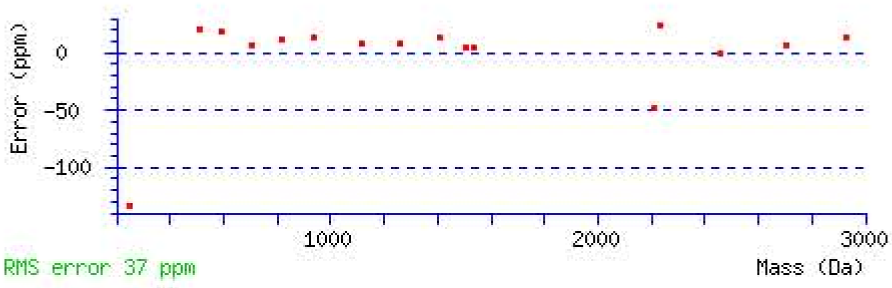
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3635.757751
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.0013
Matches : 16/292 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	100.075690	50.541483					V							27
2	199.144104	100.075690					V	3537.696565	1769.351920	3520.670016	1760.838646	3519.686000	1760.346638	26
3	298.212518	149.609897					V	3438.628151	1719.817713	3421.601602	1711.304439	3420.617586	1710.812431	25
4	458.243167	229.625222					C	3339.559737	1670.283506	3322.533188	1661.770232	3321.549172	1661.278224	24
5	897.468493	449.237885	880.441944	440.724610			Q	3179.529088	1590.268182	3162.502539	1581.754907	3161.518523	1581.262899	23
6	1026.511086	513.759181	1009.484537	505.245907	1008.500521	504.753899	E	2740.303762	1370.655519	2723.277213	1362.142244	2722.293197	1361.650236	22
7	1163.569998	582.288637	1146.543449	573.775363	1145.559433	573.283355	H	2611.261169	1306.134222	2594.234620	1297.620948	2593.250604	1297.128940	21
8	1250.602026	625.804651	1233.575477	617.291377	1232.591461	616.799369	S	2474.202257	1237.604766	2457.175708	1229.091492	2456.191692	1228.599484	20
9	1410.632675	705.819976	1393.606126	697.306701	1392.622110	696.814693	C	2387.170229	1194.088752	2370.143680	1185.575478	2369.159664	1185.083470	19
10	**1538.727638**	769.867457	1521.701089	761.354183	1520.717073	760.862175	K	2227.139580	1114.073428	2210.113031	1105.560153	2209.129015	1105.068145	18
11	1635.780402	818.393839	1618.753853	809.880565	1617.769837	809.388557	P	2099.044617	1050.025946	2082.018068	1041.512672	2081.034052	1041.020664	17
12	1692.801866	846.904571	1675.775317	838.391297	1674.791301	837.899289	G	2001.991853	1001.499564	1984.965304	992.986290	1983.981288	992.494282	16
13	2132.027192	1066.517234	2115.000643	1058.003959	2114.016627	1057.511951	Q	1944.970389	972.988832	1927.943840	964.475558	1926.959824	963.983550	15
14	**2231.095606**	1116.051441	2214.069057	1107.538166	2213.085041	1107.046158	V	***1505.745063***	753.376169	1488.718514	744.862895	1487.734498	744.370887	14
15	2391.126255	1196.066765	2374.099706	1187.553491	2373.115690	1187.061483	C	***1406.676649***	703.841962	1389.650100	695.328688	1388.666084	694.836680	13
16	2519.184833	1260.096054	2502.158284	1251.582780	2501.174268	1251.090772	Q	1246.646000	623.826638	1229.619451	615.313364	1228.635435	614.821355	12
17	2616.237597	1308.622436	2599.211048	1300.109162	2598.227032	1299.617154	P	***1118.587422***	559.797349	1101.560873	551.284074	1100.576857	550.792066	11
18	**2703.269625**	1352.138450	2686.243076	1343.625176	2685.259060	1343.133168	S	1021.534658	511.270967	1004.508109	502.757692	1003.524093	502.265684	10
19	2760.291089	1380.649182	2743.264540	1372.135908	2742.280524	1371.643900	G	***934.502630***	467.754953	917.476081	459.241678	916.492065	458.749670	9
20	2817.312553	1409.159914	2800.286004	1400.646640	2799.301988	1400.154632	G	877.481166	439.244221	860.454617	430.730946	859.470601	430.238938	8
21	**2930.396617**	1465.701946	2913.370068	1457.188672	2912.386052	1456.696664	I	***820.459702***	410.733489	803.433153	402.220214	802.449137	401.728206	7
22	3043.480681	1522.243978	3026.454132	1513.730704	3025.470116	1513.238696	L	***707.375638***	354.191457	690.349089	345.678182	689.365073	345.186174	6
23	3130.512709	1565.759993	3113.486160	1557.246718	3112.502144	1556.754710	S	***594.291574***	297.649425	577.265025	289.136150	576.281009	288.644142	5
24	3290.543358	1645.775317	3273.516809	1637.262042	3272.532793	1636.770034	C	***507.259546***	254.133411	490.232997	245.620136	489.248981	245.128128	4
25	3389.611772	1695.309524	3372.585223	1686.796249	3371.601207	1686.304241	V	347.228897	174.118086	330.202348	165.604812	329.218332	165.112804	3
26	3490.659451	1745.833363	3473.632902	1737.320089	3472.648886	1736.828081	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
27							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.9	3635.757751	0.053065	VVVCQEHSCKPGQVCQPSGGILSCVTK
23.3	3635.757751	0.053065	VVVCQEHSCKPGQVCQPSGGILSCVTK
19.5	3635.757751	0.053065	VVVCQEHSCKPGQVCQPSGGILSCVTK

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

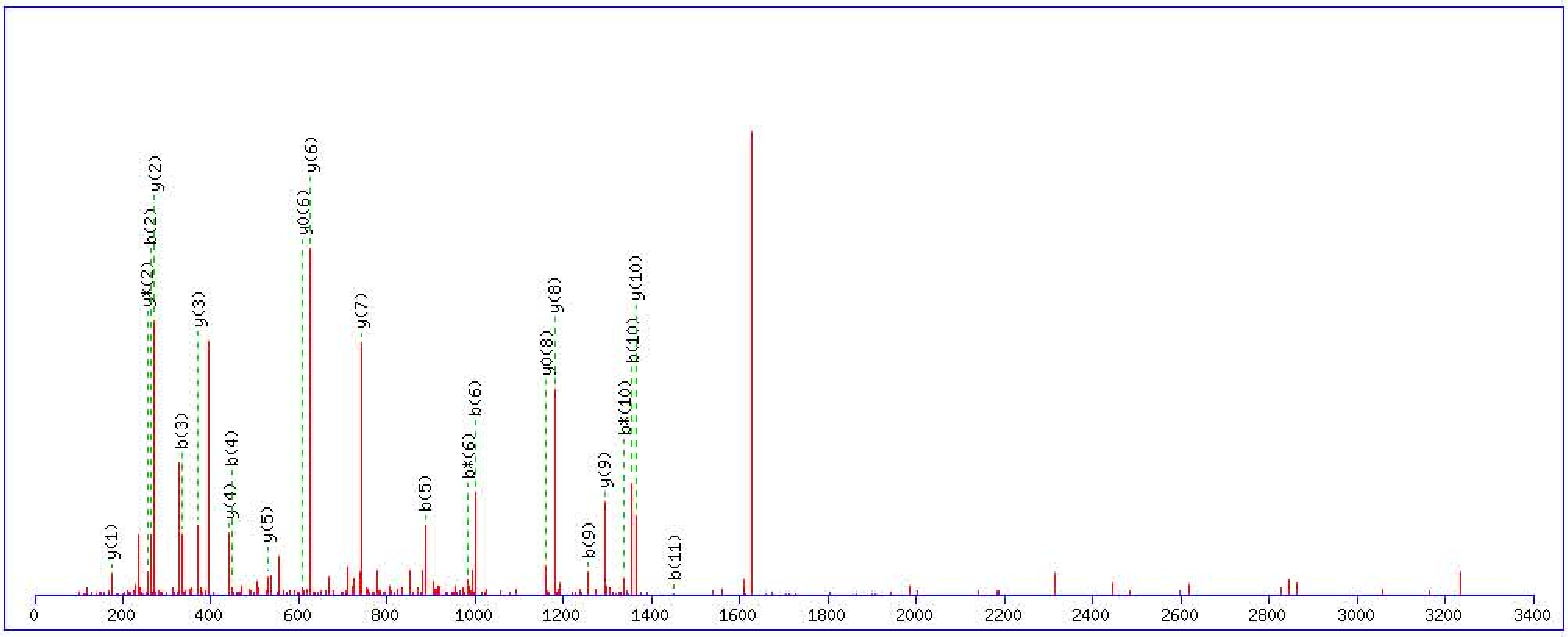
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFALQNPSAVPR**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

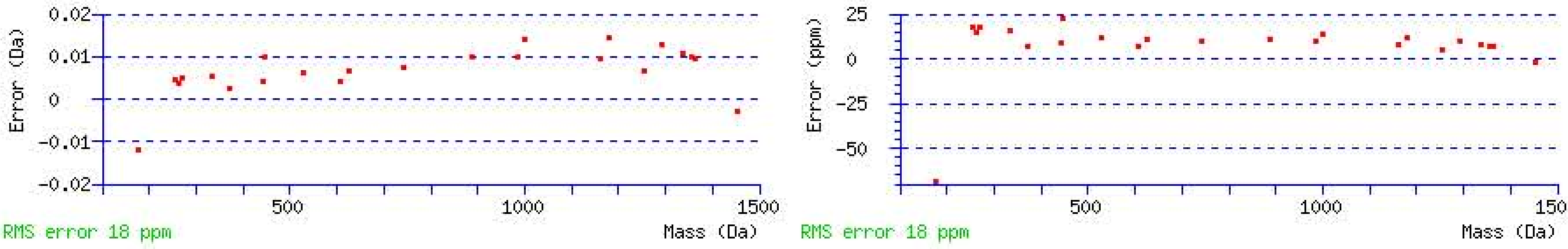
Match to Query 39930: 1624.860348 from(813.437450,2+) rtinseconds(2155) index(43290)
Title: Locus:1.1.1.3199.22 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1624.839539
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00035
Matches : 23/116 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	116.034219	58.520748			98.023654	49.515465	D							12
2	**263.102633**	132.054954			245.092068	123.049672	F	1510.819881	755.913579	1493.793332	747.400304	1492.809316	746.908296	11
3	**334.139747**	167.573512			316.129182	158.568229	A	***1363.751467***	682.379372	1346.724918	673.866097	1345.740902	673.374089	10
4	**447.223811**	224.115544			429.213246	215.110261	L	***1292.714353***	646.860815	1275.687804	638.347540	1274.703788	637.855532	9
5	**886.449137**	443.728207	869.422588	435.214932	868.438572	434.722924	Q	***1179.630289***	590.318783	1162.603740	581.805508	1161.619724	581.313500	8
6	**1000.492064**	500.749670	983.465515	492.236396	982.481499	491.744388	N	***740.404963***	370.706120	723.378414	362.192845	722.394398	361.700837	7
7	1097.544828	549.276052	1080.518279	540.762778	1079.534263	540.270770	P	***626.362036***	313.684656	609.335487	305.171382	608.351471	304.679374	6
8	1184.576856	592.792066	1167.550307	584.278792	1166.566291	583.786784	S	***529.309272***	265.158274	512.282723	256.645000	511.298707	256.152992	5
9	**1255.613970**	628.310623	1238.587421	619.797349	1237.603405	619.305341	A	***442.277244***	221.642260	425.250695	213.128986			4
10	**1354.682384**	677.844830	1337.655835	669.331556	1336.671819	668.839548	V	***371.240130***	186.123703	354.213581	177.610429			3
11	**1451.735148**	726.371212	1434.708599	717.857938	1433.724583	717.365930	P	***272.171716***	136.589496	255.145167	128.076221			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of DFALQNPSAVPR
(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	1624.839539	0.020809	DFALQNPSAVPR
19.5	1624.860672	-0.000324	VGDCVIIENPLIQR
14.9	1624.853271	0.007077	ASDPVRTGSEGLALPR
8.6	1624.864471	-0.004123	RELRSQETPEKPR
8.6	1624.871887	-0.011539	RTSSEQAVALPR
6.6	1624.875916	-0.015568	QWLEATIQLGR
2.0	1624.850784	0.009564	FCSFLQTSKVRPR
1.9	1624.879745	-0.019397	YLAIVHATNSQRPR
1.3	1624.854813	0.005535	QWVAAGGHITFK
0.5	1624.850769	0.009579	QPTWSRSSLPR

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

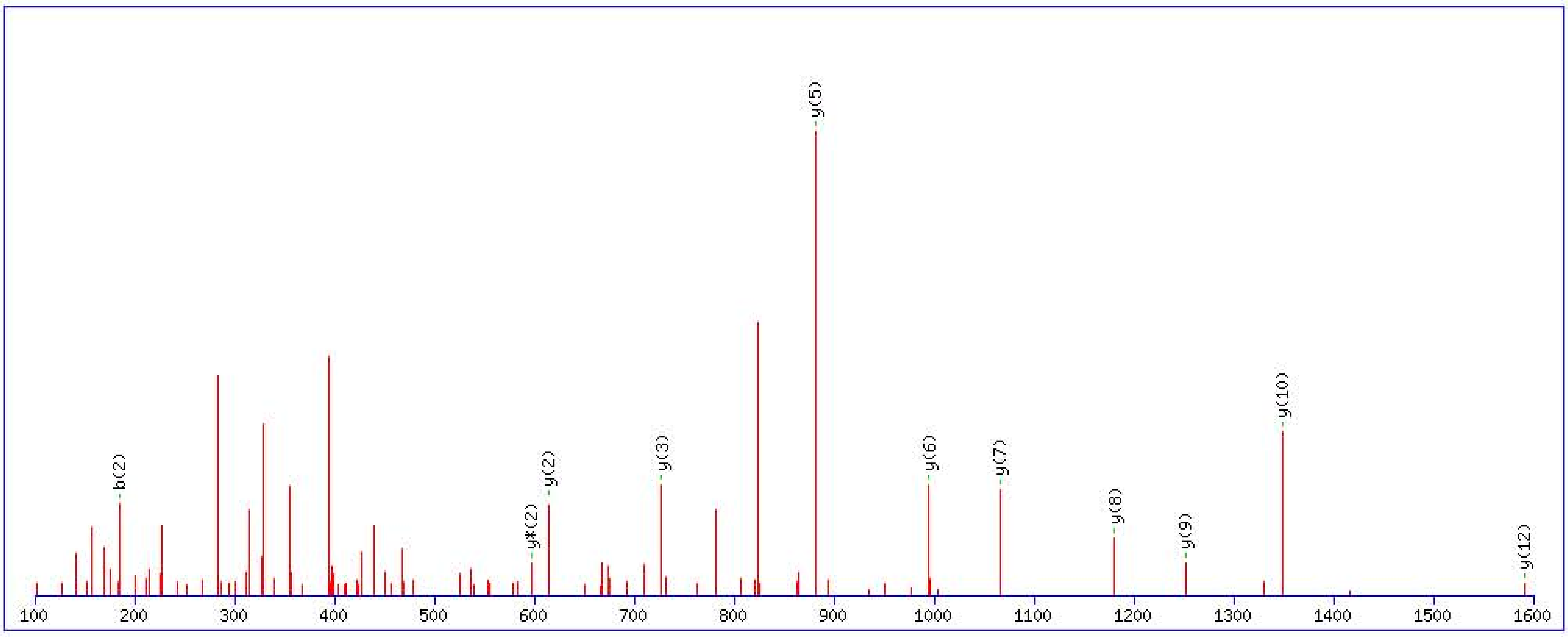
Mascot Search Results

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

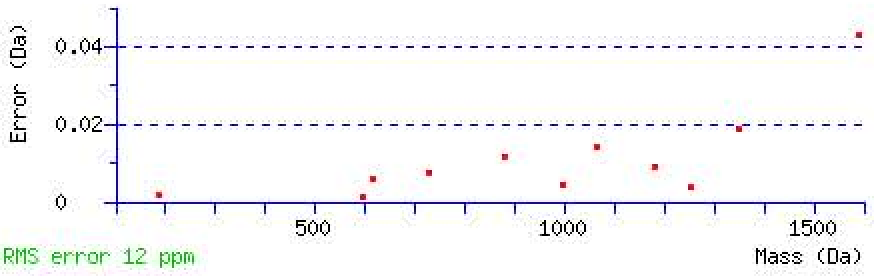
Match to Query 44651: 1774.000512 from(592.340780,3+) rtinseconds(2430) index(27610)
Title: Locus:1.1.1.2988.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

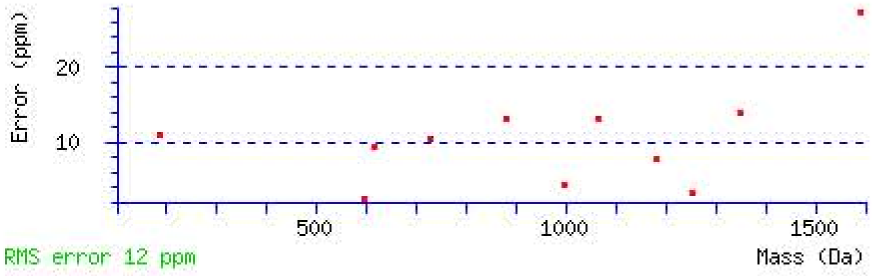
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1773.981094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 69 **Expect:** 1.3e-006
Matches : 11/114 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	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
69.2	1773.981094	0.019418	LAELPADALGPLQR
7.8	1774.014099	-0.013587	LLLQEALWPEGKLHK

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

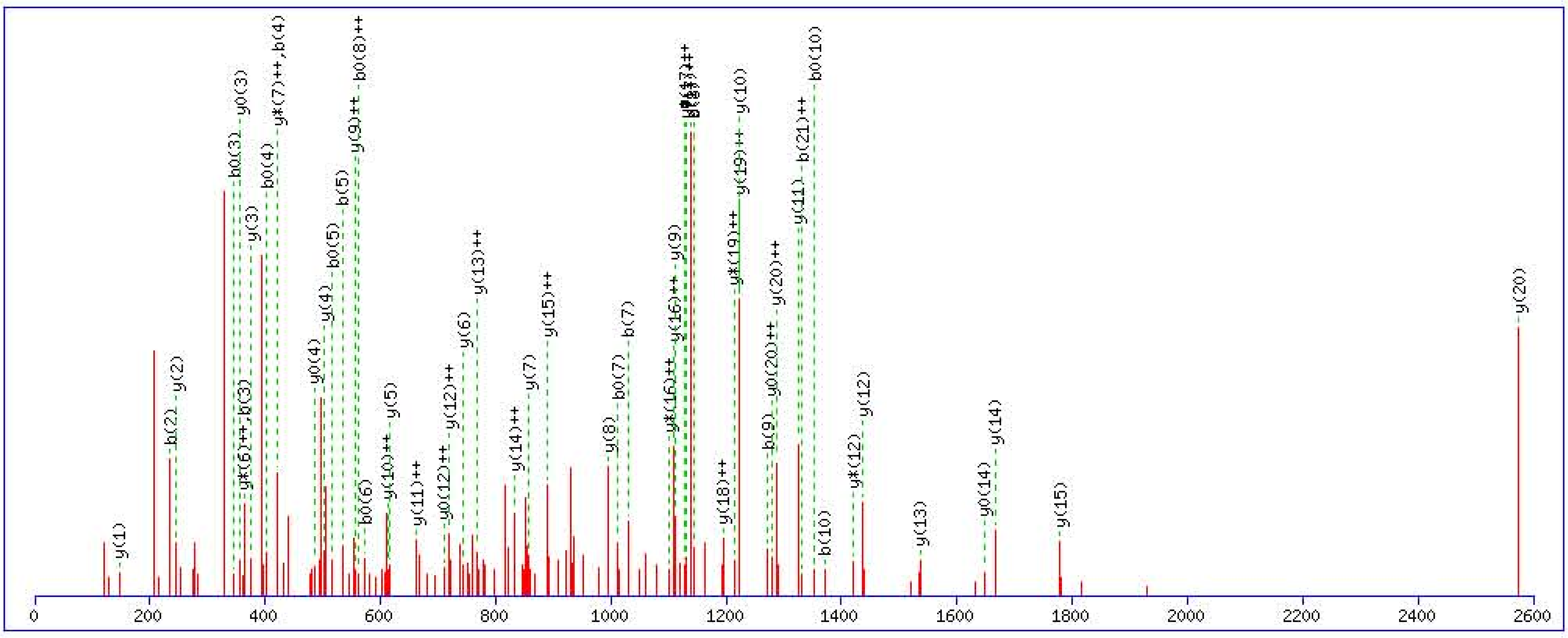
Mascot Search Results

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

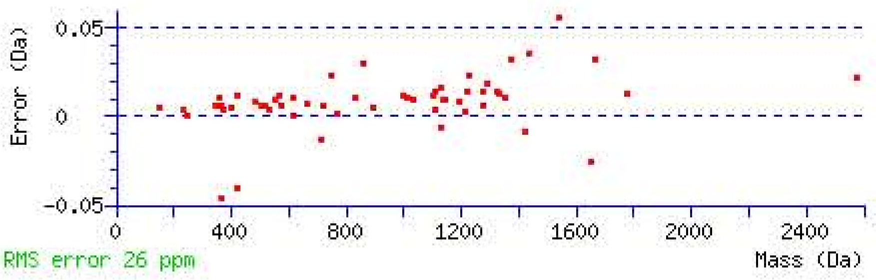
Match to Query 67246: 2807.491692 from(936.837840,3+) rtinseconds(2686) index(29281)
Title: Locus:1.1.1.3076.22 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

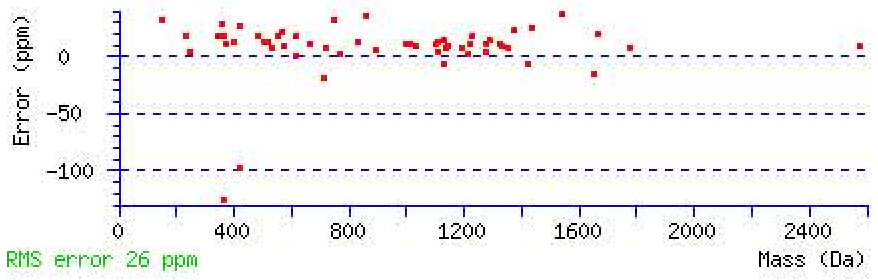
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 70 **Expect:** 1.8e-006
Matches : 56/236 fragment ions using 124 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
70.4	2807.452759	0.038933	SFEGLGQLEVLTLDHNQLQEVK
9.3	2807.452759	0.038933	SFEGLGQLEVLTLDHNQLQEVK
5.2	2807.452759	0.038933	SFEGLGQLEVLTLDHNQLQEVK

Mascot: http://www.matrixscience.com/

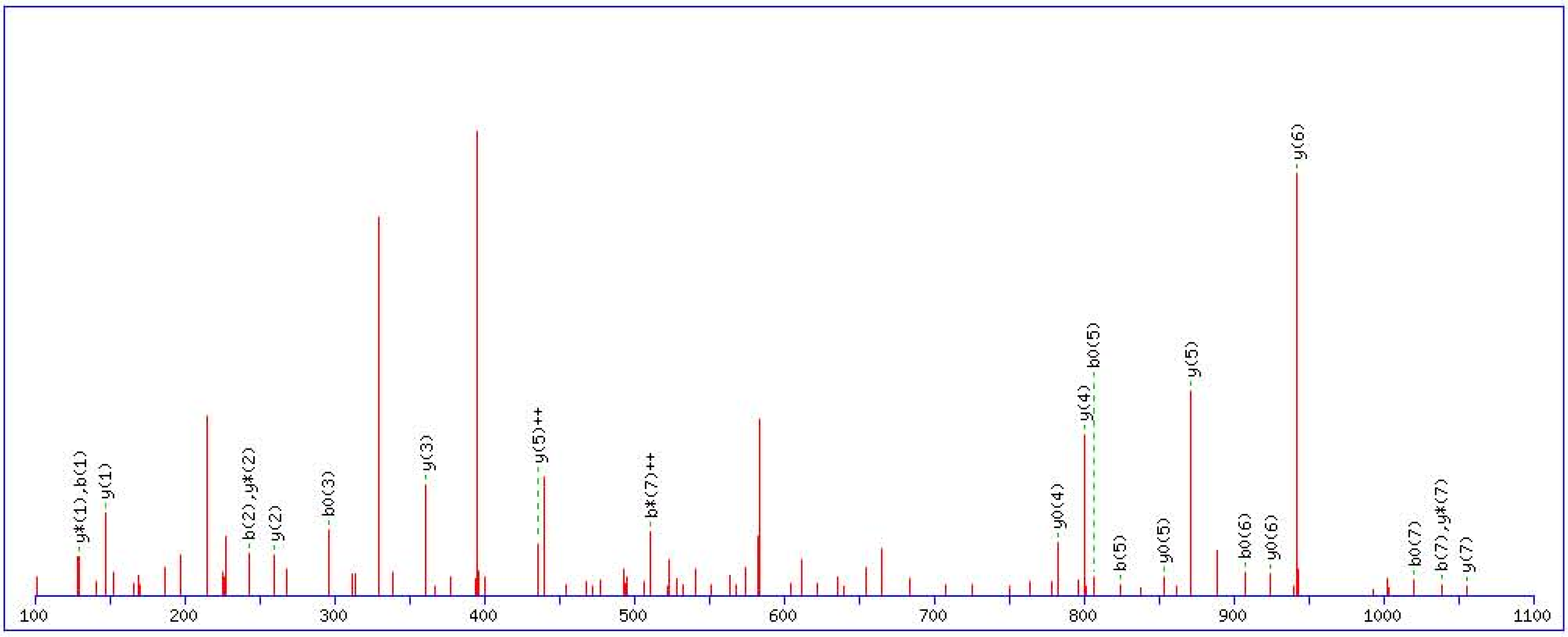
{MATRIX SCIENCE} Mascot Search Results

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

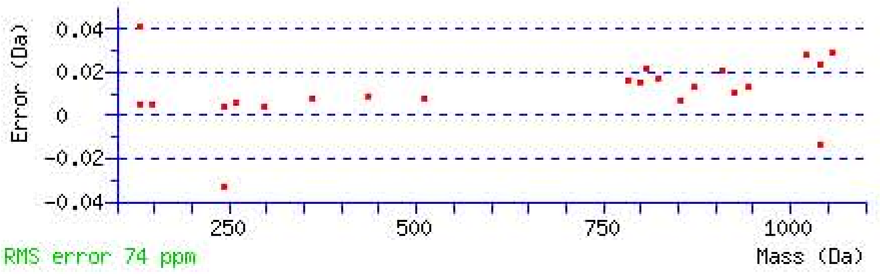
Match to Query 23223: 1183.678548 from(592.846550,2+) rtinseconds(1733) index(58861)
Title: Locus:1.1.1.3027.7 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

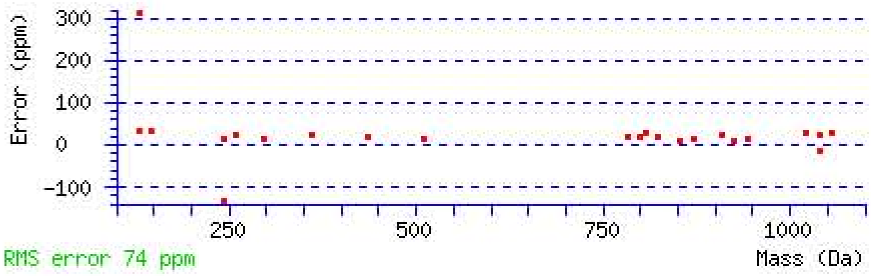
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1183.663452
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.014
Matches : 23/72 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	**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
31.2	1183.663452	0.015096	ELAAQTIK
25.1	1183.663452	0.015096	ELAAQITK
8.8	1183.692429	-0.013881	LEARLNVLEK
8.5	1183.681198	-0.002650	LEALLEAAGIGK
7.3	1183.667282	0.011266	GKQASEPALRK
6.5	1183.663467	0.015081	TQLSPSIK
6.3	1183.667297	0.011251	EPTGRVEIRK
6.2	1183.663452	0.015096	LEQAATLK
5.7	1183.674698	0.003850	TQVRELK
5.3	1183.692459	-0.013911	TLLGLQGLNQK

Mascot: http://www.matrixscience.com/

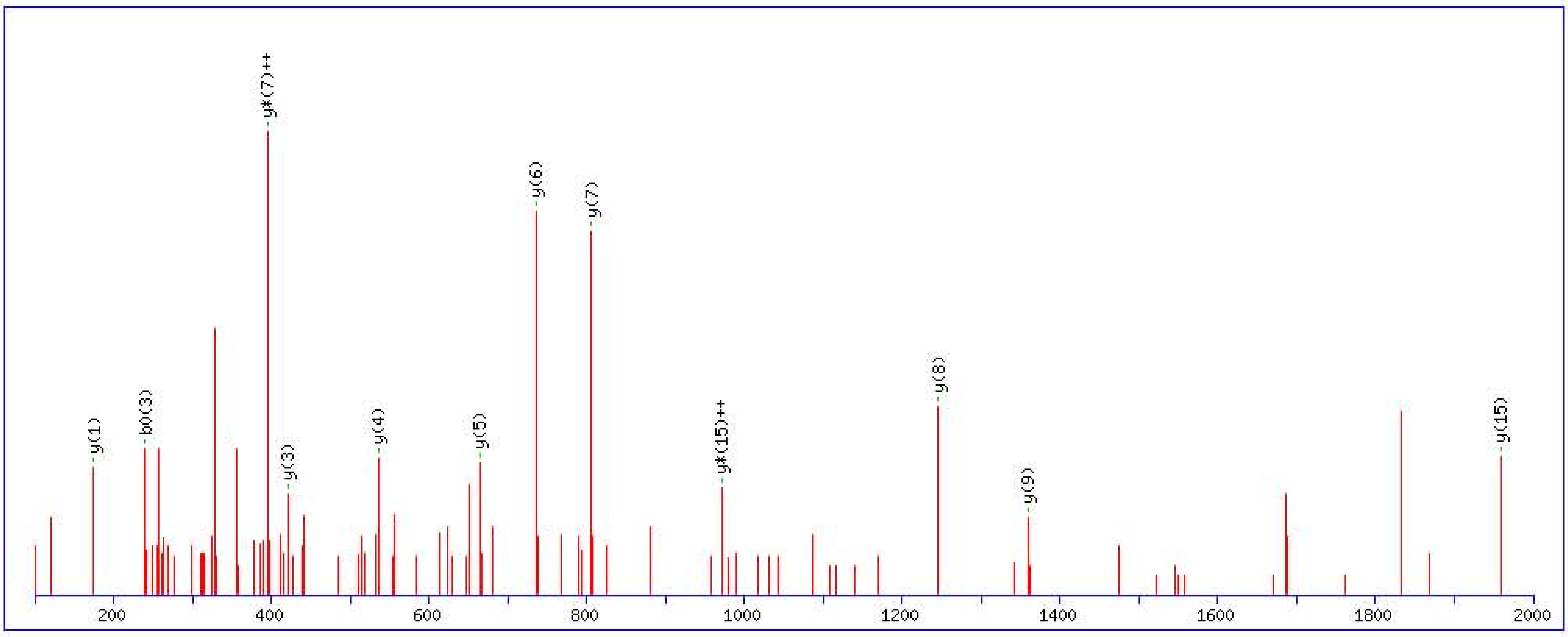
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

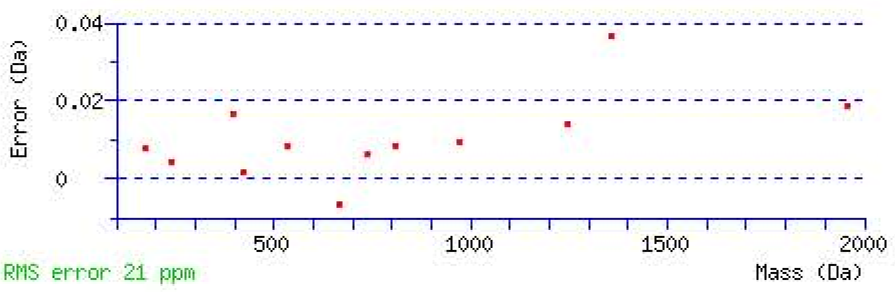
Match to Query 58356: 2314.197312 from(772.406380,3+) rtinseconds(2513) index(82263)
Title: Locus:1.1.1.2225.21 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

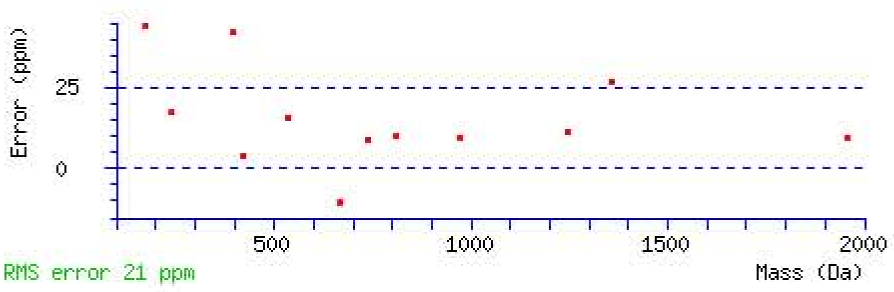
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2314.173950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 7.3e-005
Matches : 12/200 fragment ions using 19 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							19
2	145.060768	73.034022			127.050203	64.028740	S	2258.159779	1129.583527	2241.133230	1121.070253	2240.149214	1120.578245	18
3	258.144832	129.576054			240.134267	120.570772	L	2171.127751	1086.067513	2154.101202	1077.554239	2153.117186	1077.062231	17
4	357.213246	179.110261			339.202681	170.104979	V	2058.043687	1029.525481	2041.017138	1021.012207	2040.033122	1020.520199	16
5	485.271824	243.139550	468.245275	234.626276	467.261259	234.134268	Q	***1958.975273***	979.991275	1941.948724	971.478000	1940.964708	970.985992	15
6	556.308938	278.658107	539.282389	270.144833	538.298373	269.652825	A	1830.916695	915.961986	1813.890146	907.448711	1812.906130	906.956703	14
7	643.340966	322.174121	626.314417	313.660847	625.330401	313.168839	S	1759.879581	880.443429	1742.853032	871.930154	1741.869016	871.438146	13
8	772.383559	386.695418	755.357010	378.182143	754.372994	377.690135	E	1672.847553	836.927415	1655.821004	828.414140	1654.836988	827.922132	12
9	843.420673	422.213975	826.394124	413.700700	825.410108	413.208692	A	1543.804960	772.406118	1526.778411	763.892844	1525.794395	763.400836	11
10	957.463600	479.235438	940.437051	470.722164	939.453035	470.230156	N	1472.767846	736.887561	1455.741297	728.374287	1454.757281	727.882279	10
11	1070.547664	535.777470	1053.521115	527.264196	1052.537099	526.772187	L	***1358.724919***	679.866098	1341.698370	671.352823	1340.714354	670.860815	9
12	1509.772990	755.390133	1492.746441	746.876859	1491.762425	746.384851	Q	***1245.640855***	623.324066	1228.614306	614.810791	1227.630290	614.318783	8
13	1580.810104	790.908690	1563.783555	782.395416	1562.799539	781.903408	A	***806.415529***	403.711403	789.388980	395.198128	788.404964	394.706120	7
14	1651.847218	826.427247	1634.820669	817.913973	1633.836653	817.421965	A	***735.378415***	368.192846	718.351866	359.679571	717.367850	359.187563	6
15	1779.905796	890.456536	1762.879247	881.943262	1761.895231	881.451254	Q	***664.341301***	332.674289	647.314752	324.161014	646.330736	323.669006	5
16	1894.932739	947.970008	1877.906190	939.456733	1876.922174	938.964725	D	***536.282723***	268.645000	519.256174	260.131725	518.272158	259.639717	4
17	2042.001153	1021.504215	2024.974604	1012.990940	2023.990588	1012.498932	F	***421.255780***	211.131528	404.229231	202.618253			3
18	2141.069567	1071.038421	2124.043018	1062.525147	2123.059002	1062.033139	V	274.187366	137.597321	257.160817	129.084046			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GSLVQASEANLQAAQDFVR
(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	2314.173950	0.023362	GSLVQASEANLQAAQDFVR
32.4	2314.173950	0.023362	GSLVQASEANLQAAQDFVR
18.0	2314.173950	0.023362	GSLVQASEANLQAAQDFVR

Mascot: http://www.matrixscience.com/

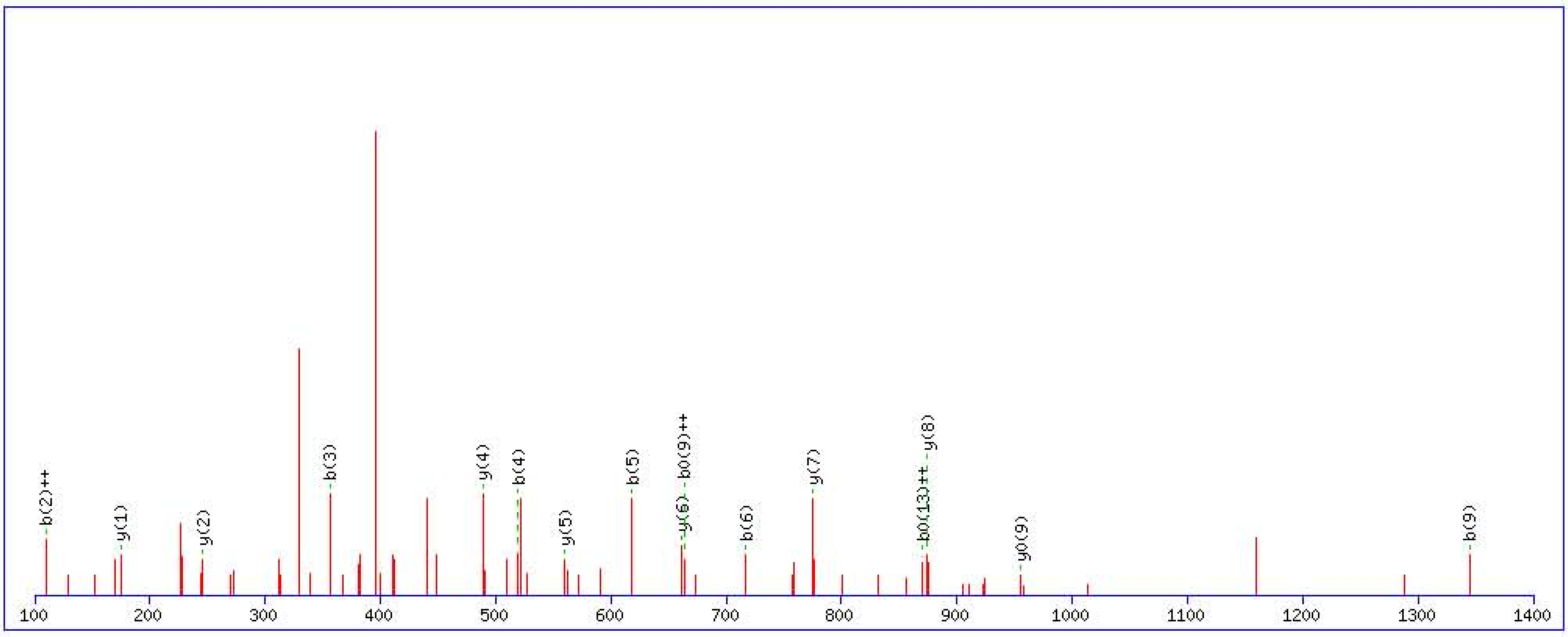
{MATRIX SCIENCE} Mascot Search Results

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

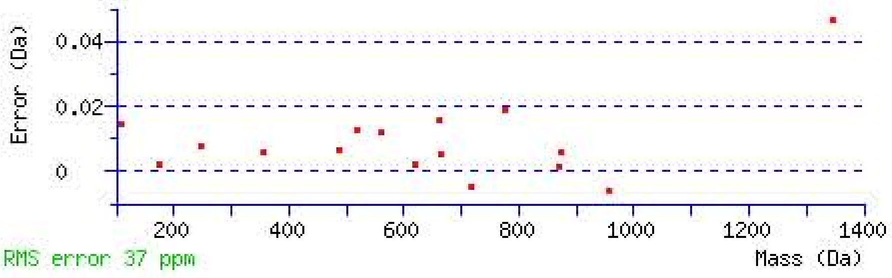
Match to Query 58409: 2316.194616 from(580.055930,4+) rtinseconds(1927) index(60233)
Title: Locus:1.1.1.3094.9 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

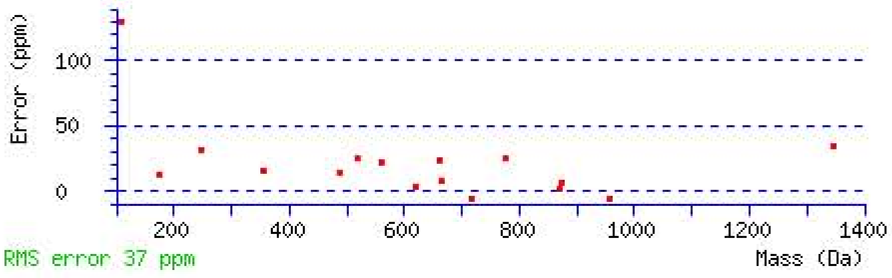
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2316.168488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.00065
Matches : 16/172 fragment ions using 31 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
39.4	2316.168488	0.026128	FAHYVVTSQVVNTANEAR
5.4	2316.201050	-0.006434	ILGKINQFFVAVFTGECVMK

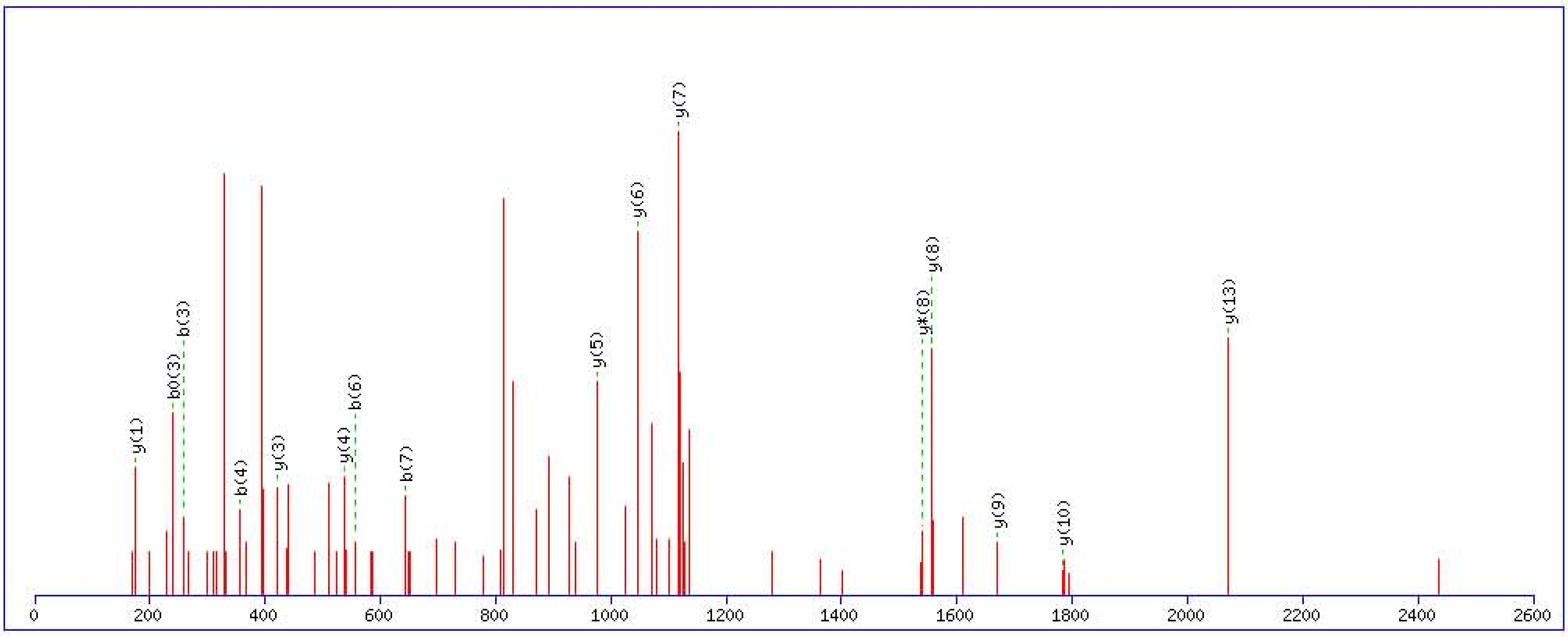
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

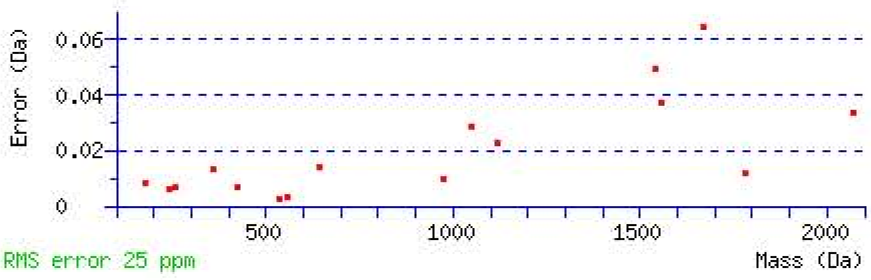
Match to Query 64811: 2625.308022 from(876.109950,3+) rtinseconds(2710) index(65470)
Title: Locus:1.1.1.3365.22 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

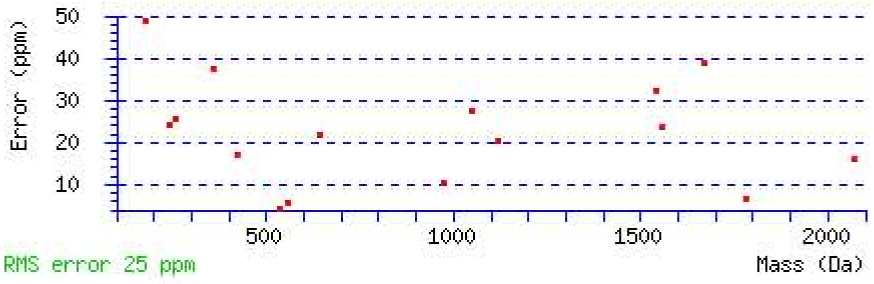


Monoisotopic mass of neutral peptide Mr(calc): 2625.340698
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.0063
Matches : 16/200 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							19
2	145.060768	73.034022			127.050203	64.028740	S	2569.326527	1285.166901	2552.299978	1276.653627	2551.315962	1276.161619	18
3	**258.144832**	129.576054			240.134267	120.570772	L	2482.294499	1241.650887	2465.267950	1233.137613	2464.283934	1232.645605	17
4	**357.213246**	179.110261			339.202681	170.104979	V	2369.210435	1185.108855	2352.183886	1176.595581	2351.199870	1176.103573	16
5	485.271824	243.139550	468.245275	234.626276	467.261259	234.134268	Q	2270.142021	1135.574648	2253.115472	1127.061374	2252.131456	1126.569366	15
6	**556.308938**	278.658107	539.282389	270.144833	538.298373	269.652825	A	2142.083443	1071.545359	2125.056894	1063.032085	2124.072878	1062.540077	14
7	**643.340966**	322.174121	626.314417	313.660847	625.330401	313.168839	S	***2071.046329***	1036.026802	2054.019780	1027.513528	2053.035764	1027.021520	13
8	772.383559	386.695418	755.357010	378.182143	754.372994	377.690135	E	1984.014301	992.510788	1966.987752	983.997514	1966.003736	983.505506	12
9	843.420673	422.213975	826.394124	413.700700	825.410108	413.208692	A	1854.971708	927.989492	1837.945159	919.476217	1836.961143	918.984209	11
10	957.463600	479.235438	940.437051	470.722164	939.453035	470.230156	N	***1783.934594***	892.470935	1766.908045	883.957660	1765.924029	883.465652	10
11	1070.547664	535.777470	1053.521115	527.264196	1052.537099	526.772187	L	***1669.891667***	835.449471	1652.865118	826.936197	1651.881102	826.444189	9
12	1509.772990	755.390133	1492.746441	746.876859	1491.762425	746.384851	Q	***1556.807603***	778.907440	1539.781054	770.394165	1538.797038	769.902157	8
13	1580.810104	790.908690	1563.783555	782.395416	1562.799539	781.903408	A	***1117.582277***	559.294776	1100.555728	550.781502	1099.571712	550.289494	7
14	1651.847218	826.427247	1634.820669	817.913973	1633.836653	817.421965	A	***1046.545163***	523.776219	1029.518614	515.262945	1028.534598	514.770937	6
15	2091.072544	1046.039910	2074.045995	1037.526635	2073.061979	1037.034627	Q	***975.508049***	488.257662	958.481500	479.744388	957.497484	479.252380	5
16	2206.099487	1103.553381	2189.072938	1095.040107	2188.088922	1094.548099	D	***536.282723***	268.644999	519.256174	260.131725	518.272158	259.639717	4
17	2353.167901	1177.087588	2336.141352	1168.574314	2335.157336	1168.082306	F	***421.255780***	211.131528	404.229231	202.618253			3
18	2452.236315	1226.621795	2435.209766	1218.108521	2434.225750	1217.616513	V	274.187366	137.597321	257.160817	129.084046			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 25 ppm



RMS error 25 ppm

NCBI **BLAST** search of GSLVQASEANLQAAQDFVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.9	2625.340698	-0.032676	GSLVQASEANLQAAQDFVR
3.7	2625.340698	-0.032676	GSLVQASEANLQAAQDFVR

Mascot: http://www.matrixscience.com/

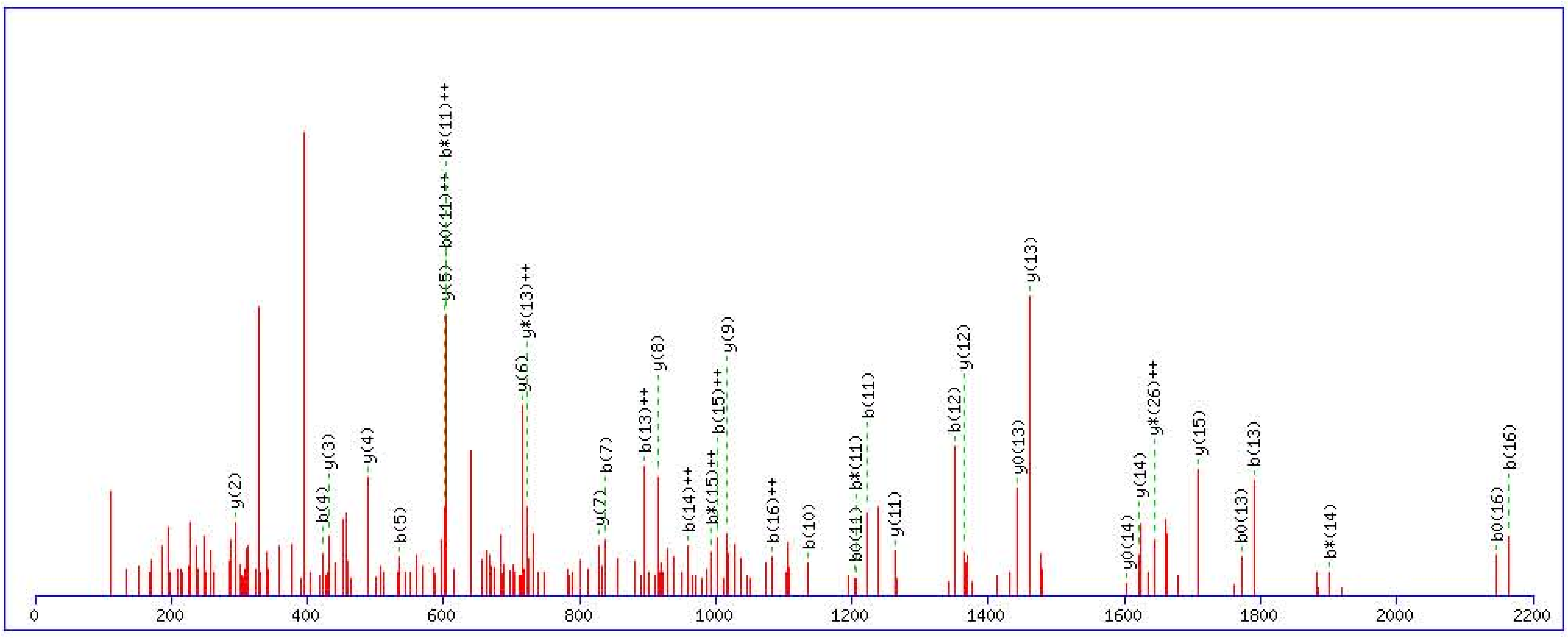
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGHVLFRPTVSQQQSCPTCSTSLLNGHFK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

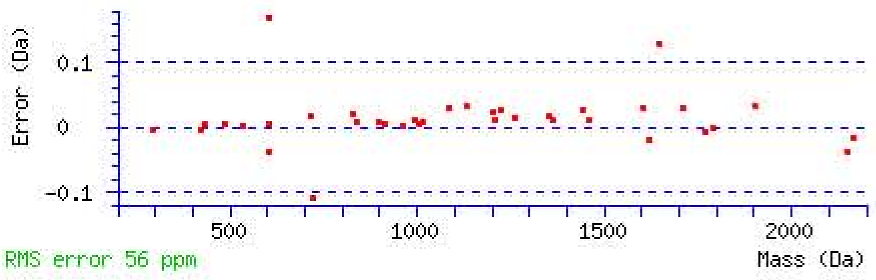
Match to Query 78799: 3624.861270 from(725.979530,5+) rtinseconds(1806) index(59398)
Title: Locus:1.1.1.3052.14 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

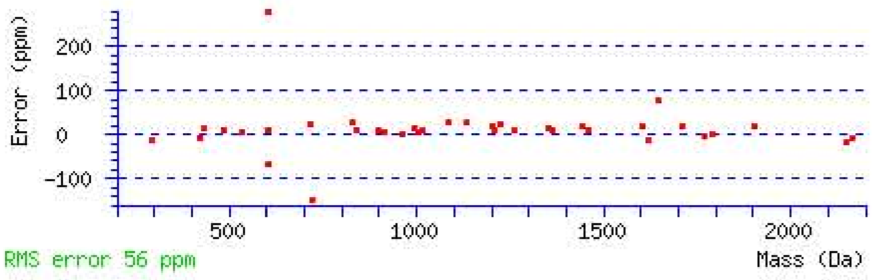
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3624.811615
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00037
Matches : 37/306 fragment ions using 97 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							29
2	186.123703	93.565489	169.097154	85.052215			G	3497.723899	1749.365587	3480.697350	1740.852313	3479.713334	1740.360305	28
3	323.182615	162.094945	306.156066	153.581671			H	3440.702435	1720.854855	3423.675886	1712.341581	3422.691870	1711.849573	27
4	***422.251029***	211.629153	405.224480	203.115878			V	3303.643523	1652.325399	3286.616974	1643.812125	3285.632958	1643.320117	26
5	***535.335093***	268.171185	518.308544	259.657910			L	3204.575109	1602.791192	3187.548560	1594.277918	3186.564544	1593.785910	25
6	682.403507	341.705392	665.376958	333.192117			F	3091.491045	1546.249160	3074.464496	1537.735886	3073.480480	1537.243878	24
7	***838.504618***	419.755947	821.478069	411.242672			R	2944.422631	1472.714953	2927.396082	1464.201679	2926.412066	1463.709671	23
8	935.557382	468.282329	918.530833	459.769054			P	2788.321520	1394.664398	2771.294971	1386.151123	2770.310955	1385.659115	22
9	1036.605061	518.806169	1019.578512	510.292894	1018.594496	509.800886	T	2691.268756	1346.138016	2674.242207	1337.624741	2673.258191	1337.132733	21
10	***1135.673475***	568.340376	1118.646926	559.827101	1117.662910	559.335093	V	2590.221077	1295.614176	2573.194528	1287.100902	2572.210512	1286.608894	20
11	***1222.705503***	611.856390	1205.678954	603.343115	1204.694938	602.851107	S	2491.152663	1246.079969	2474.126114	1237.566695	2473.142098	1237.074687	19
12	***1350.764081***	675.885679	1333.737532	667.372404	1332.753516	666.880396	Q	2404.120635	1202.563955	2387.094086	1194.050681	2386.110070	1193.558673	18
13	***1789.989407***	**895.498342**	1772.962858	886.985067	1771.978842	886.493059	Q	2276.062057	1138.534666	2259.035508	1130.021392	2258.051492	1129.529384	17
14	1918.047985	**959.527631**	1901.021436	951.014356	1900.037420	950.522348	Q	1836.836731	918.922003	1819.810182	910.408729	1818.826166	909.916721	16
15	2005.080013	**1003.043645**	1988.053464	994.530370	1987.069448	994.038362	S	***1708.778153***	854.892714	1691.751604	846.379440	1690.767588	845.887432	15
16	***2165.110662***	**1083.058969**	2148.084113	1074.545694	2147.100097	1074.053686	C	***1621.746125***	811.376700	1604.719576	802.863426	1603.735560	802.371418	14
17	2262.163426	1131.585351	2245.136877	1123.072076	2244.152861	1122.580068	P	***1461.715476***	731.361376	1444.688927	722.848101	1443.704911	722.356093	13
18	2363.211105	1182.109190	2346.184556	1173.595916	2345.200540	1173.103908	T	***1364.662712***	682.834994	1347.636163	674.321719	1346.652147	673.829711	12
19	2523.241754	1262.124515	2506.215205	1253.611240	2505.231189	1253.119232	C	***1263.615033***	632.311154	1246.588484	623.797880	1245.604468	623.305872	11
20	2610.273782	1305.640529	2593.247233	1297.127254	2592.263217	1296.635246	S	1103.584384	552.295830	1086.557835	543.782556	1085.573819	543.290548	10
21	2711.321461	1356.164368	2694.294912	1347.651094	2693.310896	1347.159086	T	***1016.552356***	508.779816	999.525807	500.266541	998.541791	499.774533	9
22	2798.353489	1399.680382	2781.326940	1391.167108	2780.342924	1390.675100	S	***915.504677***	458.255977	898.478128	449.742702	897.494112	449.250694	8
23	2911.437553	1456.222414	2894.411004	1447.709140	2893.426988	1447.217132	L	***828.472649***	414.739963	811.446100	406.226688			7
24	3024.521617	1512.764446	3007.495068	1504.251172	3006.511052	1503.759164	L	***715.388585***	358.197930	698.362036	349.684656			6
25	3138.564544	1569.785910	3121.537995	1561.272635	3120.553979	1560.780627	N	***602.304521***	301.655898	585.277972	293.142624			5
26	3195.586008	1598.296642	3178.559459	1589.783367	3177.575443	1589.291359	G	***488.261594***	244.634435	471.235045	236.121160			4
27	3332.644920	1666.826098	3315.618371	1658.312823	3314.634355	1657.820815	H	***431.240130***	216.123703	414.213581	207.610428			3
28	3479.713334	1740.360305	3462.686785	1731.847030	3461.702769	1731.355022	F	***294.181218***	147.594247	277.154669	139.080972			2
29							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KGHVLFRPTVSQQQSCPTCSTSLLNGHFK
(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	3624.811615	0.049655	KGHVLFRPTVSQQQSCPTCSTSLLNGHFK
48.3	3624.811615	0.049655	KGHVLFRPTVSQQQSCPTCSTSLLNGHFK
46.0	3624.811615	0.049655	KGHVLFRPTVSQQQSCPTCSTSLLNGHFK

Mascot: http://www.matrixscience.com/

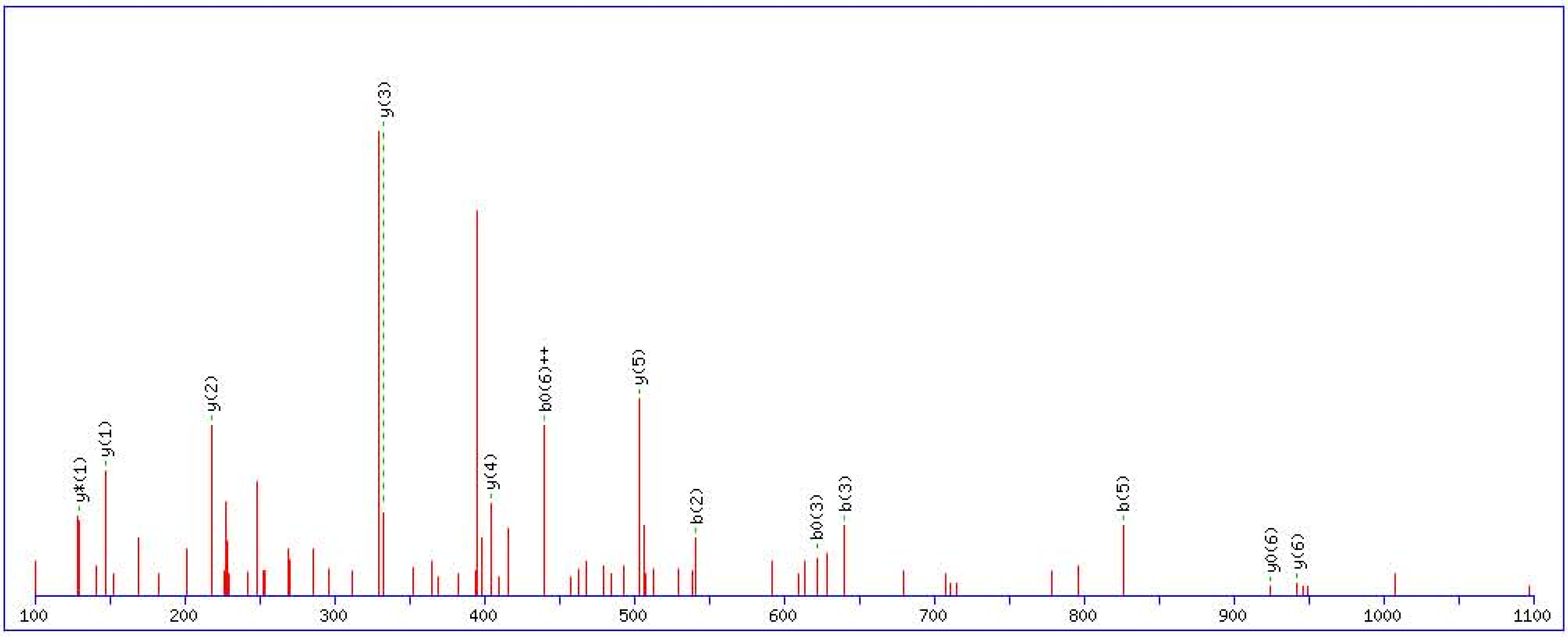
{MATRIX SCIENCE} Mascot Search Results

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

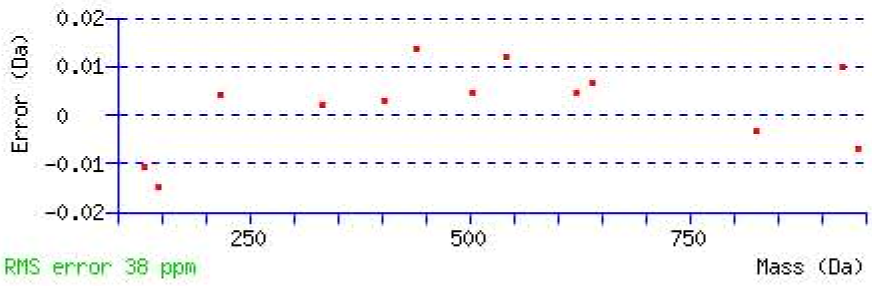
Match to Query 17318: 1042.553188 from(522.283870,2+) rtinseconds(1284) index(37232)
Title: Locus:1.1.1.2896.13 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

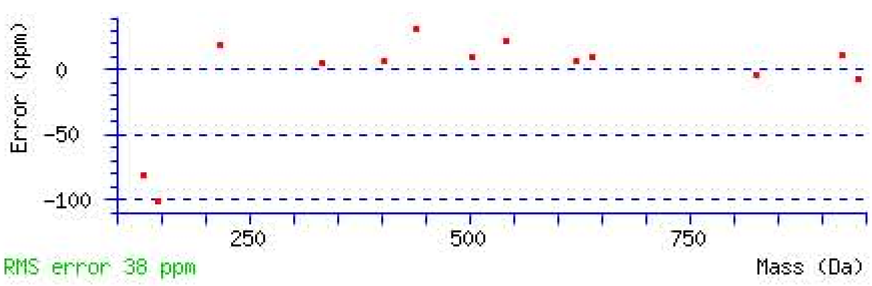
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1042.548111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0081
Matches : 13/66 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							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
34.3	1042.548111	0.005077	TQVADAK
11.3	1042.540680	0.012508	TPEERAAAAK
11.2	1042.548096	0.005092	SLQADAK
9.6	1042.540710	0.012478	SLKSPPGSDR
7.6	1042.548080	0.005108	EKEQAK
6.6	1042.540726	0.012462	KPVSEVGDGR
6.2	1042.540680	0.012508	EAEKRPADK
6.1	1042.548080	0.005108	KEQEAK
6.1	1042.548080	0.005108	KQEEAK
6.1	1042.540695	0.012493	NPREVTEAK

Mascot: http://www.matrixscience.com/

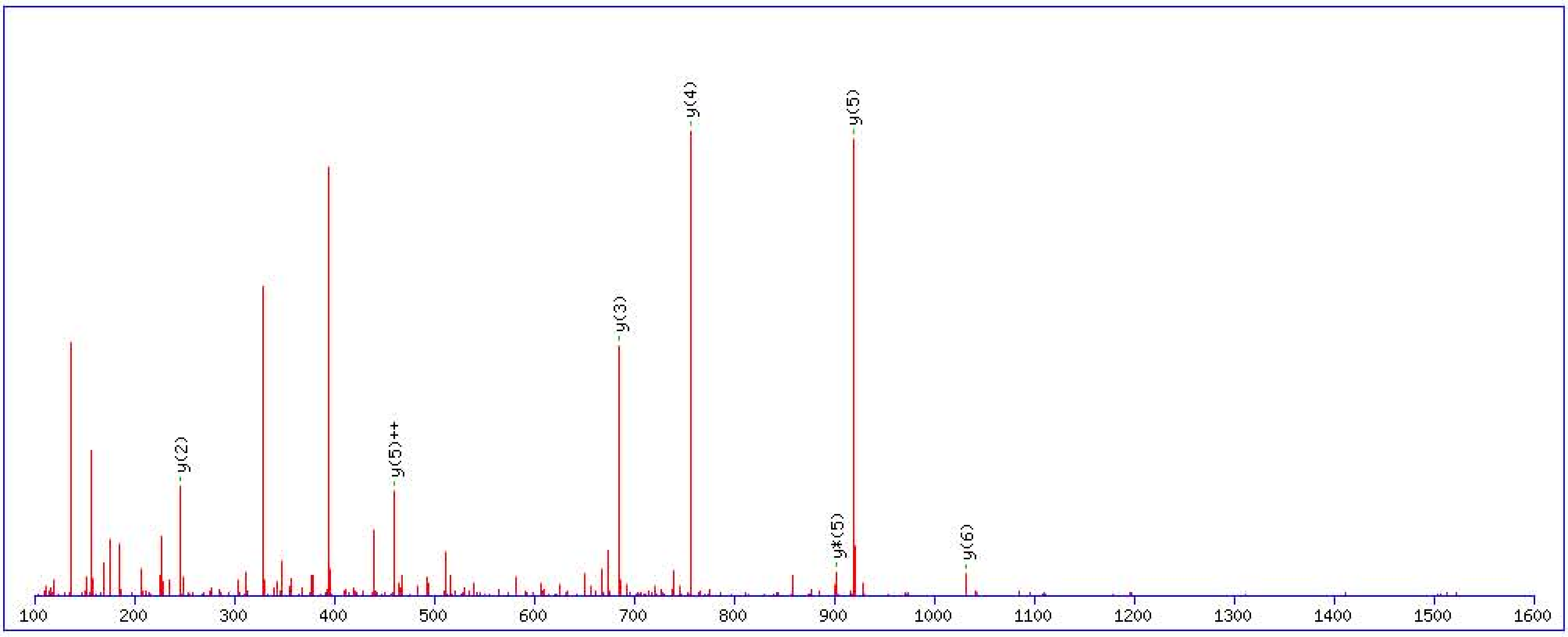
Mascot Search Results

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

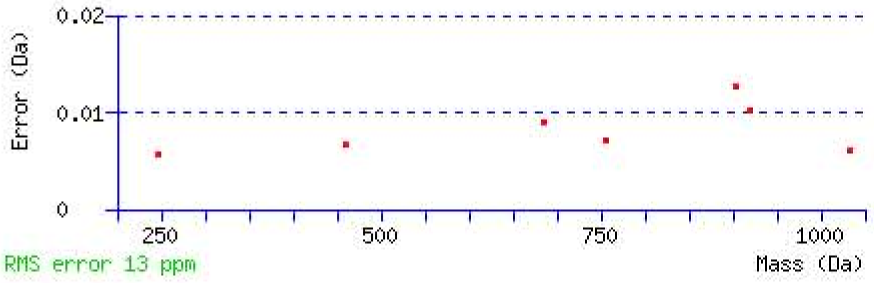
Match to Query 18980: 1102.608208 from(552.311380,2+) rtinseconds(1641) index(58232)
Title: Locus:1.1.1.2995.7 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

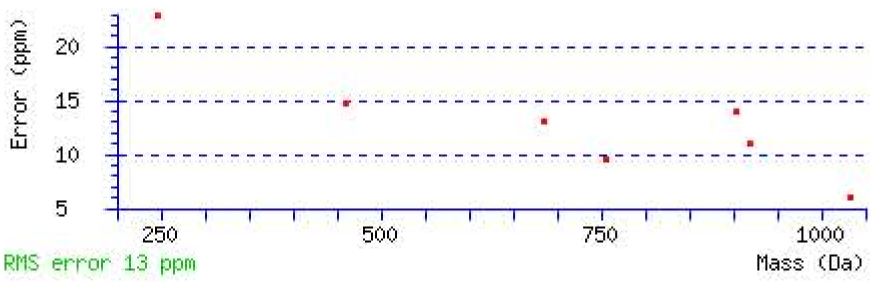
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1102.595703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.0034
Matches : 7/40 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
37.3	1102.595703	0.012505	ALYAQAR
10.3	1102.602234	0.005974	AIELGYNPVK
4.3	1102.613464	-0.005256	AIPEKYGAVR
3.8	1102.598221	0.009987	DDLKATLTAR
3.8	1102.591690	0.016518	NMEVSLVRR
3.0	1102.610321	-0.002113	ALGMMGLVRR
2.4	1102.613495	-0.005287	SFIAVPVTNR
1.9	1102.613495	-0.005287	ALTQGPLTFR
1.5	1102.602249	0.005959	AIVLFNPDSK
0.7	1102.591690	0.016518	LRCSVLEAR

Mascot: http://www.matrixscience.com/

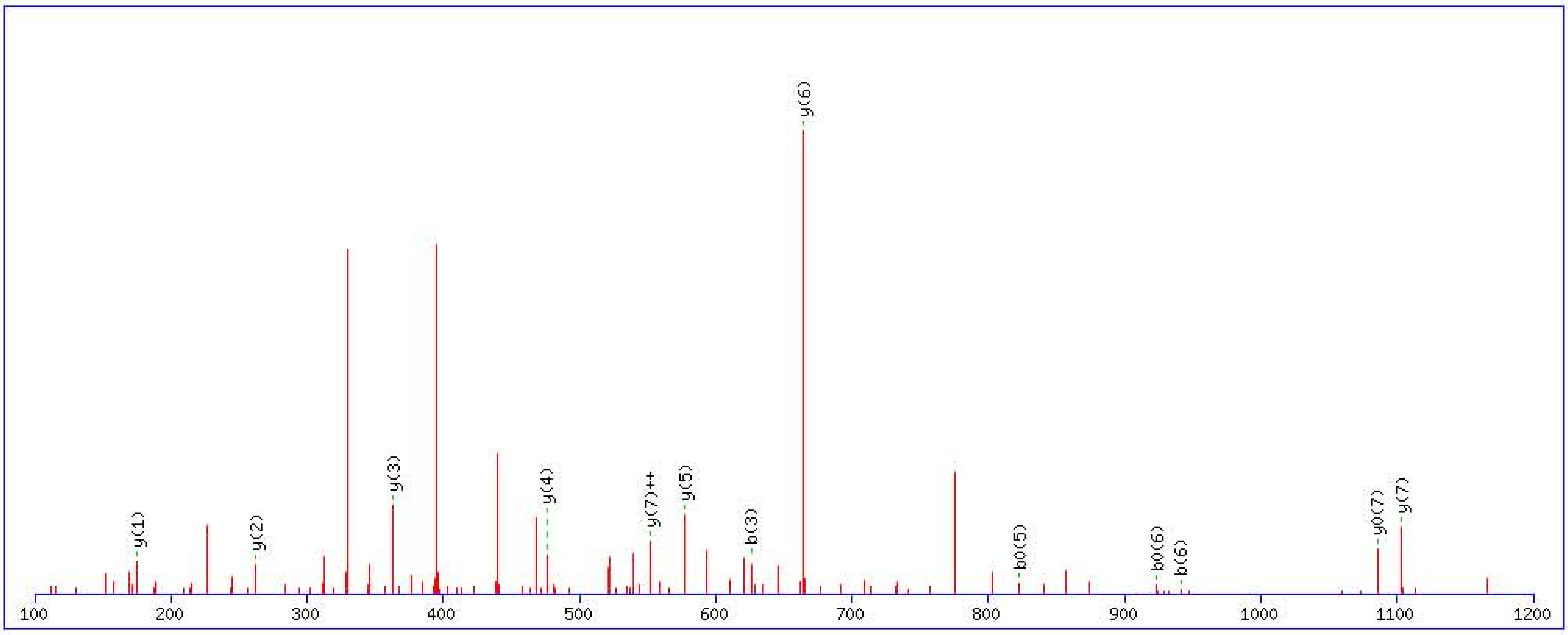
Mascot Search Results

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

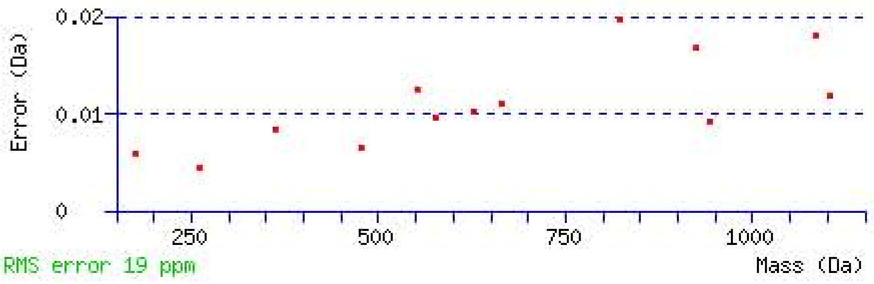
Match to Query 23733: 1201.663928 from(601.839240,2+) rtinseconds(1470) index(57058)
Title: Locus:1.1.1.2935.11 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

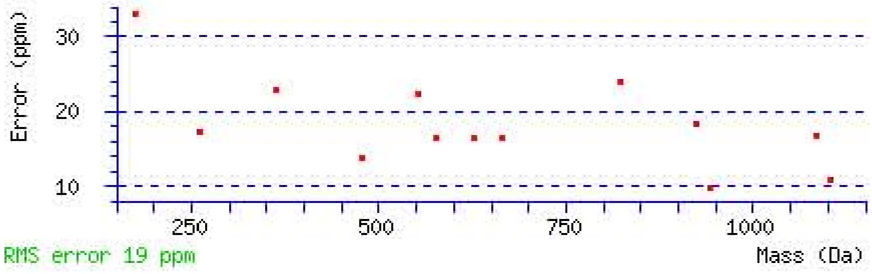
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1201.648895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 36  Expect: 0.0055
Matches : 13/76 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	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
35.9	1201.648895	0.015033	VQSTITSR
13.7	1201.677856	-0.013928	VEKLRSDLSR
0.4	1201.656769	0.007159	RVSSFTGPVPR

Mascot: http://www.matrixscience.com/

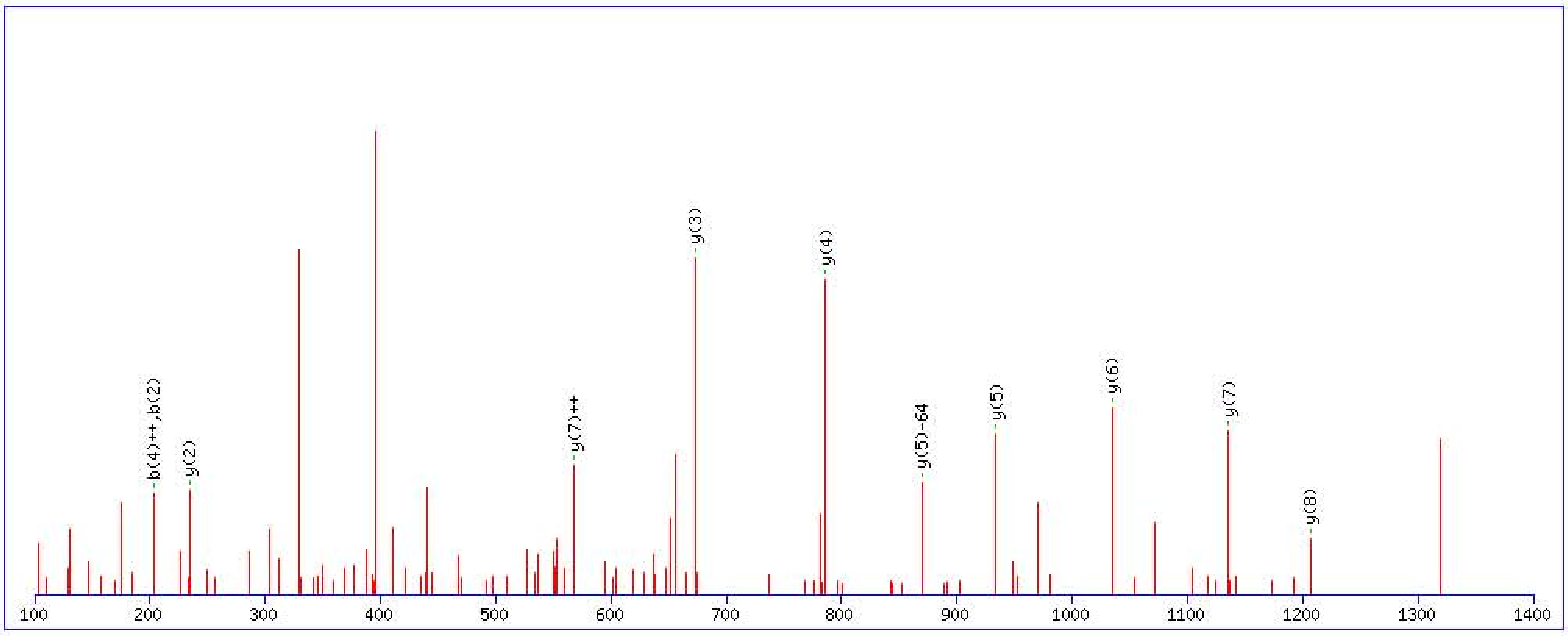
{MATRIX SCIENCE} Mascot Search Results

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

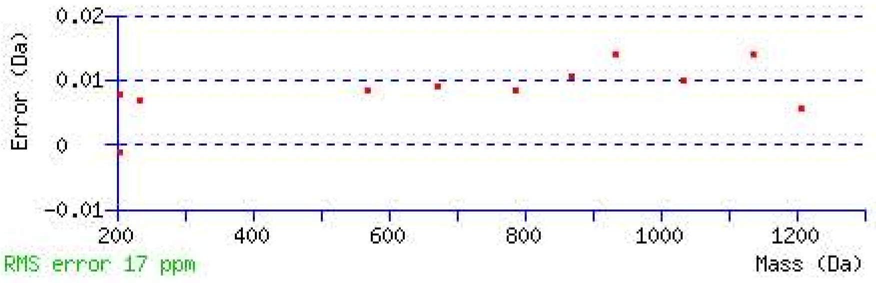
Match to Query 27761: 1336.674148 from(669.344350,2+) rtinseconds(1513) index(57350)
Title: Locus:1.1.1.2950.14 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

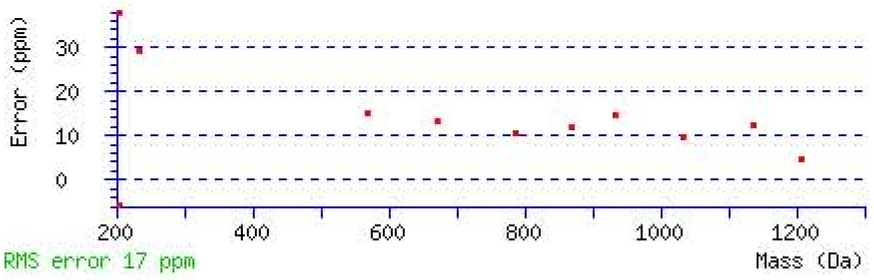
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 61  Expect: 8.6e-006
Matches : 11/122 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	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
61.0	1336.655289	0.018859	MATTMIQSK
6.7	1336.692795	-0.018647	RFTYKFNFSK
4.1	1336.662247	0.011901	KAEELQATYER
3.8	1336.662308	0.011840	KDTWGVVSSGSSK
3.8	1336.655289	0.018859	MATTMIQSK
3.8	1336.690781	-0.016633	MTASAASELILSK
2.5	1336.684937	-0.010789	QFFEIQSK
2.1	1336.684753	-0.010605	GRPSGTTKSAGYR

Mascot: http://www.matrixscience.com/

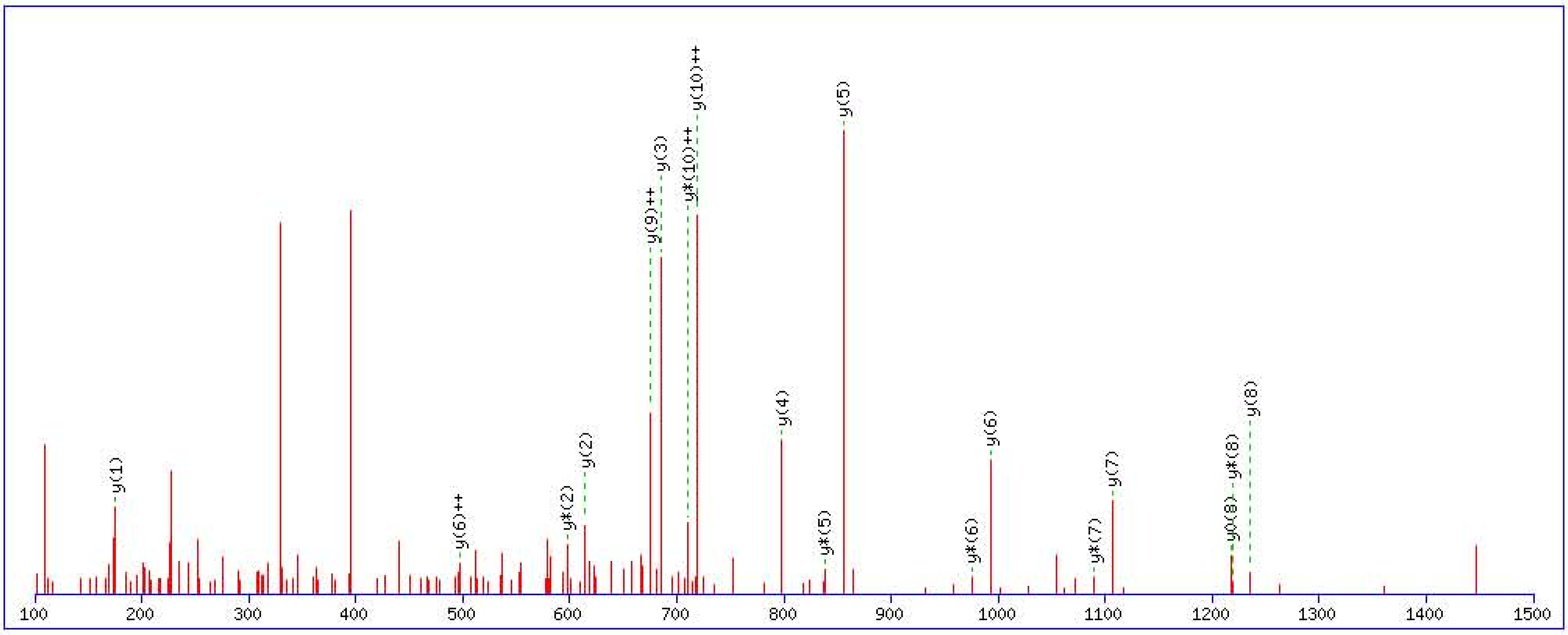
{MATRIX SCIENCE} Mascot Search Results

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

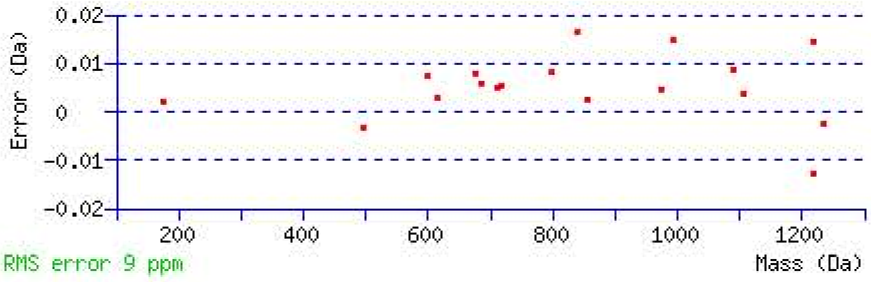
Match to Query 36420: 1548.795582 from(517.272470,3+) rtinseconds(1364) index(37770)
Title: Locus:1.1.1.2924.18 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

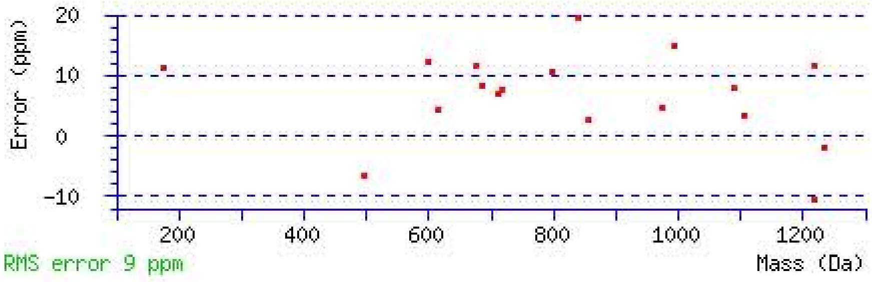
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1548.783066
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0005
Matches : 18/100 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	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
42.2	1548.783066	0.012516	LSNENHGIAQR
6.9	1548.800842	-0.005260	KGEPGEPGPKGGIGNR

Mascot: http://www.matrixscience.com/

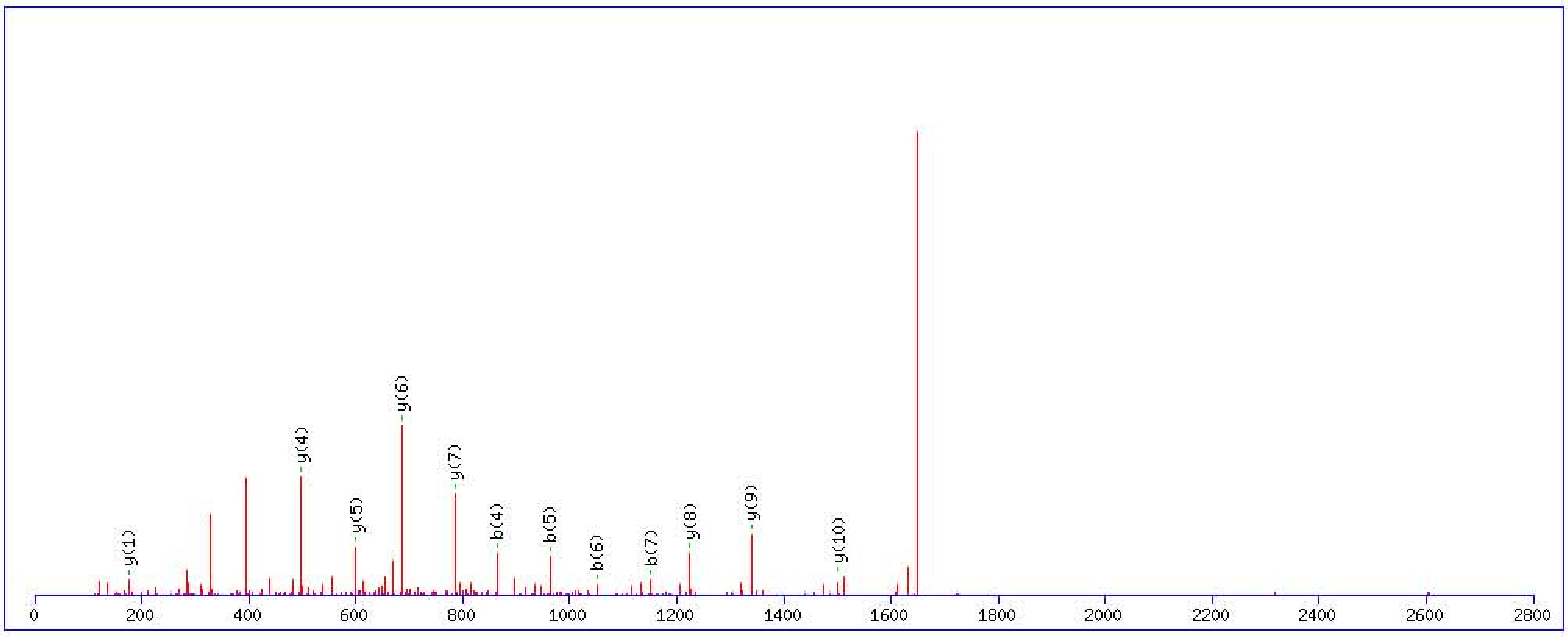
Mascot Search Results

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

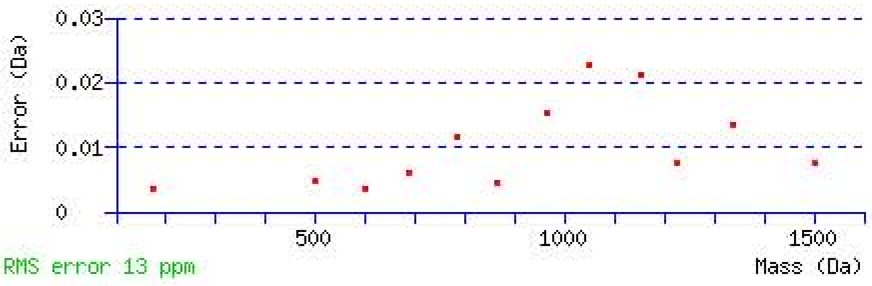
Match to Query 41112: 1647.902488 from(824.958520,2+) rtinseconds(2248) index(43972)
Title: Locus:1.1.1.3231.19 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

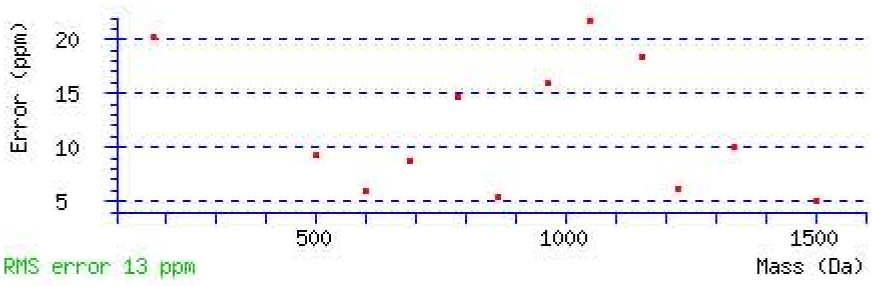
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1647.880676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 2.7e-006
Matches : 12/98 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	148.075690	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
68.0	1647.880676	0.021812	FYNQVSTPLLR
10.7	1647.895264	0.007224	MKPILLQGHER
6.0	1647.903137	-0.000649	EVRIMRWFGLVSR
5.9	1647.887878	0.014610	TLNQQLTNHIR
4.5	1647.887878	0.014610	TLNQQLTNHIR
3.1	1647.905609	-0.003121	YLRELSGSGLERLR
2.8	1647.910339	-0.007851	LMRPRREGGPPGGLR
2.5	1647.923569	-0.021081	KPSLIFLSETWSLK
2.1	1647.913040	-0.010552	CIANGVTSKVFLAIR

Mascot: http://www.matrixscience.com/

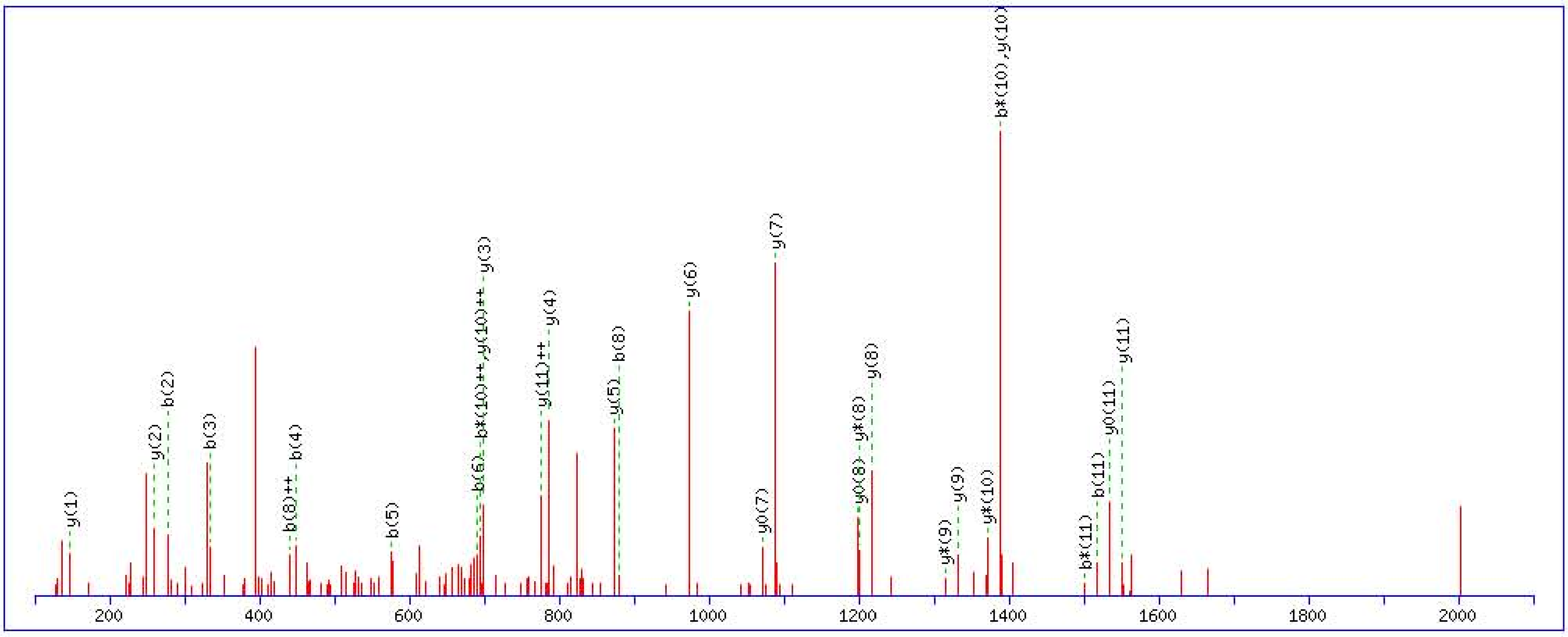
{MATRIX SCIENCE} Mascot Search Results

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

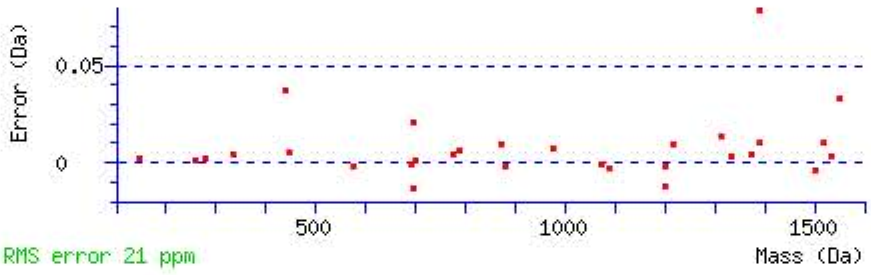
Match to Query 41580: 1663.845108 from(832.929830,2+) rtinseconds(1646) index(39712)
Title: Locus:1.1.1.3022.18 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

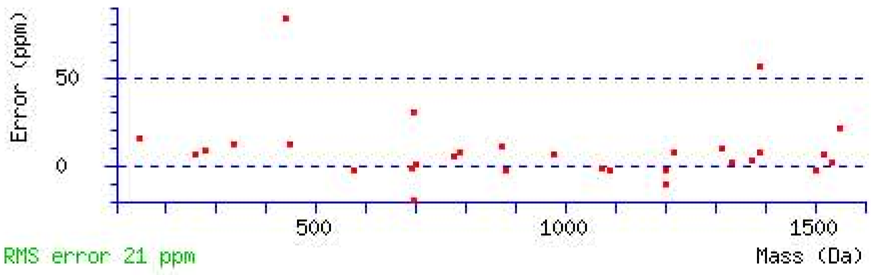
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1663.823944
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 83  Expect: 7.9e-008
Matches : 30/110 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					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
82.9	1663.823944	0.021164	IYGNQDTSSQLK
20.4	1663.823944	0.021164	IYGNQDTSSQLK
6.7	1663.863663	-0.018555	EAQKEMQKIMTSLK
5.5	1663.821442	0.023666	LYGCFLRVYMQSK
1.2	1663.845078	0.000030	LMSGVENSGKVDISTK
0.8	1663.867722	-0.022614	VEMPSFKMPKVDLK

Mascot: http://www.matrixscience.com/

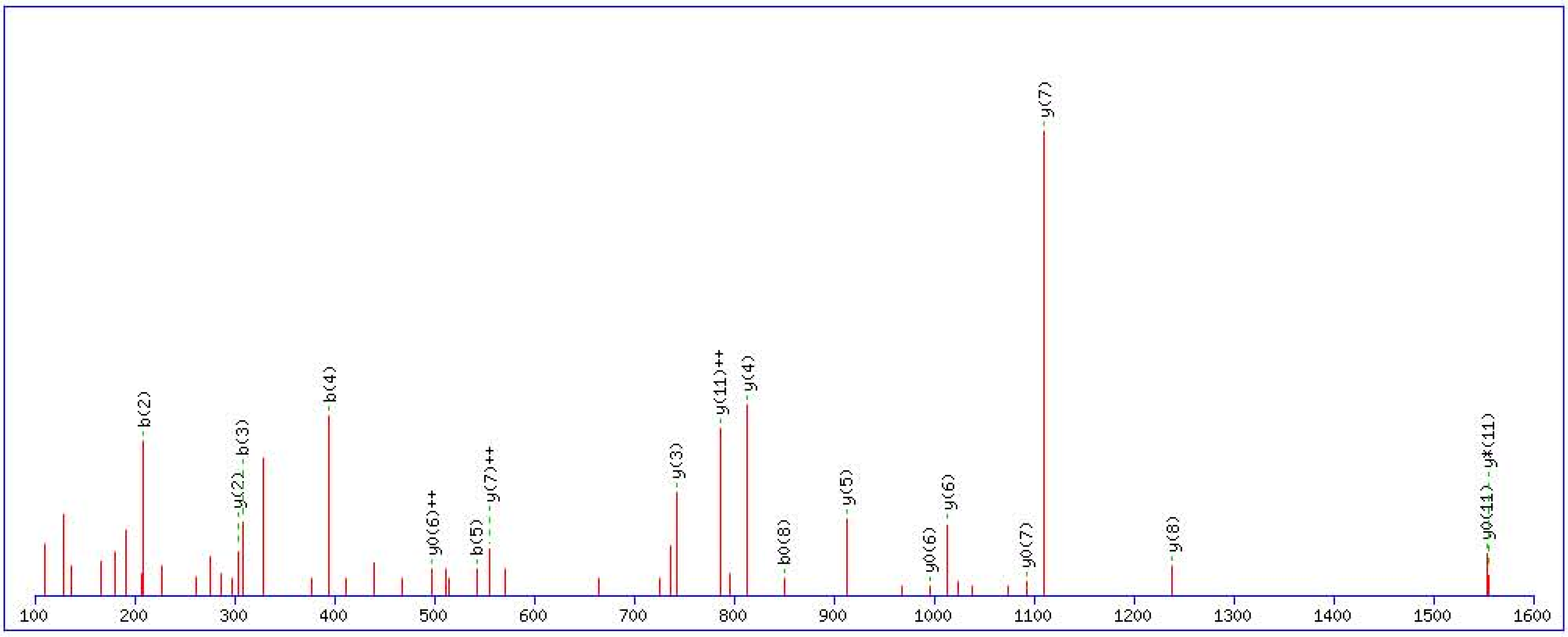
{MATRIX SCIENCE} Mascot Search Results

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

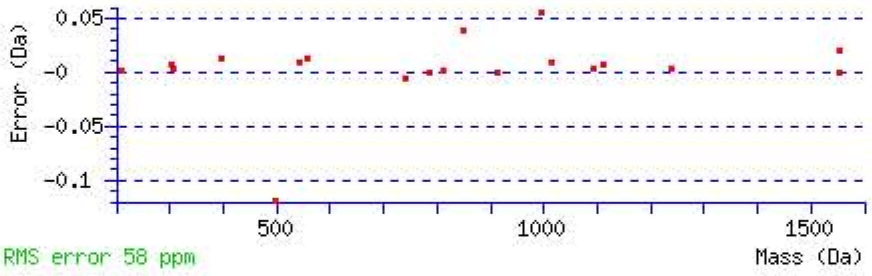
Match to Query 44746: 1778.976522 from(593.999450,3+) rtinseconds(1491) index(38704)
Title: Locus:1.1.1.2968.17 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

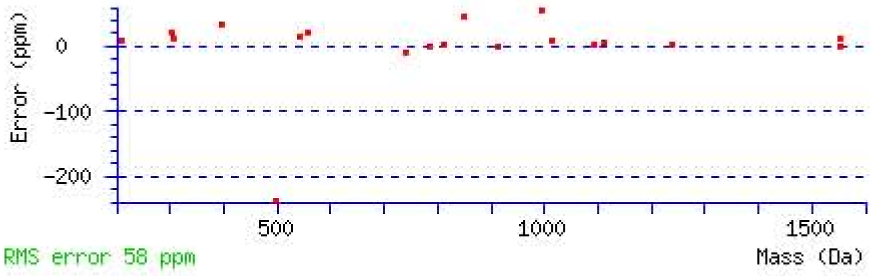
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 59 **Expect:** 2.4e-005
Matches : 19/118 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
58.7	1778.961395	0.015127	AHVSFKPTVAQQR
48.1	1778.961395	0.015127	AHVSFKPTVAQQR

Mascot: http://www.matrixscience.com/

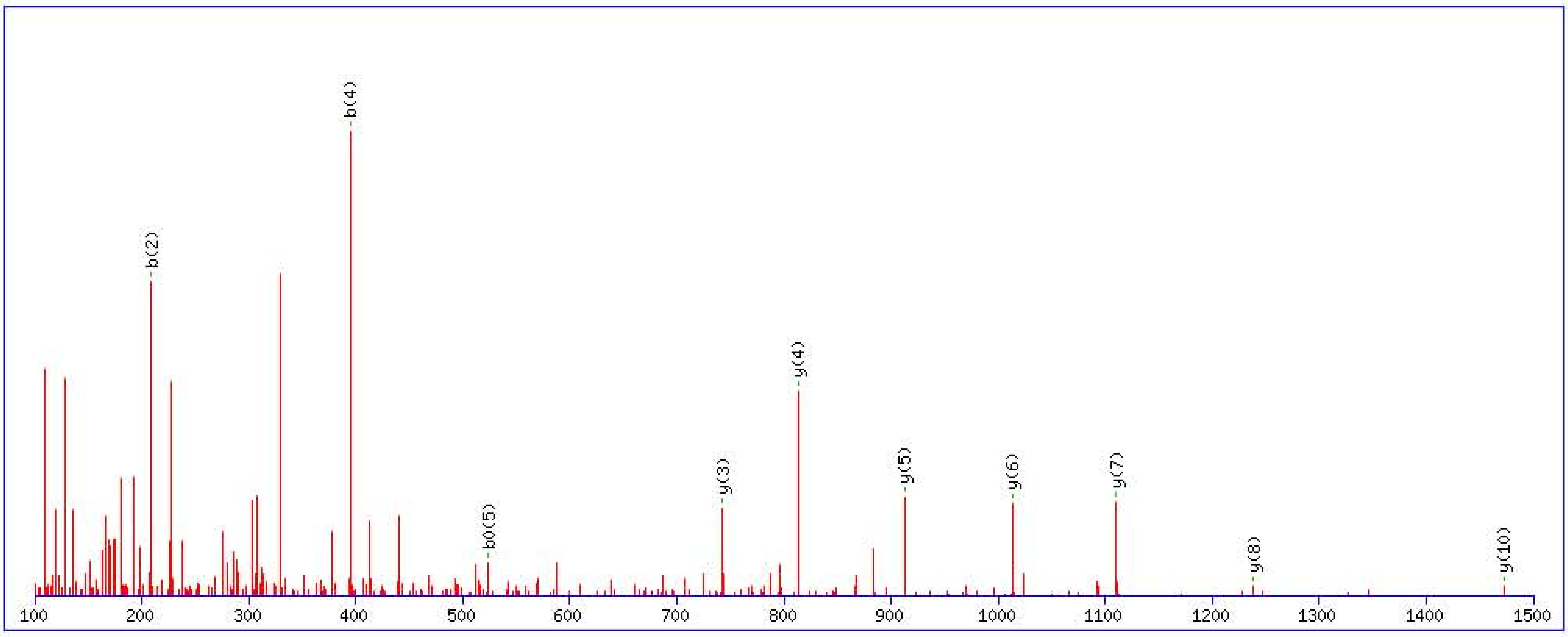
{MATRIX SCIENCE} Mascot Search Results

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

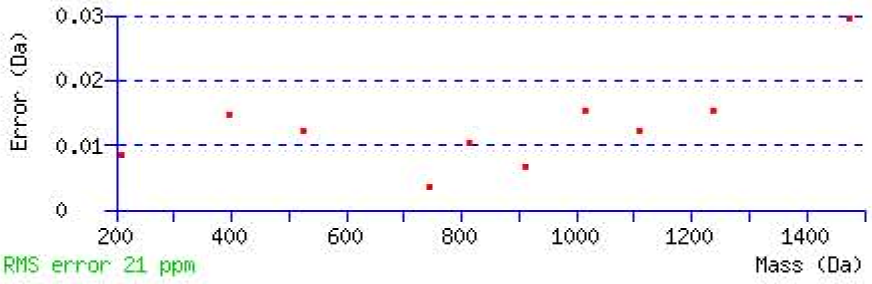
Match to Query 44749: 1778.981016 from(445.752530,4+) rtinseconds(1512) index(57342)
Title: Locus:1.1.1.2950.6 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

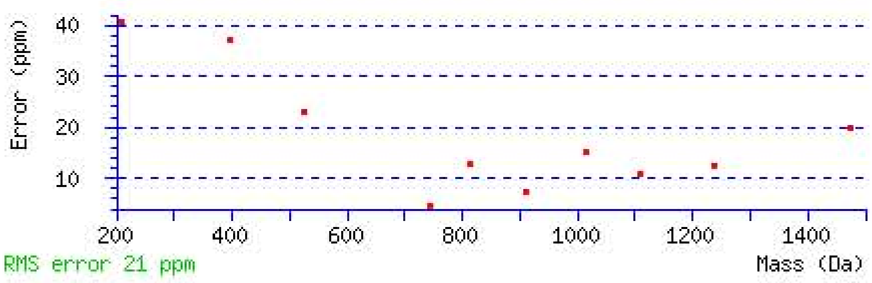
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1778.961395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00021
Matches : 10/118 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	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
48.7	1778.961395	0.019621	AHVSFKPTVAQQR
48.7	1778.961395	0.019621	AHVSFKPTVAQQR

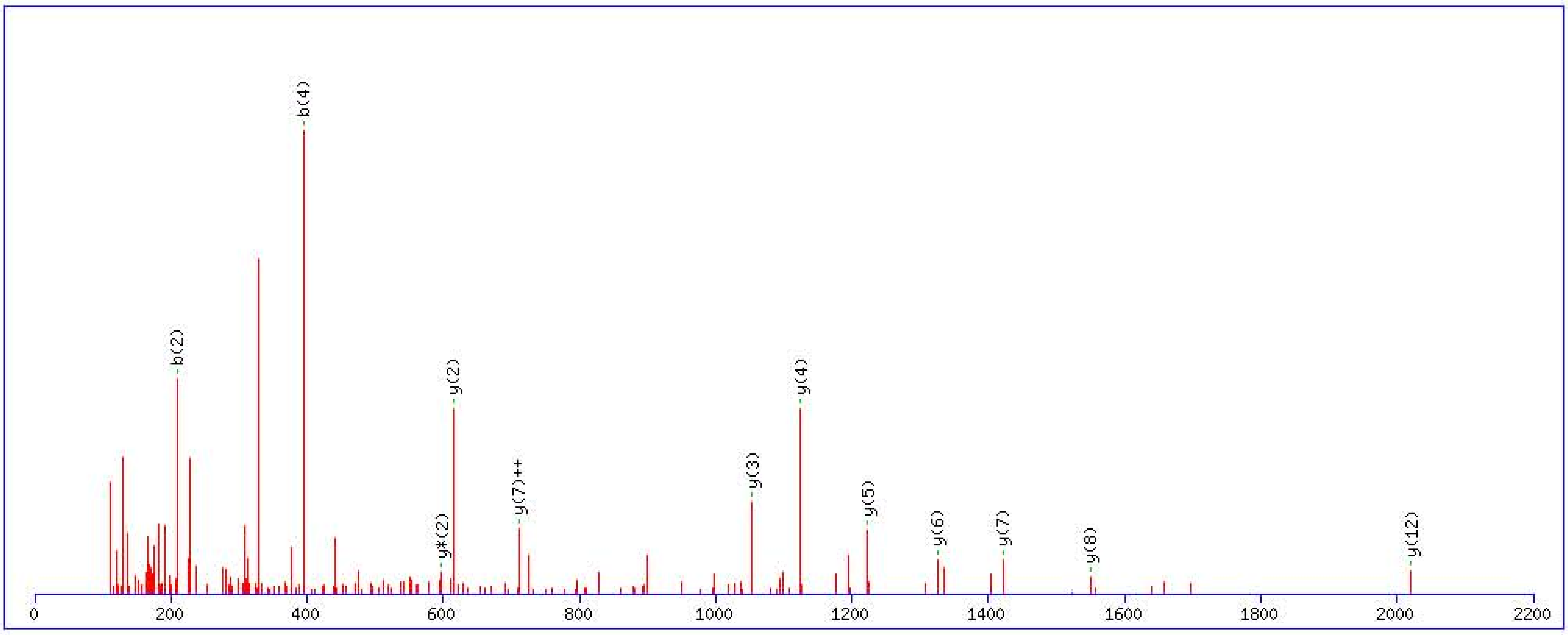
{MATRIX SCIENCE} Mascot Search Results

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

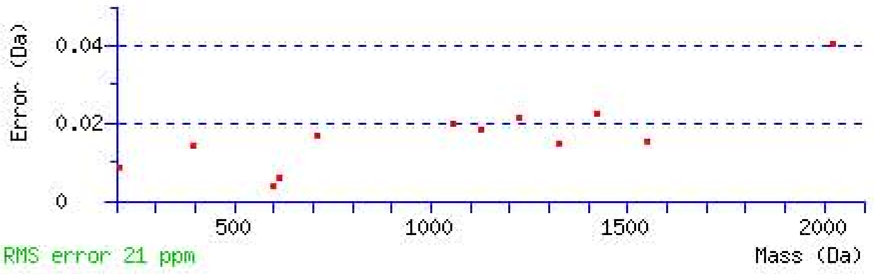
Match to Query 52933: 2090.153976 from(523.545770,4+) rtinseconds(1762) index(59069)
Title: Locus:1.1.1.3037.6 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

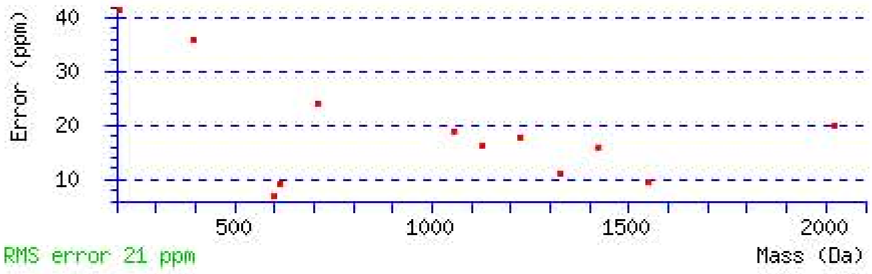
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 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: 53 **Expect:** 7.1e-005
Matches : 12/118 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							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
52.9	2090.128143	0.025833	AHVSFKPTVAQQR

Mascot: http://www.matrixscience.com/

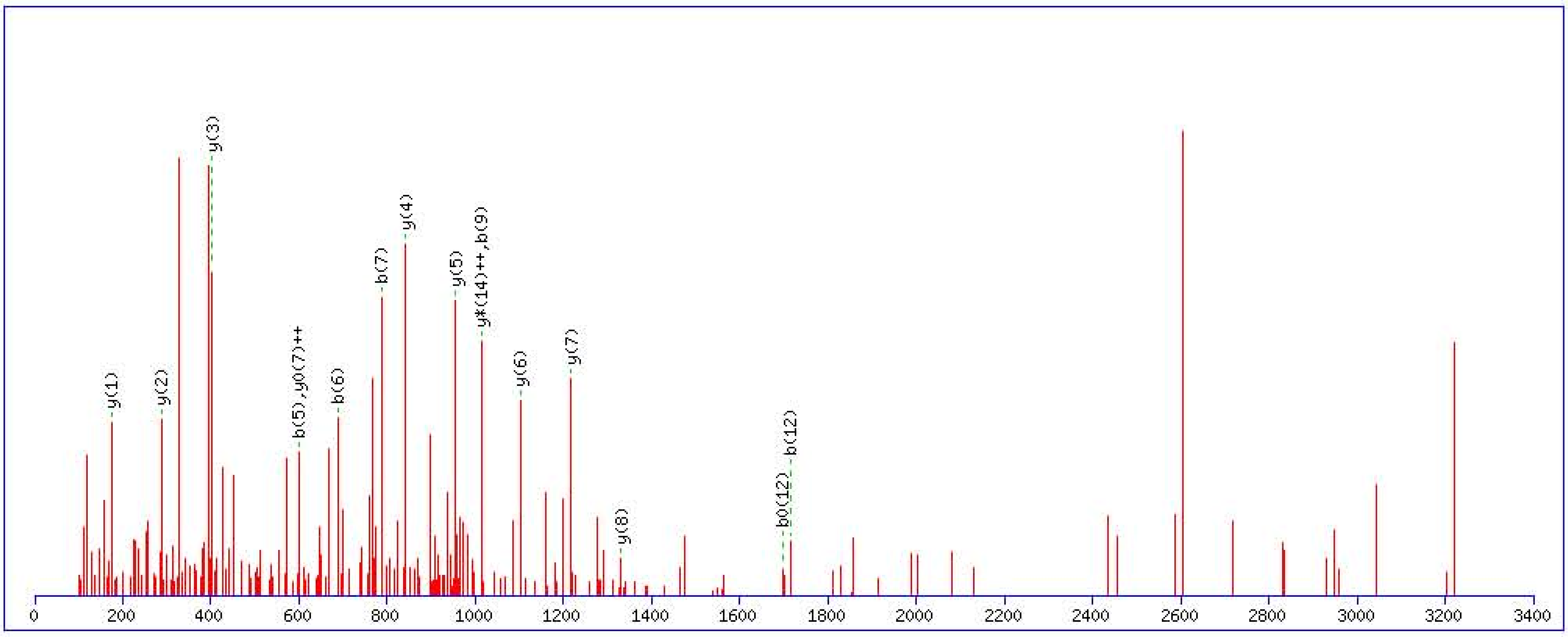
Mascot Search Results

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

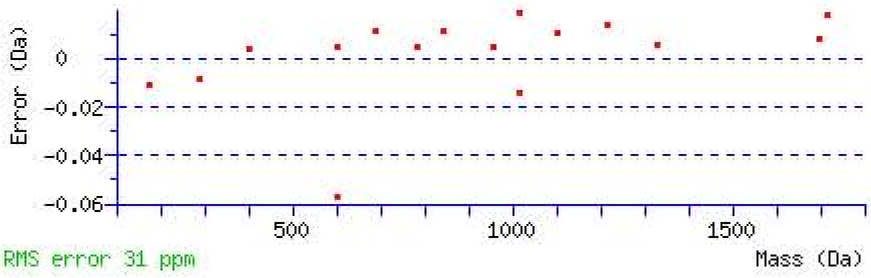
Match to Query 53416: 2115.044742 from(706.022190,3+) rtinseconds(2249) index(43982)
Title: Locus:1.1.1.3232.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

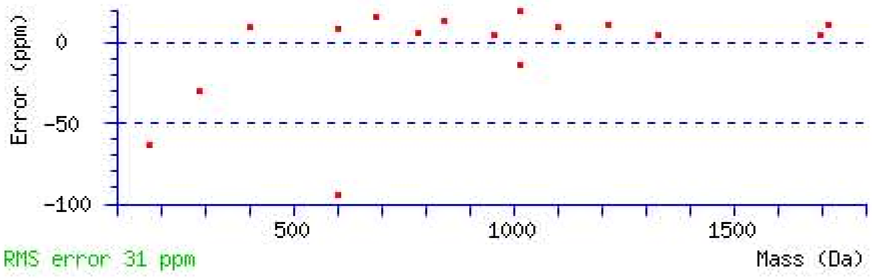
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2115.020752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 8.2e-006
Matches : 16/134 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	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
56.1	2115.020752	0.023990	AEDHFSVIDFNQNIR
1.8	2115.033981	0.010761	ESADRQVLMQEEEIK
0.4	2115.067032	-0.022290	DFEVDLLEIGGSQNLR

Mascot: http://www.matrixscience.com/

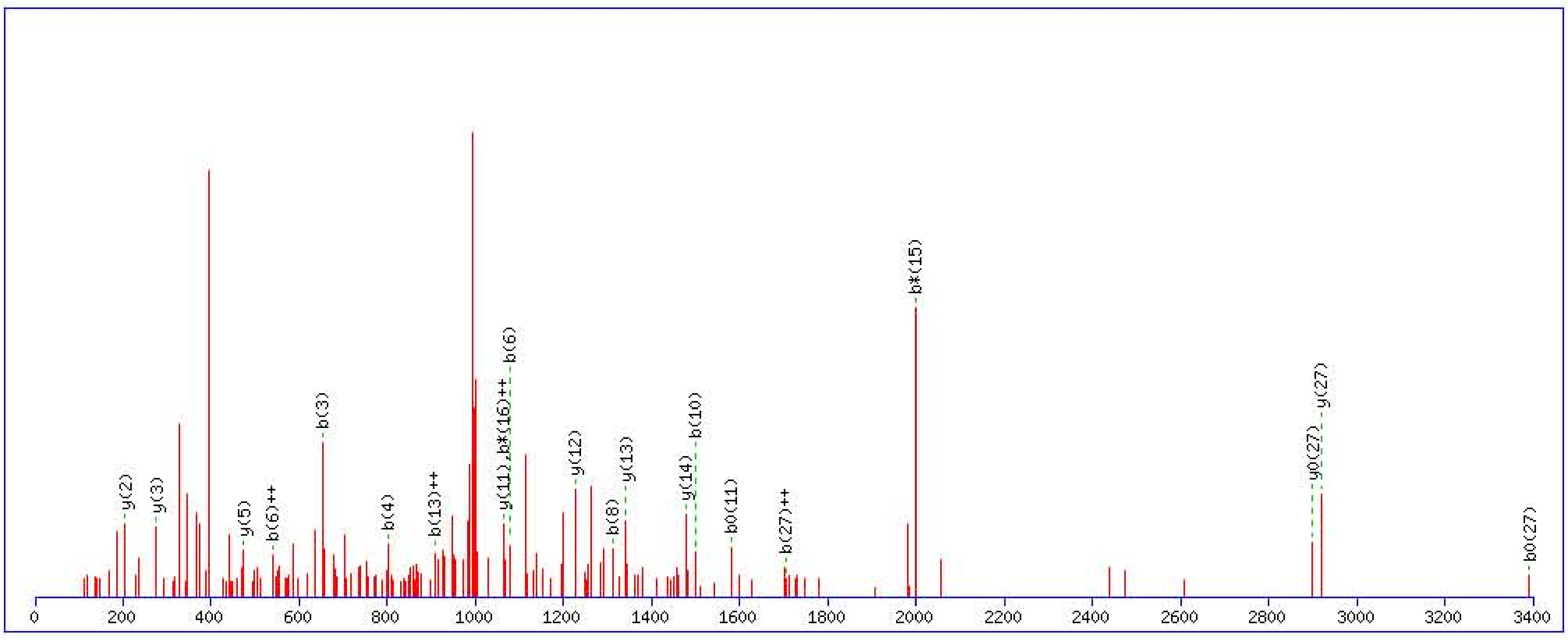
Mascot Search Results

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

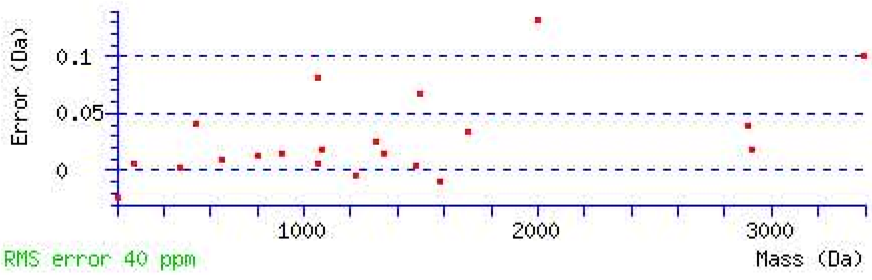
Match to Query 81125: 3993.963616 from(999.498180,4+) rtinseconds(2350) index(81242)
Title: Locus:1.1.1.2168.22 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

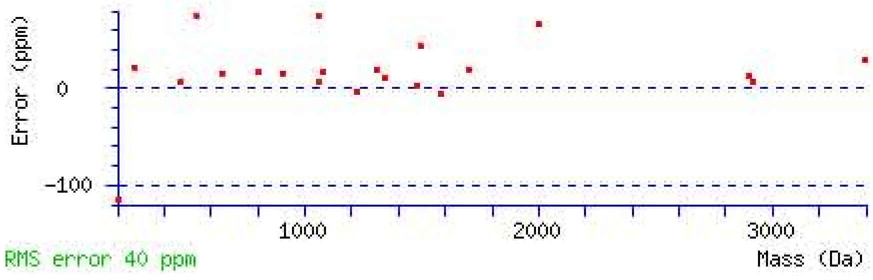
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3993.910858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.061
Matches : 21/356 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							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
25.9	3993.910858	0.052758	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK
2.5	3993.910858	0.052758	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK

Mascot: http://www.matrixscience.com/

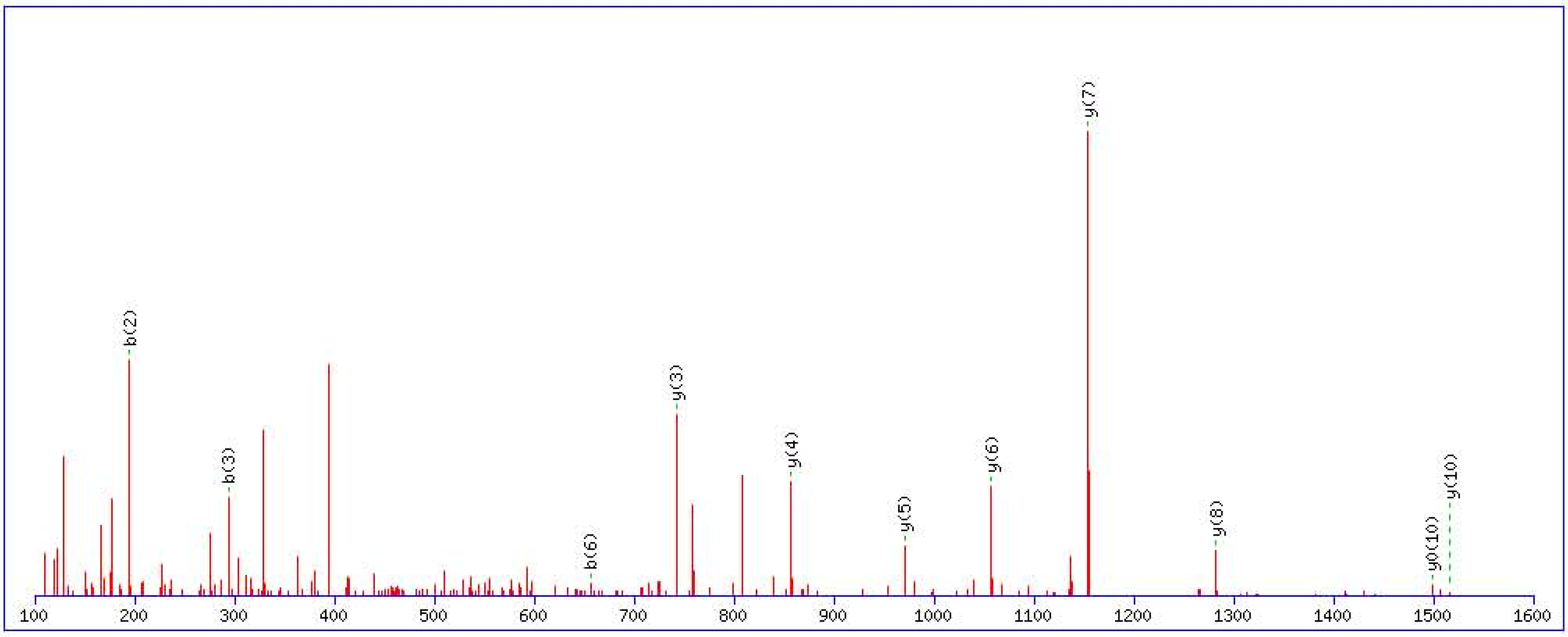
{MATRIX SCIENCE} Mascot Search Results

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

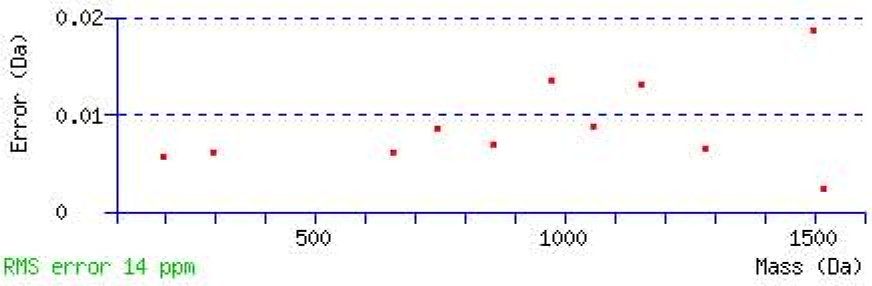
Match to Query 45521: 1808.956212 from(603.992680,3+) rtinseconds(1588) index(57930)
Title: Locus:1.1.1.2976.16 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

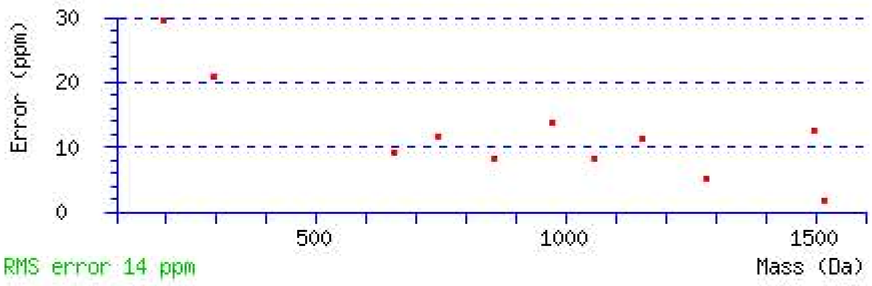
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 50  Expect: 2.3e-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





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
49.8	1808.935577	0.020635	GHVSFKPSLDQQR
49.8	1808.935577	0.020635	GHVSFKPSLDQQR
0.3	1808.946793	0.009419	IFRQNSDLVNHR

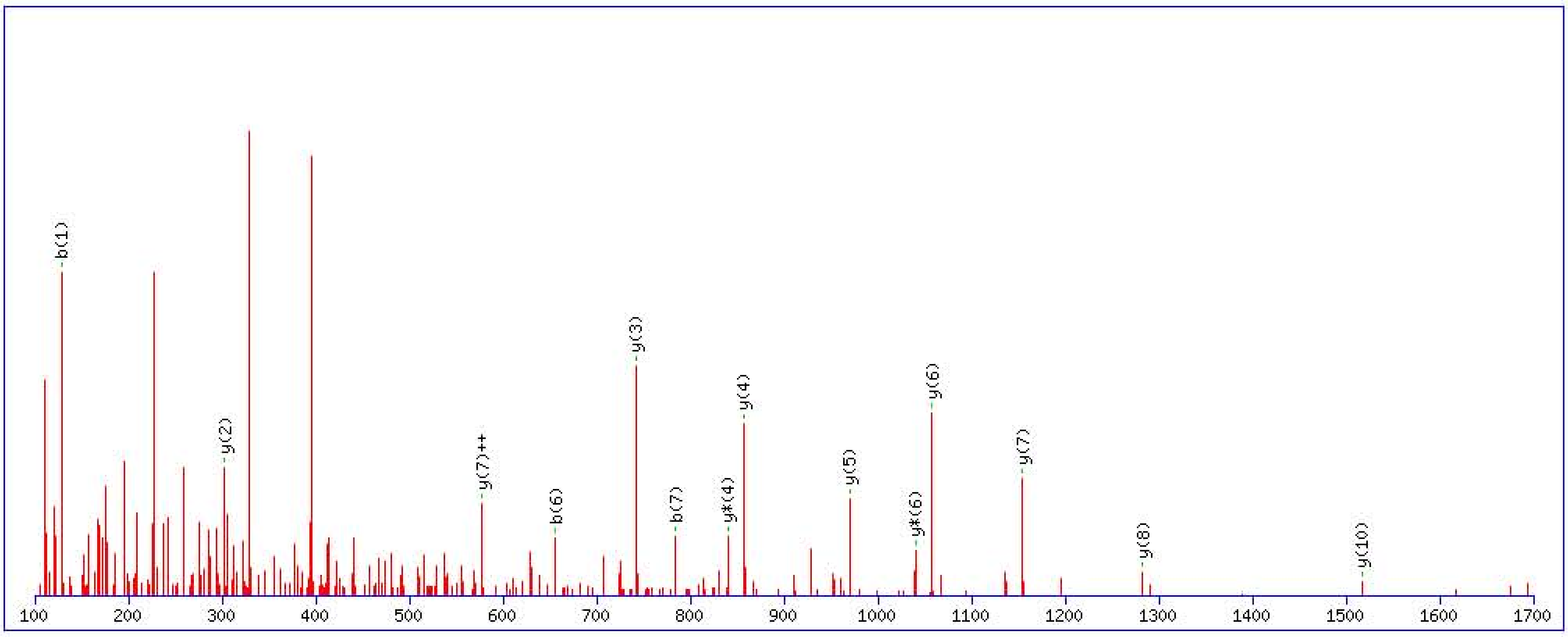
Mascot Search Results

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

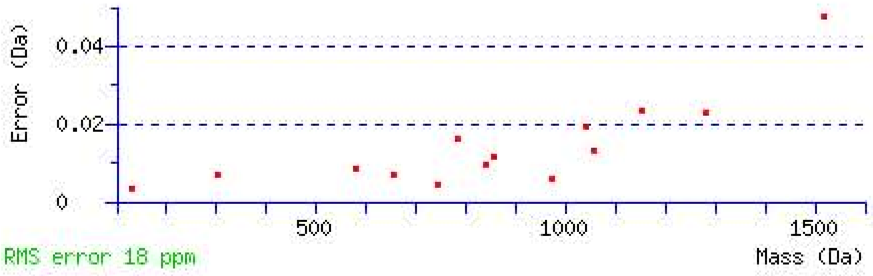
Match to Query 48421: 1937.052496 from(485.270400,4+) rtinseconds(1475) index(57083)
Title: Locus:1.1.1.2937.5 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

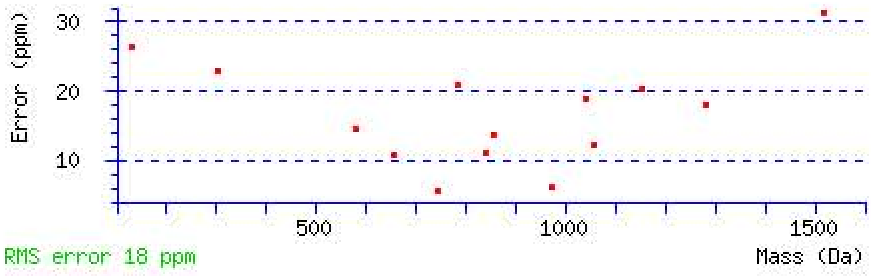
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1937.030533
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.00047
Matches : 14/142 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	**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
37.3	1937.030533	0.021963	KGHVSFKPSLDQQR
28.8	1937.030533	0.021963	KGHVSFKPSLDQQR
1.7	1937.062180	-0.009684	LLDAKSLGLKVFEDYAR

Mascot: http://www.matrixscience.com/

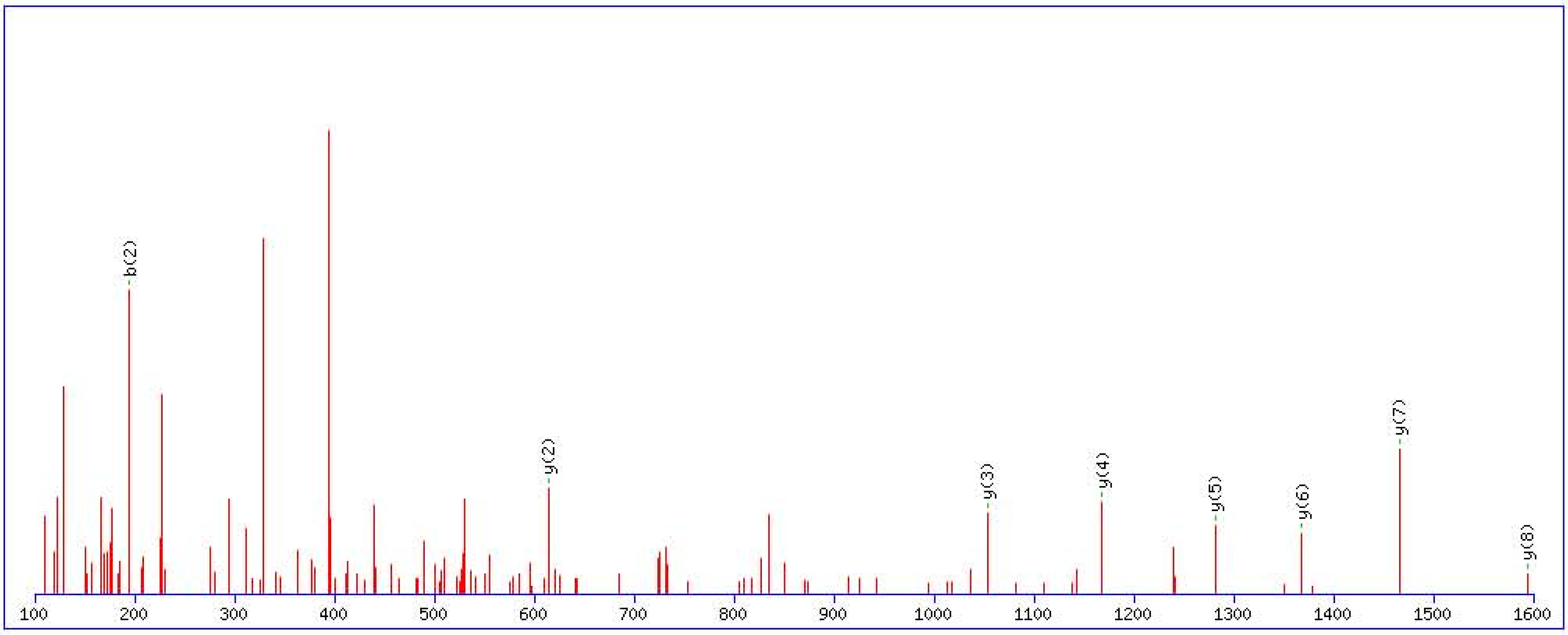
{MATRIX SCIENCE} Mascot Search Results

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

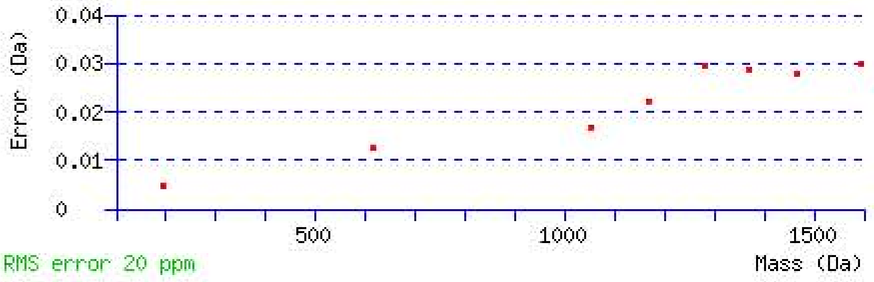
Match to Query 53497: 2120.129616 from(531.039680,4+) rtinseconds(1869) index(59758)
Title: Locus:1.1.1.3074.12 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

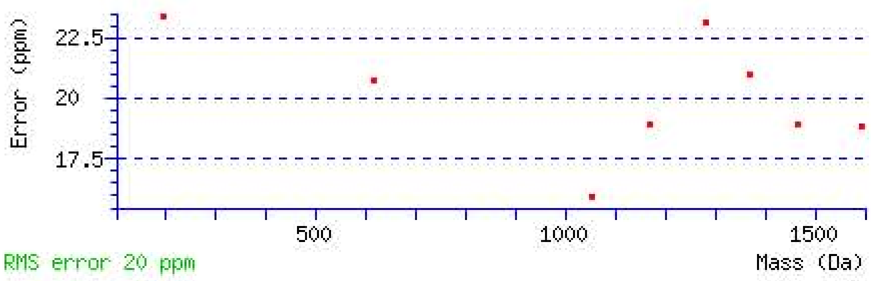
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 33  Expect: 0.013
Matches : 8/122 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	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
32.7	2120.102325	0.027291	GHVSFKPSLDQQR

Mascot: http://www.matrixscience.com/

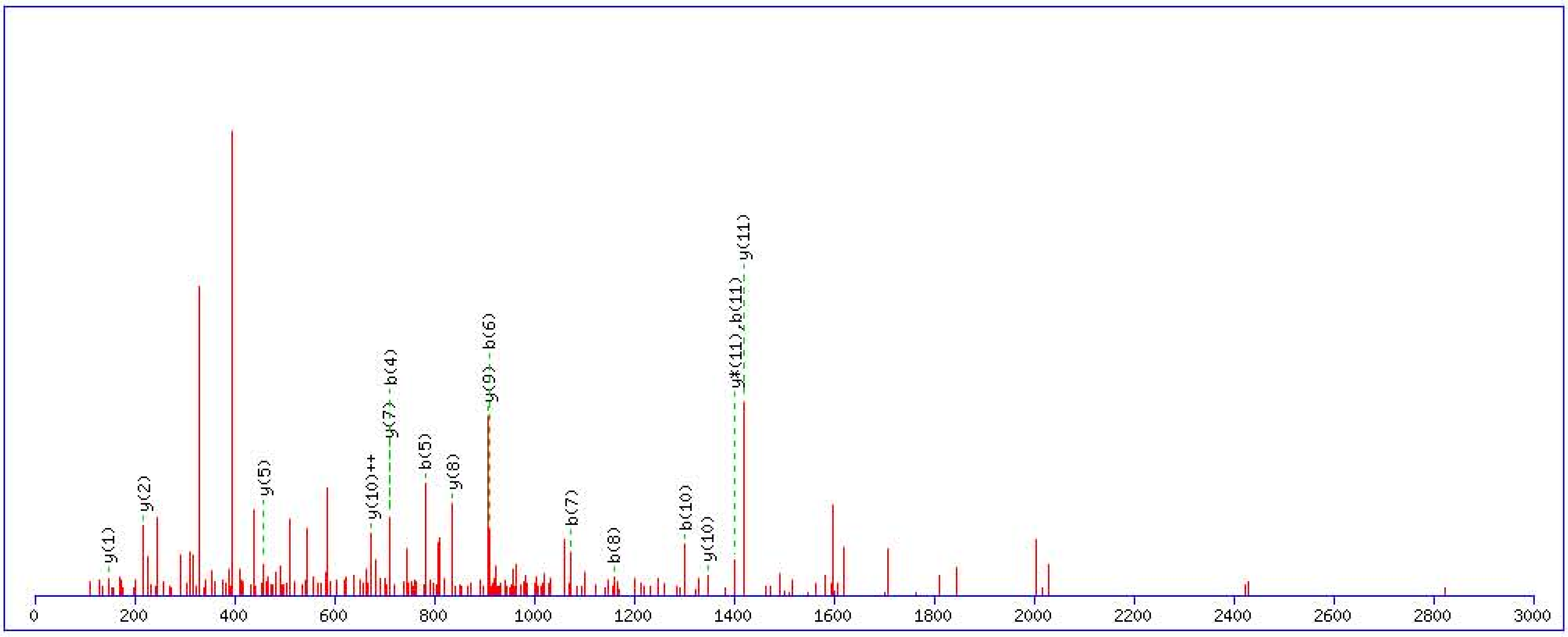
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEAQAQYSAAVAK**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

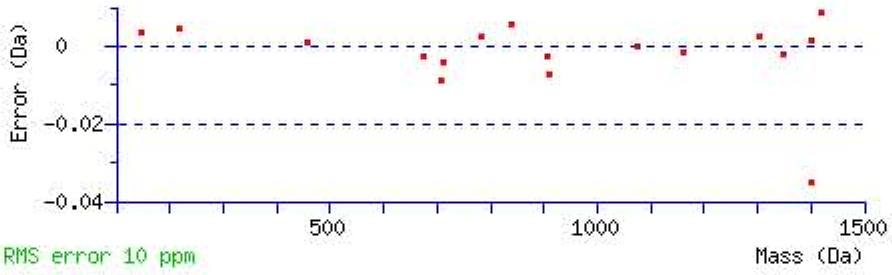
Match to Query 39577: 1617.817928 from(809.916240,2+) rtinseconds(1575) index(21574)
Title: Locus:1.1.1.2691.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

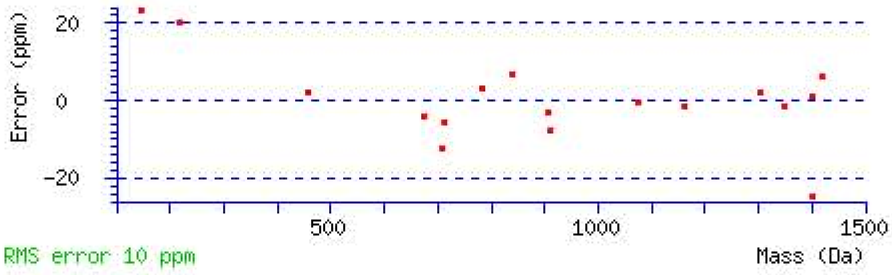
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1617.818436
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.0003
Matches : 17/126 fragment ions using 30 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							13
2	201.086983	101.047130			183.076418	92.041847	E	1547.788642	774.397959	1530.762093	765.884685	1529.778077	765.392677	12
3	272.124097	136.565687			254.113532	127.560404	A	***1418.746049***	709.876663	1401.719500	701.363388	1400.735484	700.871380	11
4	***711.349423***	356.178350	694.322874	347.665075	693.338858	347.173067	Q	***1347.708935***	674.358106	1330.682386	665.844831	1329.698370	665.352823	10
5	***782.386537***	391.696907	765.359988	383.183632	764.375972	382.691624	A	***908.483609***	454.745443	891.457060	446.232168	890.473044	445.740160	9
6	***910.445115***	455.726196	893.418566	447.212921	892.434550	446.720913	Q	***837.446495***	419.226886	820.419946	410.713611	819.435930	410.221603	8
7	***1073.508444***	537.257860	1056.481895	528.744586	1055.497879	528.252578	Y	***709.387917***	355.197597	692.361368	346.684322	691.377352	346.192314	7
8	***1160.540472***	580.773874	1143.513923	572.260600	1142.529907	571.768592	S	546.324588	273.665932	529.298039	265.152658	528.314023	264.660650	6
9	1231.577586	616.292431	1214.551037	607.779157	1213.567021	607.287149	A	***459.292560***	230.149918	442.266011	221.636643			5
10	***1302.614700***	651.810988	1285.588151	643.297714	1284.604135	642.805706	A	388.255446	194.631361	371.228897	186.118087			4
11	***1401.683114***	701.345195	1384.656565	692.831921	1383.672549	692.339913	V	317.218332	159.112804	300.191783	150.599530			3
12	1472.720228	736.863752	1455.693679	728.350478	1454.709663	727.858470	A	***218.149918***	109.578597	201.123369	101.065322			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AEAQAQYSAAVAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.4	1617.818436	-0.000508	AEAQAQYSAAVAK
37.3	1617.818436	-0.000508	AEAQAQYSAAVAK
12.1	1617.800690	0.017238	EAAQAIFPSMAR
6.2	1617.823639	-0.005711	GLHSWQKAAHGDRR
0.3	1617.800720	0.017208	TVAPMPPAQDHK

Mascot: http://www.matrixscience.com/

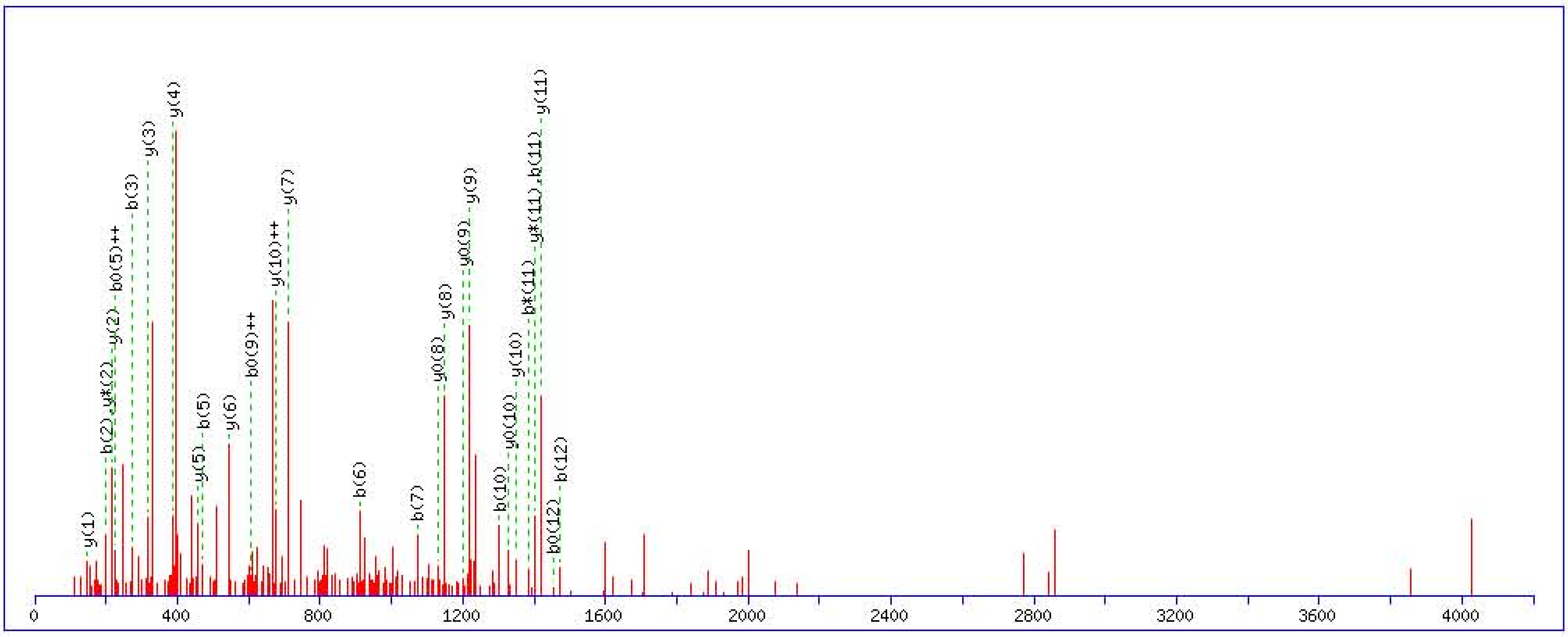
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEAQAQYSAAVAK**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

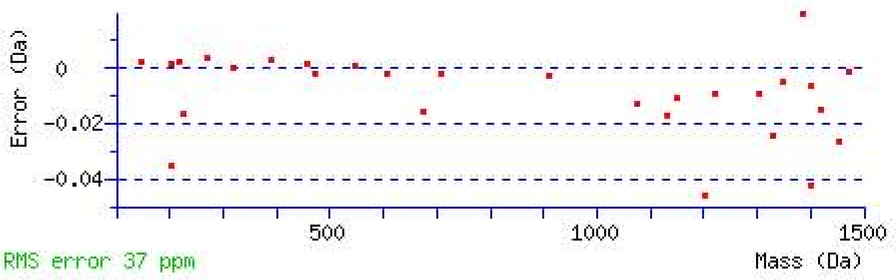
Match to Query 39579: 1617.821728 from(809.918140,2+) rtinseconds(1549) index(21393)
Title: Locus:1.1.1.2682.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

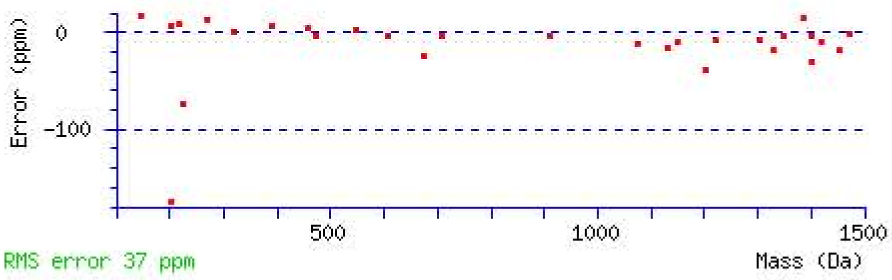


Monoisotopic mass of neutral peptide Mr(calc): 1617.818436
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 61 **Expect:** 1.3e-005
Matches : 29/126 fragment ions using 58 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							13
2	**201.086983**	101.047130			183.076418	92.041847	E	1547.788642	774.397959	1530.762093	765.884685	1529.778077	765.392677	12
3	**272.124097**	136.565687			254.113532	127.560404	A	***1418.746049***	709.876663	1401.719500	701.363388	1400.735484	700.871380	11
4	400.182675	200.594976	383.156126	192.081701	382.172110	191.589693	Q	***1347.708935***	674.358106	1330.682386	665.844831	1329.698370	665.352823	10
5	**471.219789**	236.113533	454.193240	227.600258	453.209224	227.108250	A	***1219.650357***	610.328817	1202.623808	601.815542	1201.639792	601.323534	9
6	**910.445115**	455.726196	893.418566	447.212921	892.434550	446.720913	Q	***1148.613243***	574.810260	1131.586694	566.296985	1130.602678	565.804977	8
7	**1073.508444**	537.257860	1056.481895	528.744586	1055.497879	528.252578	Y	***709.387917***	355.197597	692.361368	346.684322	691.377352	346.192314	7
8	1160.540472	580.773874	1143.513923	572.260600	1142.529907	571.768592	S	***546.324588***	273.665932	529.298039	265.152658	528.314023	264.660650	6
9	1231.577586	616.292431	1214.551037	607.779157	1213.567021	607.287149	A	***459.292560***	230.149918	442.266011	221.636643			5
10	**1302.614700**	651.810988	1285.588151	643.297714	1284.604135	642.805706	A	***388.255446***	194.631361	371.228897	186.118087			4
11	**1401.683114**	701.345195	1384.656565	692.831921	1383.672549	692.339913	V	***317.218332***	159.112804	300.191783	150.599530			3
12	**1472.720228**	736.863752	1455.693679	728.350478	1454.709663	727.858470	A	***218.149918***	109.578597	201.123369	101.065322			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 37 ppm



RMS error 37 ppm

NCBI **BLAST** search of AEAQAQYSAAVAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.1	1617.818436	0.003292	AEAQAQYSAAVAK
36.5	1617.818436	0.003292	AEAQAQYSAAVAK
8.6	1617.829681	-0.007953	NDVMIRKEAYVHK
3.8	1617.823166	-0.001438	QLRLHNDMHK
3.7	1617.843613	-0.021885	SLMESPFPAPGKTIK
2.7	1617.800720	0.021008	TVAPMPPAQDHK

Mascot: http://www.matrixscience.com/

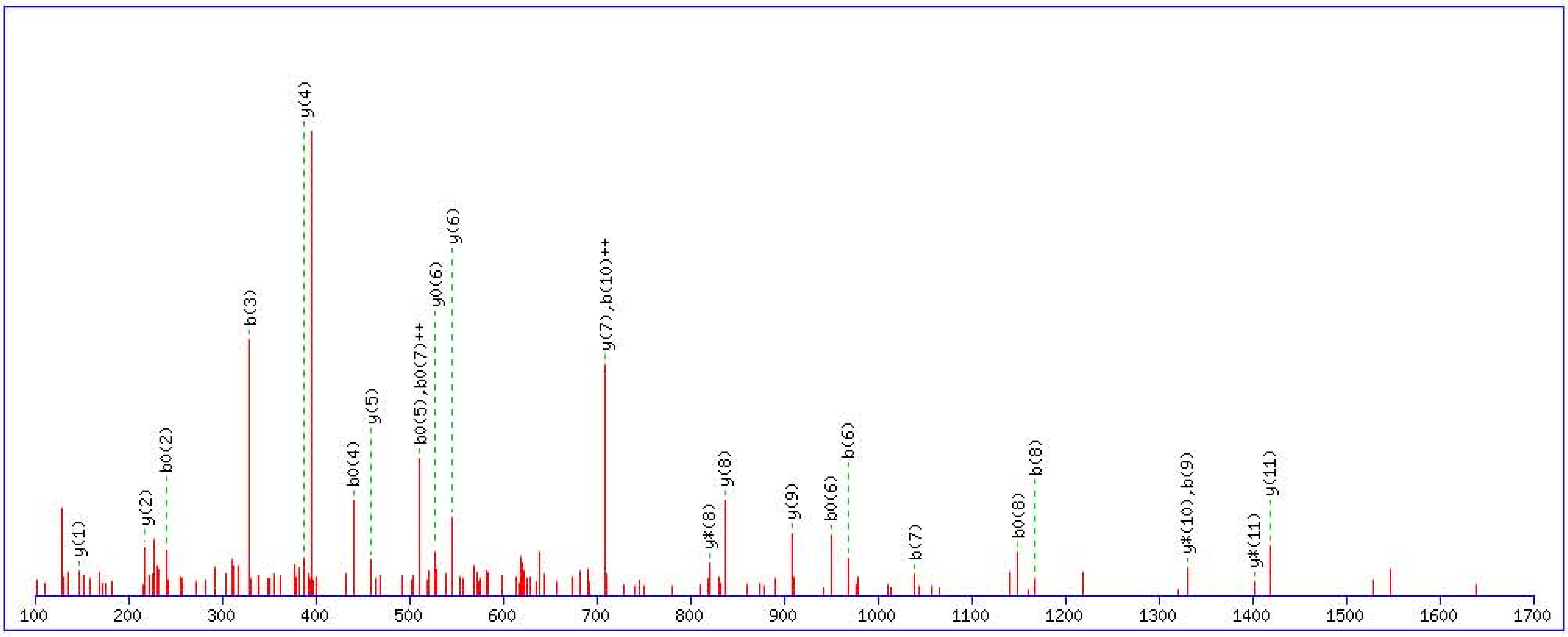
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EKAEAQAQYSAAVAK**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

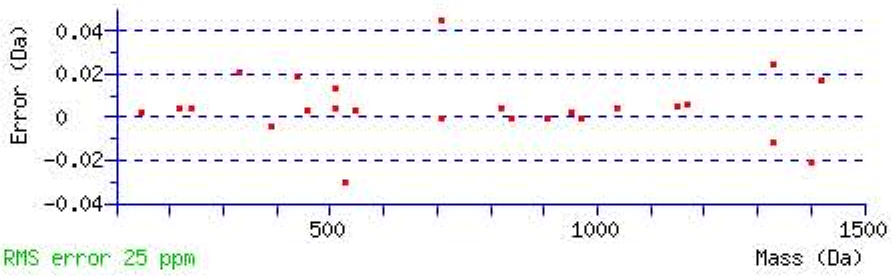
Match to Query 47085: 1874.960712 from(625.994180,3+) rtinseconds(1464) index(20728)
Title: Locus:1.1.1.2652.24 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

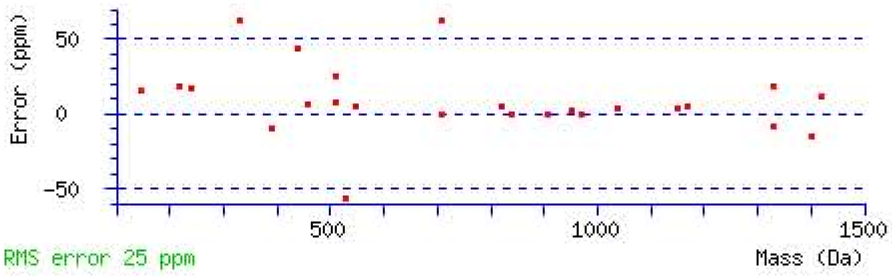
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1874.955978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 0.00013
Matches : 25/156 fragment ions using 41 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							15
2	258.144832	129.576054	241.118283	121.062780	240.134267	120.570772	K	1746.920719	873.963998	1729.894170	865.450723	1728.910154	864.958715	14
3	**329.181946**	165.094611	312.155397	156.581336	311.171381	156.089328	A	1618.825756	809.916516	1601.799207	801.403242	1600.815191	800.911233	13
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	E	1547.788642	774.397959	1530.762093	765.884685	1529.778077	765.392677	12
5	529.261653	265.134465	512.235104	256.621190	511.251088	256.129182	A	***1418.746049***	709.876663	1401.719500	701.363388	1400.735484	700.871380	11
6	**968.486979**	484.747128	951.460430	476.233853	950.476414	475.741845	Q	1347.708935	674.358106	1330.682386	665.844831	1329.698370	665.352823	10
7	**1039.524093**	520.265685	1022.497544	511.752410	1021.513528	511.260402	A	***908.483609***	454.745443	891.457060	446.232168	890.473044	445.740160	9
8	**1167.582671**	584.294973	1150.556122	575.781699	1149.572106	575.289691	Q	***837.446495***	419.226886	820.419946	410.713611	819.435930	410.221603	8
9	**1330.646000**	665.826638	1313.619451	657.313364	1312.635435	656.821355	Y	***709.387917***	355.197597	692.361368	346.684322	691.377352	346.192314	7
10	1417.678028	709.342652	1400.651479	700.829378	1399.667463	700.337370	S	***546.324588***	273.665932	529.298039	265.152658	528.314023	264.660650	6
11	1488.715142	744.861209	1471.688593	736.347935	1470.704577	735.855927	A	***459.292560***	230.149918	442.266011	221.636643			5
12	1559.752256	780.379766	1542.725707	771.866492	1541.741691	771.374484	A	***388.255446***	194.631361	371.228897	186.118087			4
13	1658.820670	829.913973	1641.794121	821.400699	1640.810105	820.908691	V	317.218332	159.112804	300.191783	150.599530			3
14	1729.857784	865.432530	1712.831235	856.919256	1711.847219	856.427248	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 EKAEAQAQYSAAVAK
(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	1874.955978	0.004734	EKAEAQAQYSAAVAK
39.3	1874.955978	0.004734	EKAEAQAQYSAAVAK
7.2	1874.940750	0.019962	LRSKGPATVEEMPSETK
4.7	1874.964783	-0.004071	AQQHWGSGVGVK

Mascot: http://www.matrixscience.com/

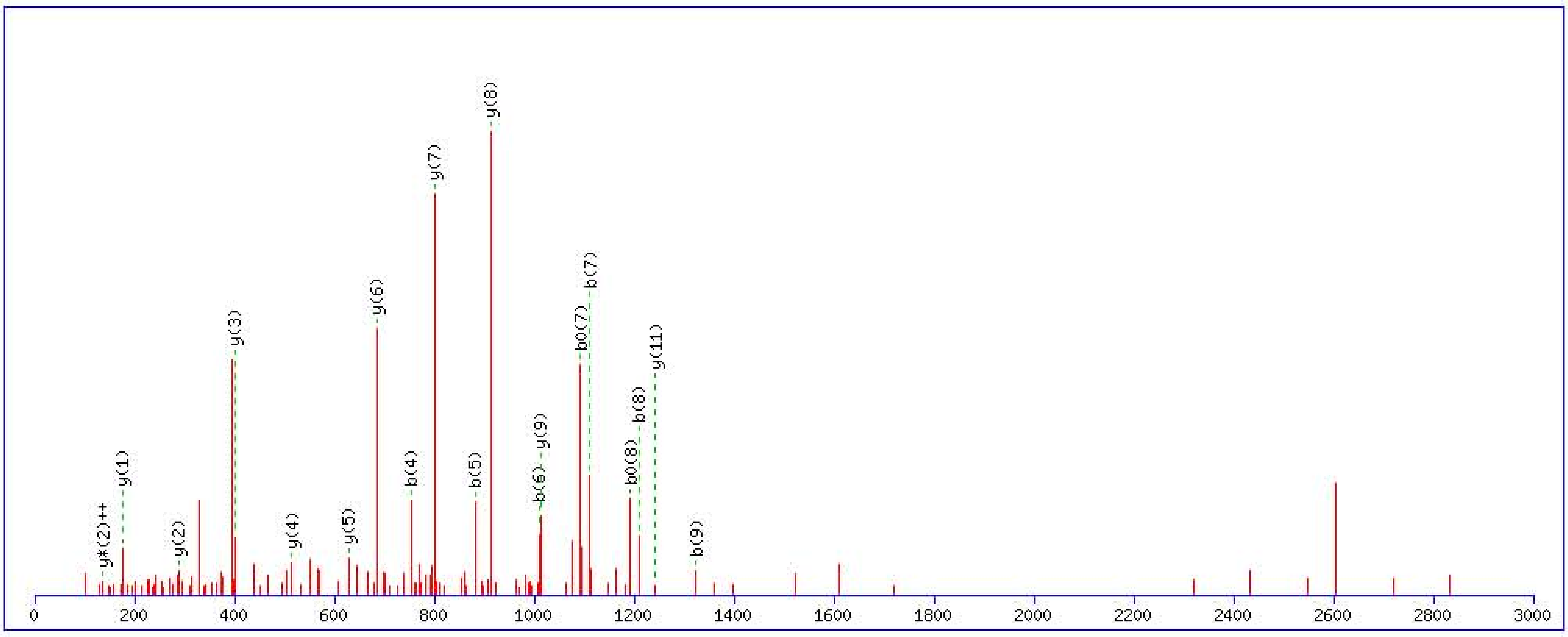
{MATRIX SCIENCE} Mascot Search Results

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

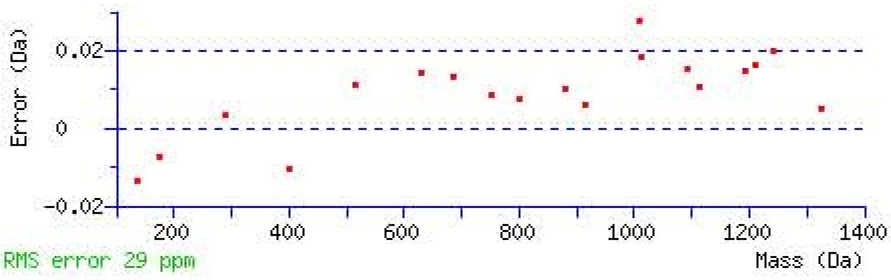
Match to Query 53547: 2122.134432 from(708.385420,3+) rtinseconds(2344) index(8817)
Title: Locus:1.1.1.3070.17 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

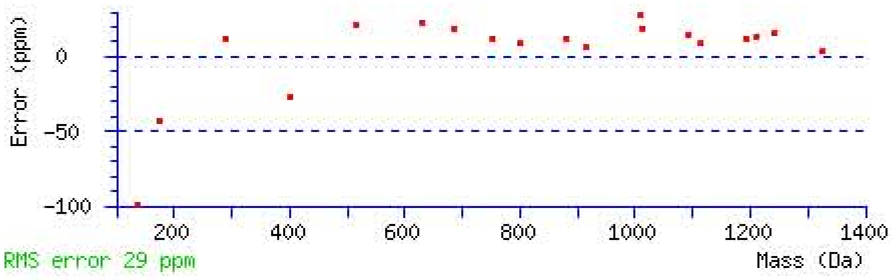
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 48  Expect: 5.4e-005
Matches : 19/162 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	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
47.8	2122.109222	0.025210	SPEQQETVLDGNLIIR
46.0	2122.109222	0.025210	SPEQQETVLDGNLIIR
2.2	2122.156799	-0.022367	AERAALEELVKLQGER
1.6	2122.139053	-0.004621	RRVYDALNVLMAMNIISK
1.6	2122.139053	-0.004621	RRVYDALNVLMAMNIISK
0.6	2122.143112	-0.008680	LYQFLLGLLTRGDMR

Mascot: http://www.matrixscience.com/

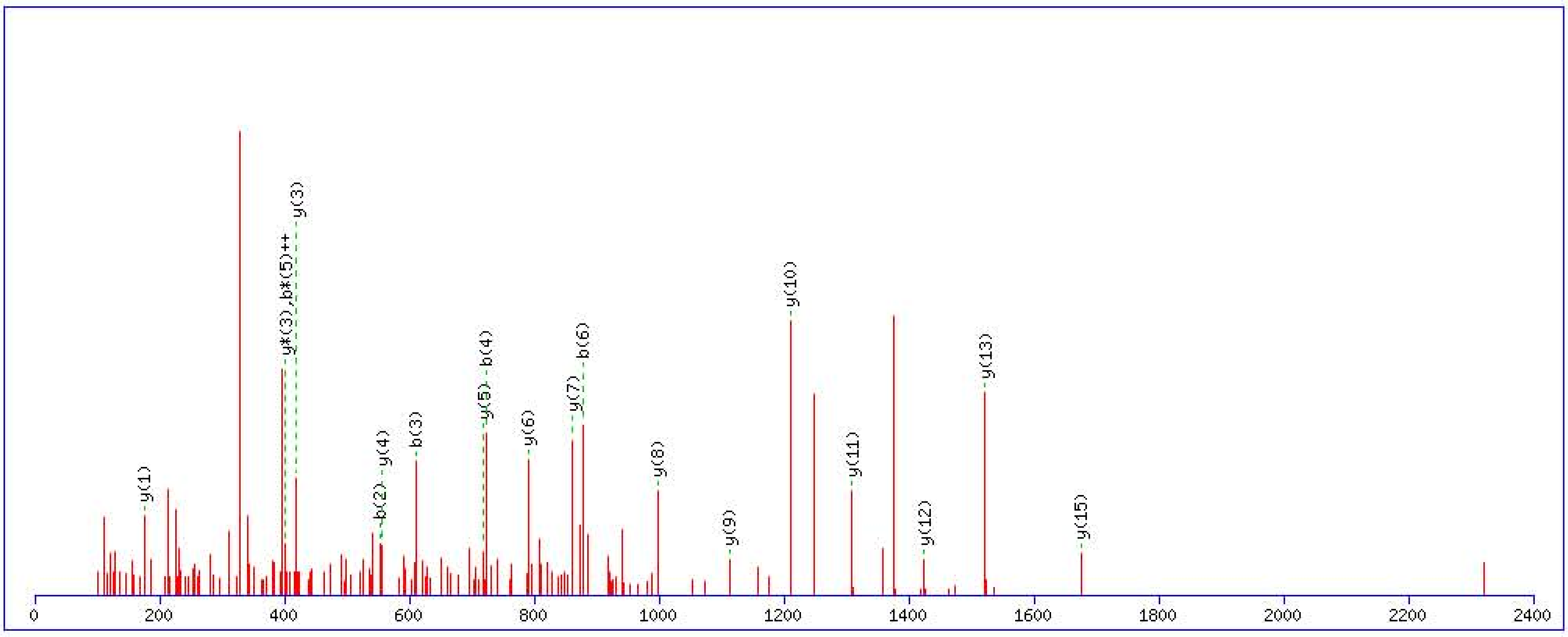
Mascot Search Results

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

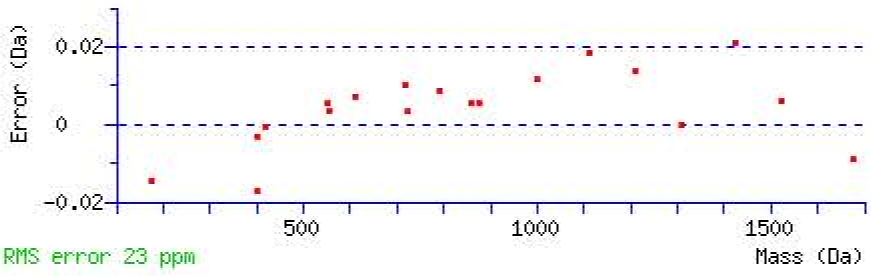
Match to Query 62930: 2494.264936 from(624.573510,4+) rtinseconds(2142) index(25685)
Title: Locus:1.1.1.2888.13 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

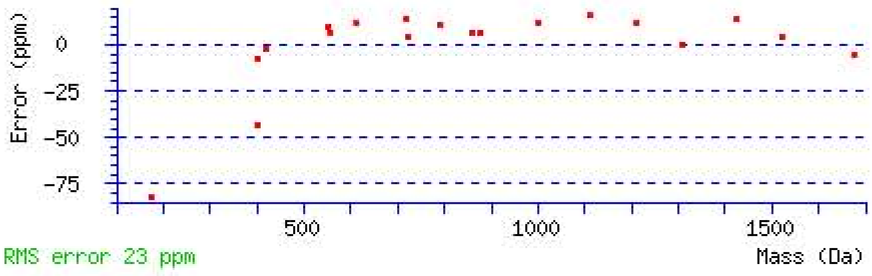
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2494.257980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1.7e-005
Matches : 19/196 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	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
62.2	2494.257980	0.006956	QLGLPGPPDVPDHAAYHPFR

Mascot: http://www.matrixscience.com/

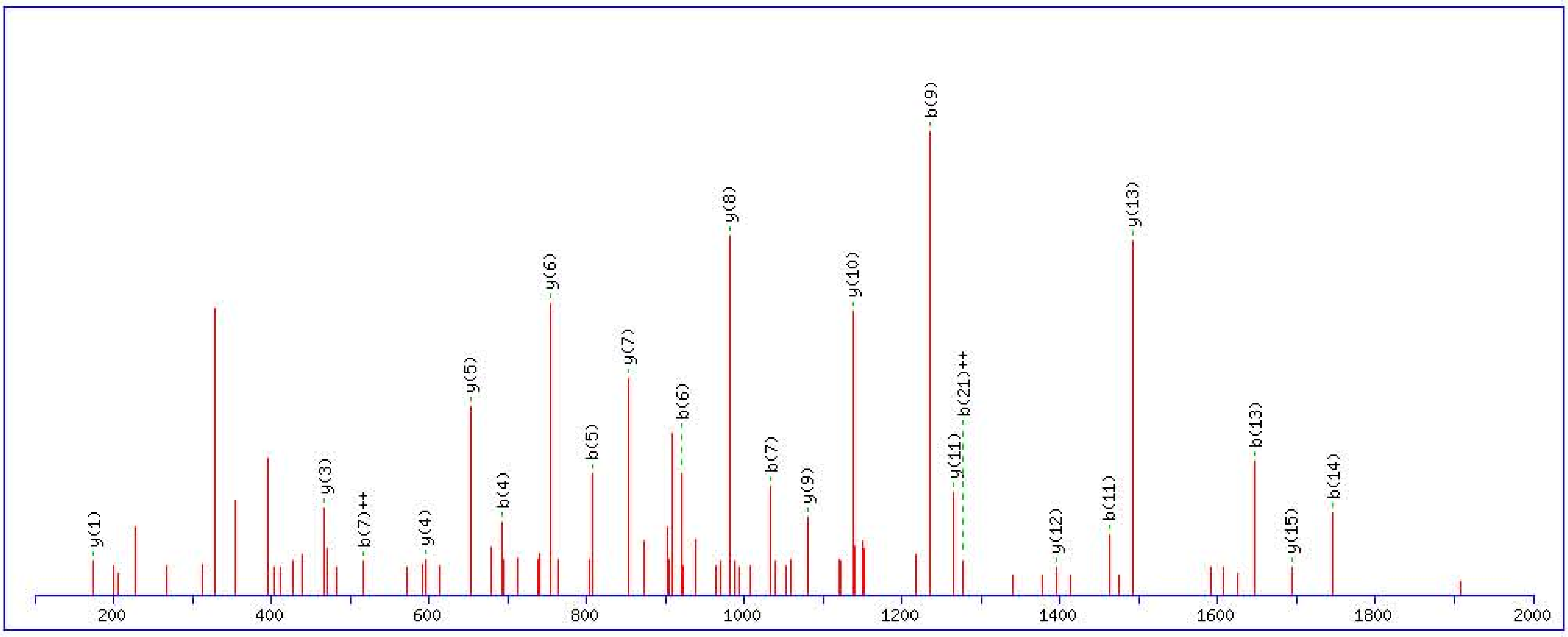
Mascot Search Results

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

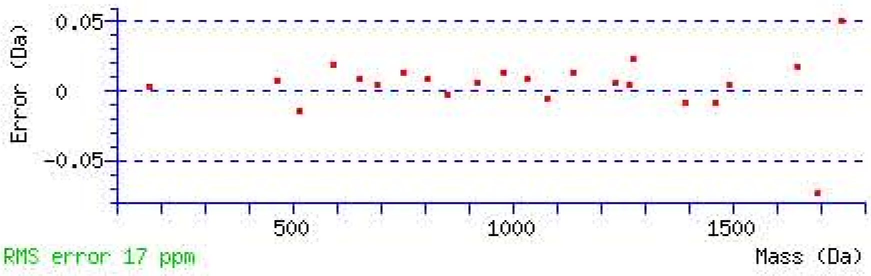
Match to Query 66071: 2725.359252 from(909.460360,3+) rtinseconds(2367) index(81389)
Title: Locus:1.1.1.2174.23 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

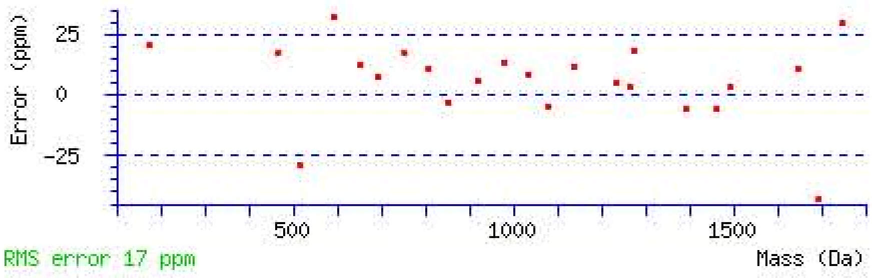
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 98  Expect: 4.6e-009
Matches : 23/236 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	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
98.0	2725.338135	0.021117	QGPVNLLSDPEQGVEVTGQYER
31.5	2725.338135	0.021117	QGPVNLLSDPEQGVEVTGQYER

Mascot: http://www.matrixscience.com/

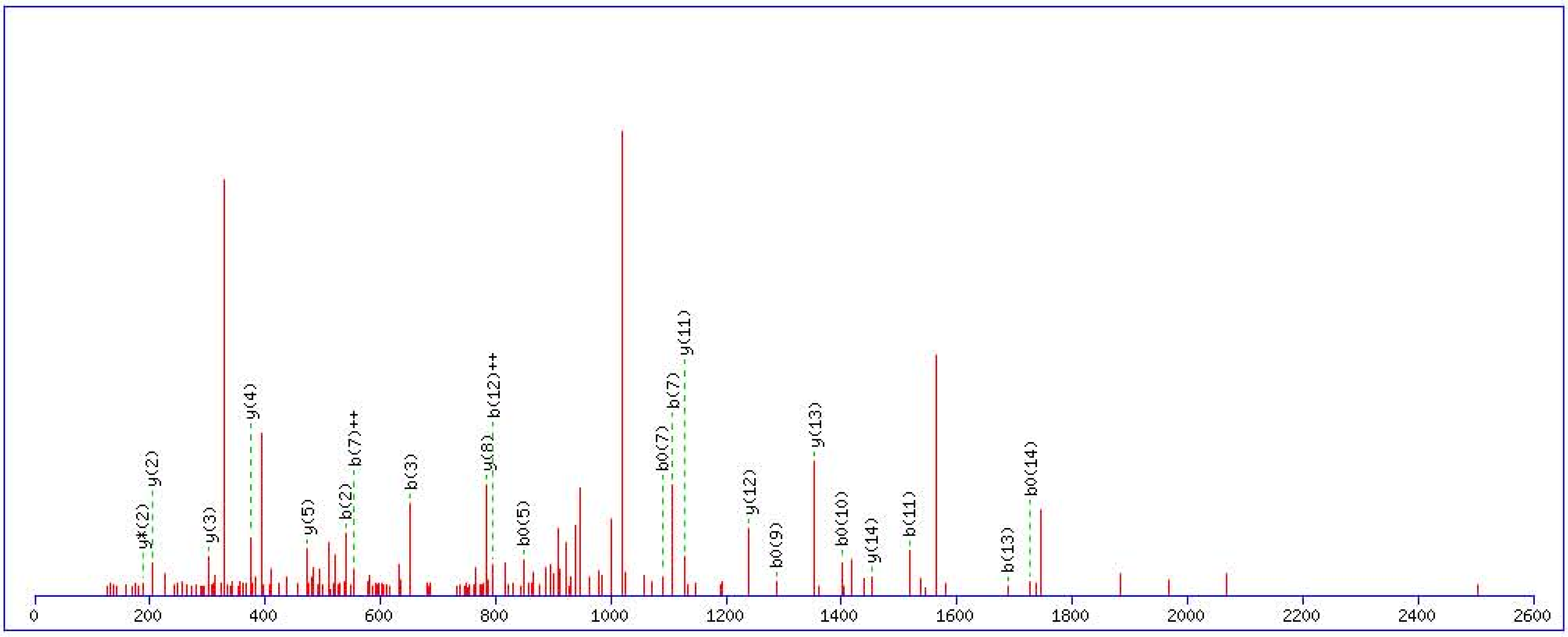
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVILTLQPTLVAVGK**
Found in **ICAM2_HUMAN**, Intercellular adhesion molecule 2 OS=Homo sapiens GN=ICAM2 PE=1 SV=2

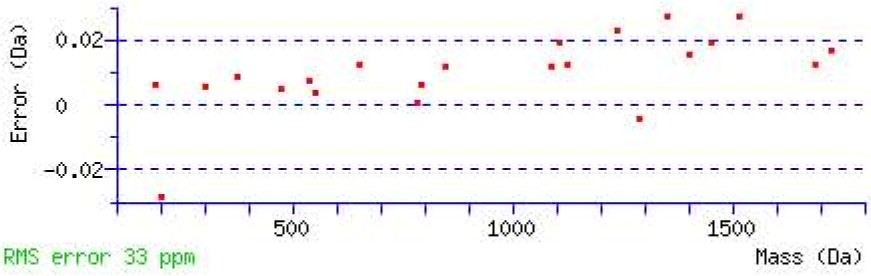
Match to Query 47323: 1890.158728 from(946.086640,2+) rtinseconds(2618) index(10440)
Title: Locus:1.1.1.3165.8 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

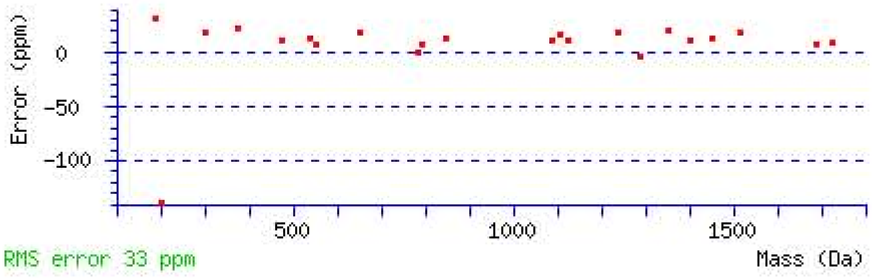
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1890.137634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.00019
Matches : 22/148 fragment ions using 49 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							15
2	**539.301016**	270.154146	522.274467	261.640872			V	***1451.919580***	726.463428	1434.893031	717.950154	1433.909015	717.458146	14
3	**652.385080**	326.696178	635.358531	318.182904			I	***1352.851166***	676.929221	1335.824617	668.415947	1334.840601	667.923939	13
4	765.469144	383.238210	748.442595	374.724936			L	***1239.767102***	620.387189	1222.740553	611.873915	1221.756537	611.381907	12
5	866.516823	433.762050	849.490274	425.248775	848.506258	424.756767	T	***1126.683038***	563.845157	1109.656489	555.331883	1108.672473	554.839874	11
6	979.600887	490.304082	962.574338	481.790807	961.590322	481.298799	L	1025.635359	513.321318	1008.608810	504.808043	1007.624794	504.316035	10
7	**1107.659465**	**554.333371**	1090.632916	545.820096	1089.648900	545.328088	Q	912.551295	456.779286	895.524746	448.266011	894.540730	447.774003	9
8	1204.712229	602.859753	1187.685680	594.346478	1186.701664	593.854470	P	***784.492717***	392.749997	767.466168	384.236722	766.482152	383.744714	8
9	1305.759908	653.383592	1288.733359	644.870318	1287.749343	644.378310	T	687.439953	344.223615	670.413404	335.710340	669.429388	335.218332	7
10	1418.843972	709.925624	1401.817423	701.412350	1400.833407	700.920341	L	586.392274	293.699775	569.365725	285.186501			6
11	**1517.912386**	759.459831	1500.885837	750.946557	1499.901821	750.454548	V	***473.308210***	237.157743	456.281661	228.644469			5
12	1588.949500	**794.978388**	1571.922951	786.465114	1570.938935	785.973105	A	***374.239796***	187.623536	357.213247	179.110261			4
13	**1688.017914**	844.512595	1670.991365	835.999321	1670.007349	835.507313	V	***303.202682***	152.104979	286.176133	143.591704			3
14	1745.039378	873.023327	1728.012829	864.510053	1727.028813	864.018044	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 QVILTLQPTLVAVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.3	1890.137634	0.021094	QVILTLQPTLVAVGK
5.8	1890.137634	0.021094	QVILTLQPTLVAVGK

Mascot: http://www.matrixscience.com/

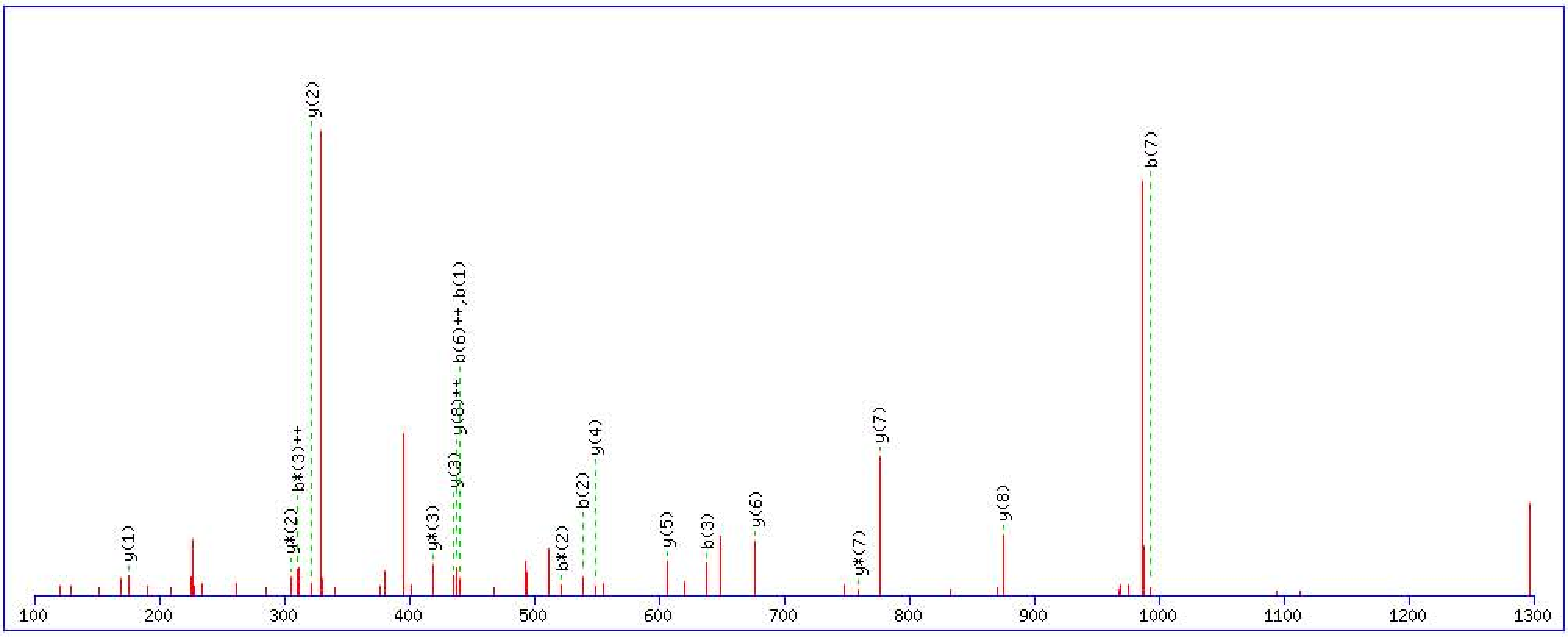
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVVAGLNFR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

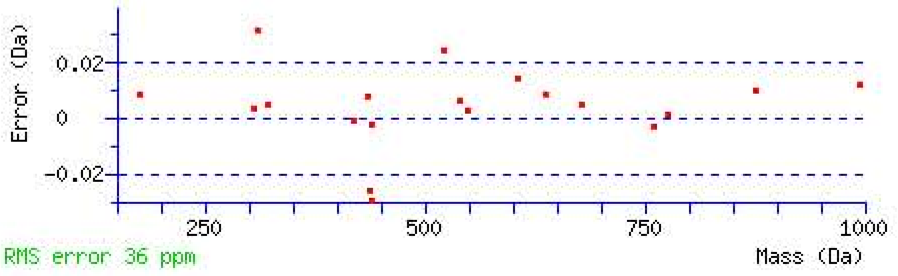
Match to Query 27240: 1313.740728 from(657.877640,2+) rtinseconds(2195) index(43589)
Title: Locus:1.1.1.3213.8 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

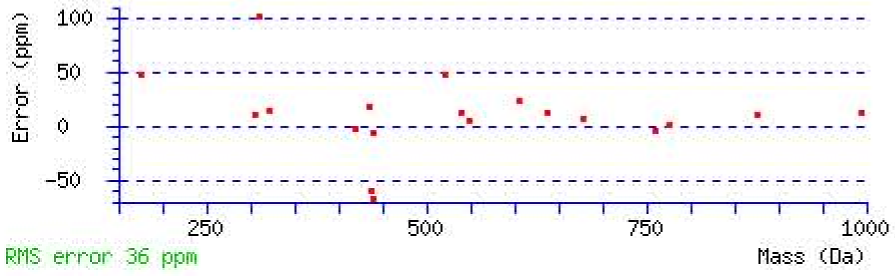
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1313.727814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0064
Matches : 19/64 fragment ions using 50 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	**440.232602**	220.619939	423.206053	212.106664	Q					9
2	**539.301016**	270.154146	522.274467	261.640872	V	***875.509763***	438.258520	858.483214	429.745245	8
3	**638.369430**	319.688353	621.342881	311.175078	V	***776.441349***	388.724313	759.414800	380.211038	7
4	709.406544	355.206910	692.379995	346.693635	A	***677.372935***	339.190106	660.346386	330.676831	6
5	766.428008	383.717642	749.401459	375.204367	G	***606.335821***	303.671549	589.309272	295.158274	5
6	879.512072	440.259674	862.485523	431.746400	L	***549.314357***	275.160817	532.287808	266.647542	4
7	**993.554999**	497.281138	976.528450	488.767863	N	***436.230293***	218.618784	419.203744	210.105510	3
8	1140.623413	570.815345	1123.596864	562.302070	F	***322.187366***	161.597321	305.160817	153.084047	2
9					R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of QVVAGLNFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.3	1313.727814	0.012914	QVVAGLNFR
11.2	1313.756805	-0.016077	KTVTHQFAVKR
3.1	1313.723755	0.016973	SSVKHRLAAMSK
3.0	1313.730286	0.010442	AKEDVLQKEVR
3.0	1313.731644	0.009084	GEPPPPVRRPGR
3.0	1313.745575	-0.004847	GSLALQPFLVGGR
3.0	1313.727798	0.012930	KSLSVWQR
3.0	1313.730301	0.010427	LSQTLQVQLER
3.0	1313.741516	-0.000788	NLTRLDLSLNR
3.0	1313.730286	0.010442	QVTKEEGLALAR

Mascot: http://www.matrixscience.com/

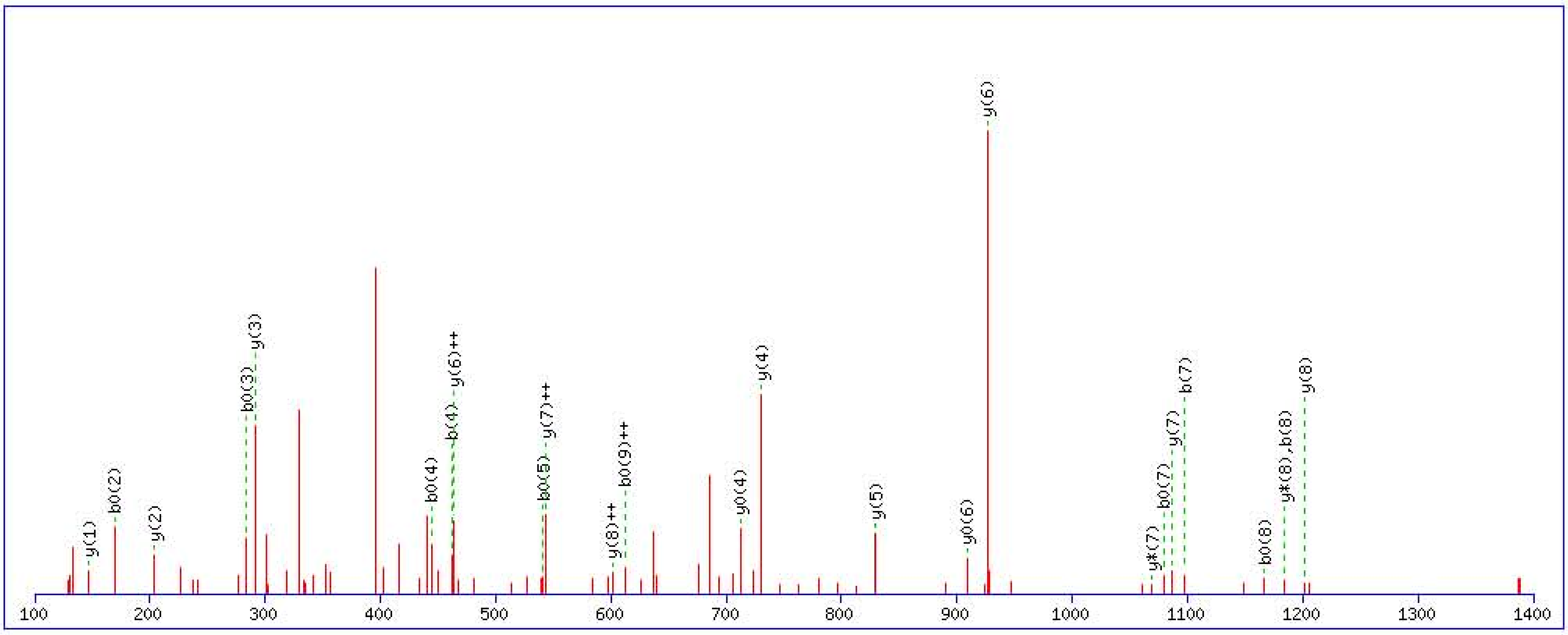
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGDCPVQSGK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

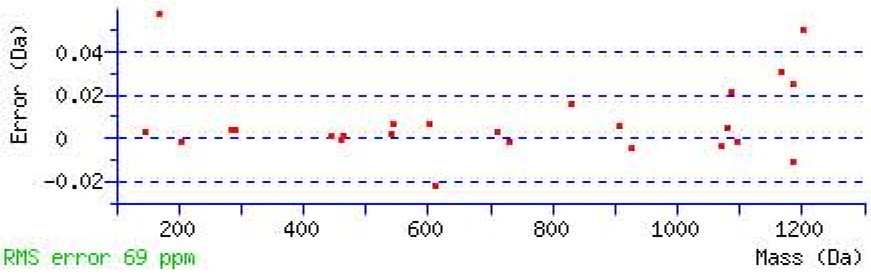
Match to Query 30115: 1386.631888 from(694.323220,2+) rtinseconds(1354) index(19900)
Title: Locus:1.1.1.2614.22 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

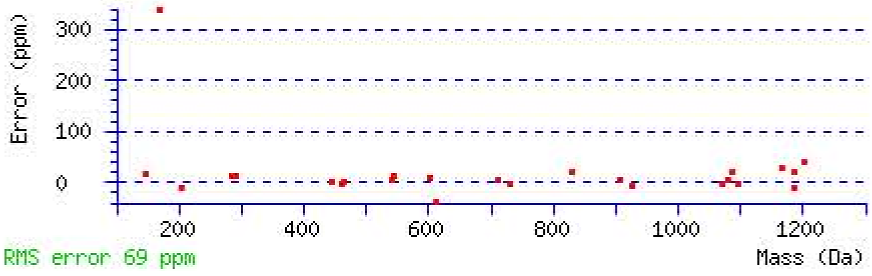
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 42  Expect: 0.00048
Matches : 25/92 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	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
42.3	1386.627182	0.004706	EGDCPVQSGK

Mascot: http://www.matrixscience.com/

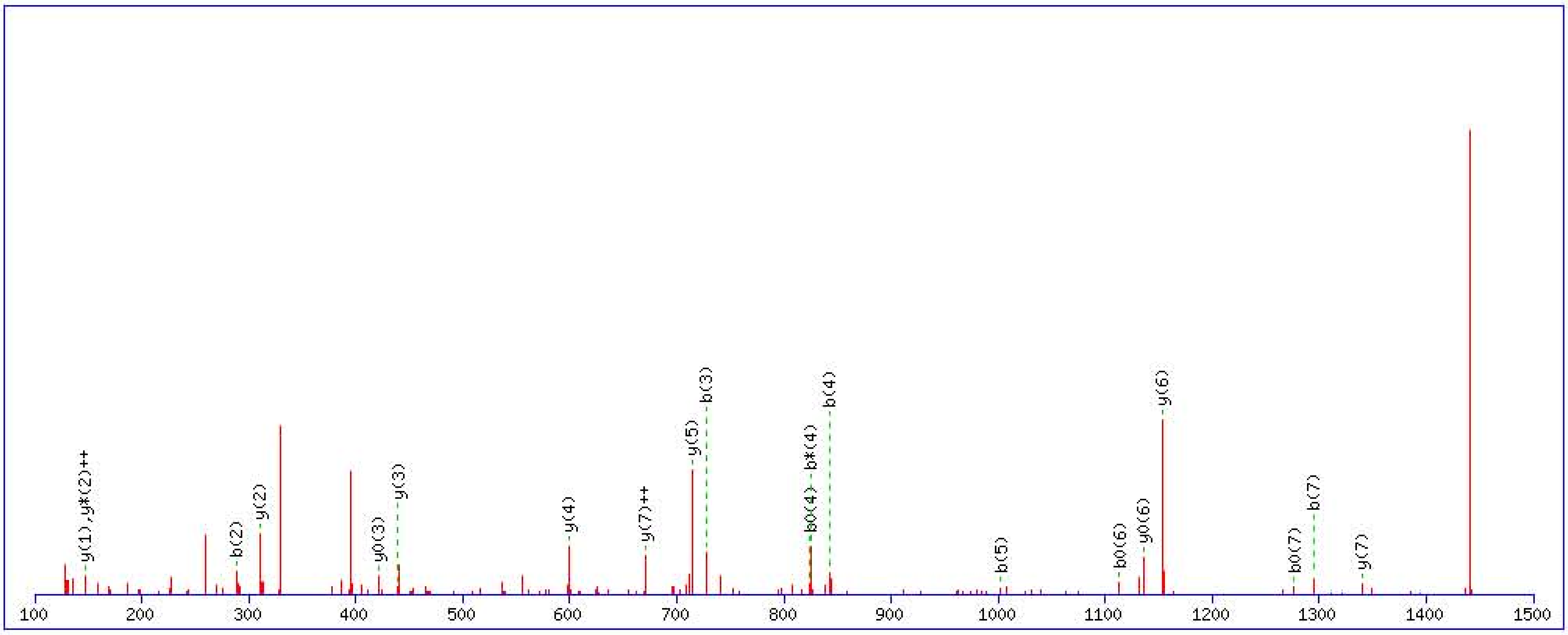
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TWQDCEYK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

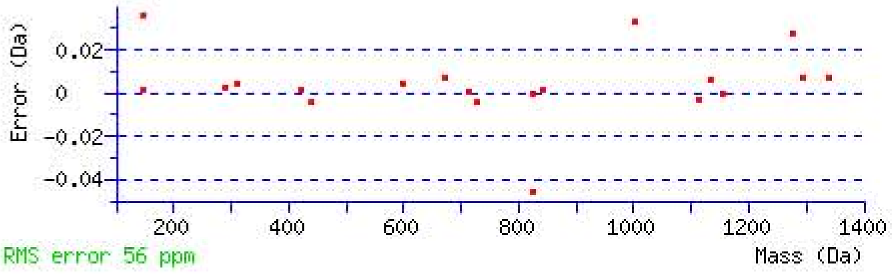
Match to Query 32988: 1439.626908 from(720.820730,2+) rtinseconds(1745) index(22830)
Title: Locus:1.1.1.2750.15 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

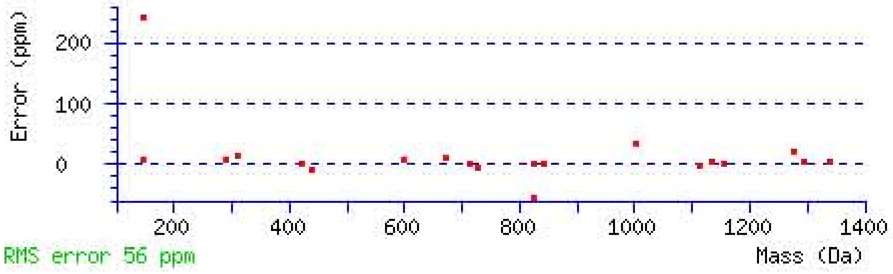
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1439.621353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.0029
Matches : 20/76 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	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
31.9	1439.621353	0.005555	TWQDCEYK

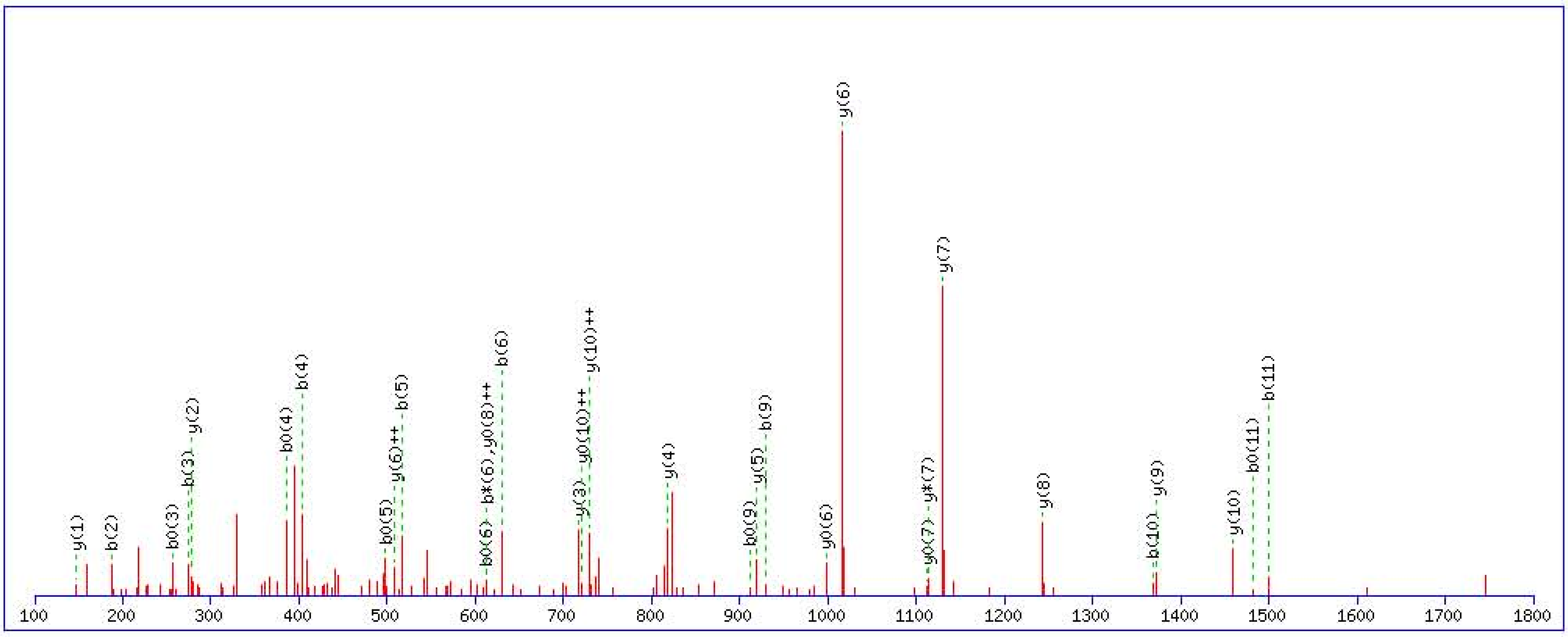
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVSEINPTTQMK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

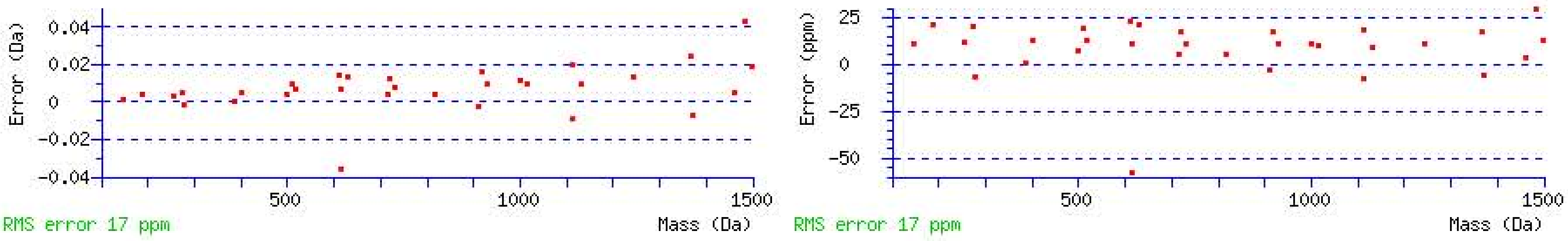
Match to Query 41042: 1644.843568 from(823.429060,2+) rtinseconds(1829) index(40936)
Title: Locus:1.1.1.3086.14 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1644.821503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 1.5e-005
Matches : 32/116 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	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
60.2	1644.821503	0.022065	SVSEINPTTQMK
8.3	1644.861710	-0.018142	VRESSCLALNDLLR
4.3	1644.850510	-0.006942	TDGIPVSGTICAKQAK
2.9	1644.854523	-0.010955	CVWSPLASPSTSILK
1.3	1644.840607	0.002961	ESGRQFCIAVTHLK
0.2	1644.861710	-0.018142	QRETSDTPIMRALK

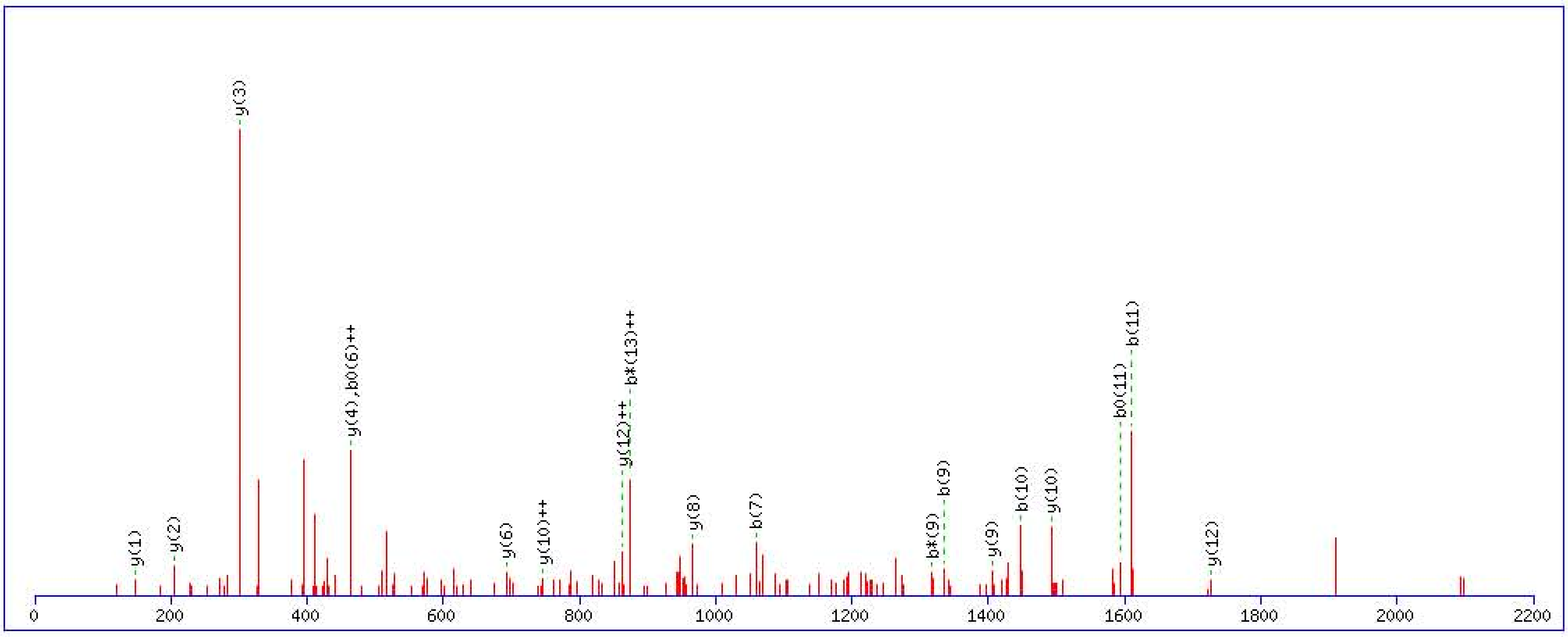
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IASFSQNCDIYPGK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

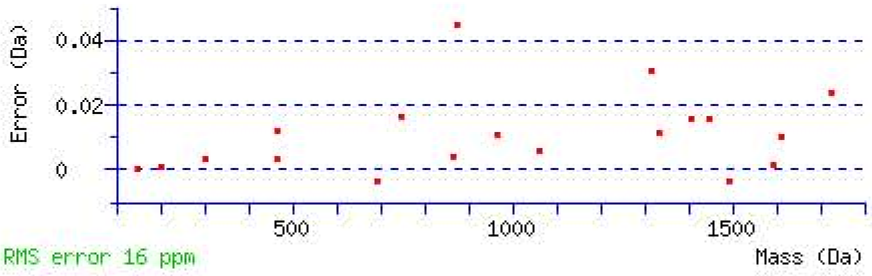
Match to Query 47783: 1909.924788 from(955.969670,2+) rtinseconds(2042) index(24997)
Title: Locus:1.1.1.2853.18 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

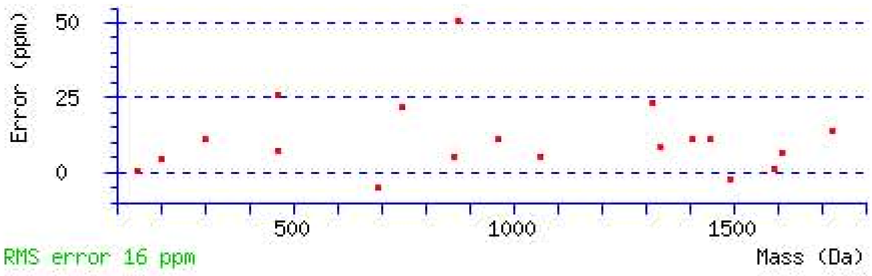
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1909.906631
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 8.3e-005
Matches : 19/132 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							14
2	185.128454	93.067865					A	1797.829854	899.418565	1780.803305	890.905291	1779.819289	890.413283	13
3	272.160482	136.583879			254.149917	127.578596	S	***1726.792740***	863.900008	1709.766191	855.386734	1708.782175	854.894726	12
4	419.228896	210.118086			401.218331	201.112803	F	1639.760712	820.383994	1622.734163	811.870720	1621.750147	811.378712	11
5	506.260924	253.634100			488.250359	244.628817	S	***1492.692298***	746.849787	1475.665749	738.336513	1474.681733	737.844505	10
6	945.486250	473.246763	928.459701	464.733488	927.475685	464.241480	Q	***1405.660270***	703.333773	1388.633721	694.820499	1387.649705	694.328491	9
7	**1059.529177**	530.268226	1042.502628	521.754952	1041.518612	521.262944	N	***966.434944***	483.721110	949.408395	475.207836	948.424379	474.715828	8
8	1219.559826	610.283551	1202.533277	601.770277	1201.549261	601.278268	C	852.392017	426.699647	835.365468	418.186372	834.381452	417.694364	7
9	**1334.586769**	667.797023	1317.560220	659.283748	1316.576204	658.791740	D	***692.361368***	346.684322	675.334819	338.171048	674.350803	337.679040	6
10	**1447.670833**	724.339054	1430.644284	715.825780	1429.660268	715.333772	I	577.334425	289.170851	560.307876	280.657576			5
11	**1610.734162**	805.870719	1593.707613	797.357445	1592.723597	796.865436	Y	***464.250361***	232.628818	447.223812	224.115544			4
12	1707.786926	854.397101	1690.760377	845.883827	1689.776361	845.391819	P	***301.187032***	151.097154	284.160483	142.583879			3
13	1764.808390	882.907833	1747.781841	874.394559	1746.797825	873.902550	G	***204.134268***	102.570772	187.107719	94.057497			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IASFSQNCDIYPGK
(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	1909.906631	0.018157	IASFSQNCDIYPGK

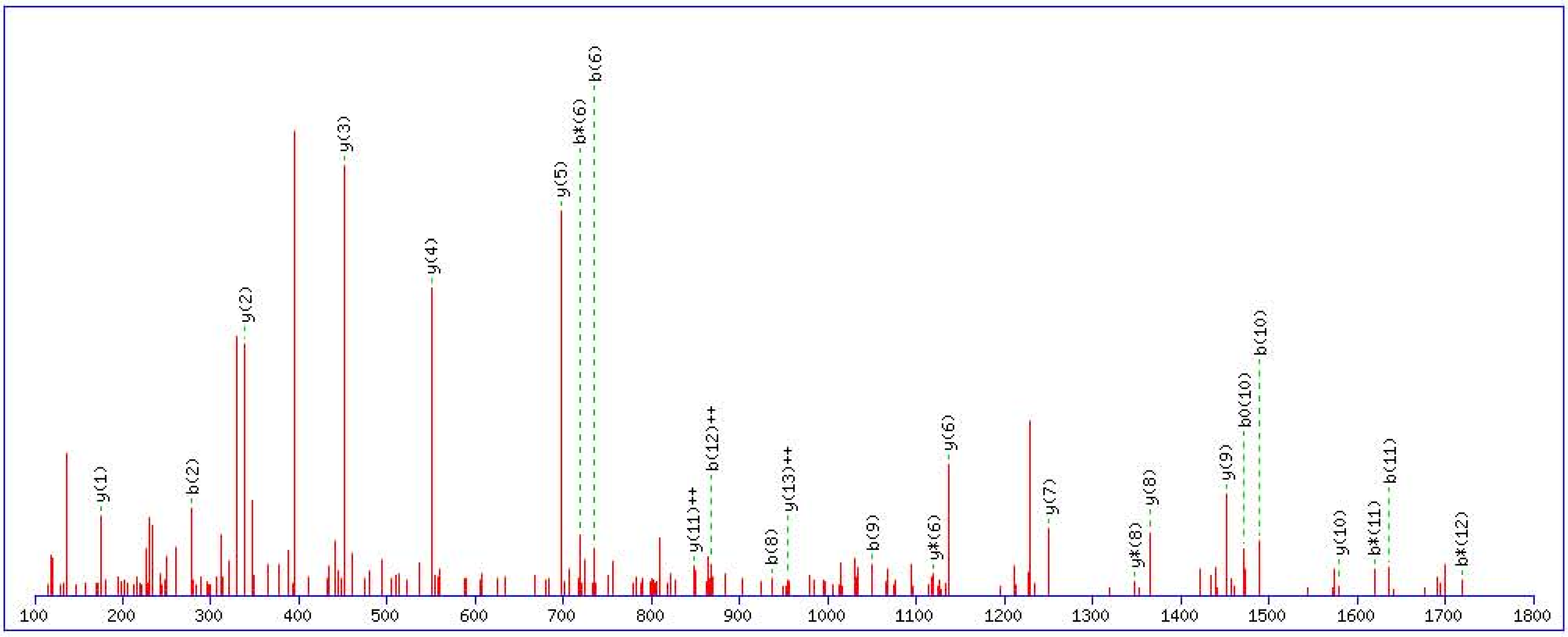
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

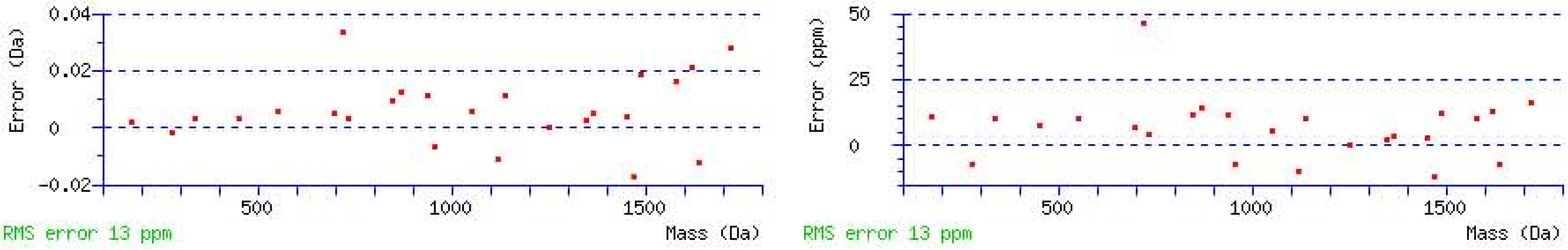
Match to Query 55039: 2185.057692 from(729.359840,3+) rtinseconds(2099) index(25392)
Title: Locus:1.1.1.2873.16 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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: 48 **Expect:** 0.00034
Matches : 25/146 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	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
47.8	2185.037445	0.020247	YNSQNQSNNQFVLYR
10.8	2185.037445	0.020247	YNSQNQSNNQFVLYR
7.1	2185.037445	0.020247	YNSQNQSNNQFVLYR

Mascot: http://www.matrixscience.com/

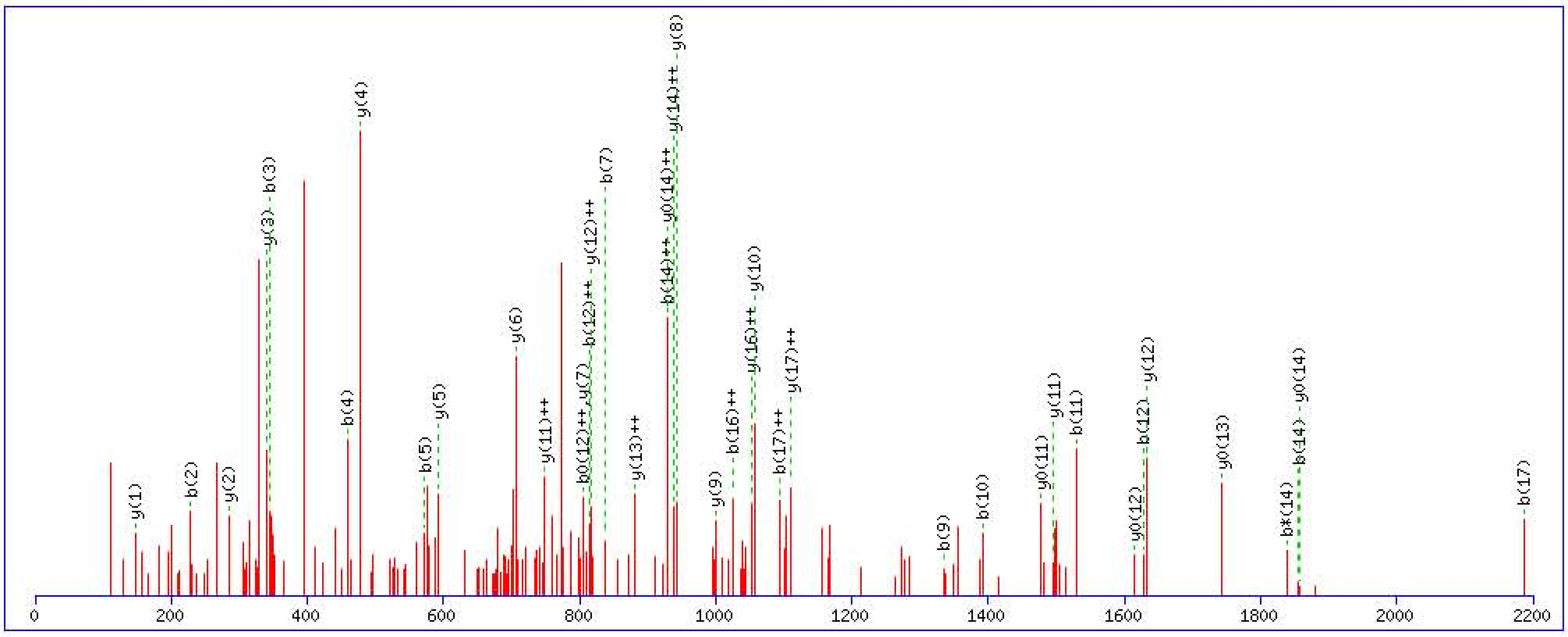
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDDDLEHQGGHVLDHGHK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

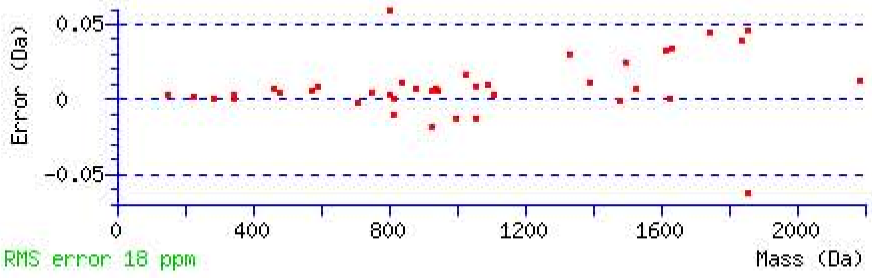
Match to Query 58836: 2332.127502 from(778.383110,3+) rtinseconds(1520) index(38923)
Title: Locus:1.1.1.2978.22 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

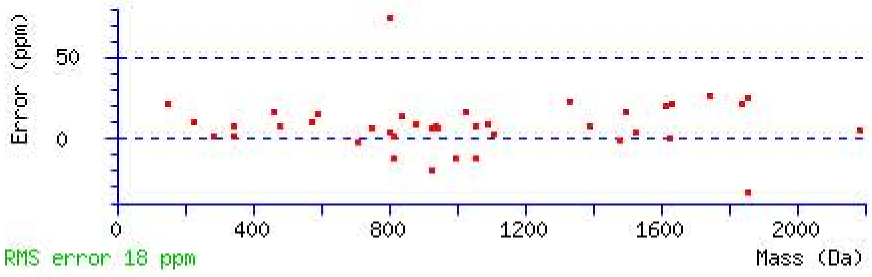
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2332.101883
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 1.6e-005
Matches : 40/180 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	114.091340	57.549308					L							18
2	***229.118283***	115.062779			211.107718	106.057497	D	2220.025077	1110.516176	2202.998528	1102.002902	2202.014512	1101.510894	17
3	***344.145226***	172.576251			326.134661	163.570968	D	2104.998134	1053.002705	2087.971585	1044.489430	2086.987569	1043.997422	16
4	***459.172169***	230.089722			441.161604	221.084440	D	1989.971191	995.489234	1972.944642	986.975959	1971.960626	986.483951	15
5	***572.256233***	286.631755			554.245668	277.626472	L	1874.944248	937.975762	1857.917699	929.462488	1856.933683	928.970480	14
6	701.298826	351.153051			683.288261	342.147769	E	1761.860184	881.433730	1744.833635	872.920456	1743.849619	872.428448	13
7	***838.357738***	419.682507			820.347173	410.677225	H	***1632.817591***	816.912434	1615.791042	808.399159	1614.807026	807.907151	12
8	1277.583064	639.295170	1260.556515	630.781896	1259.572499	630.289888	Q	***1495.758679***	748.382978	1478.732130	739.869703	1477.748114	739.377695	11
9	***1334.604528***	667.805902	1317.577979	659.292628	1316.593963	658.800620	G	***1056.533353***	528.770315	1039.506804	520.257040	1038.522788	519.765032	10
10	***1391.625992***	696.316634	1374.599443	687.803360	1373.615427	687.311352	G	***999.511889***	500.259583	982.485340	491.746308	981.501324	491.254300	9
11	***1528.684904***	764.846090	1511.658355	756.332816	1510.674339	755.840807	H	***942.490425***	471.748851	925.463876	463.235576	924.479860	462.743568	8
12	***1627.753318***	**814.380297**	1610.726769	805.867023	1609.742753	805.375015	V	***805.431513***	403.219395	788.404964	394.706120	787.420948	394.214112	7
13	1740.837382	870.922329	1723.810833	862.409055	1722.826817	861.917046	L	***706.363099***	353.685188	689.336550	345.171913	688.352534	344.679905	6
14	***1855.864325***	**928.435801**	1838.837776	919.922526	1837.853760	919.430518	D	***593.279035***	297.143156	576.252486	288.629881	575.268470	288.137873	5
15	1992.923237	996.965257	1975.896688	988.451982	1974.912672	987.959974	H	***478.252092***	239.629684	461.225543	231.116410			4
16	2049.944701	**1025.475988**	2032.918152	1016.962714	2031.934136	1016.470706	G	***341.193180***	171.100228	324.166631	162.586954			3
17	***2187.003613***	**1094.005444**	2169.977064	1085.492170	2168.993048	1085.000162	H	***284.171716***	142.589496	267.145167	134.076221			2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LDDDLEHQGGHVLDHGHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.3	2332.101883	0.025619	LDDDLEHQGGHVLDHGHK

Mascot: http://www.matrixscience.com/

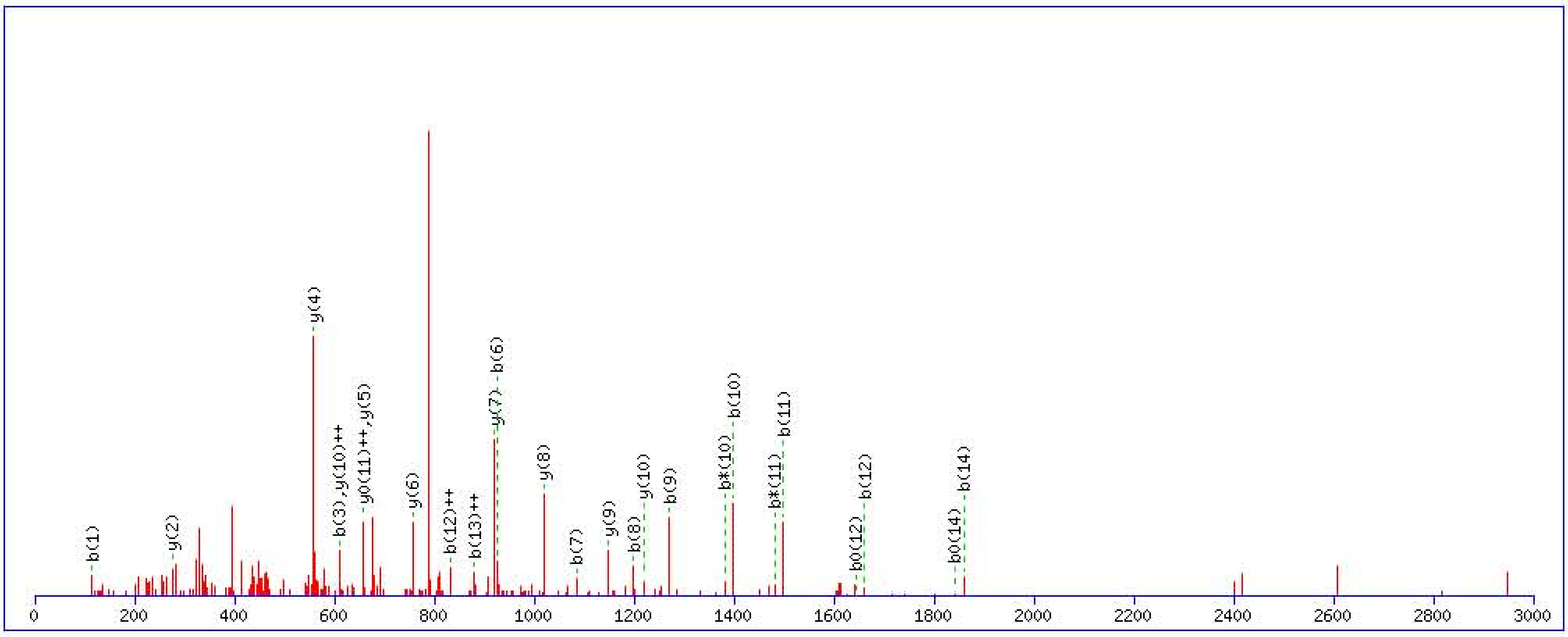
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGQSLDCNAEVYVVPWEK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

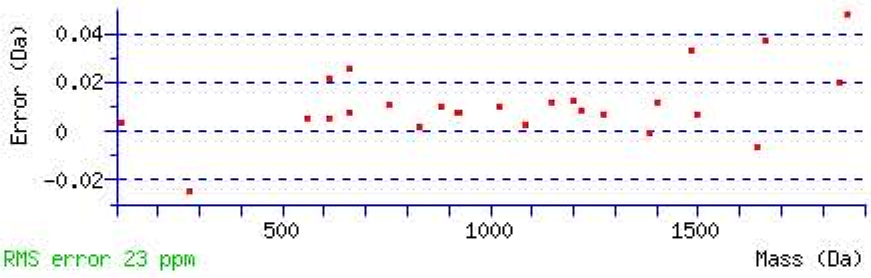
Match to Query 60493: 2417.211432 from(806.744420,3+) rtinseconds(2542) index(28312)
Title: Locus:1.1.1.3027.4 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

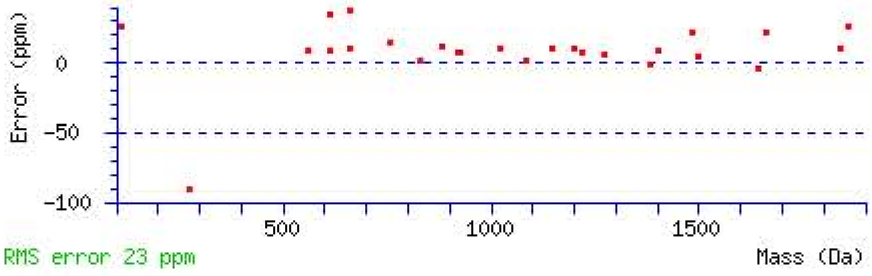
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2417.175934
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 1.7e-005
Matches : 26/192 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	***114.091340***	57.549308					L							18
2	171.112804	86.060040					G	2305.099153	1153.053214	2288.072604	1144.539940	2287.088588	1144.047932	17
3	***610.338130***	305.672703	593.311581	297.159429			Q	2248.077689	1124.542482	2231.051140	1116.029208	2230.067124	1115.537200	16
4	697.370158	349.188717	680.343609	340.675443	679.359593	340.183435	S	1808.852363	904.929820	1791.825814	896.416545	1790.841798	895.924537	15
5	810.454222	405.730749	793.427673	397.217475	792.443657	396.725467	L	1721.820335	861.413806	1704.793786	852.900531	1703.809770	852.408523	14
6	***925.481165***	463.244221	908.454616	454.730946	907.470600	454.238938	D	1608.736271	804.871774	1591.709722	796.358499	1590.725706	795.866491	13
7	***1085.511814***	543.259545	1068.485265	534.746271	1067.501249	534.254262	C	1493.709328	747.358302	1476.682779	738.845028	1475.698763	738.353020	12
8	***1199.554741***	600.281008	1182.528192	591.767734	1181.544176	591.275726	N	1333.678679	667.342978	1316.652130	658.829703	1315.668114	658.337695	11
9	***1270.591855***	635.799565	1253.565306	627.286291	1252.581290	626.794283	A	**1219.635752**	610.321514	1202.609203	601.808240	1201.625187	601.316232	10
10	***1399.634448***	700.320862	1382.607899	691.807588	1381.623883	691.315580	E	**1148.598638**	574.802957	1131.572089	566.289683	1130.588073	565.797675	9
11	***1498.702862***	749.855069	1481.676313	741.341795	1480.692297	740.849787	V	**1019.556045**	510.281661	1002.529496	501.768386	1001.545480	501.276378	8
12	***1661.766191***	**831.386734**	1644.739642	822.873459	1643.755626	822.381451	Y	**920.487631**	460.747454	903.461082	452.234179	902.477066	451.742171	7
13	1760.834605	**880.920941**	1743.808056	872.407666	1742.824040	871.915658	V	**757.424302**	379.215789	740.397753	370.702515	739.413737	370.210507	6
14	***1859.903019***	930.455148	1842.876470	921.941873	1841.892454	921.449865	V	**658.355888**	329.681582	641.329339	321.168308	640.345323	320.676300	5
15	1956.955783	978.981530	1939.929234	970.468255	1938.945218	969.976247	P	**559.287474**	280.147375	542.260925	271.634101	541.276909	271.142093	4
16	2143.035096	1072.021186	2126.008547	1063.507911	2125.024531	1063.015903	W	462.234710	231.620993	445.208161	223.107719	444.224145	222.615711	3
17	2272.077689	1136.542483	2255.051140	1128.029208	2254.067124	1127.537200	E	**276.155397**	138.581337	259.128848	130.068062	258.144832	129.576054	2
18							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LGQSLDCNAEVYVVPWEK
(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	2417.175934	0.035498	LGQSLDCNAEVYVVPWEK

Mascot: http://www.matrixscience.com/

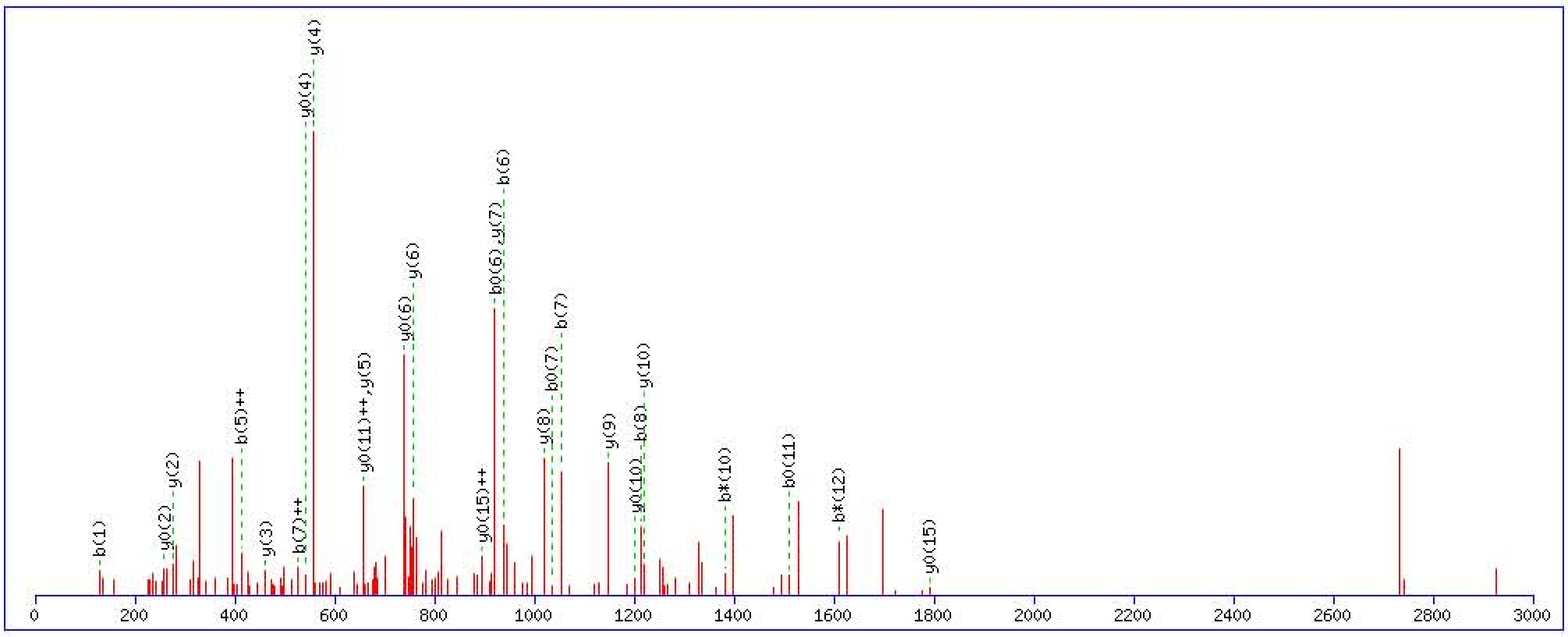
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLGQSLDCNAEVYVVPWEK**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

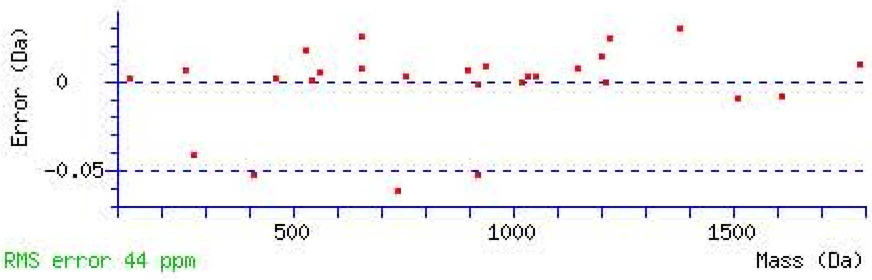
Match to Query 63830: 2545.289652 from(849.437160,3+) rtinseconds(2385) index(27412)
Title: Locus:1.1.1.2972.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

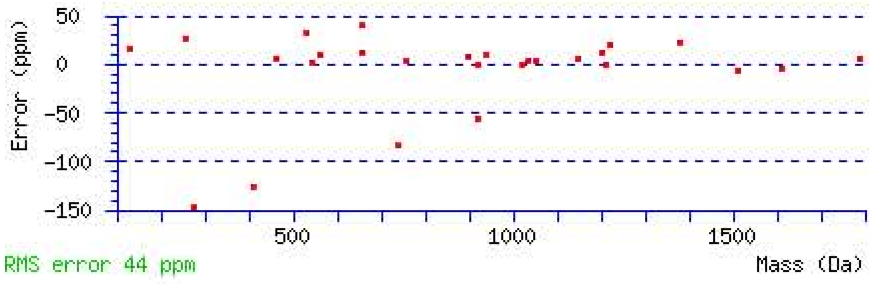


```
Monoisotopic mass of neutral peptide Mr(calc): 2545.270889
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.02
Matches : 27/206 fragment ions using 64 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							19
2	242.186303	121.596790	225.159754	113.083515			L	2418.183217	1209.595246	2401.156668	1201.081972	2400.172652	1200.589964	18
3	299.207767	150.107521	282.181218	141.594247			G	2305.099153	1153.053214	2288.072604	1144.539940	2287.088588	1144.047932	17
4	738.433093	369.720185	721.406544	361.206910			Q	2248.077689	1124.542482	2231.051140	1116.029208	2230.067124	1115.537200	16
5	825.465121	**413.236199**	808.438572	404.722924	807.454556	404.230916	S	1808.852363	904.929820	1791.825814	896.416545	1790.841798	895.924537	15
6	***938.549185***	469.778231	921.522636	461.264956	920.538620	460.772948	L	1721.820335	861.413806	1704.793786	852.900531	1703.809770	852.408523	14
7	***1053.576128***	**527.291702**	1036.549579	518.778428	1035.565563	518.286420	D	1608.736271	804.871774	1591.709722	796.358499	1590.725706	795.866491	13
8	***1213.606777***	607.307027	1196.580228	598.793752	1195.596212	598.301744	C	1493.709328	747.358302	1476.682779	738.845028	1475.698763	738.353020	12
9	1327.649704	664.328490	1310.623155	655.815216	1309.639139	655.323208	N	1333.678679	667.342978	1316.652130	658.829703	1315.668114	658.337695	11
10	1398.686818	699.847047	1381.660269	691.333773	1380.676253	690.841765	A	***1219.635752***	610.321514	1202.609203	601.808240	1201.625187	601.316232	10
11	1527.729411	764.368344	1510.702862	755.855069	1509.718846	755.363061	E	***1148.598638***	574.802957	1131.572089	566.289683	1130.588073	565.797675	9
12	1626.797825	813.902551	1609.771276	805.389276	1608.787260	804.897268	V	***1019.556045***	510.281661	1002.529496	501.768386	1001.545480	501.276378	8
13	1789.861154	895.434215	1772.834605	886.920941	1771.850589	886.428933	Y	***920.487631***	460.747454	903.461082	452.234179	902.477066	451.742171	7
14	1888.929568	944.968422	1871.903019	936.455148	1870.919003	935.963140	V	***757.424302***	379.215789	740.397753	370.702515	739.413737	370.210507	6
15	1987.997982	994.502629	1970.971433	985.989355	1969.987417	985.497347	V	***658.355888***	329.681582	641.329339	321.168308	640.345323	320.676300	5
16	2085.050746	1043.029011	2068.024197	1034.515736	2067.040181	1034.023728	P	***559.287474***	280.147375	542.260925	271.634101	541.276909	271.142093	4
17	2271.130059	1136.068667	2254.103510	1127.555393	2253.119494	1127.063385	W	***462.234710***	231.620993	445.208161	223.107719	444.224145	222.615711	3
18	2400.172652	1200.589964	2383.146103	1192.076689	2382.162087	1191.584682	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 44 ppm



RMS error 44 ppm

NCBI **BLAST** search of KLGQSLDCNAEVYVVPWEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.5	2545.270889	0.018763	KLGQSLDCNAEVYVVPWEK

Mascot: http://www.matrixscience.com/

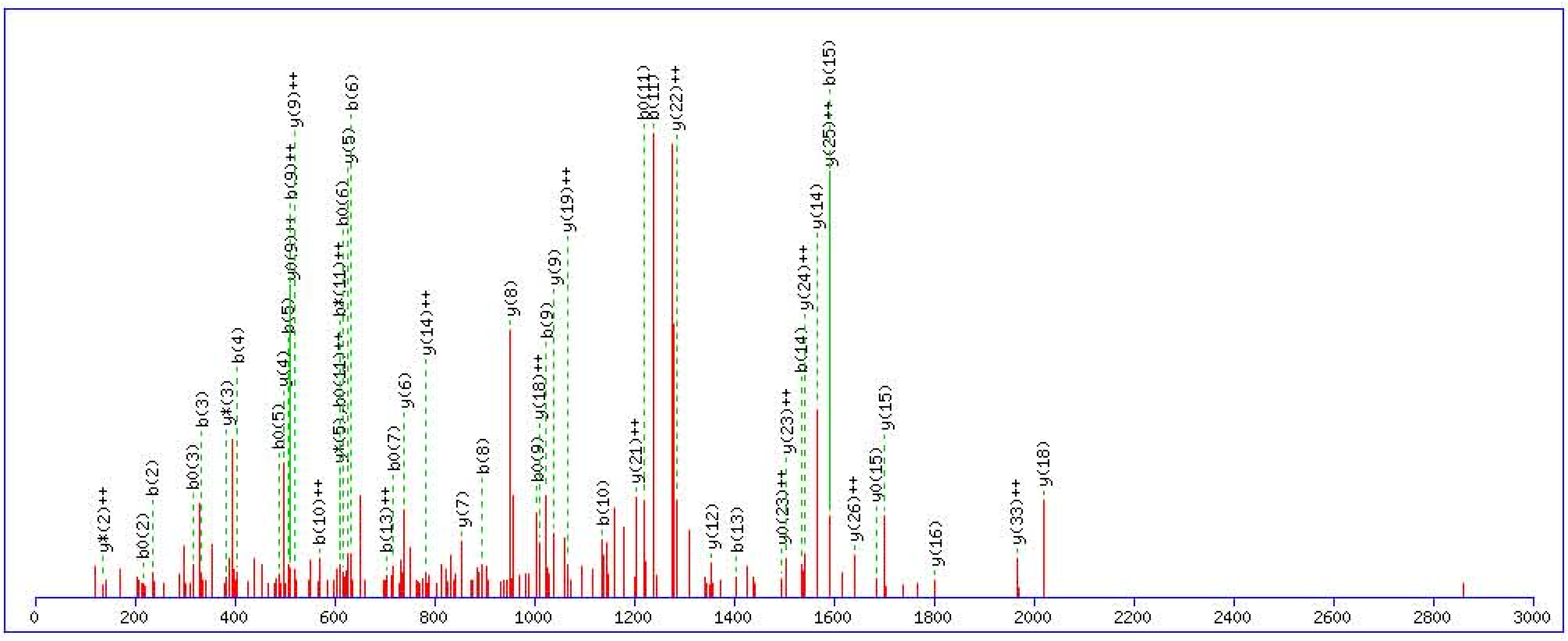
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR**
Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

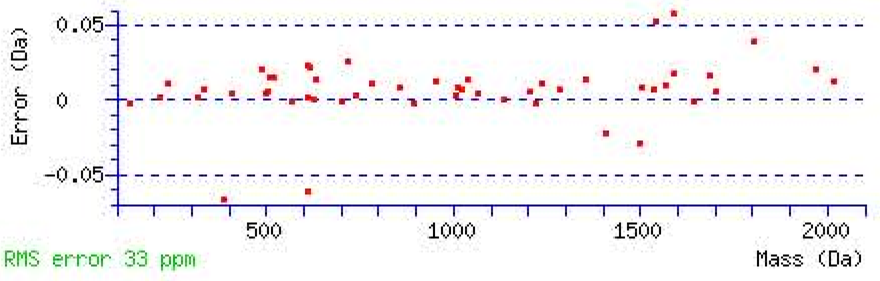
Match to Query 87839: 5066.538470 from(1014.314970,5+) rtinseconds(2651) index(28979)
Title: Locus:1.1.1.3064.20 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

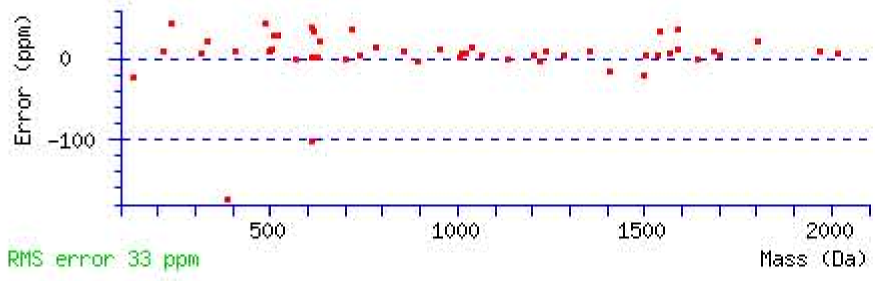
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 5066.465057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21    : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 6.9e-005
Matches : 52/484 fragment ions using 131 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
54.4	5066.465057	0.073413	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
34.0	5066.465057	0.073413	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
34.0	5066.465057	0.073413	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
24.3	5066.465057	0.073413	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR

Mascot: http://www.matrixscience.com/

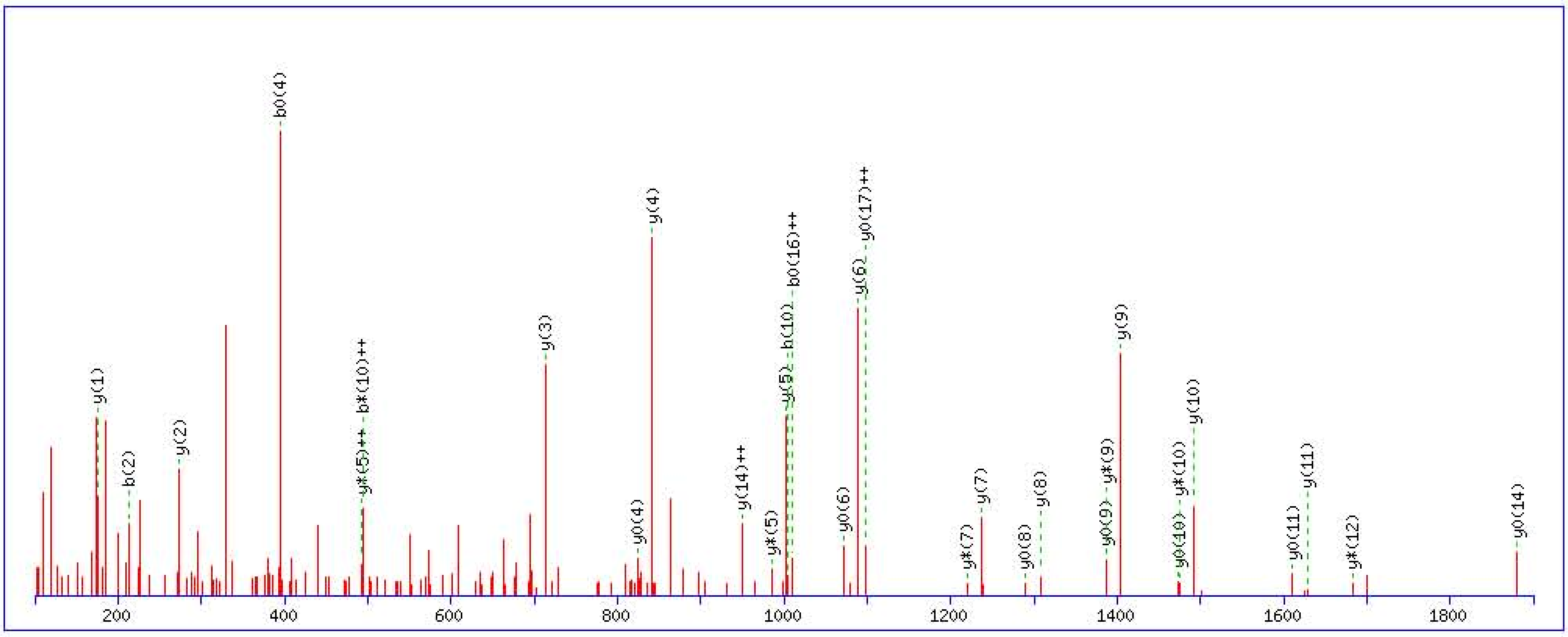
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSIAQAHSPAFSCEQVR**
Found in **CD14_HUMAN**, Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2

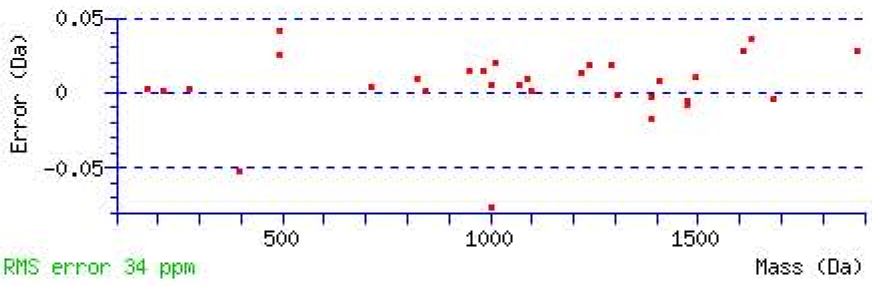
Match to Query 58277: 2310.169536 from(578.549660,4+) rtinseconds(1949) index(24350)
Title: Locus:1.1.1.2821.5 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

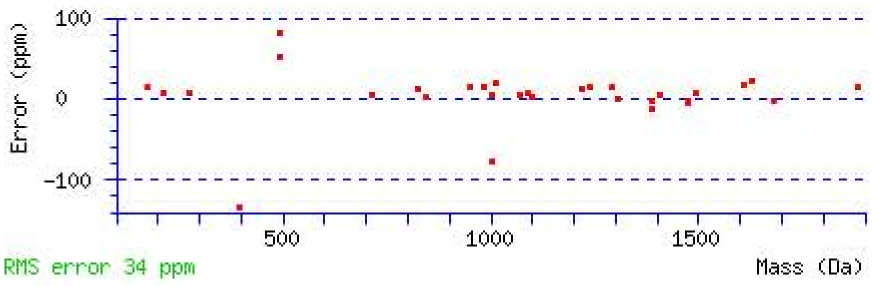
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2310.161285
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16    : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.0008
Matches : 31/184 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	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
45.5	2310.161285	0.008251	VLSIAQAHSPAFSCEQVR

Mascot: http://www.matrixscience.com/

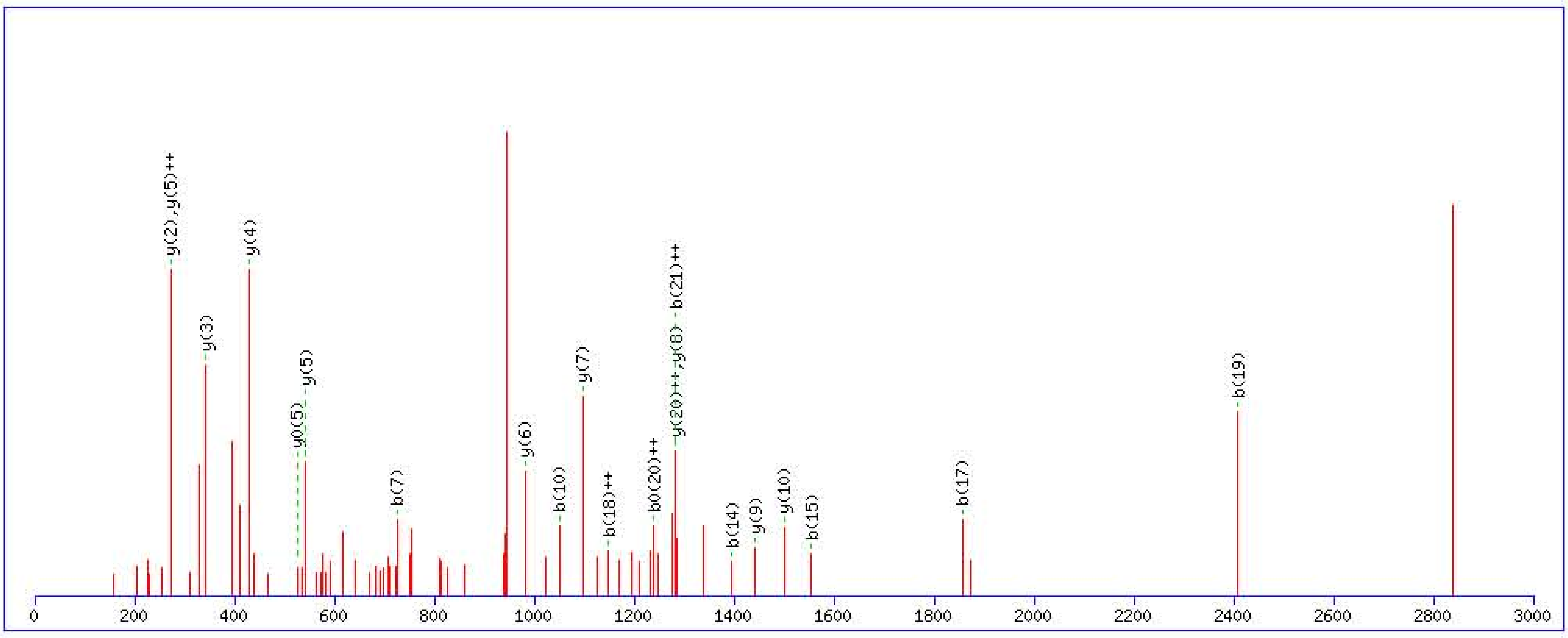
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSQTQSHPDLGTEGCWDQLSAPR**
Found in **PGRP2_HUMAN**, N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

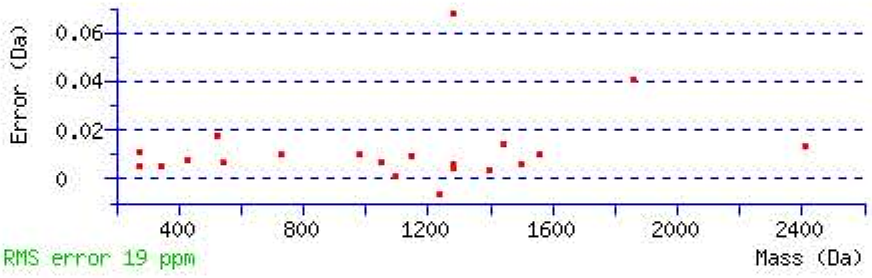
Match to Query 67766: 2837.312472 from(946.778100,3+) rtinseconds(2045) index(79163)
Title: Locus:1.1.1.2062.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

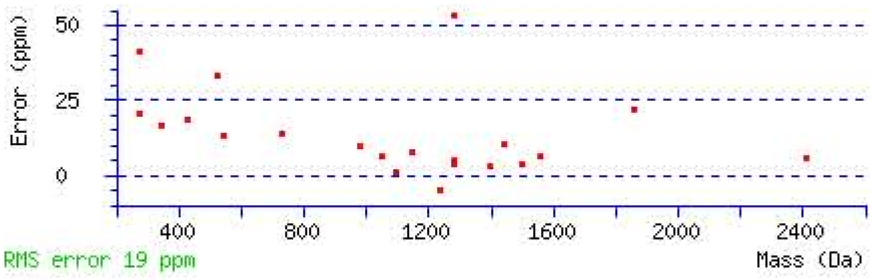
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2837.286133
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00026
Matches : 21/252 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							23
2	145.060768	73.034022			127.050203	64.028740	S	2781.271927	1391.139601	2764.245378	1382.626327	2763.261362	1382.134319	22
3	273.119346	137.063311	256.092797	128.550037	255.108781	128.058029	Q	2694.239899	1347.623587	2677.213350	1339.110313	2676.229334	1338.618305	21
4	374.167025	187.587151	357.140476	179.073876	356.156460	178.581868	T	2566.181321	1283.594298	2549.154772	1275.081024	2548.170756	1274.589016	20
5	502.225603	251.616440	485.199054	243.103165	484.215038	242.611157	Q	2465.133642	1233.070459	2448.107093	1224.557184	2447.123077	1224.065176	19
6	589.257631	295.132454	572.231082	286.619179	571.247066	286.127171	S	2337.075064	1169.041170	2320.048515	1160.527895	2319.064499	1160.035887	18
7	**726.316543**	363.661910	709.289994	355.148635	708.305978	354.656627	H	2250.043036	1125.525156	2233.016487	1117.011881	2232.032471	1116.519873	17
8	823.369307	412.188292	806.342758	403.675017	805.358742	403.183009	P	2112.984124	1056.995700	2095.957575	1048.482425	2094.973559	1047.990417	16
9	938.396250	469.701763	921.369701	461.188489	920.385685	460.696481	D	2015.931360	1008.469318	1998.904811	999.956044	1997.920795	999.464036	15
10	**1051.480314**	526.243795	1034.453765	517.730521	1033.469749	517.238512	L	1900.904417	950.955847	1883.877868	942.442572	1882.893852	941.950564	14
11	1108.501778	554.754527	1091.475229	546.241252	1090.491213	545.749244	G	1787.820353	894.413815	1770.793804	885.900540	1769.809788	885.408532	13
12	1209.549457	605.278366	1192.522908	596.765092	1191.538892	596.273084	T	1730.798889	865.903083	1713.772340	857.389808	1712.788324	856.897800	12
13	1338.592050	669.799663	1321.565501	661.286389	1320.581485	660.794380	E	1629.751210	815.379243	1612.724661	806.865969	1611.740645	806.373961	11
14	**1395.613514**	698.310395	1378.586965	689.797121	1377.602949	689.305112	G	***1500.708617***	750.857947	1483.682068	742.344672	1482.698052	741.852664	10
15	**1555.644163**	778.325719	1538.617614	769.812445	1537.633598	769.320437	C	***1443.687153***	722.347215	1426.660604	713.833940	1425.676588	713.341932	9
16	1741.723476	871.365376	1724.696927	862.852102	1723.712911	862.360093	W	***1283.656504***	642.331890	1266.629955	633.818616	1265.645939	633.326608	8
17	**1856.750419**	928.878848	1839.723870	920.365573	1838.739854	919.873565	D	***1097.577191***	549.292234	1080.550642	540.778959	1079.566626	540.286951	7
18	2295.975745	**1148.491510**	2278.949196	1139.978236	2277.965180	1139.486228	Q	***982.550248***	491.778762	965.523699	483.265488	964.539683	482.773480	6
19	**2409.059809**	1205.033542	2392.033260	1196.520268	2391.049244	1196.028260	L	***543.324922***	272.166099	526.298373	263.652825	525.314357	263.160817	5
20	2496.091837	1248.549556	2479.065288	1240.036282	2478.081272	1239.544274	S	***430.240858***	215.624067	413.214309	207.110793	412.230293	206.618785	4
21	2567.128951	**1284.068114**	2550.102402	1275.554839	2549.118386	1275.062831	A	***343.208830***	172.108053	326.182281	163.594779			3
22	2664.181715	1332.594496	2647.155166	1324.081221	2646.171150	1323.589213	P	***272.171716***	136.589496	255.145167	128.076221			2
23							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GSQTQSHPDLGTEGCWDQLSAPR
(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	2837.286133	0.026339	GSQTQSHPDLGTEGCWDQLSAPR
2.3	2837.286133	0.026339	GSQTQSHPDLGTEGCWDQLSAPR
1.9	2837.286133	0.026339	GSQTQSHPDLGTEGCWDQLSAPR

Mascot: http://www.matrixscience.com/

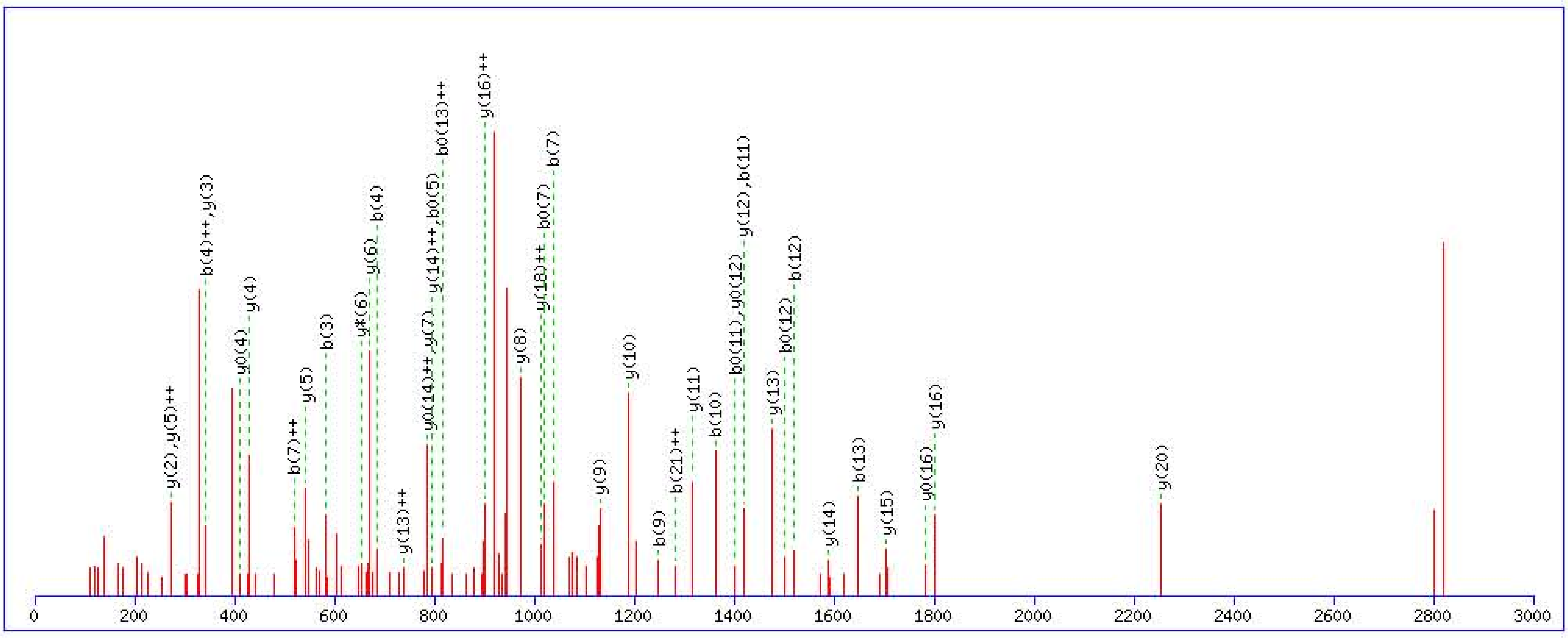
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSQTQSHPDLGTEGCWDQLSAPR**
Found in **PGRP2_HUMAN**, N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

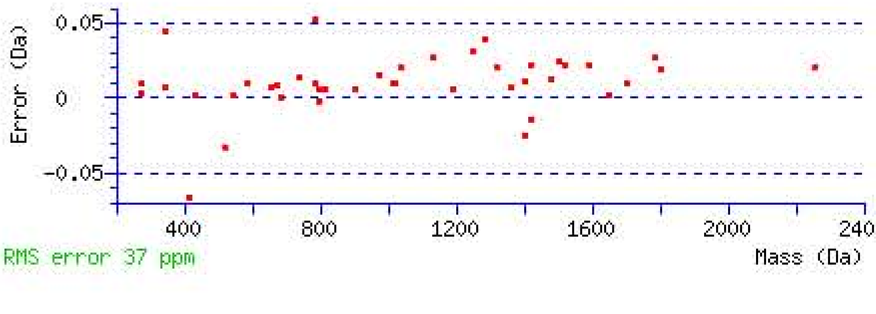
Match to Query 67768: 2837.316672 from(946.779500,3+) rtinseconds(1989) index(6468)
Title: Locus:1.1.1.2946.20 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

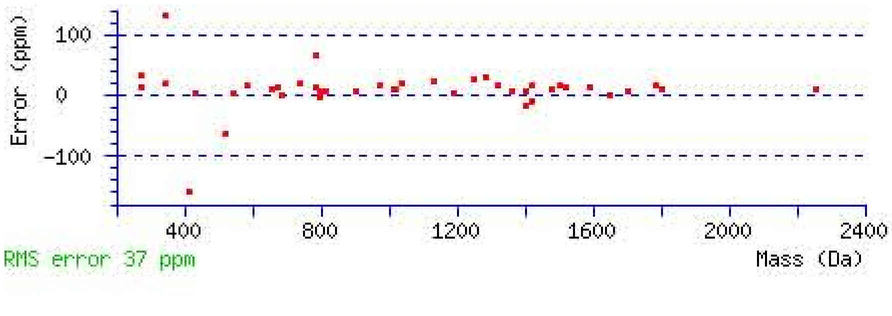
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2837.286133
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 116  Expect: 3.3e-011
Matches : 42/252 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							23
2	145.060768	73.034022			127.050203	64.028740	S	2781.271927	1391.139601	2764.245378	1382.626327	2763.261362	1382.134319	22
3	**584.286094**	292.646685	567.259545	284.133411	566.275529	283.641403	Q	2694.239899	1347.623587	2677.213350	1339.110313	2676.229334	1338.618305	21
4	**685.333773**	**343.170525**	668.307224	334.657250	667.323208	334.165242	T	***2255.014573***	1128.010924	2237.988024	1119.497650	2237.004008	1119.005642	20
5	813.392351	407.199814	796.365802	398.686539	795.381786	398.194531	Q	2153.966894	1077.487085	2136.940345	1068.973810	2135.956329	1068.481802	19
6	900.424379	450.715828	883.397830	442.202553	882.413814	441.710545	S	2025.908316	1013.457796	2008.881767	1004.944522	2007.897751	1004.452514	18
7	**1037.483291**	**519.245284**	1020.456742	510.732009	1019.472726	510.240001	H	1938.876288	969.941782	1921.849739	961.428508	1920.865723	960.936500	17
8	1134.536055	567.771666	1117.509506	559.258391	1116.525490	558.766383	P	***1801.817376***	901.412326	1784.790827	892.899052	1783.806811	892.407044	16
9	**1249.562998**	625.285137	1232.536449	616.771863	1231.552433	616.279855	D	***1704.764612***	852.885944	1687.738063	844.372670	1686.754047	843.880662	15
10	**1362.647062**	681.827169	1345.620513	673.313895	1344.636497	672.821887	L	***1589.737669***	795.372473	1572.711120	786.859198	1571.727104	786.367190	14
11	**1419.668526**	710.337901	1402.641977	701.824627	1401.657961	701.332618	G	***1476.653605***	738.830441	1459.627056	730.317166	1458.643040	729.825158	13
12	**1520.716205**	760.861741	1503.689656	752.348466	1502.705640	751.856458	T	***1419.632141***	710.319709	1402.605592	701.806434	1401.621576	701.314426	12
13	**1649.758798**	825.383037	1632.732249	816.869763	1631.748233	816.377755	E	***1318.584462***	659.795869	1301.557913	651.282595	1300.573897	650.790587	11
14	1706.780262	853.893769	1689.753713	845.380495	1688.769697	844.888487	G	***1189.541869***	595.274573	1172.515320	586.761298	1171.531304	586.269290	10
15	1866.810911	933.909094	1849.784362	925.395819	1848.800346	924.903811	C	***1132.520405***	566.763841	1115.493856	558.250566	1114.509840	557.758558	9
16	2052.890224	1026.948750	2035.863675	1018.435475	2034.879659	1017.943467	W	***972.489756***	486.748516	955.463207	478.235242	954.479191	477.743234	8
17	2167.917167	1084.462221	2150.890618	1075.948947	2149.906602	1075.456939	D	***786.410443***	393.708860	769.383894	385.195585	768.399878	384.703577	7
18	2295.975745	1148.491510	2278.949196	1139.978236	2277.965180	1139.486228	Q	***671.383500***	336.195388	654.356951	327.682114	653.372935	327.190106	6
19	2409.059809	1205.033542	2392.033260	1196.520268	2391.049244	1196.028260	L	***543.324922***	272.166099	526.298373	263.652825	525.314357	263.160817	5
20	2496.091837	1248.549556	2479.065288	1240.036282	2478.081272	1239.544274	S	***430.240858***	215.624067	413.214309	207.110793	412.230293	206.618785	4
21	2567.128951	**1284.068114**	2550.102402	1275.554839	2549.118386	1275.062831	A	***343.208830***	172.108053	326.182281	163.594779			3
22	2664.181715	1332.594496	2647.155166	1324.081221	2646.171150	1323.589213	P	***272.171716***	136.589496	255.145167	128.076221			2
23							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GSQTQSHPDLGTEGCWDQLSAPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
116.2	2837.286133	0.030539	GSQTQSHPDLGTEGCWDQLSAPR
98.7	2837.286133	0.030539	GSQTQSHPDLGTEGCWDQLSAPR

Mascot: http://www.matrixscience.com/

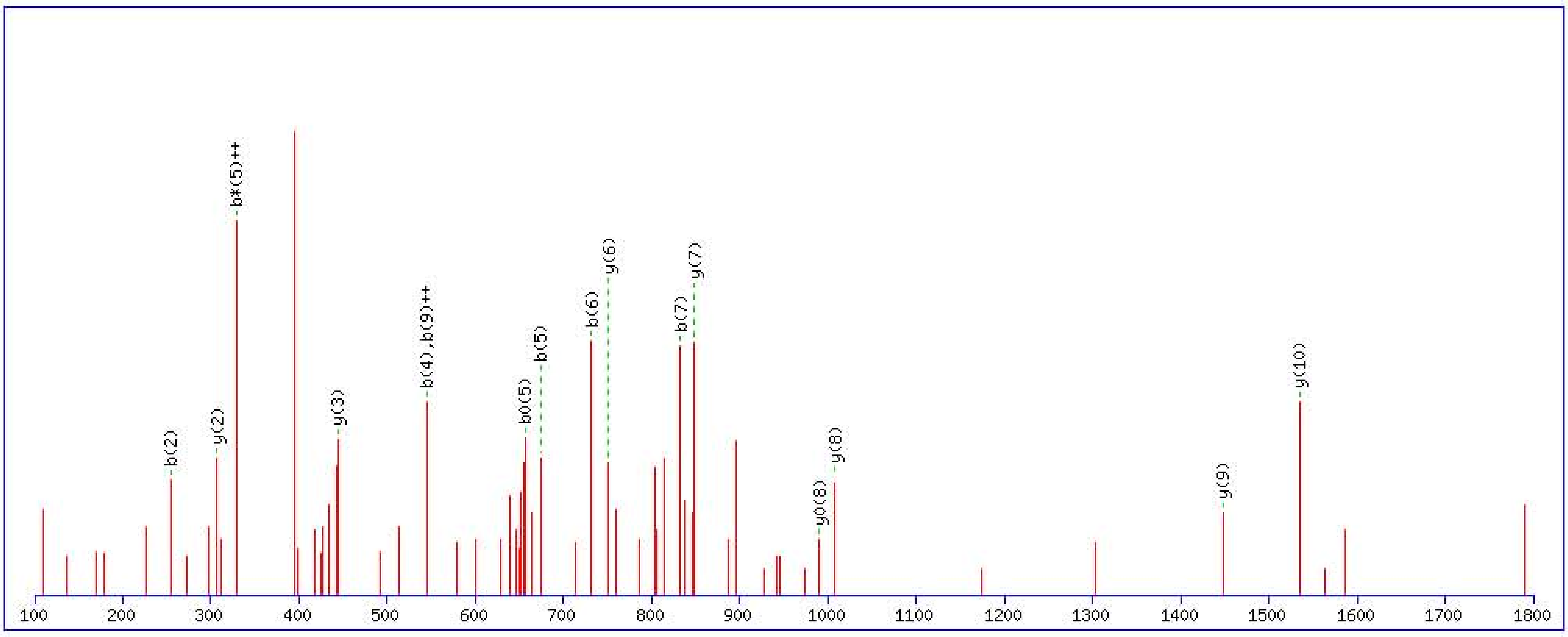
Mascot Search Results

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 64775: 2622.147296 from(656.544100,4+) rtinseconds(1325) index(37477)
Title: Locus:1.1.1.2910.12 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\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 ●



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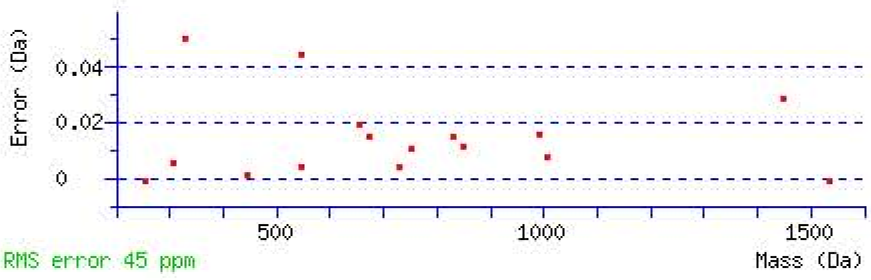
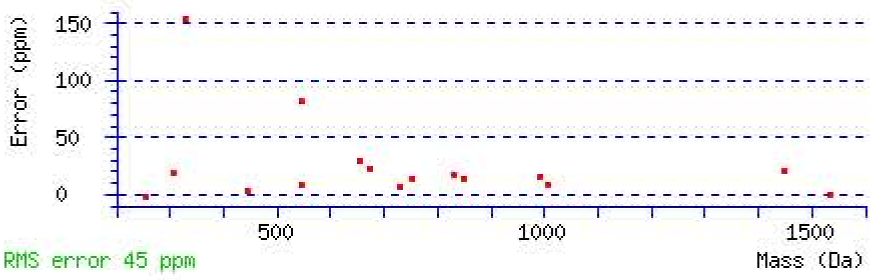
Monoisotopic mass of neutral peptide Mr(calc): 2622.123611
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00016
Matches : 16/198 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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





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
45.5	2622.123611	0.023685	RPYQEGTPCSQCPSGYHCK
3.8	2622.123611	0.023685	RPYQEGTPCSQCPSGYHCK

Mascot: http://www.matrixscience.com/

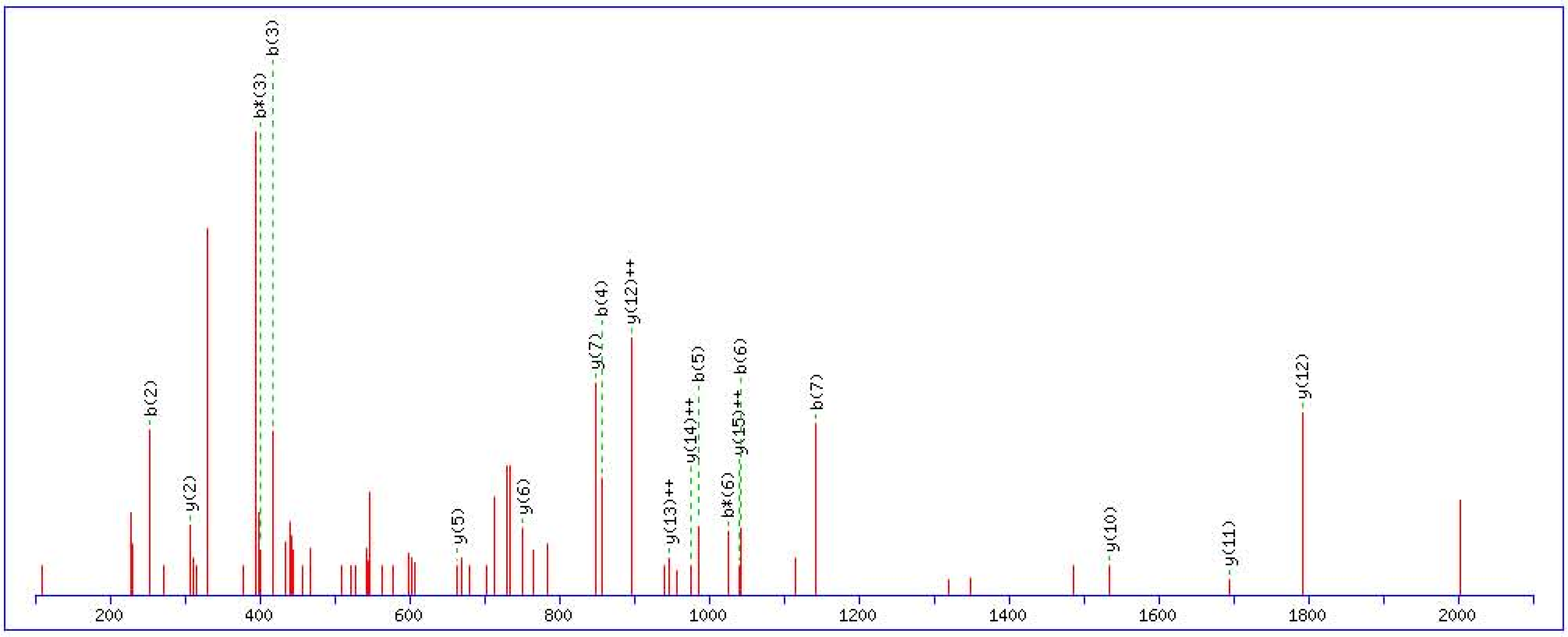
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPYQEGTPCSQCPSGYHCK**
Found in **PI16_HUMAN**, Peptidase inhibitor 16 OS=Homo sapiens GN=PI16 PE=1 SV=1

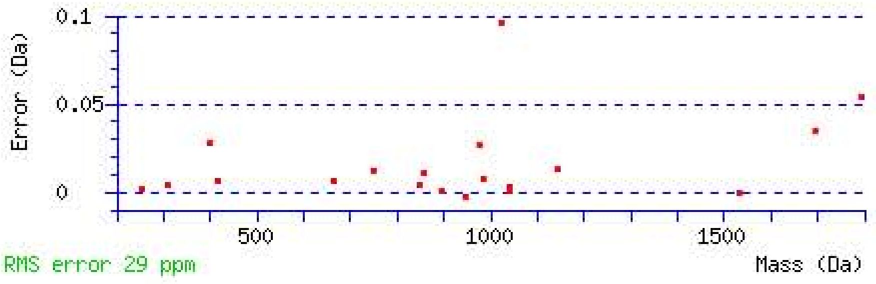
Match to Query 69551: 2933.316216 from(734.336330,4+) rtinseconds(1554) index(39188)
Title: Locus:1.1.1.2990.22 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

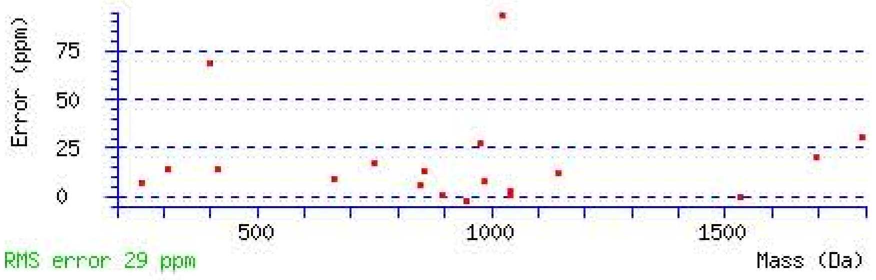
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2933.290359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Q11    : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.012
Matches : 19/198 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	157.108387	79.057831	140.081838	70.544557			R							19
2	***254.161151***	127.584213	237.134602	119.070939			P	2778.196521	1389.601898	2761.169972	1381.088624	2760.185956	1380.596616	18
3	***417.224480***	209.115878	400.197931	200.602604			Y	2681.143757	1341.075516	2664.117208	1332.562242	2663.133192	1332.070234	17
4	***856.449806***	428.728541	839.423257	420.215267			Q	2518.080428	1259.543852	2501.053879	1251.030577	2500.069863	1250.538569	16
5	***985.492399***	493.249838	968.465850	484.736563	967.481834	484.244555	E	2078.855102	1039.931189	2061.828553	1031.417914	2060.844537	1030.925906	15
6	***1042.513863***	521.760570	1025.487314	513.247295	1024.503298	512.755287	G	1949.812509	975.409893	1932.785960	966.896618	1931.801944	966.404610	14
7	***1143.561542***	572.284409	1126.534993	563.771135	1125.550977	563.279127	T	1892.791045	946.899160	1875.764496	938.385886	1874.780480	937.893878	13
8	1240.614306	620.810791	1223.587757	612.297517	1222.603741	611.805509	P	***1791.743366***	896.375321	1774.716817	887.862047	1773.732801	887.370038	12
9	1400.644955	700.826116	1383.618406	692.312841	1382.634390	691.820833	C	***1694.690602***	847.848939	1677.664053	839.335665	1676.680037	838.843656	11
10	1487.676983	744.342130	1470.650434	735.828855	1469.666418	735.336847	S	***1534.659953***	767.833614	1517.633404	759.320340	1516.649388	758.828332	10
11	1926.902309	963.954793	1909.875760	955.441518	1908.891744	954.949510	Q	1447.627925	724.317600	1430.601376	715.804326	1429.617360	715.312318	9
12	2086.932958	1043.970117	2069.906409	1035.456842	2068.922393	1034.964834	C	1008.402599	504.704937	991.376050	496.191663	990.392034	495.699655	8
13	2183.985722	1092.496499	2166.959173	1083.983224	2165.975157	1083.491216	P	***848.371950***	424.689613	831.345401	416.176338	830.361385	415.684330	7
14	2271.017750	1136.012513	2253.991201	1127.499238	2253.007185	1127.007230	S	***751.319186***	376.163231	734.292637	367.649956	733.308621	367.157948	6
15	2328.039214	1164.523245	2311.012665	1156.009970	2310.028649	1155.517962	G	***664.287158***	332.647217	647.260609	324.133942			5
16	2491.102543	1246.054909	2474.075994	1237.541635	2473.091978	1237.049627	Y	607.265694	304.136485	590.239145	295.623210			4
17	2628.161455	1314.584365	2611.134906	1306.071091	2610.150890	1305.579083	H	444.202365	222.604820	427.175816	214.091546			3
18	2788.192104	1394.599690	2771.165555	1386.086415	2770.181539	1385.594407	C	***307.143453***	154.075364	290.116904	145.562090			2
19							K	147.112804	74.060040	130.086255	65.546765			1





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
28.9	2933.290359	0.025857	RPYQEGTPCSQCPSGYHCK

Mascot: http://www.matrixscience.com/

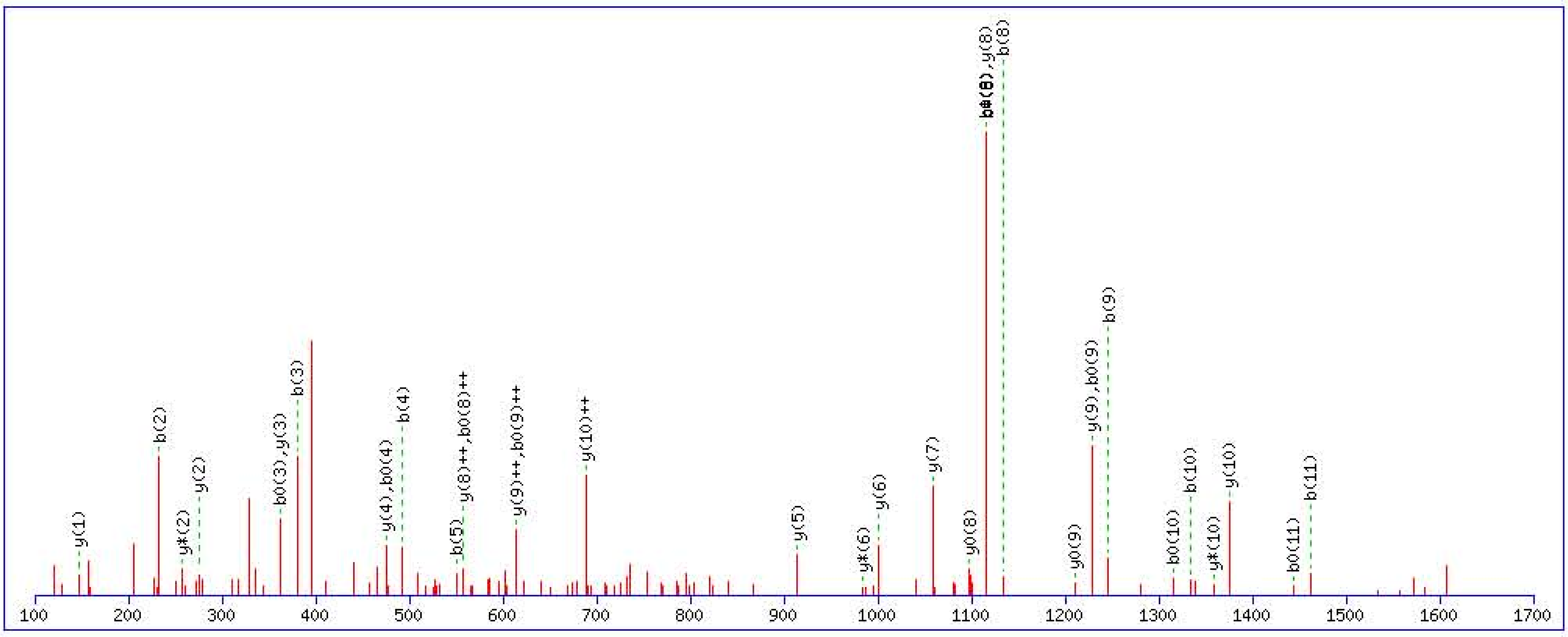
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMFIGGSQLSQK**
Found in **PHLD_HUMAN**, Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

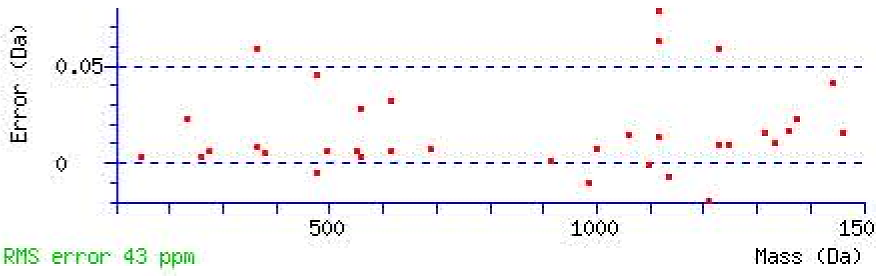
Match to Query 38994: 1606.844548 from(804.429550,2+) rtinseconds(2112) index(42979)
Title: Locus:1.1.1.3184.15 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

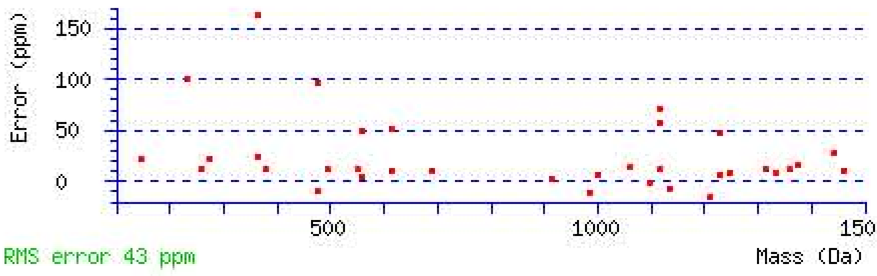
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1606.821121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 60 **Expect:** 2.3e-005
Matches : 35/114 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	102.054955	51.531116			84.044390	42.525833	T							12
2	**233.095440**	117.051358			215.084875	108.046076	M	1506.780719	753.893997	1489.754170	745.380723	1488.770154	744.888715	11
3	**380.163854**	190.585565			362.153289	181.580282	F	***1375.740234***	688.373755	1358.713685	679.860480	1357.729669	679.368472	10
4	**493.247918**	247.127597			475.237353	238.122314	I	***1228.671820***	614.839548	1211.645271	606.326273	1210.661255	605.834265	9
5	**550.269382**	275.638329			532.258817	266.633047	G	***1115.587756***	558.297516	1098.561207	549.784242	1097.577191	549.292233	8
6	607.290846	304.149061			589.280281	295.143779	G	***1058.566292***	529.786784	1041.539743	521.273509	1040.555727	520.781501	7
7	694.322874	347.665075			676.312309	338.659793	S	***1001.544828***	501.276052	984.518279	492.762777	983.534263	492.270769	6
8	**1133.548200**	567.277738	1116.521651	558.764464	1115.537635	558.272455	Q	***914.512800***	457.760038	897.486251	449.246763	896.502235	448.754755	5
9	**1246.632264**	623.819770	1229.605715	615.306495	1228.621699	614.814487	L	***475.287474***	238.147375	458.260925	229.634100	457.276909	229.142092	4
10	**1333.664292**	667.335784	1316.637743	658.822510	1315.653727	658.330501	S	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	3
11	**1461.722870**	731.365073	1444.696321	722.851798	1443.712305	722.359790	Q	***275.171382***	138.089329	258.144833	129.576054			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TMFIGGSQLSQK
(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	1606.821121	0.023427	TMFIGGSQLSQK
40.9	1606.821121	0.023427	TMFIGGSQLSQK
18.0	1606.859970	-0.015422	TMLESLIADKSGSKK
7.9	1606.842239	0.002309	ITLMSQSSTGKK
5.2	1606.838852	0.005696	GSYSLVEAQKSK
4.7	1606.838852	0.005696	QAVSMFLGAVEEAKK
3.5	1606.856628	-0.012080	TVKALEFVQTESQK
2.8	1606.831451	0.013097	RELQVLSEQYSQK
2.4	1606.850082	-0.005534	KEQHVAEQISK
2.0	1606.850082	-0.005534	GHEAVESLQAKK

Mascot: http://www.matrixscience.com/

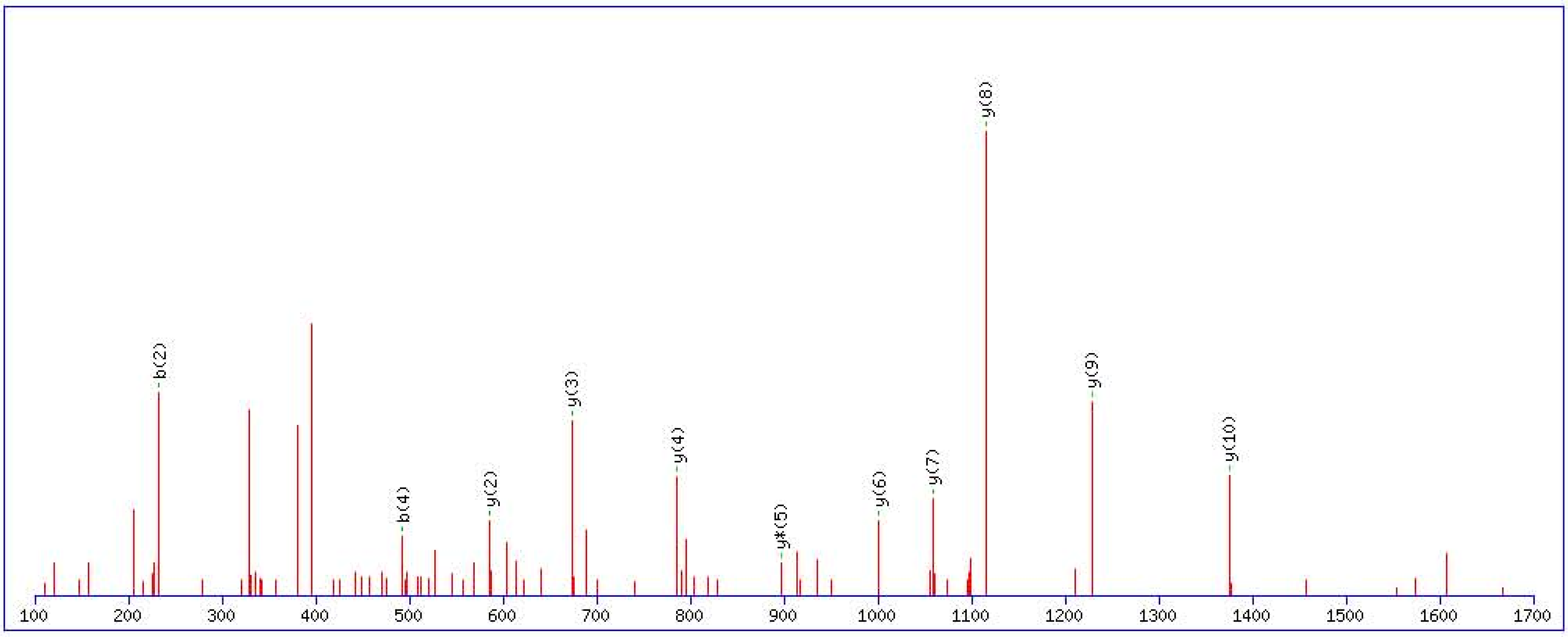
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMFIGGSQLSQK**
Found in **PHLD_HUMAN**, Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

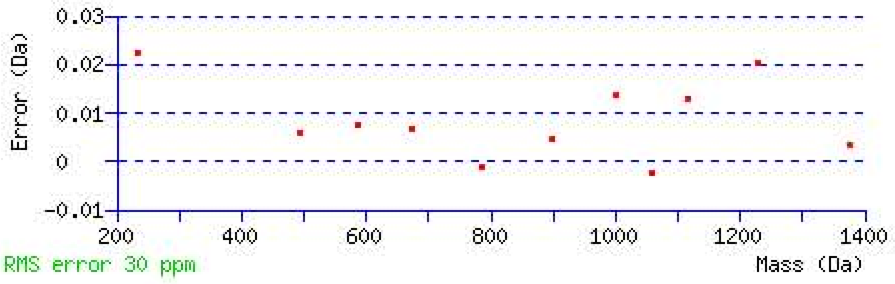
Match to Query 38995: 1606.844708 from(804.429630,2+) rtinseconds(2101) index(42901)
Title: Locus:1.1.1.3180.25 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

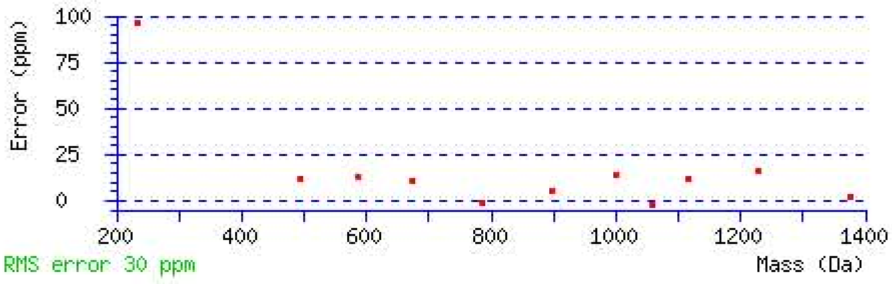
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1606.821121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 9.7e-006
Matches : 11/114 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	102.054955	51.531116			84.044390	42.525833	T							12
2	**233.095440**	117.051358			215.084875	108.046076	M	1506.780719	753.893998	1489.754170	745.380723	1488.770154	744.888715	11
3	380.163854	190.585565			362.153289	181.580282	F	***1375.740234***	688.373755	1358.713685	679.860481	1357.729669	679.368473	10
4	**493.247918**	247.127597			475.237353	238.122314	I	***1228.671820***	614.839548	1211.645271	606.326274	1210.661255	605.834266	9
5	550.269382	275.638329			532.258817	266.633047	G	***1115.587756***	558.297516	1098.561207	549.784242	1097.577191	549.292234	8
6	607.290846	304.149061			589.280281	295.143779	G	***1058.566292***	529.786784	1041.539743	521.273510	1040.555727	520.781502	7
7	694.322874	347.665075			676.312309	338.659793	S	***1001.544828***	501.276052	984.518279	492.762778	983.534263	492.270770	6
8	822.381452	411.694364	805.354903	403.181090	804.370887	402.689082	Q	914.512800	457.760038	897.486251	449.246764	896.502235	448.754756	5
9	935.465516	468.236396	918.438967	459.723122	917.454951	459.231114	L	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
10	1022.497544	511.752410	1005.470995	503.239136	1004.486979	502.747128	S	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
11	1461.722870	731.365073	1444.696321	722.851799	1443.712305	722.359791	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 TMFIGGSQLSQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.0	1606.821121	0.023587	TMFIGGSQLSQK
27.0	1606.821121	0.023587	TMFIGGSQLSQK

Mascot: http://www.matrixscience.com/

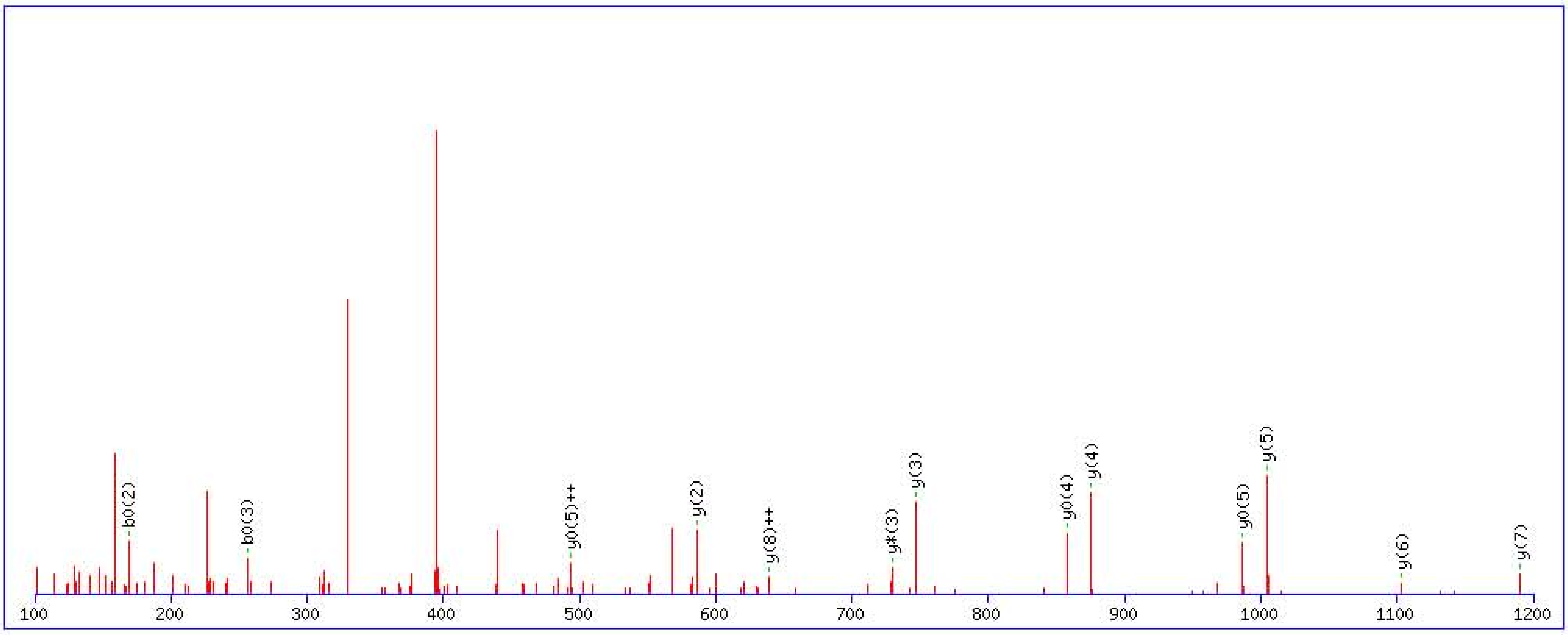
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSVEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

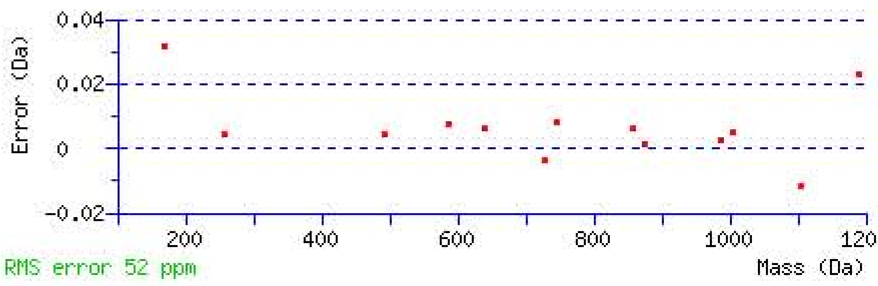
Match to Query 29762: 1375.646952 from(459.556260,3+) rtinseconds(1374) index(20065)
Title: Locus:1.1.1.2621.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

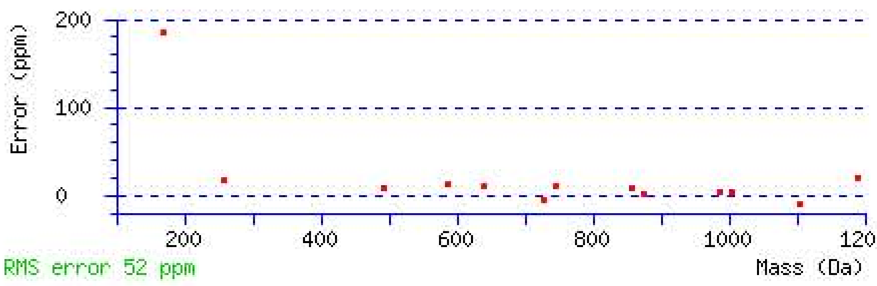
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1375.647568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.025
Matches : 13/74 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							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
27.6	1375.647568	-0.000616	VSSVEECQK

Mascot: http://www.matrixscience.com/

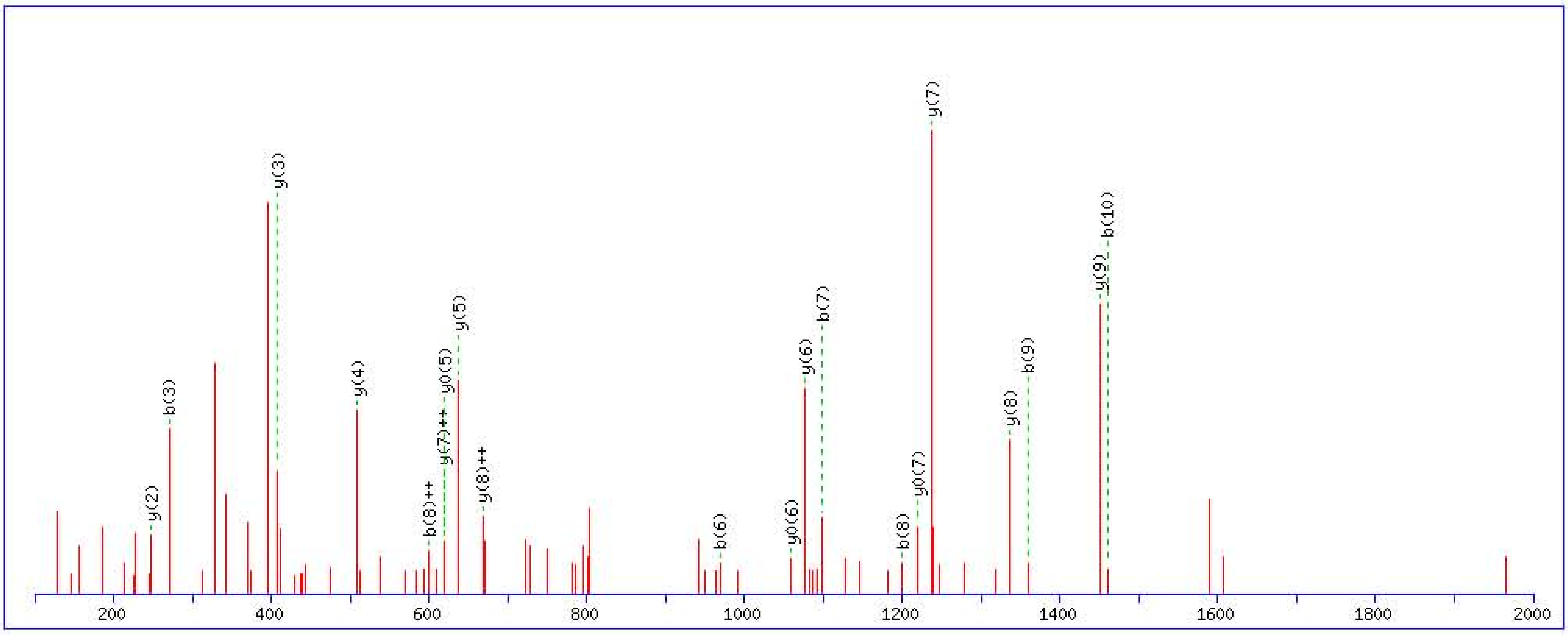
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVNVCQETCTK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

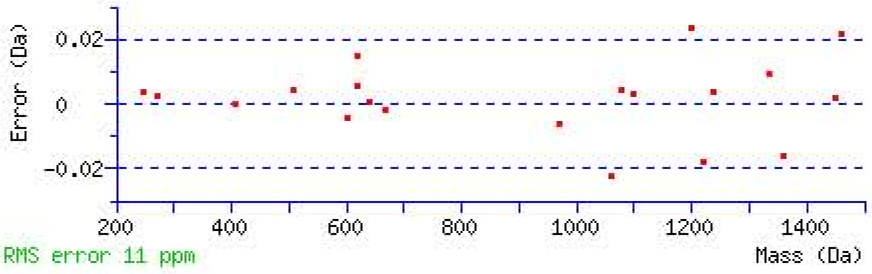
Match to Query 38959: 1605.733868 from(803.874210,2+) rtinseconds(1514) index(21100)
Title: Locus:1.1.1.2670.11 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

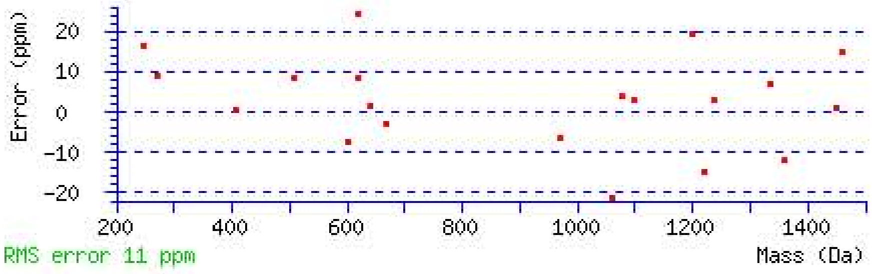
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1605.731339
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00021
Matches : 20/102 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							11
2	157.097154	79.052215					V	1549.717134	775.362205	1532.690585	766.848931	1531.706569	766.356923	10
3	**271.140081**	136.073679	254.113532	127.560404			N	***1450.648720***	725.827998	1433.622171	717.314724	1432.638155	716.822716	9
4	370.208495	185.607886	353.181946	177.094611			V	***1336.605793***	668.806535	1319.579244	660.293260	1318.595228	659.801252	8
5	530.239144	265.623210	513.212595	257.109936			C	***1237.537379***	619.272328	1220.510830	610.759053	1219.526814	610.267045	7
6	**969.464470**	485.235873	952.437921	476.722599			Q	***1077.506730***	539.257003	1060.480181	530.743729	1059.496165	530.251721	6
7	**1098.507063**	549.757170	1081.480514	541.243895	1080.496498	540.751887	E	***638.281404***	319.644340	621.254855	311.131066	620.270839	310.639058	5
8	**1199.554742**	600.281009	1182.528193	591.767735	1181.544177	591.275727	T	***509.238811***	255.123044	492.212262	246.609769	491.228246	246.117761	4
9	**1359.585391**	680.296334	1342.558842	671.783059	1341.574826	671.291051	C	***408.191132***	204.599204	391.164583	196.085930	390.180567	195.593922	3
10	**1460.633070**	730.820173	1443.606521	722.306899	1442.622505	721.814891	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GVNVCQETCTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.7	1605.731339	0.002529	GVNVCQETCTK
4.4	1605.724121	0.009747	MVFFLEDVMACTK
0.4	1605.724121	0.009747	MVFFLEDVMACTK

Mascot: http://www.matrixscience.com/

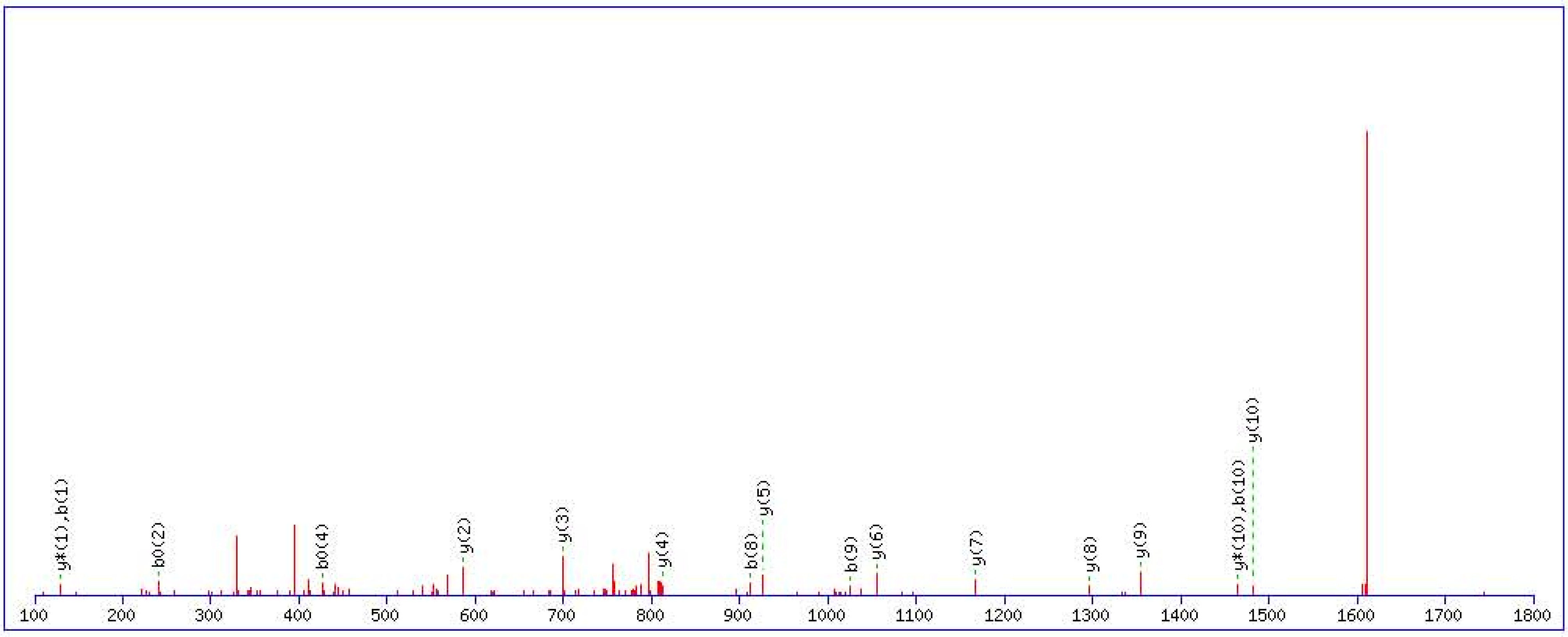
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EKGEIQNILQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

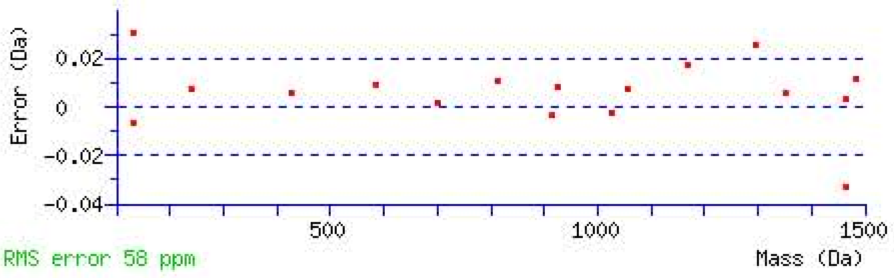
Match to Query 39160: 1609.893128 from(805.953840,2+) rtinseconds(1865) index(77858)
Title: Locus:1.1.1.2000.21 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

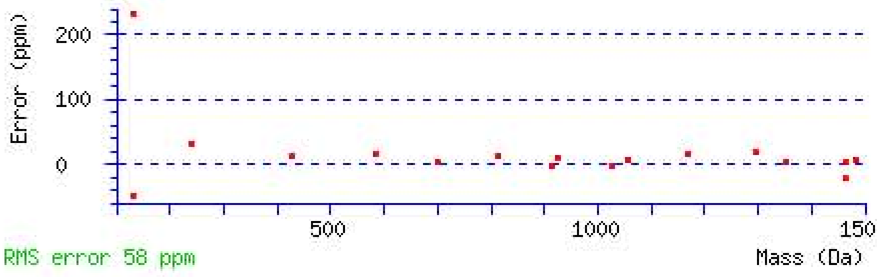
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1609.886124
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 6.6e-006
Matches : 17/104 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	**130.049869**	65.528572			112.039304	56.523290	E							11
2	258.144832	129.576054	241.118283	121.062780	240.134267	120.570772	K	***1481.850847***	741.429061	1464.824298	732.915787	1463.840282	732.423779	10
3	315.166296	158.086786	298.139747	149.573512	297.155731	149.081504	G	***1353.755884***	677.381580	1336.729335	668.868306	1335.745319	668.376297	9
4	444.208889	222.608082	427.182340	214.094808	426.198324	213.602800	E	***1296.734420***	648.870848	1279.707871	640.357574	1278.723855	639.865566	8
5	557.292953	279.150115	540.266404	270.636840	539.282388	270.144832	I	***1167.691827***	584.349552	1150.665278	575.836277			7
6	685.351531	343.179404	668.324982	334.666129	667.340966	334.174121	Q	***1054.607763***	527.807520	1037.581214	519.294245			6
7	799.394458	400.200867	782.367909	391.687592	781.383893	391.195585	N	***926.549185***	463.778231	909.522636	455.264956			5
8	**912.478522**	456.742899	895.451973	448.229625	894.467957	447.737617	I	***812.506258***	406.756767	795.479709	398.243493			4
9	**1025.562586**	513.284931	1008.536037	504.771657	1007.552021	504.279649	L	***699.422194***	350.214735	682.395645	341.701461			3
10	**1464.787912**	732.897594	1447.761363	724.384320	1446.777347	723.892312	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 EKGEIQNILQK
(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	1609.886124	0.007004	EKGEIQNILQK
14.1	1609.886124	0.007004	EKGEIQNILQK
4.1	1609.872208	0.020920	QEHGLLSLRKNGMK
3.8	1609.871521	0.021607	QESFSSILAYKIPK
3.4	1609.897354	-0.004226	ESAAINQILGRK
2.5	1609.897354	-0.004226	EQELLRQKQK
2.2	1609.889969	0.003159	QENLSLRTAVHKSK
1.2	1609.911285	-0.018157	LLTQMLPPSVAEALK
1.0	1609.872192	0.020936	QEAERALKQAR
0.9	1609.897400	-0.004272	TNLRIVDVGGQK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

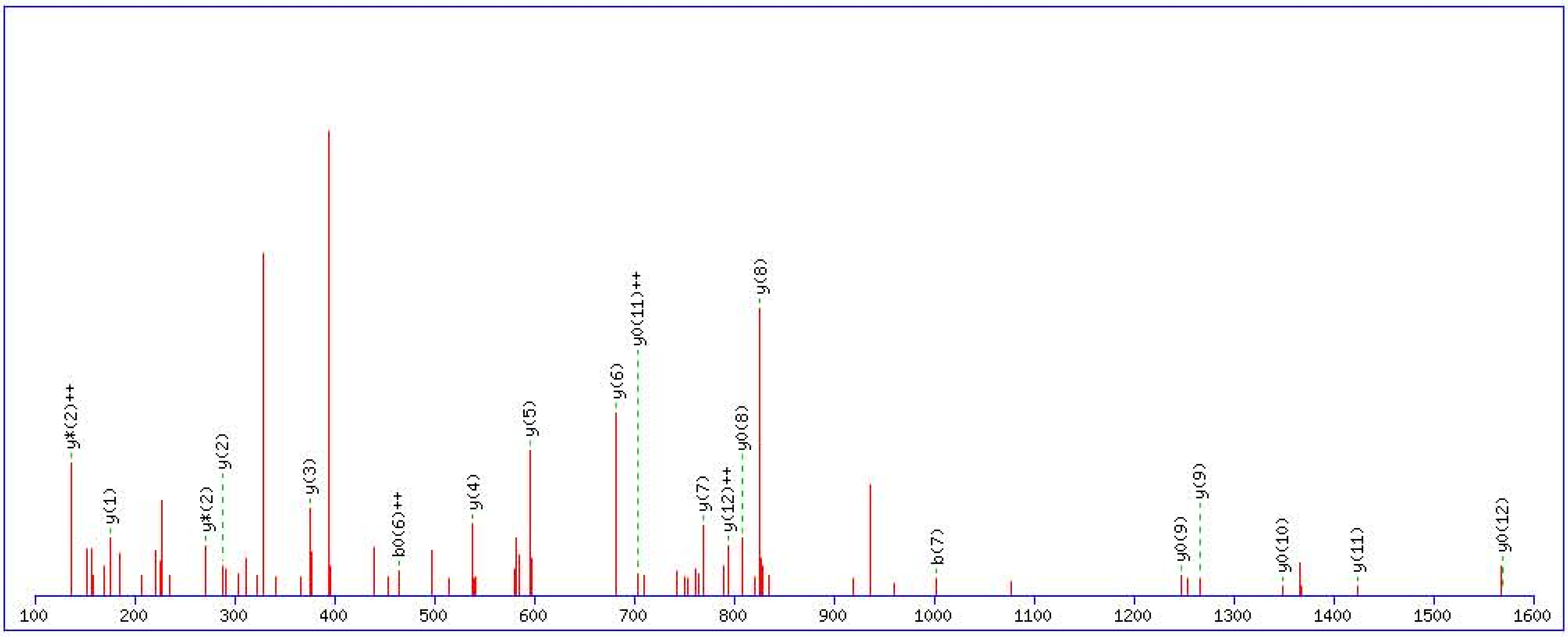
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAYGTQGSSGYSLR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

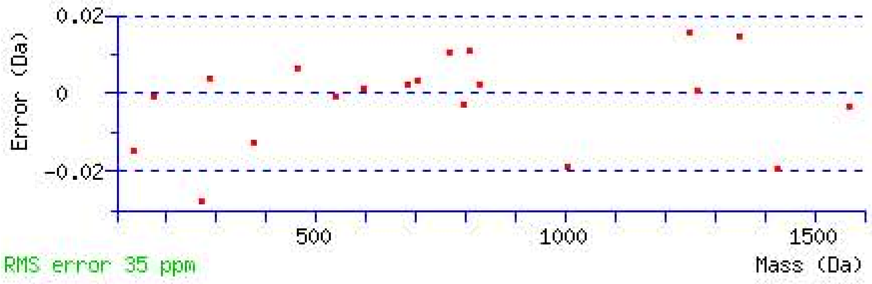
Match to Query 44473: 1769.879682 from(590.967170,3+) rtinseconds(1872) index(23739)
Title: Locus:1.1.1.2794.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

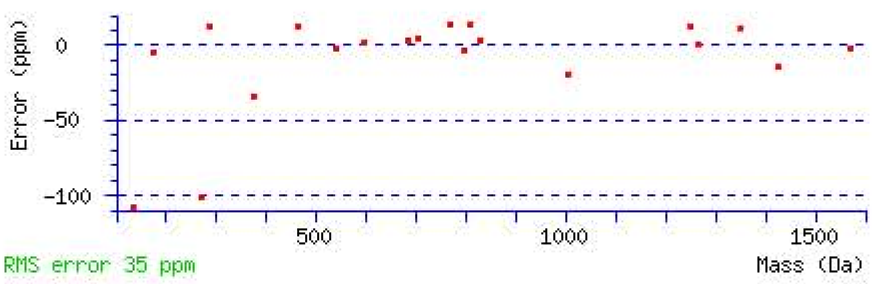
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1769.877045
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00017
Matches : 20/134 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					I							14
2	185.128454	93.067865					A	1657.800269	829.403773	1640.773720	820.890498	1639.789704	820.398490	13
3	348.191783	174.599529					Y	1586.763155	793.885216	1569.736606	785.371941	1568.752590	784.879933	12
4	405.213247	203.110261					G	***1423.699826***	712.353551	1406.673277	703.840277	1405.689261	703.348269	11
5	506.260926	253.634101			488.250361	244.628818	T	1366.678362	683.842819	1349.651813	675.329545	1348.667797	674.837537	10
6	945.486252	473.246764	928.459703	464.733490	927.475687	464.241482	Q	***1265.630683***	633.318980	1248.604134	624.805705	1247.620118	624.313697	9
7	1002.507716	501.757496	985.481167	493.244222	984.497151	492.752214	G	***826.405357***	413.706317	809.378808	405.193042	808.394792	404.701034	8
8	1089.539744	545.273510	1072.513195	536.760236	1071.529179	536.268228	S	***769.383893***	385.195585	752.357344	376.682310	751.373328	376.190302	7
9	1176.571772	588.789524	1159.545223	580.276250	1158.561207	579.784242	S	***682.351865***	341.679571	665.325316	333.166296	664.341300	332.674288	6
10	1233.593236	617.300256	1216.566687	608.786982	1215.582671	608.294974	G	***595.319837***	298.163557	578.293288	289.650282	577.309272	289.158274	5
11	1396.656565	698.831921	1379.630016	690.318646	1378.646000	689.826638	Y	***538.298373***	269.652825	521.271824	261.139550	520.287808	260.647542	4
12	1483.688593	742.347935	1466.662044	733.834660	1465.678028	733.342652	S	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
13	1596.772657	798.889967	1579.746108	790.376692	1578.762092	789.884684	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 IAYGTQGSSGYSLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.2	1769.877045	0.002637	IAYGTQGSSGYSLR

Mascot: http://www.matrixscience.com/

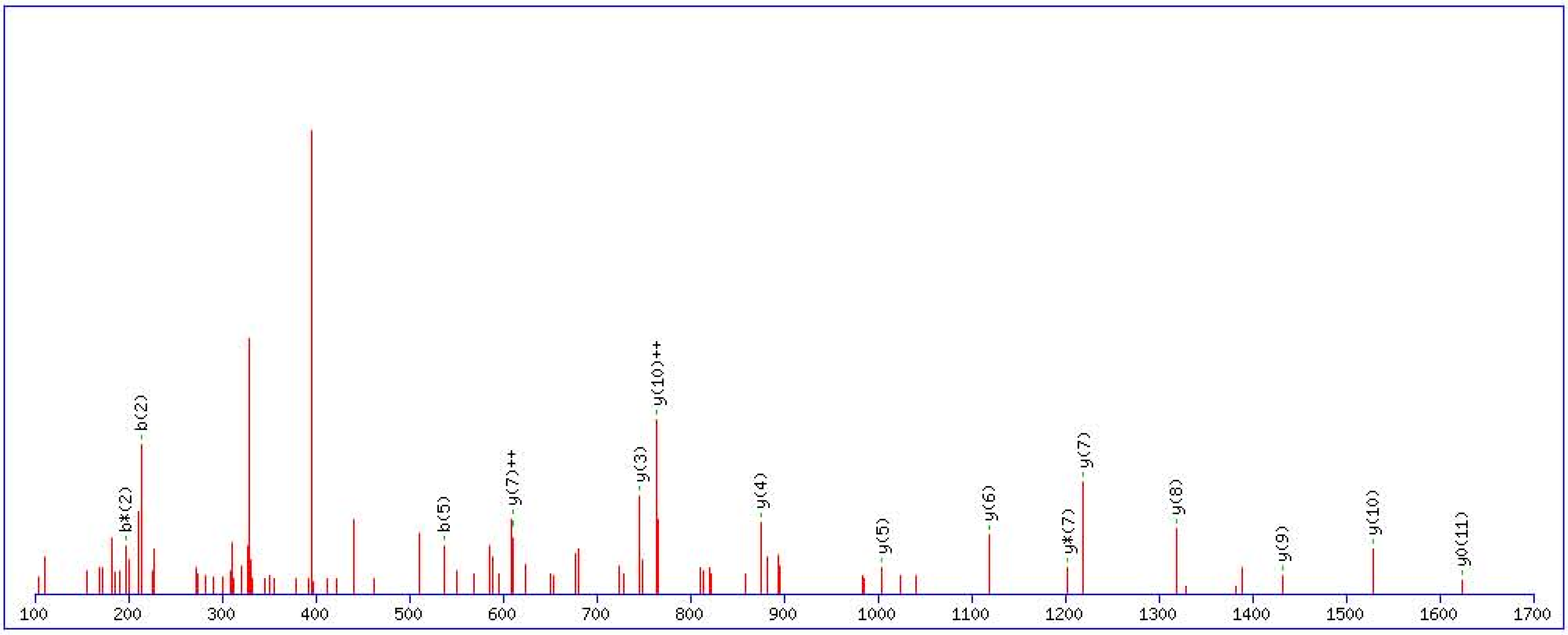
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNIPLVTNEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

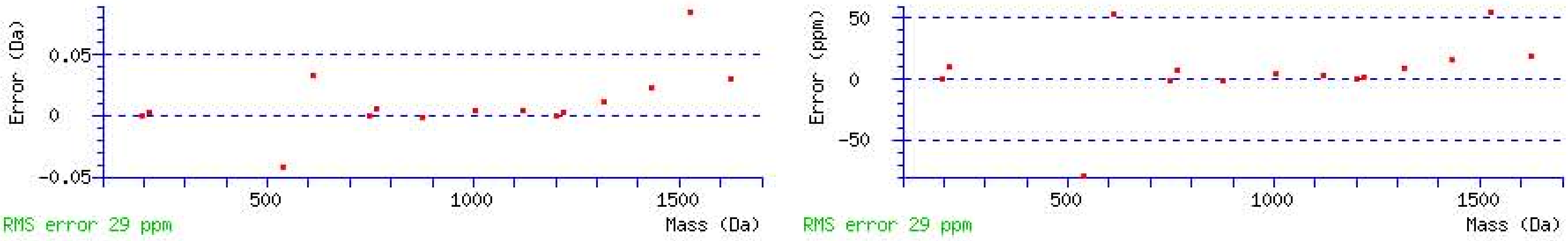
Match to Query 46667: 1853.951292 from(618.991040,3+) rtinseconds(2105) index(25443)
Title: Locus:1.1.1.2875.17 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1853.937927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 43 **Expect:** 0.0014
Matches : 15/124 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	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
42.5	1853.937927	0.013365	VNIPLVTNEECQK

Mascot: http://www.matrixscience.com/

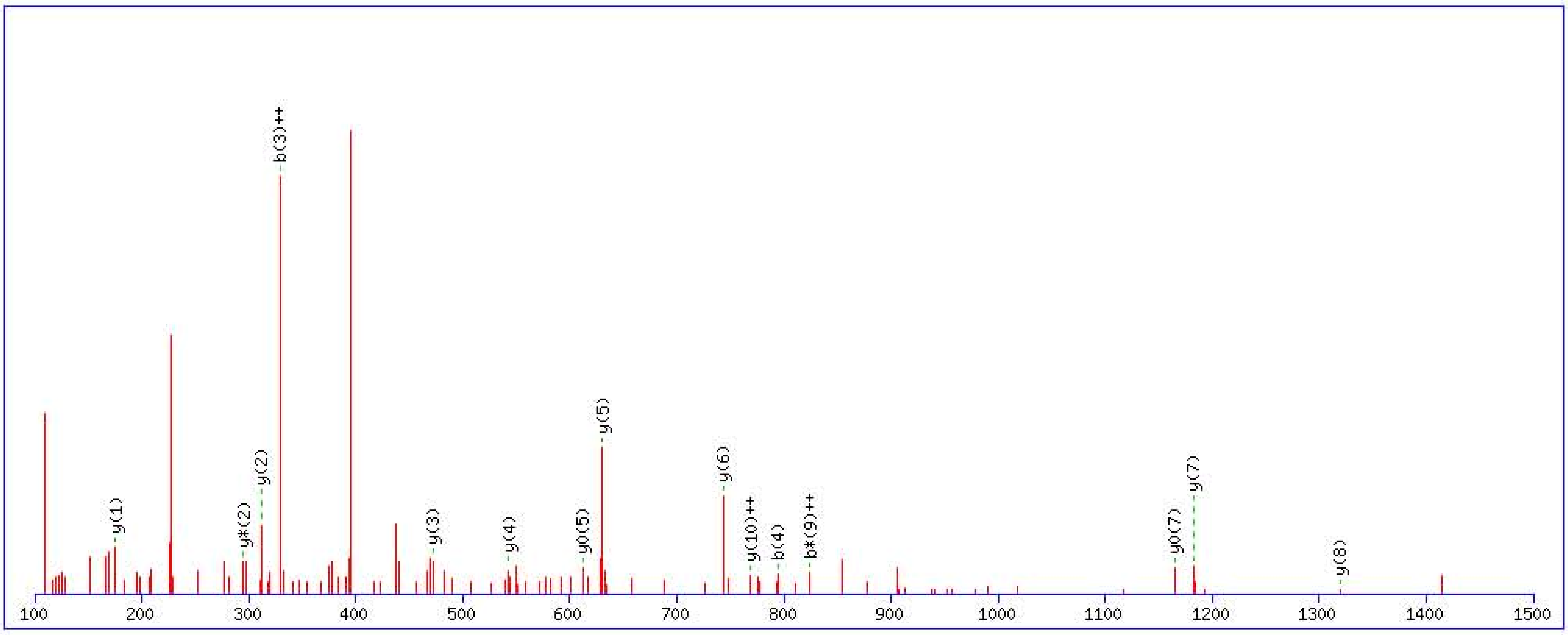
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QCGHQISACHR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

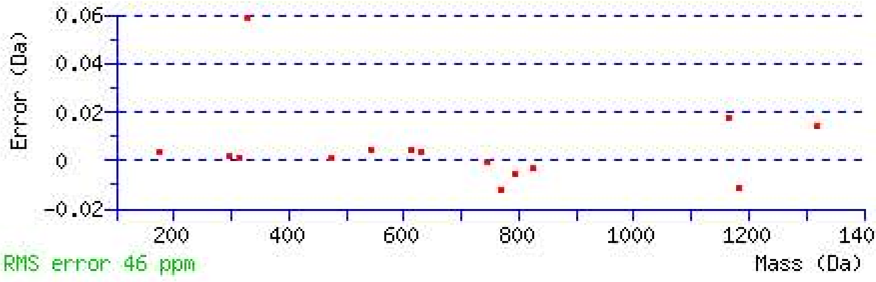
Match to Query 49353: 1974.915776 from(494.736220,4+) rtinseconds(1437) index(20524)
Title: Locus:1.1.1.2643.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

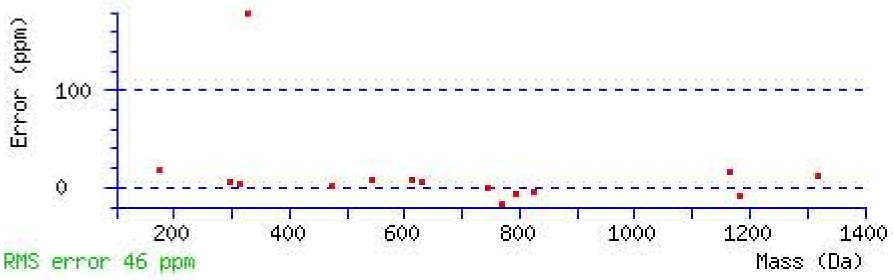
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 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: 29 **Expect:** 0.017
Matches : 15/100 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	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
28.8	1974.916122	-0.000346	QCGHQISACHR

Mascot: http://www.matrixscience.com/

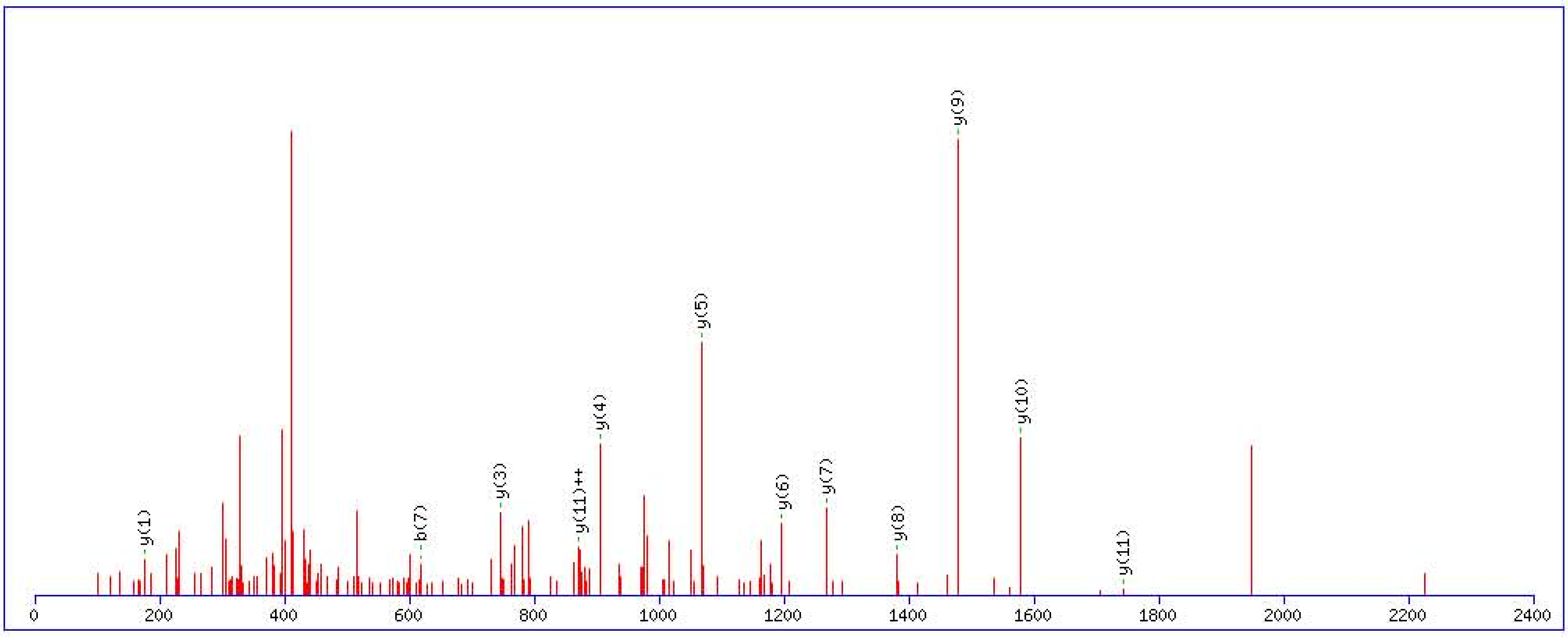
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGDVASMYTPNAQYCQMR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

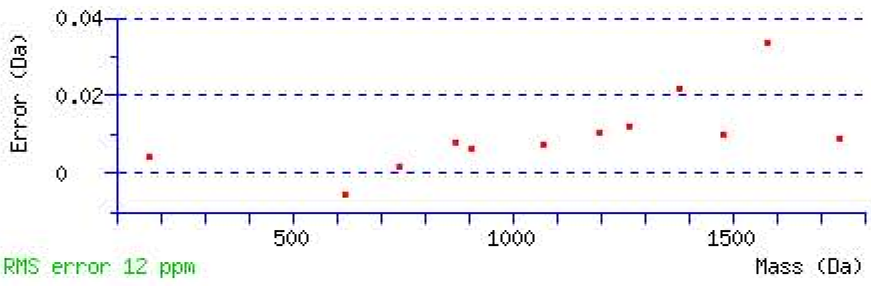
Match to Query 59245: 2359.046862 from(787.356230,3+) rtinseconds(2050) index(79199)
Title: Locus:1.1.1.2064.18 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

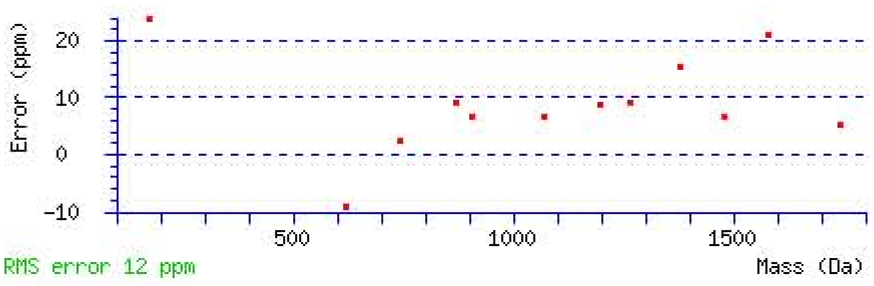
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2359.021759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 63 **Expect:** 3.9e-006
Matches : 12/162 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	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
62.5	2359.021759	0.025103	GGDVASMYTPNAQYCQMR
26.1	2359.021759	0.025103	GGDVASMYTPNAQYCQMR
5.0	2359.079300	-0.032438	TPMSVLQQAGGSMMDGPGPR

Mascot: http://www.matrixscience.com/

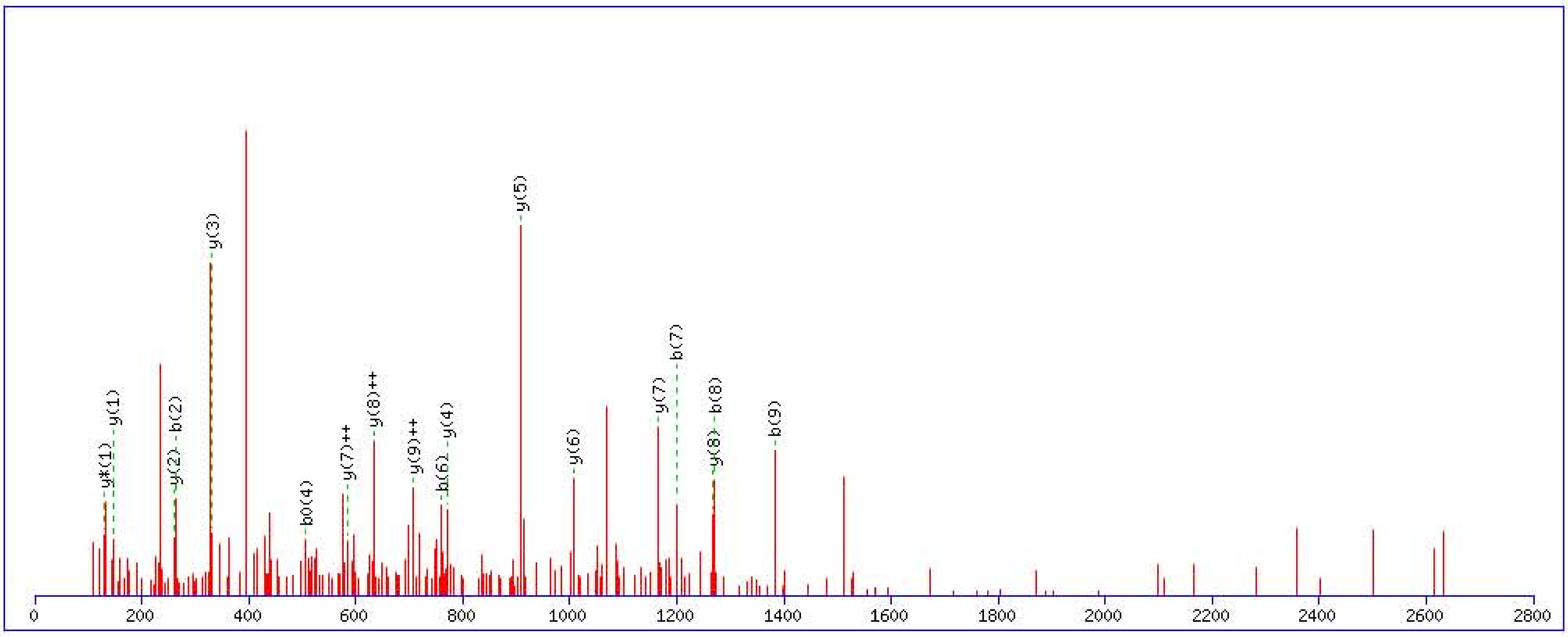
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFTCVHQALK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

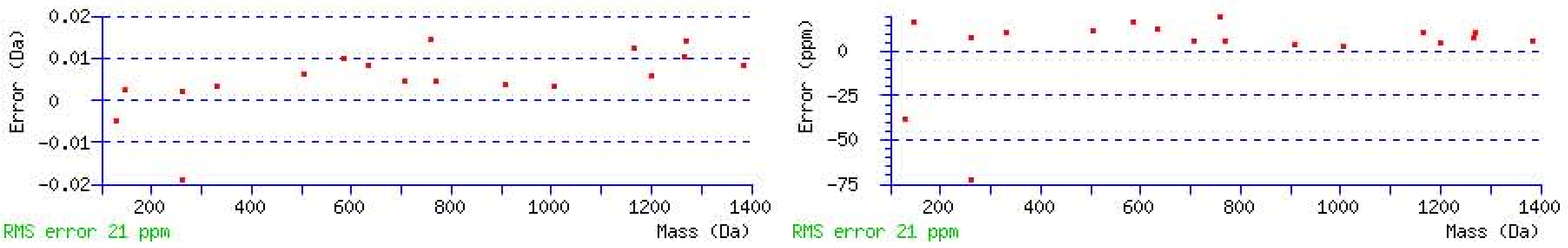
Match to Query 35927: 1528.771128 from(765.392840,2+) rtinseconds(1803) index(40807)
Title: Locus:1.1.1.3077.18 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1528.753052
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0015
Matches : 18/82 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	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
34.6	1528.753052	0.018076	DFTCVHQALK
4.4	1528.788528	-0.017400	EEQHQLAVTAYLK
2.4	1528.780685	-0.009557	EVLDQGTEISK
2.4	1528.763367	0.007761	EDQWRGLNEAAIK
1.1	1528.780670	-0.009542	EIQTLQEETK

Mascot: http://www.matrixscience.com/

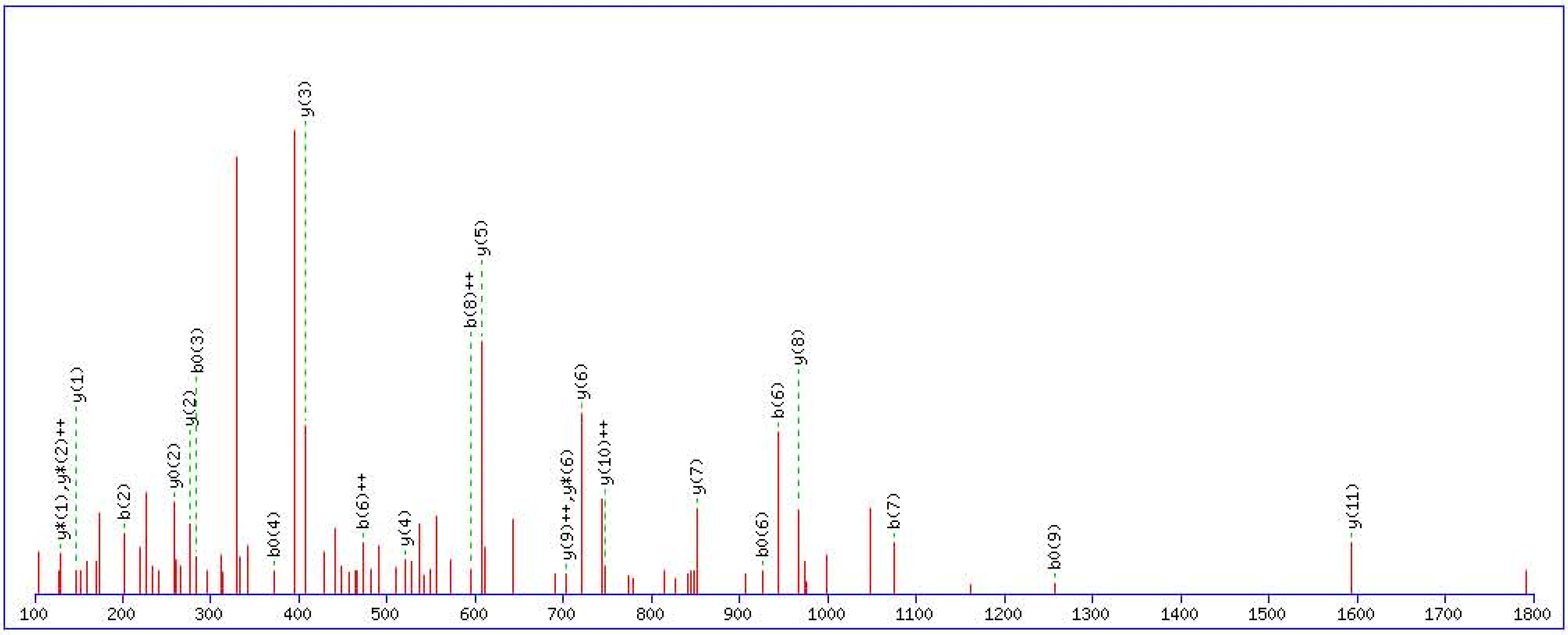
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTTSQDMLSIMEK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

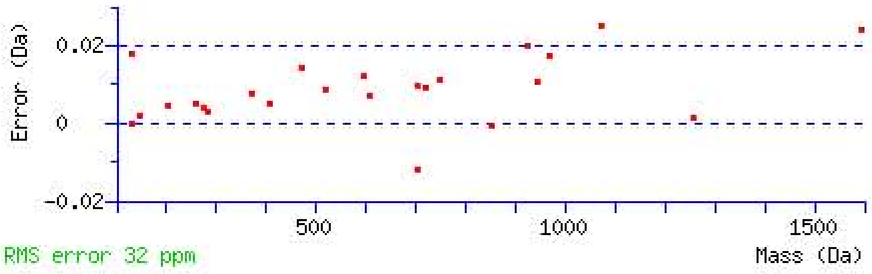
Match to Query 45097: 1792.895022 from(598.638950,3+) rtinseconds(2375) index(44830)
Title: Locus:1.1.1.3276.9 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

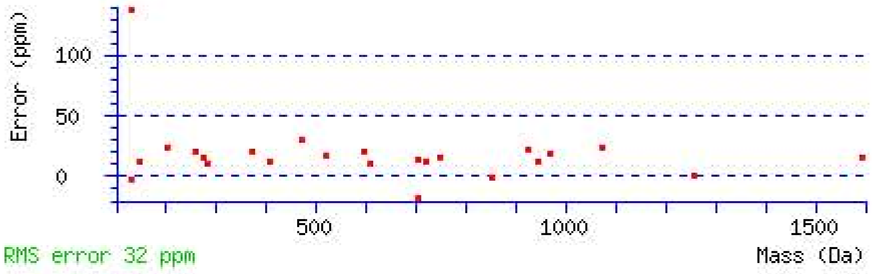
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1792.877304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.047
Matches : 24/132 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	100.075690	50.541483					V							13
2	**201.123369**	101.065322			183.112804	92.060040	T	1694.816178	847.911727	1677.789629	839.398453	1676.805613	838.906445	12
3	302.171048	151.589162			284.160483	142.583879	T	***1593.768499***	797.387888	1576.741950	788.874613	1575.757934	788.382605	11
4	389.203076	195.105176			371.192511	186.099893	S	1492.720820	746.864048	1475.694271	738.350774	1474.710255	737.858766	10
5	828.428402	414.717839	811.401853	406.204565	810.417837	405.712557	Q	1405.688792	703.348034	1388.662243	694.834760	1387.678227	694.342752	9
6	**943.455345**	**472.231311**	926.428796	463.718036	925.444780	463.226028	D	***966.463466***	483.735371	949.436917	475.222097	948.452901	474.730089	8
7	**1074.495830**	537.751553	1057.469281	529.238279	1056.485265	528.746271	M	***851.436523***	426.221900	834.409974	417.708625	833.425958	417.216617	7
8	1187.579894	**594.293585**	1170.553345	585.780311	1169.569329	585.288302	L	***720.396038***	360.701657	703.369489	352.188383	702.385473	351.696375	6
9	1274.611922	637.809599	1257.585373	629.296325	1256.601357	628.804317	S	***607.311974***	304.159625	590.285425	295.646351	589.301409	295.154343	5
10	1387.695986	694.351631	1370.669437	685.838357	1369.685421	685.346348	I	***520.279946***	260.643611	503.253397	252.130337	502.269381	251.638329	4
11	1518.736471	759.871873	1501.709922	751.358599	1500.725906	750.866591	M	***407.195882***	204.101579	390.169333	195.588305	389.185317	195.096297	3
12	1647.779064	824.393170	1630.752515	815.879896	1629.768499	815.387888	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VTTSQDMLSIMEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.1	1792.877304	0.017718	VTTSQDMLSIMEK

Mascot: http://www.matrixscience.com/

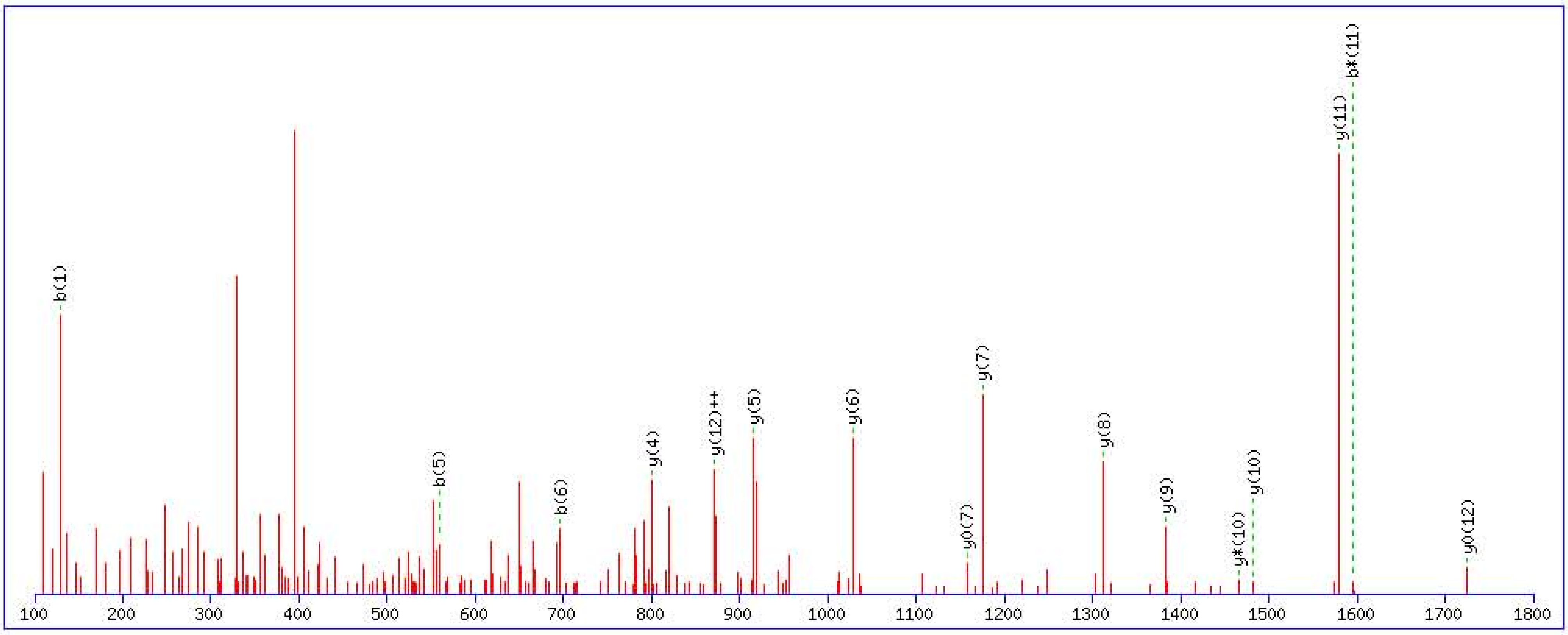
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KYPVAHFIDQTLK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

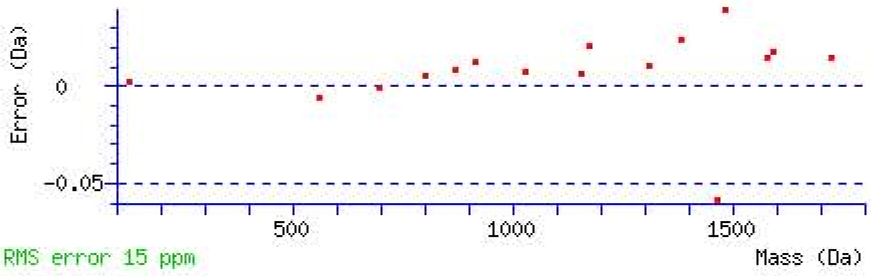
Match to Query 46972: 1870.036632 from(624.352820,3+) rtinseconds(2011) index(42282)
Title: Locus:1.1.1.3149.10 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

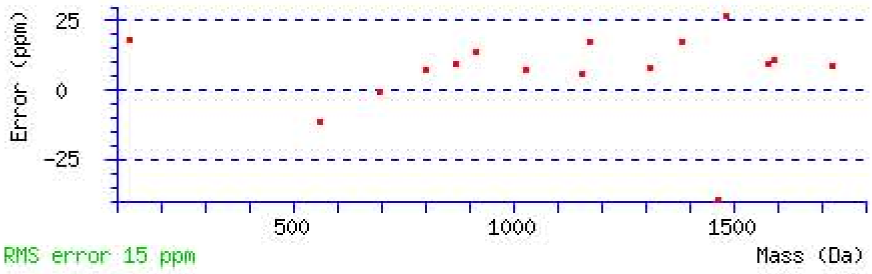
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1870.017502
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0019
Matches : 17/124 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	**129.102239**	65.054757	112.075690	56.541483			**K**							**13**
2	292.165568	146.586422	275.139019	138.073148			**Y**	1742.929827	871.968552	1725.903278	863.455277	1724.919262	862.963269	**12**
3	389.218332	195.112804	372.191783	186.599529			**P**	***1579.866498***	790.436887	1562.839949	781.923613	1561.855933	781.431605	**11**
4	488.286746	244.647011	471.260197	236.133737			**V**	***1482.813734***	741.910505	1465.787185	733.397231	1464.803169	732.905223	**10**
5	**559.323860**	280.165568	542.297311	271.652294			**A**	***1383.745320***	692.376298	1366.718771	683.863024	1365.734755	683.371016	**9**
6	**696.382772**	348.695024	679.356223	340.181750			**H**	***1312.708206***	656.857741	1295.681657	648.344467	1294.697641	647.852459	**8**
7	843.451186	422.229231	826.424637	413.715957			**F**	***1175.649294***	588.328285	1158.622745	579.815011	1157.638729	579.323003	**7**
8	956.535250	478.771263	939.508701	470.257989			**I**	***1028.580880***	514.794078	1011.554331	506.280804	1010.570315	505.788796	**6**
9	1071.562193	536.284735	1054.535644	527.771460	1053.551628	527.279452	**D**	***915.496816***	458.252046	898.470267	449.738772	897.486251	449.246764	**5**
10	1510.787519	755.897398	1493.760970	747.384123	1492.776954	746.892115	**Q**	***800.469873***	400.738575	783.443324	392.225300	782.459308	391.733292	**4**
11	1611.835198	806.421237	1594.808649	797.907963	1593.824633	797.415955	**T**	361.244547	181.125911	344.217998	172.612637	343.233982	172.120629	**3**
12	**1724.919262**	862.963269	1707.892713	854.449995	1706.908697	853.957987	**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 KYPVAHFIDQTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.9	1870.017502	0.019130	KYPVAHFIDQTLK

Mascot: http://www.matrixscience.com/

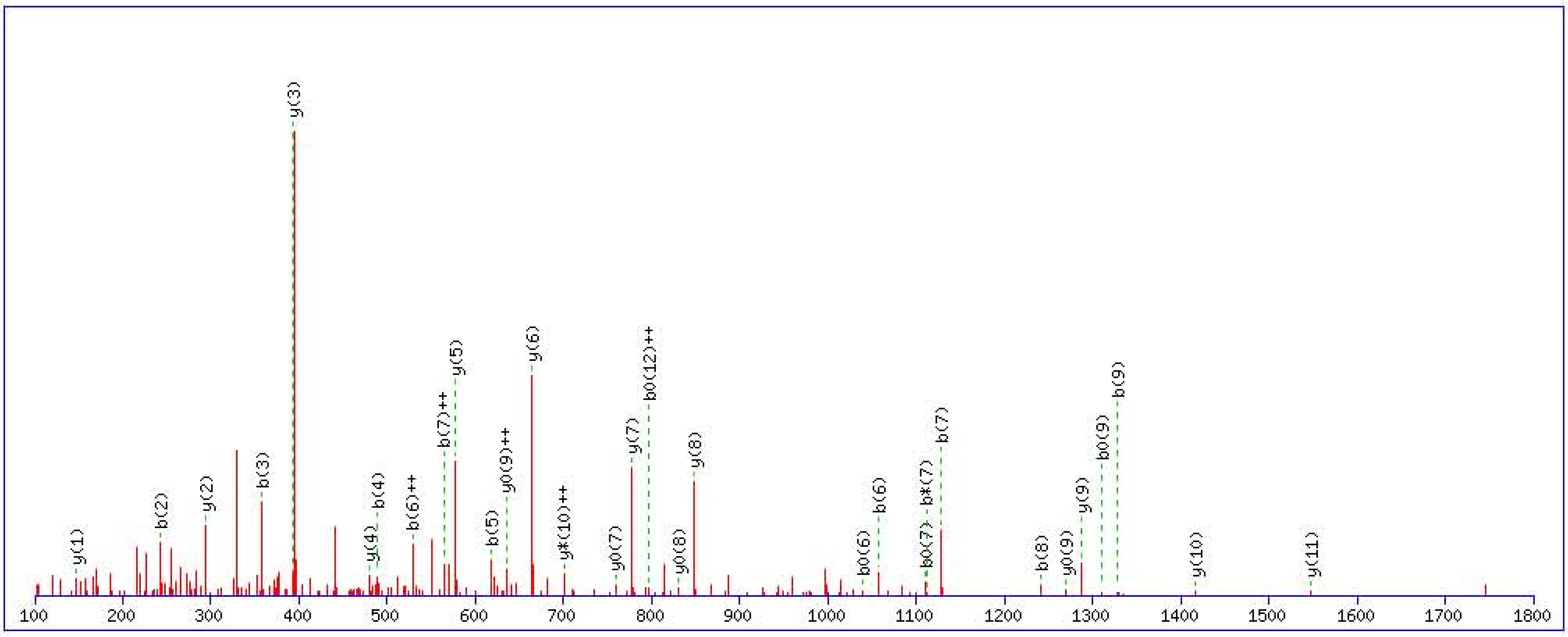
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEDMEQALSPSVFK**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

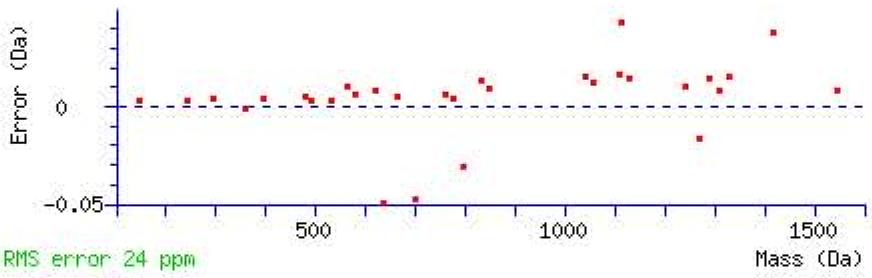
Match to Query 47546: 1903.966362 from(635.662730,3+) rtinseconds(2430) index(45160)
Title: Locus:1.1.1.3295.8 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

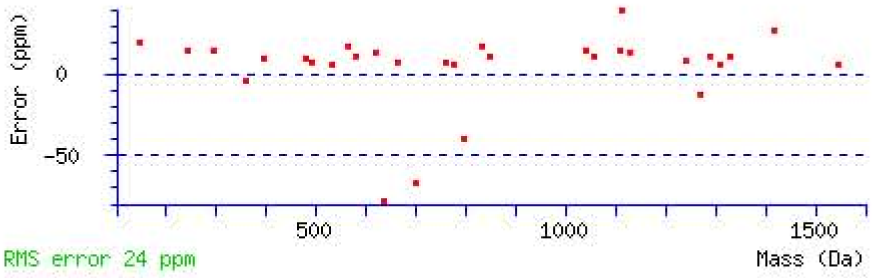
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1903.942337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 6.7e-005
Matches : 31/138 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	114.091340	57.549308					L							14
2	**243.133933**	122.070605			225.123368	113.065322	E	1791.865570	896.436423	1774.839021	887.923149	1773.855005	887.431141	13
3	**358.160876**	179.584076			340.150311	170.578794	D	1662.822977	831.915127	1645.796428	823.401852	1644.812412	822.909844	12
4	**489.201361**	245.104319			471.190796	236.099036	M	***1547.796034***	774.401655	1530.769485	765.888381	1529.785469	765.396373	11
5	**618.243954**	309.625615			600.233389	300.620333	E	***1416.755549***	708.881413	1399.729000	700.368138	1398.744984	699.876130	10
6	**1057.469280**	**529.238278**	1040.442731	520.725004	1039.458715	520.232996	Q	***1287.712956***	644.360116	1270.686407	635.846842	1269.702391	635.354834	9
7	**1128.506394**	**564.756835**	1111.479845	556.243561	1110.495829	555.751553	A	***848.487630***	424.747453	831.461081	416.234179	830.477065	415.742171	8
8	**1241.590458**	621.298867	1224.563909	612.785593	1223.579893	612.293584	L	***777.450516***	389.228896	760.423967	380.715622	759.439951	380.223614	7
9	**1328.622486**	664.814881	1311.595937	656.301607	1310.611921	655.809598	S	***664.366452***	332.686864	647.339903	324.173590	646.355887	323.681582	6
10	1425.675250	713.341263	1408.648701	704.827989	1407.664685	704.335981	P	***577.334424***	289.170850	560.307875	280.657576	559.323859	280.165568	5
11	1512.707278	756.857277	1495.680729	748.344003	1494.696713	747.851995	S	***480.281660***	240.644468	463.255111	232.131194	462.271095	231.639186	4
12	1611.775692	806.391484	1594.749143	797.878210	1593.765127	797.386202	V	***393.249632***	197.128454	376.223083	188.615180			3
13	1758.844106	879.925691	1741.817557	871.412417	1740.833541	870.920409	F	***294.181218***	147.594247	277.154669	139.080973			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LEDMEQALSPSVFK
(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	1903.942337	0.024025	LEDMEQALSPSVFK

Mascot: http://www.matrixscience.com/

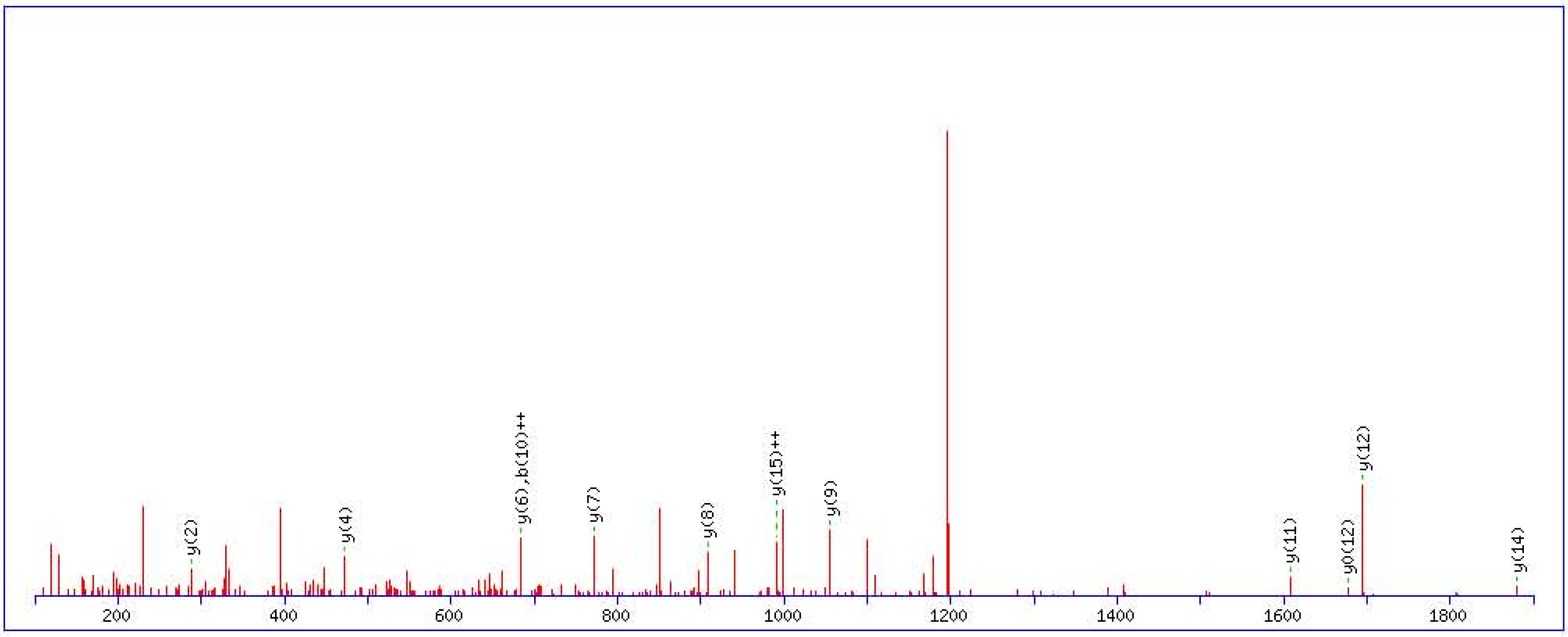
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVTSVSQIFHSPDLAIR**
Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

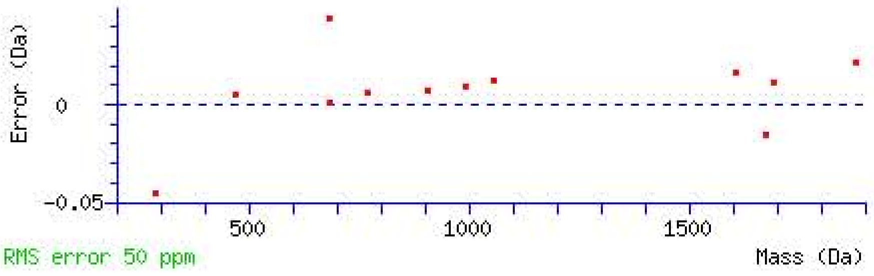
Match to Query 53897: 2137.166862 from(713.396230,3+) rtinseconds(2344) index(44573)
Title: Locus:1.1.1.3265.15 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

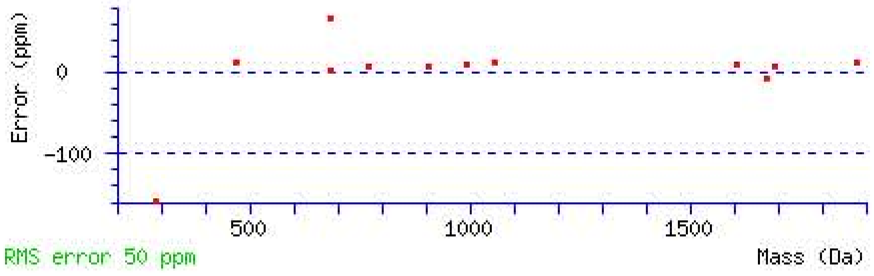
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2137.135406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.023
Matches : 12/168 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	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
28.7	2137.135406	0.031456	GVTSVSQIFHSPDLAIR

Mascot: http://www.matrixscience.com/

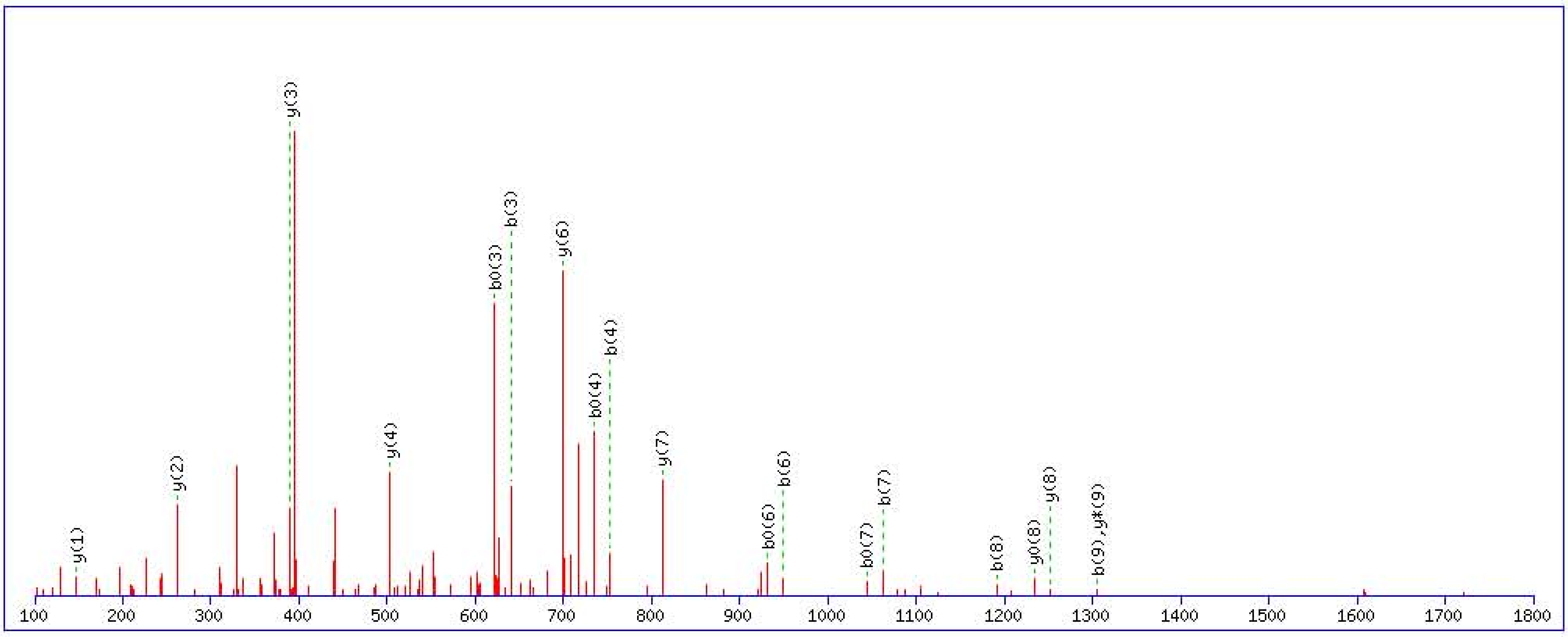
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAQLPVIENK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

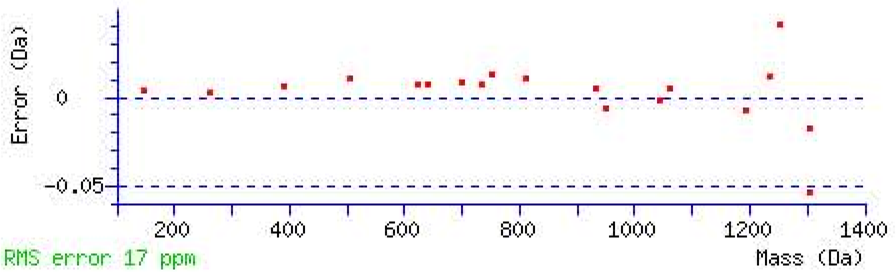
Match to Query 33371: 1450.798368 from(726.406460,2+) rtinseconds(1957) index(6278)
Title: Locus:1.1.1.2935.19 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

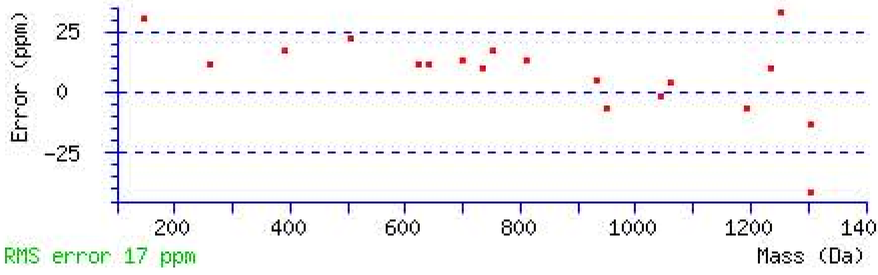
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1450.785355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0018
Matches : 19/100 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	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
35.2	1450.785355	0.013013	EAQLPVIENK
5.5	1450.790527	0.007841	QNIWRHNRLSK
5.2	1450.777985	0.020383	TVKGGFSETRIEK
4.0	1450.803986	-0.005618	QLAEQIK
4.0	1450.796600	0.001768	QISAVHKETK
0.3	1450.796585	0.001783	TKNMFLTRALEK
0.2	1450.785355	0.013013	TLQIFNIEMKSK

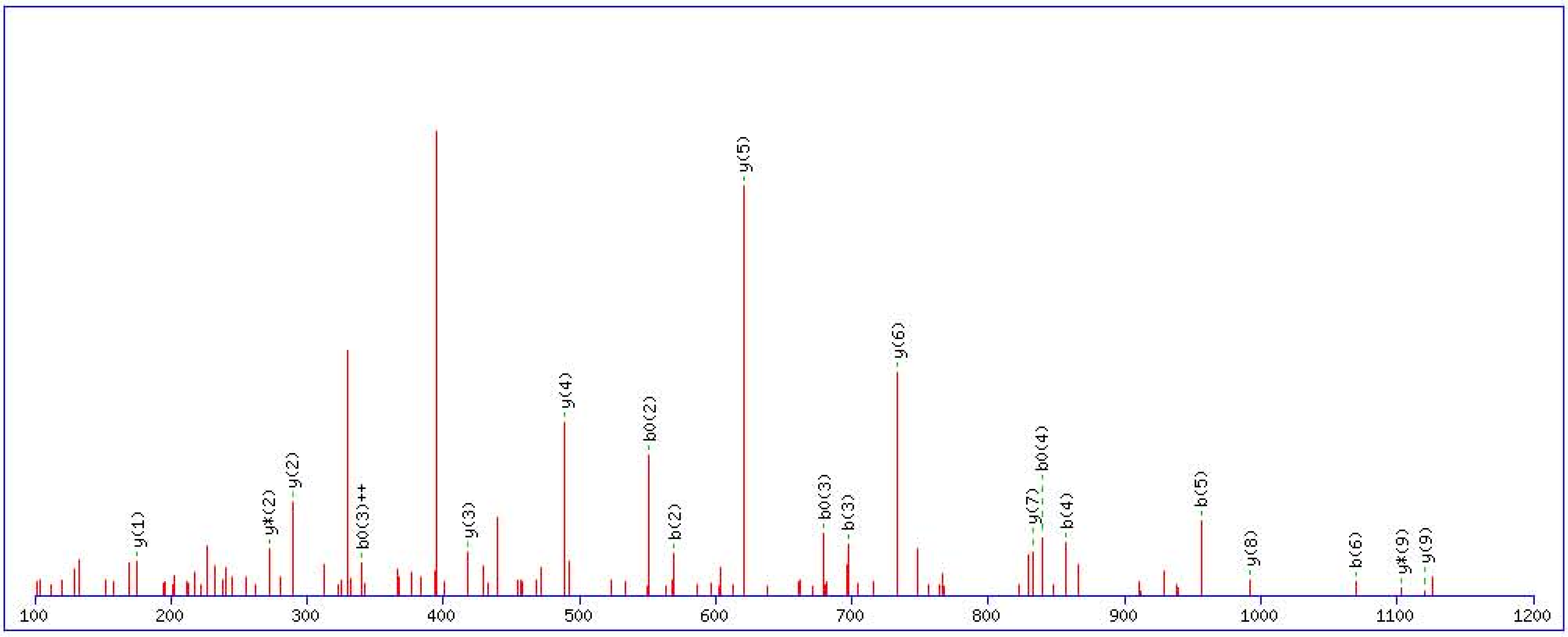
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

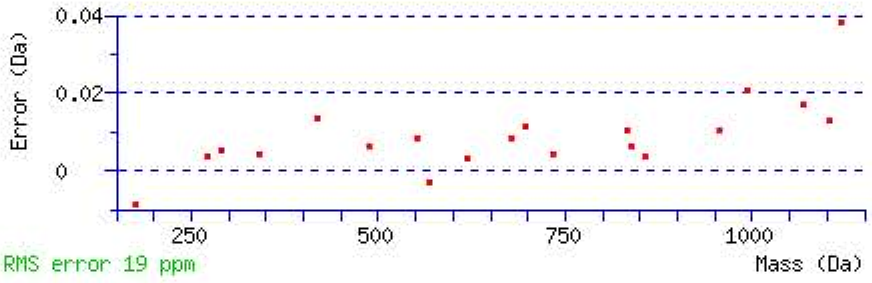
Match to Query 42170: 1687.793502 from(563.605110,3+) rtinseconds(1798) index(77540)
Title: Locus:1.1.1.1977.8 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

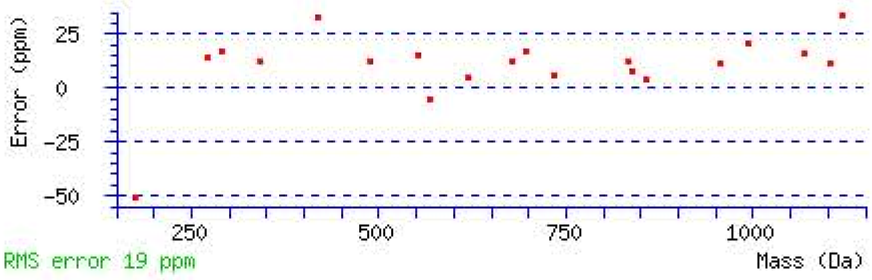
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 61  Expect: 6.7e-006
Matches : 20/114 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
61.0	1687.784393	0.009109	EQQCVIMAENR
42.9	1687.784393	0.009109	EQQCVIMAENR
5.5	1687.781006	0.012496	ELMAWNQAENR
1.0	1687.787552	0.005950	GASEDGEYFLMIRGK

Mascot: http://www.matrixscience.com/

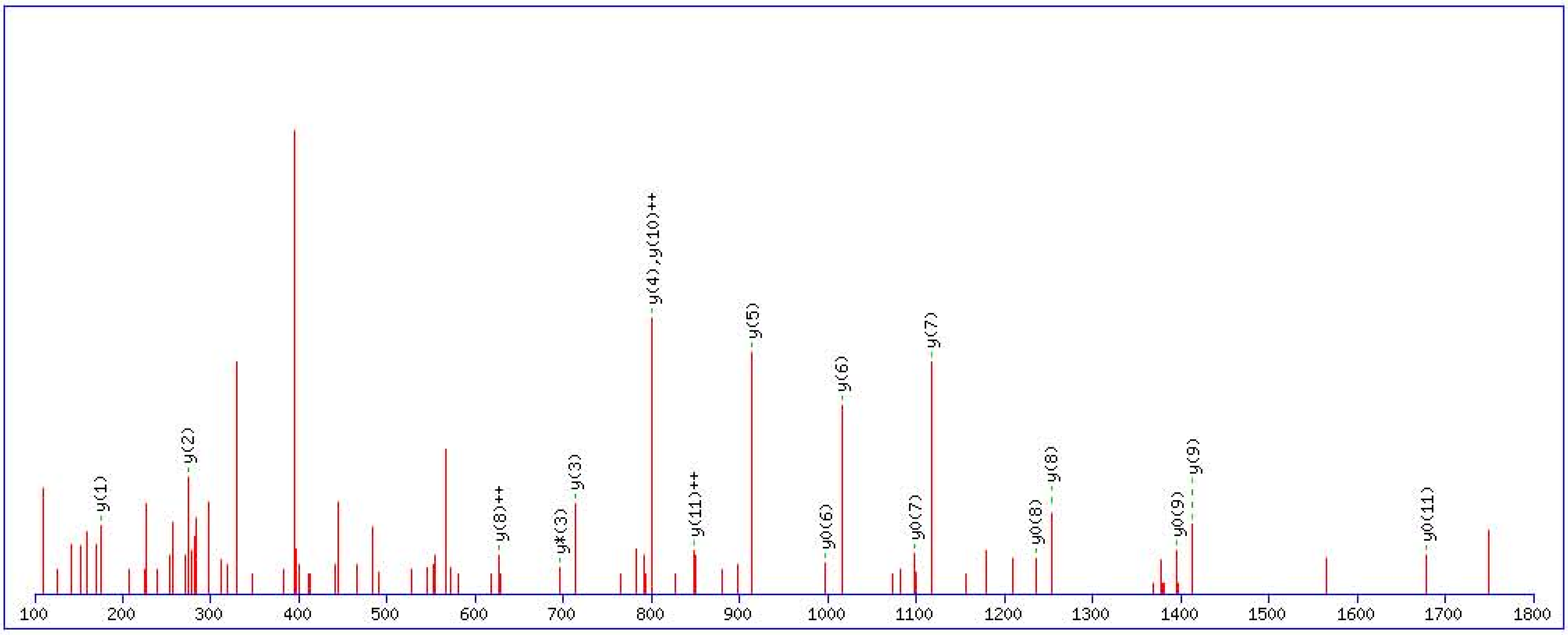
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **APWCHTTNSQVR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

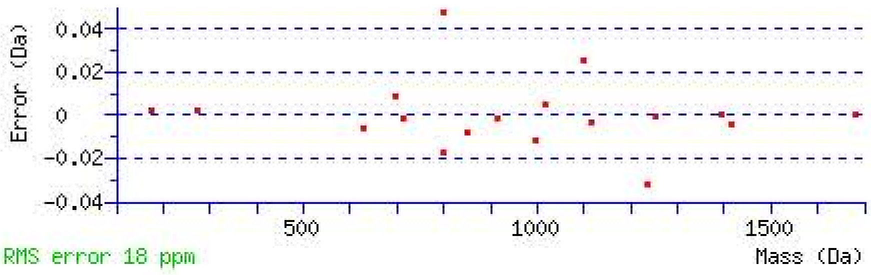
Match to Query 44343: 1766.836662 from(589.952830,3+) rtinseconds(1495) index(20948)
Title: Locus:1.1.1.2663.13 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

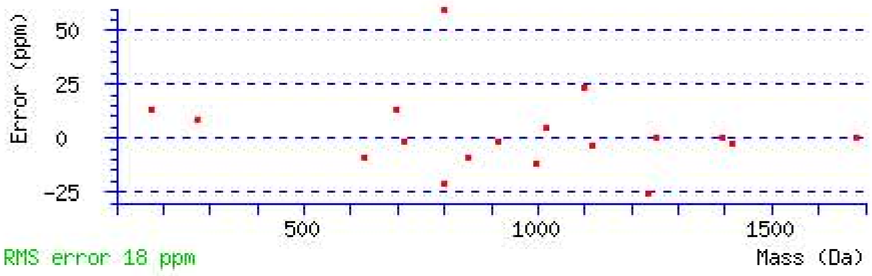
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 58  Expect: 2.9e-005
Matches : 18/102 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	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





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
57.7	1766.834488	0.002174	APWCHTTNSQVR

Mascot: http://www.matrixscience.com/

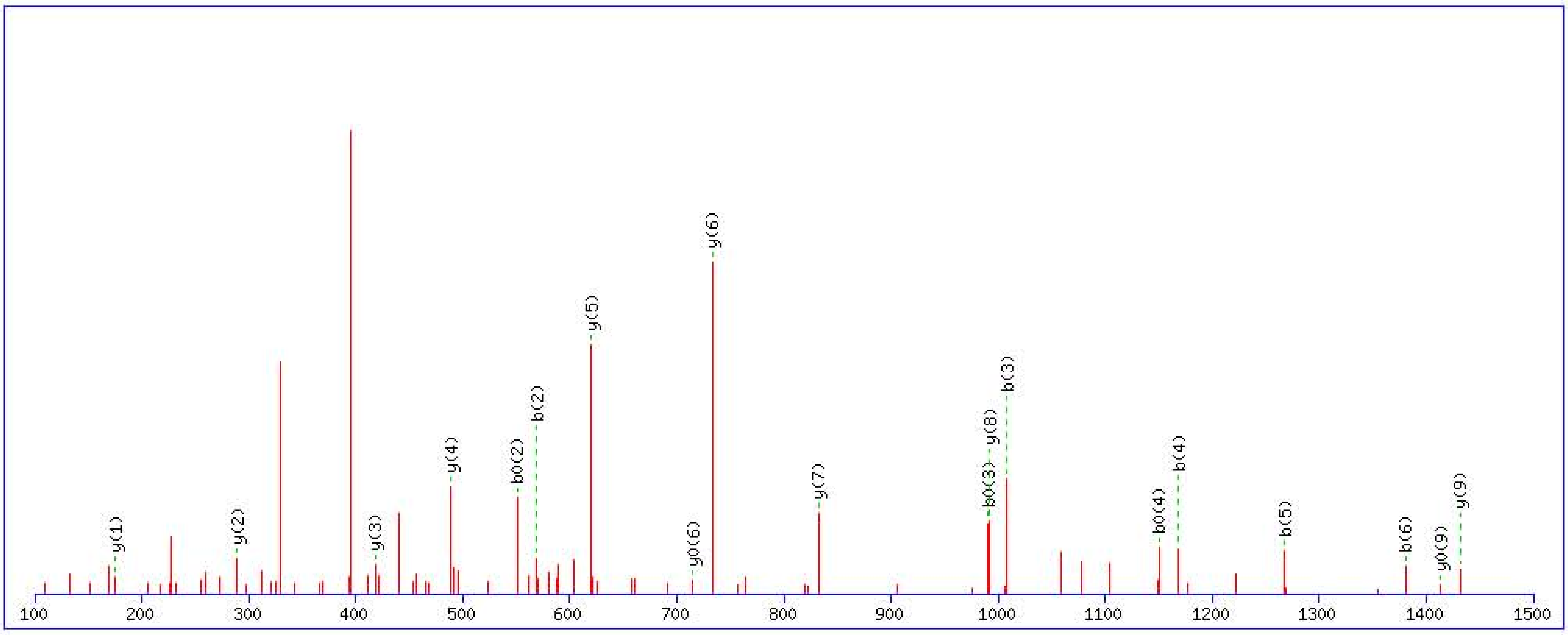
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

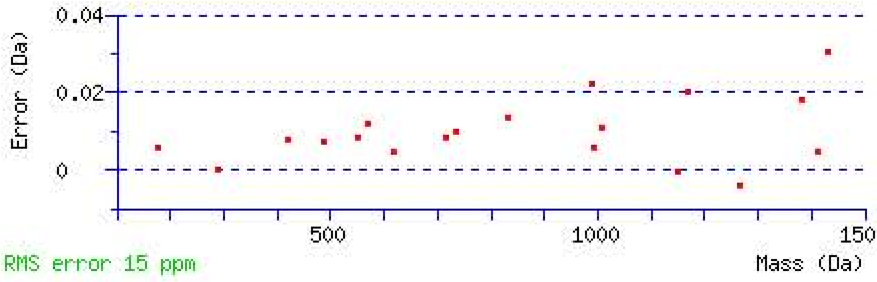
Match to Query 49935: 1998.969612 from(667.330480,3+) rtinseconds(2104) index(79569)
Title: Locus:1.1.1.2083.18 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

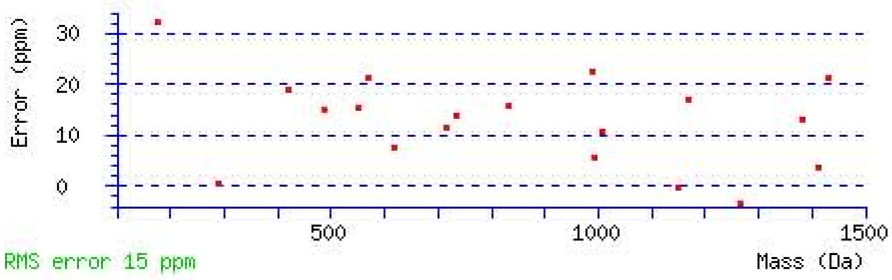
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 43  Expect: 0.00013
Matches : 19/114 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							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
43.2	1998.951141	0.018471	EQQCVIMAENR
1.7	1998.942841	0.026771	QQEEAQAAAAAASAESR

Mascot: http://www.matrixscience.com/

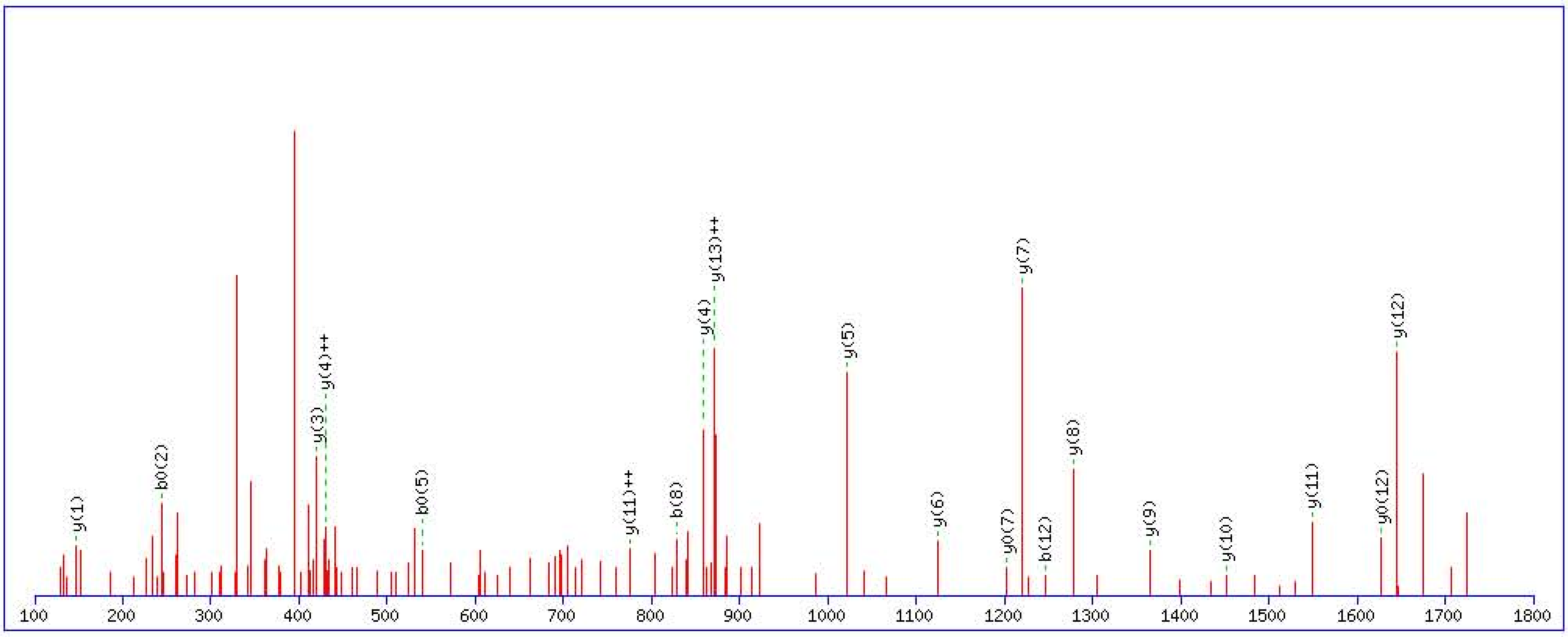
Mascot Search Results

Peptide View

MS/MS Fragmentation of CTTPPPSSGPTYQCLK
Found in PLMN_HUMAN, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

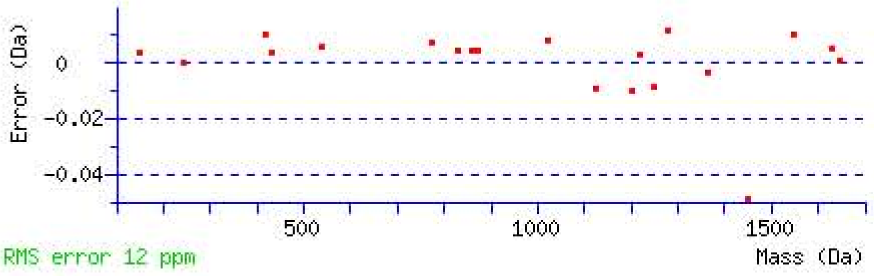
Match to Query 53270: 2103.991722 from(702.337850,3+) rtinseconds(1747) index(77216)
Title: Locus:1.1.1.1959.14 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

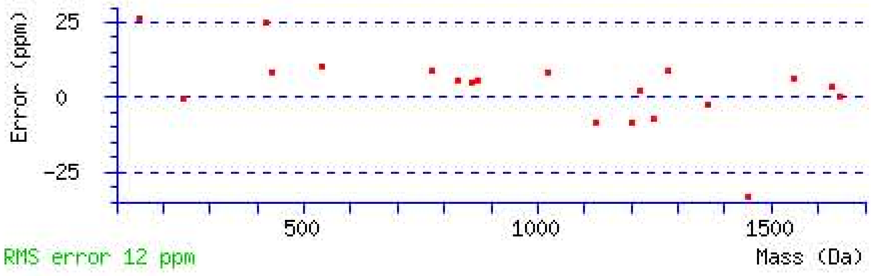


```
Monoisotopic mass of neutral peptide Mr(calc): 2103.979172
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 75  Expect: 5.6e-007
Matches : 20/144 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 12 ppm



RMS error 12 ppm

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
75.2	2103.979172	0.012550	CTTPPPSSGPTYQCLK
12.2	2103.964554	0.027168	TAADTPAIMNWDLFFTMK
0.6	2103.975754	0.015968	AEVEQMHWSYQELK

Mascot: http://www.matrixscience.com/

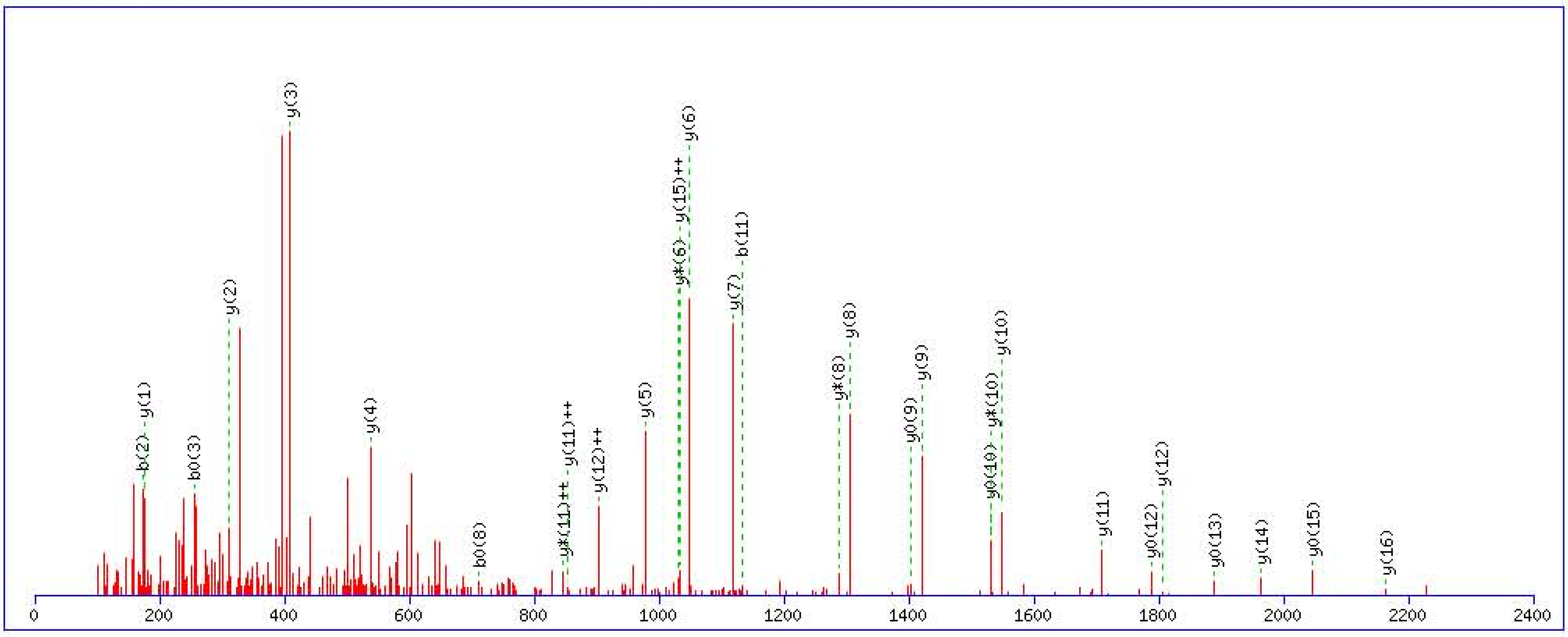
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATTVTGTPCQDWAAQEPHR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

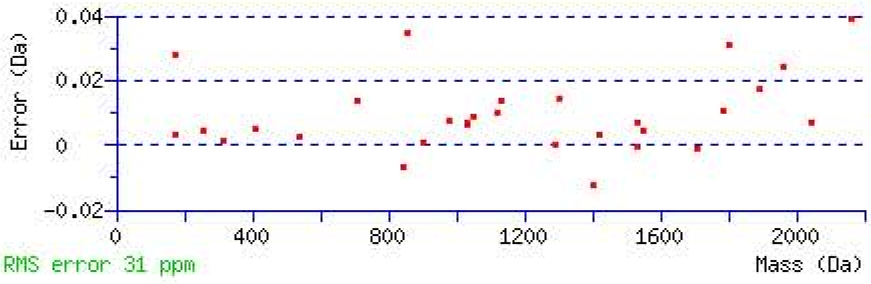
Match to Query 61092: 2436.150016 from(610.044780,4+) rtinseconds(1844) index(77741)
Title: Locus:1.1.1.1993.6 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

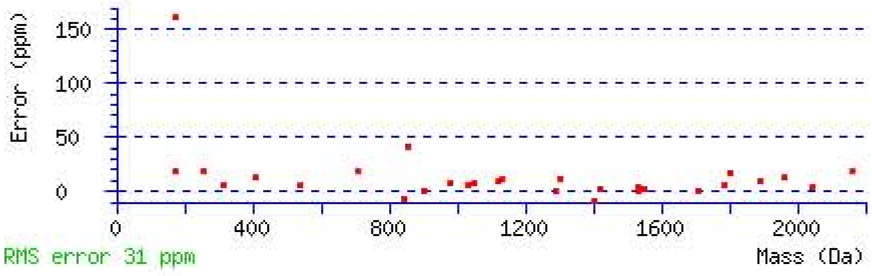
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2436.131470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15    : Biotin:Thermo-21345 (Q)
Ions Score: 82  Expect: 1.1e-007
Matches : 30/190 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	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
81.9	2436.131470	0.018546	ATTVTGTPCQDWAAQEPHR
23.8	2436.131470	0.018546	ATTVTGTPCQDWAAQEPHR

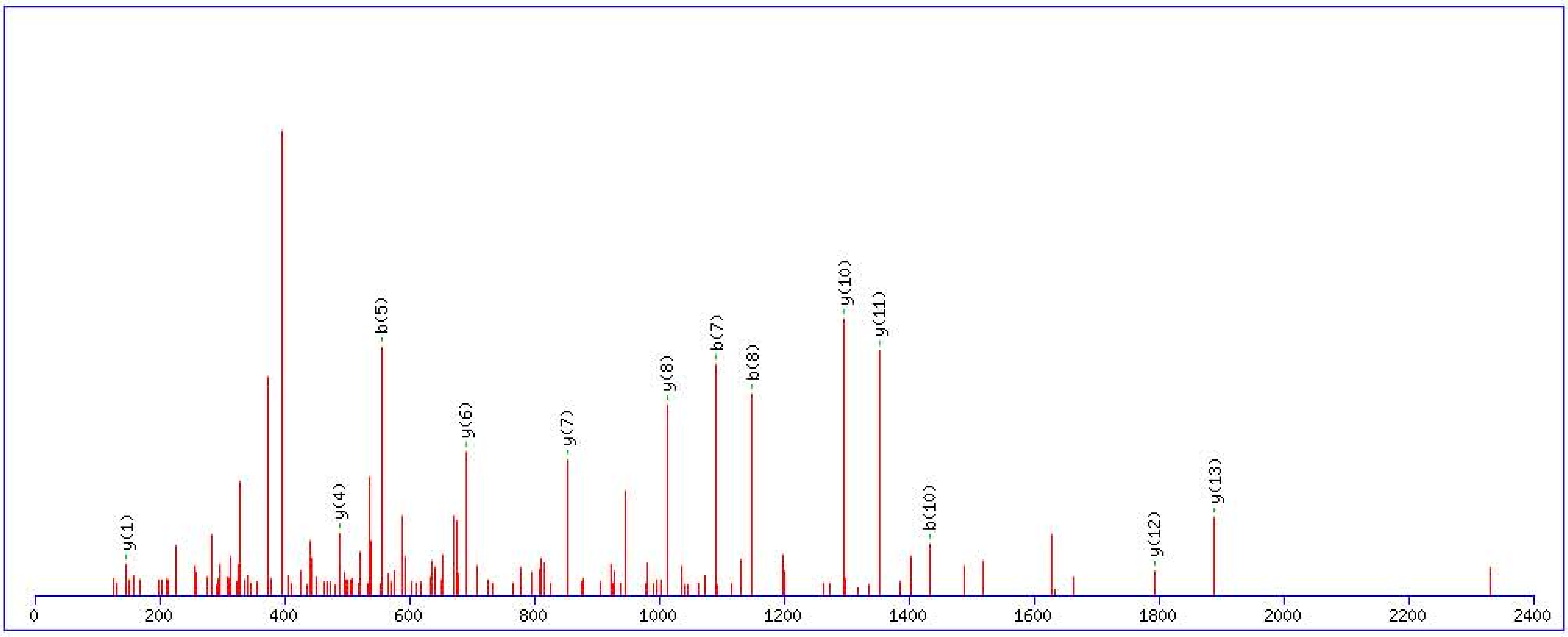
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPDNDPQGPWCYTTDPEK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

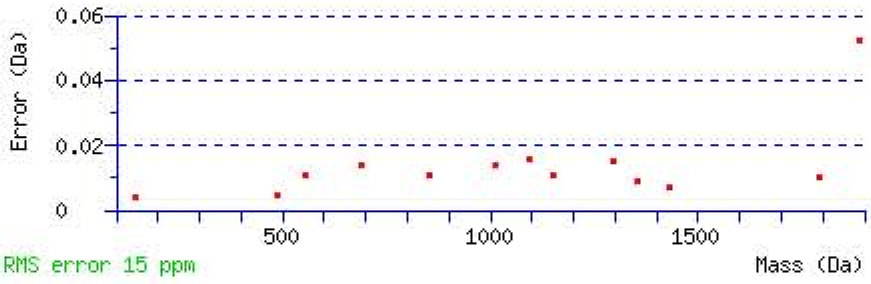
Match to Query 61283: 2444.063802 from(815.695210,3+) rtinseconds(2088) index(79459)
Title: Locus:1.1.1.2077.24 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

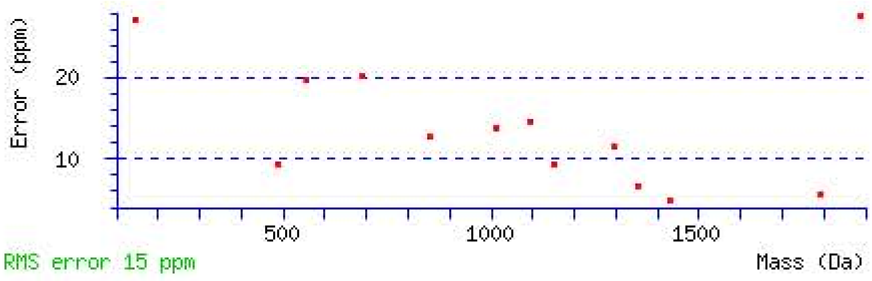
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2444.041306
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 63 **Expect:** 2.3e-006
Matches : 13/198 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	115.050203	58.028740	98.023654	49.515465			N							18
2	212.102967	106.555121	195.076418	98.041847			P	2331.005648	1166.006462	2313.979099	1157.493187	2312.995083	1157.001179	17
3	327.129910	164.068593	310.103361	155.555319	309.119345	155.063311	D	2233.952884	1117.480080	2216.926335	1108.966805	2215.942319	1108.474797	16
4	441.172837	221.090057	424.146288	212.576782	423.162272	212.084774	N	2118.925941	1059.966608	2101.899392	1051.453334	2100.915376	1050.961326	15
5	**556.199780**	278.603528	539.173231	270.090254	538.189215	269.598246	D	2004.883014	1002.945145	1987.856465	994.431871	1986.872449	993.939863	14
6	653.252544	327.129910	636.225995	318.616636	635.241979	318.124628	P	***1889.856071***	945.431673	1872.829522	936.918399	1871.845506	936.426391	13
7	**1092.477870**	546.742573	1075.451321	538.229299	1074.467305	537.737290	Q	***1792.803307***	896.905291	1775.776758	888.392017	1774.792742	887.900009	12
8	**1149.499334**	575.253305	1132.472785	566.740030	1131.488769	566.248022	G	***1353.577981***	677.292629	1336.551432	668.779354	1335.567416	668.287346	11
9	1246.552098	623.779687	1229.525549	615.266413	1228.541533	614.774404	P	***1296.556517***	648.781897	1279.529968	640.268622	1278.545952	639.776614	10
10	**1432.631411**	716.819343	1415.604862	708.306069	1414.620846	707.814061	W	1199.503753	600.255515	1182.477204	591.742240	1181.493188	591.250232	9
11	1592.662060	796.834668	1575.635511	788.321394	1574.651495	787.829385	C	***1013.424440***	507.215858	996.397891	498.702584	995.413875	498.210576	8
12	1755.725389	878.366333	1738.698840	869.853058	1737.714824	869.361050	Y	***853.393791***	427.200534	836.367242	418.687259	835.383226	418.195251	7
13	1856.773068	928.890172	1839.746519	920.376898	1838.762503	919.884889	T	***690.330462***	345.668869	673.303913	337.155595	672.319897	336.663587	6
14	1957.820747	979.414012	1940.794198	970.900737	1939.810182	970.408729	T	589.282783	295.145030	572.256234	286.631755	571.272218	286.139747	5
15	2072.847690	1036.927483	2055.821141	1028.414208	2054.837125	1027.922200	D	***488.235104***	244.621190	471.208555	236.107915	470.224539	235.615907	4
16	2169.900454	1085.453865	2152.873905	1076.940590	2151.889889	1076.448582	P	373.208161	187.107719	356.181612	178.594444	355.197596	178.102436	3
17	2298.943047	1149.975161	2281.916498	1141.461887	2280.932482	1140.969879	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
18							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NPDNDPQGPWCYTTDPEK
(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	2444.041306	0.022496	NPDNDPQGPWCYTTDPEK

Mascot: http://www.matrixscience.com/

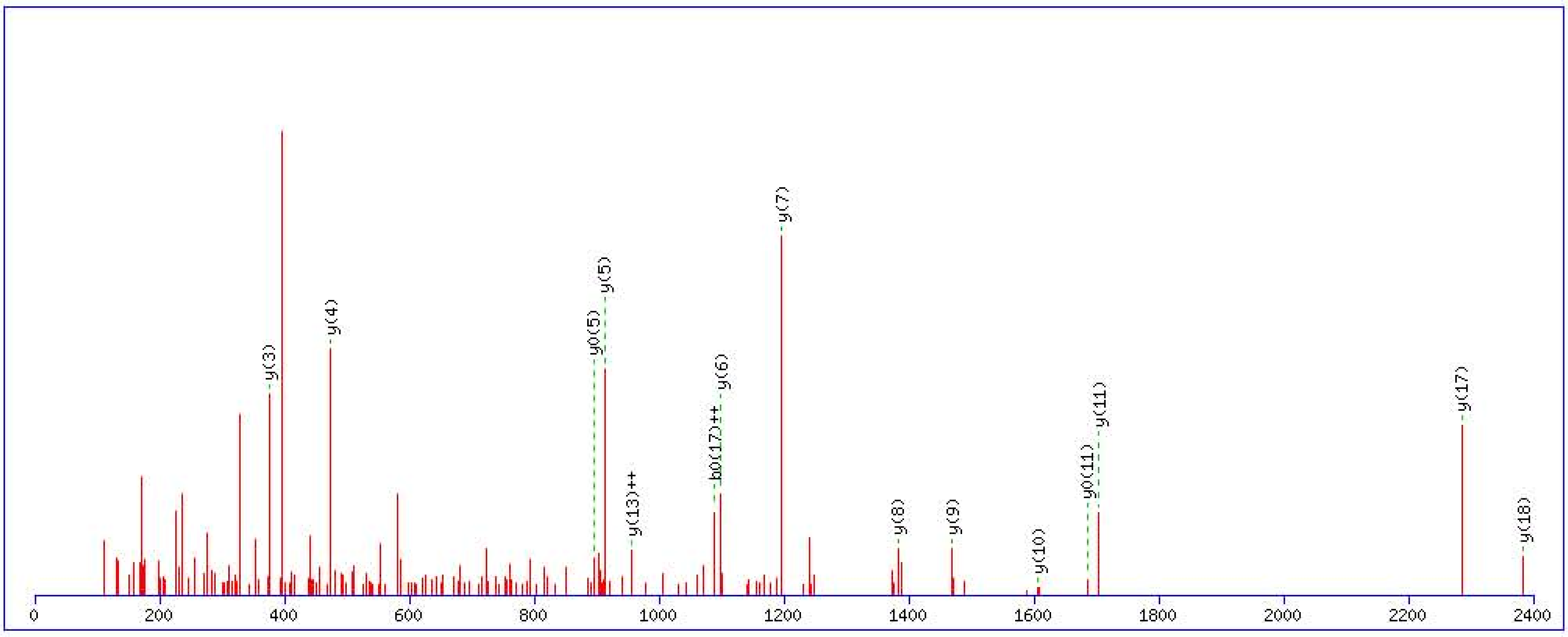
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVGGCVAHPHSWPWQVSLR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

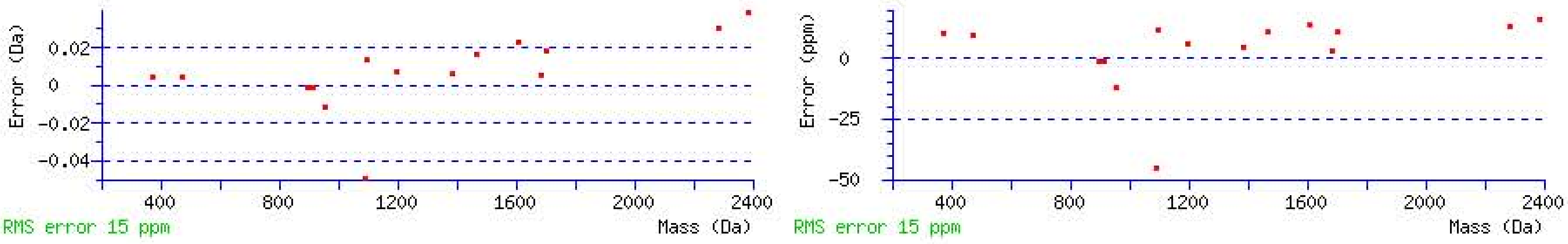
Match to Query 62389: 2482.270856 from(621.574990,4+) rtinseconds(2156) index(79925)
Title: Locus:1.1.1.2101.15 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 2482.251480
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 50 **Expect:** 0.0003
Matches : 15/164 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	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
50.1	2482.251480	0.019376	VVGGCVAHPHSWPWQVSLR

Mascot: http://www.matrixscience.com/

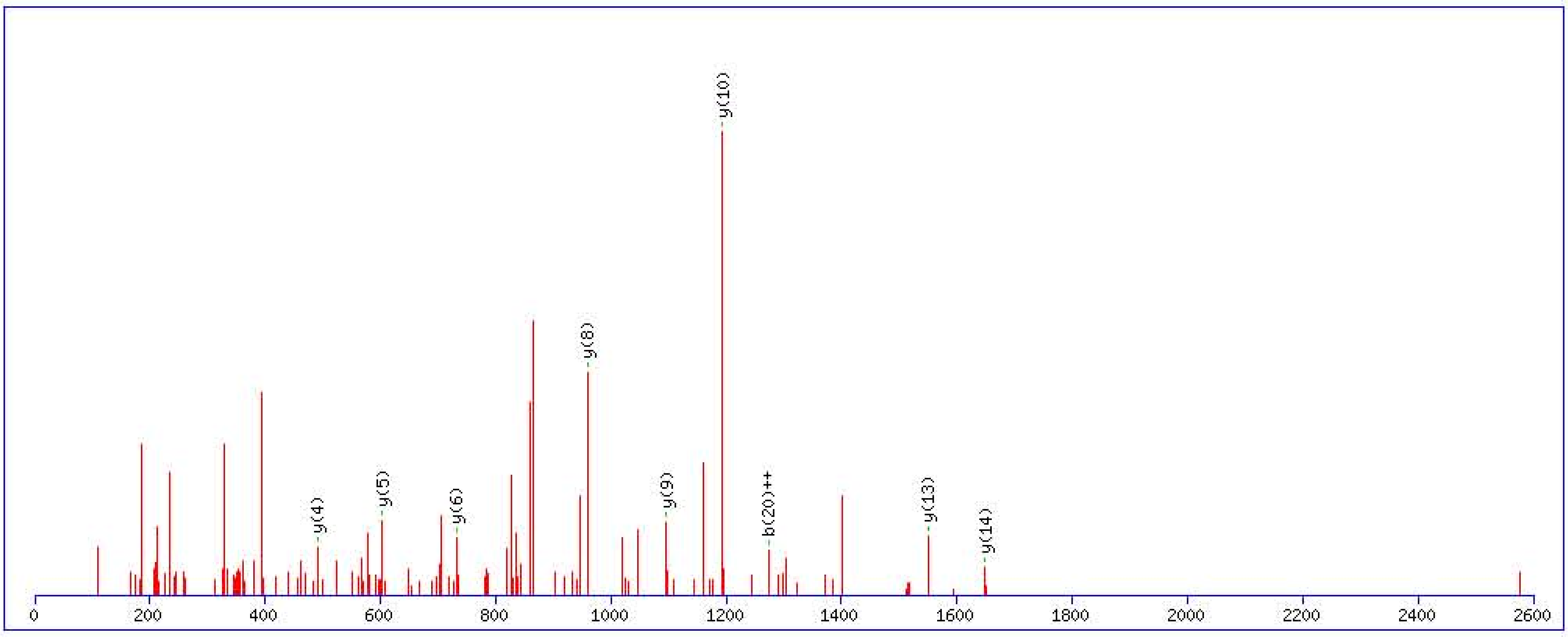
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

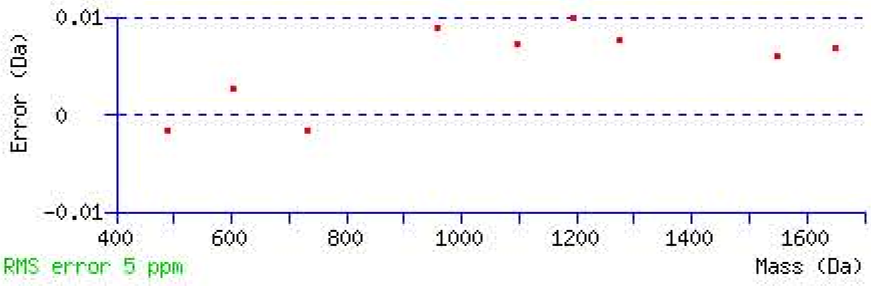
Match to Query 67237: 2806.500856 from(702.632490,4+) rtinseconds(2070) index(79339)
Title: Locus:1.1.1.2071.17 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

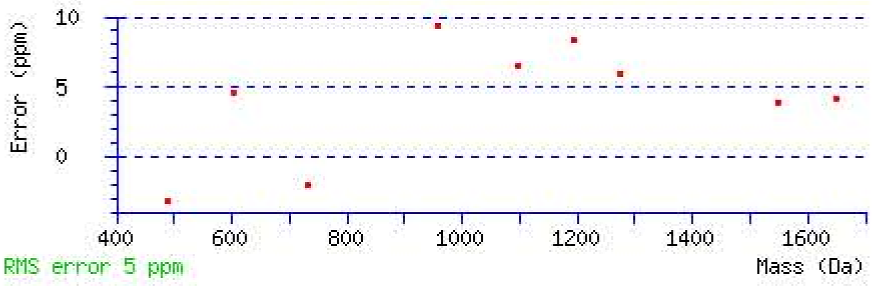
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2806.479965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0025
Matches : 9/224 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	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
38.7	2806.479965	0.020891	VILGAHQEVNLEPHVQEIEVSR

Mascot: http://www.matrixscience.com/

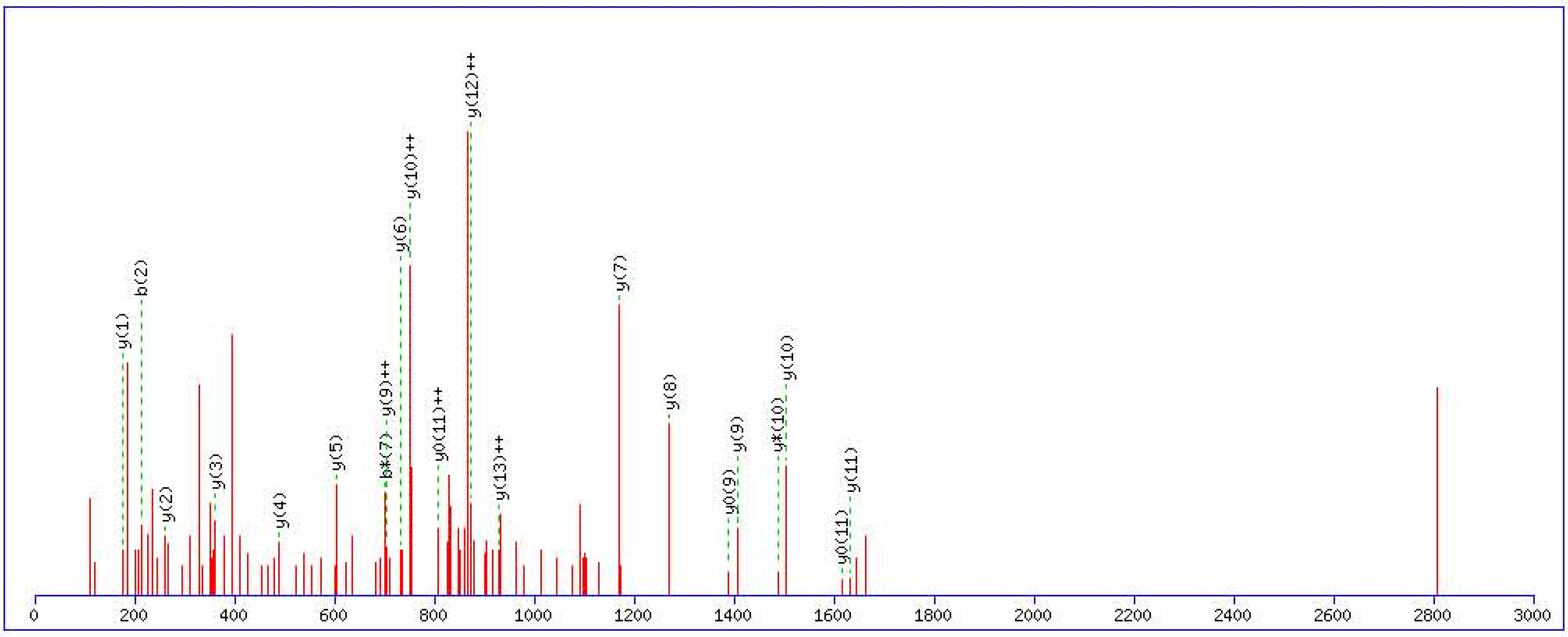
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

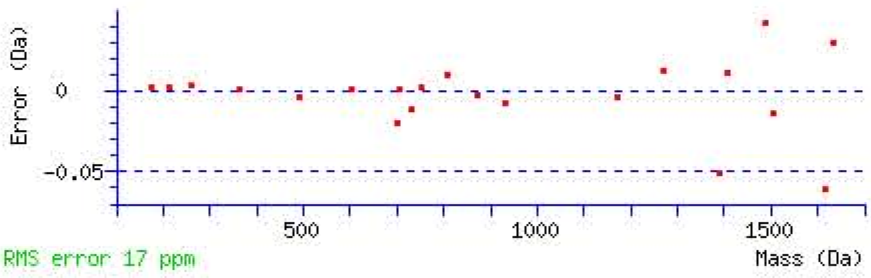
Match to Query 67239: 2806.501896 from(702.632750,4+) rtinseconds(2046) index(79175)
Title: Locus:1.1.1.2063.12 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

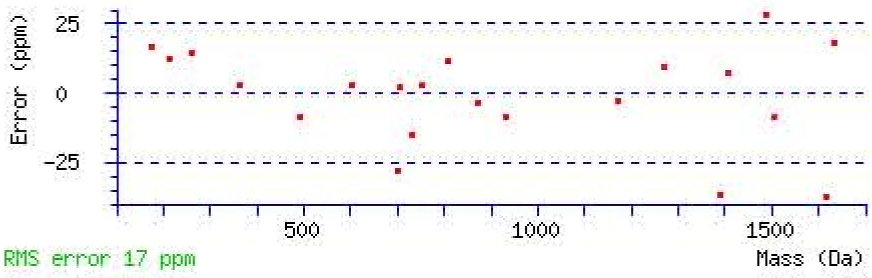
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2806.479965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 31 **Expect:** 0.015
Matches : 21/224 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	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
30.8	2806.479965	0.021931	VILGAHQEVNLEPHVQEIEVSR

Mascot: http://www.matrixscience.com/

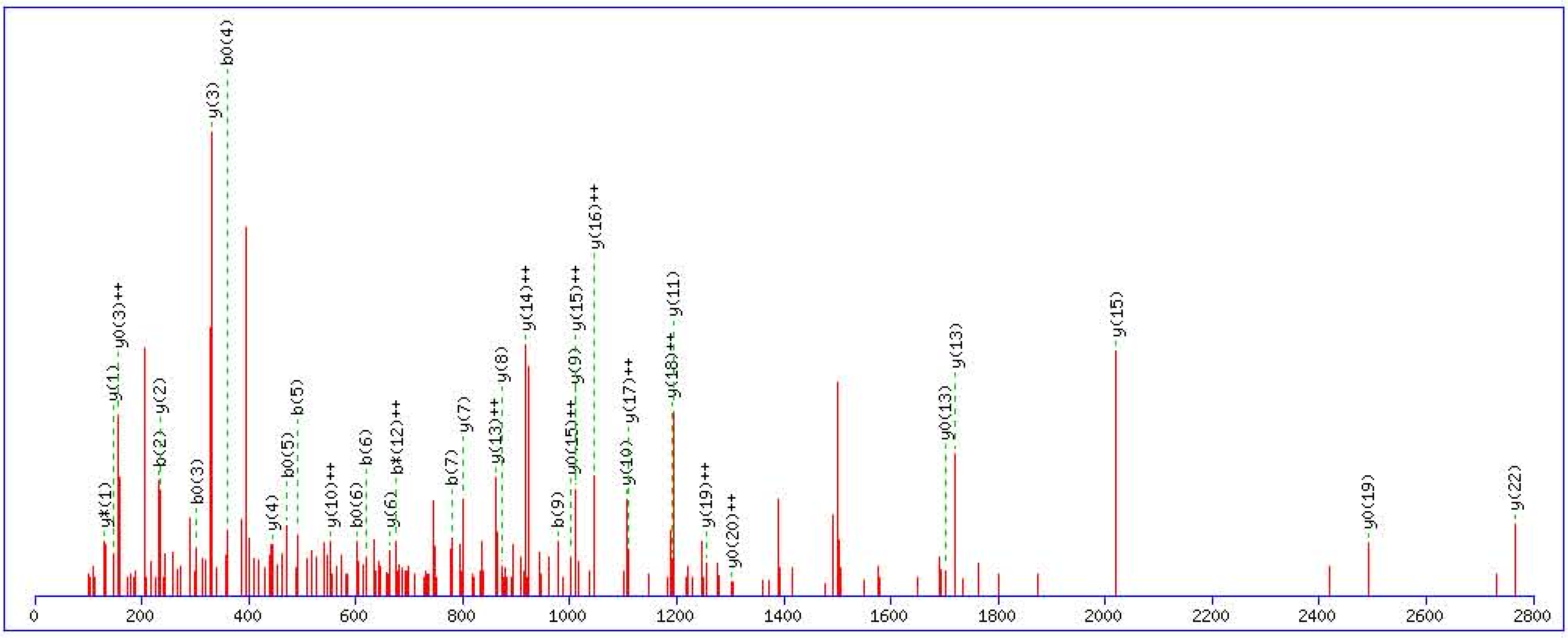
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMSGLECQAWDSQSPHAHGYIPSK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 70338: 2997.385816 from(750.353730,4+) rtinseconds(1947) index(78551)
Title: Locus:1.1.1.2028.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 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: 41  Expect: 0.0012
Matches : 37/260 fragment ions using 115 most intense peaks   (help)
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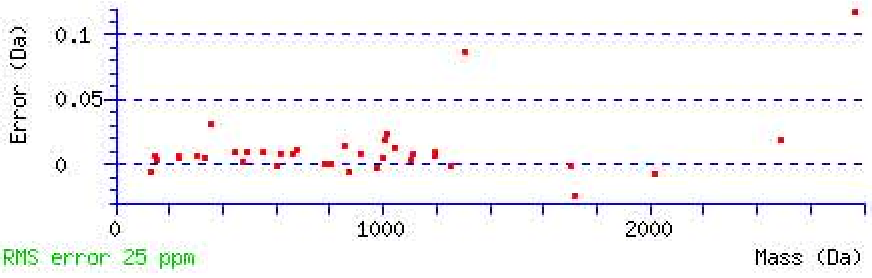
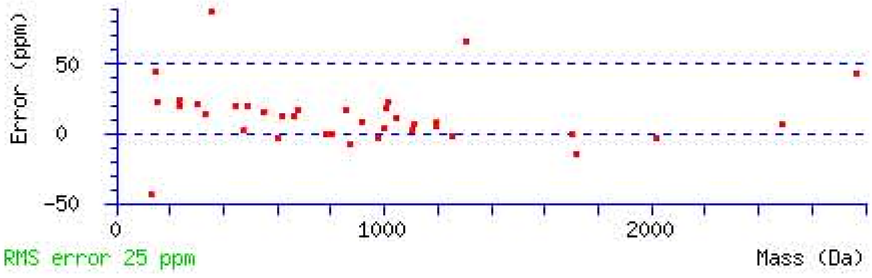
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							24
2	**233.095440**	117.051358			215.084875	108.046076	M	2897.316768	1449.162022	2880.290219	1440.648748	2879.306203	1440.156740	23
3	320.127468	160.567372			302.116903	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
40.8	2997.357162	0.028654	TMSGLECQAWDSQSPHAHGYIPSK
20.5	2997.357162	0.028654	TMSGLECQAWDSQSPHAHGYIPSK

Mascot: http://www.matrixscience.com/

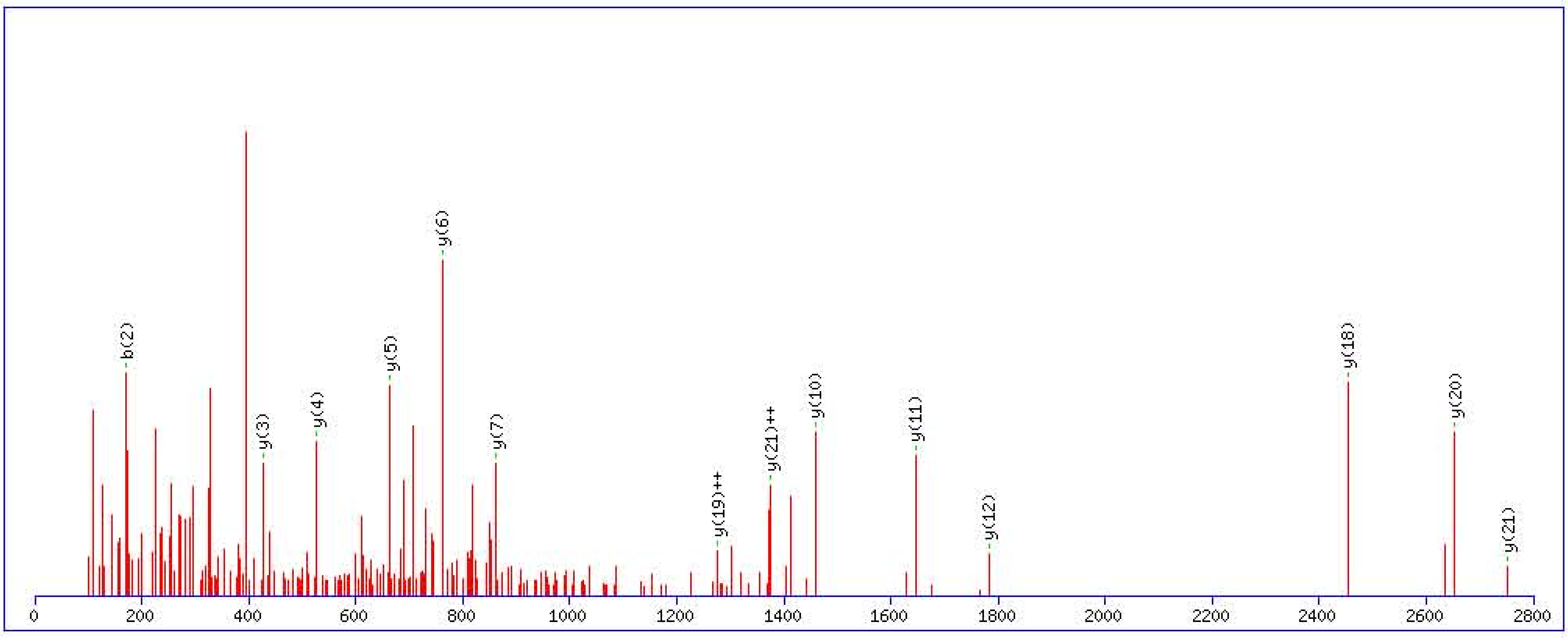
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

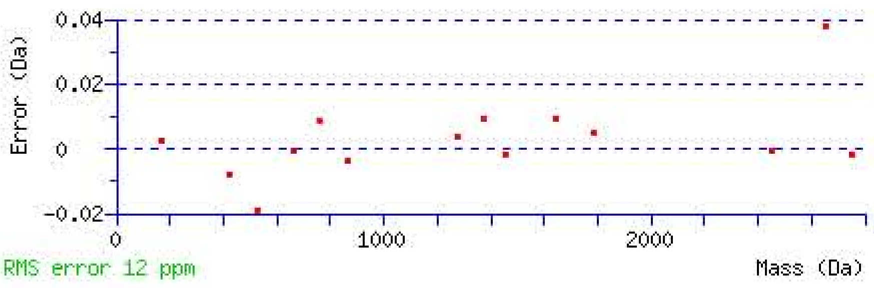
Match to Query 71292: 3092.478320 from(619.502940,5+) rtinseconds(1389) index(74877)
Title: Locus:1.1.1.1834.19 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

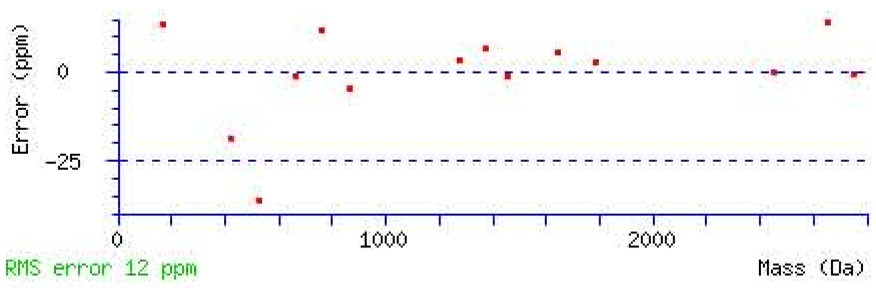
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 74 **Expect:** 8.2e-007
Matches : 14/270 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	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
74.5	3092.457016	0.021304	GNVAVTVSGHTCQHWSAQTPHTHNR
37.2	3092.457016	0.021304	GNVAVTVSGHTCQHWSAQTPHTHNR

Mascot: http://www.matrixscience.com/

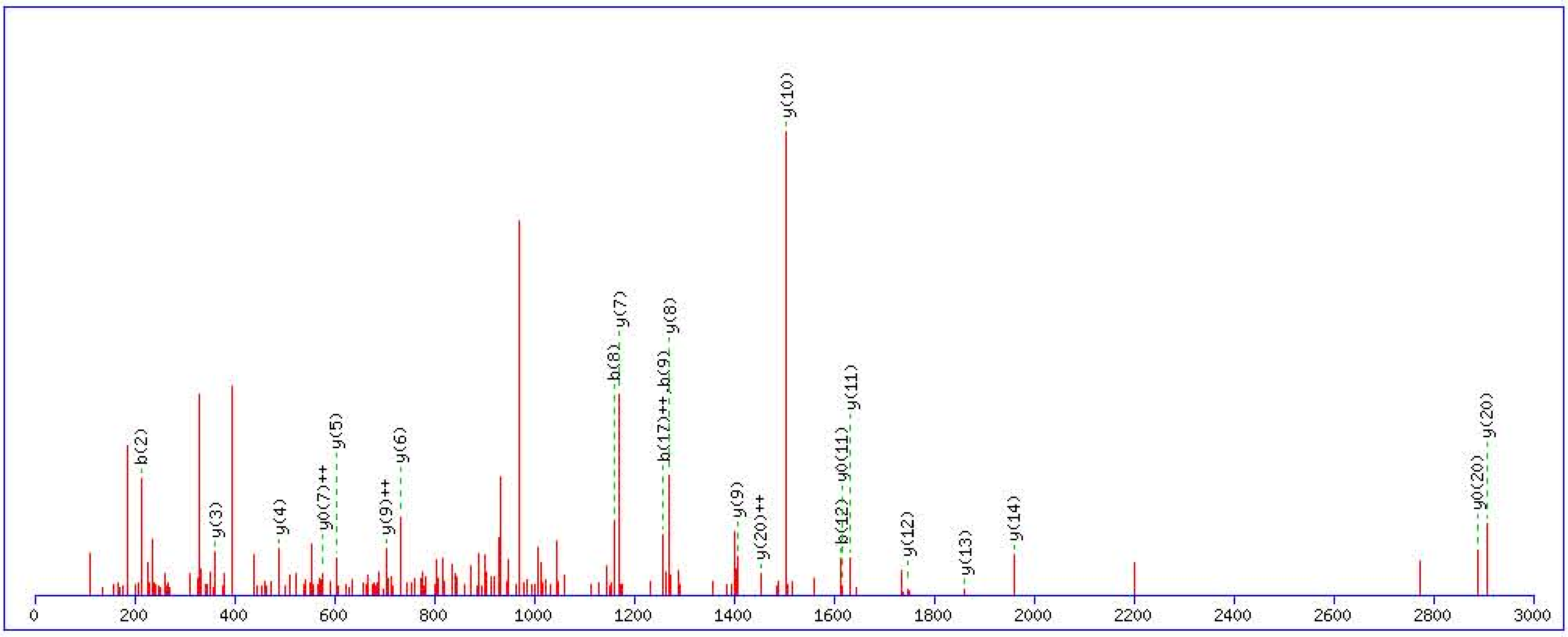
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

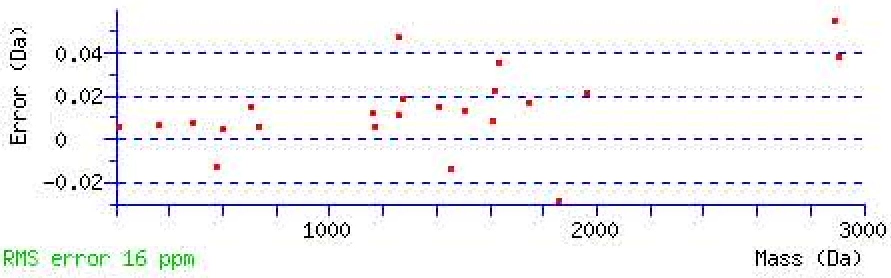
Match to Query 71449: 3117.674336 from(780.425860,4+) rtinseconds(2210) index(80324)
Title: Locus:1.1.1.2120.13 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

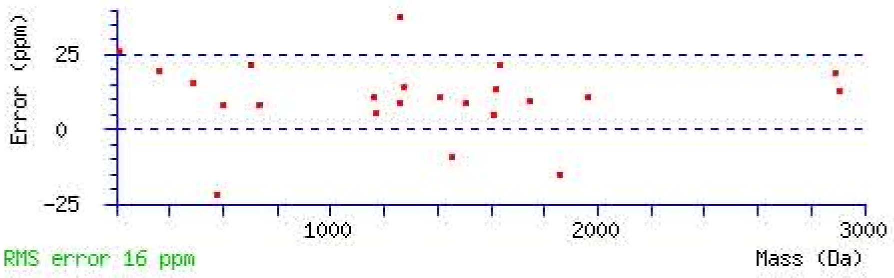
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3117.646713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 8.4e-005
Matches : 23/224 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	100.075690	50.541483					V							22
2	**213.159754**	107.083515					I	3019.585595	1510.296435	3002.559046	1501.783161	3001.575030	1501.291153	21
3	326.243818	163.625547					L	***2906.501531***	1453.754403	2889.474982	1445.241129	2888.490966	1444.749121	20
4	383.265282	192.136279					G	2793.417467	1397.212371	2776.390918	1388.699097	2775.406902	1388.207089	19
5	454.302396	227.654836					A	2736.396003	1368.701639	2719.369454	1360.188365	2718.385438	1359.696357	18
6	591.361308	296.184292					H	2665.358889	1333.183082	2648.332340	1324.669808	2647.348324	1324.177800	17
7	1030.586634	515.796955	1013.560085	507.283681			Q	2528.299977	1264.653627	2511.273428	1256.140352	2510.289412	1255.648344	16
8	**1159.629227**	580.318252	1142.602678	571.804977	1141.618662	571.312969	E	2089.074651	1045.040963	2072.048102	1036.527689	2071.064086	1036.035681	15
9	**1258.697641**	629.852459	1241.671092	621.339184	1240.687076	620.847176	V	***1960.032058***	980.519667	1943.005509	972.006393	1942.021493	971.514385	14
10	1372.740568	686.873922	1355.714019	678.360648	1354.730003	677.868640	N	***1860.963644***	930.985460	1843.937095	922.472186	1842.953079	921.980178	13
11	1485.824632	743.415954	1468.798083	734.902680	1467.814067	734.410672	L	***1746.920717***	873.963997	1729.894168	865.450722	1728.910152	864.958714	12
12	**1614.867225**	807.937251	1597.840676	799.423976	1596.856660	798.931968	E	***1633.836653***	817.421965	1616.810104	808.908690	1615.826088	808.416682	11
13	1711.919989	856.463633	1694.893440	847.950358	1693.909424	847.458350	P	***1504.794060***	752.900668	1487.767511	744.387394	1486.783495	743.895386	10
14	1848.978901	924.993089	1831.952352	916.479814	1830.968336	915.987806	H	***1407.741296***	704.374286	1390.714747	695.861012	1389.730731	695.369004	9
15	1948.047315	974.527296	1931.020766	966.014021	1930.036750	965.522013	V	***1270.682384***	635.844830	1253.655835	627.331556	1252.671819	626.839548	8
16	2387.272641	1194.139958	2370.246092	1185.626684	2369.262076	1185.134676	Q	***1171.613970***	586.310623	1154.587421	577.797349	1153.603405	577.305341	7
17	2516.315234	1258.661255	2499.288685	1250.147980	2498.304669	1249.655973	E	***732.388644***	366.697960	715.362095	358.184686	714.378079	357.692678	6
18	2629.399298	1315.203287	2612.372749	1306.690013	2611.388733	1306.198005	I	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
19	2758.441891	1379.724584	2741.415342	1371.211309	2740.431326	1370.719301	E	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
20	2857.510305	1429.258791	2840.483756	1420.745516	2839.499740	1420.253508	V	***361.219394***	181.113335	344.192845	172.600060	343.208829	172.108052	3
21	2944.542333	1472.774805	2927.515784	1464.261530	2926.531768	1463.769522	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
52.4	3117.646713	0.027623	VILGAHQEVNLEPHVQEIEVSR

Mascot: http://www.matrixscience.com/

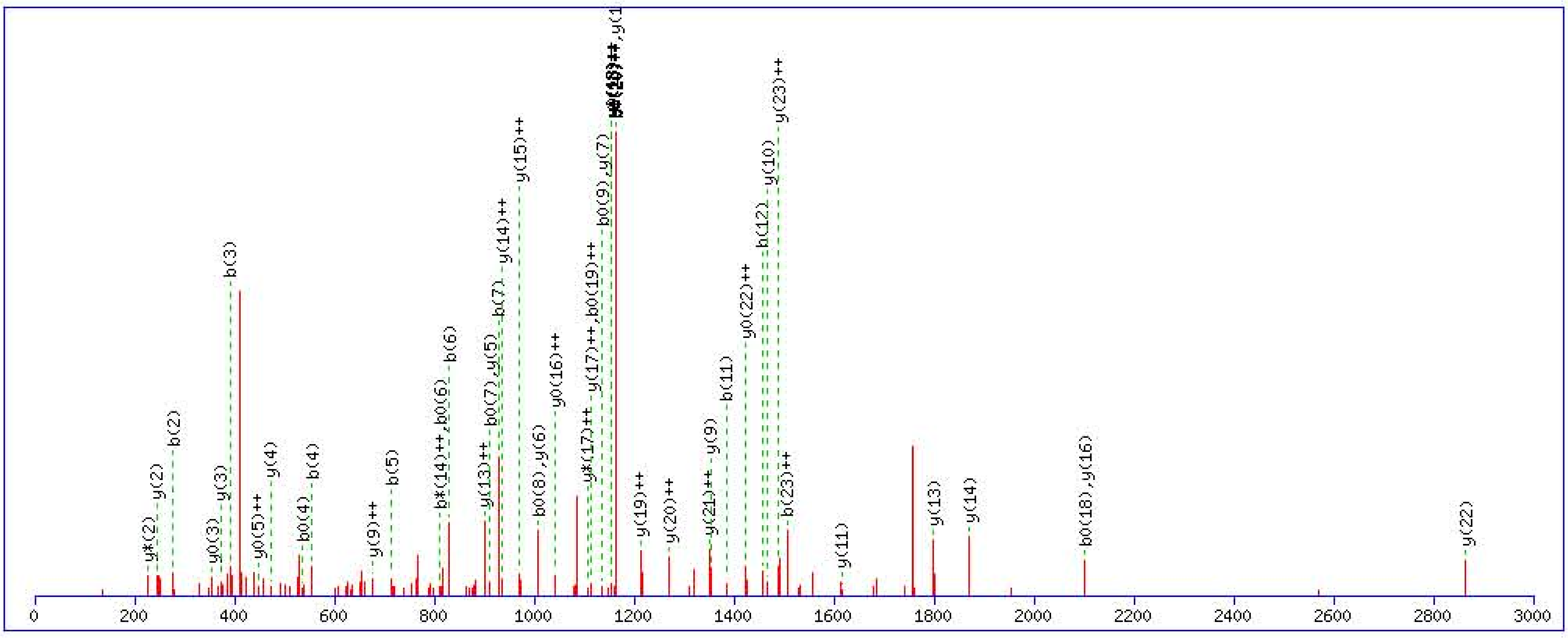
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

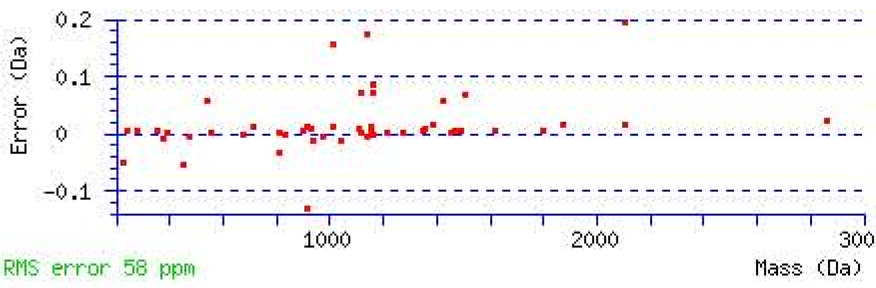
Match to Query 74290: 3254.483472 from(1085.835100,3+) rtinseconds(2033) index(79087)
Title: Locus:1.1.1.2058.23 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

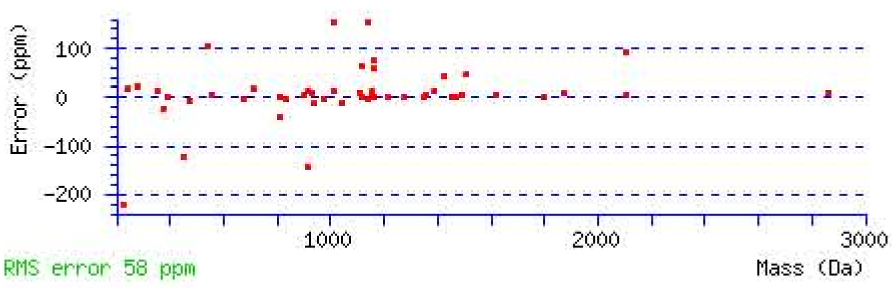
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3254.454514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00063
Matches : 50/264 fragment ions using 134 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							25
2	**277.154669**	139.080973					Y	3142.377716	1571.692496	3125.351167	1563.179221	3124.367151	1562.687213	24
3	**392.181612**	196.594444			374.171047	187.589162	D	2979.314387	1490.160831	2962.287838	1481.647557	2961.303822	1481.155549	23
4	**555.244941**	278.126109			537.234376	269.120826	Y	***2864.287444***	1432.647360	2847.260895	1424.134085	2846.276879	1423.642077	22
5	**715.275590**	358.141433			697.265025	349.136151	C	2701.224115	1351.115695	2684.197566	1342.602421	2683.213550	1342.110413	21
6	**830.302533**	415.654905			812.291968	406.649622	D	2541.193466	1271.100371	2524.166917	1262.587096	2523.182901	1262.095089	20
7	**929.370947**	465.189112			911.360382	456.183829	V	2426.166523	1213.586899	2409.139974	1205.073625	2408.155958	1204.581617	19
8	1026.423711	513.715494			1008.413146	504.710211	P	2327.098109	1164.052692	2310.071560	1155.539418	2309.087544	1155.047410	18
9	1154.482289	577.744783	1137.455740	569.231508	1136.471724	568.739500	Q	2230.045345	1115.526310	2213.018796	1107.013036	2212.034780	1106.521028	17
10	1314.512938	657.760107	1297.486389	649.246833	1296.502373	648.754825	C	***2101.986767***	1051.497021	2084.960218	1042.983747	2083.976202	1042.491739	16
11	**1385.550052**	693.278664	1368.523503	684.765390	1367.539487	684.273382	A	1941.956118	971.481697	1924.929569	962.968423	1923.945553	962.476415	15
12	**1456.587166**	728.797221	1439.560617	720.283947	1438.576601	719.791939	A	***1870.919004***	935.963140	1853.892455	927.449866	1852.908439	926.957858	14
13	1553.639930	777.323603	1536.613381	768.810329	1535.629365	768.318321	P	***1799.881890***	900.444583	1782.855341	891.931309	1781.871325	891.439301	13
14	1640.671958	820.839617	1623.645409	812.326343	1622.661393	811.834335	S	1702.829126	851.918201	1685.802577	843.404927	1684.818561	842.912919	12
15	1787.740372	894.373824	1770.713823	885.860550	1769.729807	885.368542	F	***1615.797098***	808.402187	1598.770549	799.888913	1597.786533	799.396905	11
16	1902.767315	951.887296	1885.740766	943.374021	1884.756750	942.882013	D	***1468.728684***	734.867980	1451.702135	726.354706	1450.718119	725.862698	10
17	2062.797964	1031.902620	2045.771415	1023.389346	2044.787399	1022.897338	C	***1353.701741***	677.354509	1336.675192	668.841234	1335.691176	668.349226	9
18	2119.819428	1060.413352	2102.792879	1051.900078	2101.808863	1051.408070	G	1193.671092	597.339184	1176.644543	588.825910	1175.660527	588.333902	8
19	2247.914391	1124.460834	2230.887842	1115.947559	2229.903826	1115.455551	K	***1136.649628***	568.828452	1119.623079	560.315178	1118.639063	559.823170	7
20	2344.967155	1172.987216	2327.940606	1164.473941	2326.956590	1163.981933	P	***1008.554665***	504.780971	991.528116	496.267696	990.544100	495.775688	6
21	2784.192481	1392.599879	2767.165932	1384.086604	2766.181916	1383.594596	Q	***911.501901***	456.254589	894.475352	447.741314	893.491336	447.249306	5
22	2883.260895	1442.134086	2866.234346	1433.620811	2865.250330	1433.128803	V	***472.276575***	236.641925	455.250026	228.128651	454.266010	227.636643	4
23	3012.303488	1506.655382	2995.276939	1498.142108	2994.292923	1497.650100	E	***373.208161***	187.107719	356.181612	178.594444	355.197596	178.102436	3
24	3109.356252	1555.181764	3092.329703	1546.668490	3091.345687	1546.176482	P	***244.165568***	122.586422	227.139019	114.073148			2
25							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LYDYCDVPQCAAPSFDCGKPQVEPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.8	3254.454514	0.028958	LYDYCDVPQCAAPSFDCGKPQVEPK
13.3	3254.454514	0.028958	LYDYCDVPQCAAPSFDCGKPQVEPK

Mascot: http://www.matrixscience.com/

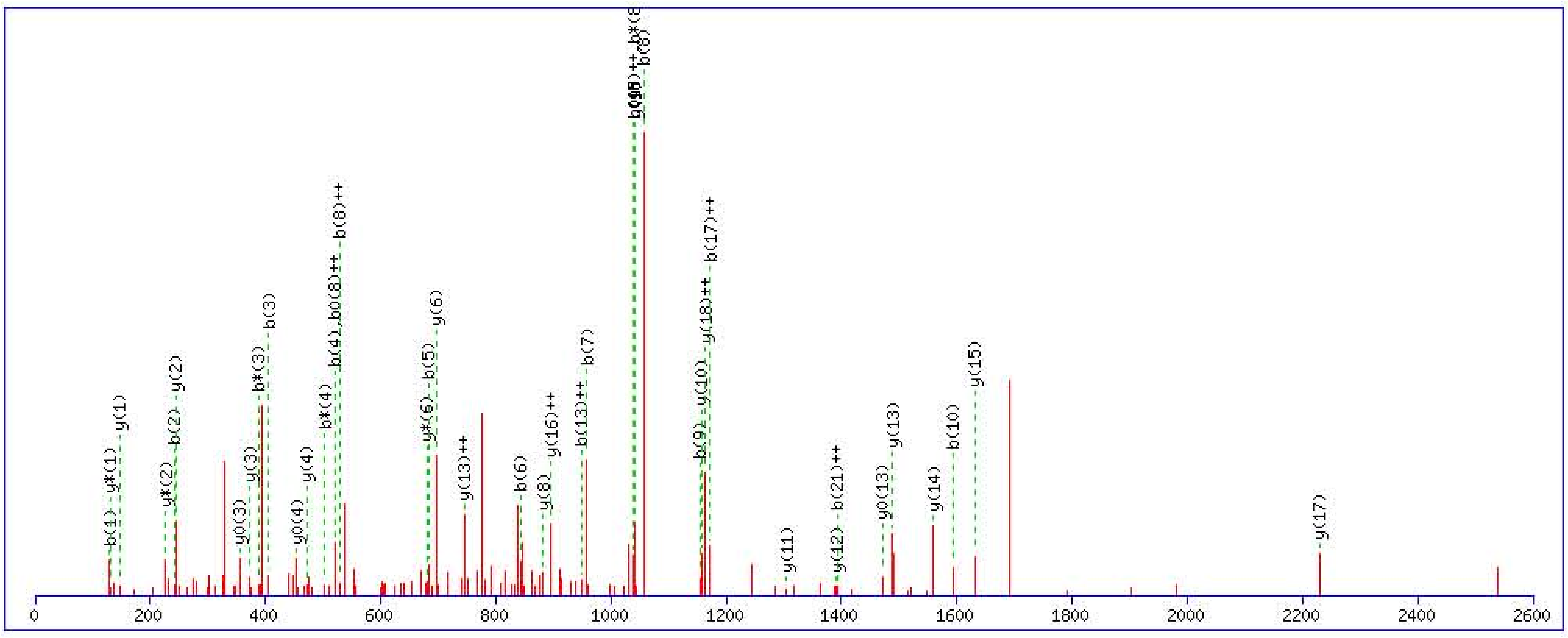
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

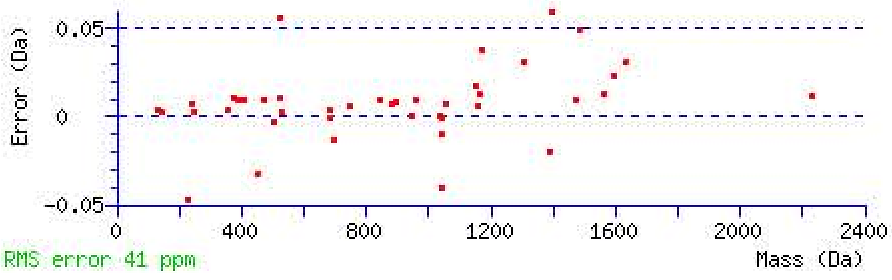
Match to Query 75900: 3382.583816 from(846.653230,4+) rtinseconds(1953) index(78600)
Title: Locus:1.1.1.2030.24 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

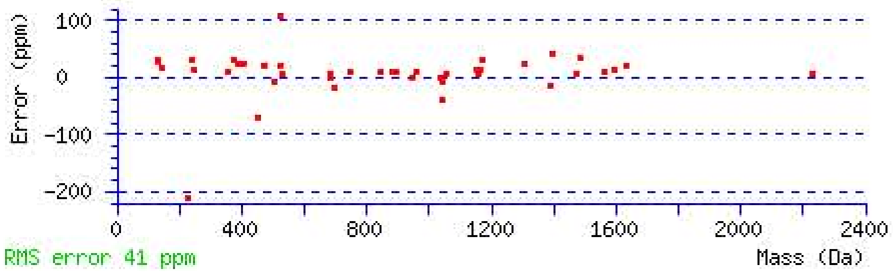
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3382.549469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 1.4e-006
Matches : 43/290 fragment ions using 113 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
64.2	3382.549469	0.034347	KLYDYCDVPQCAAPSFDCGKPQVEPK
9.3	3382.549469	0.034347	KLYDYCDVPQCAAPSFDCGKPQVEPK
1.8	3382.580414	0.003402	HLYPNTPYAYTFWTYMMNARSKNVGWR
1.8	3382.580414	0.003402	HLYPNTPYAYTFWTYMMNARSKNVGWR

Mascot: http://www.matrixscience.com/

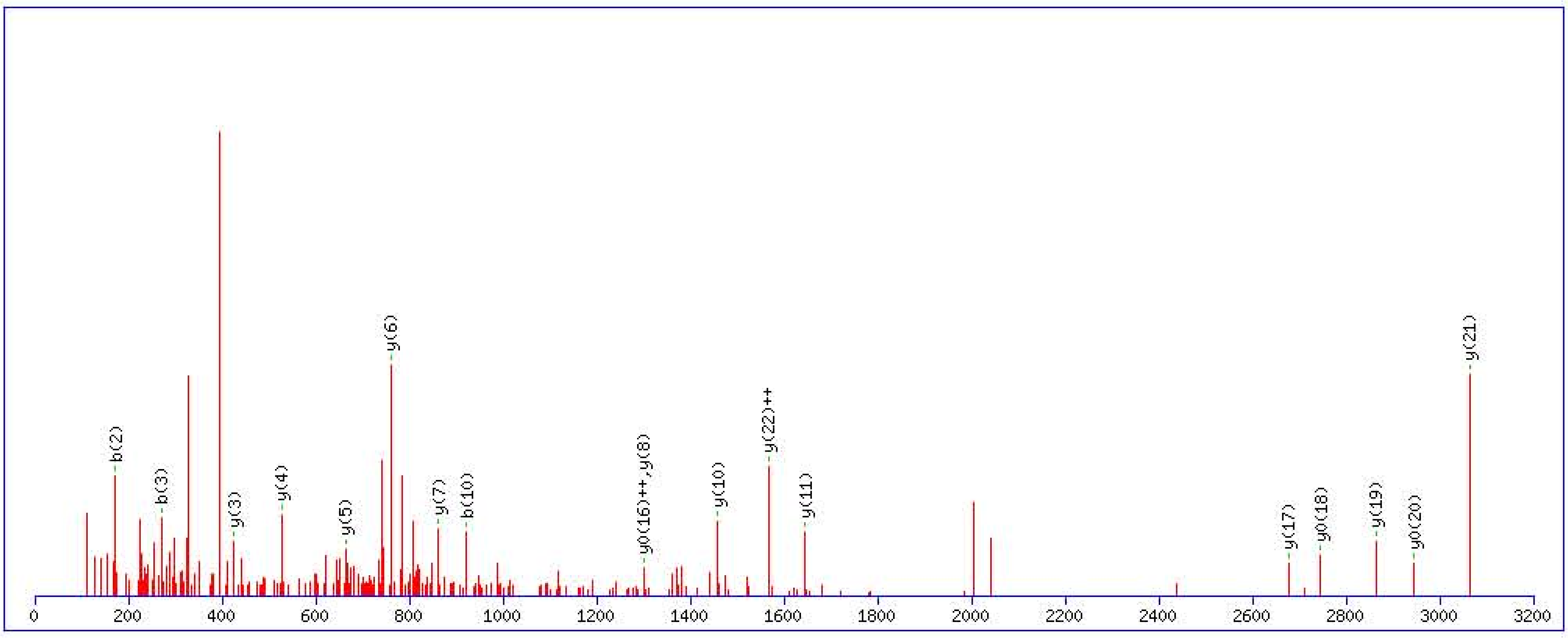
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

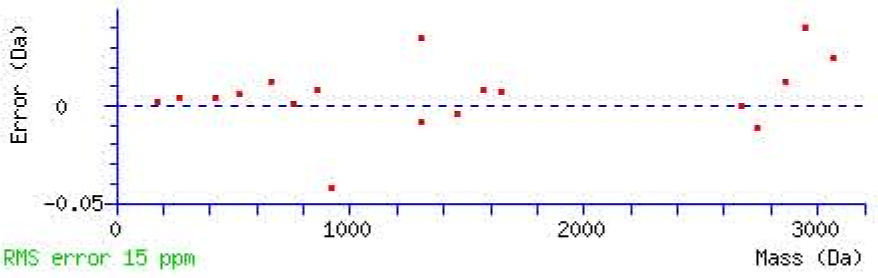
Match to Query 76232: 3403.631170 from(681.733510,5+) rtinseconds(1635) index(76543)
Title: Locus:1.1.1.1920.10 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

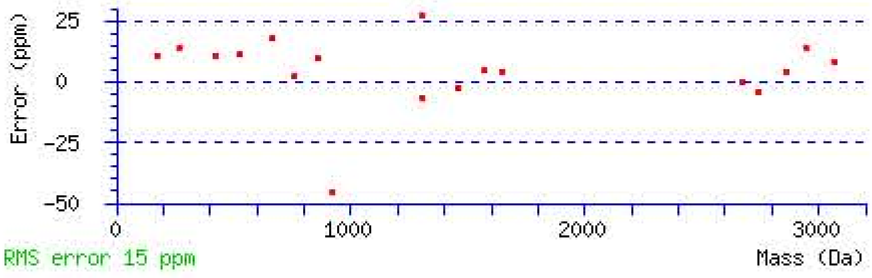
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 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: 65 **Expect:** 7.2e-006
Matches : 18/270 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	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
65.4	3403.623764	0.007406	GNVAVTVSGHTCQHWSAQTPHTHNR

Mascot: http://www.matrixscience.com/

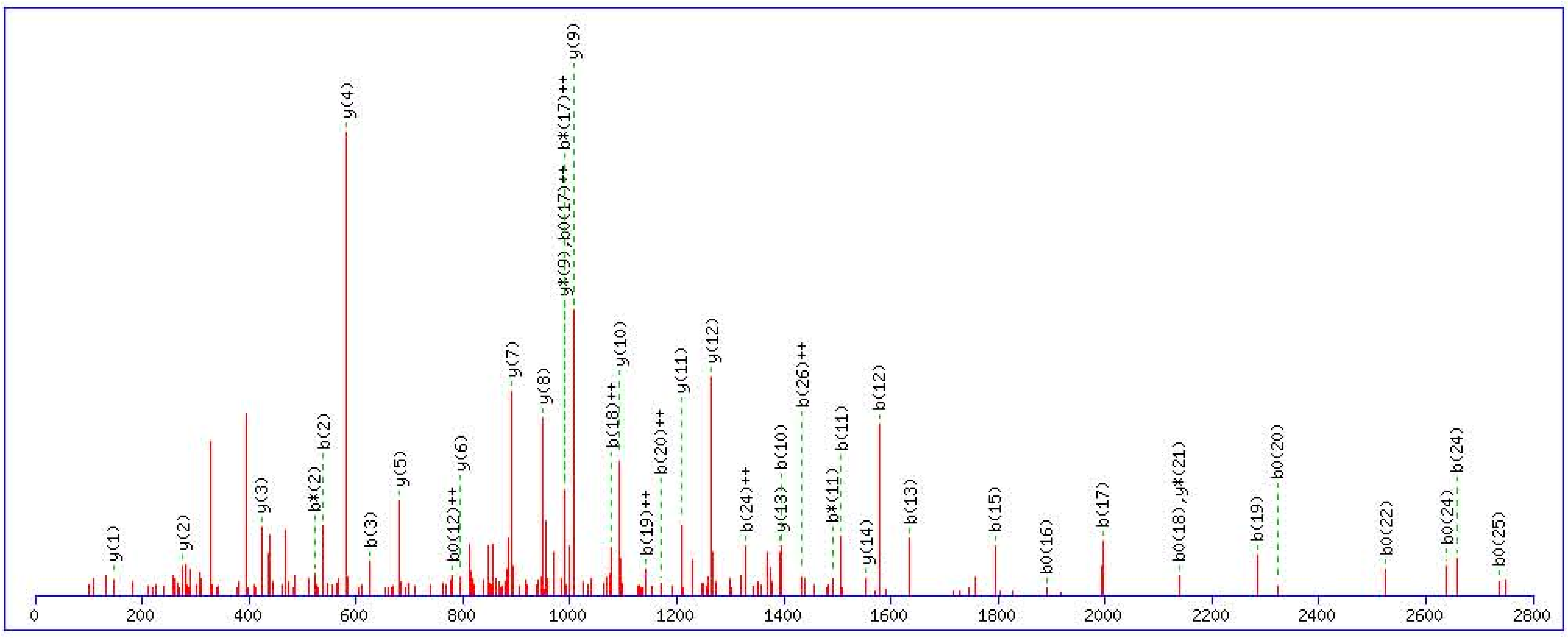
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

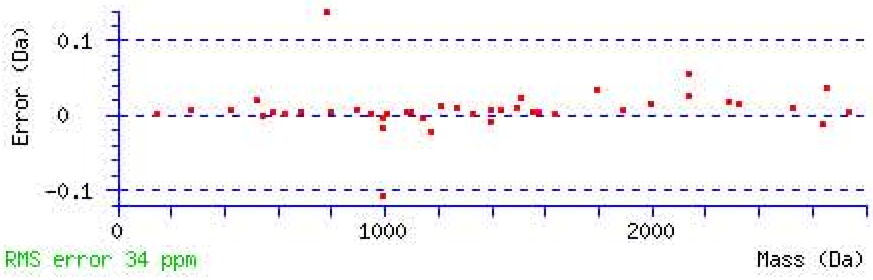
Match to Query 77947: 3547.620536 from(887.912410,4+) rtinseconds(2145) index(79834)
Title: Locus:1.1.1.2097.24 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

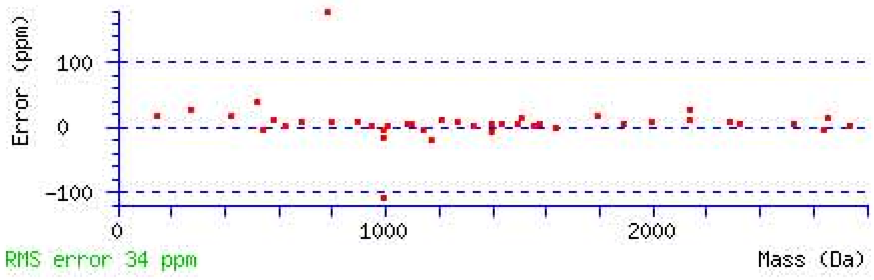
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3547.584061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 99  Expect: 1.5e-009
Matches : 42/352 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	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
98.8	3547.584061	0.036475	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK
40.8	3547.584061	0.036475	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK

Mascot: http://www.matrixscience.com/

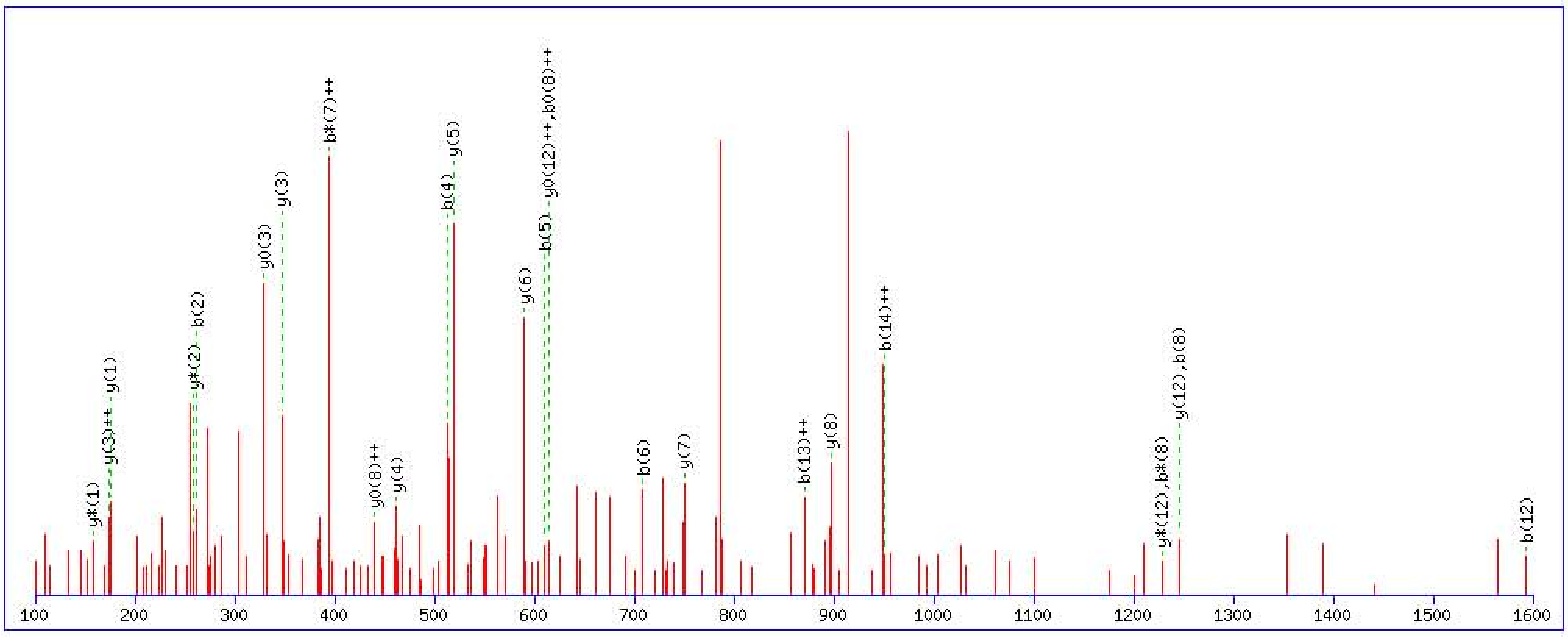
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TCNHPVPQHGGPFCAGDATR**
Found in **PROP_HUMAN**, Properdin OS=Homo sapiens GN=CFP PE=1 SV=2

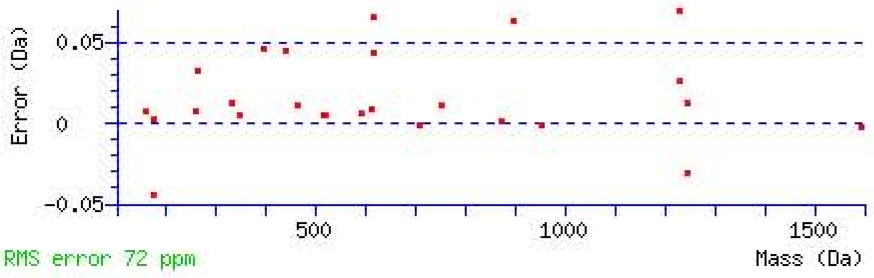
Match to Query 24971: 2489.109096 from(623.284550,4+) rtinseconds(1491) index(3265)
Title: Locus:1.1.1.2773.8 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

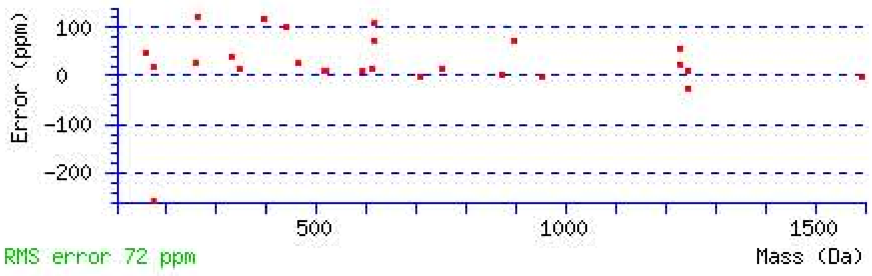
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2489.115128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.0077
Matches : 26/222 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	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
26.2	2489.115128	-0.006032	TCNHPVPQHGGPFCAGDATR

Mascot: http://www.matrixscience.com/

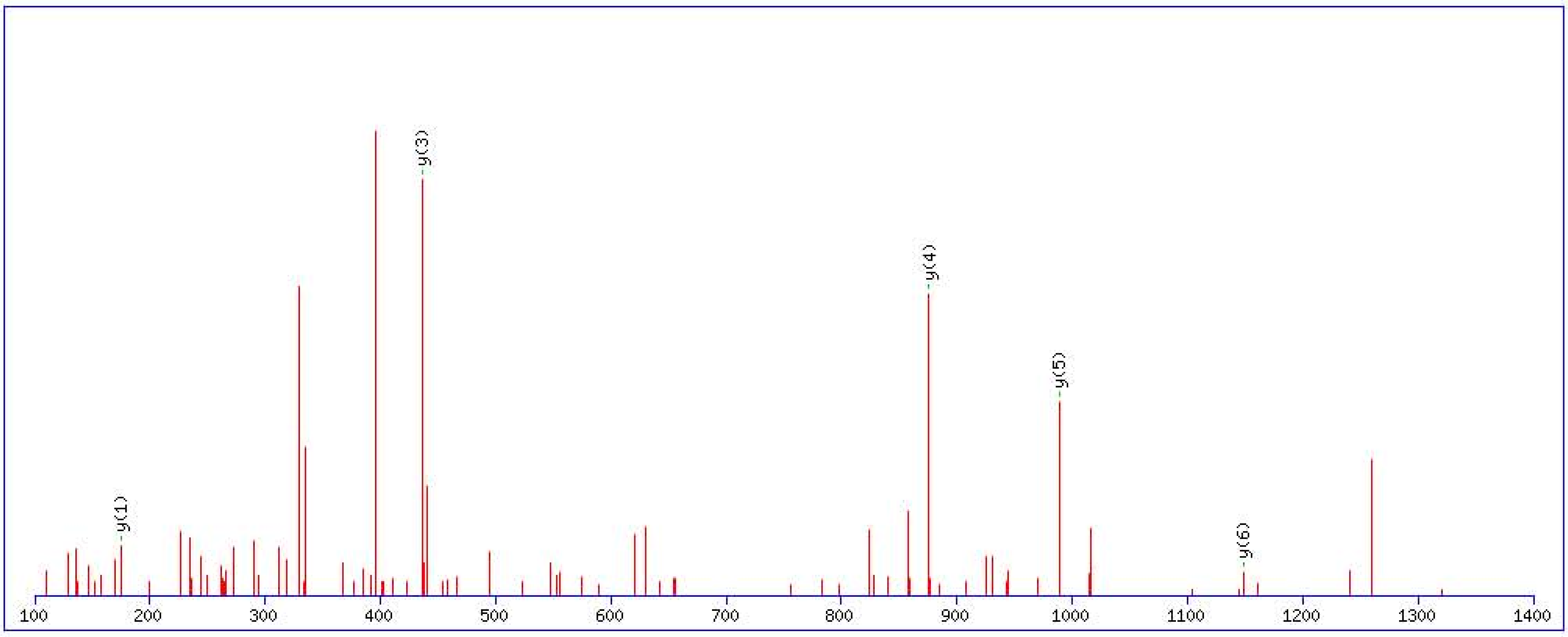
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ECLQTCR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

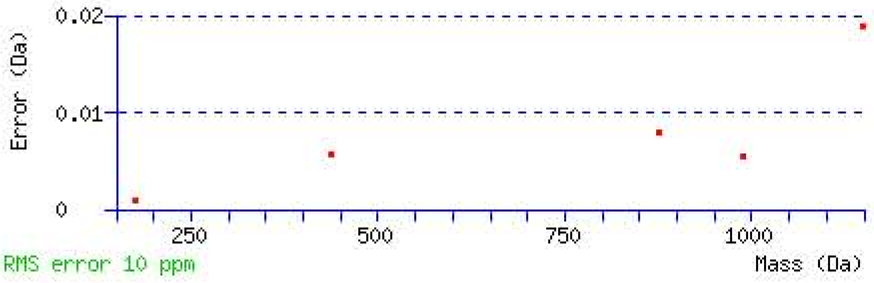
Match to Query 26115: 1276.583008 from(639.298780,2+) rtinseconds(1458) index(75418)
Title: Locus:1.1.1.1858.23 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

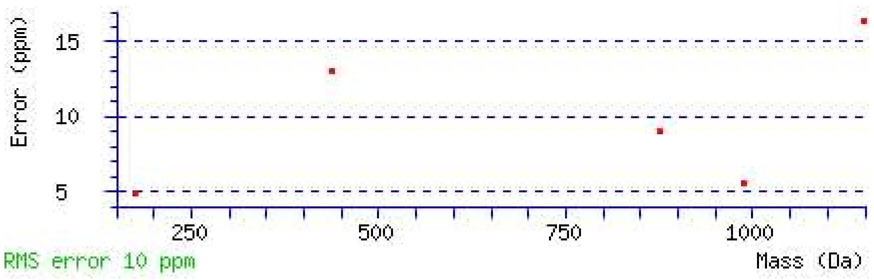
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1276.572632
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.01
Matches : 5/62 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	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
29.3	1276.572632	0.010376	ECLQTCR
8.4	1276.590393	-0.007385	TMHTSVMALDR
6.3	1276.583862	-0.000854	KMSLSCHVCR
6.1	1276.572388	0.010620	EDSYANYFIR
4.8	1276.590393	-0.007385	TMHTSVMALDR
3.5	1276.579605	0.003403	EEQRSPFNDR
3.4	1276.582977	0.000031	EMQLGREDQR
2.2	1276.590378	-0.007370	MDPCKVNELR

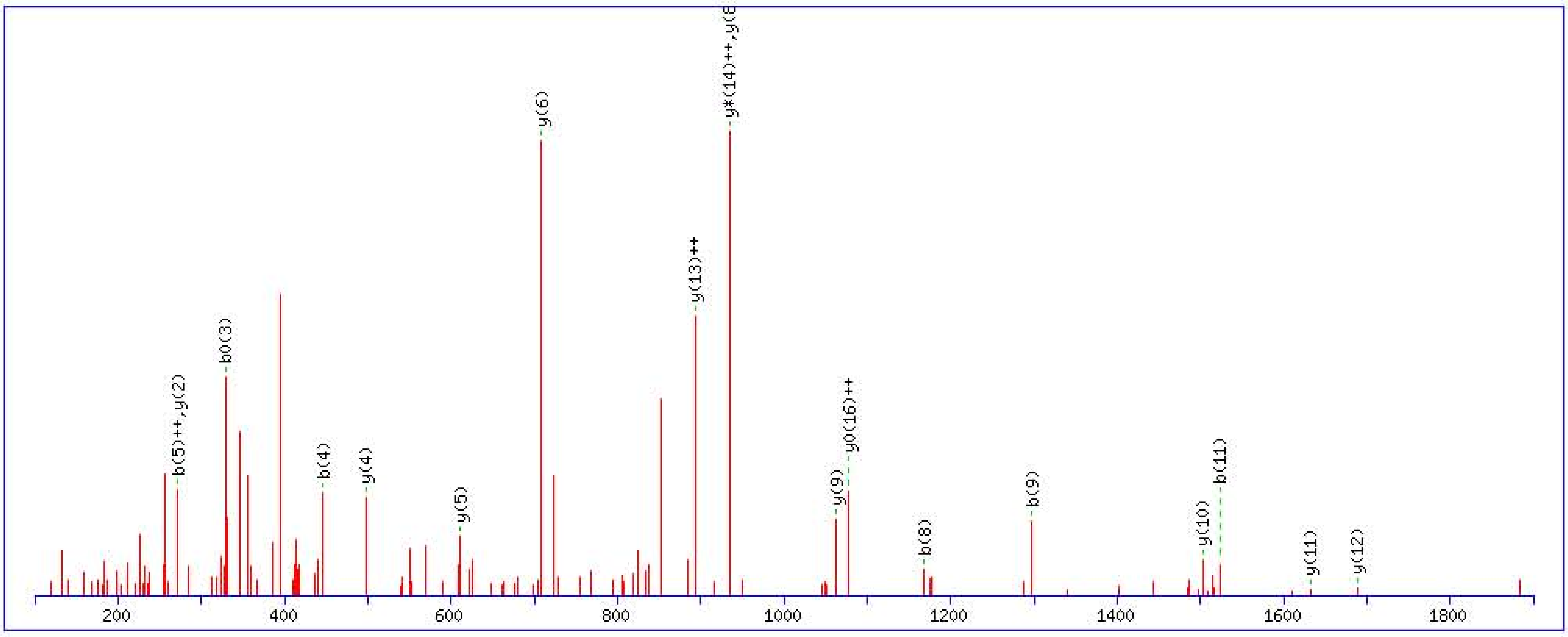
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GECVPGEQEPEPILIPR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

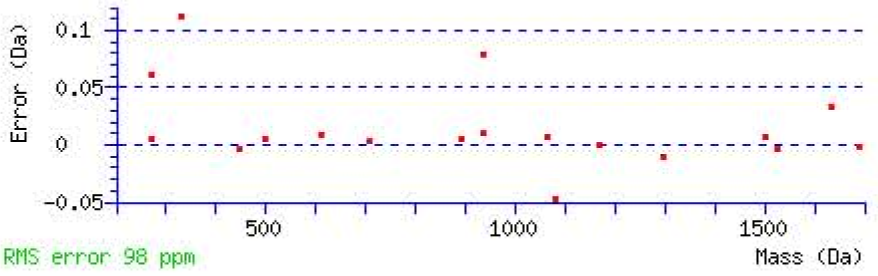
Match to Query 56210: 2230.128582 from(744.383470,3+) rtinseconds(2249) index(26550)
Title: Locus:1.1.1.2925.16 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

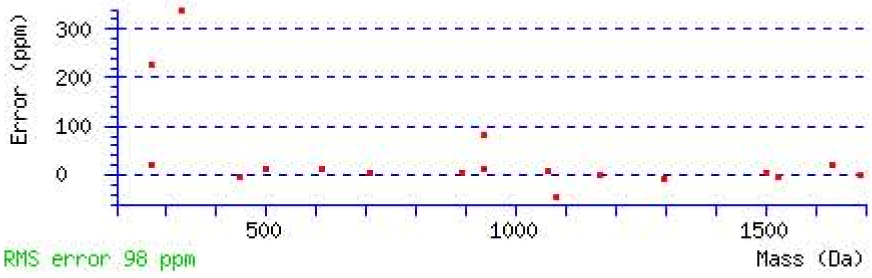
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2230.112595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00016
Matches : 18/164 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	58.028740	29.518008					G							17
2	187.071333	94.039305			169.060768	85.034022	E	2174.098425	1087.552850	2157.071876	1079.039576	2156.087860	1078.547568	16
3	347.101982	174.054629			329.091417	165.049347	C	2045.055832	1023.031554	2028.029283	1014.518279	2027.045267	1014.026271	15
4	**446.170396**	223.588836			428.159831	214.583554	V	1885.025183	943.016229	1867.998634	934.502955	1867.014618	934.010947	14
5	543.223160	272.115218			525.212595	263.109936	P	1785.956769	893.482022	1768.930220	884.968748	1767.946204	884.476740	13
6	600.244624	300.625950			582.234059	291.620668	G	***1688.904005***	844.955640	1671.877456	836.442366	1670.893440	835.950358	12
7	729.287217	365.147247			711.276652	356.141964	E	***1631.882541***	816.444908	1614.855992	807.931634	1613.871976	807.439626	11
8	**1168.512543**	584.759910	1151.485994	576.246635	1150.501978	575.754627	Q	***1502.839948***	751.923612	1485.813399	743.410337	1484.829383	742.918329	10
9	**1297.555136**	649.281206	1280.528587	640.767932	1279.544571	640.275924	E	***1063.614622***	532.310949	1046.588073	523.797674	1045.604057	523.305666	9
10	1394.607900	697.807588	1377.581351	689.294314	1376.597335	688.802306	P	***934.572029***	467.789652	917.545480	459.276378	916.561464	458.784370	8
11	**1523.650493**	762.328885	1506.623944	753.815610	1505.639928	753.323602	E	837.519265	419.263270	820.492716	410.749996	819.508700	410.257988	7
12	1620.703257	810.855267	1603.676708	802.341992	1602.692692	801.849984	P	***708.476672***	354.741974	691.450123	346.228699			6
13	1733.787321	867.397299	1716.760772	858.884024	1715.776756	858.392016	I	***611.423908***	306.215592	594.397359	297.702317			5
14	1846.871385	923.939331	1829.844836	915.426056	1828.860820	914.934048	L	***498.339844***	249.673560	481.313295	241.160285			4
15	1959.955449	980.481363	1942.928900	971.968088	1941.944884	971.476080	I	385.255780	193.131528	368.229231	184.618253			3
16	2057.008213	1029.007744	2039.981664	1020.494470	2038.997648	1020.002462	P	***272.171716***	136.589496	255.145167	128.076221			2
17							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GECVPGEQEPEPILIPR
(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	2230.112595	0.015987	GECVPGEQEPEPILIPR
1.6	2230.120468	0.008114	HVEARDLIEFGMIPEFVGR

Mascot: http://www.matrixscience.com/

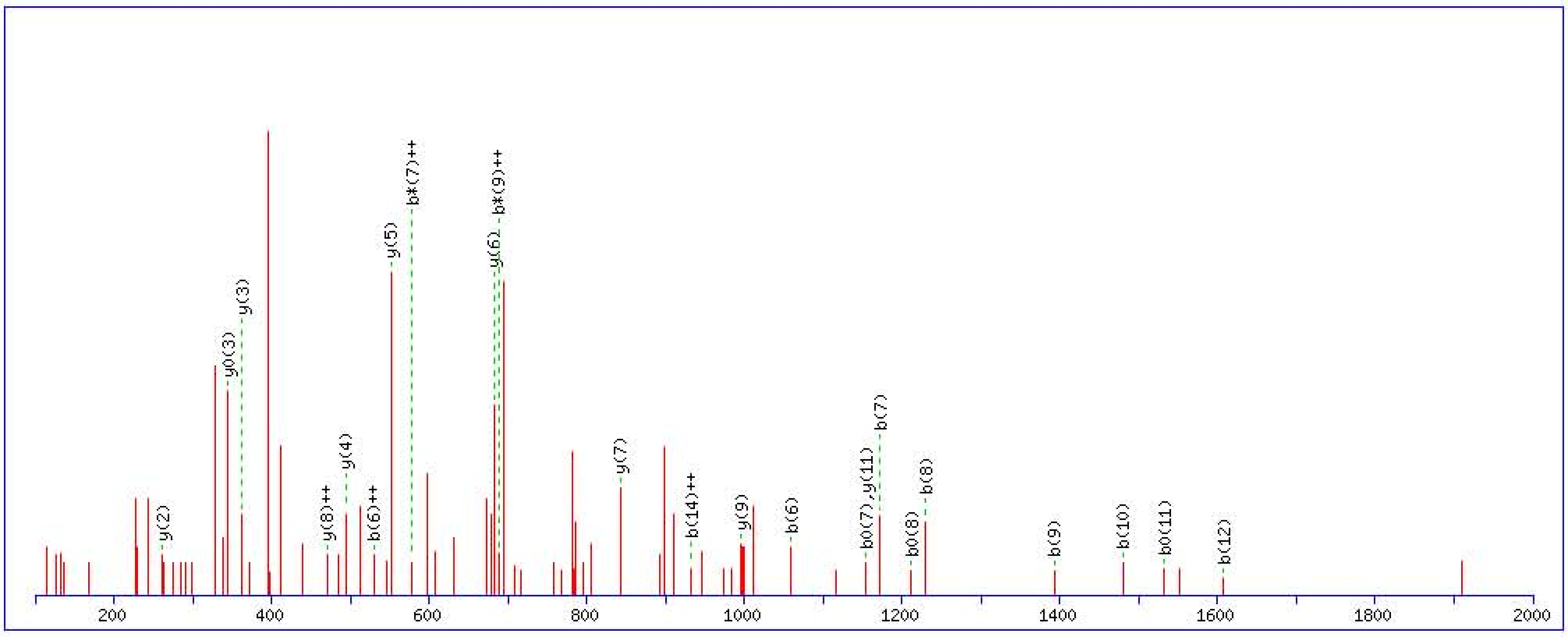
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KEDSCQLGYSAGPCMGMTSR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

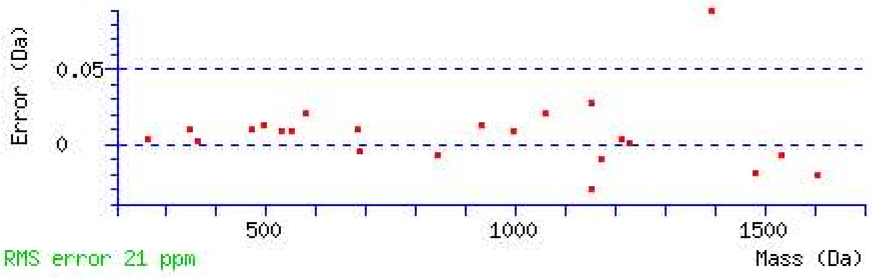
Match to Query 63822: 2545.126616 from(637.288930,4+) rtinseconds(1872) index(59789)
Title: Locus:1.1.1.3075.18 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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 ●

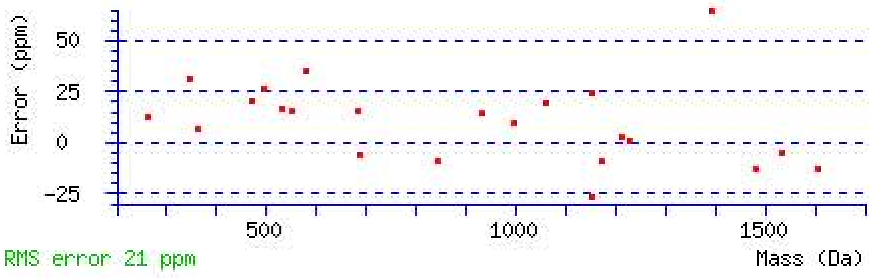


Monoisotopic mass of neutral peptide Mr(calc): 2545.089188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.012
Matches : 23/224 fragment ions using 63 most intense peaks (help)

#	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



RMS error 21 ppm



RMS error 21 ppm

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
26.9	2545.089188	0.037428	KEDSCQLGYSAGPCMGMTSR

Mascot: http://www.matrixscience.com/

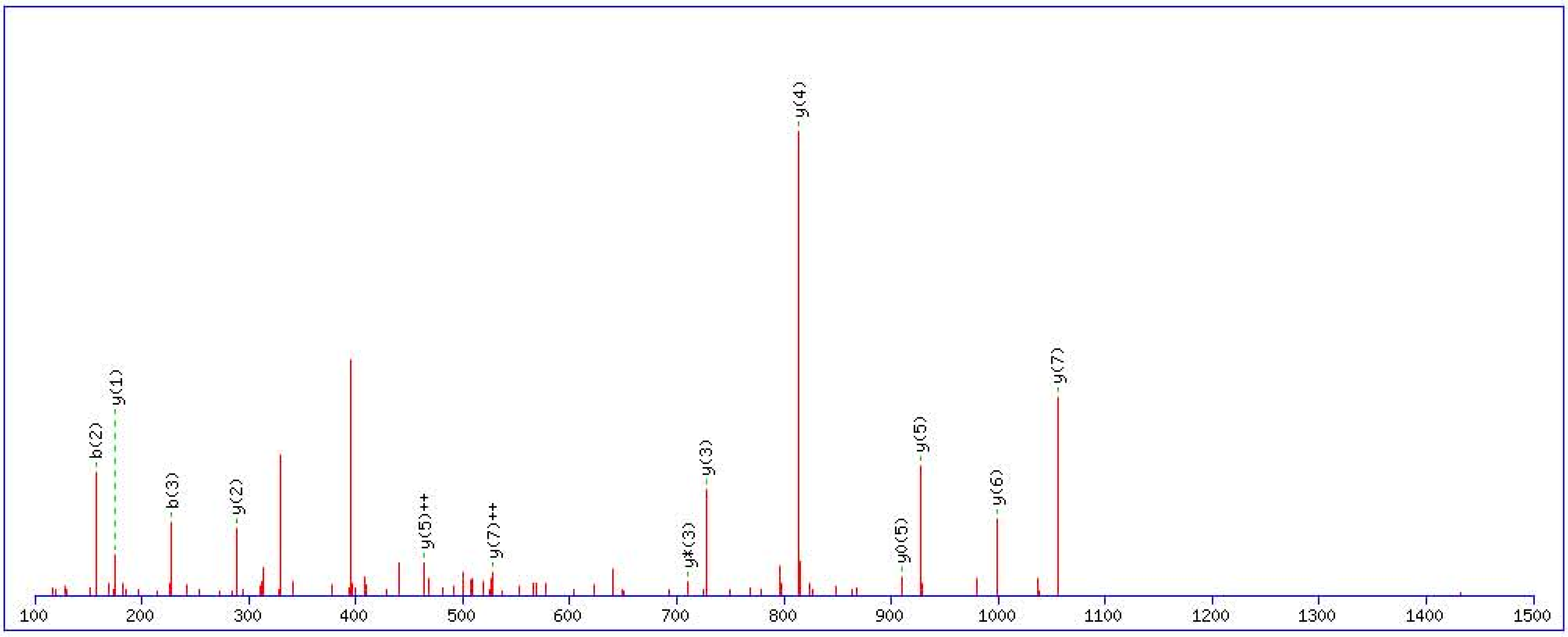
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGALSQLR**
Found in **MENT_HUMAN**, Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1

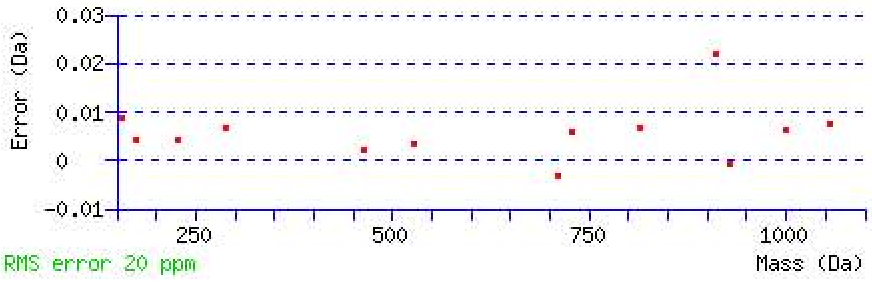
Match to Query 22013: 1153.672528 from(577.843540,2+) rtinseconds(1918) index(41581)
Title: Locus:1.1.1.3117.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

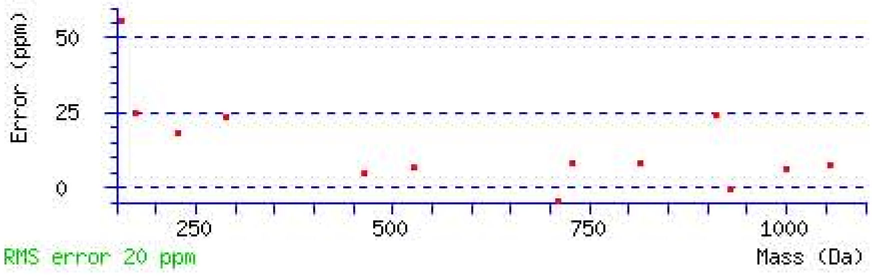
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1153.664139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 6.9e-005
Matches : 13/60 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	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
53.0	1153.664139	0.008389	VGALSQLR
19.6	1153.667953	0.004575	RANPNSIRVK
13.0	1153.675354	-0.002826	RALLSQR
13.0	1153.675369	-0.002841	RALTVQR
12.1	1153.681885	-0.009357	VQEKTALPLR
11.2	1153.664124	0.008404	VKQEALR
9.8	1153.681870	-0.009342	RALENLLPTK
5.3	1153.675369	-0.002841	QTVRALR
4.8	1153.656723	0.015805	RPSADPGKKAK
2.6	1153.664139	0.008389	VTQINLR

Mascot: http://www.matrixscience.com/

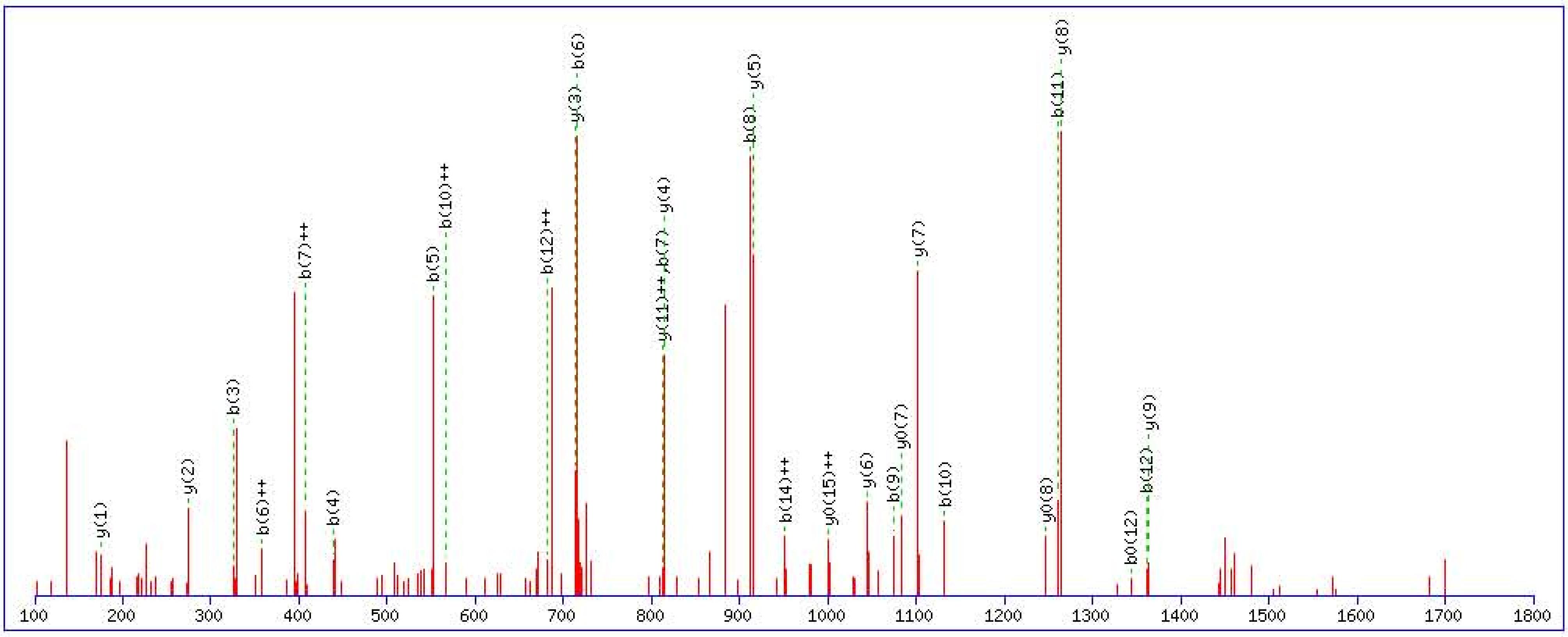
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPALNYPVYGETTQVR**
Found in **PRG4_HUMAN**, Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2

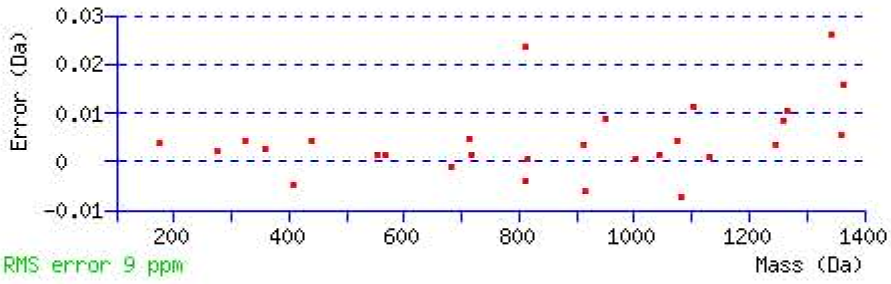
Match to Query 54788: 2174.132982 from(725.718270,3+) rtinseconds(1868) index(23714)
Title: Locus:1.1.1.2793.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

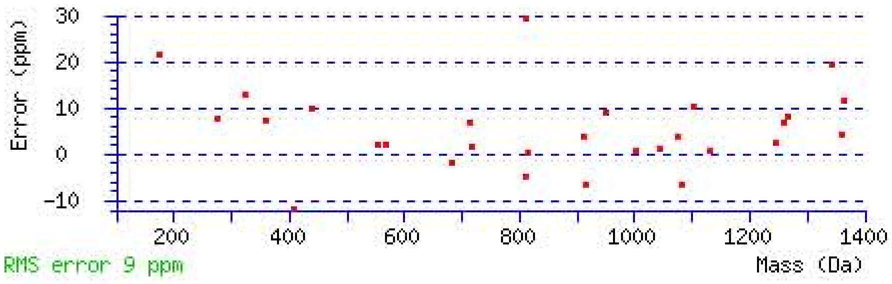
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2174.130630
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 2.8e-005
Matches : 30/154 fragment ions using 59 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							16
2	254.161151	127.584213	237.134602	119.070939			P	2019.036812	1010.022044	2002.010263	1001.508770	2001.026247	1001.016762	15
3	***325.198265***	163.102770	308.171716	154.589496			A	1921.984048	961.495662	1904.957499	952.982388	1903.973483	952.490380	14
4	***438.282329***	219.644803	421.255780	211.131528			L	1850.946934	925.977105	1833.920385	917.463831	1832.936369	916.971823	13
5	***552.325256***	276.666266	535.298707	268.152992			N	1737.862870	869.435073	1720.836321	860.921799	1719.852305	860.429791	12
6	***715.388585***	**358.197931**	698.362036	349.684656			Y	1623.819943	812.413610	1606.793394	803.900335	1605.809378	803.408327	11
7	***812.441349***	**406.724313**	795.414800	398.211038			P	1460.756614	730.881945	1443.730065	722.368671	1442.746049	721.876663	10
8	***911.509763***	456.258520	894.483214	447.745245			V	***1363.703850***	682.355563	1346.677301	673.842289	1345.693285	673.350281	9
9	***1074.573092***	537.790184	1057.546543	529.276910			Y	***1264.635436***	632.821356	1247.608887	624.308082	1246.624871	623.816074	8
10	***1131.594556***	**566.300916**	1114.568007	557.787642			G	***1101.572107***	551.289692	1084.545558	542.776417	1083.561542	542.284409	7
11	***1260.637149***	630.822212	1243.610600	622.308938	1242.626584	621.816930	E	***1044.550643***	522.778960	1027.524094	514.265685	1026.540078	513.773677	6
12	***1361.684828***	**681.346052**	1344.658279	672.832778	1343.674263	672.340769	T	***915.508050***	458.257663	898.481501	449.744389	897.497485	449.252381	5
13	1462.732507	731.869891	1445.705958	723.356617	1444.721942	722.864609	T	***814.460371***	407.733824	797.433822	399.220549	796.449806	398.728541	4
14	1901.957833	**951.482555**	1884.931284	942.969280	1883.947268	942.477272	Q	***713.412692***	357.209984	696.386143	348.696710			3
15	2001.026247	**1001.016762**	1983.999698	992.503487	1983.015682	992.011479	V	***274.187366***	137.597321	257.160817	129.084047			2
16							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of RPALNYPVYGETTQVR
(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	2174.130630	0.002352	RPALNYPVYGETTQVR
4.6	2174.133148	-0.000166	TLGGETRILAVTDFEPTQAR

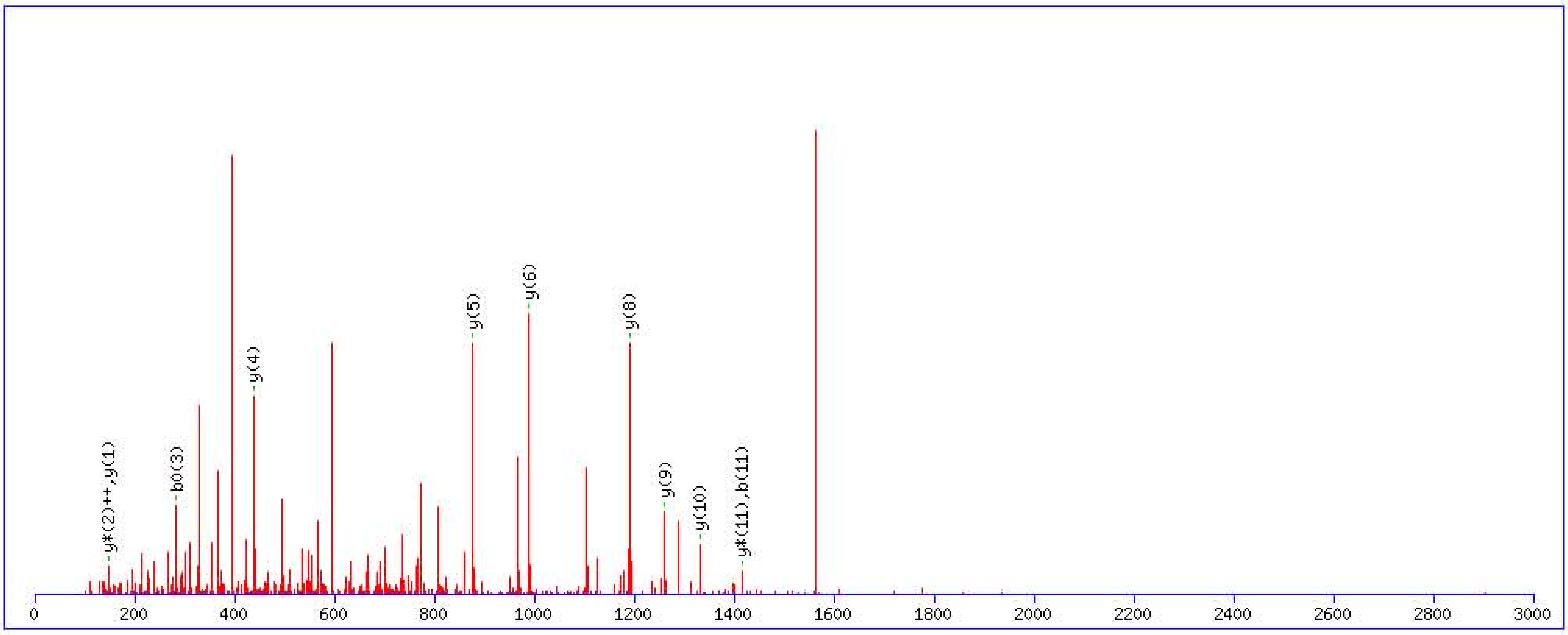
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETAASLLQAGYK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

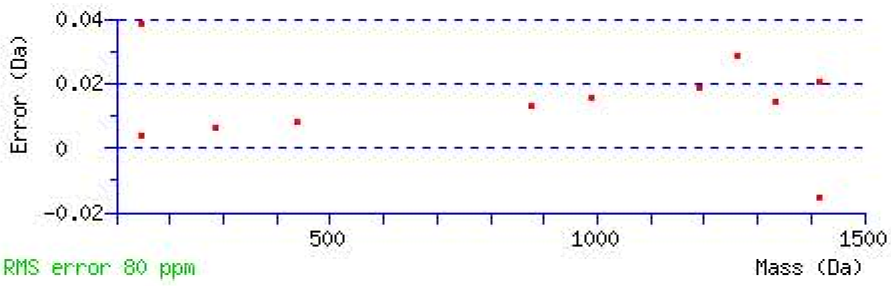
Match to Query 36750: 1561.832488 from(781.923520,2+) rtinseconds(2110) index(61492)
Title: Locus:1.1.1.3157.14 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

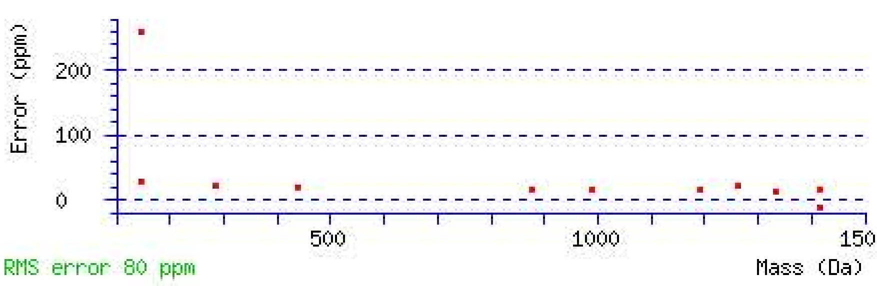
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1561.817383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.0001
Matches : 11/104 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	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
44.3	1561.817383	0.015105	ETAASLLQAGYK
1.8	1561.817398	0.015090	VLPEVLEKQCGYK

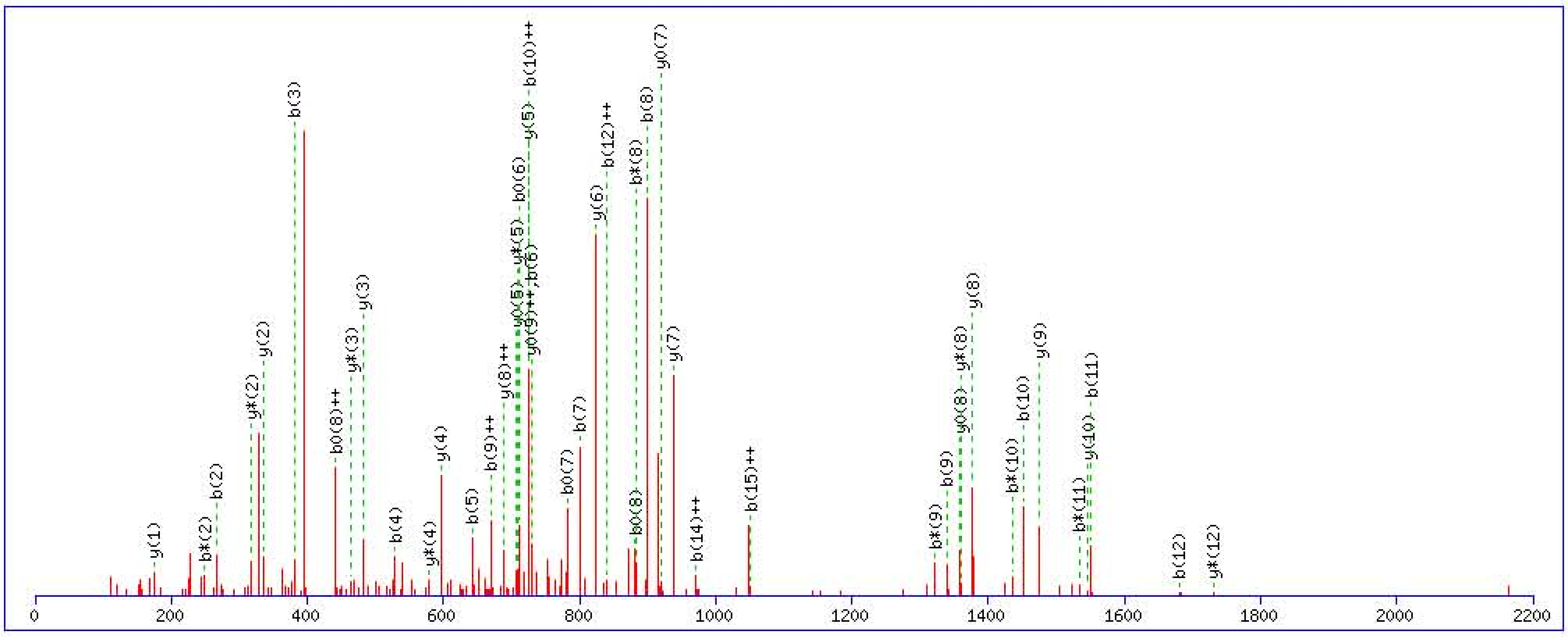
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQDFNSAVQLVENFCR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

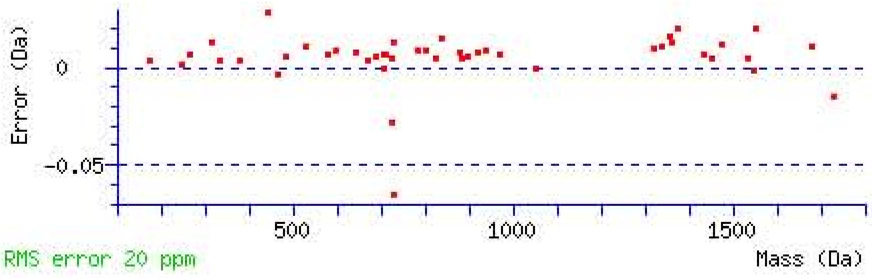
Match to Query 57320: 2274.093192 from(759.038340,3+) rtinseconds(2431) index(81734)
Title: Locus:1.1.1.2197.10 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

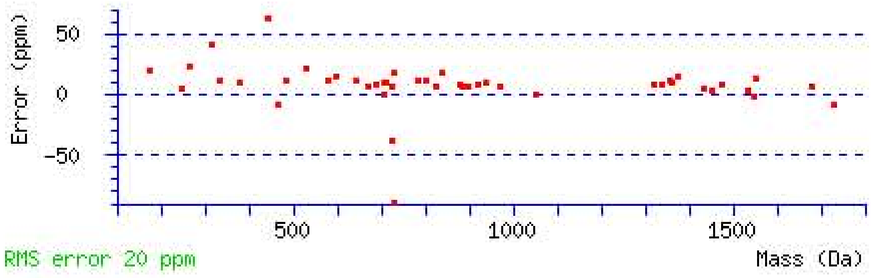
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2274.067398
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 6.1e-006
Matches : 46/166 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	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
59.0	2274.067398	0.025794	HQDFNSAVQLVENFCR
15.0	2274.067398	0.025794	HQDFNSAVQLVENFCR
3.4	2274.106277	-0.013085	EKRMTPPGGTLPGAEDVYGGSR

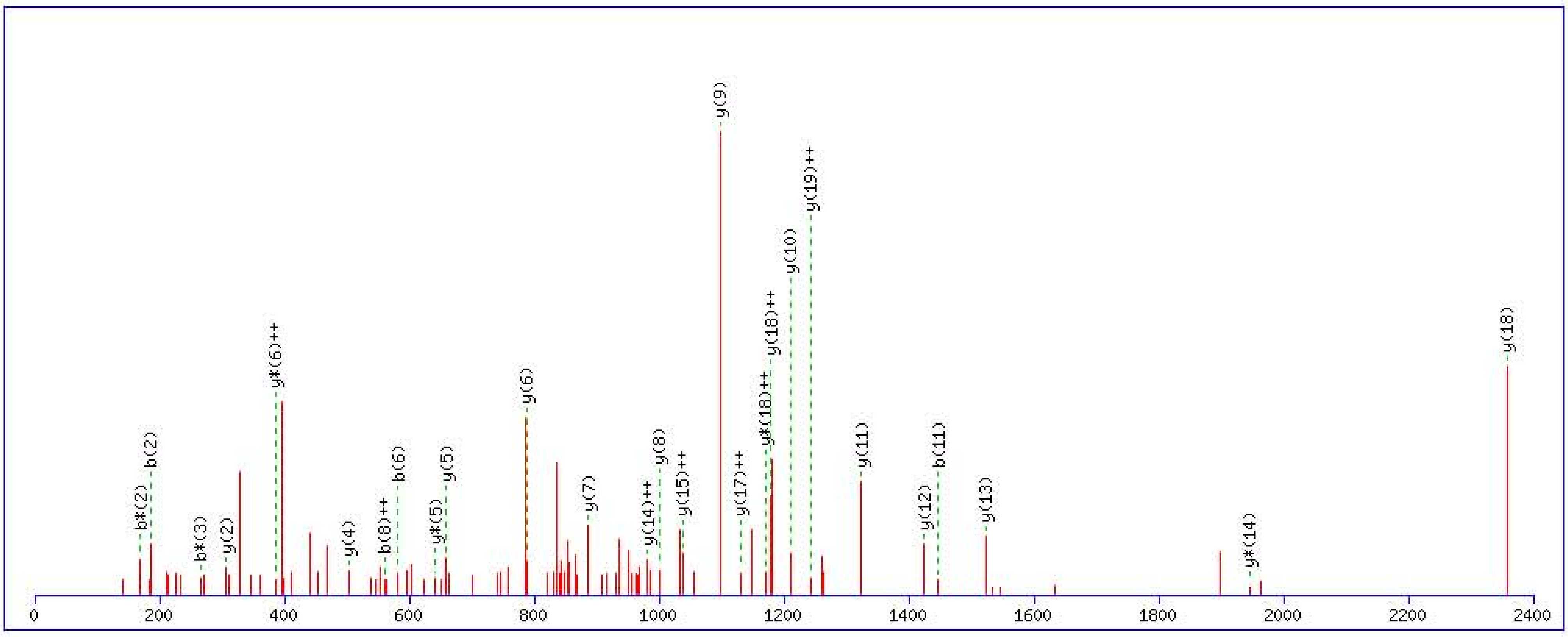
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQPSVLQVVNLPIVERPVCK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

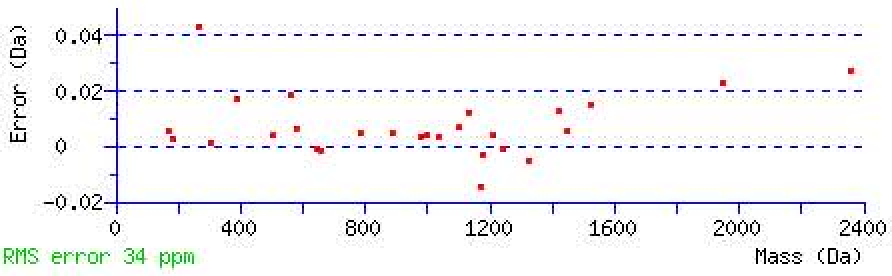
Match to Query 63771: 2542.447392 from(848.489740,3+) rtinseconds(2497) index(28027)
Title: Locus:1.1.1.3011.17 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

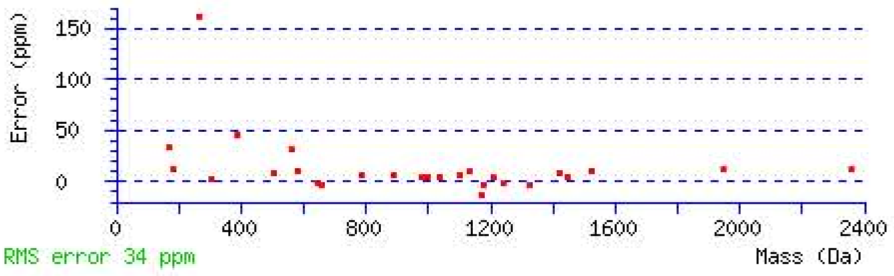
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2542.412766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.00069
Matches : 27/210 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	58.028740	29.518008					G							20
2	**186.087318**	93.547297	169.060769	85.034023			Q	2486.398570	1243.702923	2469.372021	1235.189648	2468.388005	1234.697640	19
3	283.140082	142.073679	266.113533	133.560405			P	***2358.339992***	1179.673634	2341.313443	1171.160359	2340.329427	1170.668351	18
4	370.172110	185.589693	353.145561	177.076419	352.161545	176.584411	S	2261.287228	1131.147252	2244.260679	1122.633977	2243.276663	1122.141969	17
5	469.240524	235.123900	452.213975	226.610626	451.229959	226.118618	V	2174.255200	1087.631238	2157.228651	1079.117963	2156.244635	1078.625955	16
6	**582.324588**	291.665932	565.298039	283.152658	564.314023	282.660650	L	2075.186786	1038.097031	2058.160237	1029.583756	2057.176221	1029.091748	15
7	1021.549914	511.278595	1004.523365	502.765321	1003.539349	502.273313	Q	1962.102722	981.554999	1945.076173	973.041724	1944.092157	972.549716	14
8	1120.618328	560.812802	1103.591779	552.299528	1102.607763	551.807520	V	***1522.877396***	761.942336	1505.850847	753.429061	1504.866831	752.937053	13
9	1219.686742	610.347009	1202.660193	601.833735	1201.676177	601.341727	V	***1423.808982***	712.408129	1406.782433	703.894854	1405.798417	703.402846	12
10	1333.729669	667.368473	1316.703120	658.855198	1315.719104	658.363190	N	***1324.740568***	662.873922	1307.714019	654.360647	1306.730003	653.868639	11
11	**1446.813733**	723.910505	1429.787184	715.397230	1428.803168	714.905222	L	***1210.697641***	605.852458	1193.671092	597.339184	1192.687076	596.847176	10
12	1543.866497	772.436887	1526.839948	763.923612	1525.855932	763.431604	P	***1097.613577***	549.310426	1080.587028	540.797152	1079.603012	540.305144	9
13	1656.950561	828.978918	1639.924012	820.465644	1638.939996	819.973636	I	***1000.560813***	500.784044	983.534264	492.270770	982.550248	491.778762	8
14	1756.018975	878.513126	1738.992426	869.999851	1738.008410	869.507843	V	***887.476749***	444.242012	870.450200	435.728738	869.466184	435.236730	7
15	1885.061568	943.034422	1868.035019	934.521147	1867.051003	934.029139	E	***788.408335***	394.707805	771.381786	386.194531	770.397770	385.702523	6
16	2041.162679	1021.084977	2024.136130	1012.571703	2023.152114	1012.079695	R	***659.365742***	330.186509	642.339193	321.673234			5
17	2138.215443	1069.611359	2121.188894	1061.098085	2120.204878	1060.606077	P	***503.264631***	252.135953	486.238082	243.622679			4
18	2237.283857	1119.145566	2220.257308	1110.632292	2219.273292	1110.140284	V	406.211867	203.609571	389.185318	195.096297			3
19	2397.314506	1199.160891	2380.287957	1190.647616	2379.303941	1190.155608	C	***307.143453***	154.075364	290.116904	145.562090			2
20							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GQPSVLQVVNLPIVERPVCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.5	2542.412766	0.034626	GQPSVLQVVNLPIVERPVCK
20.4	2542.412766	0.034626	GQPSVLQVVNLPIVERPVCK

Mascot: http://www.matrixscience.com/

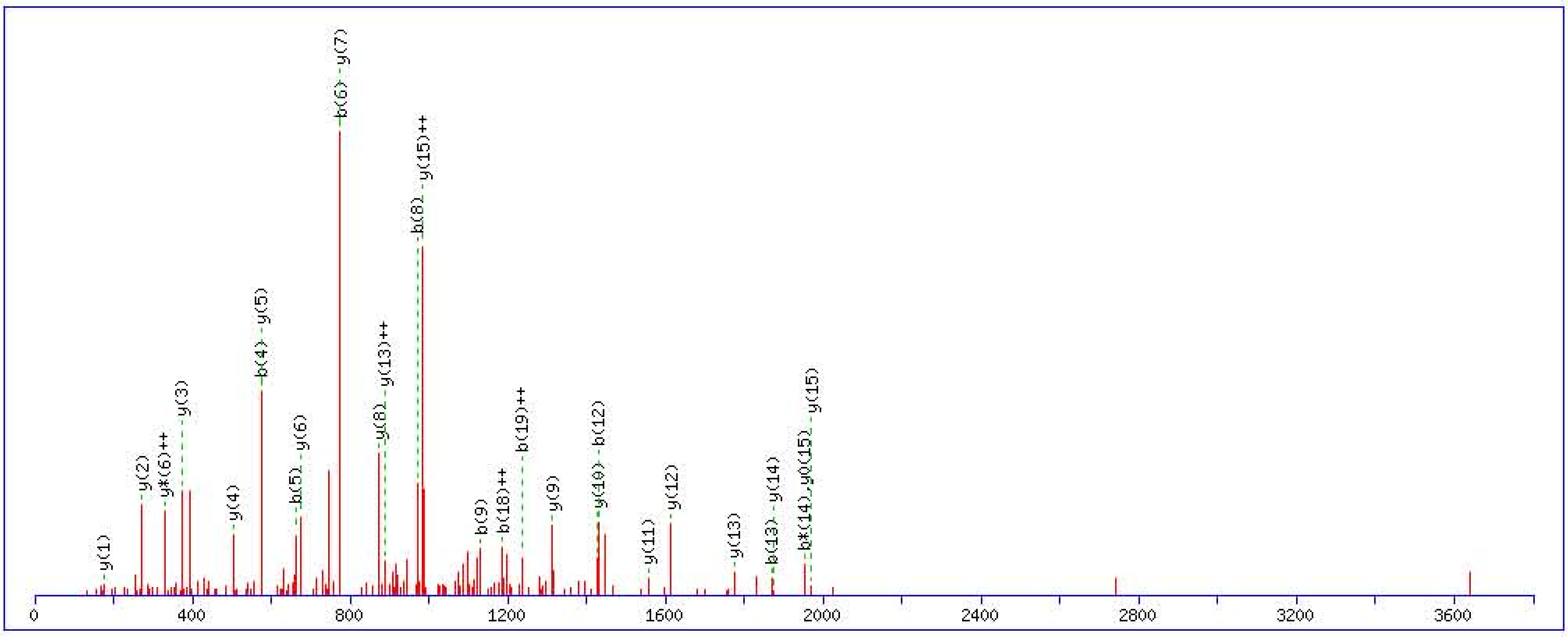
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RQECSIPVCGQDQVTVAMTPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

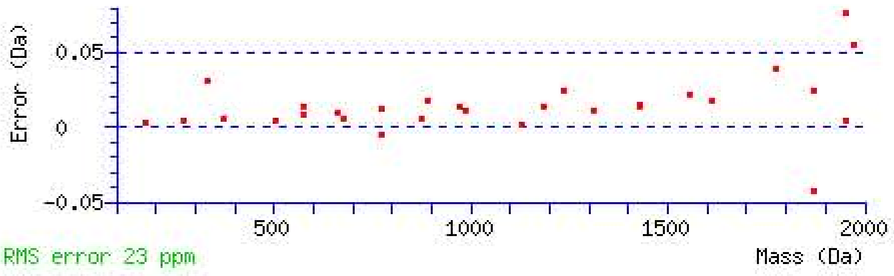
Match to Query 66258: 2742.336372 from(915.119400,3+) rtinseconds(1990) index(78837)
Title: Locus:1.1.1.2043.20 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

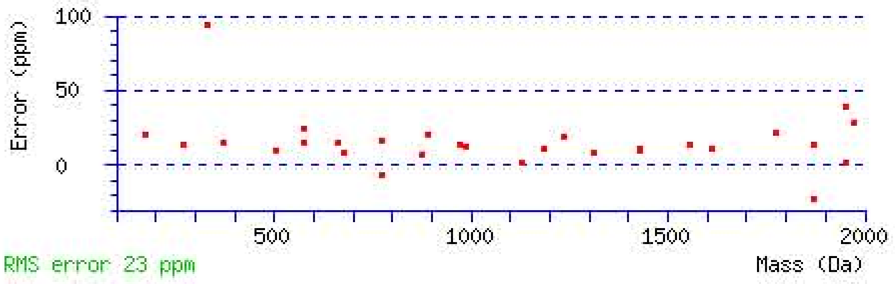
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2742.307404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 118  Expect: 4.8e-011
Matches : 29/232 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	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
117.7	2742.307404	0.028968	RQECSIPVCGQDQVTVAMTPR
87.4	2742.307404	0.028968	RQECSIPVCGQDQVTVAMTPR
25.8	2742.307404	0.028968	RQECSIPVCGQDQVTVAMTPR

Mascot: http://www.matrixscience.com/

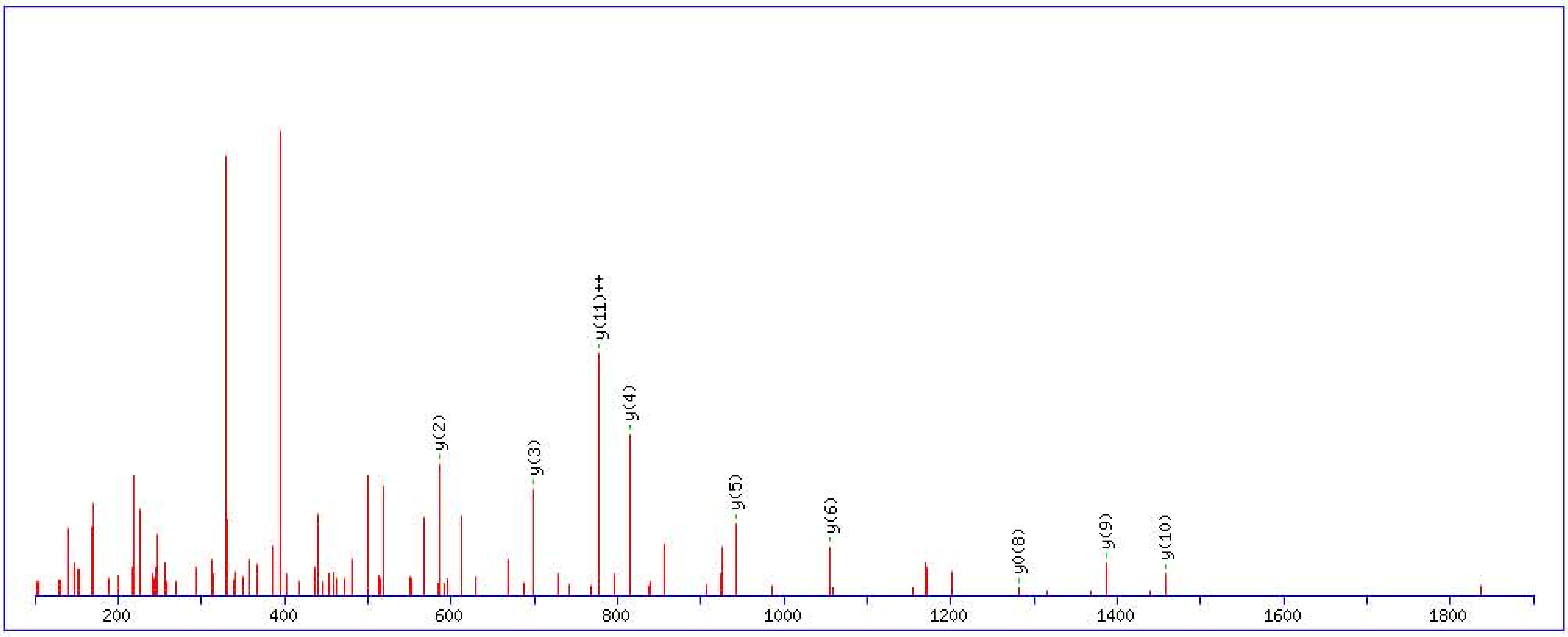
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DMPASEDLQDLQK**
Found in **SEPP1_HUMAN**, Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3

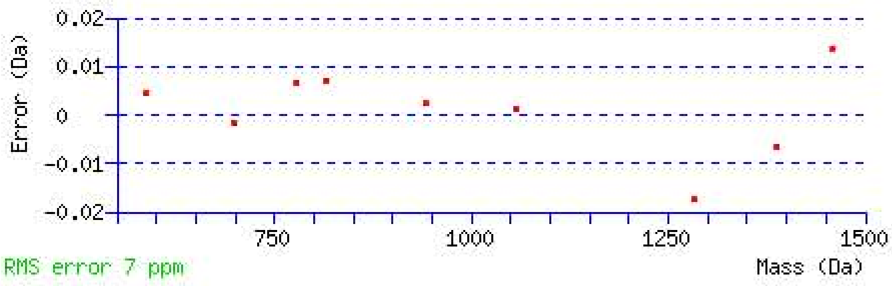
Match to Query 45287: 1799.853282 from(600.958370,3+) rtinseconds(2162) index(25854)
Title: Locus:1.1.1.2895.7 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

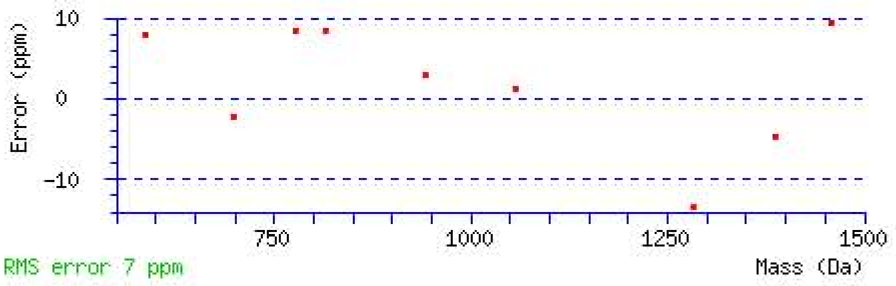
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1799.843353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 0.00071
Matches : 9/122 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
43.6	1799.843353	0.009929	DMPASEDLQDLQK
8.8	1799.843353	0.009929	DMPASEDLQDLQK

Mascot: http://www.matrixscience.com/

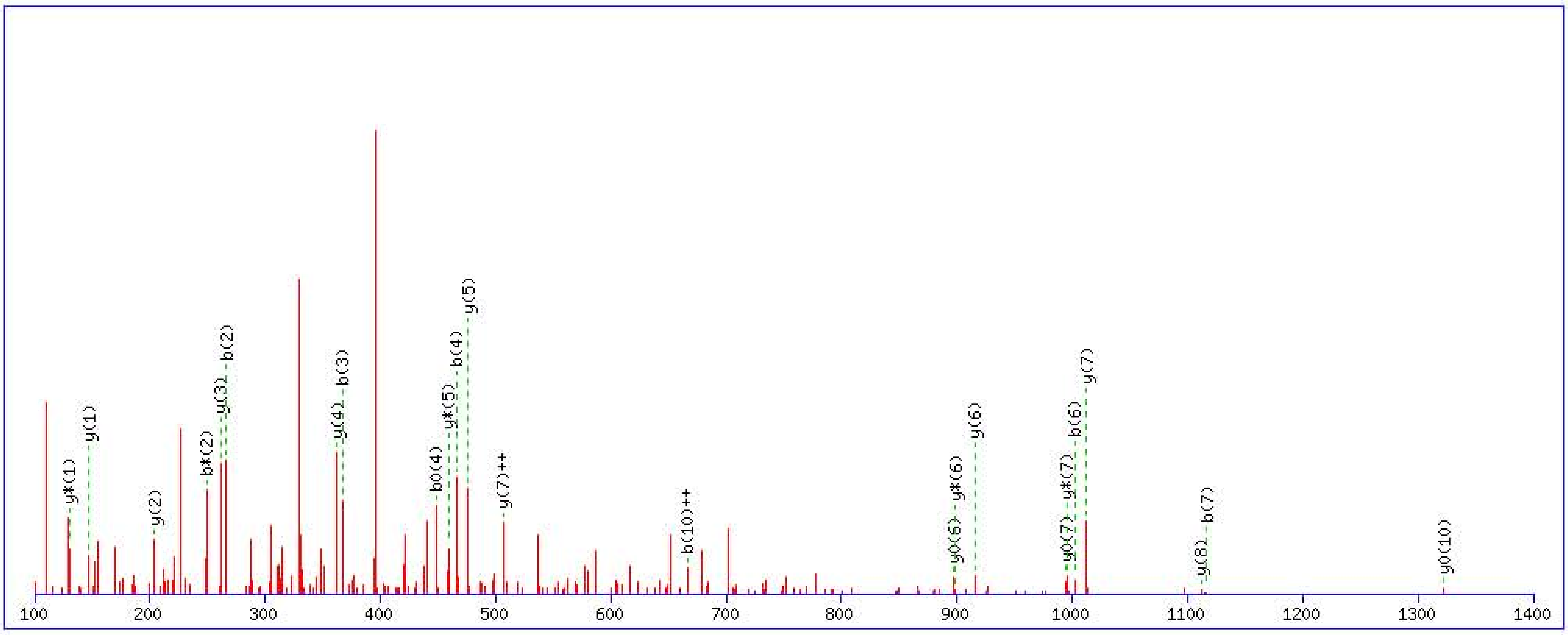
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

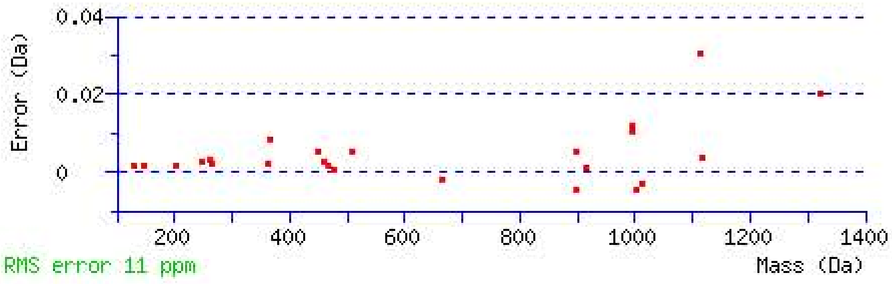
Match to Query 34208: 1476.759732 from(493.260520,3+) rtinseconds(1184) index(73548)
Title: Locus:1.1.1.1763.10 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

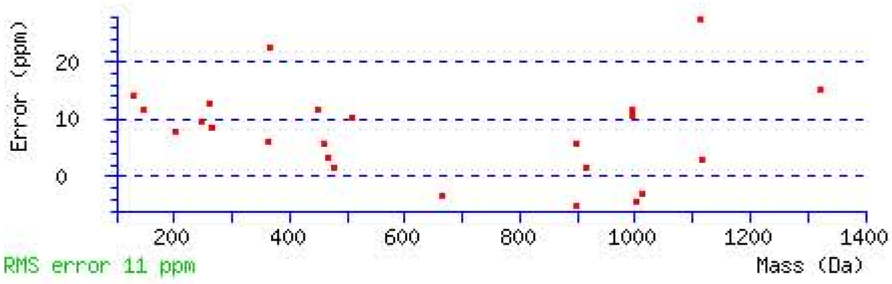
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1476.750748
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.0039
Matches : 24/108 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	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
27.4	1476.750748	0.008984	HQTVPQNTGGK
16.4	1476.750748	0.008984	HQTVPQNTGGK
1.6	1476.739487	0.020245	GPEVMAFIEQGKR

Mascot: http://www.matrixscience.com/

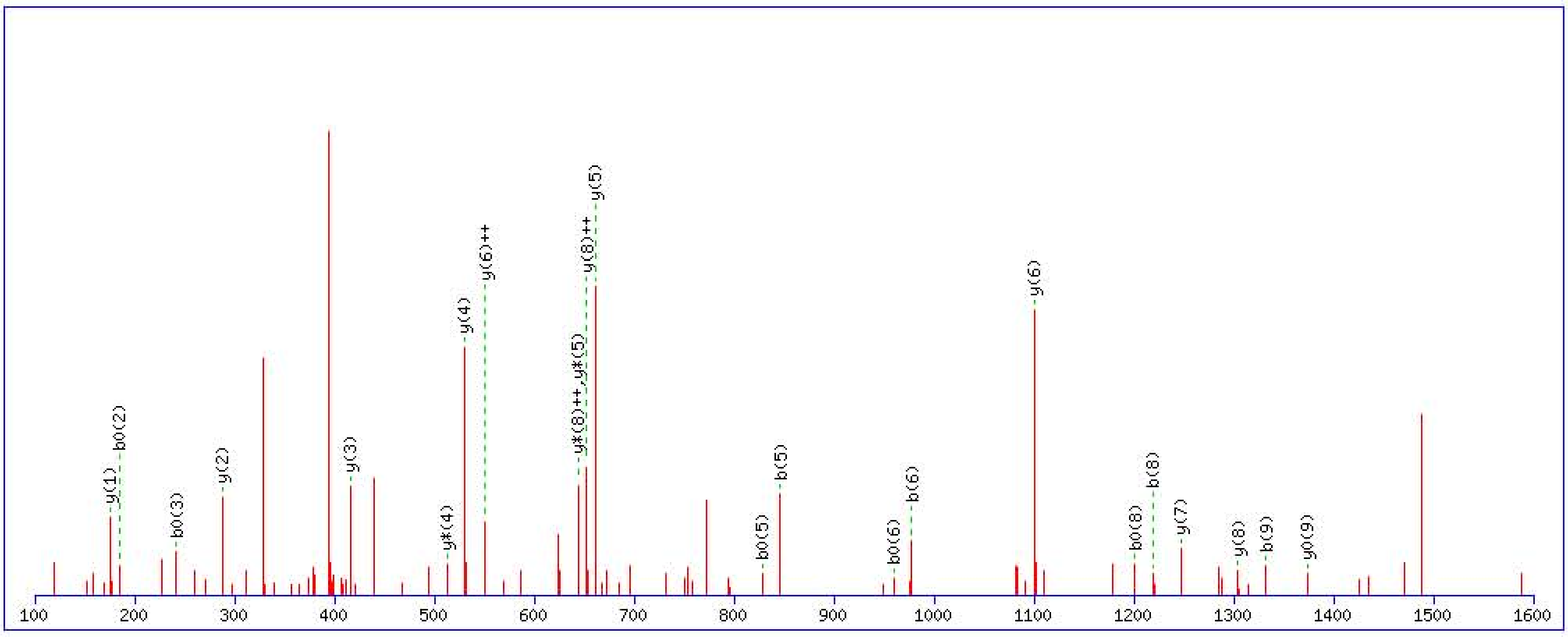
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

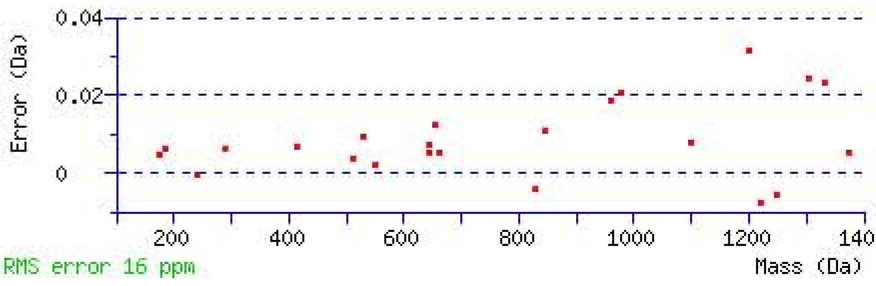
Match to Query 35137: 1505.722588 from(753.868570,2+) rtinseconds(2053) index(79227)
Title: Locus:1.1.1.2065.23 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

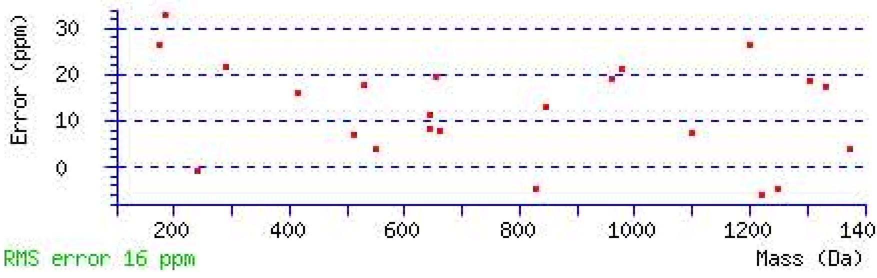
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 48 **Expect:** 0.00027
Matches : 23/84 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	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
48.5	1505.711899	0.010689	DSGFQMNQLR
15.6	1505.711899	0.010689	DSGFQMNQLR
13.9	1505.740891	-0.018303	VQTSNFPRECIR
10.2	1505.704025	0.018563	MQMEIDQLR
9.7	1505.703140	0.019448	DETMEEQDIKLR
5.7	1505.744232	-0.021644	QAKMAPSRMDSLR
3.9	1505.740891	-0.018303	GSPKCFRSVSPER
2.9	1505.730530	-0.007942	QIFCQACLR
2.9	1505.736862	-0.014274	EVMSPTGSARGRSR
2.1	1505.736877	-0.014289	AAMAVGGAGGSRVSSGR

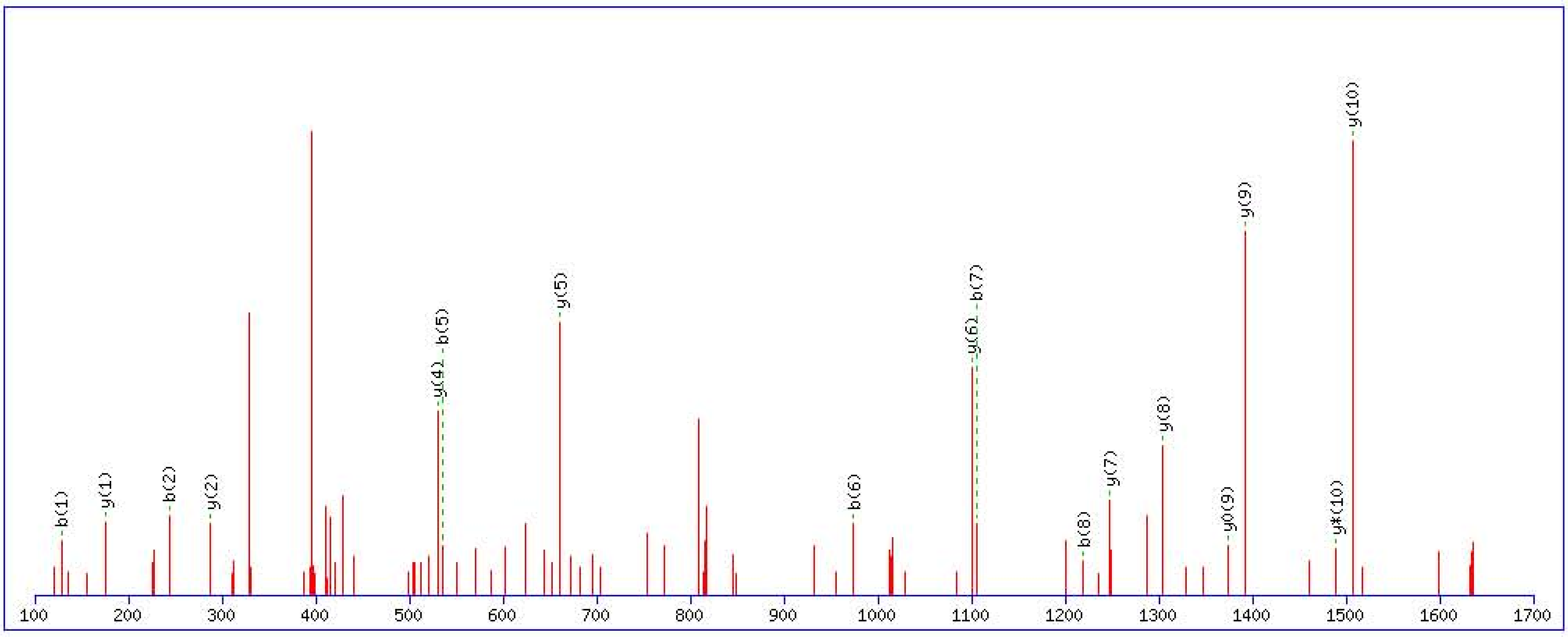
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

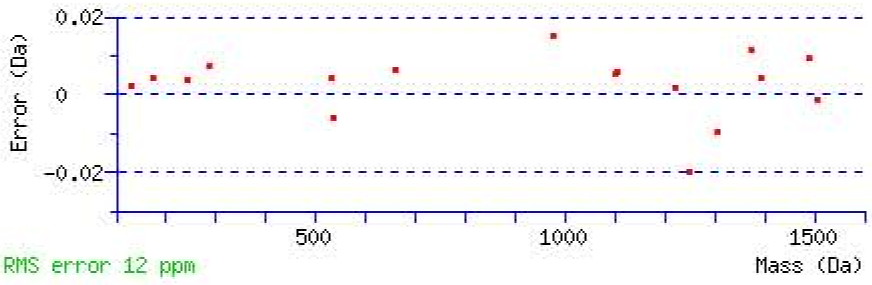
Match to Query 40673: 1633.818308 from(817.916430,2+) rtinseconds(1732) index(77123)
Title: Locus:1.1.1.1954.11 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

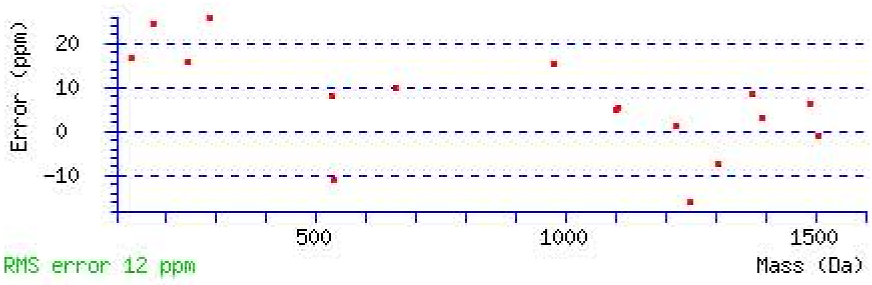
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1633.806854
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 3.3e-006
Matches : 17/102 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	**129.102239**	65.054757	112.075690	56.541483			K							11
2	**244.129182**	122.568229	227.102633	114.054955	226.118617	113.562947	D	***1506.719181***	753.863228	1489.692632	745.349954	1488.708616	744.857946	10
3	331.161210	166.084243	314.134661	157.570969	313.150645	157.078961	S	***1391.692238***	696.349757	1374.665689	687.836482	1373.681673	687.344474	9
4	388.182674	194.594975	371.156125	186.081701	370.172109	185.589693	G	***1304.660210***	652.833743	1287.633661	644.320468			8
5	**535.251088**	268.129182	518.224539	259.615908	517.240523	259.123900	F	***1247.638746***	624.323011	1230.612197	615.809736			7
6	**974.476414**	487.741845	957.449865	479.228571	956.465849	478.736563	Q	***1100.570332***	550.788804	1083.543783	542.275530			6
7	**1105.516899**	553.262088	1088.490350	544.748813	1087.506334	544.256805	M	***661.345006***	331.176141	644.318457	322.662866			5
8	**1219.559826**	610.283551	1202.533277	601.770277	1201.549261	601.278268	N	***530.304521***	265.655899	513.277972	257.142624			4
9	1347.618404	674.312840	1330.591855	665.799566	1329.607839	665.307558	Q	416.261594	208.634435	399.235045	200.121160			3
10	1460.702468	730.854872	1443.675919	722.341598	1442.691903	721.849589	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
64.5	1633.806854	0.011454	KDSGFQMNQLR
34.2	1633.806854	0.011454	KDSGFQMNQLR
5.7	1633.822128	-0.003820	QFMKGQVSWGR
5.0	1633.842361	-0.024053	QDLIPSYSLGSNKGR
3.8	1633.803482	0.014826	QLFERDWSSR
3.6	1633.824615	-0.006307	AGGAFLMAGQVAEQLR
3.2	1633.821930	-0.003622	GGRMDQQPALPHRR
2.5	1633.795609	0.022699	KFMEDEQQLR
2.4	1633.798111	0.020197	CTTVDEAEKAIELR
1.9	1633.806885	0.011423	MGVHCFLGLTATATR

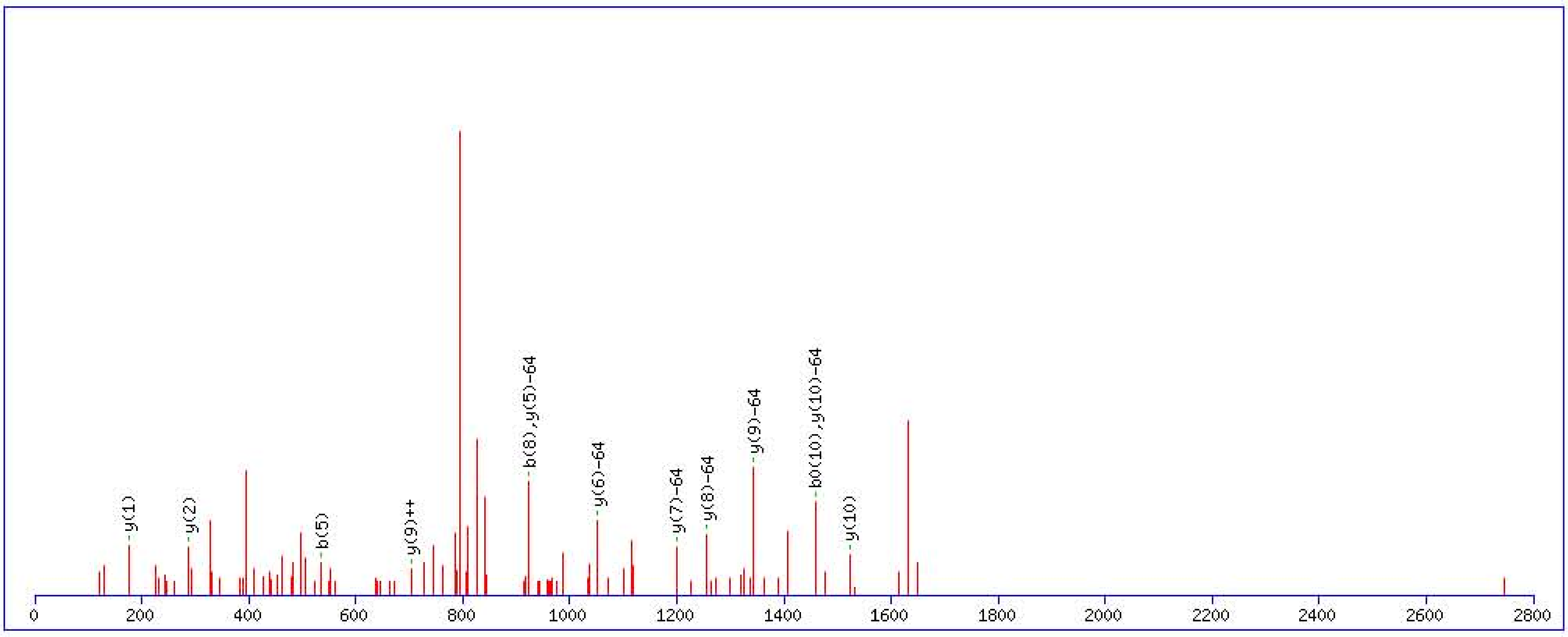
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

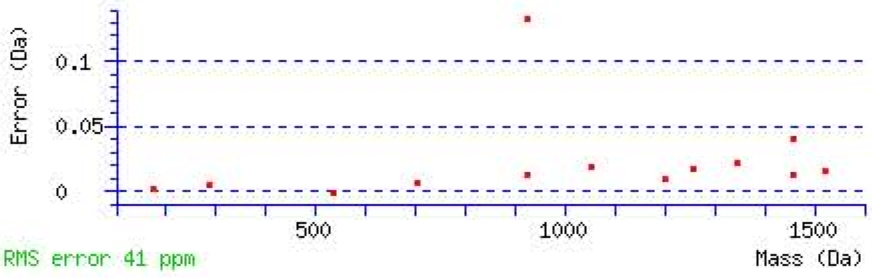
Match to Query 41157: 1649.808328 from(825.911440,2+) rtinseconds(1533) index(75941)
Title: Locus:1.1.1.1884.24 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

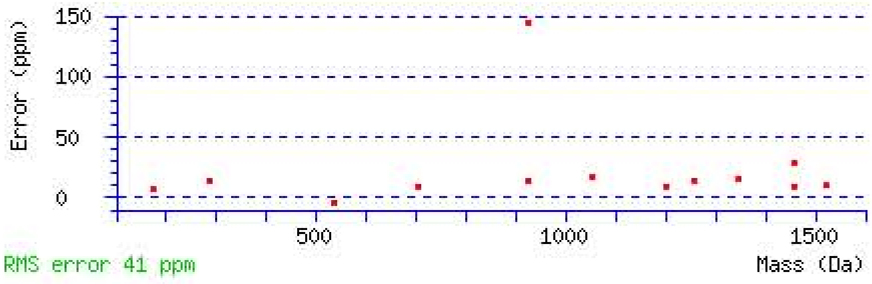
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1649.801773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7      : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 0.00013
Matches : 13/154 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							11
2	244.129182	122.568229	227.102633	114.054955	226.118617	113.562947	D	*1458.715811*	729.861544	1441.689262	721.348269	1440.705246	720.856261	10
3	331.161210	166.084243	314.134661	157.570969	313.150645	157.078961	S	*1343.688868*	672.348072	1326.662319	663.834798	1325.678303	663.342790	9
4	388.182674	194.594975	371.156125	186.081701	370.172109	185.589693	G	*1256.656840*	628.832058	1239.630291	620.318784			8
5	535.251088	268.129182	518.224539	259.615908	517.240523	259.123900	F	*1199.635376*	600.321326	1182.608827	591.808052			7
6	663.309666	332.158471	646.283117	323.645197	645.299101	323.153189	Q	*1052.566962*	526.787119	1035.540413	518.273845			6
7	746.346781	373.677029	729.320232	365.163754	728.336216	364.671746	M	*924.508384*	462.757830	907.481835	454.244556			5
8	860.389708	430.698492	843.363159	422.185218	842.379143	421.693210	N	841.471269	421.239273	824.444720	412.725998			4
9	1299.615034	650.311155	1282.588485	641.797881	1281.604469	641.305873	Q	727.428342	364.217809	710.401793	355.704535			3
10	1412.699098	706.853187	1395.672549	698.339913	1394.688533	697.847905	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
52.9	1649.801773	0.006555	KDSGFQMNQLR
39.4	1649.801773	0.006555	KDSGFQMNQLR
10.9	1649.794373	0.013955	FCSNSGRLSGPAELR
9.9	1649.790527	0.017801	KFMEDEQQLR
5.3	1649.790527	0.017801	KFMEDEQQLR
4.9	1649.793045	0.015283	EEQMDGTVTLKDLR
3.2	1649.808304	0.000024	ISPQSNVDFDLMLR
3.0	1649.824234	-0.015906	QLEQHMGQRGR
2.5	1649.830780	-0.022452	QDTVRVAFCSALQR
2.3	1649.813019	-0.004691	VHAMTQHSVQPMLR

Mascot: http://www.matrixscience.com/

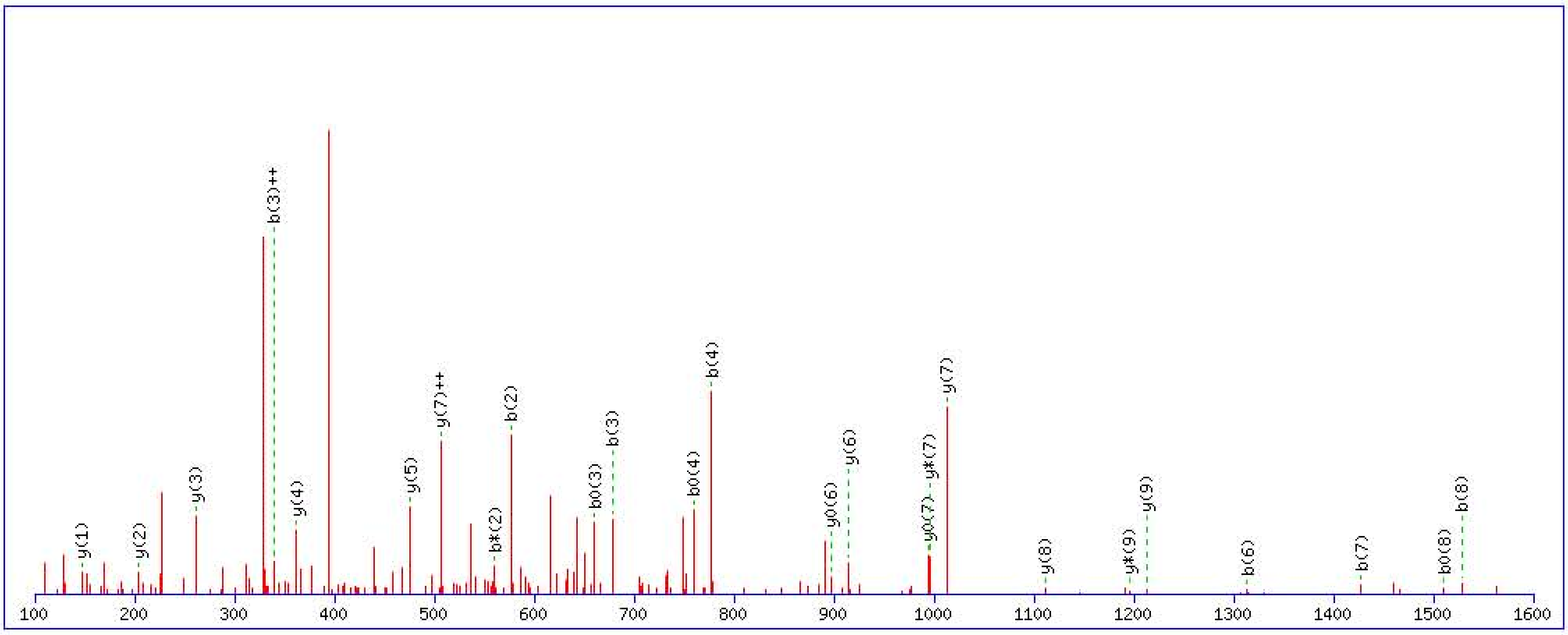
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

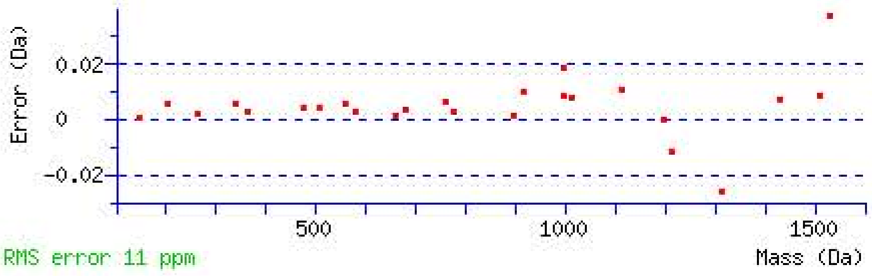
Match to Query 44955: 1787.927952 from(596.983260,3+) rtinseconds(1589) index(76331)
Title: Locus:1.1.1.1904.8 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

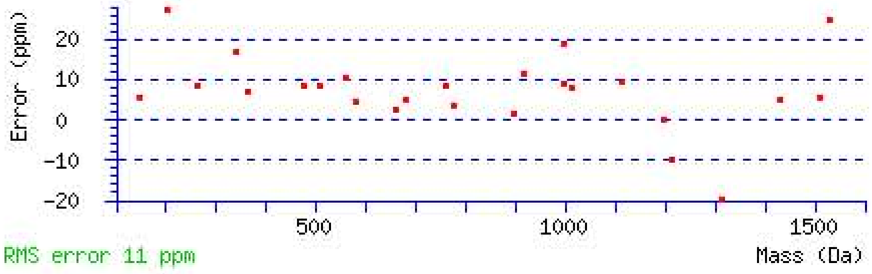
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1787.917496
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: 32 **Expect:** 0.0014
Matches : 25/108 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	138.066188	69.536732					H							11
2	**577.291514**	289.149395	560.264965	280.636121			Q	1651.865847	826.436562	1634.839298	817.923287	1633.855282	817.431279	10
3	**678.339193**	339.673235	661.312644	331.159960	660.328628	330.667952	T	***1212.640521***	606.823899	1195.613972	598.310624	1194.629956	597.818616	9
4	**777.407607**	389.207442	760.381058	380.694167	759.397042	380.202159	V	***1111.592842***	556.300059	1094.566293	547.786785	1093.582277	547.294777	8
5	874.460371	437.733824	857.433822	429.220549	856.449806	428.728541	P	***1012.524428***	506.765852	995.497879	498.252578	994.513863	497.760570	7
6	**1313.685697**	657.346487	1296.659148	648.833212	1295.675132	648.341204	Q	***915.471664***	458.239470	898.445115	449.726196	897.461099	449.234188	6
7	**1427.728624**	714.367950	1410.702075	705.854676	1409.718059	705.362668	N	***476.246338***	238.626807	459.219789	230.113532	458.235773	229.621524	5
8	**1528.776303**	764.891790	1511.749754	756.378515	1510.765738	755.886507	T	***362.203411***	181.605343	345.176862	173.092069	344.192846	172.600061	4
9	1585.797767	793.402522	1568.771218	784.889247	1567.787202	784.397239	G	***261.155732***	131.081504	244.129183	122.568229			3
10	1642.819231	821.913254	1625.792682	813.399979	1624.808666	812.907971	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
31.6	1787.917496	0.010456	HQTVPQNTGGK
1.2	1787.923996	0.003956	VPLQGFAALEGMNGIQK

Mascot: http://www.matrixscience.com/

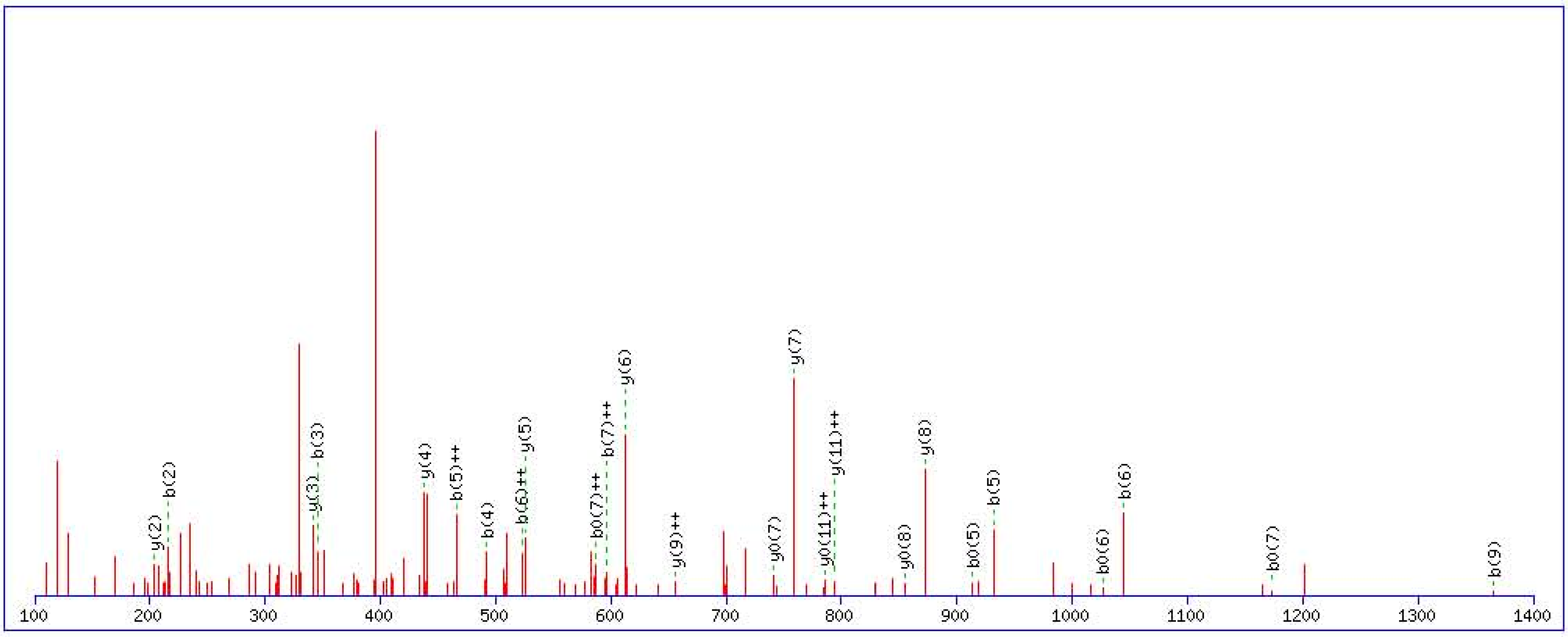
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SKEFQLFSSPHGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

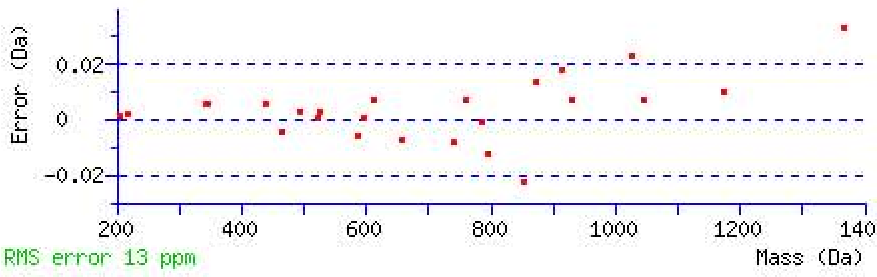
Match to Query 45333: 1801.931322 from(601.651050,3+) rtinseconds(1761) index(77338)
Title: Locus:1.1.1.1964.16 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

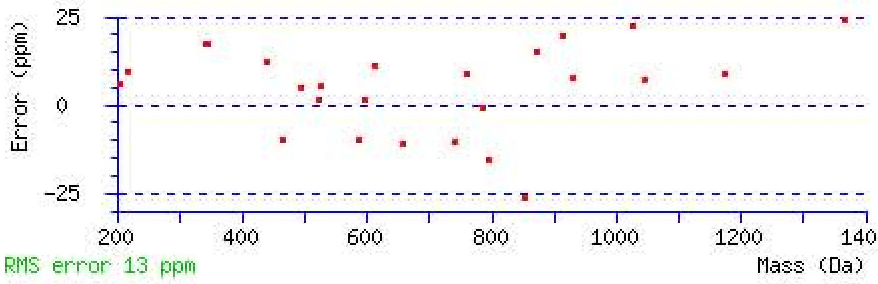
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1801.918518
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.0039
Matches : 25/134 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							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
29.0	1801.918518	0.012804	SKEFQLFSSPHGK
3.1	1801.914536	0.016786	QTVMTVVYGVTRYGGR
0.9	1801.905701	0.025621	DAEAAEATAEGALKAEKK
0.5	1801.924332	0.006990	MIQQEEIRKLEEEK

Mascot: http://www.matrixscience.com/

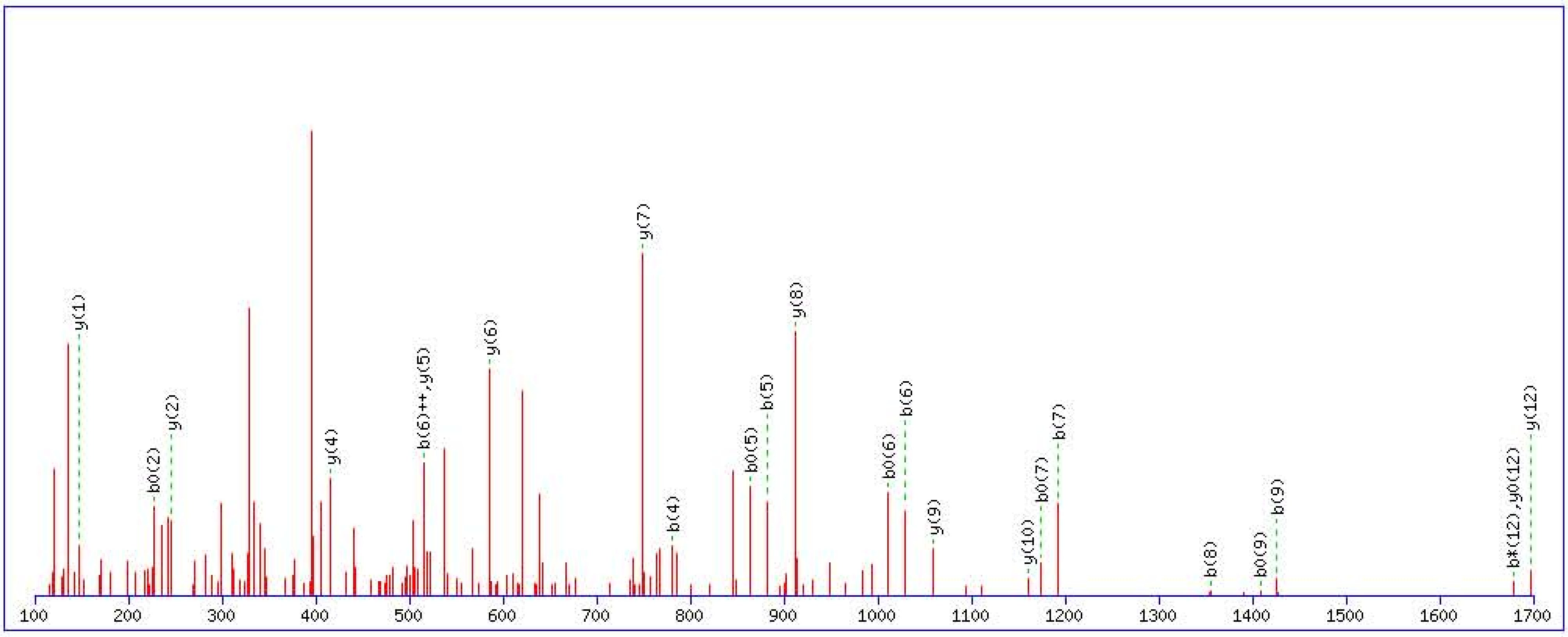
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDPQTFYYAVAVVK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

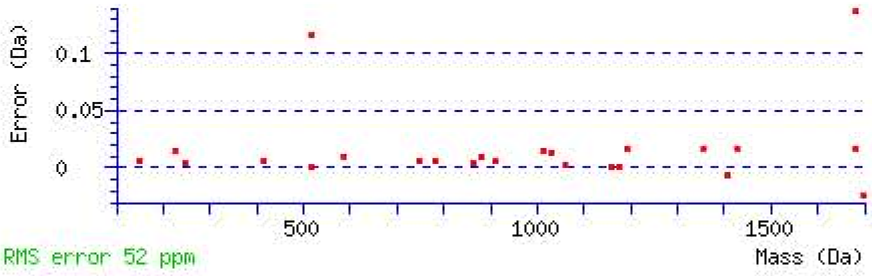
Match to Query 48485: 1939.997082 from(647.672970,3+) rtinseconds(2547) index(82435)
Title: Locus:1.1.1.2237.8 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

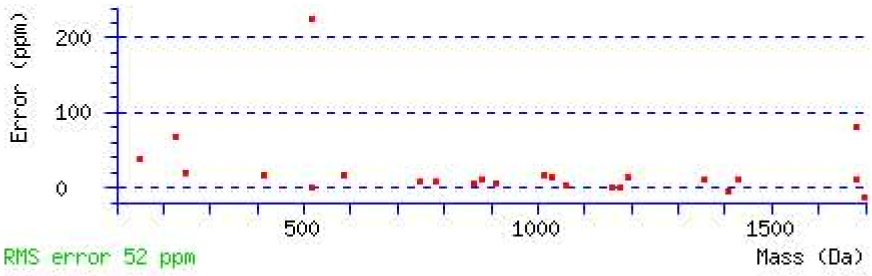
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1939.975372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00095
Matches : 24/132 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							14
2	245.076812	123.042044			227.066247	114.036762	D	1811.940058	906.473667	1794.913509	897.960393	1793.929493	897.468385	13
3	342.129576	171.568426			324.119011	162.563144	P	***1696.913115***	848.960196	1679.886566	840.446921	1678.902550	839.954913	12
4	**781.354902**	391.181089	764.328353	382.667815	763.344337	382.175807	Q	1599.860351	800.433814	1582.833802	791.920539	1581.849786	791.428531	11
5	**882.402581**	441.704929	865.376032	433.191654	864.392016	432.699646	T	***1160.635025***	580.821151	1143.608476	572.307876	1142.624460	571.815868	10
6	**1029.470995**	515.239136	1012.444446	506.725861	1011.460430	506.233853	F	***1059.587346***	530.297311	1042.560797	521.784037			9
7	**1192.534324**	596.770800	1175.507775	588.257526	1174.523759	587.765518	Y	***912.518932***	456.763104	895.492383	448.249830			8
8	**1355.597653**	678.302465	1338.571104	669.789190	1337.587088	669.297182	Y	***749.455603***	375.231440	732.429054	366.718165			7
9	**1426.634767**	713.821022	1409.608218	705.307747	1408.624202	704.815739	A	***586.392274***	293.699775	569.365725	285.186501			6
10	1525.703181	763.355229	1508.676632	754.841954	1507.692616	754.349946	V	***515.355160***	258.181218	498.328611	249.667944			5
11	1596.740295	798.873786	1579.713746	790.360511	1578.729730	789.868503	A	***416.286746***	208.647011	399.260197	200.133737			4
12	1695.808709	848.407993	1678.782160	839.894718	1677.798144	839.402710	V	345.249632	173.128454	328.223083	164.615180			3
13	1794.877123	897.942200	1777.850574	889.428925	1776.866558	888.936917	V	***246.181218***	123.594247	229.154669	115.080973			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EDPQTFYYAVAVVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	1939.975372	0.021710	EDPQTFYYAVAVVK

Mascot: http://www.matrixscience.com/

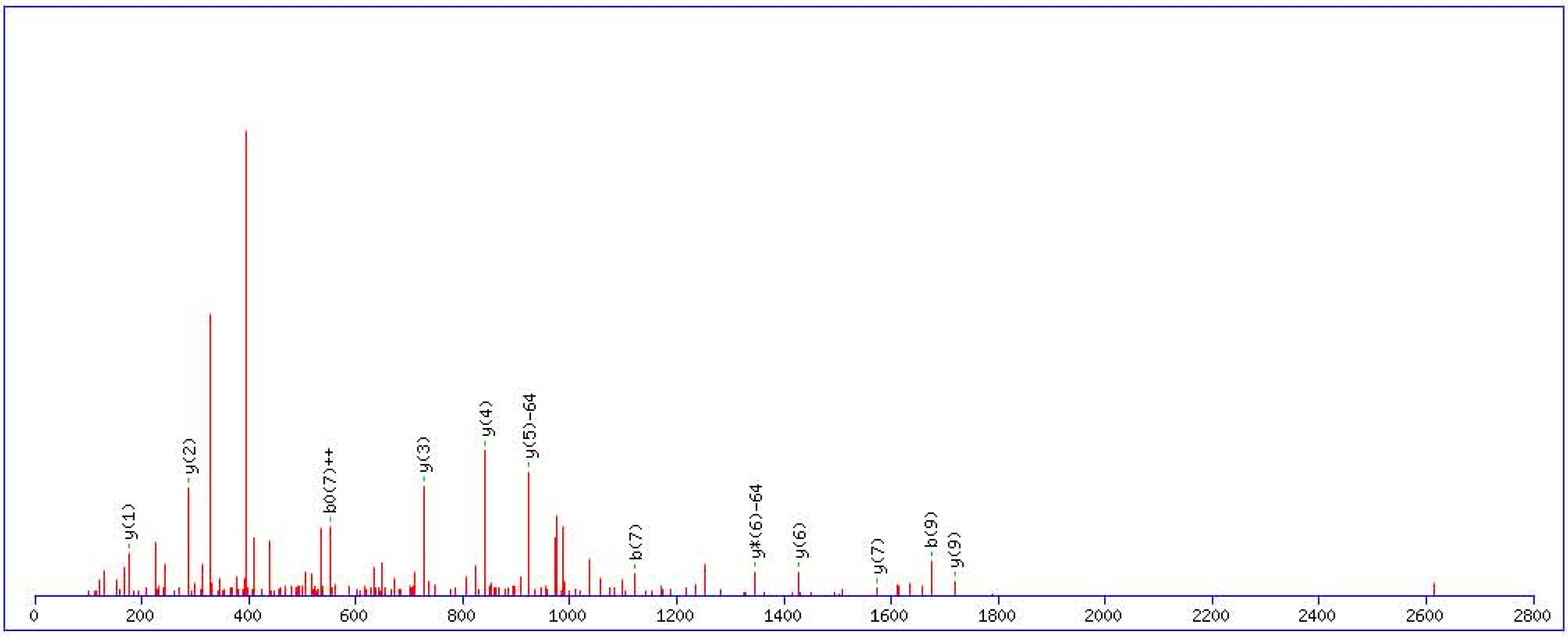
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

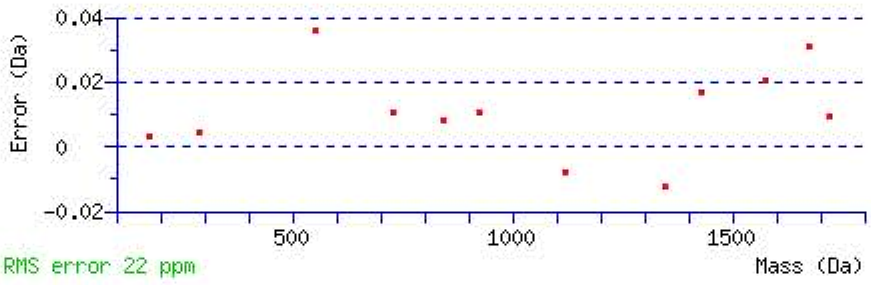
Match to Query 48961: 1960.982292 from(654.668040,3+) rtinseconds(1880) index(77974)
Title: Locus:1.1.1.2005.23 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

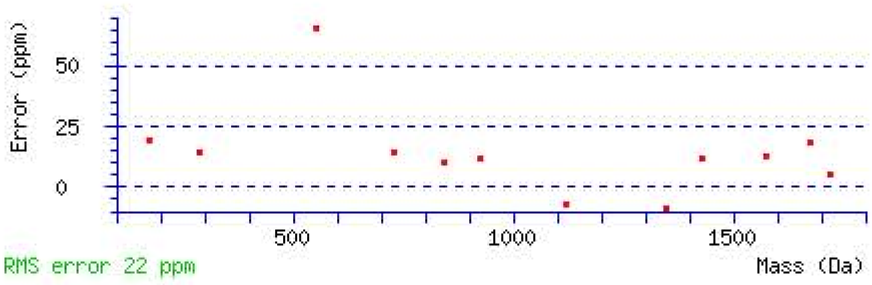
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1960.968521
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
M7      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00041
Matches : 12/154 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	129.102239	65.054757	112.075690	56.541483			K							11
2	244.129182	122.568229	227.102633	114.054955	226.118617	113.562947	D	1833.880844	917.444060	1816.854295	908.930785	1815.870279	908.438777	10
3	331.161210	166.084243	314.134661	157.570969	313.150645	157.078961	S	*1718.853901*	859.930588	1701.827352	851.417314	1700.843336	850.925306	9
4	388.182674	194.594975	371.156125	186.081701	370.172109	185.589693	G	1631.821873	816.414574	1614.795324	807.901300			8
5	535.251088	268.129182	518.224539	259.615908	517.240523	259.123900	F	*1574.800409*	787.903842	1557.773860	779.390568			7
6	974.476414	487.741845	957.449865	479.228571	956.465849	478.736563	Q	*1427.731995*	714.369635	1410.705446	705.856361			6
7	**1121.511814**	561.259545	1104.485265	552.746271	1103.501249	552.254262	M	988.506669	494.756972	971.480120	486.243698			5
8	1235.554741	618.281008	1218.528192	609.767734	1217.544176	609.275726	N	*841.471269*	421.239272	824.444720	412.725998			4
9	**1674.780067**	837.893671	1657.753518	829.380397	1656.769502	828.888389	Q	*727.428342*	364.217809	710.401793	355.704534			3
10	1787.864131	894.435703	1770.837582	885.922429	1769.853566	885.430421	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
41.8	1960.968521	0.013771	KDSGFQMNQLR
5.3	1960.967636	0.014656	QLSEFDTEREQLR
2.4	1960.963608	0.018684	GSPSSQSIPEKNSKSLCR
1.8	1960.961609	0.020683	FDNTGDQHQIPQRHLR
0.2	1961.011414	-0.029122	NLCNIFPSNIVLAVMEK

Mascot: http://www.matrixscience.com/

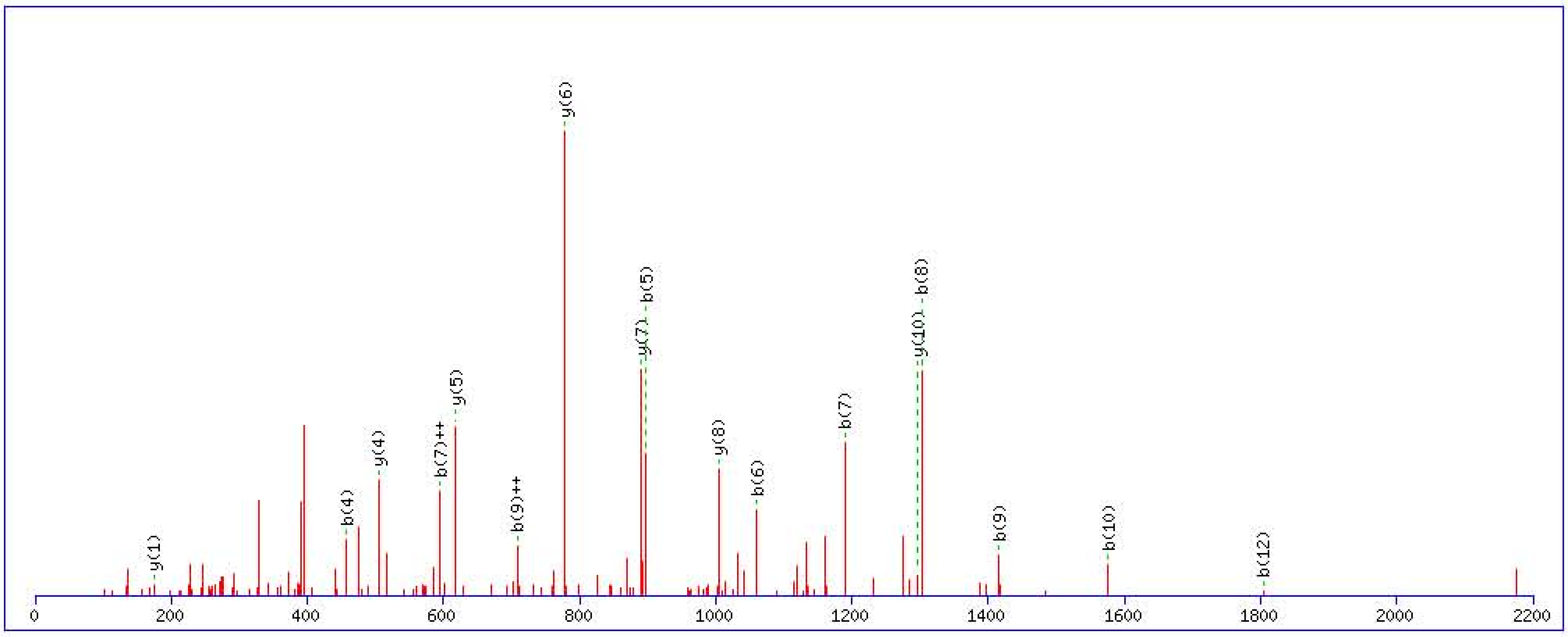
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADRDQYELLCLDNTR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

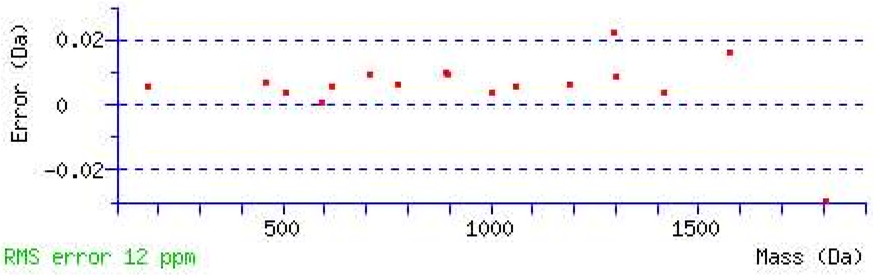
Match to Query 55208: 2192.055072 from(731.692300,3+) rtinseconds(2173) index(80072)
Title: Locus:1.1.1.2107.14 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

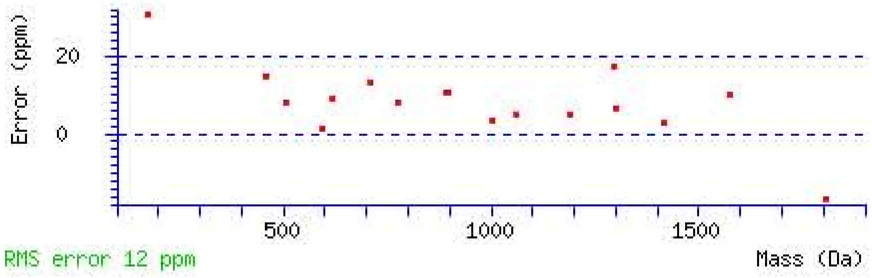
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2192.035400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00024
Matches : 17/160 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	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
49.4	2192.035400	0.019672	ADRDQYELLCLDNTR

Mascot: http://www.matrixscience.com/

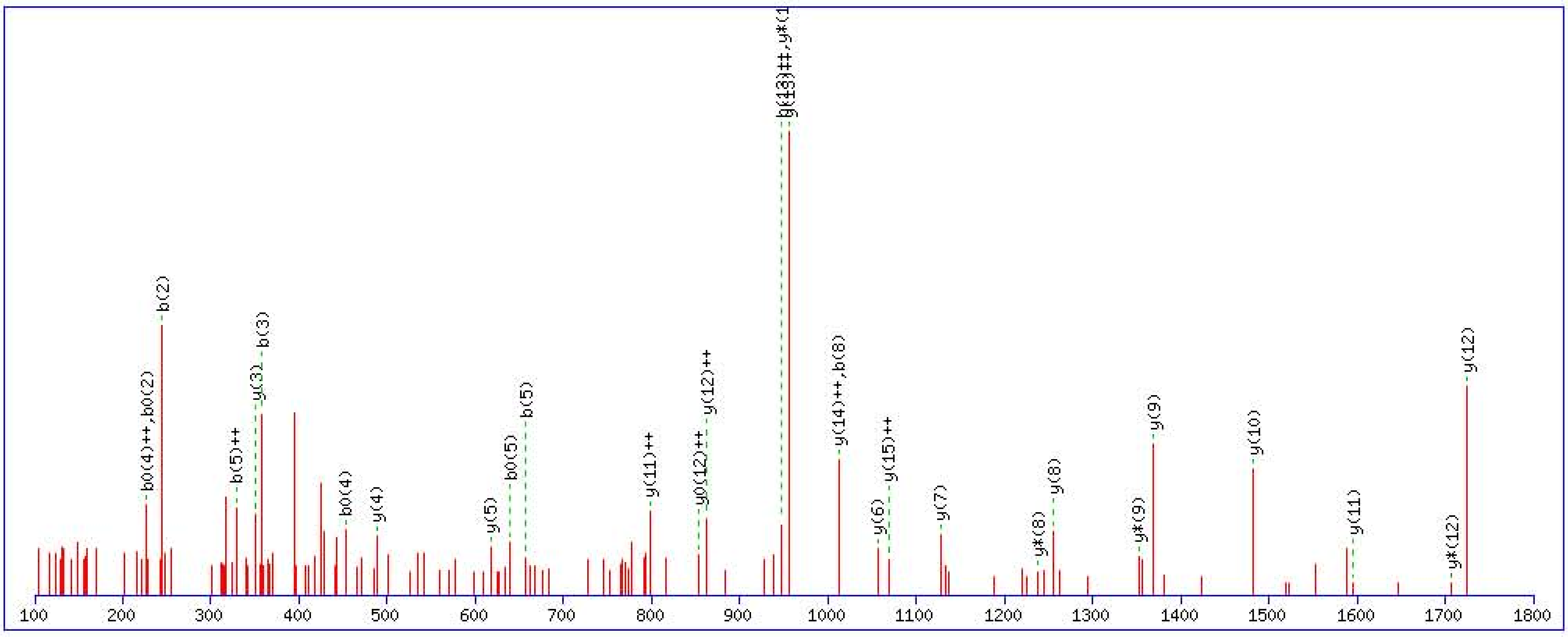
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDLIWELLNQAQEHFGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

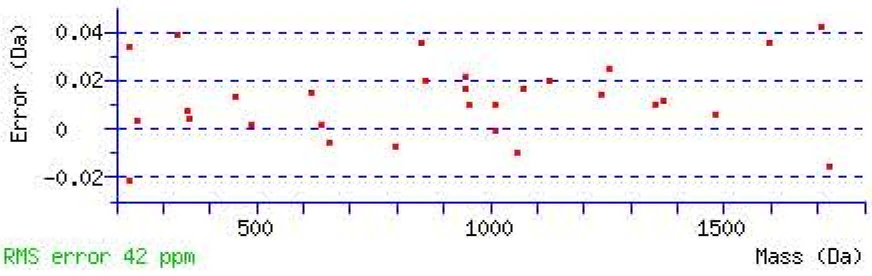
Match to Query 59490: 2380.212252 from(794.411360,3+) rtinseconds(3258) index(87601)
Title: Locus:1.1.1.2479.11 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

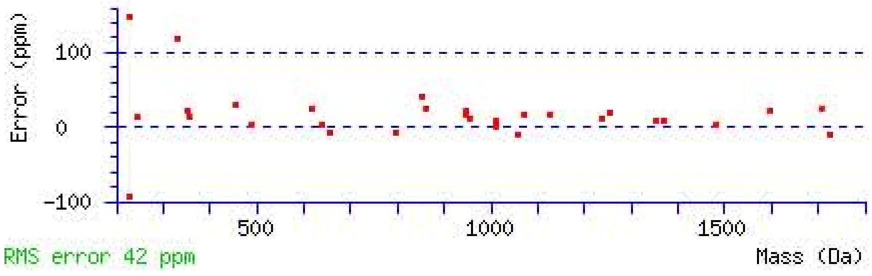
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2380.188522
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 33 **Expect:** 0.00087
Matches : 30/168 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	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	1254.636479	627.821878	1237.609930	619.308603	1236.625914	618.816595	Q	***1255.625205***	628.316240	1238.598656	619.802966	1237.614640	619.310958	8
11	1325.673593	663.340435	1308.647044	654.827160	1307.663028	654.335152	A	***1127.566627***	564.286951	1110.540078	555.773677	1109.556062	555.281669	7
12	1764.898919	882.953098	1747.872370	874.439823	1746.888354	873.947815	Q	***1056.529513***	528.768395	1039.502964	520.255120	1038.518948	519.763112	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
32.8	2380.188522	0.023730	EDLIWELLNQAQEHFGK
28.5	2380.188522	0.023730	EDLIWELLNQAQEHFGK
0.2	2380.199814	0.012438	GEPGLQGFPGKPGFLGEVGPPGMR

Mascot: http://www.matrixscience.com/

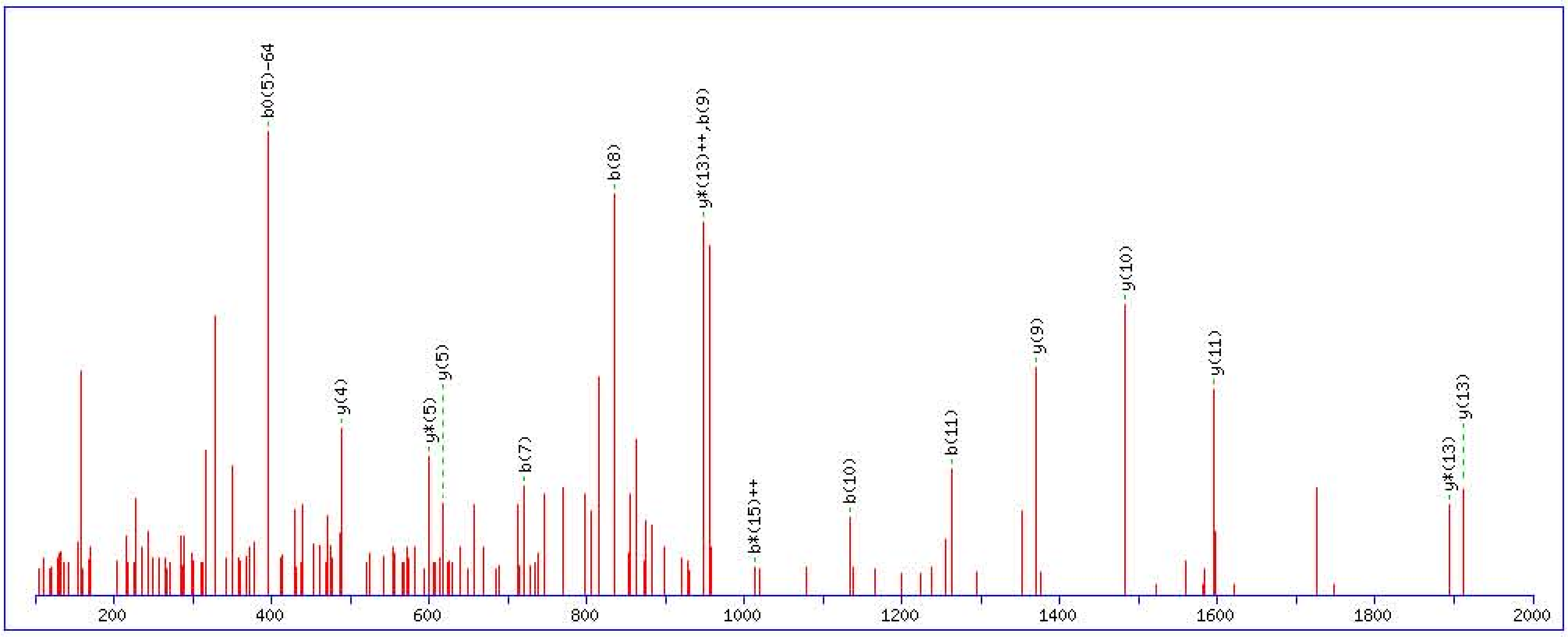
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SMGGKEDLIWELLNQAQEHFGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

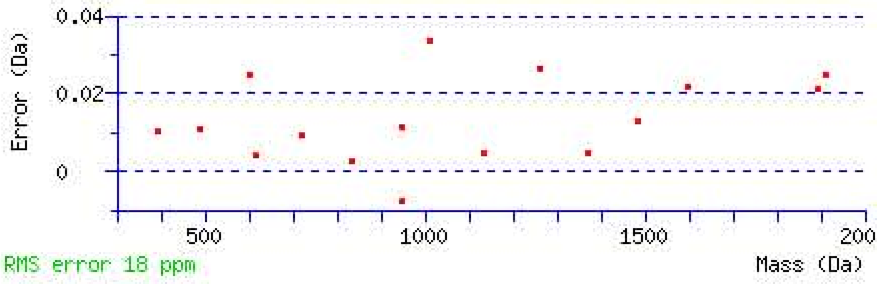
Match to Query 68325: 2856.426576 from(715.113920,4+) rtinseconds(2911) index(85150)
Title: Locus:1.1.1.2361.10 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

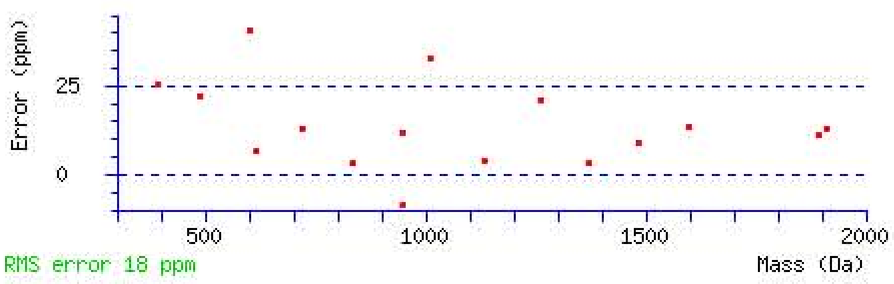
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2856.393845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q15    : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0023
Matches : 16/356 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							22
2	235.074704	118.040990			217.064139	109.035707	M	2770.369121	1385.688198	2753.342572	1377.174924	2752.358556	1376.682916	21
3	292.096168	146.551722			274.085603	137.546439	G	2623.333721	1312.170498	2606.307172	1303.657224	2605.323156	1303.165216	20
4	349.117632	175.062454			331.107067	166.057171	G	2566.312257	1283.659766	2549.285708	1275.146492	2548.301692	1274.654484	19
5	477.212595	239.109935	460.186046	230.596661	459.202030	230.104653	K	2509.290793	1255.149034	2492.264244	1246.635760	2491.280228	1246.143752	18
6	606.255188	303.631232	589.228639	295.117958	588.244623	294.625950	E	2381.195830	1191.101553	2364.169281	1182.588278	2363.185265	1182.096270	17
7	***721.282131***	361.144704	704.255582	352.631429	703.271566	352.139421	D	2252.153237	1126.580256	2235.126688	1118.066982	2234.142672	1117.574974	16
8	***834.366195***	417.686736	817.339646	409.173461	816.355630	408.681453	L	2137.126294	1069.066785	2120.099745	1060.553510	2119.115729	1060.061502	15
9	***947.450259***	474.228768	930.423710	465.715493	929.439694	465.223485	I	2024.042230	1012.524753	2007.015681	1004.011479	2006.031665	1003.519471	14
10	***1133.529572***	567.268424	1116.503023	558.755150	1115.519007	558.263142	W	***1910.958166***	955.982721	1893.931617	947.469447	1892.947601	946.977439	13
11	***1262.572165***	631.789721	1245.545616	623.276446	1244.561600	622.784438	E	1724.878853	862.943065	1707.852304	854.429790	1706.868288	853.937782	12
12	1375.656229	688.331753	1358.629680	679.818478	1357.645664	679.326470	L	***1595.836260***	798.421768	1578.809711	789.908494	1577.825695	789.416486	11
13	1488.740293	744.873785	1471.713744	736.360510	1470.729728	735.868502	L	***1482.752196***	741.879736	1465.725647	733.366462	1464.741631	732.874454	10
14	1602.783220	801.895248	1585.756671	793.381974	1584.772655	792.889966	N	***1369.668132***	685.337704	1352.641583	676.824430	1351.657567	676.332422	9
15	2042.008546	1021.507911	2024.981997	1012.994637	2023.997981	1012.502629	Q	1255.625205	628.316241	1238.598656	619.802966	1237.614640	619.310958	8
16	2113.045660	1057.026468	2096.019111	1048.513193	2095.035095	1048.021186	A	816.399879	408.703578	799.373330	400.190303	798.389314	399.698295	7
17	2241.104238	1121.055757	2224.077689	1112.542483	2223.093673	1112.050475	Q	745.362765	373.185021	728.336216	364.671746	727.352200	364.179738	6
18	2370.146831	1185.577054	2353.120282	1177.063779	2352.136266	1176.571771	E	***617.304187***	309.155732	600.277638	300.642457	599.293622	300.150449	5
19	2507.205743	1254.106510	2490.179194	1245.593235	2489.195178	1245.101227	H	***488.261594***	244.634435	471.235045	236.121160			4
20	2654.274157	1327.640717	2637.247608	1319.127442	2636.263592	1318.635434	F	351.202682	176.104979	334.176133	167.591704			3
21	2711.295621	1356.151449	2694.269072	1347.638174	2693.285056	1347.146166	G	204.134268	102.570772	187.107719	94.057497			2
22							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of SMGGKEDLIWELLNQAQEHFGK
(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	2856.393845	0.032731	SMGGKEDLIWELLNQAQEHFGK
38.3	2856.393845	0.032731	SMGGKEDLIWELLNQAQEHFGK

Mascot: http://www.matrixscience.com/

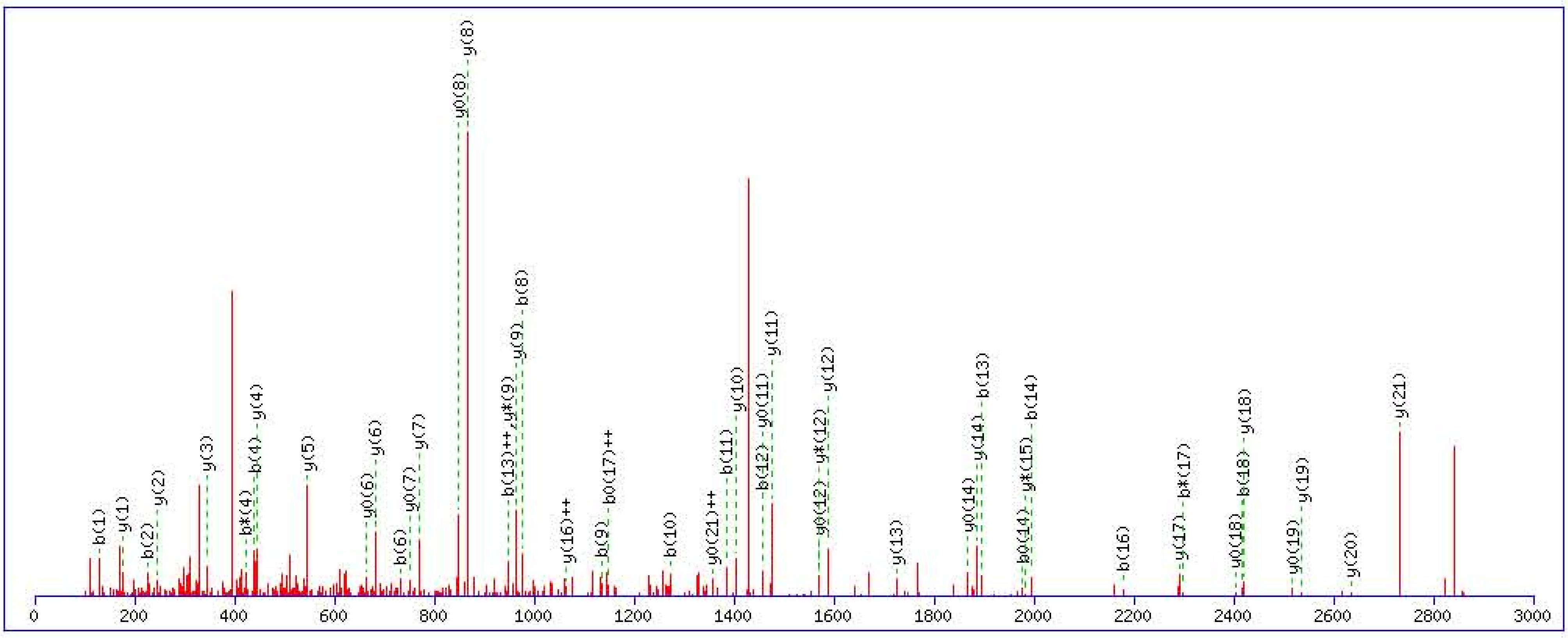
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVDEYKDCHLAQVPSHTVVAR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

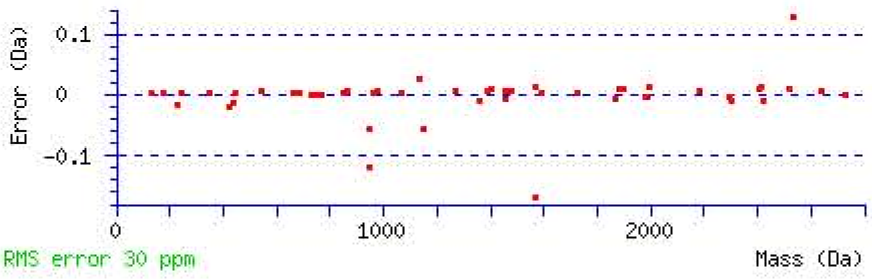
Match to Query 68410: 2859.474296 from(715.875850,4+) rtinseconds(1492) index(75675)
Title: Locus:1.1.1.1870.12 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

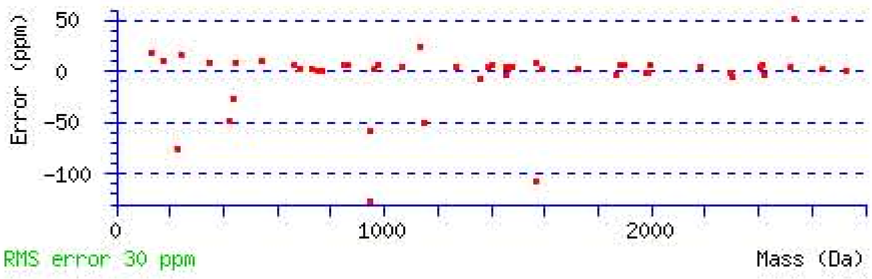
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [3000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2859.452393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 100  Expect: 8e-010
Matches : 50/238 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	**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
99.9	2859.452393	0.021903	KPVDEYKDCHLAQVPSHTVVAR
2.7	2859.504028	-0.029732	KIFGSVHPVRPMRLESFSACIWVK
0.5	2859.516418	-0.042122	QPAKEVTKASDGSLLGDLGHTPLSK

Mascot: http://www.matrixscience.com/

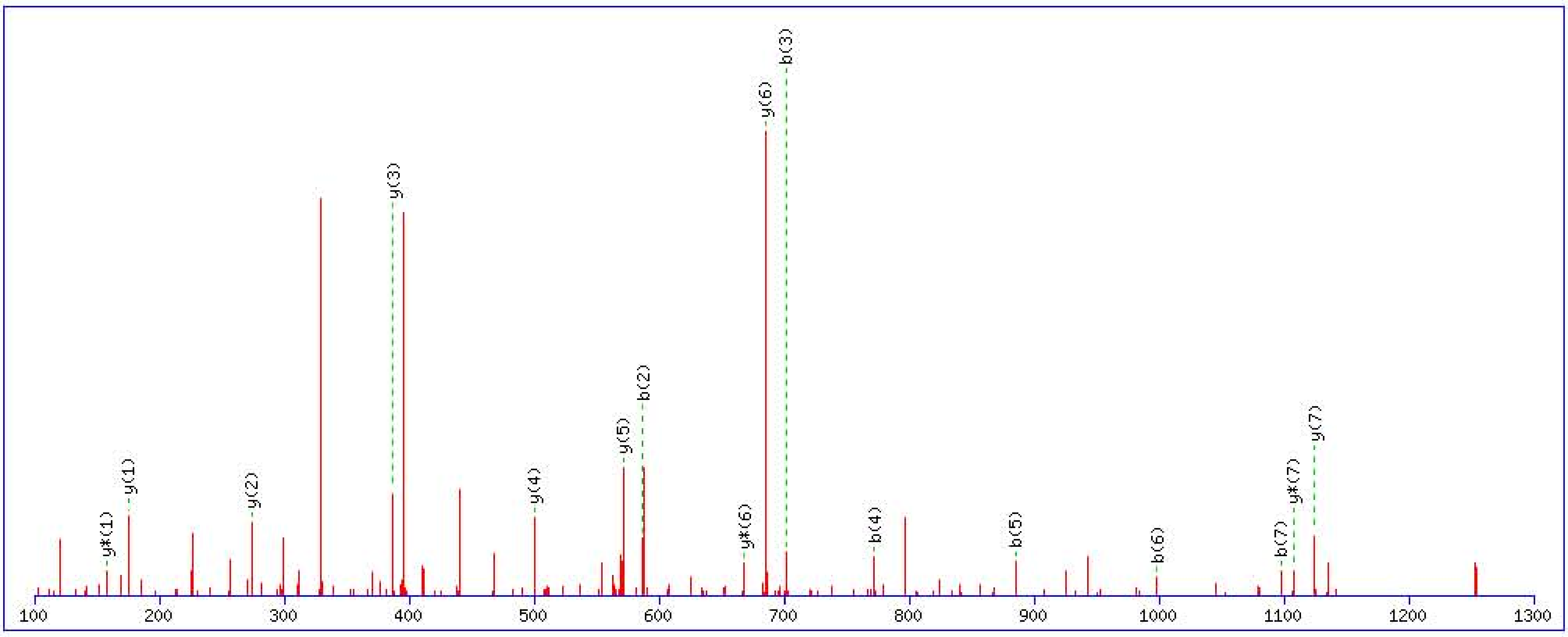
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQNALLVR**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

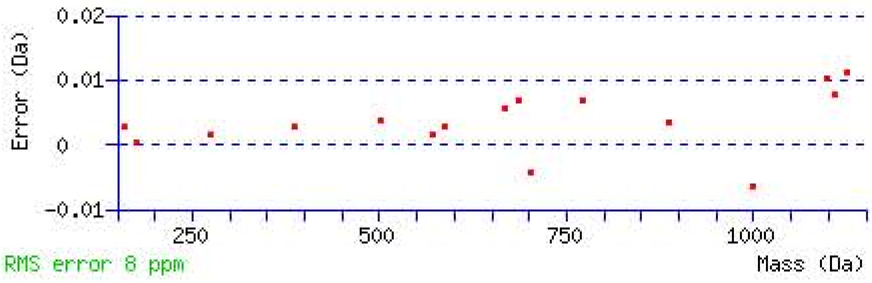
Match to Query 25947: 1270.729188 from(636.371870,2+) rtinseconds(2084) index(25280)
Title: Locus:1.1.1.2868.8 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

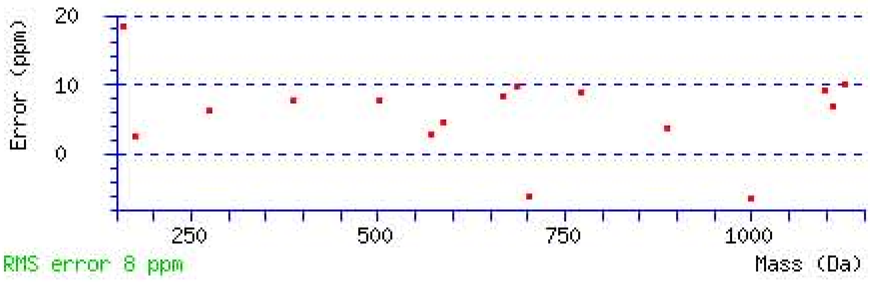
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1270.721985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0027
Matches : 16/54 fragment ions using 35 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
37.5	1270.721985	0.007203	FQNALLVR
16.6	1270.722000	0.007188	FQIAQVVR
12.9	1270.735687	-0.006499	KEAELRSGIIR
10.9	1270.733215	-0.004027	MFHIRAVILR
7.2	1270.733215	-0.004027	FQRQILR
6.8	1270.725357	0.003831	QKVMAIVR
5.7	1270.735687	-0.006499	LKKLSNLNADR
4.1	1270.735733	-0.006545	EILGRGVSSVVR
4.0	1270.717957	0.011231	QLSRTLSR
3.8	1270.739761	-0.010573	QVVNIPSFIVR

Mascot: http://www.matrixscience.com/

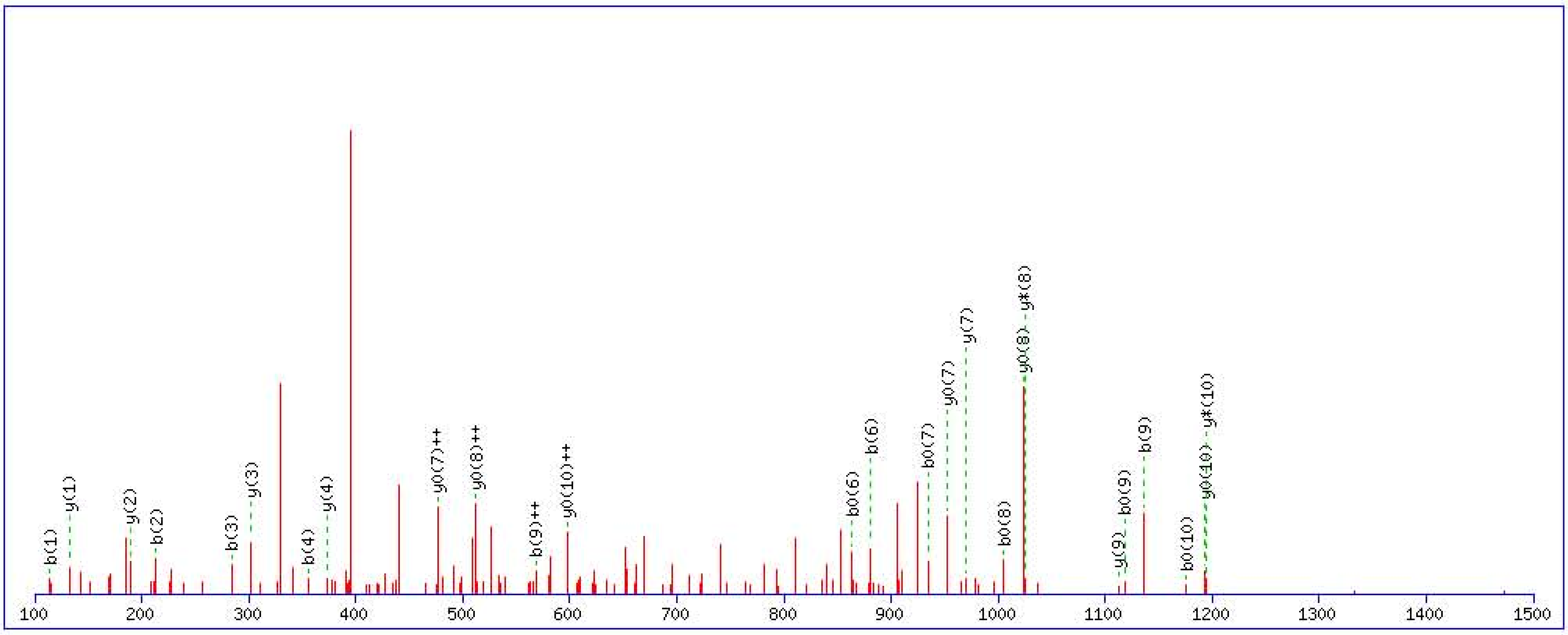
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVAASQAALGL**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

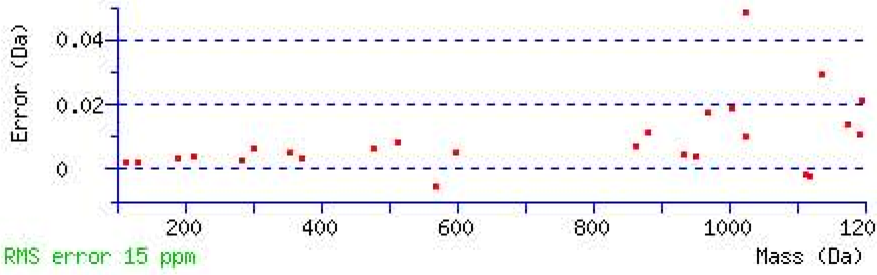
Match to Query 27457: 1323.770968 from(662.892760,2+) rtinseconds(2520) index(28224)
Title: Locus:1.1.1.3019.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

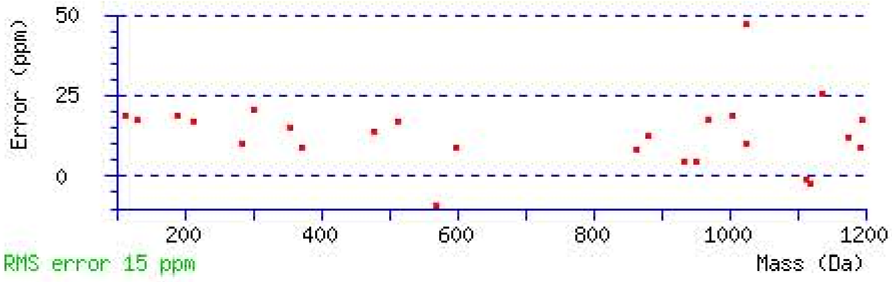
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1323.758423
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0012
Matches : 32/80 fragment ions using 80 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	***213.159754***	107.083515					V	1211.681657	606.344466	1194.655108	597.831192	1193.671092	597.339184	10
3	***284.196868***	142.602072					A	**1112.613243**	556.810259	1095.586694	548.296985	1094.602678	547.804977	9
4	***355.233982***	178.120629					A	1041.576129	521.291702	1024.549580	512.778428	1023.565564	512.286420	8
5	442.266010	221.636643			424.255445	212.631361	S	**970.539015**	485.773145	953.512466	477.259871	952.528450	476.767863	7
6	***881.491336***	441.249306	864.464787	432.736032	863.480771	432.244024	Q	883.506987	442.257131	866.480438	433.743857			6
7	***952.528450***	**476.767863**	935.501901	468.254589	934.517885	467.762581	A	444.281661	222.644468					5
8	***1023.565564***	**512.286420**	1006.539015	503.773146	1005.554999	503.281138	A	**373.244547**	187.125911					4
9	***1136.649628***	**568.828452**	1119.623079	560.315178	1118.639063	559.823169	L	**302.207433**	151.607354					3
10	***1193.671092***	**597.339184**	1176.644543	588.825909	1175.660527	588.333901	G	**189.123369**	95.065322					2
11							L	**132.101905**	66.554590					1





NCBI **BLAST** search of LVAASQAALGL
(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	1323.758423	0.012545	LVAASQAALGL
3.3	1323.780899	-0.009931	MLGVPANRIVVR

Mascot: http://www.matrixscience.com/

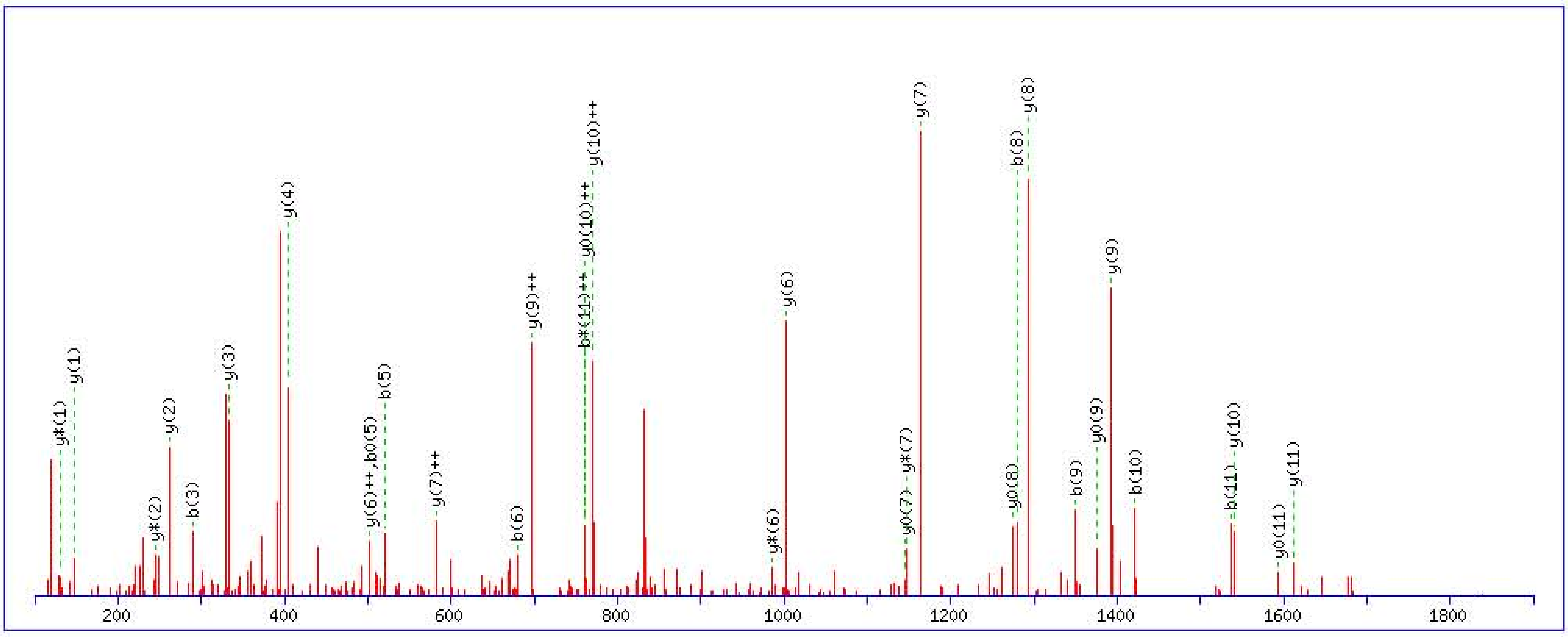
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAFTECCQAADK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

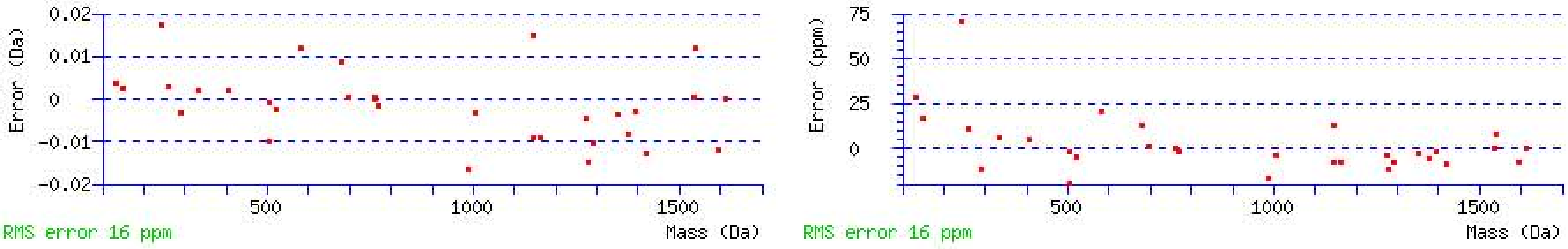
Match to Query 42027: 1681.733248 from(841.873900,2+) rtinseconds(1585) index(21636)
Title: Locus:1.1.1.2694.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1681.726227
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 7.7e-006
Matches : 32/110 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	72.044390	36.525833					A							12
2	143.081504	72.044390					A	***1611.696399***	806.351838	1594.669850	797.838563	1593.685834	797.346555	11
3	**290.149918**	145.578597					F	***1540.659285***	770.833281	1523.632736	762.320006	1522.648720	761.827998	10
4	391.197597	196.102437			373.187032	187.097154	T	***1393.590871***	697.299074	1376.564322	688.785799	1375.580306	688.293791	9
5	**520.240190**	260.623733			502.229625	251.618451	E	***1292.543192***	646.775234	1275.516643	638.261960	1274.532627	637.769952	8
6	**680.270839**	340.639058			662.260274	331.633775	C	***1163.500599***	582.253938	1146.474050	573.740663	1145.490034	573.248655	7
7	840.301488	420.654382			822.290923	411.649100	C	***1003.469950***	502.238613	986.443401	493.725339	985.459385	493.233331	6
8	**1279.526814**	640.267045	1262.500265	631.753771	1261.516249	631.261763	Q	843.439301	422.223289	826.412752	413.710014	825.428736	413.218006	5
9	**1350.563928**	675.785602	1333.537379	667.272328	1332.553363	666.780320	A	***404.213975***	202.610626	387.187426	194.097351	386.203410	193.605343	4
10	**1421.601042**	711.304159	1404.574493	702.790885	1403.590477	702.298877	A	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	3
11	**1536.627985**	768.817631	1519.601436	760.304356	1518.617420	759.812348	D	***262.139747***	131.573512	245.113198	123.060237	244.129182	122.568229	2
12							K	***147.112804***	74.060040	130.086255	65.546765			1



NCBI **BLAST** search of AAFTECCQAADK
(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	1681.726227	0.007021	AAFTECCQAADK
1.6	1681.757706	-0.024458	ESRSTCLKTNDEDK
1.0	1681.737442	-0.004194	CENCGNAYKQK

Mascot: http://www.matrixscience.com/

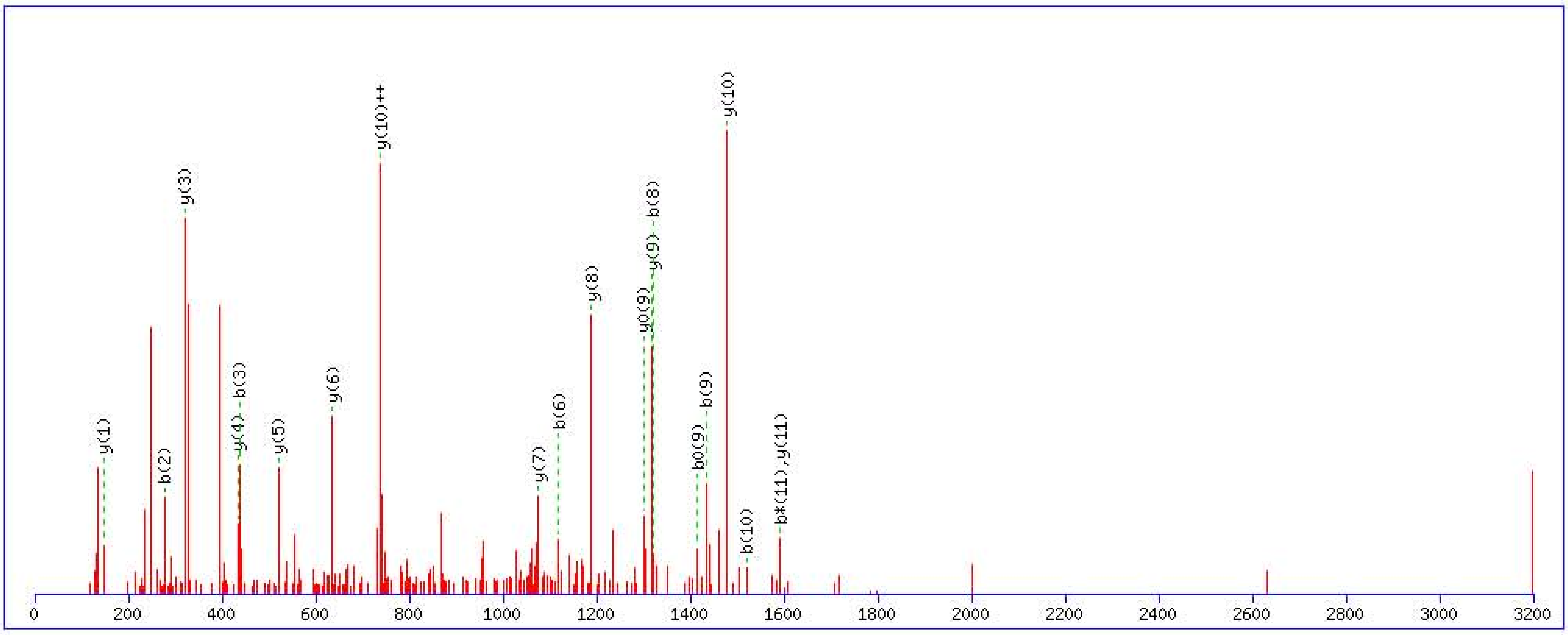
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YICENQDSISSK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

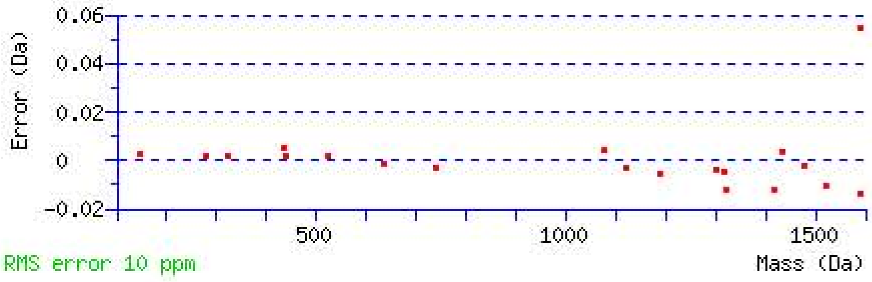
Match to Query 43980: 1753.809808 from(877.912180,2+) rtinseconds(1641) index(21975)
Title: Locus:1.1.1.2714.17 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

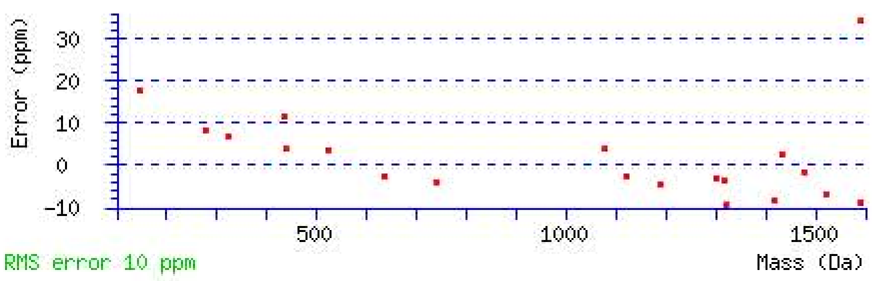
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1753.801483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 73 **Expect:** 6.5e-007
Matches : 20/116 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	164.070605	82.538940					Y							12
2	**277.154669**	139.080973					I	***1591.745454***	796.376365	1574.718905	787.863091	1573.734889	787.371083	11
3	**437.185318**	219.096297					C	***1478.661390***	739.834333	1461.634841	731.321059	1460.650825	730.829051	10
4	566.227911	283.617594			548.217346	274.612311	E	***1318.630741***	659.819009	1301.604192	651.305734	1300.620176	650.813726	9
5	680.270838	340.639057	663.244289	332.125783	662.260273	331.633775	N	***1189.588148***	595.297712	1172.561599	586.784438	1171.577583	586.292430	8
6	**1119.496164**	560.251720	1102.469615	551.738446	1101.485599	551.246437	Q	***1075.545221***	538.276249	1058.518672	529.762974	1057.534656	529.270966	7
7	1234.523107	617.765192	1217.496558	609.251917	1216.512542	608.759909	D	***636.319895***	318.663586	619.293346	310.150311	618.309330	309.658303	6
8	**1321.555135**	661.281206	1304.528586	652.767931	1303.544570	652.275923	S	***521.292952***	261.150114	504.266403	252.636840	503.282387	252.144832	5
9	**1434.639199**	717.823238	1417.612650	709.309963	1416.628634	708.817955	I	***434.260924***	217.634100	417.234375	209.120826	416.250359	208.628818	4
10	**1521.671227**	761.339252	1504.644678	752.825977	1503.660662	752.333969	S	***321.176860***	161.092068	304.150311	152.578794	303.166295	152.086786	3
11	1608.703255	804.855266	1591.676706	796.341991	1590.692690	795.849983	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





NCBI **BLAST** search of YICENQDSISSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.7	1753.801483	0.008325	YICENQDSISSK

Mascot: http://www.matrixscience.com/

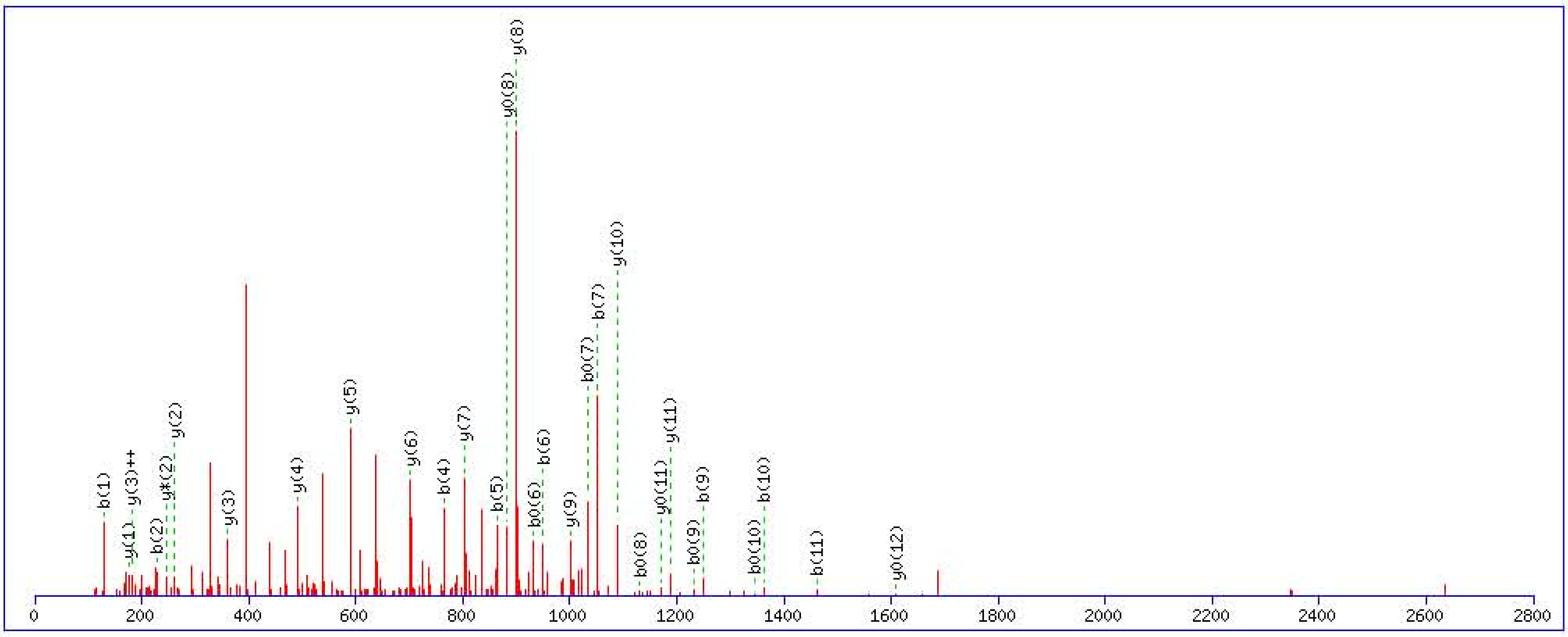
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVPQVSTPTLVEVSR**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

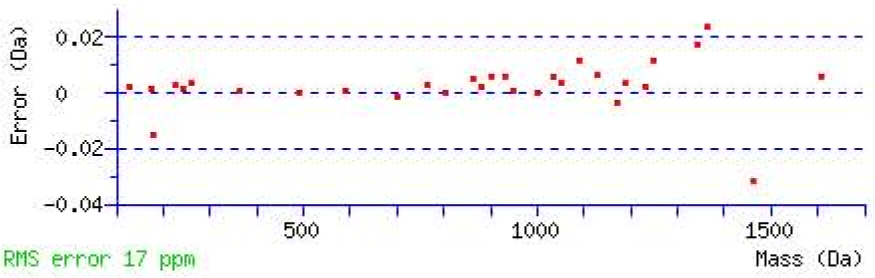
Match to Query 48701: 1950.107352 from(651.043060,3+) rtinseconds(1938) index(24273)
Title: Locus:1.1.1.2817.12 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

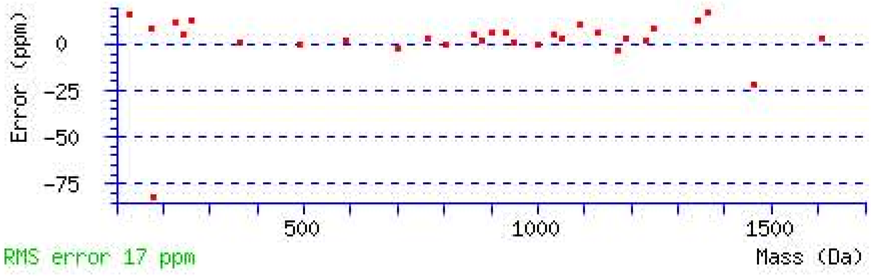
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1950.097229
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 6.1e-005
Matches : 30/156 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	***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
52.1	1950.097229	0.010123	KVPQVSTPTLVEVSR

Mascot: http://www.matrixscience.com/

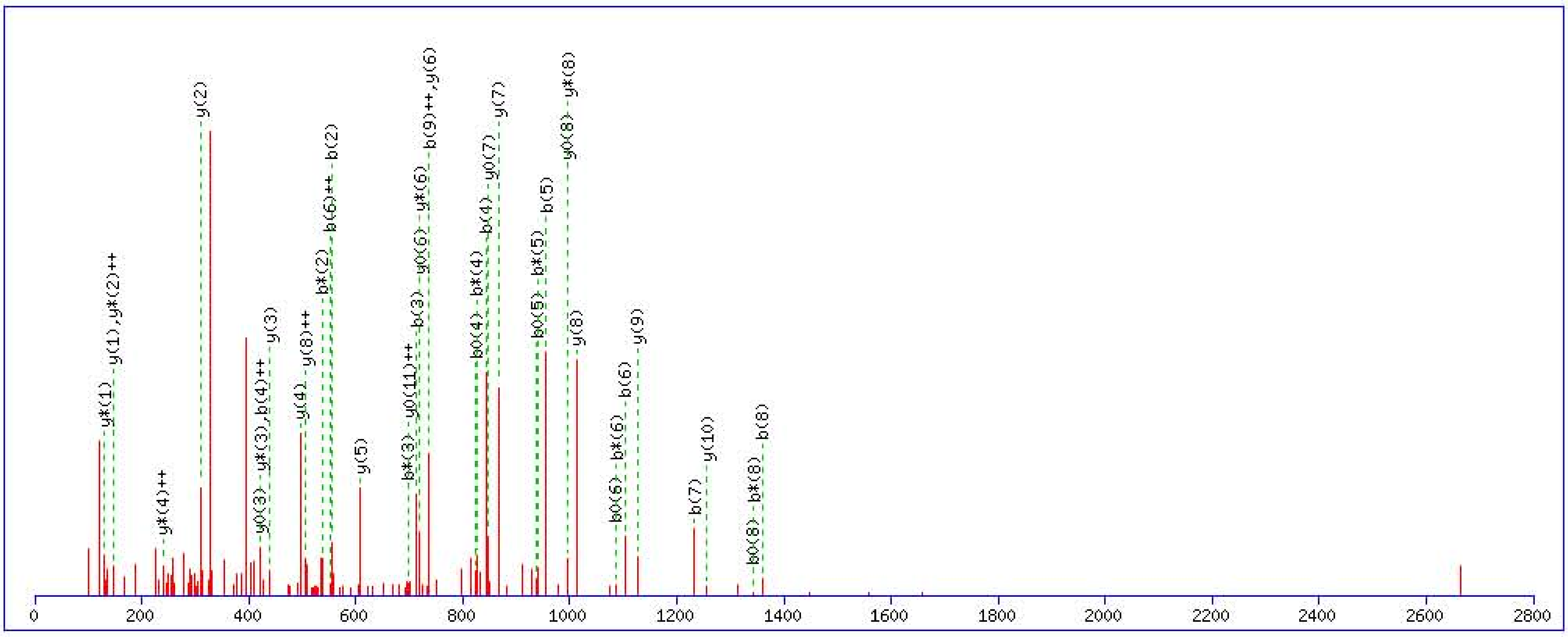
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QNCELFEQLGEYK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

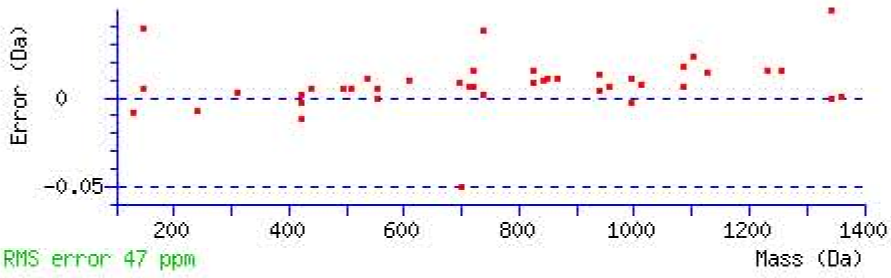
Match to Query 49205: 1967.929872 from(656.983900,3+) rtinseconds(2373) index(27329)
Title: Locus:1.1.1.2968.13 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

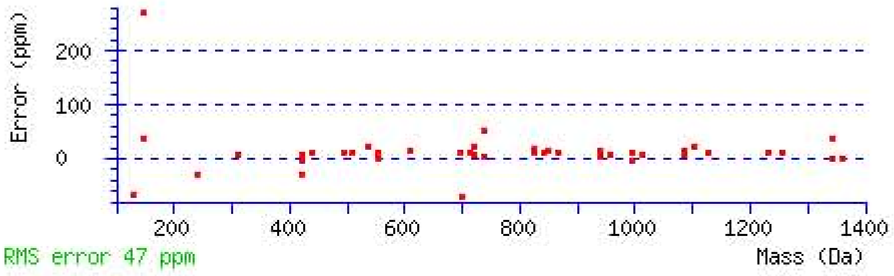
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1967.912094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00028
Matches : 42/134 fragment ions using 81 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							13
2	**554.275529**	277.641403	537.248980	269.128128			N	1529.694072	765.350674	1512.667523	756.837400	1511.683507	756.345392	12
3	**714.306178**	357.656727	697.279629	349.143453			C	1415.651145	708.329211	1398.624596	699.815936	1397.640580	699.323928	11
4	**843.348771**	**422.178024**	826.322222	413.664749	825.338206	413.172741	E	***1255.620496***	628.313886	1238.593947	619.800612	1237.609931	619.308604	10
5	**956.432835**	478.720056	939.406286	470.206781	938.422270	469.714773	L	***1126.577903***	563.792590	1109.551354	555.279315	1108.567338	554.787307	9
6	**1103.501249**	**552.254263**	1086.474700	543.740988	1085.490684	543.248980	F	***1013.493839***	507.250558	996.467290	498.737283	995.483274	498.245275	8
7	**1232.543842**	616.775559	1215.517293	608.262285	1214.533277	607.770277	E	***866.425425***	433.716351	849.398876	425.203076	848.414860	424.711068	7
8	**1360.602420**	680.804848	1343.575871	672.291574	1342.591855	671.799566	Q	***737.382832***	369.195054	720.356283	360.681780	719.372267	360.189772	6
9	1473.686484	**737.346880**	1456.659935	728.833606	1455.675919	728.341598	L	***609.324254***	305.165765	592.297705	296.652490	591.313689	296.160482	5
10	1530.707948	765.857612	1513.681399	757.344338	1512.697383	756.852330	G	***496.240190***	248.623733	479.213641	240.110458	478.229625	239.618450	4
11	1659.750541	830.378909	1642.723992	821.865634	1641.739976	821.373626	E	***439.218726***	220.113001	422.192177	211.599726	421.208161	211.107718	3
12	1822.813870	911.910573	1805.787321	903.397299	1804.803305	902.905291	Y	***310.176133***	155.591705	293.149584	147.078430			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of QNCELFEQLGEYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.9	1967.912094	0.017778	QNCELFEQLGEYK
5.1	1967.930069	-0.000197	TQQRMKEMESVMK
5.1	1967.930069	-0.000197	TQQRMKEMESVMK

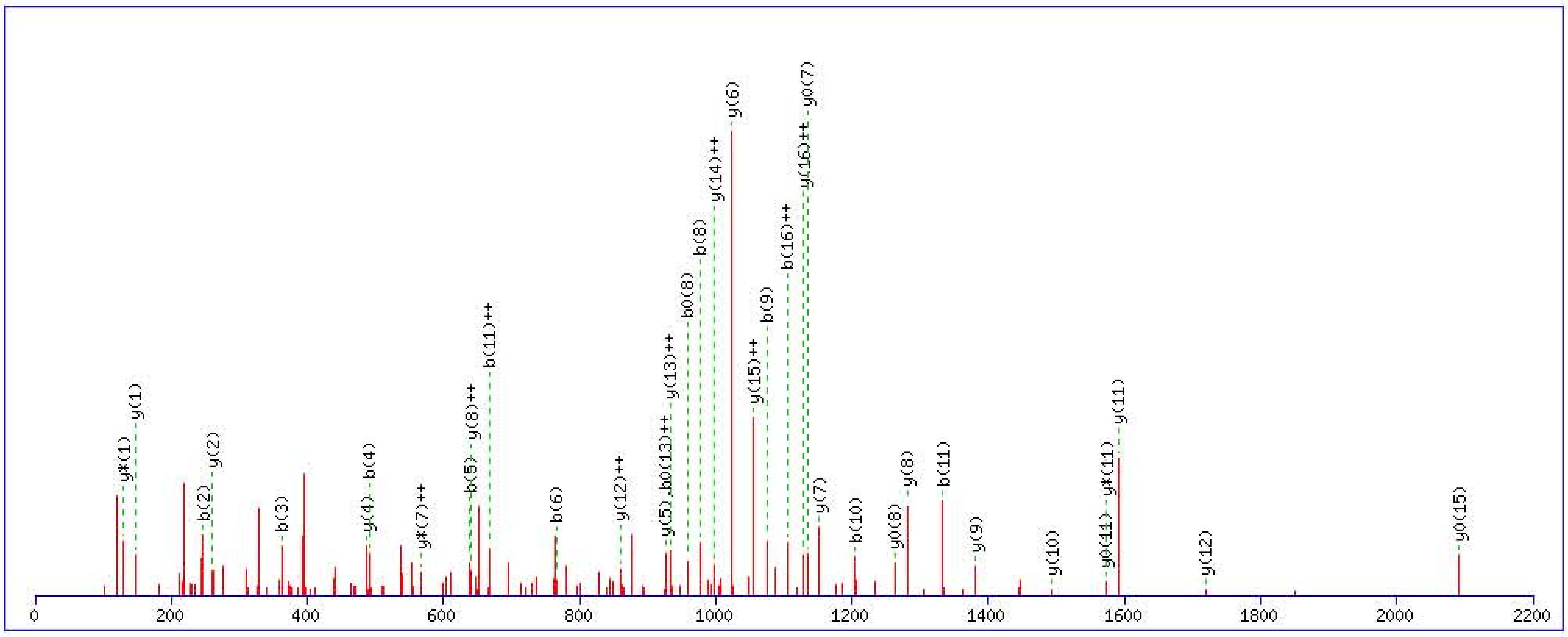
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFDEFKPLVEEPQNLIK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

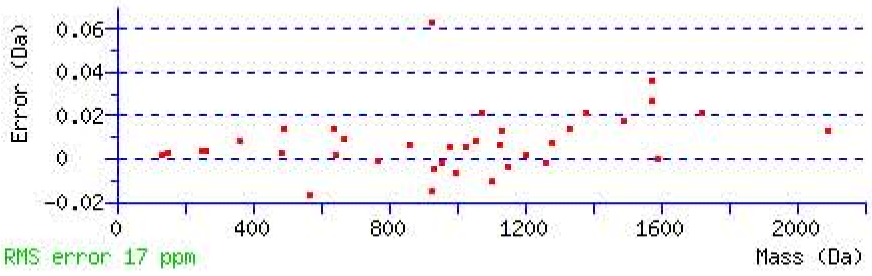
Match to Query 59169: 2355.281652 from(786.101160,3+) rtinseconds(2598) index(28675)
Title: Locus:1.1.1.3046.14 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

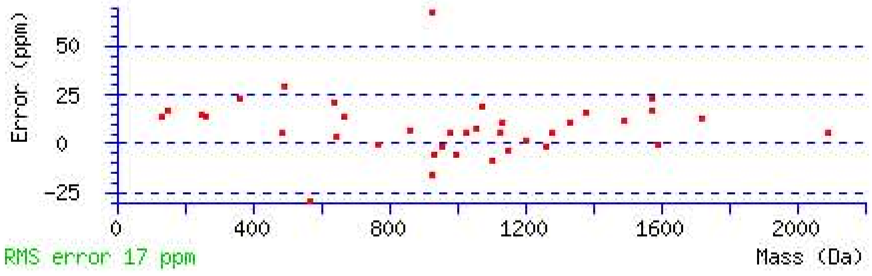
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2355.254822
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 4.3e-005
Matches : 37/166 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	100.075690	50.541483					V							17
2	***247.144104***	124.075690					F	2257.193704	1129.100490	2240.167155	1120.587216	2239.183139	1120.095208	16
3	***362.171047***	181.589161			344.160482	172.583879	D	2110.125290	1055.566283	2093.098741	1047.053008	2092.114725	1046.561000	15
4	***491.213640***	246.110458			473.203075	237.105176	E	1995.098347	998.052812	1978.071798	989.539537	1977.087782	989.047529	14
5	***638.282054***	319.644665			620.271489	310.639383	F	1866.055754	933.531515	1849.029205	925.018241	1848.045189	924.526233	13
6	***766.377017***	383.692147	749.350468	375.178872	748.366452	374.686864	K	***1718.987340***	859.997308	1701.960791	851.484034	1700.976775	850.992026	12
7	863.429781	432.218529	846.403232	423.705254	845.419216	423.213246	P	***1590.892377***	795.949827	1573.865828	787.436552	1572.881812	786.944544	11
8	***976.513845***	488.760561	959.487296	480.247286	958.503280	479.755278	L	***1493.839613***	747.423445	1476.813064	738.910170	1475.829048	738.418162	10
9	***1075.582259***	538.294768	1058.555710	529.781493	1057.571694	529.289485	V	***1380.755549***	690.881413	1363.729000	682.368138	1362.744984	681.876130	9
10	***1204.624852***	602.816064	1187.598303	594.302790	1186.614287	593.810782	E	***1281.687135***	641.347206	1264.660586	632.833931	1263.676570	632.341923	8
11	***1333.667445***	**667.337361**	1316.640896	658.824086	1315.656880	658.332078	E	***1152.644542***	576.825909	1135.617993	568.312635	1134.633977	567.820627	7
12	1430.720209	715.863743	1413.693660	707.350468	1412.709644	706.858460	P	***1023.601949***	512.304613	1006.575400	503.791338			6
13	1869.945535	935.476406	1852.918986	926.963131	1851.934970	926.471123	Q	***926.549185***	463.778231	909.522636	455.264956			5
14	1983.988462	992.497869	1966.961913	983.984595	1965.977897	983.492587	N	***487.323859***	244.165568	470.297310	235.652293			4
15	2097.072526	1049.039901	2080.045977	1040.526627	2079.061961	1040.034619	L	373.280932	187.144104	356.254383	178.630830			3
16	2210.156590	**1105.581933**	2193.130041	1097.068659	2192.146025	1096.576651	I	***260.196868***	130.602072	243.170319	122.088798			2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VFDEFKPLVEEPQNLIK
(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	2355.254822	0.026830	VFDEFKPLVEEPQNLIK
4.8	2355.254166	0.027486	MDSTACLKSLLLTVSQYKAVK

Mascot: http://www.matrixscience.com/

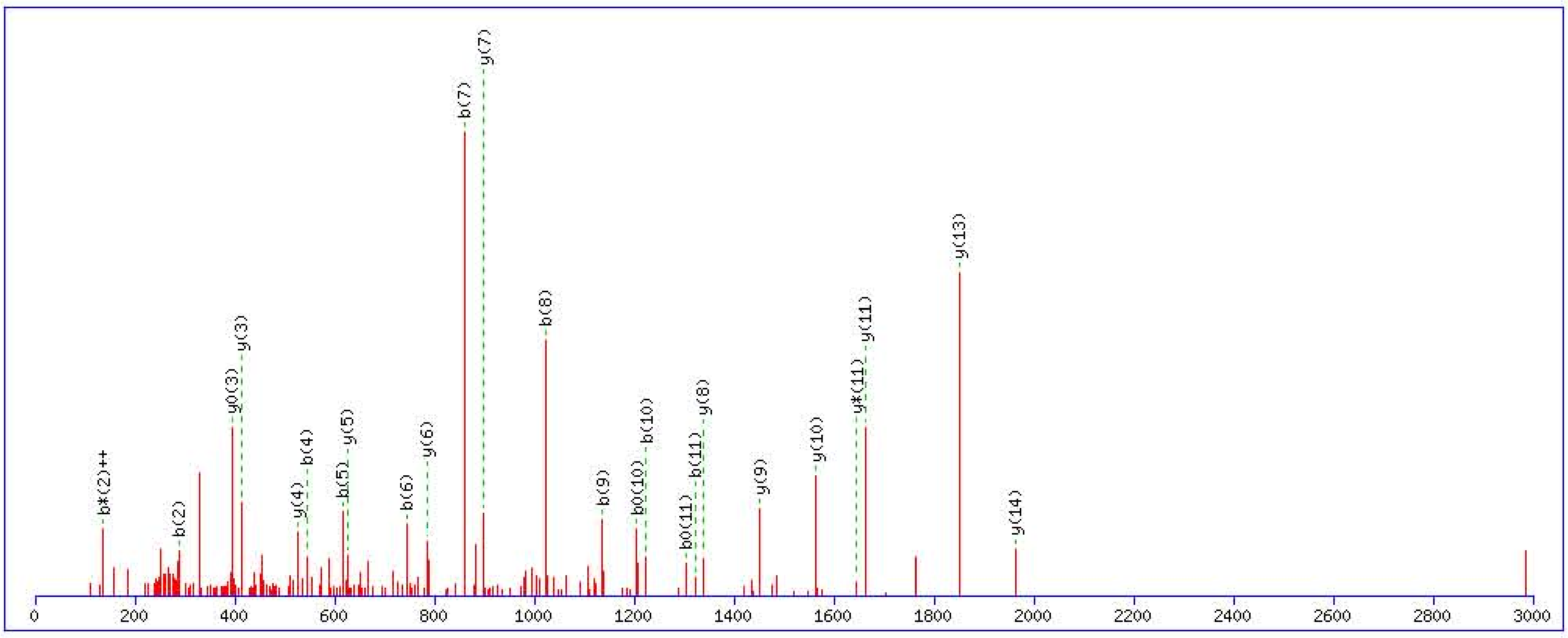
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RMPCAEDYLSVVLNQLCVLHEK**
Found in **ALBU_HUMAN**, Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

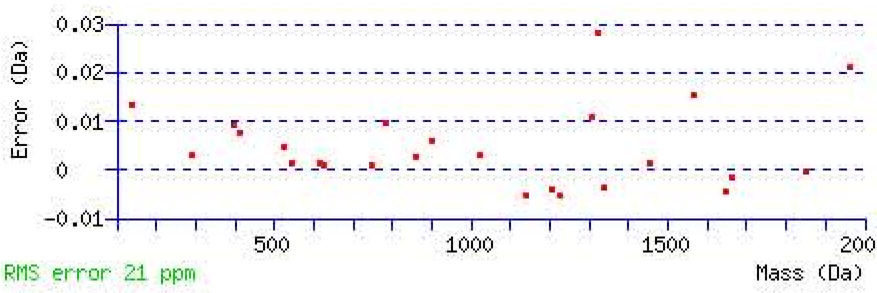
Match to Query 70246: 2984.504896 from(747.133500,4+) rtinseconds(3047) index(31738)
Title: Locus:1.1.1.3200.8 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

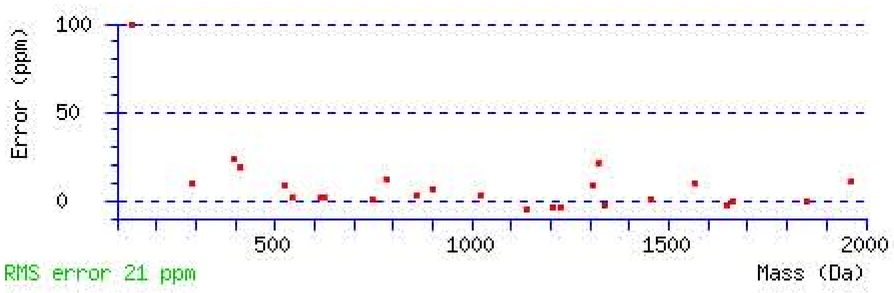
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2984.474426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15    : Biotin:Thermo-21345 (Q)
Ions Score: 92  Expect: 2e-008
Matches : 25/240 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	157.108387	79.057831	140.081838	70.544557			R							22
2	***288.148872***	144.578074	271.122323	136.064799			M	2829.380614	1415.193945	2812.354065	1406.680670	2811.370049	1406.188662	21
3	385.201636	193.104456	368.175087	184.591181			P	2698.340129	1349.673702	2681.313580	1341.160428	2680.329564	1340.668420	20
4	***545.232285***	273.119781	528.205736	264.606506			C	2601.287365	1301.147320	2584.260816	1292.634046	2583.276800	1292.142038	19
5	***616.269399***	308.638338	599.242850	300.125063			A	2441.256716	1221.131996	2424.230167	1212.618721	2423.246151	1212.126713	18
6	***745.311992***	373.159634	728.285443	364.646360	727.301427	364.154352	E	2370.219602	1185.613439	2353.193053	1177.100164	2352.209037	1176.608156	17
7	***860.338935***	430.673106	843.312386	422.159831	842.328370	421.667823	D	2241.177009	1121.092142	2224.150460	1112.578868	2223.166444	1112.086860	16
8	***1023.402264***	512.204770	1006.375715	503.691496	1005.391699	503.199488	Y	2126.150066	1063.578671	2109.123517	1055.065396	2108.139501	1054.573388	15
9	***1136.486328***	568.746802	1119.459779	560.233528	1118.475763	559.741519	L	***1963.086737***	982.047007	1946.060188	973.533732	1945.076172	973.041724	14
10	***1223.518356***	612.262816	1206.491807	603.749542	1205.507791	603.257534	S	***1850.002673***	925.504975	1832.976124	916.991700	1831.992108	916.499692	13
11	***1322.586770***	661.797023	1305.560221	653.283749	1304.576205	652.791741	V	1762.970645	881.988961	1745.944096	873.475686	1744.960080	872.983678	12
12	1421.655184	711.331230	1404.628635	702.817956	1403.644619	702.325948	V	***1663.902231***	832.454754	1646.875682	823.941479	1645.891666	823.449471	11
13	1534.739248	767.873262	1517.712699	759.359988	1516.728683	758.867980	L	***1564.833817***	782.920547	1547.807268	774.407272	1546.823252	773.915264	10
14	1648.782175	824.894726	1631.755626	816.381451	1630.771610	815.889443	N	***1451.749753***	726.378515	1434.723204	717.865240	1433.739188	717.373232	9
15	2088.007501	1044.507388	2070.980952	1035.994114	2069.996936	1035.502106	Q	***1337.706826***	669.357051	1320.680277	660.843777	1319.696261	660.351769	8
16	2201.091565	1101.049421	2184.065016	1092.536146	2183.081000	1092.044138	L	***898.481500***	449.744388	881.454951	441.231114	880.470935	440.739106	7
17	2361.122214	1181.064745	2344.095665	1172.551470	2343.111649	1172.059462	C	***785.397436***	393.202356	768.370887	384.689081	767.386871	384.197073	6
18	2460.190628	1230.598952	2443.164079	1222.085677	2442.180063	1221.593669	V	***625.366787***	313.187032	608.340238	304.673757	607.356222	304.181749	5
19	2573.274692	1287.140984	2556.248143	1278.627709	2555.264127	1278.135701	L	***526.298373***	263.652825	509.271824	255.139550	508.287808	254.647542	4
20	2710.333604	1355.670440	2693.307055	1347.157165	2692.323039	1346.665157	H	***413.214309***	207.110793	396.187760	198.597518	395.203744	198.105510	3
21	2839.376197	1420.191736	2822.349648	1411.678462	2821.365632	1411.186454	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
22							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of RMPCAEDYLSVVLNQLCVLHEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
91.7	2984.474426	0.030470	RMPCAEDYLSVVLNQLCVLHEK
10.3	2984.466171	0.038725	QQMNGLTSFLDASTVYGSSPALERQLR
0.7	2984.506546	-0.001650	LEDHEYKPLDPKDIRLPPPMPPSER

Mascot: http://www.matrixscience.com/

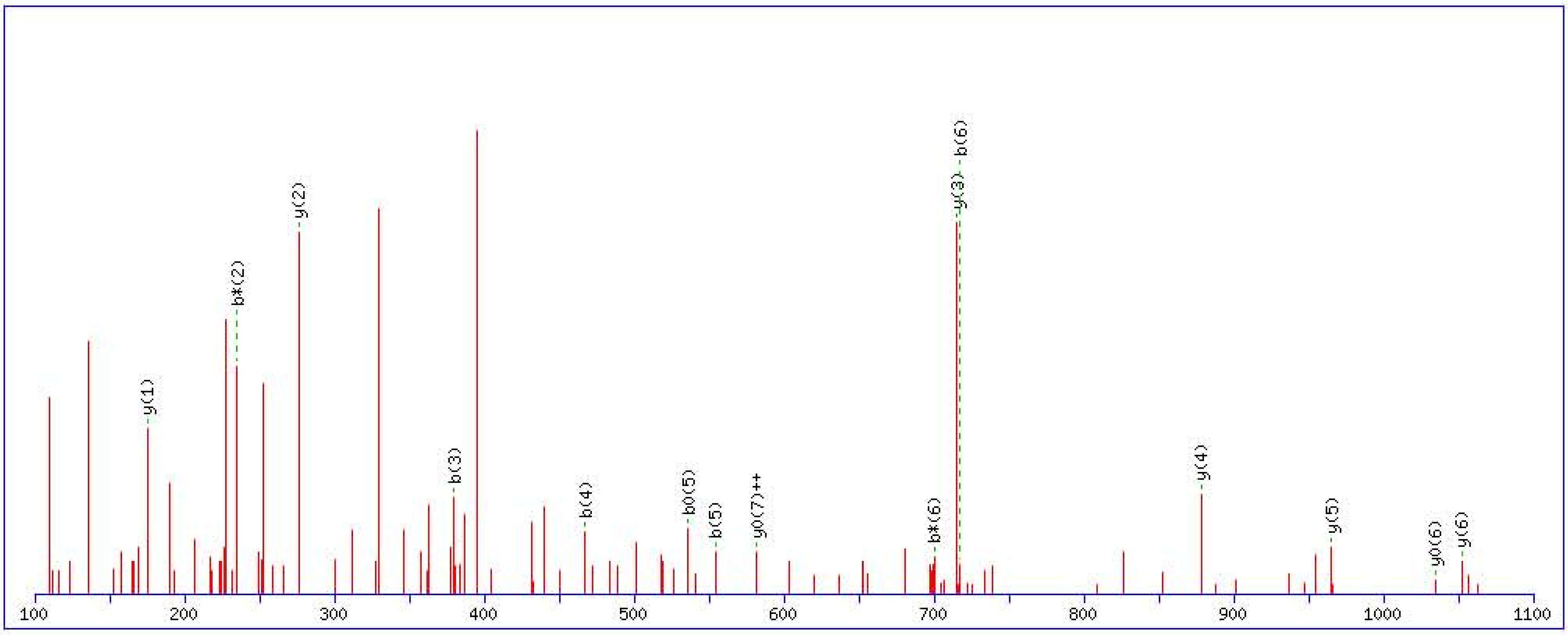
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NHQSSYQTR**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

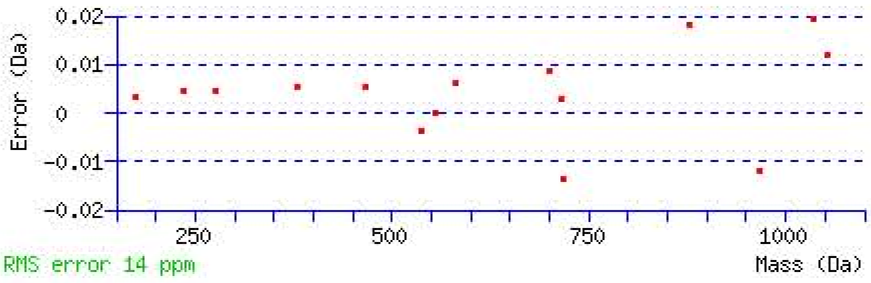
Match to Query 32658: 1430.680812 from(477.900880,3+) rtinseconds(1146) index(36386)
Title: Locus:1.1.1.2848.7 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

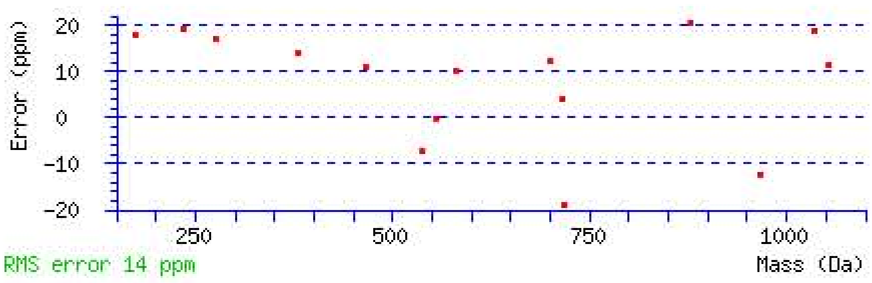
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1430.672470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.013
Matches : 15/88 fragment ions using 30 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							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
27.3	1430.672470	0.008342	NHQSSYQTR
7.1	1430.689743	-0.008931	QKPSGSEMEK

Mascot: http://www.matrixscience.com/

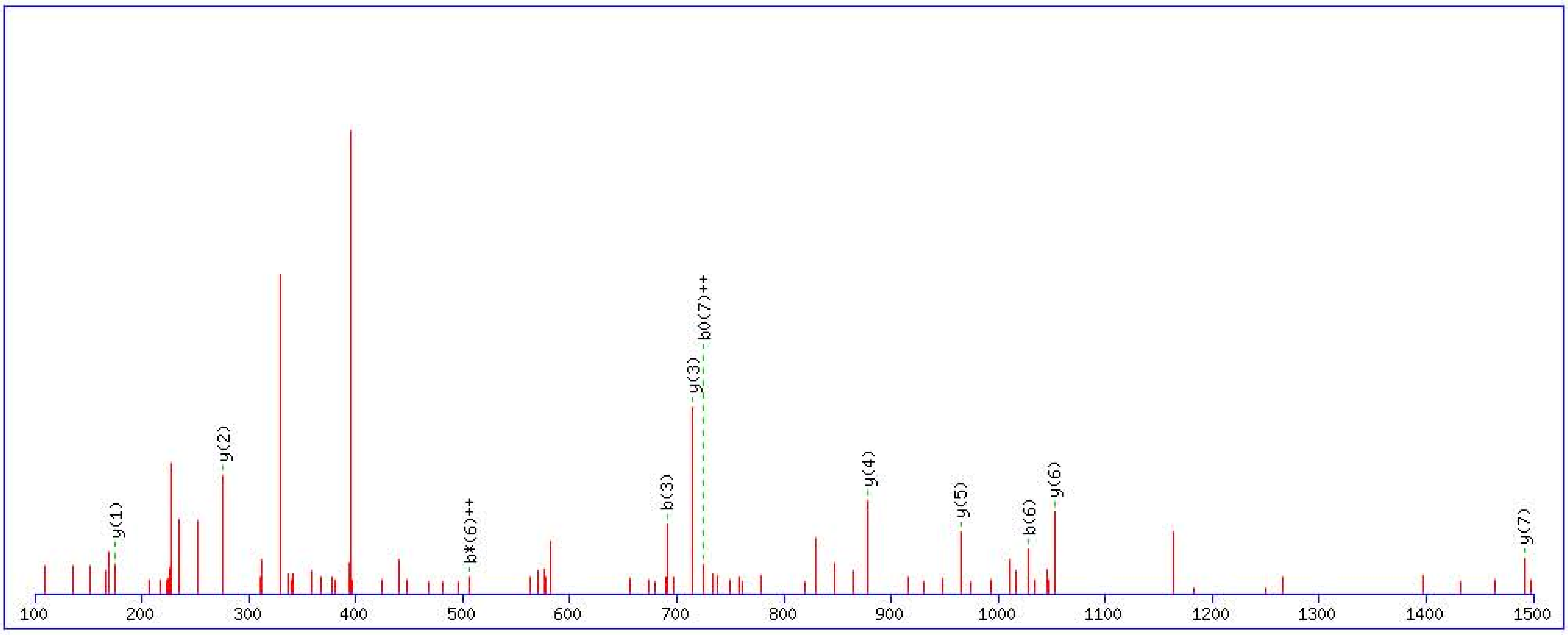
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NHQSSYQTR**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

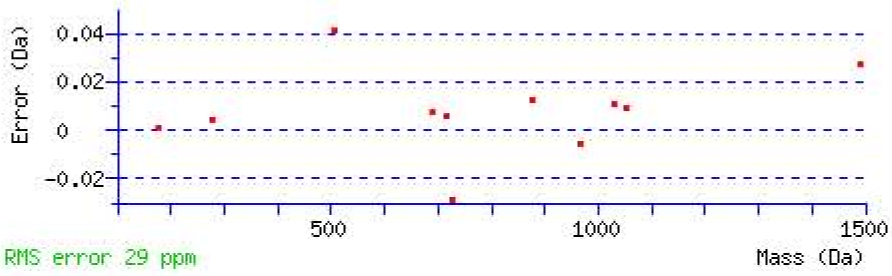
Match to Query 43506: 1741.854612 from(581.625480,3+) rtinseconds(1536) index(39041)
Title: Locus:1.1.1.2984.16 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

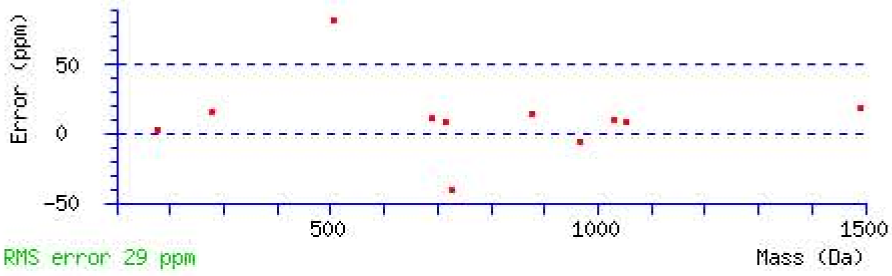
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1741.839218
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 28 **Expect:** 0.0087
Matches : 11/88 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	115.050203	58.028740	98.023654	49.515465			N							9
2	252.109115	126.558195	235.082566	118.044921			H	1628.803580	814.905428	1611.777031	806.392154	1610.793015	805.900146	8
3	**691.334441**	346.170859	674.307892	337.657584			Q	***1491.744668***	746.375972	1474.718119	737.862698	1473.734103	737.370690	7
4	778.366469	389.686872	761.339920	381.173598	760.355904	380.681590	S	***1052.519342***	526.763309	1035.492793	518.250035	1034.508777	517.758027	6
5	865.398497	433.202886	848.371948	424.689612	847.387932	424.197604	S	***965.487314***	483.247295	948.460765	474.734021	947.476749	474.242013	5
6	**1028.461826**	514.734551	1011.435277	506.221276	1010.451261	505.729268	Y	***878.455286***	439.731281	861.428737	431.218007	860.444721	430.725999	4
7	1467.687152	734.347214	1450.660603	725.833940	1449.676587	725.341932	Q	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
8	1568.734831	784.871054	1551.708282	776.357779	1550.724266	775.865771	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
28.3	1741.839218	0.015394	NHQSSYQTR
6.3	1741.878082	-0.023470	TLEESNSGPLMKKHR

Mascot: http://www.matrixscience.com/

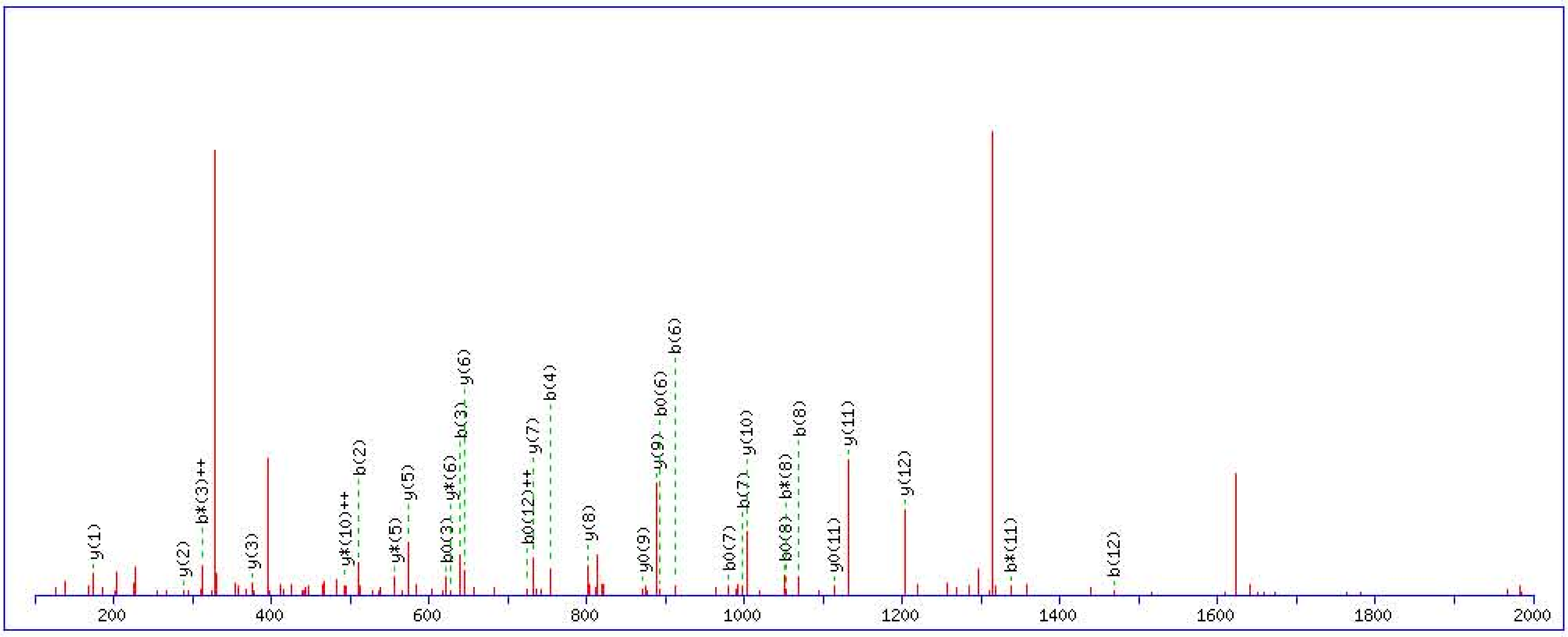
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QAEISASAPTSLR**
Found in **SHBG_HUMAN**, Sex hormone-binding globulin OS=Homo sapiens GN=SHBG PE=1 SV=2

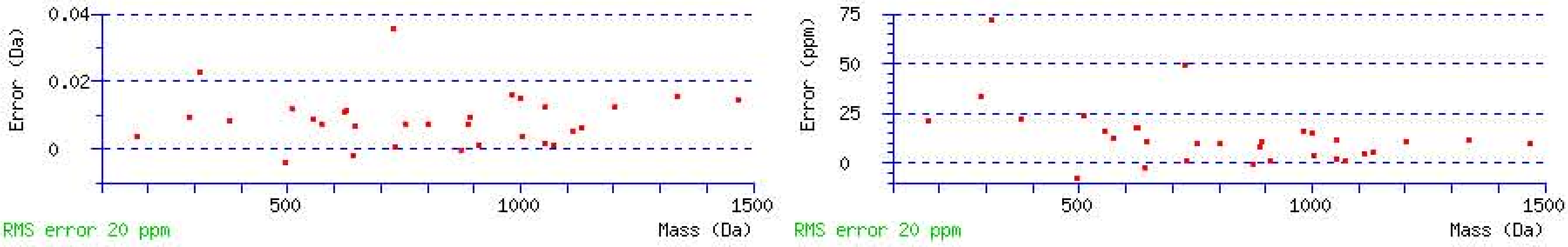
Match to Query 40964: 1640.871228 from(821.442890,2+) rtinseconds(1853) index(5478)
Title: Locus:1.1.1.2899.18 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1640.855560
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 3.8e-005
Matches : 31/136 fragment ions using 78 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							13
2	**511.269716**	256.138496	494.243167	247.625221			A	***1202.637542***	601.822409	1185.610993	593.309135	1184.626977	592.817126	12
3	**640.312309**	320.659793	623.285760	312.146518	622.301744	311.654510	E	***1131.600428***	566.303852	1114.573879	557.790578	1113.589863	557.298569	11
4	**753.396373**	377.201825	736.369824	368.688550	735.385808	368.196542	I	***1002.557835***	501.782556	985.531286	493.269281	984.547270	492.777273	10
5	840.428401	420.717839	823.401852	412.204564	822.417836	411.712556	S	***889.473771***	445.240523	872.447222	436.727249	871.463206	436.235241	9
6	**911.465515**	456.236396	894.438966	447.723121	893.454950	447.231113	A	***802.441743***	401.724510	785.415194	393.211235	784.431178	392.719227	8
7	**998.497543**	499.752410	981.470994	491.239135	980.486978	490.747127	S	***731.404629***	366.205953	714.378080	357.692678	713.394064	357.200670	7
8	**1069.534657**	535.270966	1052.508108	526.757692	1051.524092	526.265684	A	***644.372601***	322.689939	627.346052	314.176664	626.362036	313.684656	6
9	1166.587421	583.797349	1149.560872	575.284074	1148.576856	574.792066	P	***573.335487***	287.171382	556.308938	278.658107	555.324922	278.166099	5
10	1267.635100	634.321188	1250.608551	625.807914	1249.624535	625.315905	T	476.282723	238.644999	459.256174	230.131725	458.272158	229.639717	4
11	1354.667128	677.837202	1337.640579	669.323928	1336.656563	668.831920	S	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
12	**1467.751192**	734.379234	1450.724643	725.865960	1449.740627	725.373951	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 QAEISASAPTSLR
(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	1640.855560	0.015668	QAEISASAPTSLR
6.5	1640.885422	-0.014194	LLKKDLCNTHLMR
3.7	1640.866791	0.004437	QAQAGGSKKAEQK
3.5	1640.852188	0.019040	EPPKEKEFQSPGLR
3.0	1640.849030	0.022198	AQEMEAAVGRLR
1.8	1640.879364	-0.008136	MAHRAGLLPNHRPR
1.6	1640.884521	-0.013293	EAQKKPAESQKIER
1.1	1640.855530	0.015698	QAKLEKEEAER
0.9	1640.870804	0.000424	FLMSAERYDKLLR
0.8	1640.848160	0.023068	LQRILEGEGNQEAGK

Mascot: http://www.matrixscience.com/

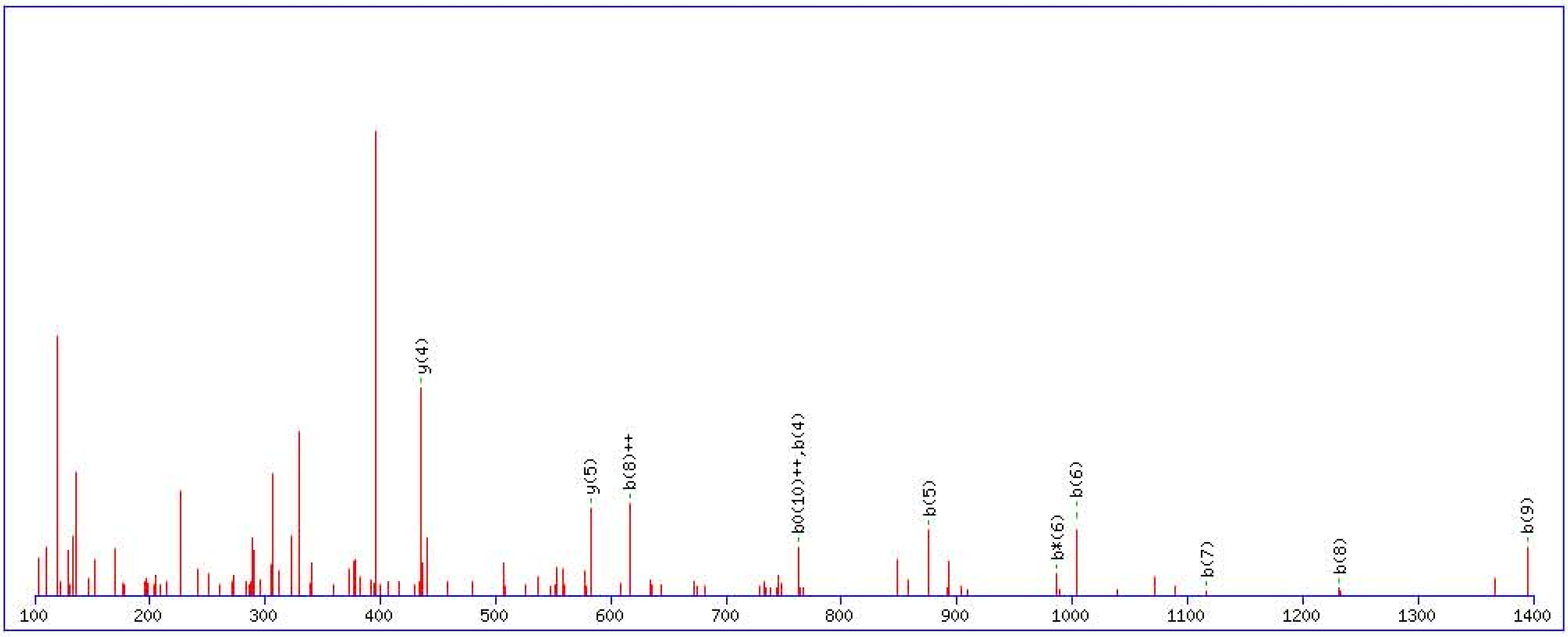
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGHQLQLDYFGACK**
Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

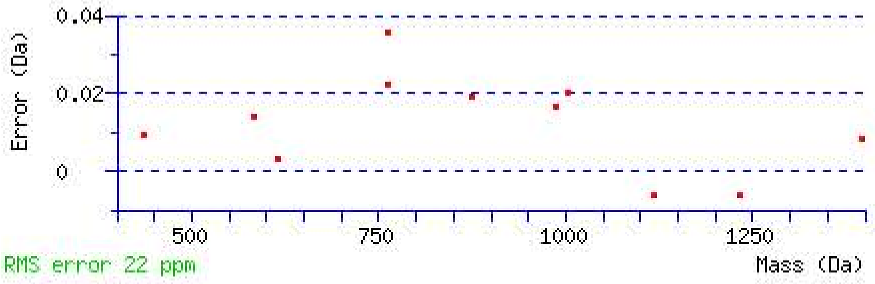
Match to Query 49361: 1975.000976 from(494.757520,4+) rtinseconds(1924) index(60205)
Title: Locus:1.1.1.3093.6 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

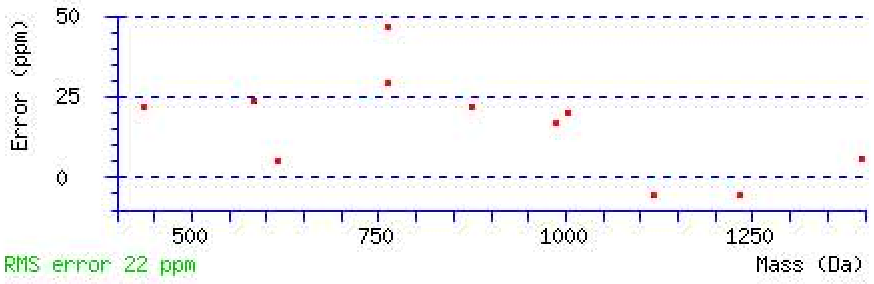
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1974.980804
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0003
Matches : 11/130 fragment ions using 13 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							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
38.5	1974.980804	0.020172	KGHQLQLDYFGACK
17.2	1974.980804	0.020172	KGHQLQLDYFGACK
0.9	1975.015823	-0.014847	AEKTFSVYEIMCKILK

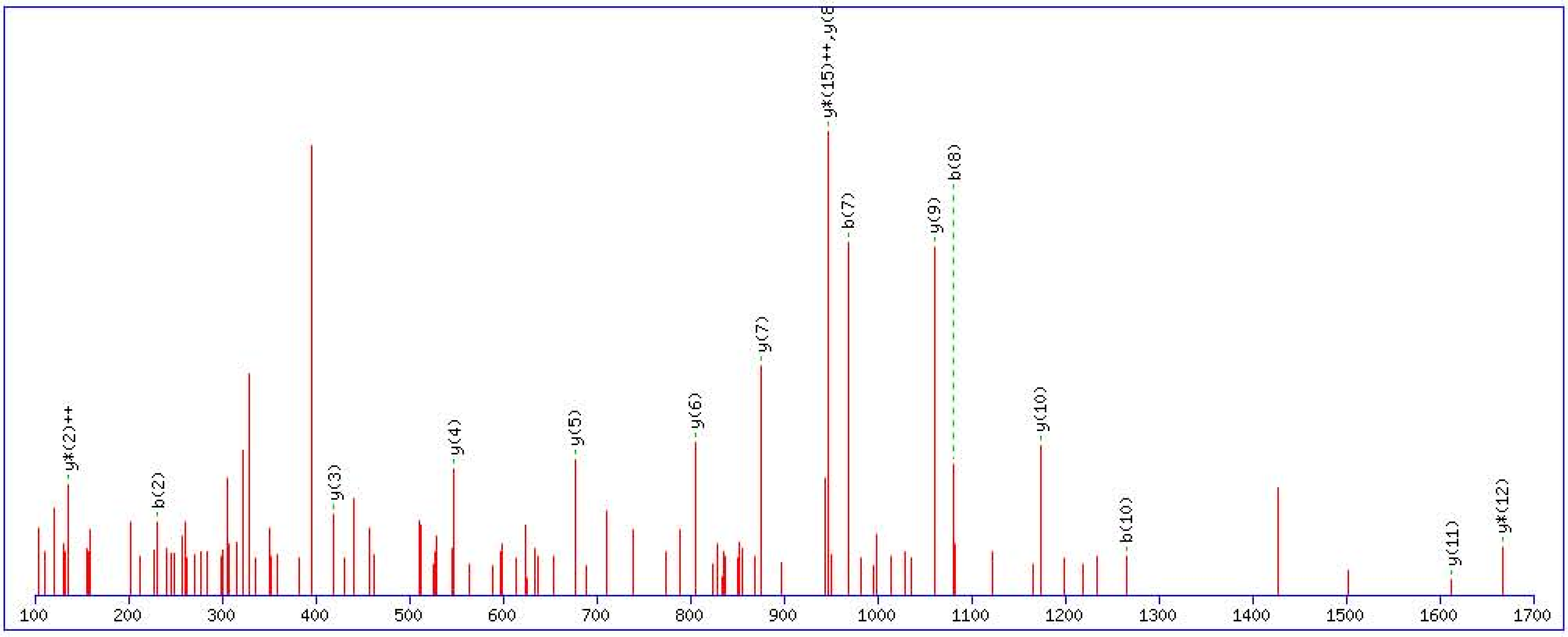
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVGGIAQIIAAQEEMLR**
Found in **TLN1_HUMAN**, Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3

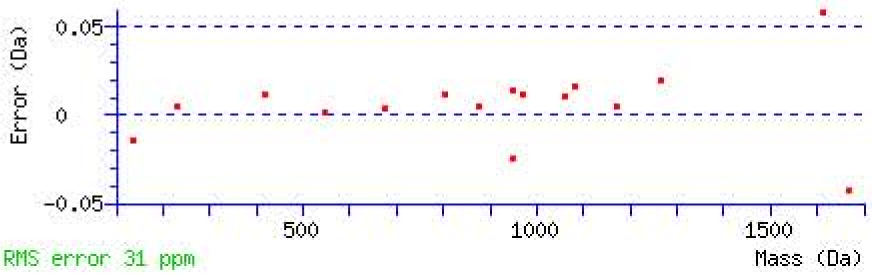
Match to Query 53942: 2140.152642 from(714.391490,3+) rtinseconds(2998) index(49404)
Title: Locus:1.1.1.3489.7 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

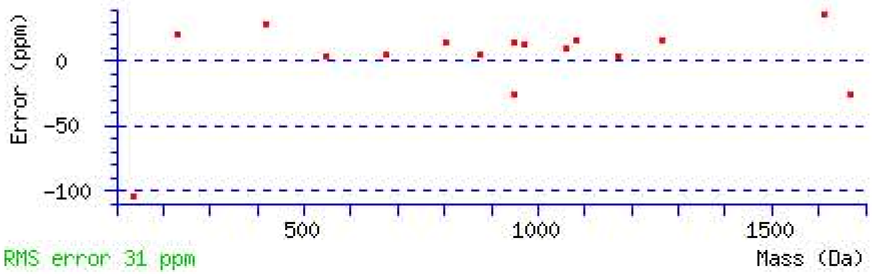
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2140.120636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 2.4e-005
Matches : 16/150 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	132.047761	66.527518					M							17
2	**231.116175**	116.061725					V	2010.087467	1005.547372	1993.060918	997.034097	1992.076902	996.542089	16
3	288.137639	144.572457					G	1911.019053	956.013165	1893.992504	947.499890	1893.008488	947.007882	15
4	345.159103	173.083189					G	1853.997589	927.502433	1836.971040	918.989158	1835.987024	918.497150	14
5	458.243167	229.625221					I	1796.976125	898.991701	1779.949576	890.478426	1778.965560	889.986418	13
6	529.280281	265.143779					A	1683.892061	842.449669	1666.865512	833.936394	1665.881496	833.444386	12
7	**968.505607**	484.756442	951.479058	476.243167			Q	***1612.854947***	806.931112	1595.828398	798.417837	1594.844382	797.925829	11
8	**1081.589671**	541.298474	1064.563122	532.785199			I	***1173.629621***	587.318449	1156.603072	578.805174	1155.619056	578.313166	10
9	1194.673735	597.840505	1177.647186	589.327231			I	***1060.545557***	530.776417	1043.519008	522.263142	1042.534992	521.771134	9
10	**1265.710849**	633.359062	1248.684300	624.845788			A	***947.461493***	474.234385	930.434944	465.721110	929.450928	465.229102	8
11	1336.747963	668.877619	1319.721414	660.364345			A	***876.424379***	438.715828	859.397830	430.202553	858.413814	429.710545	7
12	1464.806541	732.906908	1447.779992	724.393634			Q	***805.387265***	403.197271	788.360716	394.683996	787.376700	394.191988	6
13	1593.849134	797.428205	1576.822585	788.914930	1575.838569	788.422922	E	***677.328687***	339.167982	660.302138	330.654707	659.318122	330.162699	5
14	1722.891727	861.949502	1705.865178	853.436227	1704.881162	852.944219	E	***548.286094***	274.646685	531.259545	266.133411	530.275529	265.641403	4
15	1853.932212	927.469744	1836.905663	918.956470	1835.921647	918.464461	M	***419.243501***	210.125389	402.216952	201.612114			3
16	1967.016276	984.011776	1949.989727	975.498501	1949.005711	975.006493	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of MVGGIAQIIAAQEEMLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.4	2140.120636	0.032006	MVGGIAQIIAAQEEMLR
0.4	2140.120636	0.032006	MVGGIAQIIAAQEEMLR
0.1	2140.135010	0.017632	RMLEESNLSFLKELLFR

Mascot: http://www.matrixscience.com/

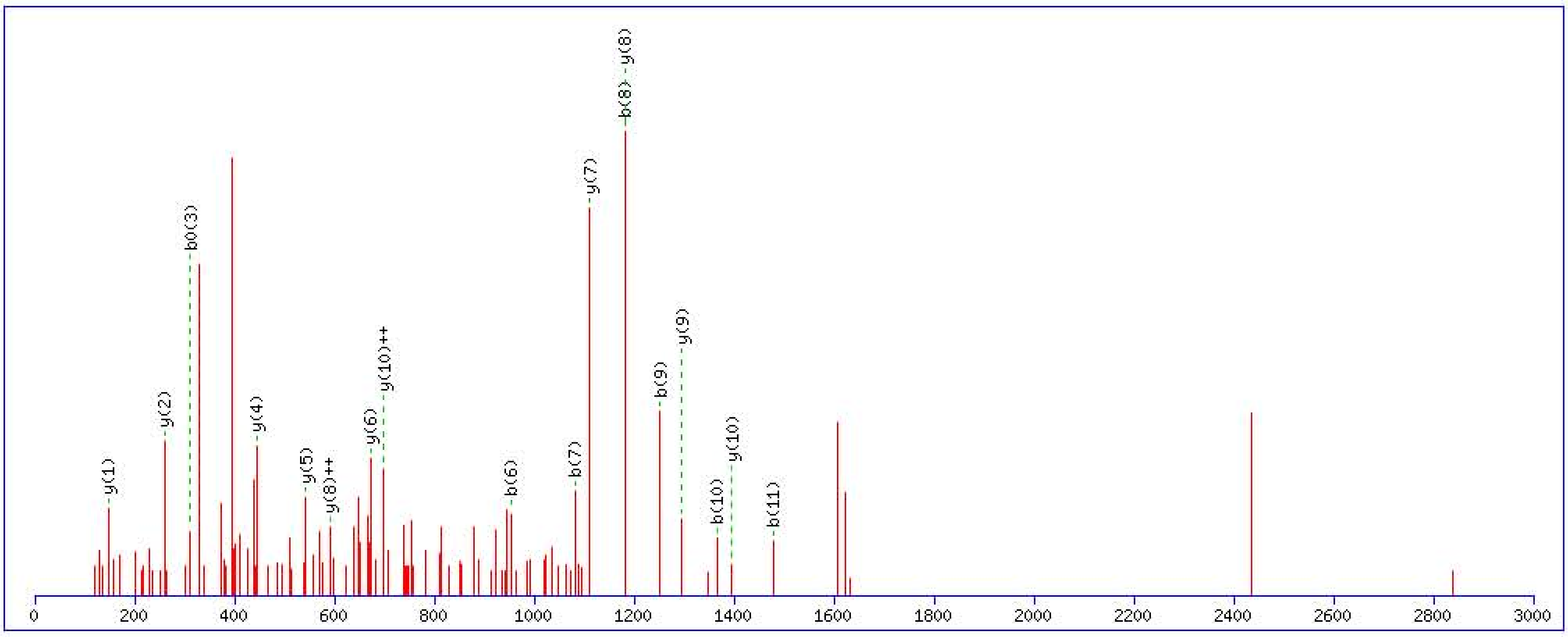
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDTLAQEVALLK**
Found in **TETN_HUMAN**, Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3

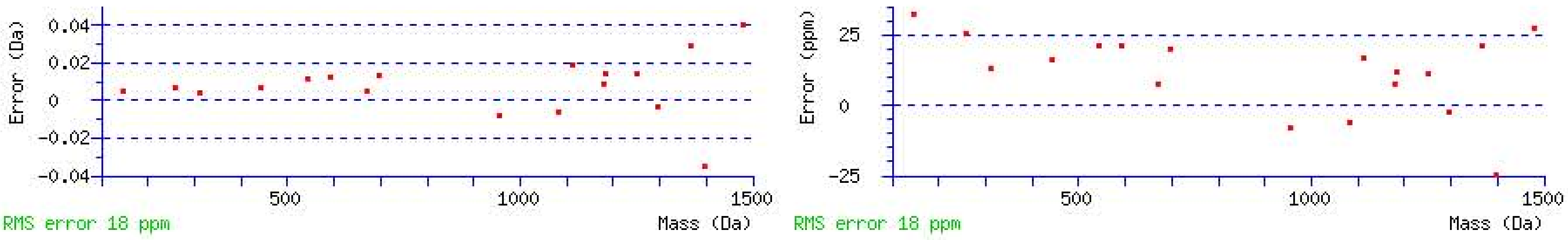
Match to Query 39903: 1623.943148 from(812.978850,2+) rtinseconds(2563) index(10096)
Title: Locus:1.1.1.3146.16 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1623.926941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 2.2e-006
Matches : 18/110 fragment ions using 28 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	114.091340	57.549308					L							12
2	229.118283	115.062779			211.107718	106.057497	D	1511.850179	756.428728	1494.823630	747.915453	1493.839614	747.423445	11
3	330.165962	165.586619			312.155397	156.581336	T	***1396.823236***	698.915256	1379.796687	690.401982	1378.812671	689.909973	10
4	443.250026	222.128651			425.239461	213.123369	L	***1295.775557***	648.391416	1278.749008	639.878142	1277.764992	639.386134	9
5	514.287140	257.647208			496.276575	248.641926	A	***1182.691493***	591.849385	1165.664944	583.336110	1164.680928	582.844102	8
6	**953.512466**	477.259871	936.485917	468.746597	935.501901	468.254589	Q	***1111.654379***	556.330827	1094.627830	547.817553	1093.643814	547.325545	7
7	**1082.555059**	541.781168	1065.528510	533.267893	1064.544494	532.775885	E	***672.429053***	336.718165	655.402504	328.204890	654.418488	327.712882	6
8	**1181.623473**	591.315375	1164.596924	582.802100	1163.612908	582.310092	V	***543.386460***	272.196868	526.359911	263.683593			5
9	**1252.660587**	626.833932	1235.634038	618.320657	1234.650022	617.828649	A	***444.318046***	222.662661	427.291497	214.149386			4
10	**1365.744651**	683.375964	1348.718102	674.862689	1347.734086	674.370681	L	373.280932	187.144104	356.254383	178.630829			3
11	**1478.828715**	739.917995	1461.802166	731.404721	1460.818150	730.912713	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 LDTLAQEVALLK
(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	1623.926941	0.016207	LDTLAQEVALLK
7.2	1623.942001	0.001147	ESKPGGLPRRSSIIK
3.8	1623.957260	-0.014112	IFRPKHTRISELK
2.7	1623.934799	0.008349	FIQKFSQASSKILK
2.7	1623.928284	0.014864	LCHAAFLPSVRLLK
2.7	1623.942200	0.000948	LLPVQENFLLK
2.2	1623.928268	0.014880	EVQRLYHKLK

Mascot: http://www.matrixscience.com/

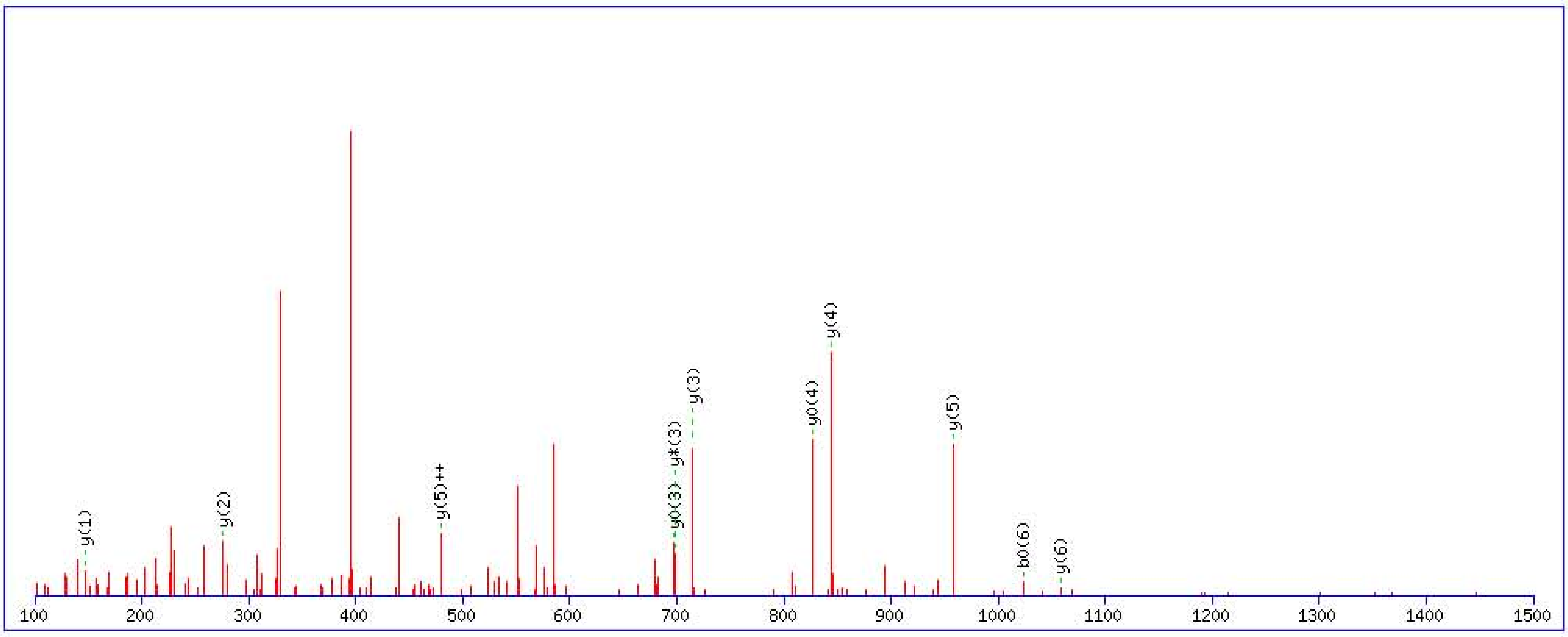
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETIEQEK**
Found in **TYB10_HUMAN**, Thymosin beta-10 OS=Homo sapiens GN=TMSB10 PE=1 SV=2

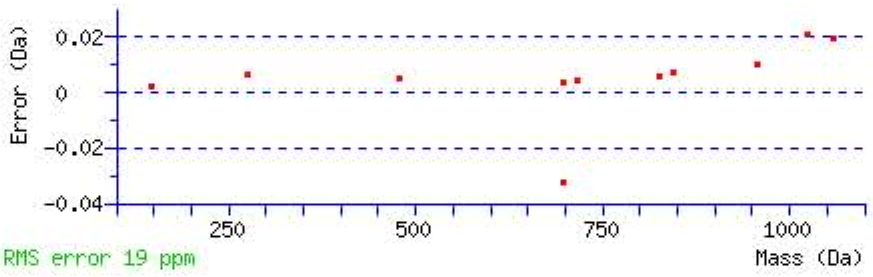
Match to Query 23329: 1186.597268 from(594.305910,2+) rtinseconds(1438) index(75254)
Title: Locus:1.1.1.1851.12 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

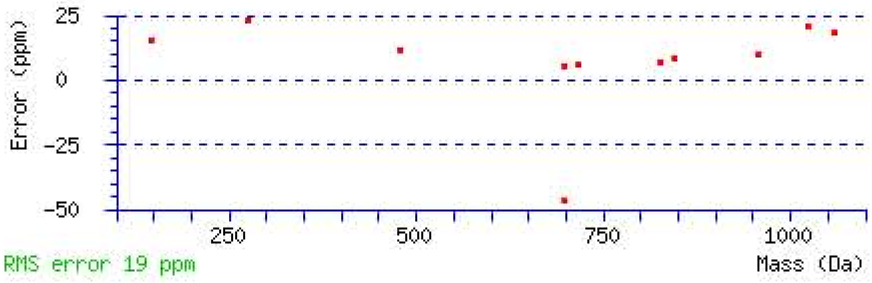
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1186.590347
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0066
Matches : 11/62 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	231.097548	116.052412			213.086983	107.047130	T	***1058.555059***	529.781168	1041.528510	521.267893	1040.544494	520.775885	6
3	344.181612	172.594444			326.171047	163.589162	I	***957.507380***	479.257328	940.480831	470.744054	939.496815	470.252046	5
4	473.224205	237.115741			455.213640	228.110458	E	***844.423316***	422.715296	827.396767	414.202022	826.412751	413.710014	4
5	912.449531	456.728404	895.422982	448.215129	894.438966	447.723121	Q	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
6	1041.492124	521.249700	1024.465575	512.736426	1023.481559	512.244418	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 ETIEQEK
(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	1186.590347	0.006921	ETIEQEK
9.7	1186.612808	-0.015540	TLEKMEKHR
6.5	1186.591721	0.005547	KTVGFHSHMK
4.3	1186.601578	-0.004310	TNEKQEK
3.1	1186.605606	-0.008338	MEPPNLYPVK
2.8	1186.590347	0.006921	QEEELTK
2.7	1186.601578	-0.004310	QEQKESK
2.6	1186.613464	-0.016196	WAEHFIKEK
1.9	1186.609436	-0.012168	KNHKEEFQK
0.7	1186.594223	0.003045	EPGRGGTETVGK

Mascot: http://www.matrixscience.com/

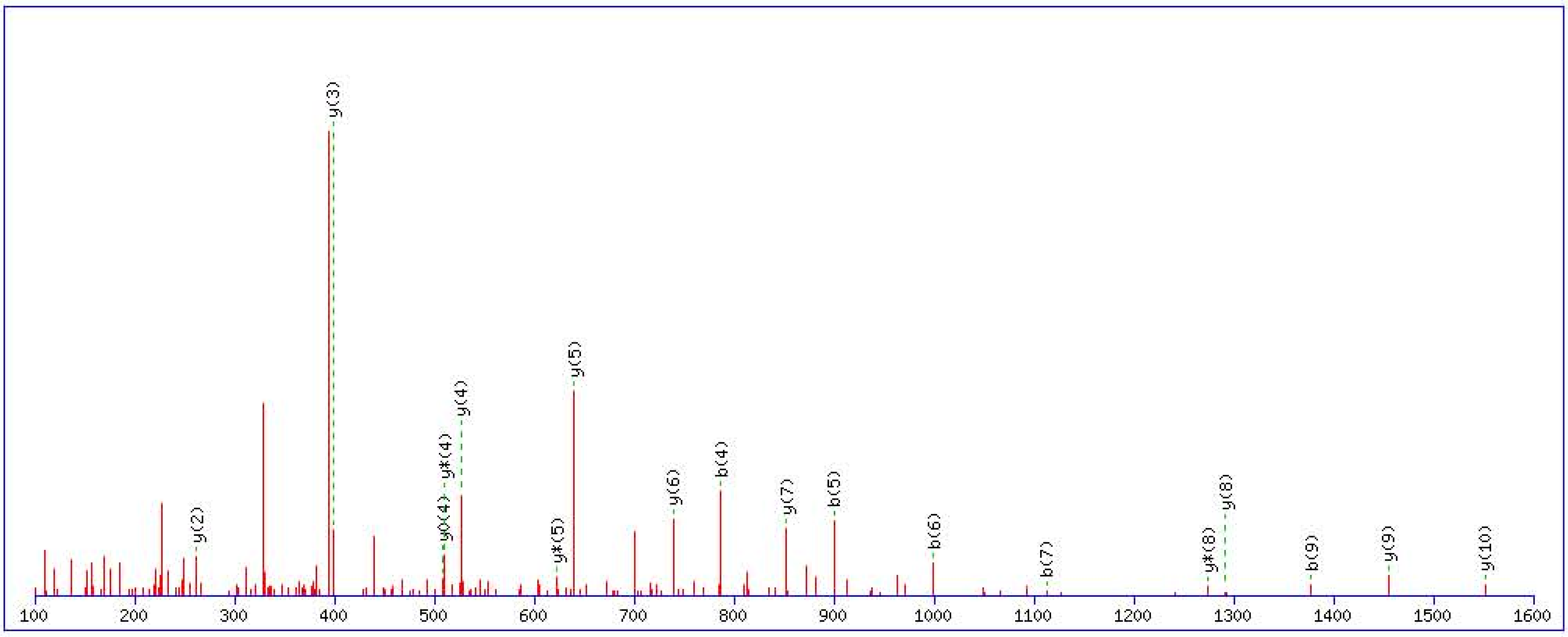
{MATRIX}{SCIENCE} Mascot Search Results

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

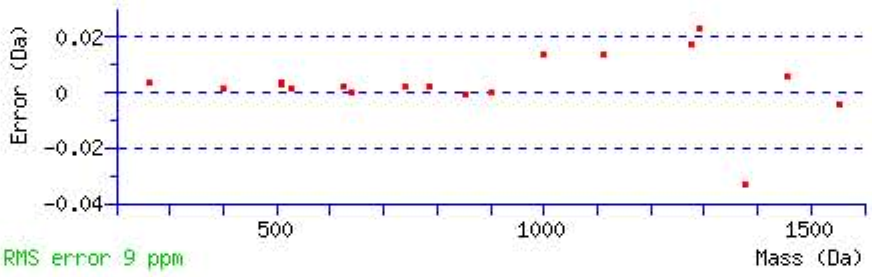
Match to Query 40836: 1637.873922 from(546.965250,3+) rtinseconds(1865) index(23694)
Title: Locus:1.1.1.2792.9 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

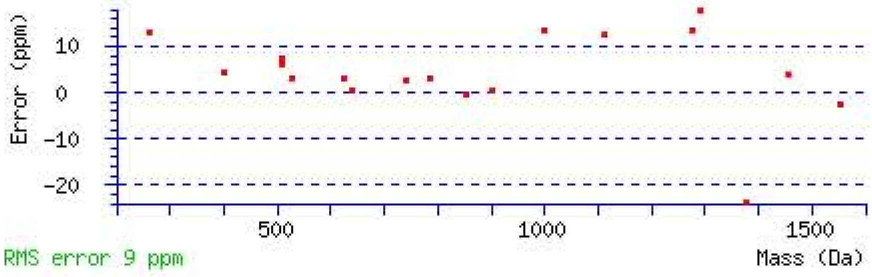
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1637.871170
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 5.9e-005
Matches : 18/112 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	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
46.4	1637.871170	0.002752	SPYQLVLQHSR
3.5	1637.871170	0.002752	SPYQLVLQHSR
1.3	1637.855911	0.018011	RTAYSGVPMTILSSR

Mascot: http://www.matrixscience.com/

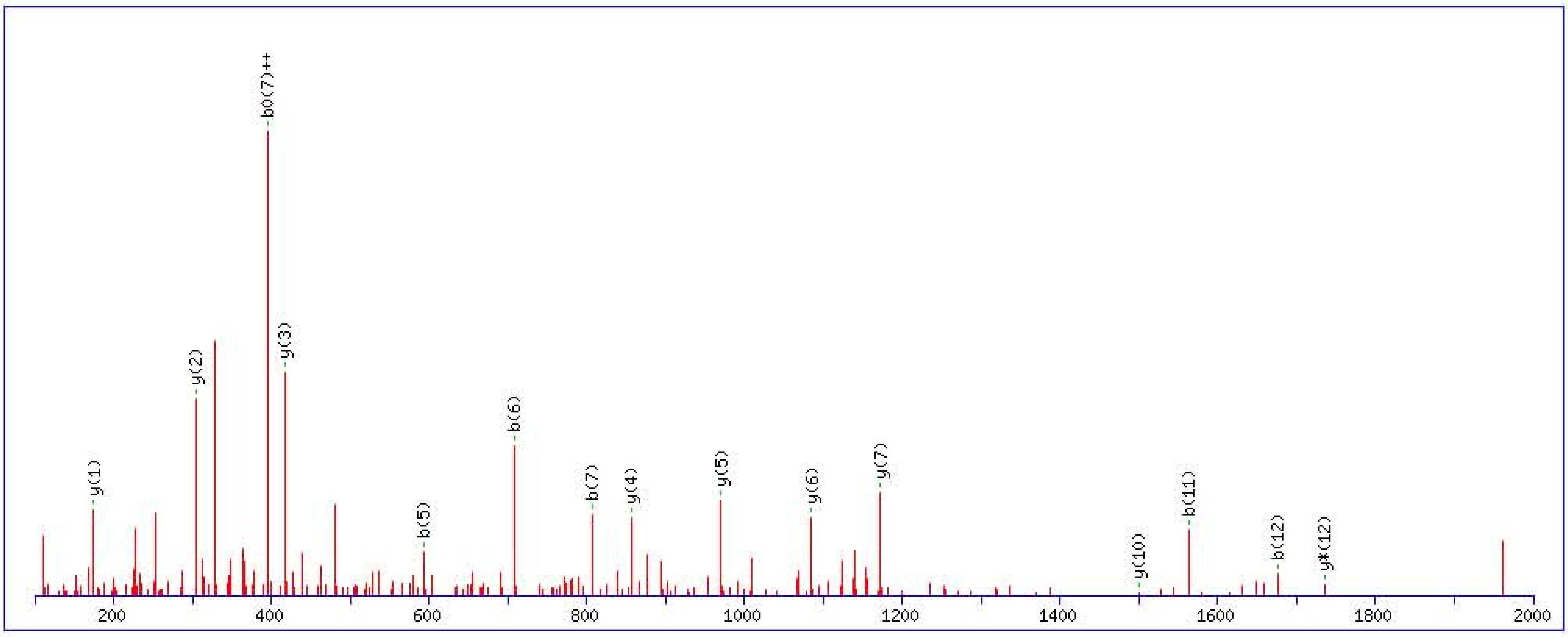
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLHDLDVSDNQLER**
Found in **VASN_HUMAN**, Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

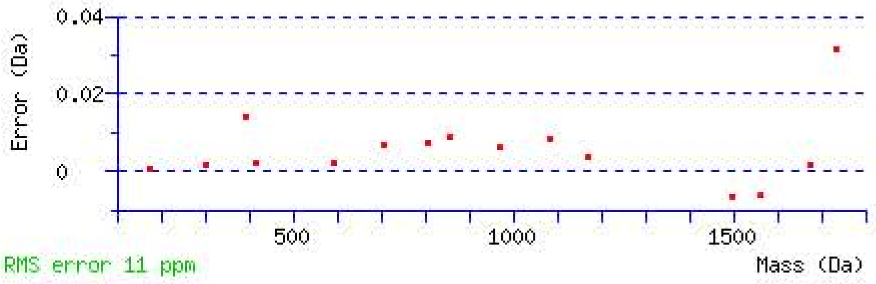
Match to Query 49407: 1977.967902 from(660.329910,3+) rtinseconds(1918) index(24106)
Title: Locus:1.1.1.2810.6 File:"2013-07-02 CLN FXIII 180 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

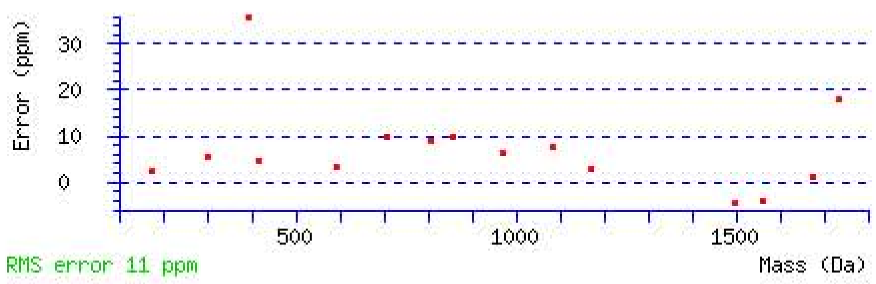
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 70 **Expect:** 2.8e-007
Matches : 15/148 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	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
70.0	1977.957809	0.010093	NLHDLDVSDNQLER
0.1	1977.979813	-0.011911	TMPRTVPGSTMKMGSLER

Mascot: http://www.matrixscience.com/

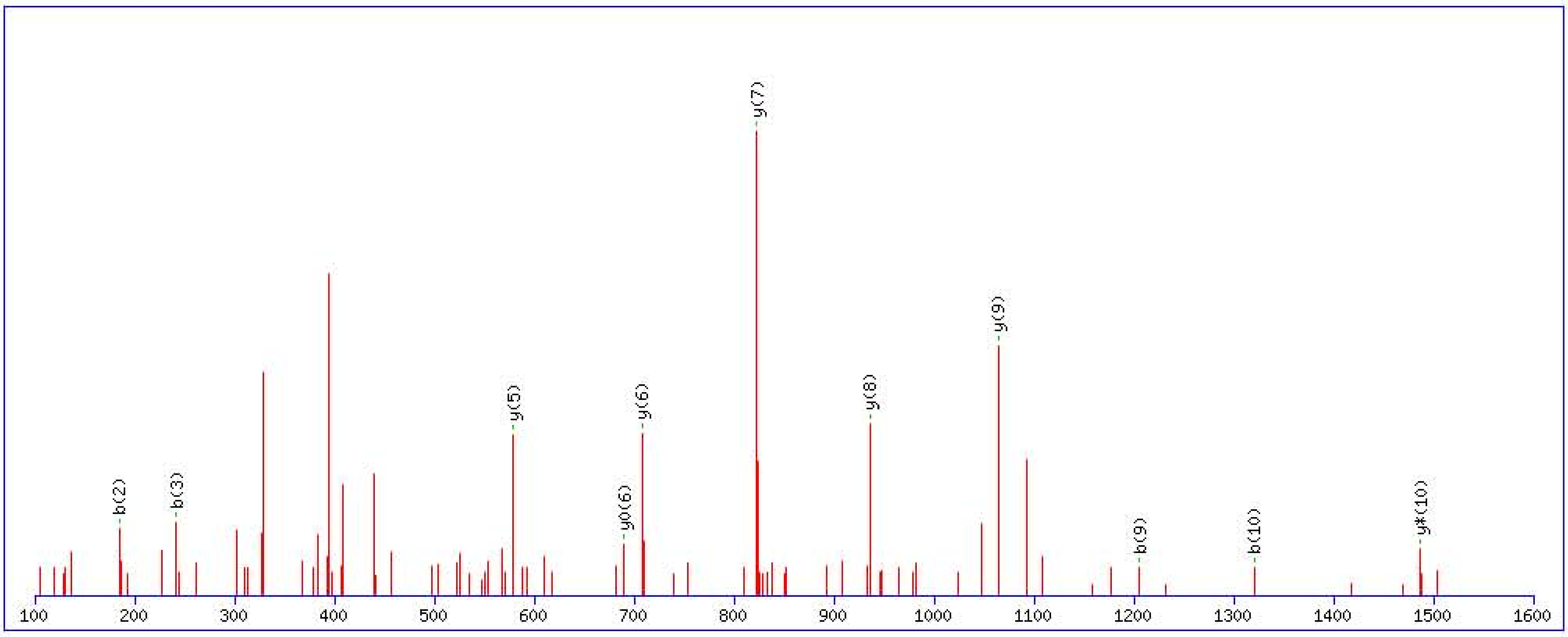
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAGLGLQQLDEGLFSR**
Found in **VASN_HUMAN**, Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

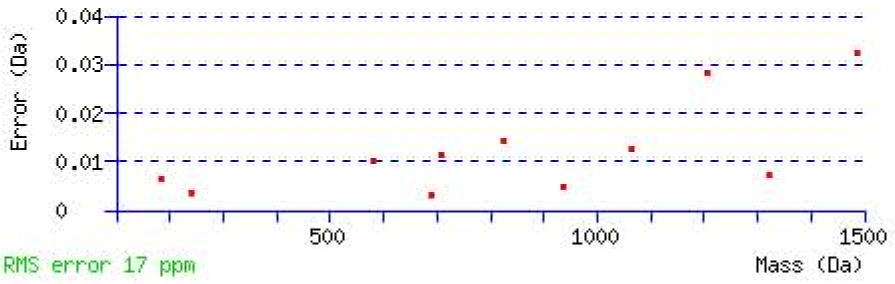
Match to Query 51460: 2027.116512 from(676.712780,3+) rtinseconds(2791) index(11539)
Title: Locus:1.1.1.3225.14 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

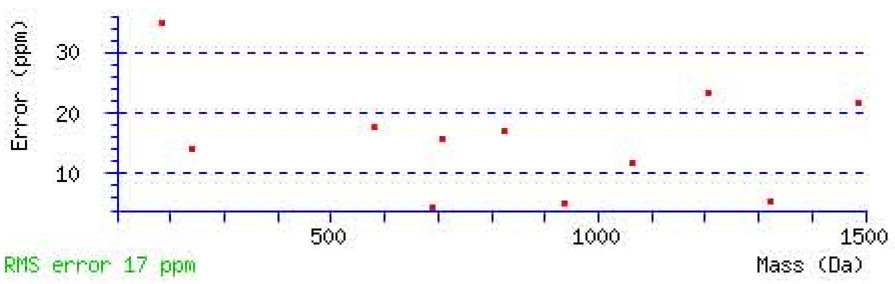
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.087372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0033
Matches : 11/148 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							16
2	***185.128454***	93.067865					A	1915.010596	958.008936	1897.984047	949.495662	1897.000031	949.003654	15
3	***242.149918***	121.578597					G	1843.973482	922.490379	1826.946933	913.977105	1825.962917	913.485097	14
4	355.233982	178.120629					L	1786.952018	893.979647	1769.925469	885.466373	1768.941453	884.974364	13
5	412.255446	206.631361					G	1673.867954	837.437615	1656.841405	828.924341	1655.857389	828.432333	12
6	525.339510	263.173393					L	1616.846490	808.926883	1599.819941	800.413609	1598.835925	799.921601	11
7	964.564836	482.786056	947.538287	474.272782			Q	1503.762426	752.384851	1486.735877	743.871577	1485.751861	743.379569	10
8	1092.623414	546.815345	1075.596865	538.302071			Q	***1064.537100***	532.772188	1047.510551	524.258914	1046.526535	523.766906	9
9	***1205.707478***	603.357377	1188.680929	594.844102			L	***936.478522***	468.742899	919.451973	460.229625	918.467957	459.737617	8
10	***1320.734421***	660.870848	1303.707872	652.357574	1302.723856	651.865566	D	***823.394458***	412.200867	806.367909	403.687593	805.383893	403.195585	7
11	1449.777014	725.392145	1432.750465	716.878871	1431.766449	716.386863	E	***708.367515***	354.687396	691.340966	346.174121	690.356950	345.682113	6
12	1506.798478	753.902877	1489.771929	745.389603	1488.787913	744.897594	G	***579.324922***	290.166099	562.298373	281.652825	561.314357	281.160817	5
13	1619.882542	810.444909	1602.855993	801.931634	1601.871977	801.439626	L	522.303458	261.655367	505.276909	253.142093	504.292893	252.650085	4
14	1766.950956	883.979116	1749.924407	875.465842	1748.940391	874.973833	F	409.219394	205.113335	392.192845	196.600061	391.208829	196.108053	3
15	1853.982984	927.495130	1836.956435	918.981856	1835.972419	918.489848	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
16							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LAGLGLQQLDEGLFSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.0	2027.087372	0.029140	LAGLGLQQLDEGLFSR
27.8	2027.087372	0.029140	LAGLGLQQLDEGLFSR

Mascot: http://www.matrixscience.com/

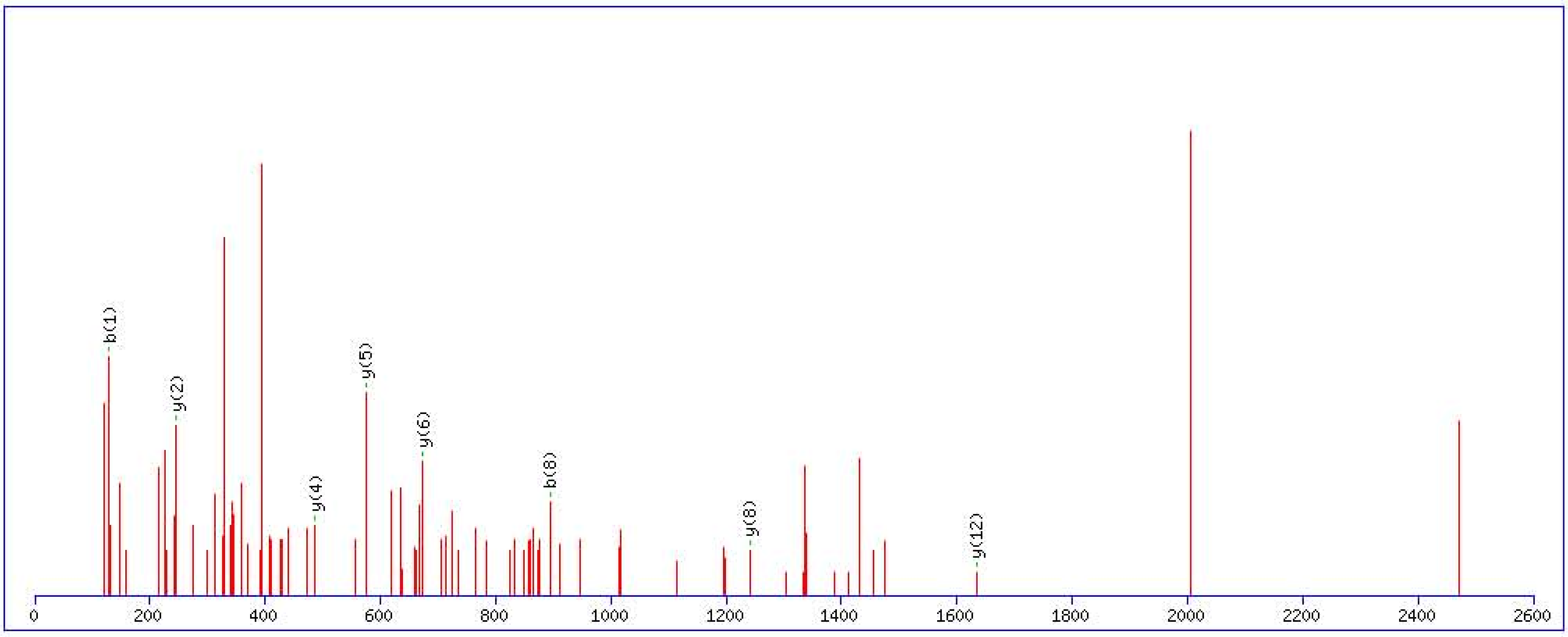
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KFPSGTFEQVSQLVK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

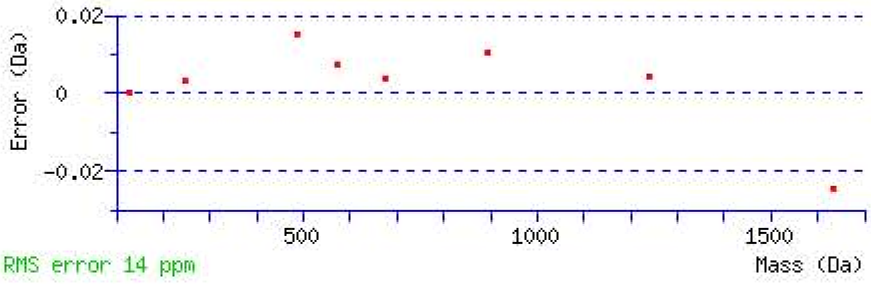
Match to Query 27767: 2005.056282 from(669.359370,3+) rtinseconds(2348) index(81230)
Title: Locus:1.1.1.2168.10 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

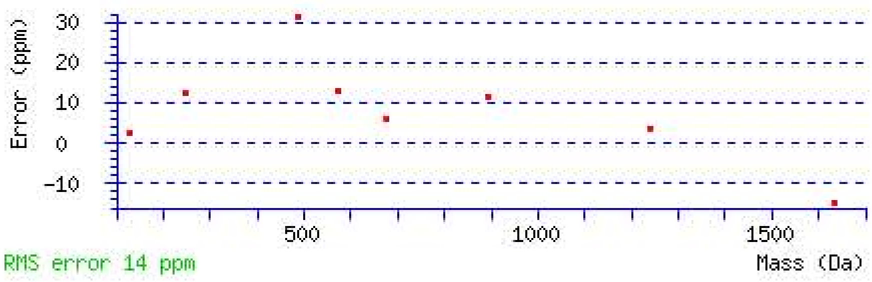
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2005.070679
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.0057
Matches : 8/154 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							15
2	276.170653	138.588964	259.144104	130.075690			F	1877.982984	939.495130	1860.956435	930.981856	1859.972419	930.489848	14
3	373.223417	187.115346	356.196868	178.602072			P	1730.914570	865.960923	1713.888021	857.447649	1712.904005	856.955641	13
4	460.255445	230.631360	443.228896	222.118086	442.244880	221.626078	S	***1633.861806***	817.434541	1616.835257	808.921267	1615.851241	808.429259	12
5	517.276909	259.142093	500.250360	250.628818	499.266344	250.136810	G	1546.829778	773.918527	1529.803229	765.405253	1528.819213	764.913245	11
6	618.324588	309.665932	601.298039	301.152658	600.314023	300.660650	T	1489.808314	745.407795	1472.781765	736.894521	1471.797749	736.402513	10
7	765.393002	383.200139	748.366453	374.686865	747.382437	374.194857	F	1388.760635	694.883955	1371.734086	686.370681	1370.750070	685.878673	9
8	**894.435595**	447.721436	877.409046	439.208161	876.425030	438.716153	E	***1241.692221***	621.349749	1224.665672	612.836474	1223.681656	612.344466	8
9	1333.660921	667.334098	1316.634372	658.820824	1315.650356	658.328816	Q	1112.649628	556.828452	1095.623079	548.315178	1094.639063	547.823169	7
10	1432.729335	716.868306	1415.702786	708.355031	1414.718770	707.863023	V	***673.424302***	337.215789	656.397753	328.702515	655.413737	328.210507	6
11	1519.761363	760.384320	1502.734814	751.871045	1501.750798	751.379037	S	***574.355888***	287.681582	557.329339	279.168308	556.345323	278.676300	5
12	1647.819941	824.413609	1630.793392	815.900334	1629.809376	815.408326	Q	***487.323860***	244.165568	470.297311	235.652293			4
13	1760.904005	880.955640	1743.877456	872.442366	1742.893440	871.950358	L	359.265282	180.136279	342.238733	171.623004			3
14	1859.972419	930.489848	1842.945870	921.976573	1841.961854	921.484565	V	***246.181218***	123.594247	229.154669	115.080973			2
15							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KFPSGTFEQVSQLVK
(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	2005.070679	-0.014397	KFPSGTFEQVSQLVK
4.8	2005.070679	-0.014397	KFPSGTFEQVSQLVK
3.3	2005.048874	0.007408	KTMSKPGNGQPPVPEK

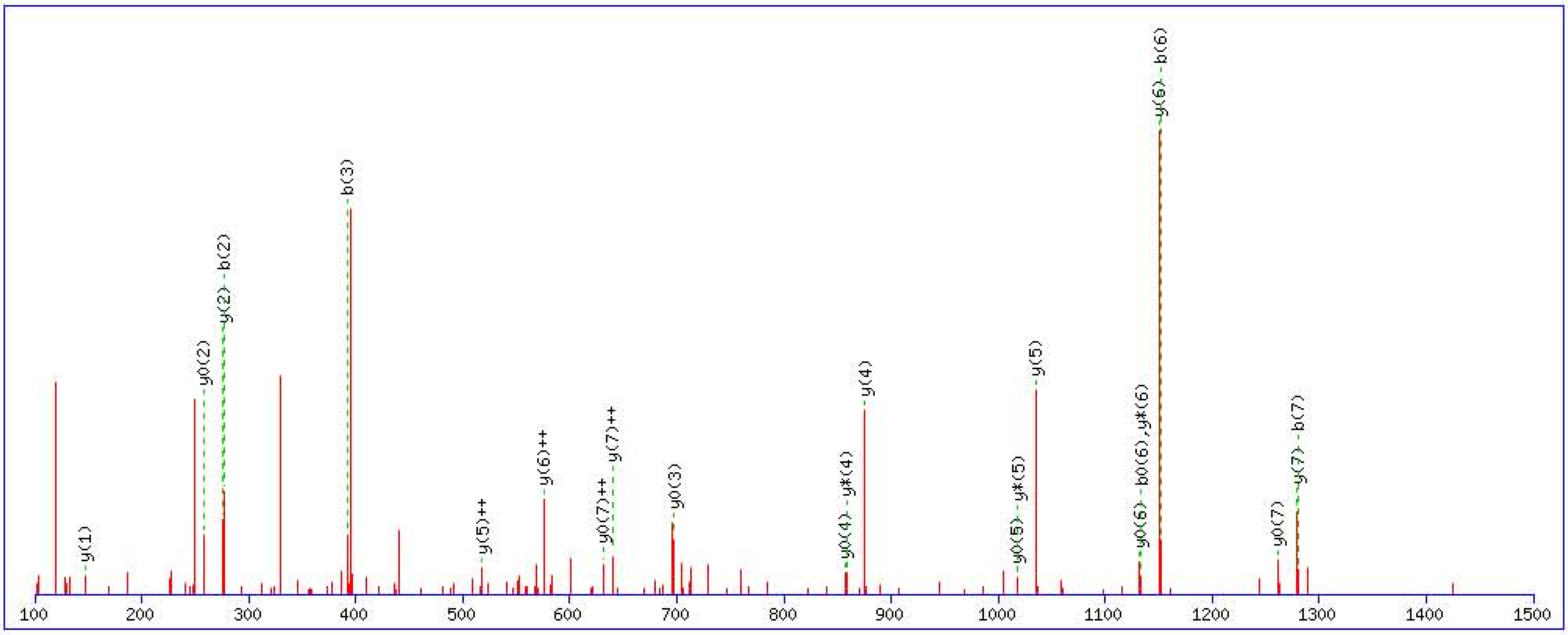
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FEDCCQEK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

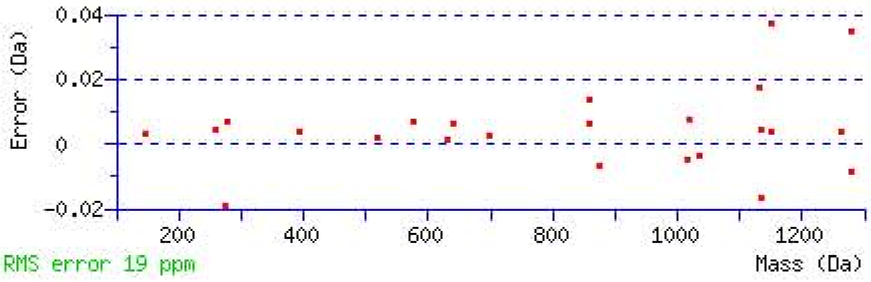
Match to Query 32479: 1425.579948 from(713.797250,2+) rtinseconds(1446) index(2928)
Title: Locus:1.1.1.2757.24 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

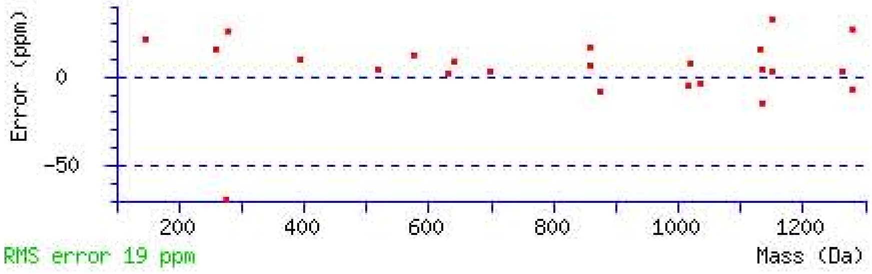
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1425.572693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.0035
Matches : 24/70 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	148.075690	74.541483					F							8
2	**277.118283**	139.062779			259.107718	130.057497	E	***1279.511557***	640.259417	1262.485008	631.746142	1261.500992	631.254134	7
3	**392.145226**	196.576251			374.134661	187.570968	D	***1150.468964***	575.738120	1133.442415	567.224846	1132.458399	566.732838	6
4	552.175875	276.591576			534.165310	267.586293	C	***1035.442021***	518.224649	1018.415472	509.711374	1017.431456	509.219366	5
5	712.206524	356.606900			694.195959	347.601618	C	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
6	**1151.431850**	576.219563	1134.405301	567.706289	1133.421285	567.214281	Q	715.380723	358.194000	698.354174	349.680725	697.370158	349.188717	3
7	**1280.474443**	640.740860	1263.447894	632.227585	1262.463878	631.735577	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FEDCCQEK
(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	1425.572693	0.007255	FEDCCQEK

Mascot: http://www.matrixscience.com/

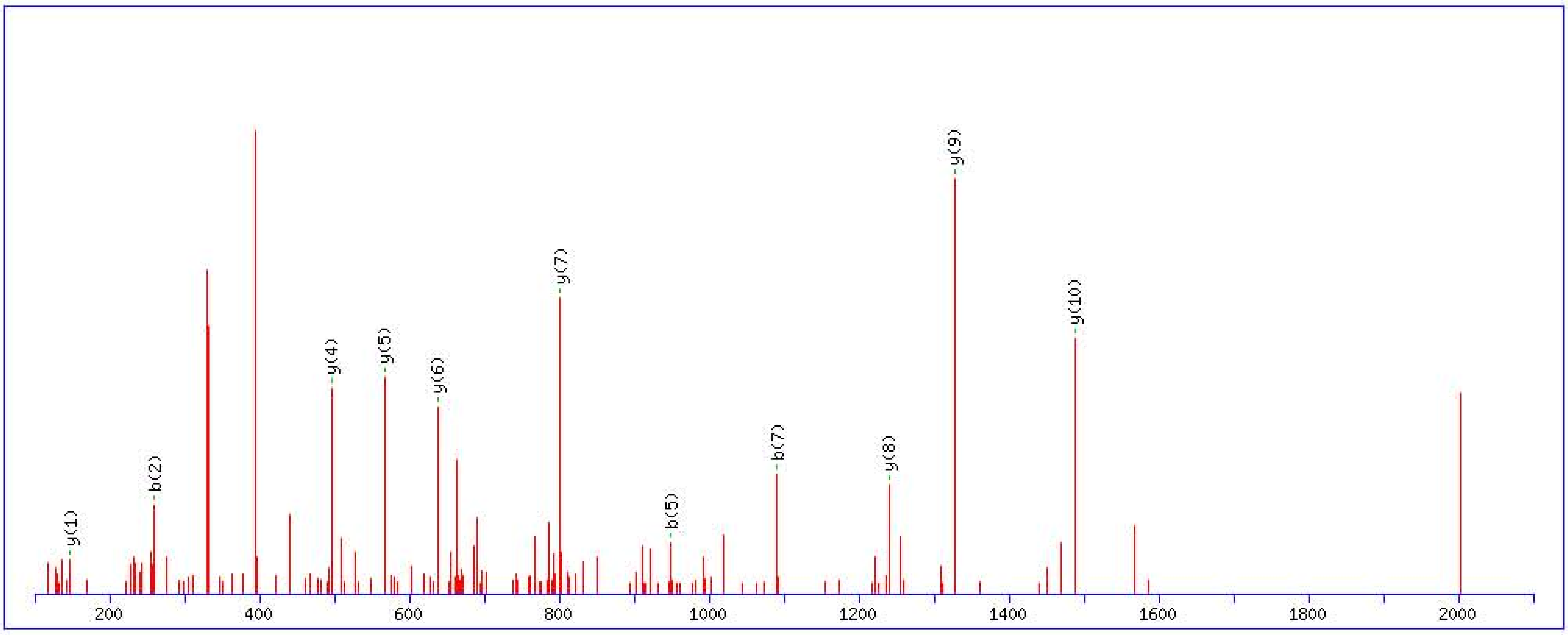
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VCSQYAAYGEK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

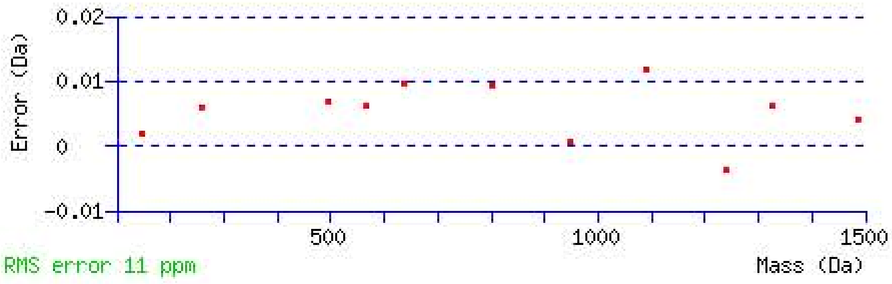
Match to Query 38013: 1585.733788 from(793.874170,2+) rtinseconds(1636) index(4155)
Title: Locus:1.1.1.2823.14 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

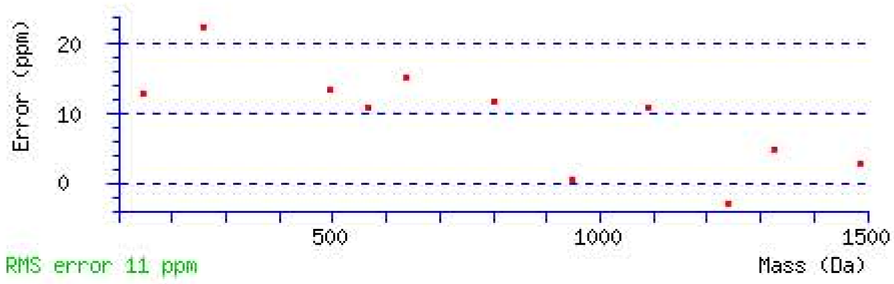
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1585.726868
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 67 **Expect:** 2.3e-006
Matches : 11/108 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	100.075690	50.541483					V							11
2	**260.106339**	130.556807					C	***1487.665750***	744.336513	1470.639201	735.823239	1469.655185	735.331231	10
3	347.138367	174.072821			329.127802	165.067539	S	***1327.635101***	664.321189	1310.608552	655.807914	1309.624536	655.315906	9
4	786.363693	393.685485	769.337144	385.172210	768.353128	384.680202	Q	***1240.603073***	620.805175	1223.576524	612.291900	1222.592508	611.799892	8
5	**949.427022**	475.217149	932.400473	466.703875	931.416457	466.211867	Y	***801.377747***	401.192512	784.351198	392.679237	783.367182	392.187229	7
6	1020.464136	510.735706	1003.437587	502.222432	1002.453571	501.730424	A	***638.314418***	319.660847	621.287869	311.147573	620.303853	310.655565	6
7	**1091.501250**	546.254263	1074.474701	537.740989	1073.490685	537.248981	A	***567.277304***	284.142290	550.250755	275.629016	549.266739	275.137008	5
8	1254.564579	627.785928	1237.538030	619.272653	1236.554014	618.780645	Y	***496.240190***	248.623733	479.213641	240.110459	478.229625	239.618451	4
9	1311.586043	656.296660	1294.559494	647.783385	1293.575478	647.291377	G	333.176861	167.092069	316.150312	158.578794	315.166296	158.086786	3
10	1440.628636	720.817956	1423.602087	712.304682	1422.618071	711.812674	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VCSQYAAYGEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.9	1585.726868	0.006920	VCSQYAAYGEK
18.2	1585.744614	-0.010826	MSVNYAAGLSPYADK
1.9	1585.747986	-0.014198	MKMGQEFVESKEK

Mascot: http://www.matrixscience.com/

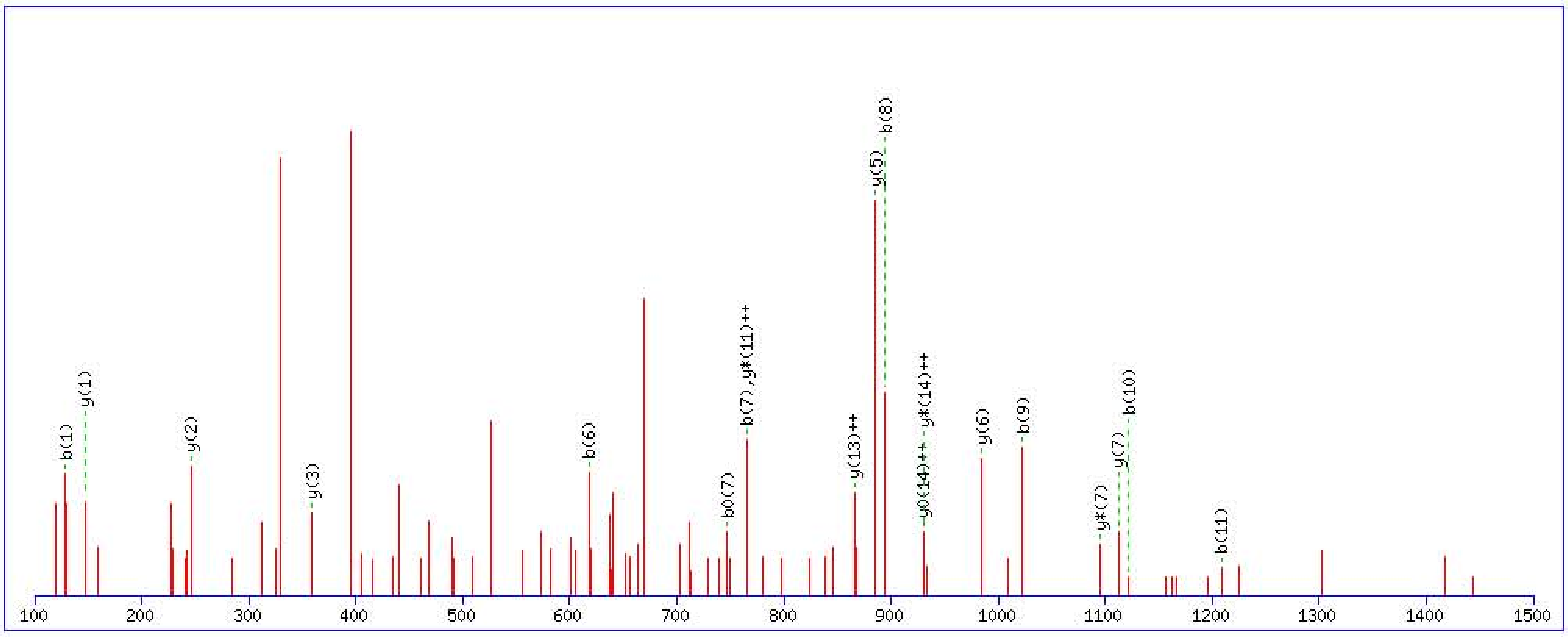
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KFPSGTFEQVSQLVK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

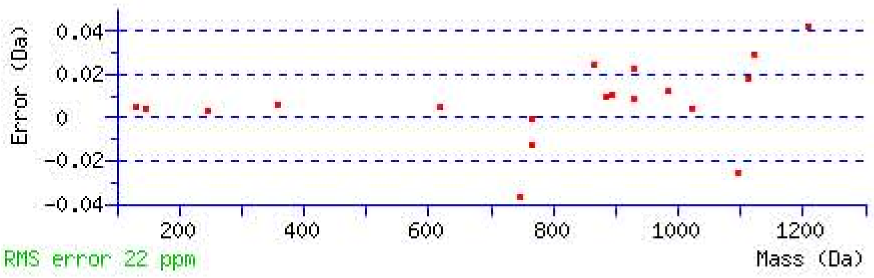
Match to Query 50938: 2005.087182 from(669.369670,3+) rtinseconds(2228) index(80469)
Title: Locus:1.1.1.2126.14 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

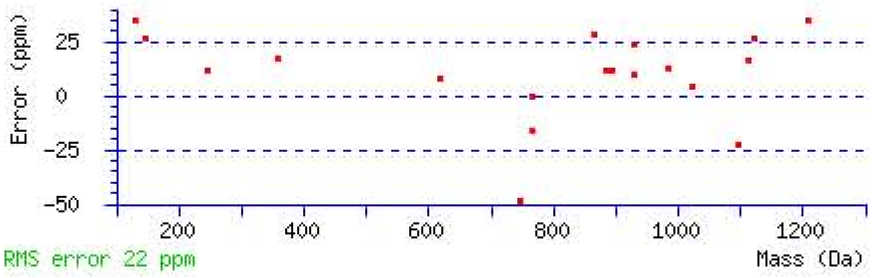
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2005.070679
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0076
Matches : 20/154 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	***129.102239***	65.054757	112.075690	56.541483			K							15
2	276.170653	138.588964	259.144104	130.075690			F	1877.982984	939.495130	1860.956435	930.981856	1859.972419	930.489848	14
3	373.223417	187.115346	356.196868	178.602072			P	1730.914570	865.960923	1713.888021	857.447649	1712.904005	856.955641	13
4	460.255445	230.631360	443.228896	222.118086	442.244880	221.626078	S	1633.861806	817.434541	1616.835257	808.921267	1615.851241	808.429259	12
5	517.276909	259.142093	500.250360	250.628818	499.266344	250.136810	G	1546.829778	773.918527	1529.803229	765.405253	1528.819213	764.913245	11
6	***618.324588***	309.665932	601.298039	301.152658	600.314023	300.660650	T	1489.808314	745.407795	1472.781765	736.894521	1471.797749	736.402513	10
7	***765.393002***	383.200139	748.366453	374.686865	747.382437	374.194857	F	1388.760635	694.883956	1371.734086	686.370681	1370.750070	685.878673	9
8	***894.435595***	447.721436	877.409046	439.208161	876.425030	438.716153	E	1241.692221	621.349749	1224.665672	612.836474	1223.681656	612.344466	8
9	***1022.494173***	511.750725	1005.467624	503.237450	1004.483608	502.745442	Q	***1112.649628***	556.828452	1095.623079	548.315178	1094.639063	547.823170	7
10	***1121.562587***	561.284932	1104.536038	552.771657	1103.552022	552.279649	V	***984.591050***	492.799163	967.564501	484.285889	966.580485	483.793881	6
11	***1208.594615***	604.800946	1191.568066	596.287671	1190.584050	595.795663	S	***885.522636***	443.264956	868.496087	434.751682	867.512071	434.259674	5
12	1647.819941	824.413609	1630.793392	815.900334	1629.809376	815.408326	Q	798.490608	399.748942	781.464059	391.235668			4
13	1760.904005	880.955641	1743.877456	872.442366	1742.893440	871.950358	L	***359.265282***	180.136279	342.238733	171.623004			3
14	1859.972419	930.489848	1842.945870	921.976573	1841.961854	921.484565	V	***246.181218***	123.594247	229.154669	115.080973			2
15							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KFPSGTFEQVSQLVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.9	2005.070679	0.016503	KFPSGTFEQVSQLVK
8.7	2005.070679	0.016503	KFPSGTFEQVSQLVK

Mascot: http://www.matrixscience.com/

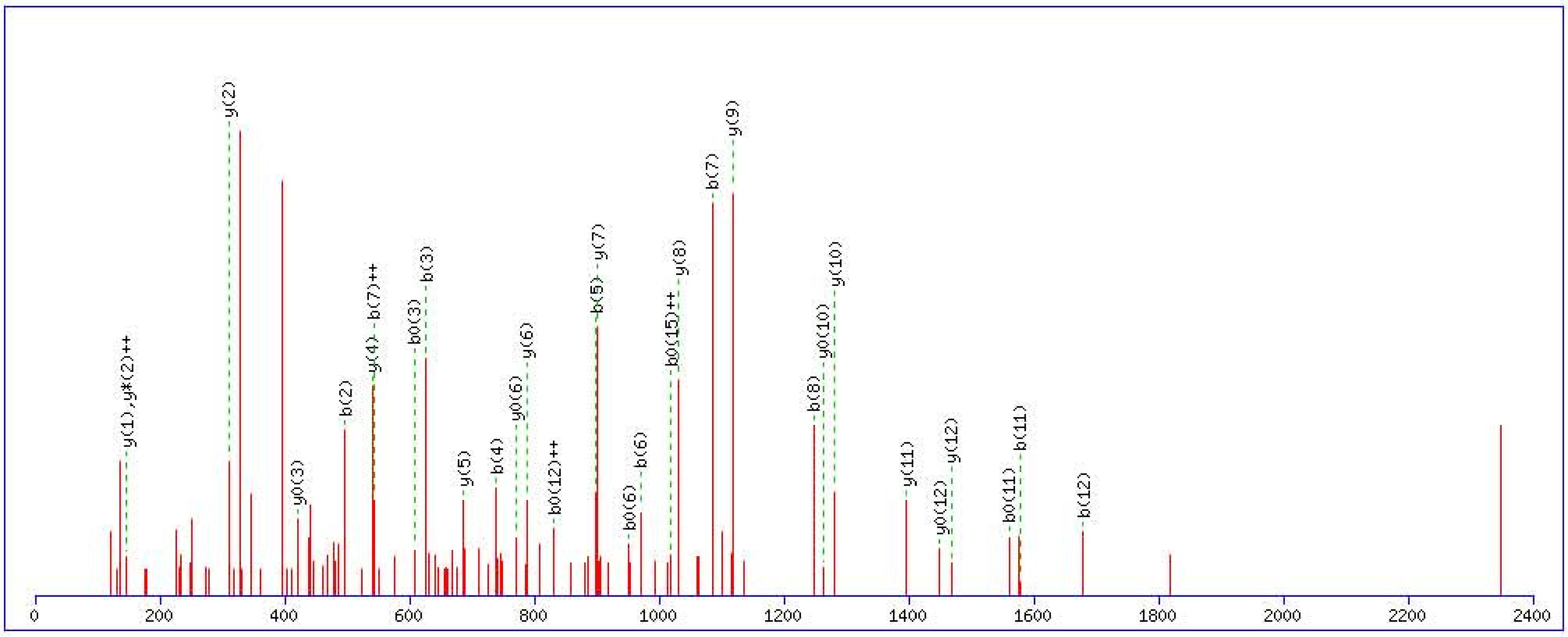
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQELCADYSENTFTEYK**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

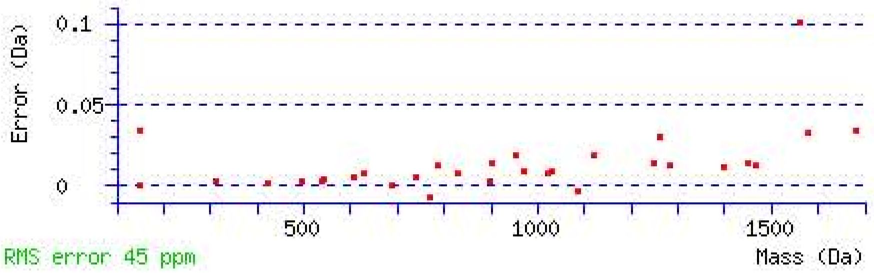
Match to Query 59312: 2365.047012 from(789.356280,3+) rtinseconds(2160) index(79957)
Title: Locus:1.1.1.2102.22 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

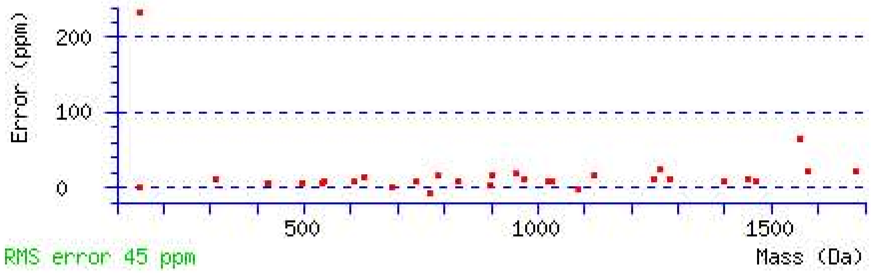
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 81 **Expect:** 4.3e-008
Matches : 31/182 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	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
81.3	2365.024231	0.022781	GQELCADYSENTFTEYK

Mascot: http://www.matrixscience.com/

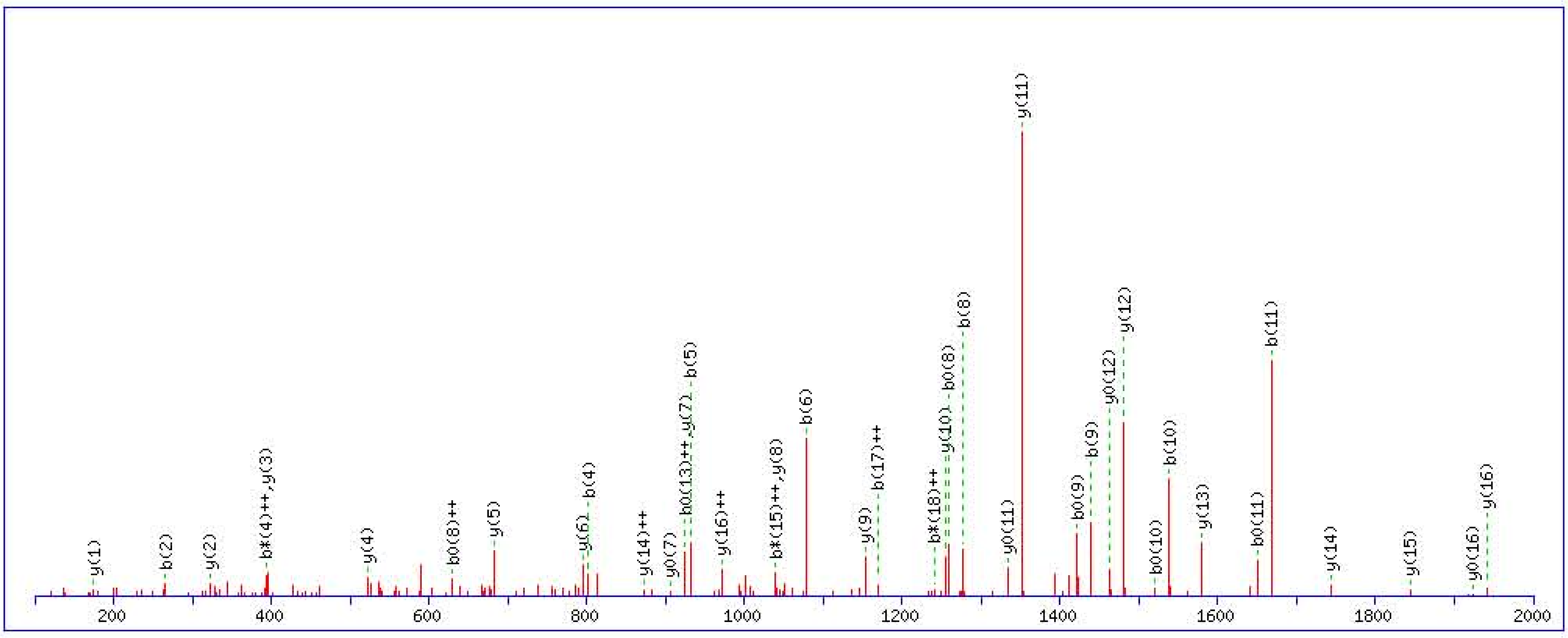
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQPQEFPTYVEPTNDEICEAFR**
Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

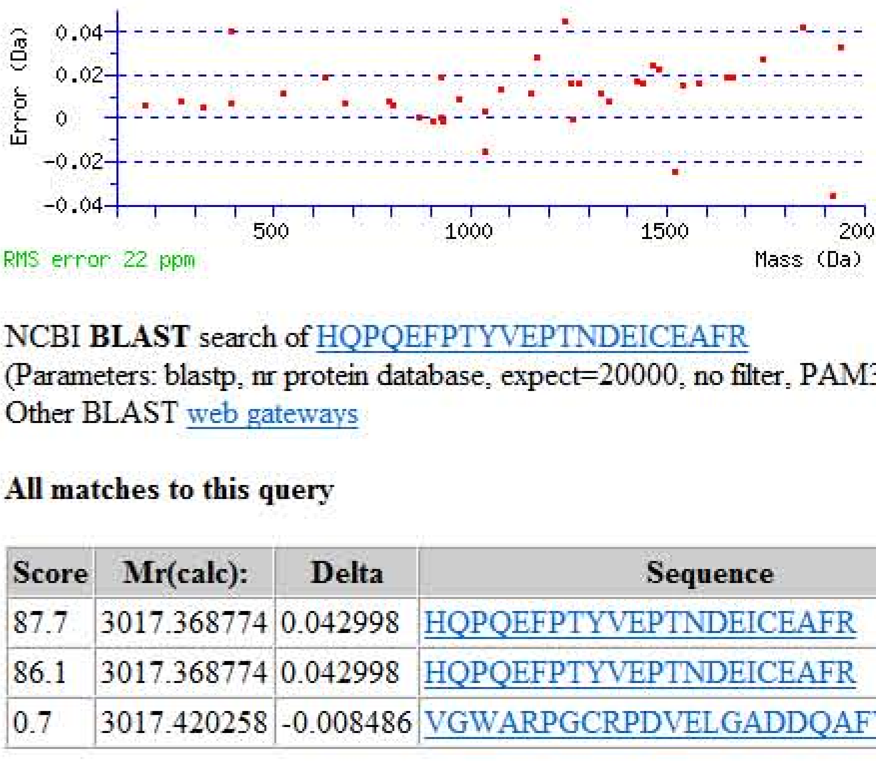
Match to Query 70546: 3017.411772 from(1006.811200,3+) rtinseconds(2329) index(81122)
Title: Locus:1.1.1.2161.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

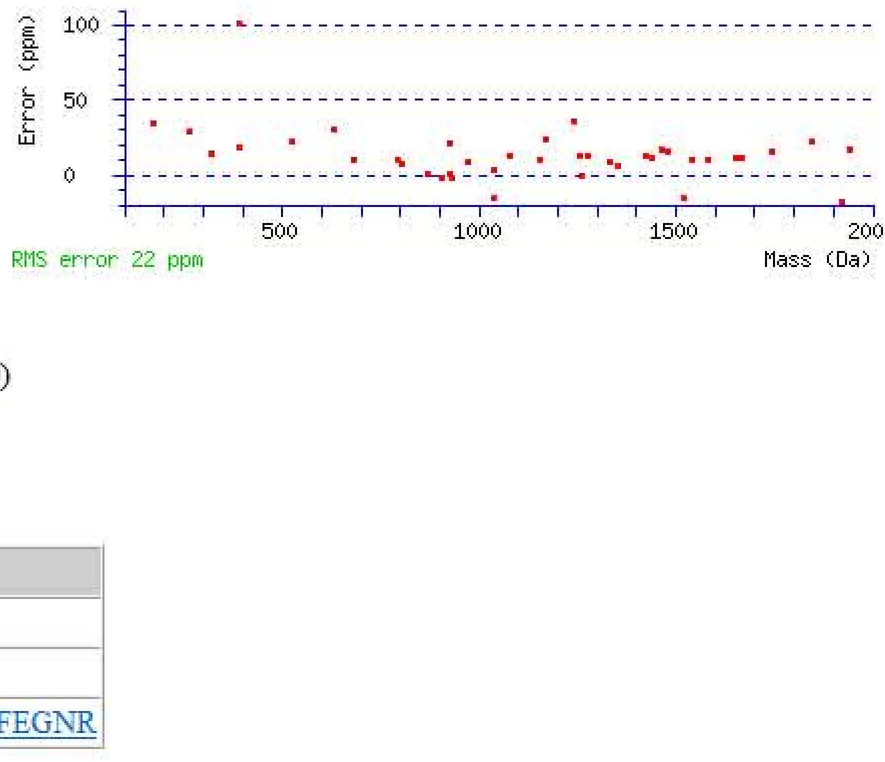
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3017.368774
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 88 **Expect:** 7e-009
Matches : 40/236 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	138.066188	69.536732					H							22
2	**266.124766**	133.566021	249.098217	125.052746			Q	2881.317146	1441.162211	2864.290597	1432.648936	2863.306581	1432.156928	21
3	363.177530	182.092403	346.150981	173.579129			P	2753.258568	1377.132922	2736.232019	1368.619647	2735.248003	1368.127639	20
4	**802.402856**	401.705066	785.376307	393.191792			Q	2656.205804	1328.606540	2639.179255	1320.093265	2638.195239	1319.601257	19
5	**931.445449**	466.226363	914.418900	457.713088	913.434884	457.221080	E	2216.980478	1108.993877	2199.953929	1100.480602	2198.969913	1099.988594	18
6	**1078.513863**	539.760570	1061.487314	531.247295	1060.503298	530.755287	F	2087.937885	1044.472580	2070.911336	1035.959306	2069.927320	1035.467298	17
7	1175.566627	588.286952	1158.540078	579.773677	1157.556062	579.281669	P	***1940.869471***	970.938374	1923.842922	962.425099	1922.858906	961.933091	16
8	**1276.614306**	638.810791	1259.587757	630.297517	1258.603741	629.805509	T	***1843.816707***	922.411992	1826.790158	913.898717	1825.806142	913.406709	15
9	**1439.677635**	720.342456	1422.651086	711.829181	1421.667070	711.337173	Y	***1742.769028***	871.888152	1725.742479	863.374878	1724.758463	862.882870	14
10	**1538.746049**	769.876663	1521.719500	761.363388	1520.735484	760.871380	V	***1579.705699***	790.356488	1562.679150	781.843213	1561.695134	781.351205	13
11	**1667.788642**	834.397959	1650.762093	825.884685	1649.778077	825.392677	E	***1480.637285***	740.822281	1463.610736	732.309006	1462.626720	731.816998	12
12	1764.841406	882.924341	1747.814857	874.411067	1746.830841	873.919059	P	***1351.594692***	676.300984	1334.568143	667.787710	1333.584127	667.295702	11
13	1865.889085	933.448181	1848.862536	924.934906	1847.878520	924.442898	T	***1254.541928***	627.774602	1237.515379	619.261328	1236.531363	618.769320	10
14	1979.932012	990.469644	1962.905463	981.956370	1961.921447	981.464362	N	***1153.494249***	577.250763	1136.467700	568.737488	1135.483684	568.245480	9
15	2094.958955	1047.983115	2077.932406	1039.469841	2076.948390	1038.977833	D	***1039.451322***	520.229299	1022.424773	511.716025	1021.440757	511.224017	8
16	2224.001548	1112.504412	2206.974999	1103.991137	2205.990983	1103.499130	E	***924.424379***	462.715828	907.397830	454.202553	906.413814	453.710545	7
17	2337.085612	1169.046444	2320.059063	1160.533170	2319.075047	1160.041162	I	***795.381786***	398.194531	778.355237	389.681257	777.371221	389.189249	6
18	2497.116261	1249.061769	2480.089712	1240.548494	2479.105696	1240.056486	C	***682.297722***	341.652499	665.271173	333.139225	664.287157	332.647217	5
19	2626.158854	1313.583065	2609.132305	1305.069791	2608.148289	1304.577783	E	***522.267073***	261.637175	505.240524	253.123900	504.256508	252.631892	4
20	2697.195968	1349.101622	2680.169419	1340.588348	2679.185403	1340.096340	A	***393.224480***	197.115878	376.197931	188.602603			3
21	2844.264382	1422.635829	2827.237833	1414.122555	2826.253817	1413.630547	F	***322.187366***	161.597321	305.160817	153.084046			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of HQPQEFPTYVEPTNDEICEAFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.7	3017.368774	0.042998	HQPQEFPTYVEPTNDEICEAFR
86.1	3017.368774	0.042998	HQPQEFPTYVEPTNDEICEAFR
0.7	3017.420258	-0.008486	VGWARPGCRPDVELGADDQAFVFEGNR

Mascot: http://www.matrixscience.com/

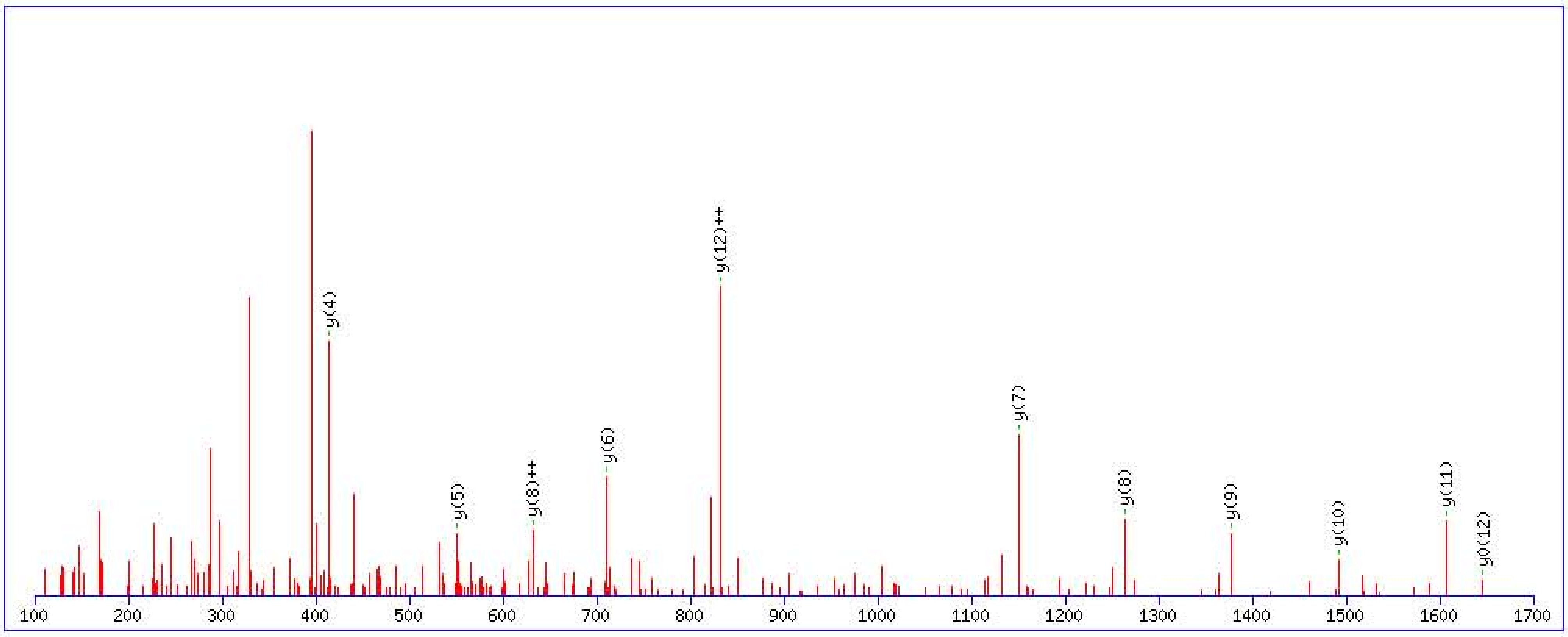
Mascot Search Results

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

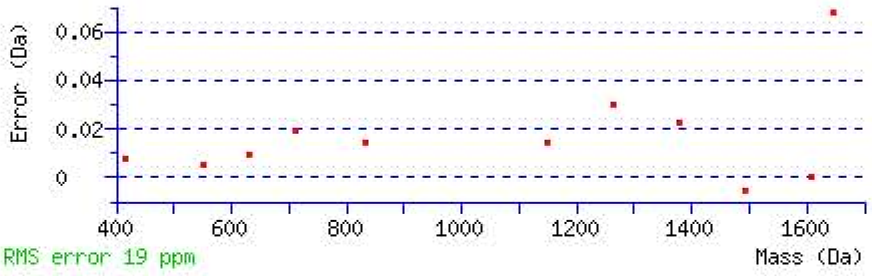
Match to Query 44686: 1775.930352 from(592.984060,3+) rtinseconds(1945) index(60388)
Title: Locus:1.1.1.3100.14 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

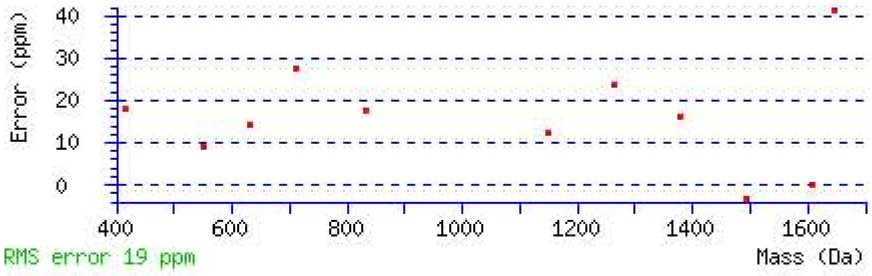
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 57  Expect: 4.5e-006
Matches : 11/110 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
57.3	1775.906250	0.024102	LGDDLLQCHPAVK
0.2	1775.935852	-0.005500	KRSPYNYLQVAYFK

Mascot: http://www.matrixscience.com/

{MATRIX}
{SCIENCE}

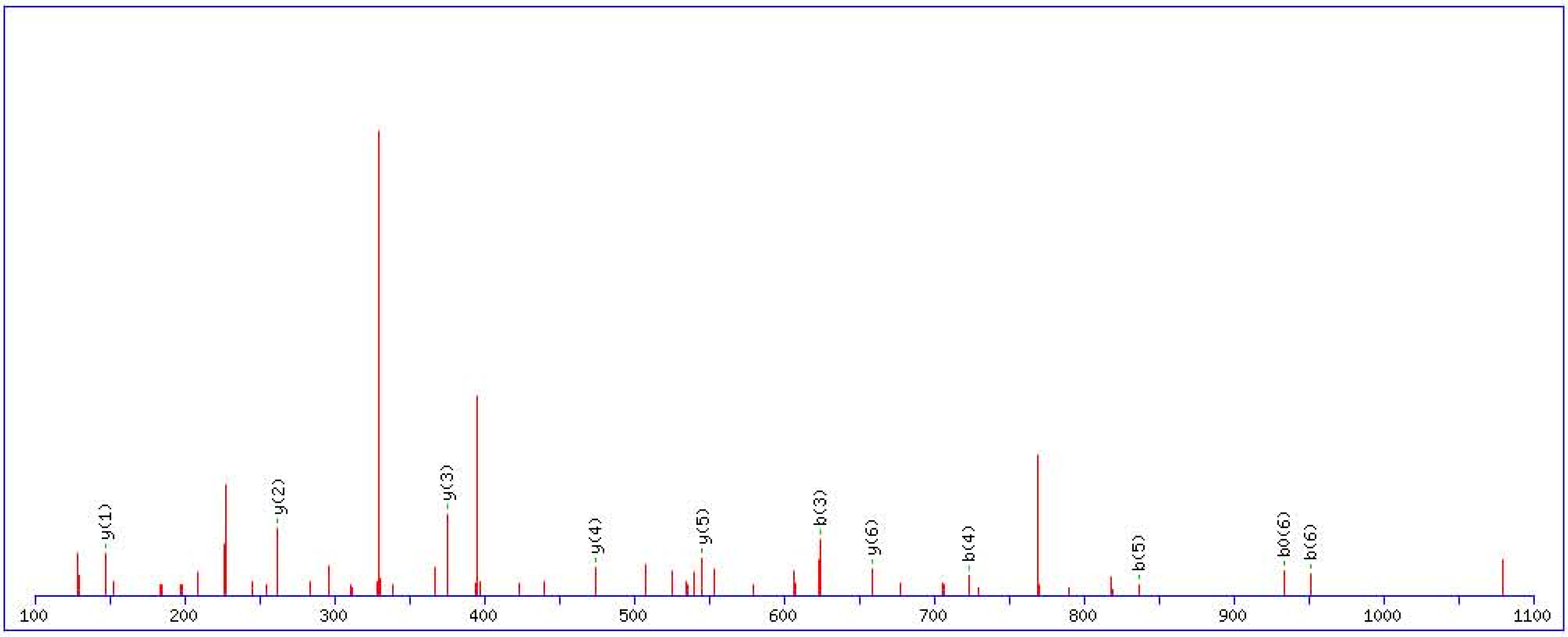
Mascot Search Results

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

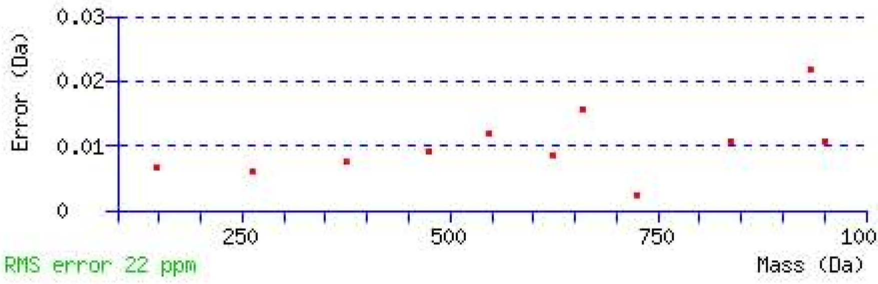
Match to Query 18865: 1096.645548 from(549.330050,2+) rtinseconds(1959) index(60506)
Title: Locus:1.1.1.3105.7 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

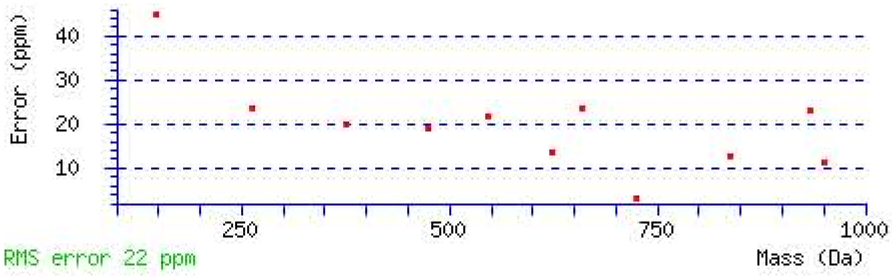
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 30  Expect: 0.01
Matches : 11/60 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	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
30.4	1096.631439	0.014109	QLAVLDK
8.6	1096.631439	0.014109	GILQLDK
7.5	1096.639297	0.006251	AHVSPLFKAK
4.5	1096.660416	-0.014868	EPVLRKDLK
3.9	1096.631439	0.014109	QIDVAIK
2.1	1096.635269	0.010279	SSSLVIHKAR
1.7	1096.660431	-0.014883	SLKVVPEGIR
1.0	1096.646500	-0.000952	KPDQARVRK

Mascot: http://www.matrixscience.com/

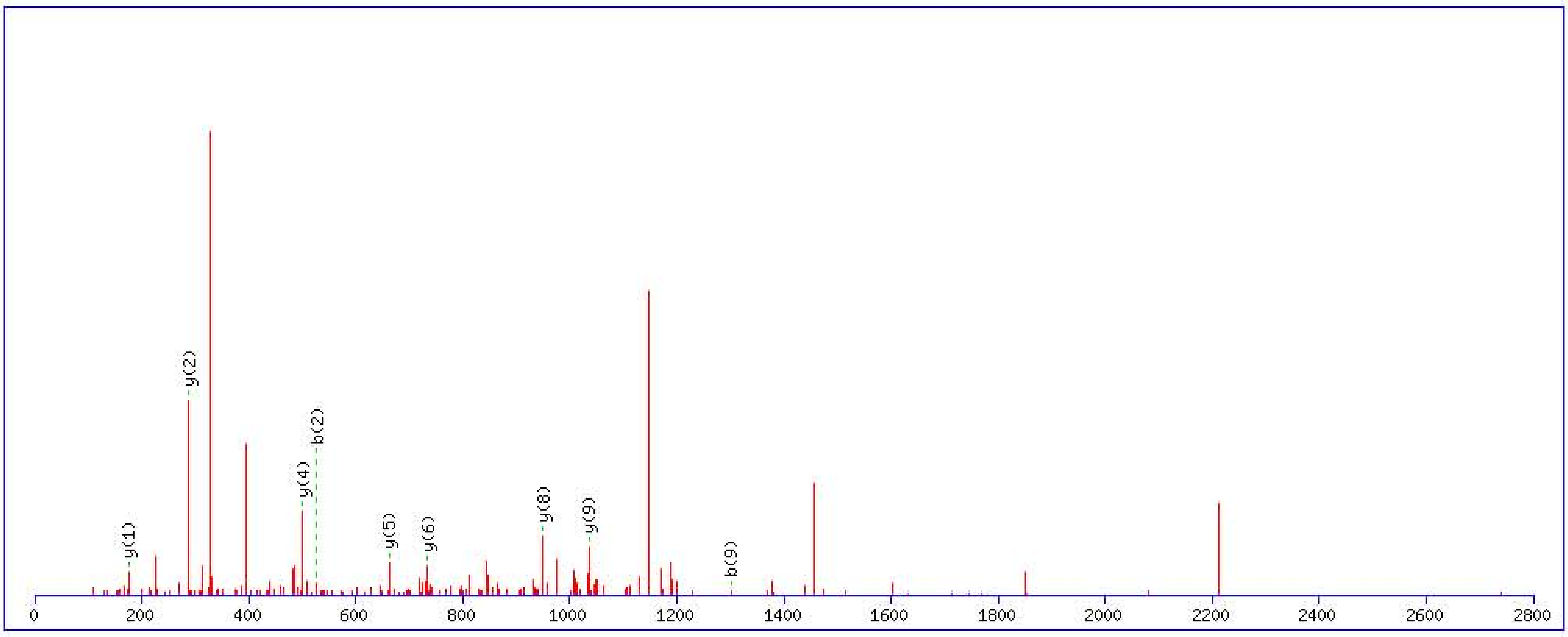
{MATRIX SCIENCE} Mascot Search Results

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

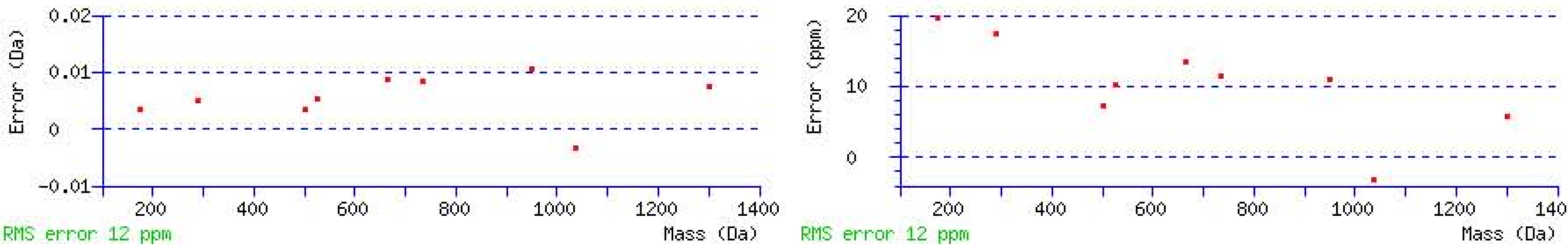
Match to Query 34119: 1474.734608 from(738.374580,2+) rtinseconds(1757) index(40488)
Title: Locus:1.1.1.3061.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1474.723831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 0.00019
Matches : 9/102 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	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	0.010777	QSTNAYPDLR
10.6	1474.741592	-0.006984	SSLEHGSDVYLLR
9.6	1474.721161	0.013447	QSTHGERGHR
9.0	1474.744934	-0.010326	LSKEELIQNMDR
6.3	1474.731033	0.003575	RGDGGKMAAAGALER
5.3	1474.746307	-0.011699	DAVQHERGPR
5.2	1474.748779	-0.014171	LQSESTNNGKNKR
4.0	1474.742462	-0.007854	QCKSEFPIR
4.0	1474.753708	-0.019100	QRPSFTCLR
2.5	1474.735092	-0.000484	GTVAPHDQSPR

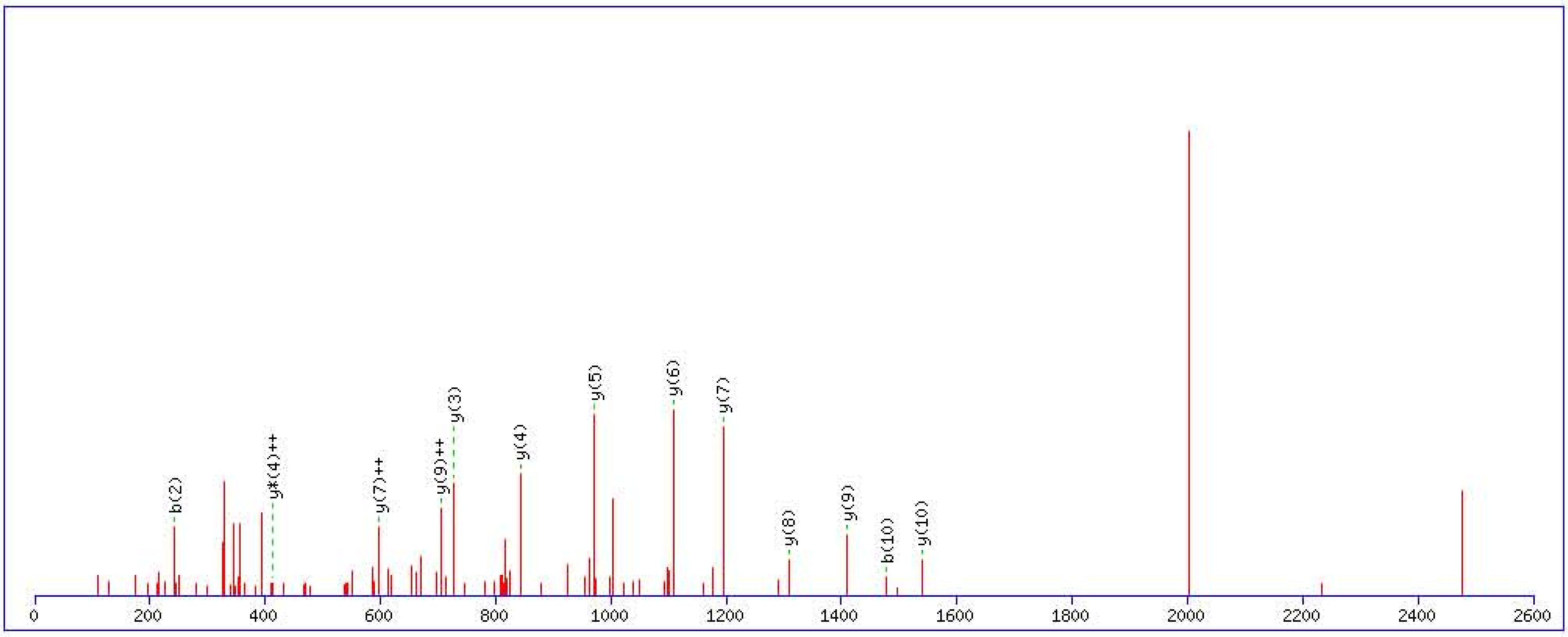
{MATRIX SCIENCE} Mascot Search Results

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

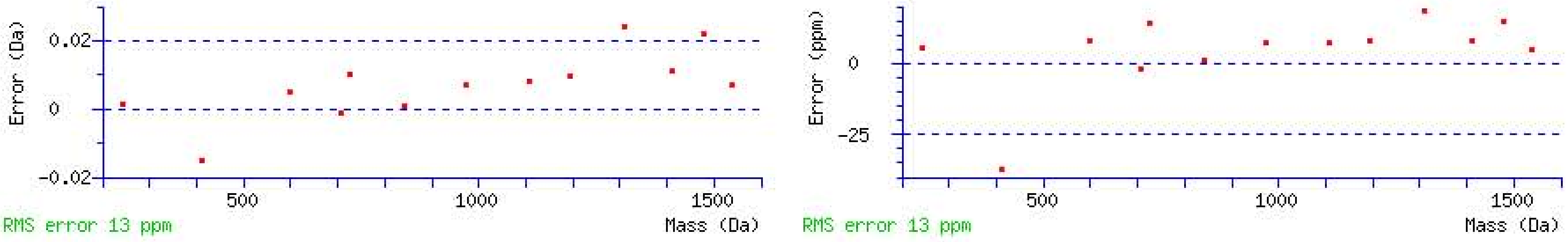
Match to Query 41217: 1650.860728 from(826.437640,2+) rtinseconds(1631) index(39647)
Title: Locus:1.1.1.3017.15 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1650.839920
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 71  Expect: 1.2e-006
Matches : 13/94 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	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
71.3	1650.839920	0.020808	IETISHEDLQR
7.9	1650.858551	0.002177	LQQEQDLR
5.5	1650.868896	-0.008168	LELLELDHEQTRR
4.9	1650.870239	-0.009511	LFRSNSHLKEHQR
3.6	1650.863037	-0.002309	NQFLPNALREFFR
2.2	1650.884171	-0.023443	NKSTLEAFRSPVFR
2.1	1650.855164	0.005564	KKEYNFLDQR

Mascot: http://www.matrixscience.com/

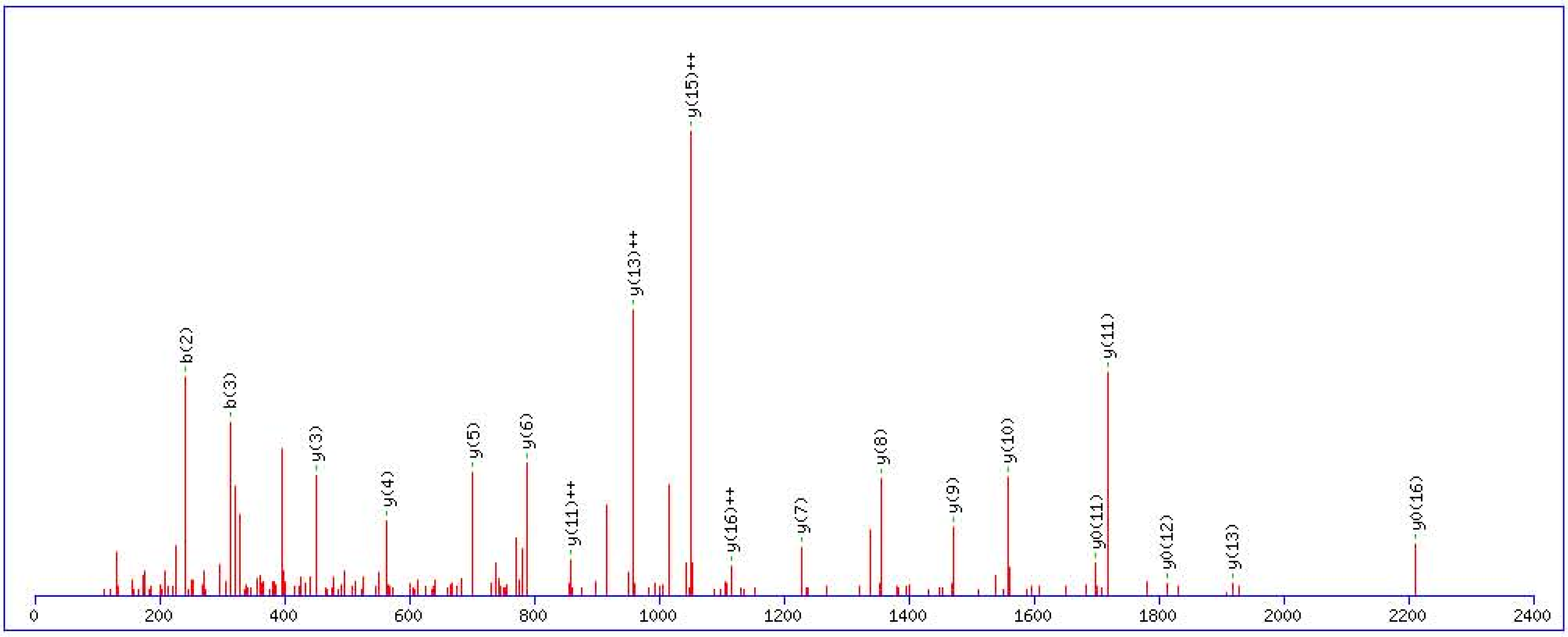
Mascot Search Results

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

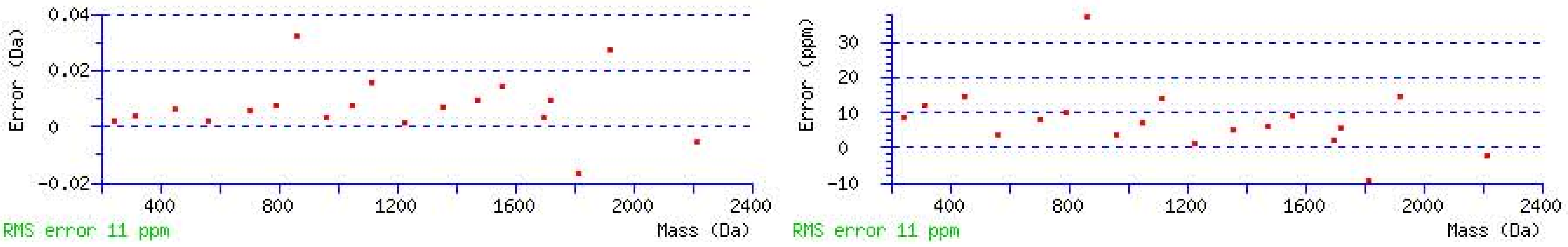
Match to Query 58967: 2342.172372 from(781.731400,3+) rtinseconds(2148) index(79860)
Title: Locus:1.1.1.2098.25 File:"2013-07-02 CLN FXIII 180 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 2342.151108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 93  Expect: 1.7e-008
Matches : 19/178 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
92.6	2342.151108	0.021264	IQALSLCSDQQSHLEFR
76.0	2342.151108	0.021264	IQALSLCSDQQSHLEFR

Mascot: http://www.matrixscience.com/

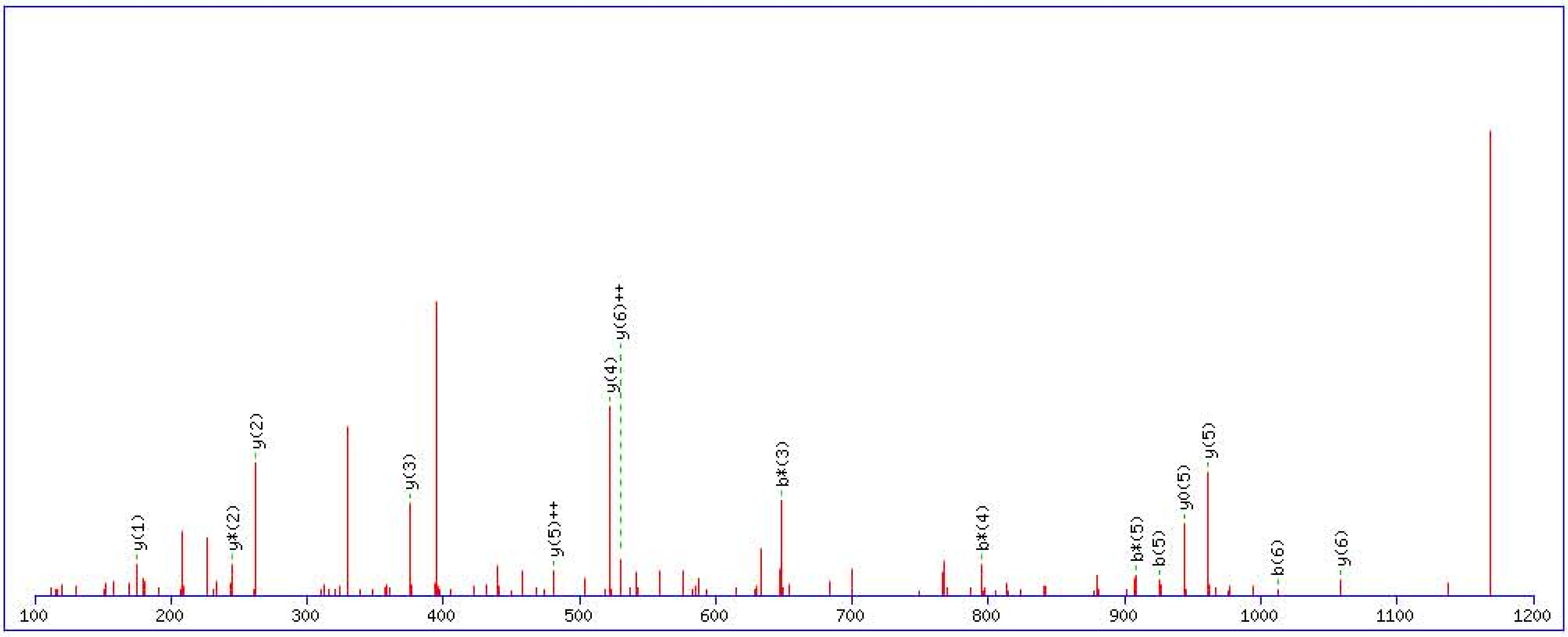
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QPQFISR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

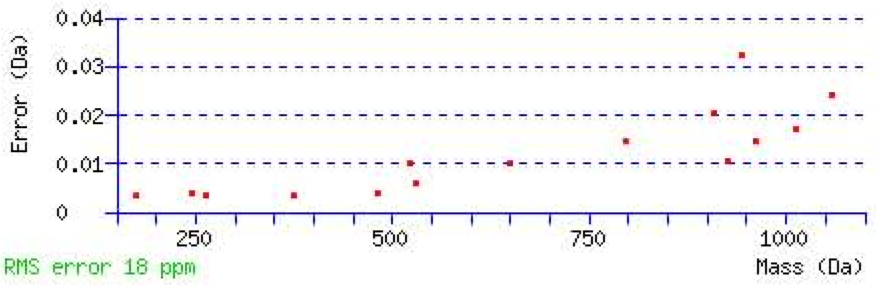
Match to Query 23311: 1185.649788 from(593.832170,2+) rtinseconds(1760) index(59049)
Title: Locus:1.1.1.3036.10 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

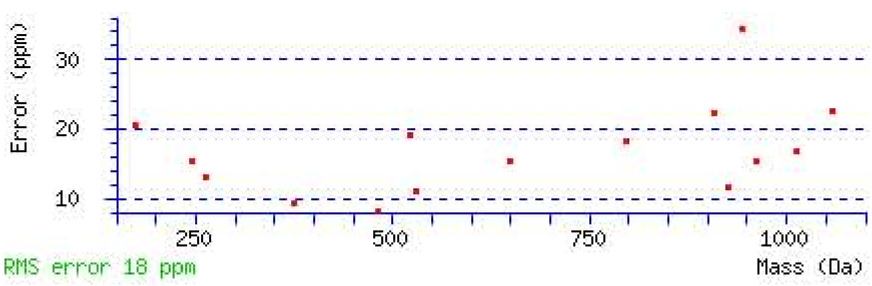
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1185.632843
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.014
Matches : 15/60 fragment ions using 31 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							7
2	226.118618	113.562947	209.092069	105.049673			P	***1058.581548***	529.794412	1041.554999	521.281138	1040.570983	520.789129	6
3	665.343944	333.175610	648.317395	324.662336			Q	***961.528784***	481.268030	944.502235	472.754755	943.518219	472.262747	5
4	812.412358	406.709817	795.385809	398.196543			F	***522.303458***	261.655367	505.276909	253.142092	504.292893	252.650084	4
5	**925.496422**	463.251849	908.469873	454.738575			I	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
6	**1012.528450**	506.767863	995.501901	498.254589	994.517885	497.762581	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 QPQFISR
(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	1185.632843	0.016945	QPQFISR
18.5	1185.646561	0.003227	KPIDSLRDSR
13.5	1185.632843	0.016945	QPQFISR
10.5	1185.653961	-0.004173	LSGALPLCLSR
7.0	1185.636200	0.013588	QIAAVMSR
5.8	1185.657806	-0.008018	RLRLVDGDSR
4.9	1185.650604	-0.000816	KPVTENVPFR
4.8	1185.653946	-0.004158	NMEIPKGLIR
4.6	1185.646561	0.003227	APSAKKPSTGSR
4.4	1185.653976	-0.004188	TQITLGSR

Mascot: http://www.matrixscience.com/

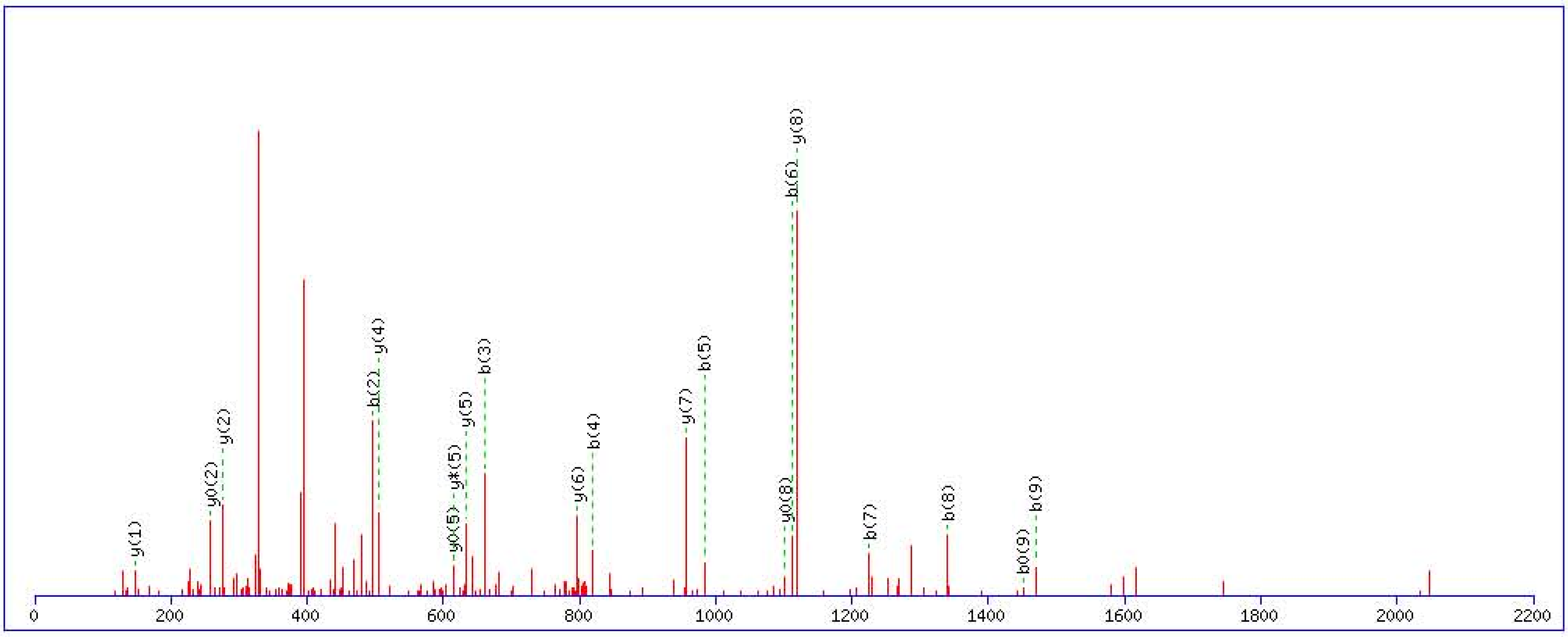
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQYCYELDEK**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

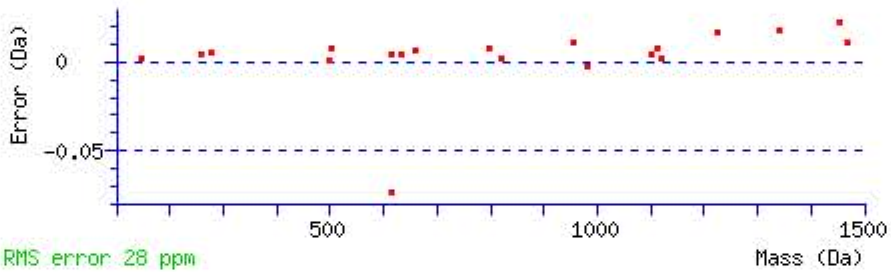
Match to Query 39359: 1614.728188 from(808.371370,2+) rtinseconds(1861) index(41099)
Title: Locus:1.1.1.3097.14 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

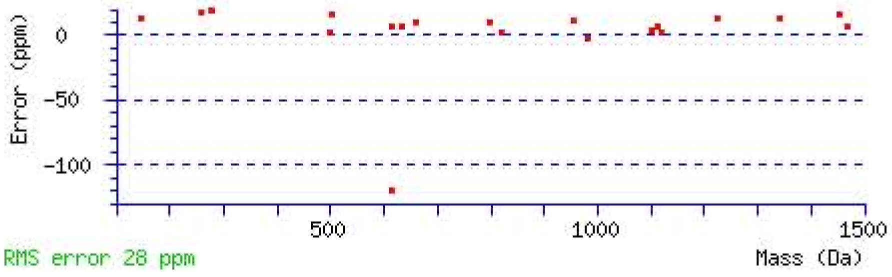
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 57 **Expect:** 1.1e-005
Matches : 20/94 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							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
57.4	1614.705795	0.022393	GQYCYELDEK
10.9	1614.748520	-0.020332	TRAPAEEGAEGPSDTK
7.1	1614.717010	0.011178	EYFRMELMHAEK
4.8	1614.738129	-0.009941	EKAKADAECYTAMK
3.3	1614.738174	-0.009986	MDSCIEAFGTTKQK
1.3	1614.748535	-0.020347	VDNSSLTGESEPQPR
1.1	1614.748489	-0.020301	EPGNSALEEREQEK
0.6	1614.738174	-0.009986	KFCNETDVSQMLK

Mascot: http://www.matrixscience.com/

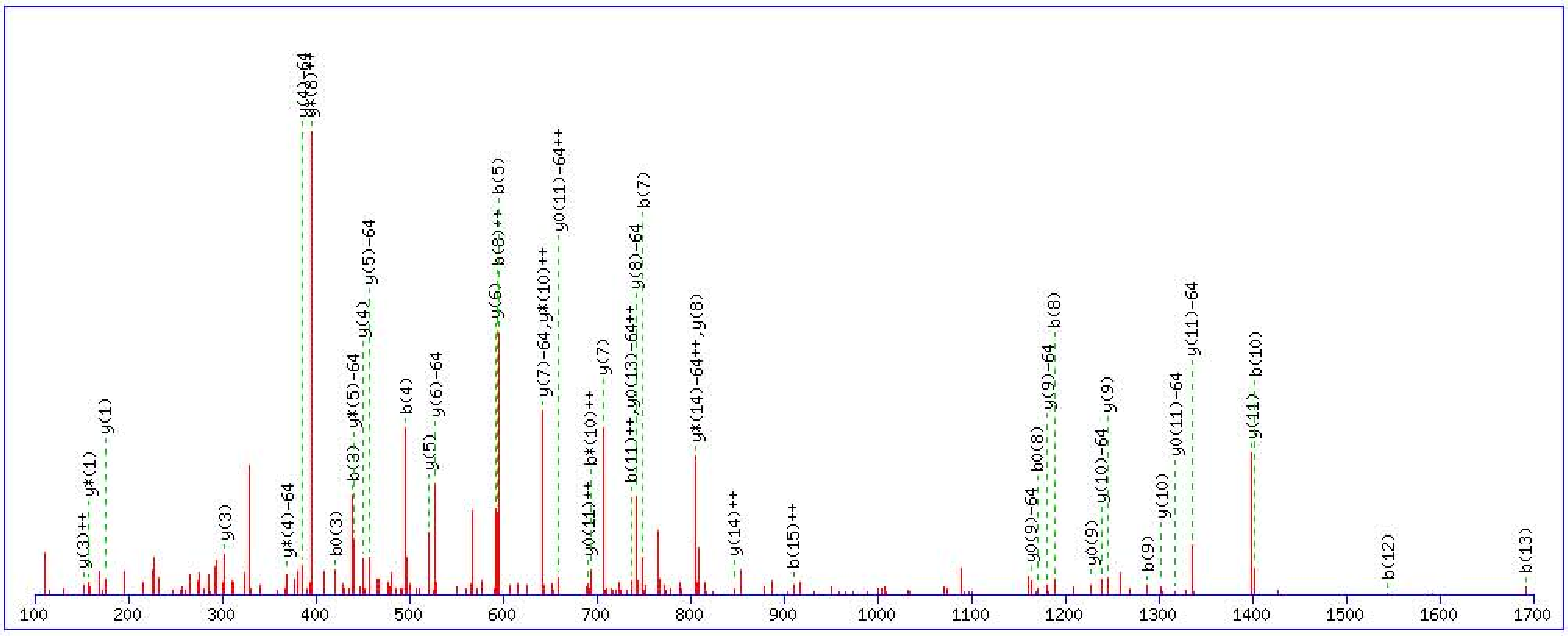
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DWHGVPGQVDAAMAGR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

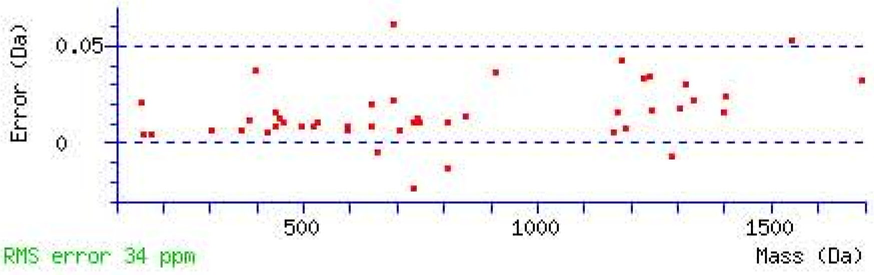
Match to Query 49704: 1992.957522 from(665.326450,3+) rtinseconds(1928) index(60240)
Title: Locus:1.1.1.3094.16 File:"2013-07-02 CLN FXIII 180 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

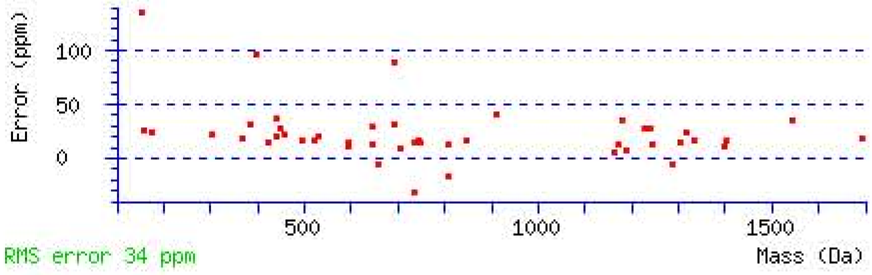
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1992.929855
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
M13     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 40  Expect: 0.0002
Matches : 47/238 fragment ions using 94 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	302.113532	151.560404			284.102967	142.555122	W	1878.910172	939.958724	1861.883623	931.445450	1860.899607	930.953441	15
3	***439.172444***	220.089860			421.161879	211.084577	H	1692.830859	846.919067	1675.804310	838.405793	1674.820294	837.913785	14
4	***496.193908***	248.600592			478.183343	239.595309	G	1555.771947	778.389612	1538.745398	769.876337	1537.761382	769.384329	13
5	***595.262322***	298.134799			577.251757	289.129517	V	1498.750483	749.878880	1481.723934	741.365605	1480.739918	740.873597	12
6	692.315086	346.661181			674.304521	337.655899	P	***1399.682069***	700.344673	1382.655520	691.831398	1381.671504	691.339390	11
7	***749.336550***	375.171913			731.325985	366.166631	G	***1302.629305***	651.818290	1285.602756	643.305016	1284.618740	642.813008	10
8	***1188.561876***	**594.784576**	1171.535327	586.271302	1170.551311	585.779293	Q	***1245.607841***	623.307558	1228.581292	614.794284	1227.597276	614.302276	9
9	***1287.630290***	644.318783	1270.603741	635.805509	1269.619725	635.313501	V	***806.382515***	403.694896	789.355966	395.181621	788.371950	394.689613	8
10	***1402.657233***	701.832255	1385.630684	693.318980	1384.646668	692.826972	D	***707.314101***	354.160688	690.287552	345.647414	689.303536	345.155406	7
11	1473.694347	**737.350812**	1456.667798	728.837537	1455.683782	728.345529	A	***592.287158***	296.647217	575.260609	288.133942			6
12	***1544.731461***	772.869369	1527.704912	764.356094	1526.720896	763.864086	A	***521.250044***	261.128660	504.223495	252.615385			5
13	***1691.766861***	846.387069	1674.740312	837.873794	1673.756296	837.381786	M	***450.212930***	225.610103	433.186381	217.096828			4
14	1762.803975	881.905626	1745.777426	873.392351	1744.793410	872.900343	A	***303.177530***	152.092403	286.150981	143.579128			3
15	1819.825439	**910.416358**	1802.798890	901.903083	1801.814874	901.411075	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
39.9	1992.929855	0.027667	DWHGVPGQVDAAMAGR
0.4	1992.973892	-0.016370	RTHTFNSGEARPGDRHR

Mascot: http://www.matrixscience.com/

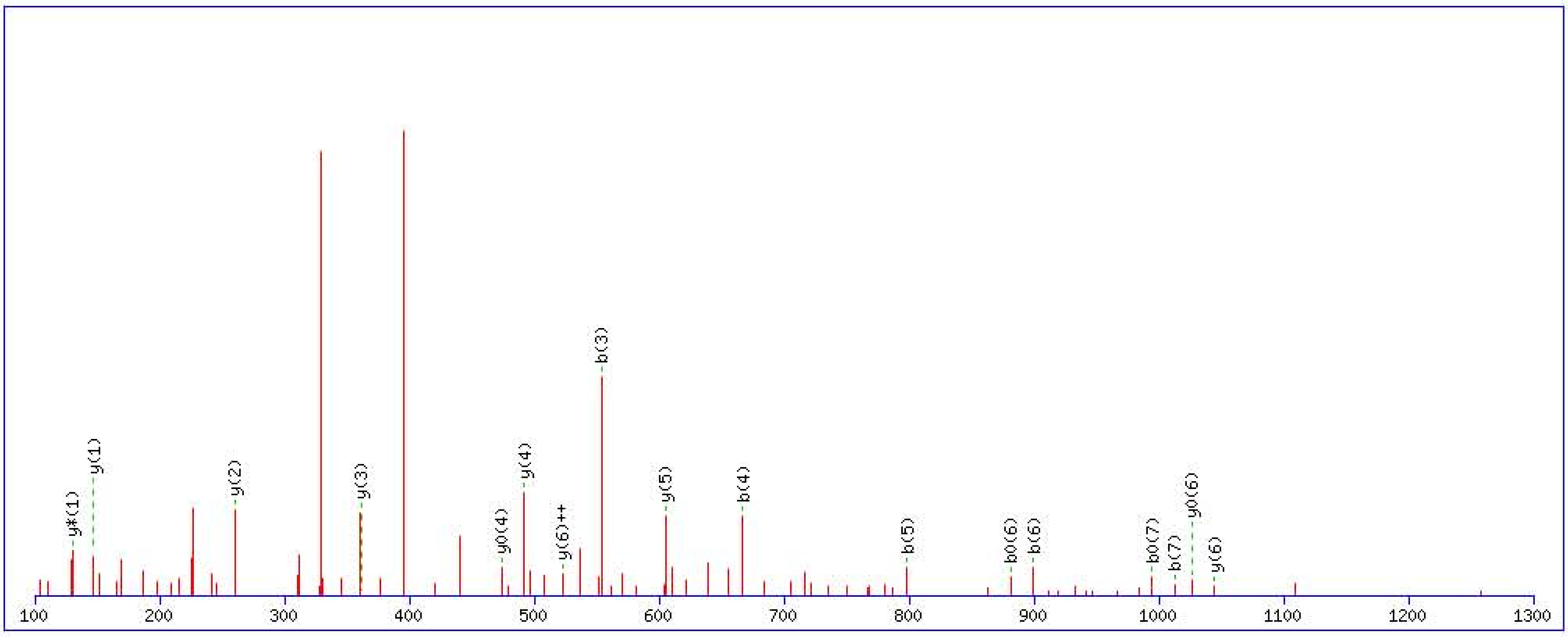
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGQIMTLK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

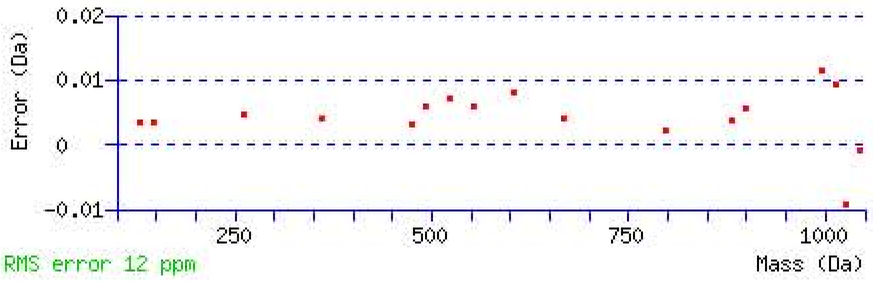
Match to Query 22101: 1157.641928 from(579.828240,2+) rtinseconds(1906) index(41483)
Title: Locus:1.1.1.3113.13 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

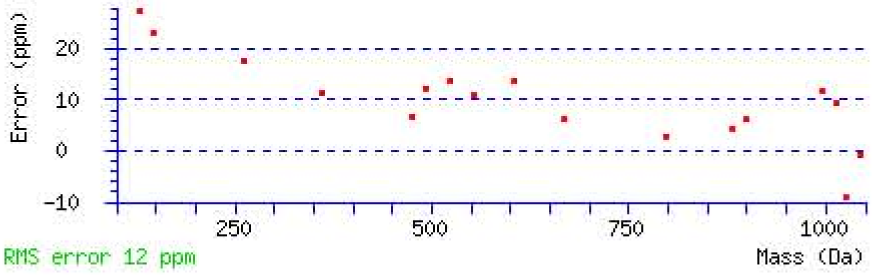
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1157.630066
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.024
Matches : 17/66 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							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
30.2	1157.630066	0.011862	GGQIMTLK
14.3	1157.630051	0.011877	QLSQMLK
11.6	1157.647827	-0.005899	ALVGGTAPMTIK
9.9	1157.640411	0.001517	SPGKNSSIQLK
7.7	1157.647827	-0.005899	IMVPINGSVTK
6.2	1157.640411	0.001517	AQQLLSSGNLK
5.9	1157.636566	0.005362	ILVEEMAPLK
5.9	1157.629196	0.012732	EPQTITQLTK
5.2	1157.630081	0.011847	CVTLVQK
4.2	1157.636566	0.005362	LLAIMPDELK

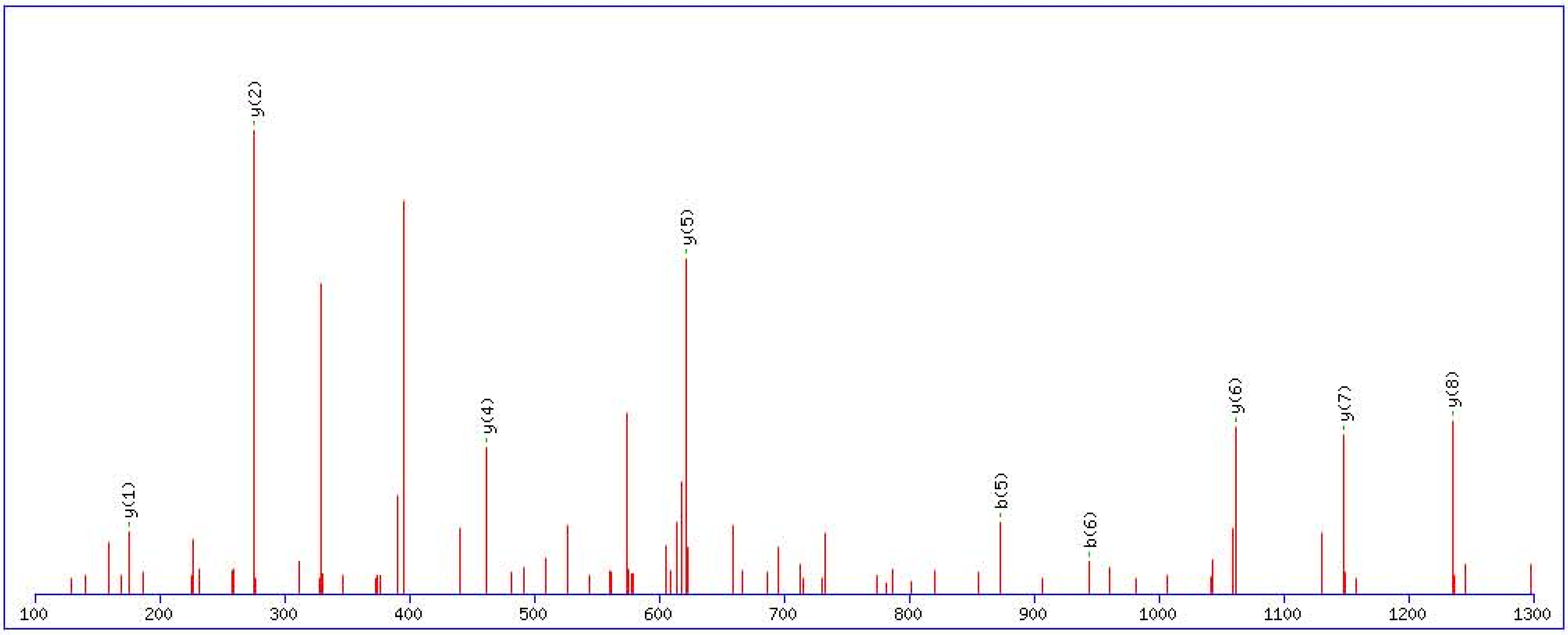
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSQCADTR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

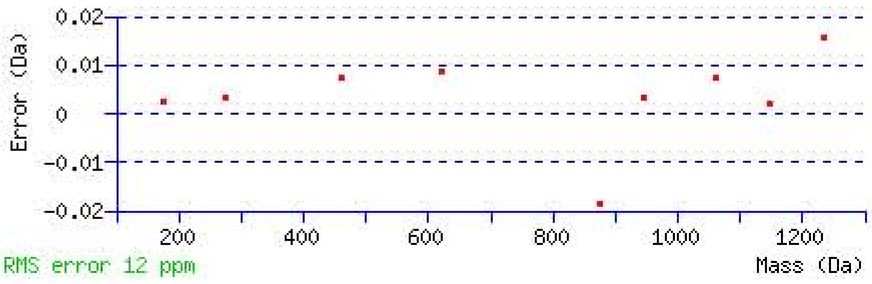
Match to Query 27657: 1333.624628 from(667.819590,2+) rtinseconds(1259) index(37085)
Title: Locus:1.1.1.2887.23 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

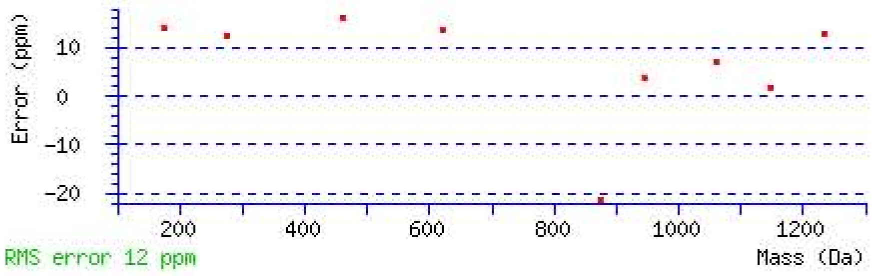
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1333.611862
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 61 **Expect:** 1e-005
Matches : 9/86 fragment ions using 12 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
61.2	1333.611862	0.012766	VSSQCADTR
9.2	1333.633606	-0.008978	LIYNTHMADEK
5.1	1333.636108	-0.011480	VSEEKEVTEER
3.2	1333.636993	-0.012365	VSPSAEMVMIDR
2.8	1333.607117	0.017511	GEIEIESDAPMK

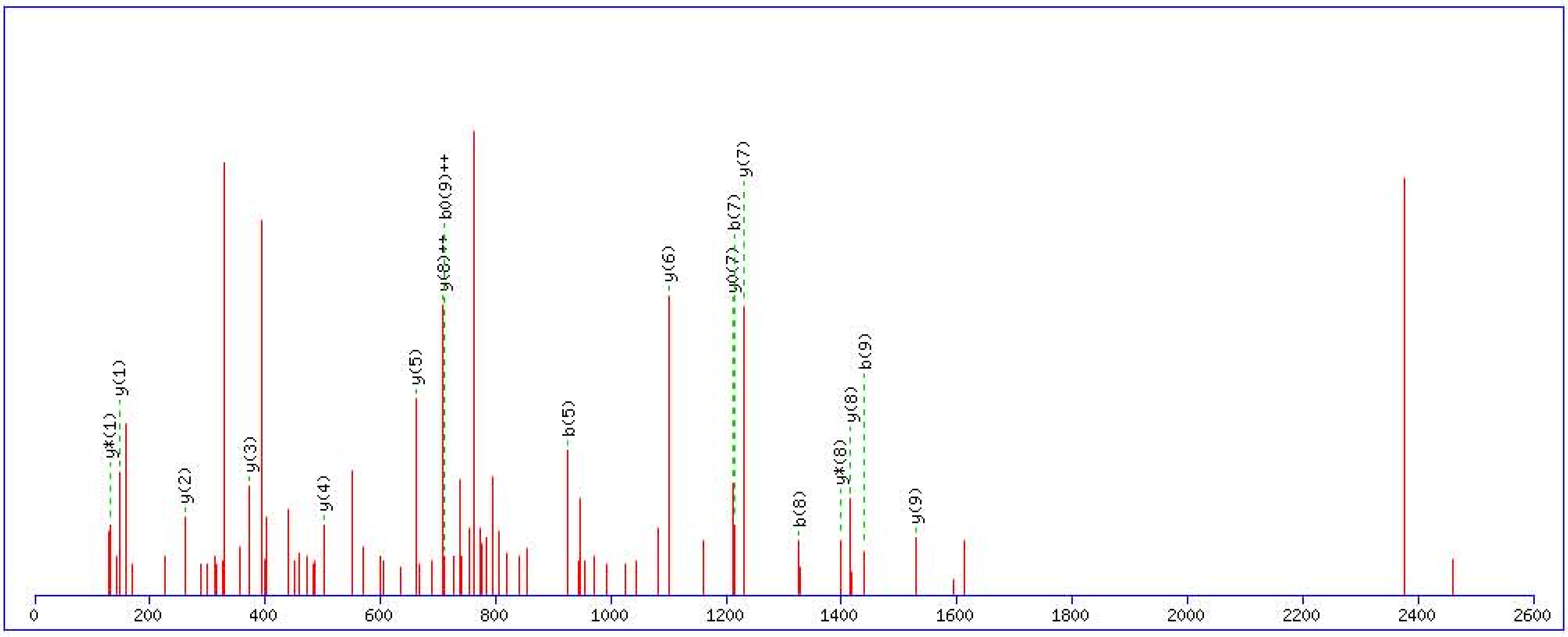
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLWEQCQLLK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

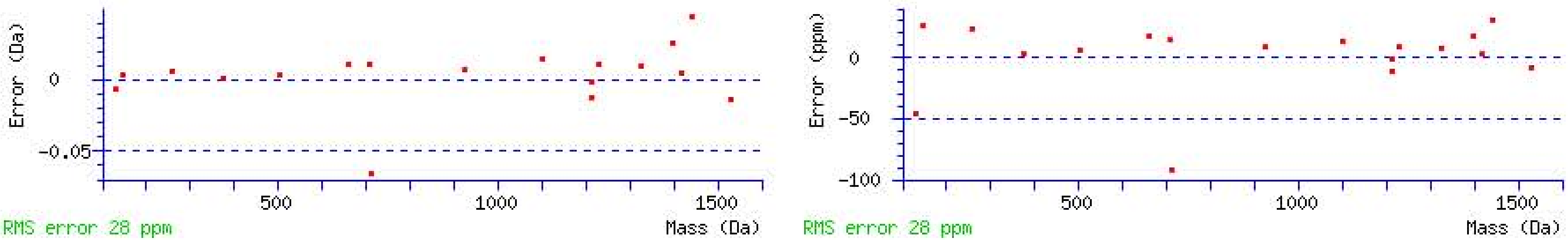
Match to Query 37980: 1584.838228 from(793.426390,2+) rtinseconds(2382) index(44891)
Title: Locus:1.1.1.3278.20 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

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): 1584.815628
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.0013
Matches : 18/82 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							10
2	171.112804	86.060040					L	***1528.801455***	764.904366	1511.774906	756.391091	1510.790890	755.899083	9
3	357.192117	179.099696					W	***1415.717391***	708.362333	1398.690842	699.849059	1397.706826	699.357051	8
4	486.234710	243.620993			468.224145	234.615711	E	***1229.638078***	615.322677	1212.611529	606.809403	1211.627513	606.317394	7
5	**925.460036**	463.233656	908.433487	454.720382	907.449471	454.228374	Q	***1100.595485***	550.801381	1083.568936	542.288106			6
6	1085.490685	543.248981	1068.464136	534.735706	1067.480120	534.243698	C	***661.370159***	331.188718	644.343610	322.675443			5
7	**1213.549263**	607.278270	1196.522714	598.764995	1195.538698	598.272987	Q	***501.339510***	251.173393	484.312961	242.660118			4
8	**1326.633327**	663.820302	1309.606778	655.307027	1308.622762	654.815019	L	***373.280932***	187.144104	356.254383	178.630829			3
9	**1439.717391**	720.362333	1422.690842	711.849059	1421.706826	711.357051	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 GLWEQCQLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.3	1584.815628	0.022600	GLWEQCQLLK
21.7	1584.815628	0.022600	GLWEQCQLLK
10.7	1584.836746	0.001482	EQVAAMQAGLLK
6.1	1584.824615	0.013613	EADETKLAEEIPLK
5.3	1584.836746	0.001482	EQVAAMQAGLLK
4.0	1584.858337	-0.020109	GAKTQAQEREVIQK
3.5	1584.818130	0.020098	VTRAFSTSMEISIK
3.0	1584.858322	-0.020094	QRNSTIEAANLAGLK
2.5	1584.858322	-0.020094	EAERASKLGQLQQK
2.0	1584.858353	-0.020125	QLDGLAGLKGEGSRGK

Mascot: http://www.matrixscience.com/

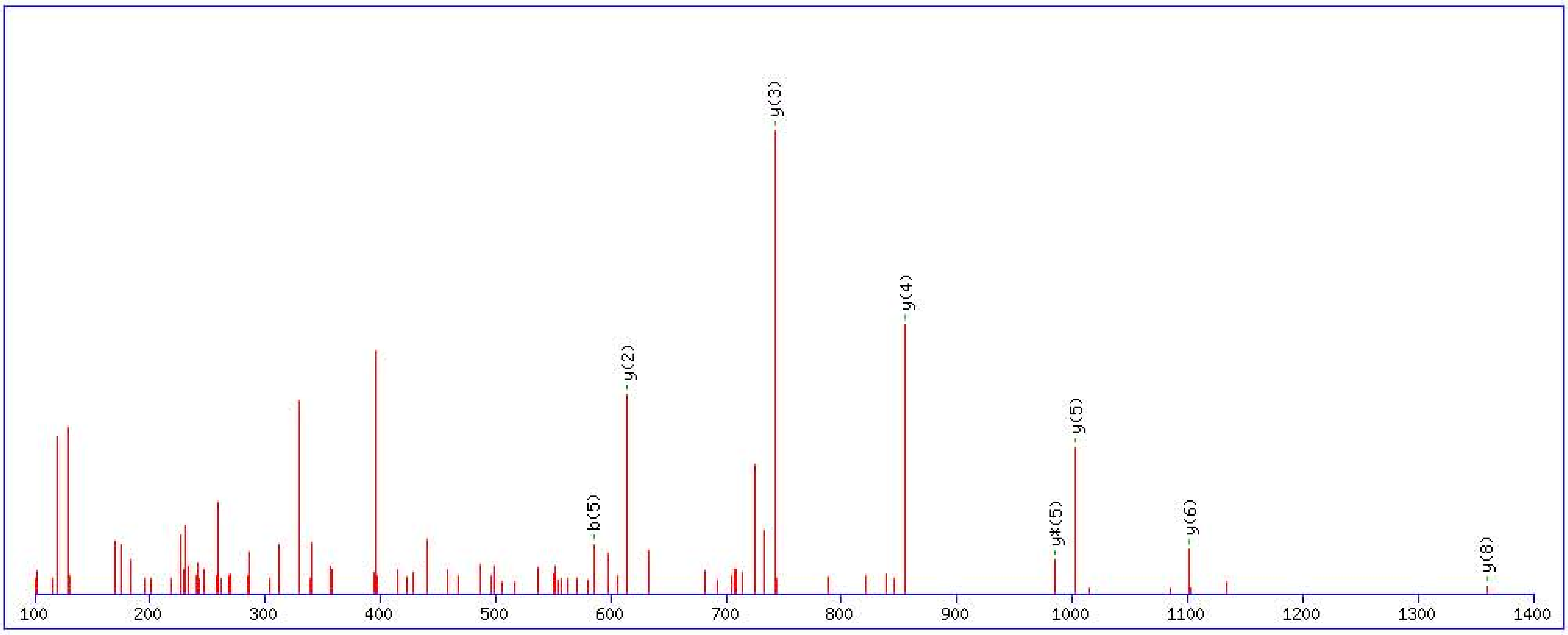
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VKEEVFIQQR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

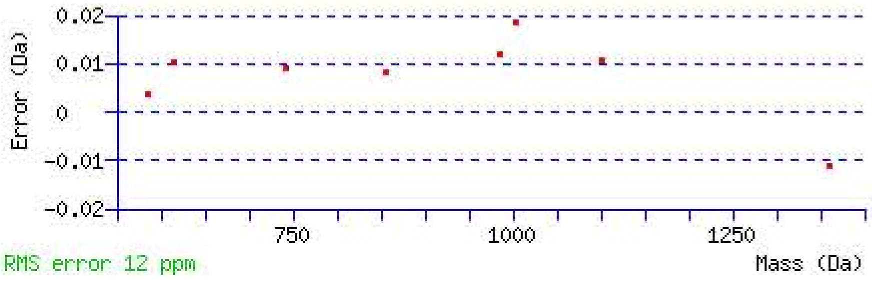
Match to Query 38034: 1585.878102 from(529.633310,3+) rtinseconds(1767) index(40564)
Title: Locus:1.1.1.3065.6 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

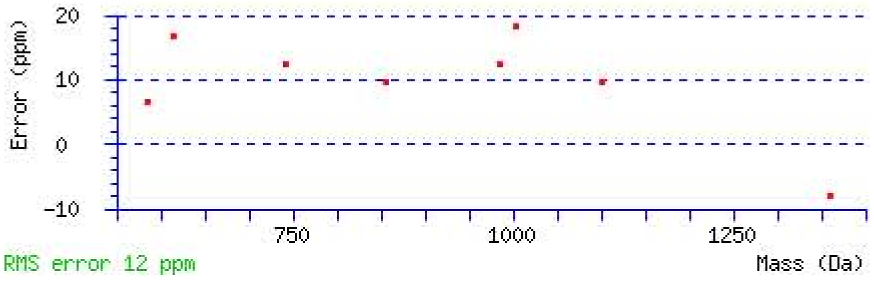
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
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: 40  Expect: 0.0011
Matches : 8/90 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							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
39.6	1585.865021	0.013081	VKEEVFIQQR
26.5	1585.865021	0.013081	VKEEVFIQQR
7.9	1585.893524	-0.015422	QDLIKSLAMLK
3.7	1585.857605	0.020497	QEEVAGIRAKFPNK

Mascot: http://www.matrixscience.com/

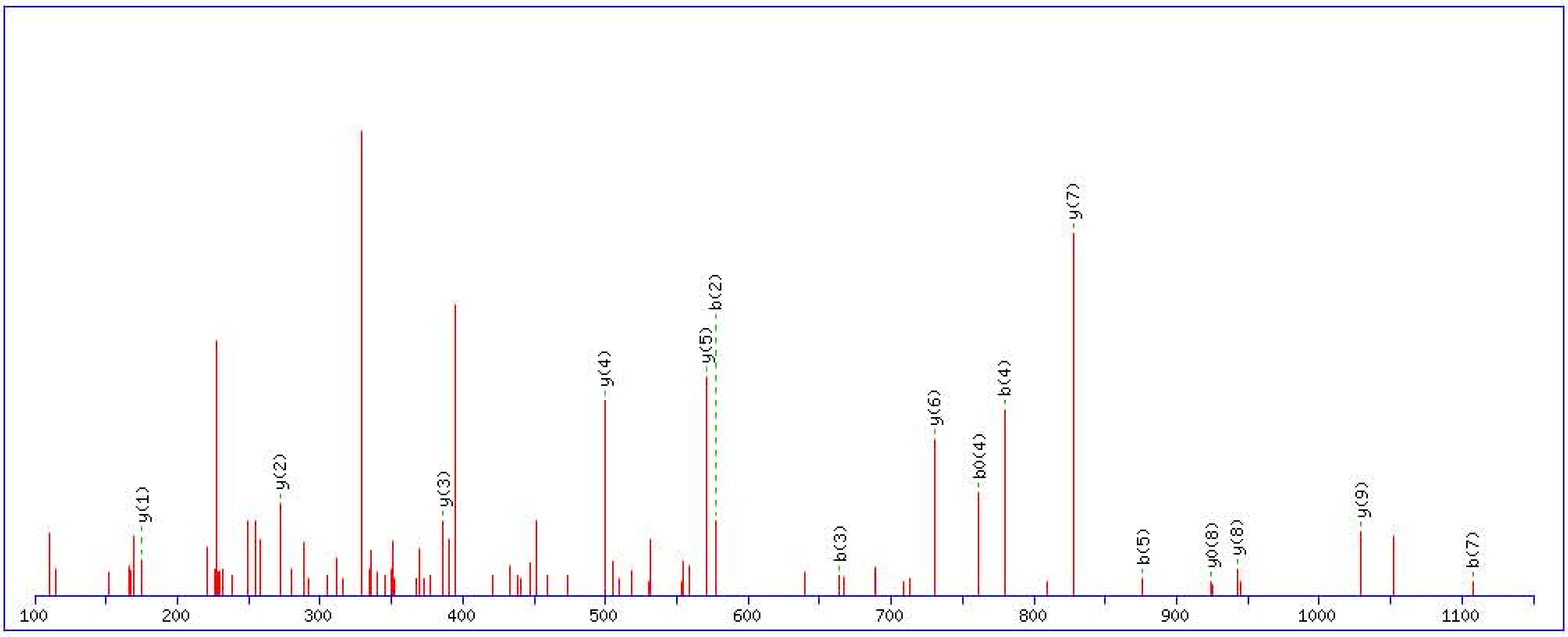
{MATRIX SCIENCE}
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QHSDPCALNPR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

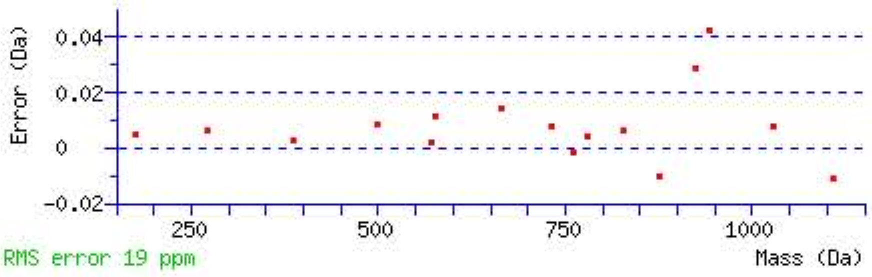
Match to Query 38908: 1604.762922 from(535.928250,3+) rtinseconds(1418) index(38115)
Title: Locus:1.1.1.2943.11 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

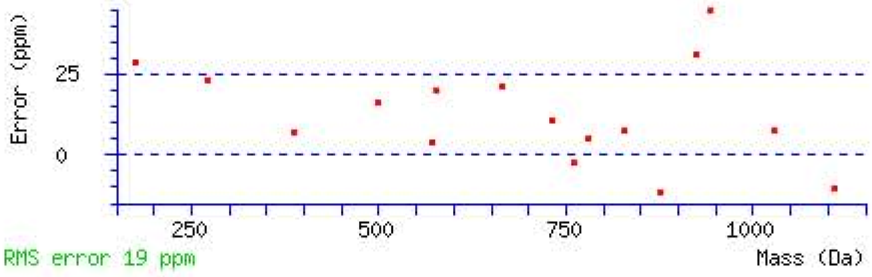
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1604.755157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 3.4e-005
Matches : 16/102 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	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
57.0	1604.755157	0.007765	QHSDPCALNPR
10.4	1604.782806	-0.019884	QEQIINTMTQDLR
4.8	1604.747070	0.015852	NGYAEFPPSPSNPTK
2.0	1604.754288	0.008634	GPSPASSSSSPPAHPR

Mascot: http://www.matrixscience.com/

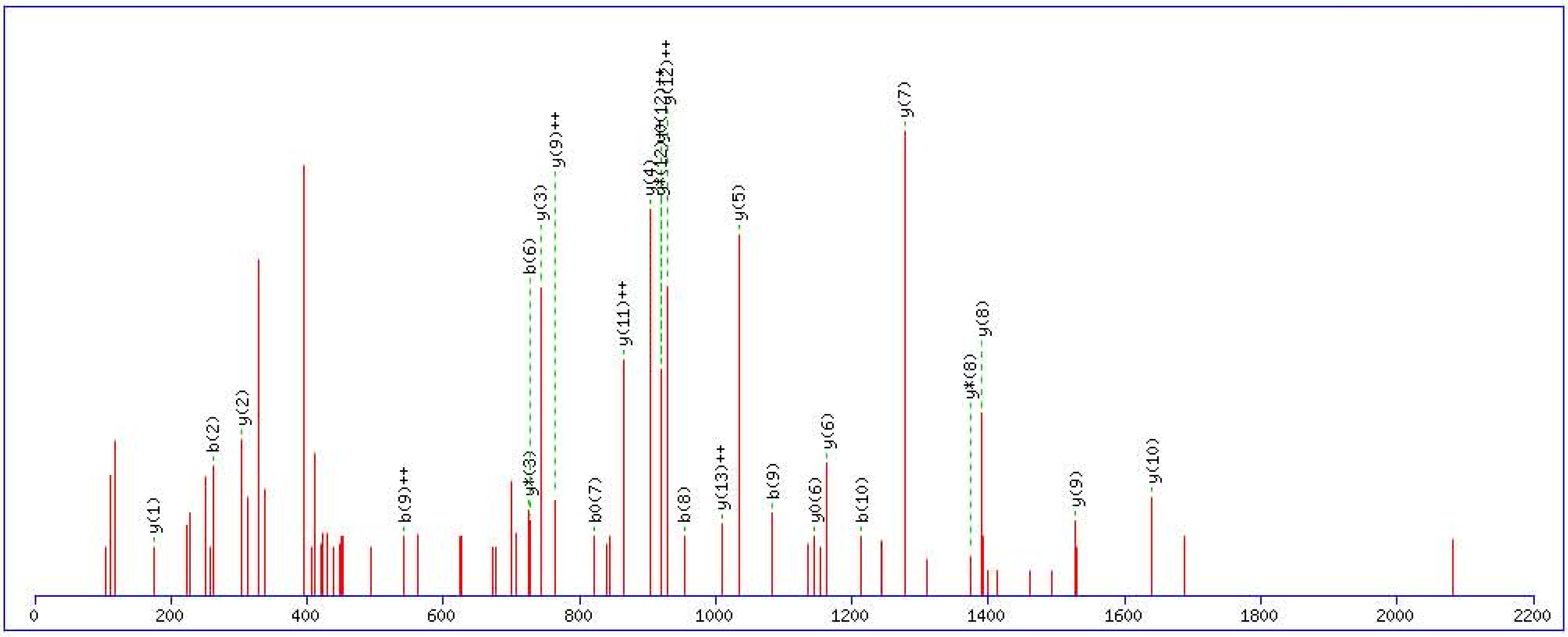
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TCQSLHINEMCQER**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

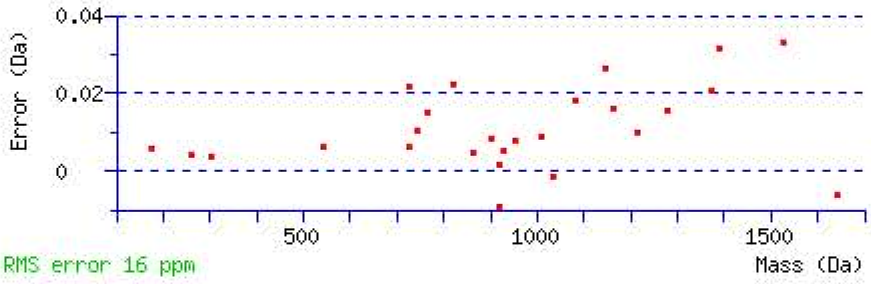
Match to Query 53432: 2115.956562 from(706.326130,3+) rtinseconds(1726) index(40235)
Title: Locus:1.1.1.3050.17 File:"2013-07-02 CLN FXIII 180 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\mascot_daemon_merge.mgf

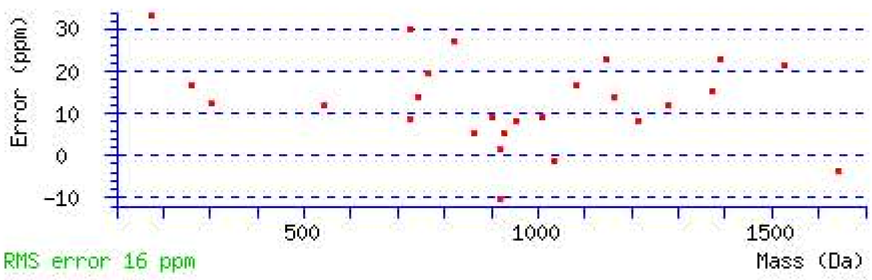
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2115.932205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00016
Matches : 26/150 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	102.054955	51.531116			84.044390	42.525833	T							14
2	**262.085604**	131.546440			244.075039	122.541158	C	2015.891820	1008.449548	1998.865271	999.936274	1997.881255	999.444266	13
3	390.144182	195.575729	373.117633	187.062455	372.133617	186.570447	Q	1855.861171	928.434224	1838.834622	919.920949	1837.850606	919.428941	12
4	477.176210	239.091743	460.149661	230.578469	459.165645	230.086461	S	1727.802593	864.404935	1710.776044	855.891660	1709.792028	855.399652	11
5	590.260274	295.633775	573.233725	287.120501	572.249709	286.628493	L	***1640.770565***	820.888921	1623.744016	812.375646	1622.760000	811.883638	10
6	**727.319186**	364.163231	710.292637	355.649957	709.308621	355.157949	H	***1527.686501***	764.346889	1510.659952	755.833614	1509.675936	755.341606	9
7	840.403250	420.705263	823.376701	412.191989	822.392685	411.699981	I	***1390.627589***	695.817433	1373.601040	687.304158	1372.617024	686.812150	8
8	**954.446177**	477.726727	937.419628	469.213452	936.435612	468.721444	N	***1277.543525***	639.275401	1260.516976	630.762126	1259.532960	630.270118	7
9	**1083.488770**	542.248023	1066.462221	533.734749	1065.478205	533.242741	E	***1163.500598***	582.253937	1146.474049	573.740663	1145.490033	573.248655	6
10	**1214.529255**	607.768266	1197.502706	599.254991	1196.518690	598.762983	M	***1034.458005***	517.732641	1017.431456	509.219366	1016.447440	508.727358	5
11	1374.559904	687.783590	1357.533355	679.270316	1356.549339	678.778308	C	***903.417520***	452.212398	886.390971	443.699124	885.406955	443.207116	4
12	1813.785230	907.396253	1796.758681	898.882979	1795.774665	898.390971	Q	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
13	1942.827823	971.917550	1925.801274	963.404275	1924.817258	962.912267	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TCQSLHINEMCQER
(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	2115.932205	0.024357	TCQSLHINEMCQER
4.3	2115.981628	-0.025066	DKPASSMSDDEMPVLEIPR

Mascot: http://www.matrixscience.com/

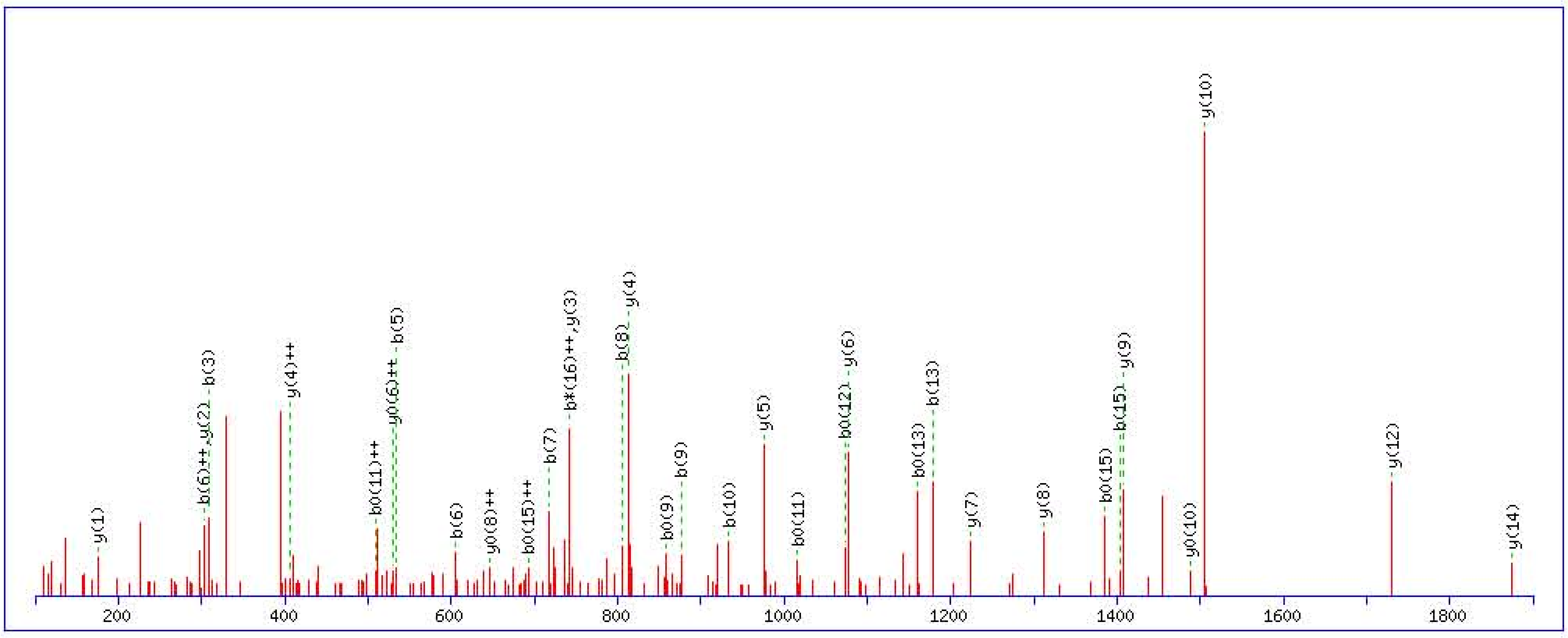
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGHPEALSAGTGSPQPPSFTYAQQR**
Found in **ZYX_HUMAN**, Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1

Match to Query 69152: 2907.459896 from(727.872250,4+) rtinseconds(1997) index(6501)
Title: Locus:1.1.1.2949.14 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 min 1st\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): 2907.433762

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

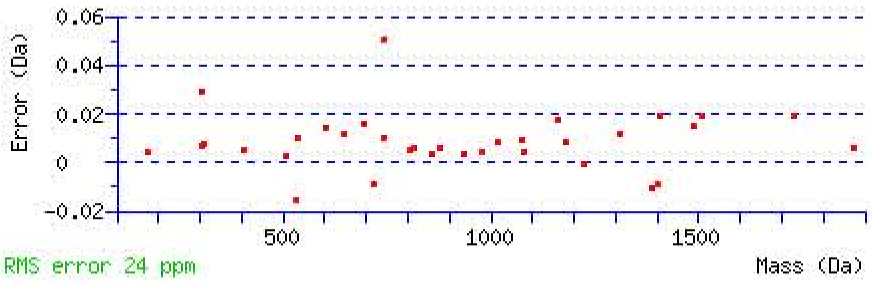
Variable modifications:

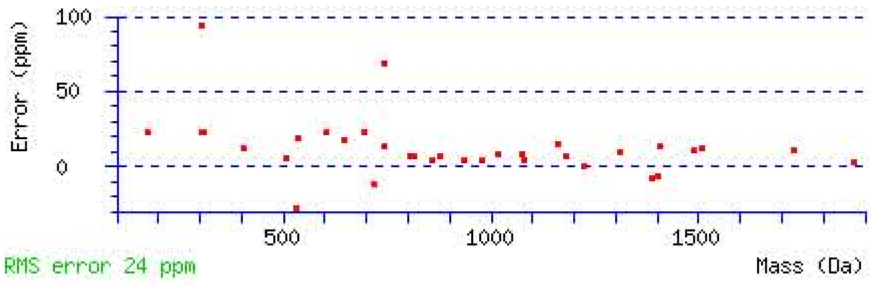
Q23 : Biotin:Thermo-21345 (Q)

Ions Score: 72 **Expect:** 2.1e-006

Matches : 34/242 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	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	2606.270788	1303.639032	2589.244239	1295.125758	2588.260223	1294.633750	Q	***742.402856***	371.705066	725.376307	363.191792			3
24	2734.329366	1367.668321	2717.302817	1359.155047	2716.318801	1358.663039	Q	***303.177530***	152.092403	286.150981	143.579129			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
71.5	2907.433762	0.026134	LGHPEALSAGTGSPQPPSFTYAQQR
71.4	2907.433762	0.026134	LGHPEALSAGTGSPQPPSFTYAQQR
17.5	2907.433762	0.026134	LGHPEALSAGTGSPQPPSFTYAQQR

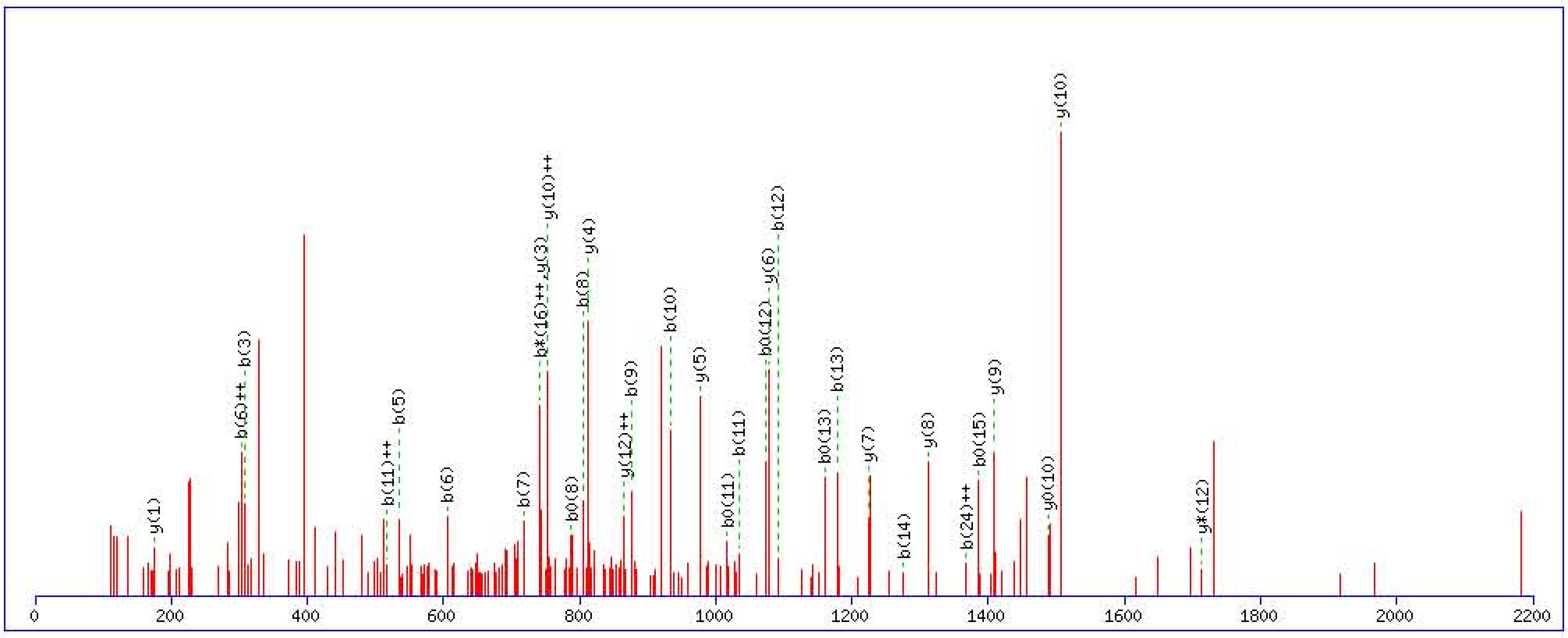
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGHPEALSAGTGSPQPPSFTYAQQR**
Found in **ZYX_HUMAN**, Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1

Match to Query 69153: 2907.459896 from(727.872250,4+) rtinseconds(1992) index(6474)
Title: Locus:1.1.1.2947.6 File:"2013-07-02 CLN FXIII 180 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\7 FXIII 180 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): 2907.433762
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q24 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 0.00023
Matches : 33/242 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							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
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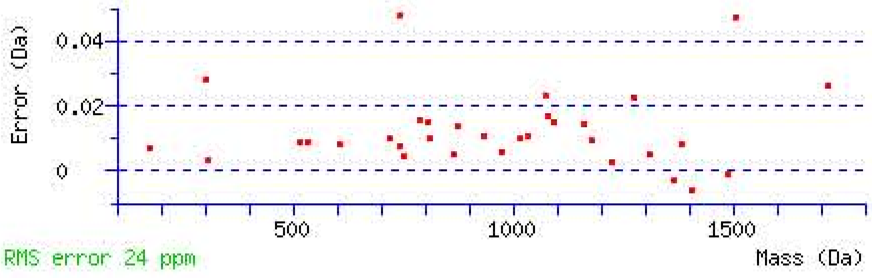
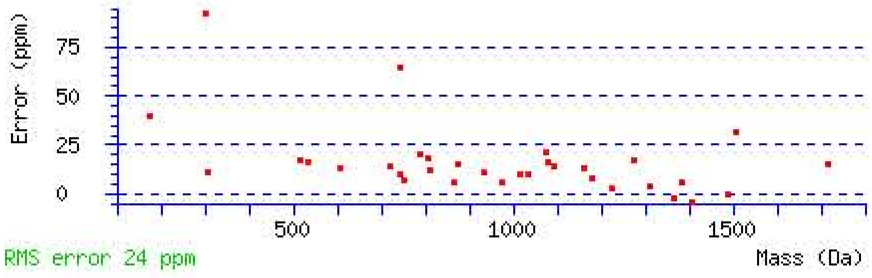
22	2167.045462	1084.026369	2150.018913	1075.513095	2149.034897	1075.021087	A	***813.439970***	407.223623	796.413421	398.710349			4
23	2295.104040	1148.055658	2278.077491	1139.542384	2277.093475	1139.050376	Q	***742.402856***	371.705066	725.376307	363.191792			3
24	2734.329366	**1367.668321**	2717.302817	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
51.2	2907.433762	0.026134	LGHPEALSAGTGSPQPPSFTYAQQR
48.8	2907.433762	0.026134	LGHPEALSAGTGSPQPPSFTYAQQR
16.0	2907.433762	0.026134	LGHPEALSAGTGSPQPPSFTYAQQR

Mascot: http://www.matrixscience.com/